STATEMENT OF JUSTIN ANTHONY HOWES

I, Justin Anthony Howes, care of Queensland Health Forensic and Scientific Service, Team Leader, do solemnly and sincerely declare that:

1. I am employed by Queensland Health Forensic and Scientific Service ('QHFSS').

2. I hold the position of Team Leader at QHFSS at Coopers Plains.

3. I hold a Master of Science in Forensic Science (Griffith University -2000), a Bachelor of Arts in Human Movement Science (University of Qld – 1997), and a Bachelor of Science in Molecular Biology (University of Qld -1995). I also have a Diploma of Management (TAFE Qld – 2015) and a Certificate IV in Workplace Training and Assessment – 2005.

4. On 19 August 2022, under s 5(d)(1) of the *Commissions of Inquiry Act 1950,* Commissioner Sofronoff QC issued Notice 2022/104 ('the Notice') to me. I am required to provide a statement as to whether I agree or disagree with a number of matters as set out in paragraphs A to E of the Notice. If I disagree to any extent with any of the matters, I have been requested to state the nature of my disagreement and to explain in detail the reasons for such disagreement.

5. I have also been asked to make a submission concerning any recommendation that, in my view, ought to be made in the event the Commissioner Sofronoff QC, concludes that the matters set out in Paragraphs A to E are substantially correct, including in particular a recommendation as follows:

   (a) *That FSS issues addendum statements to all those issued since November 2015 that have stated that "DNA was not detected in these samples" where the sample had a quantitation value above 0 and below 0.001ng/µL reporting the actual facts referable to such samples such as "A very low quantity of DNA may have been detected in this sample. It is possible but unlikely that further work might result in a useable profile".*

[redacted]

Justin Howes

Witness

LUKE RYAN

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Responses to paragraphs A to E

Paragraph A

Since approximately November 2015, formal witness statements for samples that returned a quantitation value less than 0.001ng/µL have been reported using words to the effect 'DNA was not detected in these samples and therefore they were not tested further.'

6. I agree with the proposition in part

7. Since the implementation of the Quant-Trio DNA Quantification Kit (Quant Trio) in November 2015, samples that quantify less than the validated Limit of Detection (LOD) value of 0.001ng/µL are reported per exhibit via the Forensic Register (FR) as 'No DNA Detected'. It is my understanding that when this result is received by the Queensland Police Service (QPS) in the FR, the line 'No DNA detected' expands as the comment below which is an excerpt from the Standard Operating Procedure (SOP) 23008v14 – Explanations of Exhibit Report Results (**JH-1**) and the internal spreadsheet (**JH-2**):

> **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.
> Mnemonic = NDNAD
> (PP21 or P+)
>
> For Powerplex 21: This comment is entered into the EXH when the quantitation value is less than the limit of detection (LOD) for quantitation, and there is no indication of inhibition. This sample will not proceed to amplification. QPS can request processing of the sample to restart should they require it.

8. If a statement is requested for a case, the Reporting Scientist can use their discretion in determining the wording for all results. The statement is then subjected to a peer-review by another competent Reporting Scientist. There are suggested wording phrases that Reporting Scientists may elect to use as per the Standard Operating Procedure

[redacted]

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17119v14 for Release of Results (**JH-3**) that was included in the next version of this SOP after the implementation of Quant Trio. The suggested wording for 'No DNA Detected' is as written in Paragraph A. As this is suggested wording and the Reporting Scientist may elect to use different wording prior to peer-review, I agree in part to Paragraph A.

Paragraph B

A quantitation value between 0 and 0.001ng/µL falls below the manufacturer's limit of detection for the quantitation equipment which has been used by the laboratory since 2015.

9. I agree in part to paragraph B.

10. To answer this, I have agreed in part as I have assumed that what is mentioned in Paragraph B to be the 'manufacturer's limit of detection' is the same as what is mentioned in the User Guide as their 'Assay Sensitivity' (**JH-6 p299**).

11. The internal validation of Quantifiler Trio DNA Quantification Kit in 2015 showed that 'Quantifiler Trio can reliably detect DNA down to concentrations of 1pg/µL' (or 0.001ng/µL) (**JH-4 p203**). This was using the 7500 Real-Time PCR instrument. Further, the validation report found that there were inaccuracies at low DNA concentrations (ie. nearing 1pg/µL) and this was not unexpected given the manufacturer had reported that Quantifiler Trio has single source sensitivity only down to 5ng/µL (**JH-4**). The validation report recommended the LOD for sample workflow to be set at 0.001ng/µL.

12. The 7500 instrument was replaced with the QuantStudio 5 Real-Time PCR System (QS5) in 2019. The validation of the QS5 showed that the Limit of Detection value of 0.001ng/µL was supported by the internal testing (**JH-5**).

[redacted]

Justin Howes　　　　　　　　　　Witness

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13. The LOD, according to the internal validation, is lower than the assay sensitivity reported by the manufacturer (**JH-6**). The internal LOD equates to being able to theoretically detect less than one diploid cell, which has approximately 6pg of DNA (**JH-7**). This compares to the manufacturer's assay sensitivity which explains that when '2.0uL of a sample at the lowest concentration standard (5pg/µL) is loaded in a reaction, the well contains approximately 1.5 diploid human genome equivalents.'(**JH-6**). Practically, this means that more samples in the laboratory are afforded the opportunity to proceed to DNA amplification in an attempt to obtain useable DNA profiles, compared with if the manufacturer's assay sensitivity was used to direct workflow. Having said that, while the workflow currently does not direct samples in this range to amplification after obtaining a quantification below the LOD (0.001ng/µL), samples are reported to QPS and are available for further testing, as per the exhibit report result explanatory material quoted in Paragraph A (**JH-1 and JH-2**). In these situations, the workflow permits further work as there has not been any amplification or concentration steps prior to the reporting of 'No DNA Detected'; therefore, there is DNA extract that could be processed upon request.

Paragraph C

A quantitation value above 0 and below 0.001ng/µL indicates the detection of some fluorescence, which might indicate DNA but might also be the result of something that is not DNA.

14. I agree in part with paragraph C.

15. According to Butler (**2012 – JH-8 p367**):

> '…in spite of the sensitivity of qPCR, some studies have shown that STR typing results can be obtained even when a "zero" quantitative value is observed (Cupples et al 2009). Stochastic variation with low amounts of DNA is the reason for such observations'

[redacted]

Justin Howes Witness

Luke Ryan

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16. Butler (**2012 -JH-8 p368**) continues to describe that 'stochastic variation can limit the reliability of qPCR results'. The manufacturer's guide (**JH-6**) describes that 'at concentrations <5pg/µL, stochastic effects, or the statistical effect of random sampling of alleles present at a very low copy number, can produce significant variability in assay results.' Further, it describes that:

> 'detection of such a low quantity of DNA can vary from amplification to amplification based on stochastic effects. Such levels may be considered background signal and may vary from laboratory to laboratory, and may not produce detectable product when the STR Kits are used'

17. I agree that background fluorescence could be present below the low quant value of 0.001ng/µL and agree that there might be the presence of DNA that is not registered as a 'detection' according to the internal validation. In my opinion, we can't say that there is 'no DNA' below the LOD, all we can mention is that it is not detected according to our validation work. If DNA is not detected, it could be for the reasons described by Butler (2012) relating to stochastic effects. As he mentions (**JH-8 p367**), it could be that 'while there is DNA present in such samples, the qPCR result is very low or zero due to the PCR primers failing to find sufficient target to amplify'.

Paragraph D

It may be possible to obtain a useable DNA profile from some samples with a quantitation value above 0 and below 0.001ng/µL.

18. I agree in part with paragraph D.

19. To answer this Paragraph, I have assumed that a 'useable' DNA profile is one that is 'suitable for comparison', that is, a DNA profile that could be compared to other samples in the matter or to DNA profiles held on the National Criminal Investigation DNA Database (NCIDD).

[redacted]

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20. As above within the response to Paragraph C, Butler (2012 **JH-8 p368**) describes stochastic effects and provides further reasons where DNA results may be obtained when the quantification result is less than the LOD. This is based on the quantification process using less sample to provide the estimate of concentration in the DNA extract compared to the amount added to the next process being DNA amplification: '

> 'Second, remember that there are different volumes of input DNA being used. Many qPCR assays require 2μL of input DNA while STR typing PCR reactions can take 10μL or more of input DNA (*NB. FSS uses up to 15μL of input DNA*). Thus, because five times as much DNA extraction volume can be included in the STR amplification reaction, more input DNA can be included giving rise to a result when the qPCR value was "zero."'

21. The question is whether a useable DNA profile could be obtained for samples with a quantitation value above 0 and below 0.001ng/μL. In my opinion, this finding cannot be excluded, and this view is consistent with a view on science from eminent scientist Dr Peter Gill where he was recently quoted in Chemistry World (July 2022) in saying: 'We don't deal with the definitive. In fact, no scientist does"' (**JH-9 – Page ~~377~~** 376).

JH 25/08/2022

22. Having said that, it is important to look at the evidence, and in in-house data compiled in 2017 it was found that of the 49 samples with quantification values up to and including 0.001ng/μL where they were concentrated in an attempt to obtain a useable profile, there were no findings of results other that what could broadly be described as 'unsuitable for interpretation' (**JH-10 'Combined' worksheet**). With this data, it is important to mention that there were DNA profiles obtained after concentration, but no evidence to indicate there were 'useable' DNA profiles in the dataset.

Paragraph E

In the premises, it is not true to say for every such sample that "DNA was not detected".

23. I disagree with paragraph E.

[redacted]

Justin Howes

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24. According to the internal validation of Quant Trio (**JH-5**), DNA extracts that quantify below 0.001ng/µL are found to be below the validated LOD. For these samples, the results are reported per exhibit in a simple format as 'No DNA Detected' to QPS, which carries the expanded comment of: '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' (**JH-1 and JH-2**). Further, there is suggested wording for statements (**JH-3**) which Reporting Scientists could opt to use. This wording is 'DNA was not detected in these samples and therefore they were not tested further' (**JH-3**). Reporting Scientists may alternatively elect to use their own version of wording to explain the result. An example of other wording is 'DNA was not detected in this sample during the initial (sic) stages of DNA analysis and as such this sample was not submitted for DNA profiling' (**JH-11**). In all situations, the wording for this and every result detailed in statements are subject to a peer review.

25. This follows then that it is true that results in this range are reported to QPS in a summary form of 'No DNA Detected' as the result is below the validated LOD. This is not to say that DNA is not present in a definitive sense, it is saying that the validation findings are such that for these samples, the quantification values are below the LOD.

Submissions on recommendations

26. I will accept any recommendation that the Commission makes, including using the wording suggested from the Commissioner in this Notice moving forward.

27. The wording currently used in statements summarises the results reported to QPS on an exhibit-base. My understanding is that the result in the QPS system expands to a comment that is made available to the Investigating Officer. If the QPS then require a statement, for these results the Reporting Scientist can use their discretion to describe the results with suggested wording provided in a Standard Operating Procedure.

28. My view is that the wording used in statements has not been made untruthfully as it is not incorrect. It has always been open for questioning in court or in pre-trial conference

[redacted]

Justin Howes

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and I am not aware if any wording has caused confusion to the courts in any particular matter.

[redacted]

Justin Howes

Witness

LUKE RYAN

JUSTICE OF THE PEACE (QUALIFIED)
Reg.No.: 113602
DEPT. OF JUSTICE & ATTORNEY-GENERAL

All the facts and circumstances declared in my statement, are within my own knowledge and belief, except for the facts and circumstances declared from information only, and where applicable, my means of knowledge and sources of information are contained in this statement.

I make this solemn declaration conscientiously believing the same to be true and by virtue of the provisions of the *Oaths Act 1867*.

TAKEN AND DECLARED before me at Brisbane in the State of Queensland this ninth day of 25August 2022

[redacted]

Justice of the Peace (Qualified)
Reg. No. 13802
Dept. of Justice & Attorney-General

Justin Howes

Witness
LUKE RYAN

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Explanations of Exhibit Report Results

Not Current

1. Purpose

To provide explanations for the results available for the EXR/EXH result/status field

2. Scope

AUSLAB is the case management computer system used within the DNA Analysis section. AUSLAB utilises EXR/EXH pages to report information relating to exhibits to the Queensland Police Service (QPS). This document provides clear explanations for the results available for the EXR/EXH result/status field, which are available for DNA Analysis staff, and also QPS DNA Results Management Unit (DRMU).

3. ASSOCIATED DOCUMENTS

16004 AUSLAB Users Manual – DNA Analysis
17117 Procedure for Case Management

4. EXPLANATIONS

4.1 Blood Examination

1 **Presumptive blood test neg. Submitted for cells**
This item/sample tested negative to a presumptive test for blood (TMB). This item was submitted for general cell DNA testing.
Mnemonic = PBNSC

2 **Presumptive blood test pos. Submitted-results pending**
This item/sample tested positive to a presumptive test for blood (TMB) and was submitted for DNA testing. Results are pending.
Mnemonic = 1BPPSR

3 **Presumptive blood test neg.**
This item/sample tested negative to a presumptive test for blood (TMB).
Mnemonic = PBTN

4 **Presumptive blood test positive**
This item/sample tested positive to a presumptive test for blood (TMB).
Mnemonic = PREBT

4.2 Seminal Fluid Examination

1 **Presump. PSA test positive, submitted - results pending**
This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was submitted for DNA testing. Results are pending.
Mnemonic = PAPPRP

2 **Presump. AP test positive, submitted - results pending**
This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Results are pending.
Mnemonic = PPSRP

3 **Presump. PSA test positive, no sperm found**
This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. No spermatozoa were detected by microscopy. This item was submitted for DNA testing. Results are pending.
Mnemonic = PPSANS

4 **Micro positive for sperm. Submitted-results pending**
Spermatozoa were detected on this item/sample by microscopy. This item/sample was submitted for DNA testing. Results are pending.
Mnemonic = SPPDNA

5 **Micro neg for sperm**
Spermatozoa were not detected on this item/sample by microscopy.
Mnemonic = MNS

6 **Semen not detected**
Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. QHFSS recommends QPS to commence further examination on items relating to this case if applicable.
Mnemonic = SEMND

Not Current

4.3 Saliva Examination

1 **Presump saliva positive. Submitted-results pending**
This item/sample tested positive to a presumptive test for saliva (Phadebas) and was submitted for DNA testing. Results are pending.
Mnemonic = PSPSRP

2 **Presump saliva negative. Submitted for cells**
This item/sample tested negative to a presumptive test for saliva (Phadebas). This item/sample was submitted for general cell DNA testing.
Mnemonic = PSNSC

3 **Submitted as cells, Presump saliva test pending**
This item/sample was submitted for general cell DNA testing. The item/sample will be tested with the presumptive test for saliva (Phadebas). Results are pending.
Mnemonic = SACPSP

4 **Presump saliva test negative**
This item/sample tested negative to a presumptive test for saliva (Phadebas).
Mnemonic = PSTN

5 **Presump saliva test positive**
This item/sample tested positive to a presumptive test for saliva (Phadebas).
Mnemonic = PSTP

4.4 Hair Examination

1 **Hair located. Not suitable for analysis**
Hair/s were located on this item/sample. They were observed using microscopy and deemed unsuitable for DNA testing due to no observed cellular material, or possible animal origin.
Mnemonic = HLNSA

2 **Hair located. Submitted results pending**
Hair/s were located on this item/sample. These hairs have been submitted for DNA testing. Results are pending.
Mnemonic = HLSRP

3 **No hair located. No further examination conducted**
The item/sample was examined for the presence of hair and none was located. This could be due to no hair present or item is substance other than hair. No further testing for hair was conducted on this item.
Mnemonic = NHLNE

This comment can be used when examinations were undertaken on items but no hair was located or the item was a substance other than hair, and therefore no further examination was conducted e.g. A4 tapelifts, clothing.

4.5 General Examination

1 **Submitted-results pending**
This item/sample was submitted for DNA testing. Results are pending.
Mnemonic = SRP

2 **Sample unsuitable for analysis**
This item/sample is unsuitable for DNA testing due to, but not limited to: excess dirt, or the presence of mould.
Mnemonic = UNSS

3 **Items Prioritised. Not examined at this time**
This item/sample has been prioritised based on case information provided by QPS. Examinations may be conducted in the future.
Mnemonic = IPNE

4 **Items prioritised, not submitted at this time**
This item/sample has been prioritised and as such samples taken from this exhibit have not been submitted at this time.
Mnemonic = IPNST

5 **Submitted as cells**
This item/sample was submitted for general cell DNA testing.
Mnemonic = SAC

Not Current

6 **Sample pooled and processed under**
This item/sample was pooled and submitted for DNA testing under the barcode sent with this exhibit report. The final results will be reported under the barcode.
Mnemonic = SPP

7 **Entire sample consumed**
The entire item/sample was consumed during examination.
Mnemonic= ESCD

8 **Sample processed and final results under**
This item/sample was processed under the barcode sent with this exhibit report. The final results will be reported under that barcode.
Mnemonic = SPFRU

This comment should be used when the original barcode has undergone further processing under a new barcode, and the reported profile result is under this new barcode, which needs to be reported to QPS.

9 **Multiple items - not all tested**
This exhibit consisted of multiple items packaged together under one exhibit barcode, of which not all were selected for examination. If more or all of the remaining items are required to be examined, this can be completed upon request.
Mnemonic = MINAL

This comment can be used when multiple items were received together under one exhibit barcode, of which only some of the items were selected for examination.

10 **All items now tested**
All items for this exhibit have now been examined.
Mnemonic = AINT

This comment must follow “Multiple items – not all tested”

11 **No further examinations conducted**
This item/sample was tested for the possible presence of biological material and none were detected. No further testing was conducted on this item.
Mnemonic = NFEC

This comment can be used when examinations were undertaken on items, but no biological material was detected, and therefore no samples were submitted for DNA testing.

12 **Sample required manual intervention prior to extraction**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the extraction process.
Mnemonic = SRMI

This comment can be used when manipulation of an item examined by QPS were undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated. This EXR/EXH line should be used for general manipulation only. More specific EXH lines are listed below.

Not Current

13 **Sample required manual intervention – swab stick too long**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the swab stick was too long and required shortening to enable downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process. The ideal stick length should be no more than 24mm total length (swab stick plus swab head).
Mnemonic = MISSTL

This comment can be used when manipulation of a swab submitted by QPS was undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated, due to the swab stick being too long.

14 **Sample required manual intervention – excess substrate**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as excess substrate was contained within the tube. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.
Mnemonic = MIES

This comment can be used when manipulation of an item examined by QPS was undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated, due to excess substrate.

15 **Sample reqd manual intervention– tlift rolled incorrectly**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the tapelift was rolled incorrectly, impeding downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.
Mnemonic = MITRI

This comment can be used when manipulation of a tapelift examined by QPS was undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated, due to the tapelift being rolled incorrectly.

16 **Sample on hold, awaiting advice**
This item/sample has been placed on hold and is awaiting additional information from QPS before processing can recommence. This information may relate to, but is not limited to; examination priority, screening requirements.
Mnemonic = SOHAA

This comment can be used when a sample is to be placed on hold until advice is received from QPS before any examination can commence.

Not Current

4.6 Exception reporting to QPS for Evidence Recovery

The following EXR/EXHs should be used in place of a FERRO when items are submitted incorrectly by QPS for DNA testing.

1 **Hair located on the outside of an in-tube submission**
A hair was located either outside the tube or partially hanging in and out of the tube. It is unclear if this hair was part of the collected item or incorrectly transferred during collection. This hair/hair portion has been stored and will only be analysed if a request is provided.
Mnemonic = HOIS

Not Current

2 **Multiple items incorrectly submitted under single barcode**
Multiple items, or multiple AP positive areas have been submitted under a single barcode identifier. Each item requires its own unique barcode, as the barcode is used for reporting purposes to both the forensic register and the National Criminal Investigation DNA Database. Each item will be allocated a new barcode for processing and reporting purposes.
Mnemonic = MIISB

3 **Labelling discrepancy**
There is a labelling discrepancy (Occurrence number or sample description) between the exhibit packaging and the AUSLAB/Forensic Register interface records. This sample can not be processed until the labelling discrepancy is resolved. The discrepancy will be highlighted to the QPS Sample Management Unit for clarification in the first instance, and if unable to be resolved, will be referred to the appropriate QPS officer for resolution. Please ensure all labelling details are correct before submission to the DNA Analysis Laboratory
Mnemonic = LDIS

4 **No barcode on sample**
The item/sample provided in a tube was not labelled with a barcode. A barcode is required for the processing of the item and for continuity purposes. A barcode the same as that attached to the packaging has been affixed to the item.
Mnemonic = NBOS

5 **On hold - Insufficient information provided for testing**
There was insufficient information provided with this submission to determine what type of analysis is required for this item/sample e.g., saliva, semen. This sample is to be placed on hold until further information on the testing requirements for this sample is provided.
Mnemonic = OHII

6 **Incorrect submission of cigarette butt**
This cigarette butt was received in a tube. Items provided in a tube are intended to be submitted directly for DNA processing with minimal manual intervention. This sample required further examination as it was received as a whole cigarette butt. Please submit whole cigarette butts in a Crime Scene Sample envelope or as a sub-sample of the filter paper.
Mnemonic = ISCB

FINAL RESULTS

Note 1: The following final results cover samples processed using the Profiler® Plus (P+) and Powerplex® 21 (PP21) amplification kits. Some EXH lines are to be used for one kit only. Other EXHs are generic and can be used for either kit. At the end of each comment, the kit or kits that the EXH can be used with be denoted in brackets.

Note 2: The first result line will refer to the final DNA profile result e.g. Single source DNA profile (with the LR if a reference evidence sample compared) or 2 person or 3 person mixed DNA profile (with a subsequent EXH line referring to an LR if a reference evidence sample compared). See examples 1 and 2 below.

Note 3: For single source profiles ONLY, the unknown designation or the reference sample barcode (for LR calculations) will only be entered into the Linked number field for the DNA profile result. No designations will be added to the NCIDD upload lines for single source profiles.

e.g. 1
Single source DNA profile

Lab No.	Result/Status	Linked No.	Warm link name
123456789	Single Source DNA profile	ukm1	
987654321	NCIDD upload single source DNA profile		

e.g. 2
Single source DNA profile – reference sample

Lab No.	Result/Status	Linked No.	Warm link name
123456789	Single Source 20 loci DNA profile >100 billion	564219762	SMITH
987654321	NCIDD upload single source DNA profile		

Note 4: For two or three person mixed DNA profiles, the first line will designate the DNA profile result regardless if a LR for a reference evidence sample comparison has been calculated. The following line will refer to the LR or non-contribution line (if calculated). The next line whether a sample is deconvoluted and a profile is available for upload to NCIDD.

e.g. 3
Deconvoluted mixed DNA profile – reference sample

Lab No.	Result/Status	Linked No.	Warm link name
123456789	2 person mixed DNA profile		
987654321	NCIDD upload - mixed DNA profile	Ukm1	

e.g. 4
Deconvoluted mixed DNA profile – reference sample

Lab No.	Result/Status	Linked No.	Warm link name
123456789	2 person mixed DNA profile		
123456789	2 person mixt, LR >100 billion	564219762	SMITH
987654321	NCIDD upload - mixed DNA profile	564219762	

Note 5: For all final results containing a match to a reference barcode, the QPS DRMU update the expanded comments as per the following example:

Not Current

Examples:
PowerPlex® 21 and STRmix^{TM}: *SS DNA profile less than 9 loci LR > 100 billion -* This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from **[QPS inserts barcode of ref sample and other details such as name and DOB]**. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.

Profiler Plus: *9 loci DNA profile. Uploaded to NCIDD* – This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from **[QPS inserts barcode of ref sample and other details such as name and DOB].** The DNA profile obtained from barcode **[QPS inserts barcode number of the crime scene sample]** has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.

POWERPLEX® 21 and STRmix RESULTS

The follow comments are for use results processed using PowerPlex® 21 and interpreted with the STRmix^{TM} Expert System.

4.7 Single Source DNA profiles (PP21)

1 **Single Source DNA profile**
The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
Mnemonic = 1SS
(PP21)

This comment will be used for unknown contributors and for DNA profiles where the matching reference sample has been reported with an LR on at least one other sample within the case. This comment can be used for DNA profiles with 12 or more alleles.

2 **Single Source- low support for contribution**
This item/sample provided a partial DNA profile which indicated the presence of one contributor. Only limited information has been obtained and this information matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. Statistically, this DNA profile provides low support that the associated barcode sent with this exhibit report is the donor of this DNA. Further information can be provided if required.
Mnemonic = 1SSLOW
(PP21)

3 **Single source DNA profile < 9 loci LR 100 – 1000**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile

Not Current

matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L1
(PP21)

4 **Single source DNA profile < 9 loci LR 1000 - 10 000**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L2
(PP21)

5 **Single source DNA profile < 9 loci LR 10 000 - 100 000**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L3
(PP21)

6 **Single source DNA profile < 9 loci LR 100 000 - 1 million**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L4
(PP21)

7 **SS DNA profile < 9 loci LR 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L5
(PP21)

8 **SS DNA profile < 9 loci LR 1 billion - 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA

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information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L6
(PP21)

9 **SS DNA profile less than 9 loci LR > 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L7
(PP21)

10 **SS DNA profile 9 loci and above LR 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L8
(PP21)

11 **SS DNA profile 9 loci and above LR 1 billion- 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L9
(PP21)

12 **SS DNA profile 9 loci and above LR > 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1S9L10
(PP21)

13 **Single source 20 loci DNA profile LR > 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It obtained all of the DNA information potentially available. This DNA profile matched

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the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS20L
(PP21)

14 **Single Source DNA profile - assumed known contributor**
This item/sample provided a DNA profile that indicated the presence of one contributor. The associated barcode matches this DNA profile. Based on information provided to the laboratory, it has been assumed that the associated barcode is the donor of this DNA. Given this assumption, no statistical interpretation has been performed.
Mnemonic = 1SSAKN
(PP21)

The following comments will be applied when a single source DNA profile is selected for loading to the National Criminal Investigation DNA Database (NCIDD). These are not stand alone comments and should be preceded by a final result for the profile e.g. Single Source DNA Profile.

15 **NCIDD upload single source DNA profile**
A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.
Mnemonic = 1SSNCD
(PP21)

The following two comments are to be used when a sample has been selected for loading to NCIDD for <u>Intelligence purposes only</u>, and should only be used after consultation with a Senior Scientist.

Comment 16 should be used when a single source profile is obtained which is less than the stringency for reporting a match on NCIDD (<12 alleles).

16 **NCIDD Intel upload - single source partial profile**
This item/sample gave an incomplete single source DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes. This incomplete DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be statistically evaluated and reported as a likelihood ratio. Depending on the amount of information in this DNA profile, the strength of the support for inclusion will vary.
Mnemonic = 1SSIND
(PP21)

Comment 17 should be used when a single source profile is obtained which is undergoing rework, however a profile has been selected for loading to NCIDD for intelligence purposes.

17 **NCIDD Intel upload - interim single source profile**
This item/sample gave an interim result of an apparent single source DNA profile. This DNA profile has been selected for loading to NCIDD for intelligence purposes, as this

Not Current

sample is currently undergoing further processing. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that the final result may vary. Any reference samples subsequently received will be statistically evaluated against the final DNA profile and reported as a likelihood ratio.
Mnemonic = 1SSINI
(PP21)

The following comments will be applied when a single source DNA profile is unable to be loaded to NCIDD (if an EXH is required if the only sample in a case).

18 **Single source DNA profile < NCIDD matching stringency**
The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile was below the QHSS stringency for reporting a match on NCIDD, and has therefore not been loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
Mnemonic = 1SSLND
(PP21)

This EXH line should be used when the DNA profile consists of 6-11 alleles for both unknowns and reference sample comparisons.

19 **Single source DNA profile- unsuitable for NCIDD searching**
The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile contained insufficient information for searching on NCIDD, and is therefore unable to be loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
Mnemonic = 1SSUND
(PP21)

This EXH line should be used when the DNA profile consists of 1-5 alleles for both unknowns and reference sample comparisons.

4.8 Mixed DNA profiles (PP21)

The following comment will be used when a mixed DNA profile is likely to produce a similar result to one already reported from the same scene and is a stand alone EXH. This DNA profile will not be deconvoluted in STRmix.

20 **Similar result to previous DNA profile**
This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. This DNA profile has been assessed and is considered

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to provide similar information to the DNA profile obtained from the sample barcode sent with this exhibit report and therefore has not been statistically evaluated at this time. Please contact the laboratory if you require a more detailed interpretation of this DNA profile.
Mnemonic = SRPP
(PP21)

The following comment will be used for three person mixed DNA profiles with a priority of 3 only and is a stand alone EXH.

21 **3 person mixed DNA profile not deconvoluted**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from three contributors. This mixed DNA profile has been assessed and it is considered that, if the DNA profile were to be deconvoluted, it may provide sufficient information for upload to NCIDD. Deconvolution of this DNA profile has not been performed at this time. Please contact the laboratory if further interpetation is required.
Mnemonic = 3MXND
(PP21)

The following comments will be used as the first line for all two or three person mixtures. These lines describe the DNA profile result obtained. Subsequent lines will refer to, including, but not limited to: reference samples matches, non contribution lines, deconvolution lines, NCIDD upload lines.

1 **Two person mixed DNA profile**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Mnemonic = 2MX
(PP21)

2 **Three person mixed DNA profile**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.
Mnemonic = 3MX
(PP21)

The following comments will be used for unknown contributors only where there is no reference sample for comparison and provision of a LR and no DNA profile for upload to NCIDD. This line will follow the EXH line “Two person mixed DNA profile” or “Three person mixed DNA profile”.

3 **No statistical interpretation performed**
In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.
Mnemonic = NSIP
(PP21)

Non-conditioned EXHs

The following comments will be used when a reference evidence sample/s is/are provided for comparison. These lines will follow the EXH line “Two person mixed DNA profile” or “Three person mixed DNA profile”.

4 **2 person mix - low support for contribution**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. The DNA profile provides low support for the proposition that the

Not Current

associated barcode is a contributor of DNA to this mixed DNA profile. Please contact DNA Analysis if further information is required.
Mnemonic = 2MXLOW
(PP21)

5 **2 person mix - support for contribution 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX1
(PP21)

6 **2 person mix - support for contribution 1000 to 10 000**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX2
(PP21)

7 **2 person mix, support for contrib 10 000 - 100 000**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX3
(PP21)

8 **2 person mix- support for contrib 100 000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX4
(PP21)

9 **2 person mix - support for contrib 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX5
(PP21)

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10 **2 person mix- support for contrib 1 billion - 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX6
(PP21)

11 **2 person mix profile - support for contrib > 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX7
(PP21)

12 **3 person mix - low support for contribution**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
Mnemonic = 3MXLOW
(PP21)

13 **3 person mix - support for contribution 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX1
(PP21)

14 **3 person mix - support for contribution 1000 to 10 000**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX2
(PP21)

15 **3 person mix - support for contrib 10 000 - 100 000**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.

Not Current

Mnemonic = 3MX3
(PP21)

16 **3 person mix - support for contrib 100 000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX4
(PP21)

17 **3 person mix - support for contrib 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX5
(PP21)

18 **3 person mix- support for contrib 1 billion - 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX6
(PP21)

19 **3 person mix profile - support for contrib > 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX7
(PP21)

The following comments will be used when there are numerous reference samples in the case to describe the LRs produced for a group of reference samples. There will be no information in the linked number field. If reference samples are excluded then EMDP will be used.

20 **Mixture - low support for contrib or supports non contrib**
This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.

Not Current

Mnemonic = MLSONC
(PP21)

Conditioned/Remaining Mixed DNA profile EXHs

The following comments will be used when a reference evidence sample/s is/are provided for conditioning a two or three person mixed DNA profile. These lines will follow the EXH line "Two person mixed DNA profile" or "Three person mixed DNA profile".

21 **2 person mixed profile - conditioned on**
This item/sample provided a DNA profile that indicated the presence of two contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.
Mnemonic = 2MXCON
(PP21)

22 **3 person mixed profile - conditioned on**
This item/sample provided a DNA profile that indicated the presence of three contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.
Mnemonic = 3MXCON
(PP21)

23 **2 person mix remaining - low support for contrib.**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
Mnemonic = 2MXRL
(PP21)

24 **2 person mix remaining - support for contrib 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR1
(PP21)

25 **2 person mix remaining- support for contrib 1000 to 10000**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.

Not Current

Mnemonic = 2MXR2
(PP21)

26 **2 person mix rem - support for contrib 10 000 to 100 000**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR3
(PP21)

27 **2 person mix rem- support for contrib 100000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR4
(PP21)

28 **2 person rem- support for contrib 1 million to 1 billion**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR5
(PP21)

29 **2 person rem - support for contrib 1 billion -100 billion**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR6
(PP21)

30 **2 person mix rem - support for contribution > 100 billion**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.

Not Current

Mnemonic = 2MXR7
(PP21)

31 **3 person mix remaining - low support for contrib.**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
Mnemonic = 3MXRL
(PP21)

32 **3 person mix remaining - support for contrib 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR1
(PP21)

33 **3 person mix remaining- support for contrib 1000 to 10000**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR2
(PP21)

34 **3 person mix rem - support for contrib 10 000 to 100 000**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR3
(PP21)

35 **3 person mix rem- support for contrib 100000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR4
(PP21)

Not Current

36 **3 person rem - support for contrib 1 million to 1 billion**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR5
(PP21)

37 **3 person rem - support for contrib 1 billion-100 billion**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR6
(PP21)

38 **3 person mix rem - support for contribution > 100 billion**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR7
(PP21)

Not Current

The following comment will be used when there are numerous reference samples in the case to describe the LRs produced for a group of reference samples. There will be no information in the linked number field. If reference samples are excluded then EMDP will be used.

39 **Cond mix rem - low supp for contrib or supp non contrib**
This item/sample provided a DNA profile that indicated the presence of two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately. When conditioning on the assumed known contributor, then the DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.
Mnemonic = CMLSNC
(PP21)

The following comment will be used where a remaining contribution from a 2 person conditioned profile matches a previously identified unknown DNA profile.

40 **2 pers mix remaining consistent with unknown**
The mixed DNA profile result for this sample indicated the presence of DNA from two contributors and has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. This remaining contribution is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. This unknown is therefore a possible donor of DNA to the 'remaining' contribution. It is important to note that this information is provided for intelligence purposes only and a statistical evaulation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.
Mnemonic = 2MXRCU
(PP21)

<u>NCIDD loading</u>

The following comments will be applied when a contribution of DNA from a mixed DNA profile (2 or 3 person mixture) is deconvoluted and selected for <u>loading to NCIDD</u>.

41 **NCIDD upload - mixed DNA profile**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXNCD
(PP21)

This comment should be used when a two or three person mixed DNA profile has been obtained, from which a DNA contribution has been fully deconvoluted and selected for loading to NCIDD.

42 **NCIDD upload - conditioned contribution**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The conditioned contribution described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA

Not Current

profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.
Mnemonic = 2MXCND
(PP21)

43 **NCIDD upload remaining contribution**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. The associated barcode/unknown designation sent with this exhibit report is a possible donor of DNA to the 'remaining contribution’. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXRND
(PP21)

This comment should be used when a two person mixed DNA profile has been conditioned on a reference sample, and the remaining contributor has been selected for loading to NCIDD.

44 **3 person mixed profile, mixture remaining NCIDD**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 3MXRND
(PP21)

This comment should be used when a three person mixed DNA profile has been conditioned on a reference sample, and the remaining contribution consists of more than one contributor, from which a DNA profile has been fully deconvoluted for loading to NCIDD.

Not Current

The following comments will be applied when a remaining DNA profile is unable to be loaded to NCIDD (if an EXH is required if the only sample in a case). An unknown designation will not accompany these EXH lines.

45 **Mix Rem DNA contrib < NCIDD matching stringency**
The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This remaining contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXRLM
(PP21)

46 **Mix Rem DNA contrib unsuitable for NCIDD searching**
The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin and has therefore been designated as unknown. This remaining contribution is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXUNS
(PP21)

The following EXH line should be used in conjunction with either 2MXRLM or 2MXUNS only, in the situation where the remaining component after conditioning indicates male origin.

47 **Remaining contribution indicates male origin**
The remaining contribution separated after conditioning the mixed DNA profile indicates male origin.
Mnemonic = 2MXUNM
(PP21)

Powerplex® 21 INTEL EXHs

These EXR/EXH lines indicate a profile has been interpreted for the purposes of loading a DNA profile to NCIDD for intelligence purposes only. These lines will follow an EXH line that describes the DNA profile result: e.g. “Two person mixed DNA profile” or “Three person mixed DNA profile”.

Please see section 4.15 for additional Intel EXH comments for P+ and PP21.

48 **NCIDD upload - Intel mixed DNA profile**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted

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in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXIND
(PP21)

This comment should be used for a two or three person mixture when a contribution of DNA has been deconvoluted by STRmix, however all loci have not been fully deconvoluted to greater than or equal to 99%. The profile selected for loading to NCIDD much have at least 6 loci fully deconvoluted.

49 **2 person mixed profile - conditioned on – Intel**
This item/sample provided a DNA profile that indicated the presence of two contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
Mnemonic = 2MXCI
(PP21)

This comment should be used for a two person mixture when the mixed DNA profile has been conditioned on an unknown or reference sample for intelligence purposes only. For example, conditioned on an unknown female profile from a SAIK (sexual assault investigation kit), or an intelligence reference sample for a victim in the absence of an evidence reference sample.

50 **3 person mixed profile - conditioned on - Intel**
This item/sample provided a DNA profile that indicated the presence of three contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
Mnemonic = 3MXCI
(PP21)

This comment should be used for a three person mixture when the mixed DNA profile has been conditioned on an unknown or reference sample for intelligence purposes only. For example, conditioned on an unknown female profile from a SAIK (sexual assault investigation kit), or an intelligence reference sample for a victim in the absence of an evidence reference sample.

51 **2 person mixed profile - remaining Intel – NCIDD**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor for intelligence

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purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXRIN
(PP21)

This comment should be used for a two person mixture when the mixed DNA profile has been conditioned on an unknown or reference sample for intelligence purposes only (e.g. uk f1 from a SAIK, or an Intel reference sample), and the remaining profile is to be loaded to NCIDD. This EXH should follow the EXH line 2MXCI.

52 **3 pers mix, intel cond, remaining intel NCIDD**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 3MXRIN
(PP21)

This comment should be used for a three person mixture when the mixed DNA profile has been conditioned on an unknown (e.g. uk f1 from a SAIK, or an Intel reference sample), and the remaining profile is to be loaded to NCIDD. The remaining profile may be either fully or partially deconvoluted, either way it is an intelligence upload. This EXH should follow the EXH line 3MXCI.

53 **3 pers mixed profile, mix remaining intel NCIDD**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.

Not Current

Mnemonic = 3MXIND
(PP21)

This comment should be used for a three person mixture when the mixed DNA profile has been conditioned, and the remaining profile consists of more than one contributor, from which a profile has been partially deconvoluted for loading to NCIDD for intelligence purposes only.

54 **3 person mixed profile, mixture remaining NCIDD**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 3MXRND
(PP21)

This comment should be used for a three person mixture when the mixed DNA profile has been conditioned, and the remaining profile consists of more than one contributor, from which a profile has been fully deconvoluted for loading to NCIDD.

55 **Mixture contribution loaded to NCIDD - see Intel report**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. A DNA contribution was able to be deconvoluted for loading to NCIDD, and further information about this will follow in an intelligence report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile the, strength of the support for contribution will vary.
Mnemonic = 2MXNIR
(PP21)

The comment will be used when an Intelligence Report is required to explain the interpretations made in order to load a contributor of DNA to NCIDD. This EXH line will generally be used when no other EXH is suitable, or when the interpretation cannot be appropriately explained by EXH lines.

Not Current

Non-contribution Mixture EXHs

These following comments will be applied when the Likelihood ratio calculated by STRmix^{TM} is <1. These lines will follow the EXH line “Two person mixed DNA profile” or “Three person mixed DNA profile”. See also MLSONC.

56 **2 person mix - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 2MXNC
(PP21)

57 **3 person mix - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 3MXNC
(PP21)

58 **2 person mix remaining - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of two contributors. If it is assumed that the barcode sent with the above exhibit report (2 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 2MXRNC
(PP21)

59 **3 person mix remaining - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of three contributors. If it is assumed that the barcode sent with the above exhibit report (3 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 3MXRNC
(PP21)

60 **Excluded from mixed DNA profile**
This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately. The statistical interpretation shows that some or all of the donors of the reference DNA profiles associated with this case are excluded as having contributed to this mixed DNA profile.
Mnemonic = EMDP
(PP21)

This comment will be used for all mixtures types where some or all of the reference samples are excluded as potential contributors. The linked no. field will remain blank for this line.

Not Current

Not Current

Inconclusive Mixture EXHs

These following comments will be applied when the Likelihood ratio calculated by STRmix^{TM} equals 1. These lines will follow the EXH line “Two person mixed DNA profile” or “Three person mixed DNA profile”.

61 **2 person mixed DNA profile - inconclusive**
This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.
Mnemonic = 2MXINC
(PP21)

62 **3 person mixed DNA profile - inconclusive**
This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.
Mnemonic = 3MXINC
(PP21)

4.9 NSD or no further processing Final Results (PP21 and P+)

1 **No DNA profile**
A DNA profile was not obtained from this item/sample, due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = NOPROF
(PP21 or P+)

This comment will be used when there are no peaks observed in the DNA profile obtained.

2 **No DNA profile – possible sub-threshold peaks**
A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This could be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = NDPPTP
(P+)

This comment will be used when there are no peaks above threshold in profile obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed, but does not meet the thresholds for comparing and reporting.

3 **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.
Mnemonic = NDNAD
(PP21 or P+)

For Powerplex 21: This comment is entered into the EXH when the quantitation value is less than the limit of detection (LOD) for quantitation, and there is no indication of inhibition. This sample will not proceed to amplification. QPS can request processing of the sample to restart should they require it.
For Profiler Plus, this comment is entered into the EXH for Volume Crime Priority 3 samples only when the quantitation value is undetermined, and there is no indication of inhibition.

4 **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 DNA Analysis if further information is required.
Mnemonic = DIFP
(PP21)

This comment is entered for Priority 3 samples only when the quantitation value falls below the point at which the results would be considered unreliable for interpretation. These samples will not proceed to amplification. See 17117 *Procedure for Case Management* for details.

5 **No reportable DNA profile**
A DNA profile above QHFSS standard reporting thresholds was not obtained from this sample/item. This may be due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = NRDP
(P+)

This comment will be used for Priority 3 Volume Crime samples processed using Profiler® Plus only. This comment encompasses instances when no DNA profile is obtained, and no DNA profile, possible sub threshold peaks are obtained. This comment indicates to QPS that for Volume Priority 3 samples, no reportable DNA profile was obtained.

4.10 Suspect Check Results (PP21 and P+)

These lines will follow an EXH line that describes the DNA profile result: e.g. "Two person mixed DNA profile" or "Three person mixed DNA profile".

1 **Suspect check Action - No Match**
The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.
Mnemonic = SCANM
(PP21 or P+)

This comment will be used when the barcode of a nominated suspect has been provided for an intelligence reference sample from the QPS DRMU, and it does NOT match or can be excluded as a contributor of DNA to the crime scene profile.

Not Current

2 **Suspect check - insufficient information to compare**
There was insufficient information in the DNA profile obtained from this item/sample to determine if the nominated suspect could be a potential contributor.
Mnemonic = SCII
(PP21 or P+)

This comment will be used when the barcode of a nominated suspect has been provided for an intelligence reference sample from the QPS DRMU, and there is insufficient information in the DNA profile obtained from the crime scene sample to determine if the nominated person could be a potential contributor.

The following comments will be used with STRmix^{TM} for comparisons of provided intelligence reference samples against mixed DNA profiles obtained from crime scene samples (where the profile is suitable for comparison). These lines will follow the EXH lines "Two person mixed DNA profile" or "Three person mixed DNA profile".

Not Current

3 **Suspect check - low support for contribution**
The DNA profile provides low support for the proposition that the nominated suspect is a possible donor of DNA to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCLOW
(PP21)

4 **Suspect check - support for contribution 100 to 1000**
This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC1
(PP21)

5 **Suspect check - support for contribution 1000 to 10 000**
This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC2
(PP21)

6 **Suspect check- support for contribution 10 000 to 100 000**
This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC3
(PP21)

7 **Suspect check - support for contrib 100 000 - 1 million**
This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile,

rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC4
(PP21)

8 **Suspect check- support for contrib 1 million - 1 billion**
This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC5
(PP21)

9 **Suspect check- support for contrib 1 billion- 100 billion**
This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC6
(PP21)

10 **Suspect check - support for contribution > 100 billion**
This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC7
(PP21)

Not Current

4.11 General Final Results (PP21 and P+)

11 **Possible sub-threshold information**
The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.
Mnemonic = PSTI
(PP21)

This comment should be used there is an indication of possible additional DNA observed below the limit of reporting (LOR). This should indicate to QPS that there was something observed along with the reportable DNA profile, but does not meet the thresholds for comparing and reporting.

12 **No further work required as per advice from QPS**
QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.
Mnemonic = NWQPS
(PP21 or P+)

This comment will be used when QPS have advised they do not require testing on an item.

13 **QPS advised no further work required – results available**
QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA testing and results are available, however these have not been interpreted at this stage. QPS can submit a request to QHFSS for an interpretation of the DNA results if required.
Mnemonic = NWQPSR
(PP21 or P+)

This comment will be used when QPS have advised they do not require testing, but a DNA profile has been obtained. This comment will indicate to QPS that the sample has undergone DNA testing; however no interpretation was performed as per their advice.

14 **Testing restarted on advice from QPS**
QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.
Mnemonic = TRQ
(PP21 or P+)

This comment will be used when information has been obtained from the Queensland Police Service that testing is now required for an item.

15 **DNA profile removed from NCIDD**
The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.
Mnemonic = PRNCID
(PP21 or P+)

This comment will be used when a DNA profile previously reported as uploaded to NCIDD is removed from NCIDD due to information provided by the police, or other circumstances in which the DNA profile should not be on NCIDD, such as a change in NCIDD category, or the DNA profile is replaced by better profile from a different barcode.

16 **This sample has undergone further processing**
This item/sample has undergone further processing and an improved DNA profile has been obtained.
Mnemonic = SUFP
(PP21 or P+)

This comment is to be used when a final result has already been reported (e.g. partial profile) for that sample but for whatever reason it has undergone further reworking and a new final result needs to be reported (e.g. full profile).

17 **No further work able to be conducted on this sample**
This item/sample has been assessed and it has been determined that no further processing can be conducted on this sample, due to, but not limited to: no DNA extract left for further testing, current DNA profile improvement processes have already been exhausted.
Mnemonic = NFWA
(PP21 or P+)

Not Current

This comment can be used when a request has come from QPS for further work on a sample to be conducted. This line will be used when there is no further processing that can be undertaken e.g. no extract left after microcon, current processes have already been exhausted, or computer software programs are not compatible (e.g. 3100 to GMIDX).

PROFILER® PLUS RESULTS

The following comments are for the majority to be used with results processed using Profiler® Plus and interpreted with the Kinship statistical software. Please note: there are some EXHs below that can be used for both PP21 and P+, as indicated by the kit in brackets after the comment.

4.12 Full Profile Final Results (P+)

63 **9 loci DNA profile. Uploaded to NCIDD**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = FUPNPN
(P+)

This comment should be used when a full DNA profile was obtained from the sample and this profile is to be uploaded to NCIDD.

64 **9 loci DNA profile**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = FUPROF
(P+)

This comment should be used when a full DNA profile was obtained from the sample. This sample will not be uploaded to NCIDD.

65 **9 loci DNA profile- NCIDD- possible sub-threshold peaks**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = DPNPTP
(P+)

This comment should be used when a full DNA profile was obtained from the sample and this profile is to be uploaded to NCIDD, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

Not Current

66 **9 loci DNA profile - possible sub-threshold peaks**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained.
Mnemonic = DPPTP
(P+)

This comment should be used when a full DNA profile was obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

4.13 Partial Profile Final Results (PP21 and P+)

1 **Partial DNA profile**
This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = PDNA
(P+)

This comment should be used when a partial DNA profile was obtained from the sample, greater than the stringency for reporting a match on NCIDD (12 alleles or greater). This sample will not be uploaded to NCIDD.

2 **Partial DNA profile. Uploaded to NCIDD**
This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This partial DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = PAPNPN
(P+)

This comment should be used when a partial DNA profile was obtained from the sample and this profile is to be uploaded to NCIDD (12 alleles or greater).

3 **Partial DNA profile. Insufficient for NCIDD matching**
This item/sample gave a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PDNAIN
(P+)

Not Current

This comment should be used when a partial DNA profile was obtained from the sample which is less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5 alleles). This indicates to the QPS DRMU that a partial DNA profile was obtained that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

4 **Partial DNA profile unsuitable for comparison purposes**
This item/sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information within the DNA profile. This may be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = PPUCP
(PP21 or P+)

This comment should be used when a partial DNA profile was obtained which has very little information and is considered insufficient for informative comparison. This indicates to the QPS DRMU that a partial DNA profile was obtained that should not be used for comparison to a reference sample.

5 **Partial DNA profile- NCIDD- possible sub-threshold peaks**
This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained, which has been selected for loading to NCIDD. This partial DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = PDNPTP
(P+)

This comment should be used when a partial DNA profile (12 alleles or greater) was obtained from the sample and this profile is to be uploaded to NCIDD, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

6 **Partial DNA profile - possible sub-threshold peaks**
This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained.
Mnemonic = PDPTP
(P+)

This comment should be used when a partial DNA profile (12 alleles or greater) was obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

Not Current

7 **Partial profile, insuff NCIDD- pos. sub-threshold peaks**
This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained. This partial DNA profile was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PPINPT
(P+)

This comment should be used when a partial DNA profile (less than 12 alleles and greater than 5 alleles) was obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the partial DNA profile, but does not meet the thresholds for comparing and reporting. It will also inform QPS DRMU that the partial DNA profile could be used for comparison to other DNA profiles, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

8 **Partial DNA profile, 3 of 18 DNA components**
This item/sample gave a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PD3C
(P+)

This comment should be used when a partial DNA profile was obtained which has 3 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

9 **Partial DNA profile, 4 of 18 DNA components**
This item/sample gave a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PD4C
(P+)

Not Current

This comment should be used when a partial DNA profile was obtained which has 4 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

10 **Partial DNA profile, 5 of 18 DNA components**
This item/sample gave a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PD5C
(P+)

This comment should be used when a partial DNA profile was obtained which has 5 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

4.14 Mixed DNA Profile Final Results

Major DNA profile (P+)

1 **Mixed DNA profile. Major component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MIPMAC
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the major DNA profile was a full DNA profile. The major DNA profile will not be uploaded to NCIDD.

2 **Mixed DNA profile. Major component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MIPMUN
(P+)

Not Current

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This major DNA profile was a full DNA profile and will be uploaded to NCIDD.

3 **Mixed profile, partial major component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MPPMA
(P+)

This comment should be used when a partial mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This partial major DNA profile will not be uploaded to NCIDD, however this comment should be used when the major DNA profile is 12 alleles or greater.

4 **Mixed DNA profile, partial major component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MPPMAN
(P+)

This comment should be used when a partial mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This partial major DNA profile will be uploaded to NCIDD.

5 **Mixed profile, major component insuff for NCIDD matching**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMAIN
(P+)

This comment should be used when a partial mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This major DNA profile was a partial DNA profile less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5). This indicates to the QPS DRMU that the major DNA profile was a partial DNA

Not Current

profile that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

Minor DNA profiles (P+)

6 **Mixed DNA profile. Minor Component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MIPMIC
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile was a full DNA profile. This minor DNA profile will not be uploaded to NCIDD.

7 **Mixed profile, minor component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been loaded to NCIDD. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MPMINC
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile obtained a full DNA profile. This minor DNA profile will be uploaded to NCIDD.

8 **Mixed profile, partial minor component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MPPMI
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile was a partial DNA profile that contained information which could be used for comparison purposes. This minor DNA profile will not be uploaded to NCIDD, however this comment should be used when the minor DNA profile is 12 alleles or greater.

9 **Mixed DNA profile, partial minor component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor

Not Current

DNA profiles. The minor DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MPPMIN
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile obtained information that could be reported as a cold link on NCIDD (12 alleles or greater). This partial minor DNA profile will be uploaded to NCIDD.

10 **Mixed profile, minor component insuff for NCIDD matching**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMIIN
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This minor DNA profile was a partial DNA profile less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5). This indicates to the QPS DRMU that the minor DNA profile was a partial DNA profile that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

11 **Mixed profile- Minor component unsuitable for comparison**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained.
Mnemonic = MPMUC
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This minor DNA profile was a partial DNA profile which has very little information and is considered insufficient for informative comparison.

12 **Mixed DNA profile, complex minor component cannot exclude**
This item/sample gave a mixed DNA profile DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to the minor component of this mixed DNA profile.

Not Current

Mnemonic = MDNA1
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor Components. This minor component was a mixed DNA profile from two or more contributors. An evidence sample or unknown contributor (e.g. uk m1) could not be excluded as a contributor to this mixed DNA profile. There will always be a name associated with this sample in the *Linked No.* field of the EXR/EXH.

13 **Mixed profile, complex mixed minor component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.
Mnemonic = MPRO
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This minor component was a mixed DNA profile from two or more contributors. At this stage, the minor component cannot be interpreted further as no reference sample was obtained that when compared, could be ‘included’ (i.e. not excluded) as having contributed to the complex minor DNA profile, or comparison with additional reference sample may be possible if forthcoming. There will be no name associated with this line in the *Linked No.* field of the EXR/EXH.

14 **Mixed profile- complex minor unsuit for interp or compar.**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile is too complex for meaningful interpretation or comparison purposes due to the unknown number of potential contributors and/or the limited amount of information within the minor DNA profile.
Mnemonic = MPCMU
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor Components. This minor component was a mixed DNA profile from two or more contributors. Due to the unknown number of contributors or the partial nature of the minor DNA profile, no meaningful interpretation or comparison could be performed. There will be no name associated with this sample in the *Linked No.* field of the EXR/EXH.

15 **Mixed profile, minor profile insuff – indicated male origin**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile did not contain sufficient information for comparison purposes other that to say it indicated it was of male origin.
Mnemonic = MPMPIM
(P+)

Not Current

This comment is for the rare occurrence where the major is female and the minor is only a Y (no STRs). DRMU will occasionally call to ask whether the minor DNA profile indicated male origin, and this EXH line will provide this information.

16 **Mixed profile, minor comp. 3 of 18 DNA components**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMC3
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into major and minor DNA profiles. This minor DNA profile was a partial DNA profile which obtained 3 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial minor DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

17 **Mixed profile, minor comp. 4 of 18 DNA components**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMC4
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into major and minor DNA profiles. This minor DNA profile was a partial DNA profile which obtained 4 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial minor DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

18 **Mixed profile, minor comp. 5 of 18 DNA components**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds.

Not Current

There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMC5
(P+)

This comment should be used when a mixed DNA profile was obtained from this sample that could be separated into major and minor DNA profiles. This minor DNA profile was a partial DNA profile which obtained 5 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial minor DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

Complex Mixed DNA profiles (more than 2 contributors) (P+ or PP21)

19 **Complex mixed DNA profile – cannot exclude**
This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.
Mnemonic = CMPCE
(P+)

This comment should be used when a full or partial mixed DNA profile was obtained from at least two contributors which were unable to be resolved into distinct DNA contributions (e.g. major and minor DNA profiles or conditioned DNA profiles). This may include an indication of a low-level DNA contribution that is affecting the interpretation of the DNA profile (i.e.. it is preventing the DNA profile from being able to be separated into major and minor DNA profiles). An evidence sample or unknown contributor (e.g. uk m1) could not be excluded as a contributor to this mixed DNA profile. There will always be a name associated with this sample in the *Linked No.* field of the EXR/EXH.

20 **Complex mixed DNA profile. Unable to load to NCIDD**
This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. This complex mixed DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.
Mnemonic = CMPULN
(P+)

This comment should be used when a full or partial mixed DNA profile was obtained from at least two contributors which were unable to be resolved into distinct DNA contributions (e.g. major and minor DNA profiles or conditioned DNA profiles). This may include an indication of a low-level DNA contribution that is affecting the interpretation of the DNA profile (i.e.. it is preventing the DNA

Not Current

profile from being able to be separated into major and minor DNA profiles). There should be no name associated with this sample in the *Linked No.* field of the EXR/EXH as there are no reference samples/unknown profiles to compare to within the case.

21 **Complex mixed profile unsuitable for interp or comparison**
This item/sample gave a complex Mixed DNA profile with multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.
Mnemonic = CMPU
(PP21 or P+)

This comment should be used when a mixed DNA profile was obtained from multiple contributors. Due to the unknown number of contributors or the partial nature of the mixed DNA profile, no meaningful interpretation or comparison could be performed. There will be no name associated with this sample in the *Linked No.* field of the EXR/EXH.

Not Current

No major/minor DNA profiles / Even Mixed DNA profiles (2 contributors) (P+)

22 **Mixed profile, No major/minor. Unable to load to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. In the absence of reference samples, no further interpretation can be conducted; or comparison with additional reference samples may be possible if forthcoming.
Mnemonic = MPNMUN
(P+)

This comment should be used when a full or partial even mixed DNA profile was obtained from this sample which indicated the presence of DNA from two people. The mixed DNA profile could not be separated into major and minor DNA profiles. There should be no name associated with this sample in the *Linked No.* field of the EXR/EXH.

23 **Mixed profile, No major/minor – cannot exclude**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.
Mnemonic = MPNMM
(P+)

This is comment should be used when a mixed DNA profile was obtained from this sample which could not be separated into major and minor DNA profiles. An evidence sample or unknown contributor (e.g. uk m1) could not be excluded as a contributor to this mixed DNA profile. There will always be a name associated with this sample in the *Linked No.* field of the EXR/EXH.

Conditioned Mixed DNA profiles (P+)

24 **Mixed DNA profile conditioned on**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”
Mnemonic = MPCO
(P+)

This comment should be used when a full or partial mixed DNA profile consistent with coming from two contributors was obtained which could not be separated into major and minor contributions. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. This comment must always be followed by MPRP, MIPPRO, or MPRPAC.

25 **Mixed DNA profile. Remaining profile after conditioning**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MPRP
(P+)

This comment should be used when a full or partial mixed DNA profile consistent with coming from two contributors was obtained which could not be separated into major and minor contributions. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. This comment must always follow MPCO, or MIPDNA.

26 **Mixed DNA profile conditioned on – NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MIPDNA
(P+)

This comment should be used when a full or partial mixed DNA profile consistent with coming from two contributors was obtained which could not be separated into major and minor contributions. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The known contributor to this DNA profile will be uploaded to NCIDD. This comment must always be followed by MPRP, MIPPRO, or MPRPAC.

27 **Mixed profile. Remaining profile after conditioning – NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the

Not Current

presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this report. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MIPPRO
(P+)

This comment should be used when a full or partial mixed DNA profile which indicates the presence of DNA from two contributors was obtained, which could not be separated into major and minor DNA profiles. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The profile remaining after conditioning will be uploaded to NCIDD. This comment must always follow MPCO, or MIPDNA.

28 **Mixed profile. Remain profile after cond – insuff NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This remaining DNA profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPRPAC
(P+)

This comment should be used when a full or partial mixed DNA profile which indicates the presence of DNA from two contributors was obtained, which could not be separated into major and minor DNA profiles. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The profile remaining after conditioning was a partial DNA profile which contained information less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5). This indicates to the QPS DRMU that a partial DNA profile was obtained that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD. This comment must always follow MPCO, or MIPDNA.

29 **Mixed profile. Remain profile after cond– unsuitable NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which contained insufficient information for searching on NCIDD, and therefore is unable to be loaded to NCIDD. This remaining DNA profile may contain enough information to compare to other DNA profiles for either inclusion or exclusionary purposes. Where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPRPC

Not Current

(P+)

This comment should be used when a full or partial mixed DNA profile which indicates the presence of DNA from two contributors was obtained which could not be separated into major and minor DNA profiles. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The profile remaining after conditioning was a partial DNA profile which has less than 6 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS DRMU that a partial minor DNA profile was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes. This sample should not be uploaded to NCIDD. This comment must always follow MPCO, or MIPDNA.

4.15 Intelligence Results (PP21 or P+)

These EXR/EXH lines indicate a profile is to be loaded to NCIDD for intelligence purposes only, and further interpretations need to be made in a statement. These comments should only be used when there are no reference samples for a case and should not be used if a better profile exists that can be loaded.

These profiles are loaded to NCIDD in order to provide intelligence information to Queensland Police Service to aid in their investigations. Where possible, an unknown designation should be associated to the Intelligence EXH lines.

1 **Mixture Interp reqd - Intel profile loaded to NCIDD**
This item/sample gave a mixed DNA profile that has been interpreted for intelligence purposes only. This interpretation may not be able to be used for evidentiary purposes. This means that we may have lowered our routine interpretational or NCIDD matching guidelines in order to assist with the generation of intelligence information. This intelligence DNA profile has been selected for loading to NCIDD and further explanation of the interpretations made will follow in an intelligence report. It should be noted that the interpretation provided within this intelligence report may not meet the stringent court reporting guidelines and therefore wording within an evidential statement may be different. The Intelligence DNA profile loaded to NCIDD will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It will be outlined in the Intelligence report that this mixed DNA profile may be reported differently in an evidentiary statement.
Mnemonic = MIRIN
(P+)

2 **Partial profile Interp reqd – Intel profile loaded NCIDD**
This item/sample gave a partial DNA profile which contained an indication of DNA at a level less than the laboratorys standard reporting threshold. This profile was submitted for further analysis below QHFSS standard reporting thresholds for intelligence purposes. The subsequent profile has been selected for loading to NCIDD for intelligence purposes only and further explanation of the interpretations made will follow in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
Mnemonic = PIRIN
(P+)

3 **Partial profile – Intel profile loaded NCIDD**

Not Current

This item/sample gave a partial DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. This profile may also have indications of DNA at a level less than the laboratorys standard reporting threshold, therefore the profile may have been submitted for further analysis below standard reporting thresholds for intelligence purposes. The profile has been selected for loading to NCIDD for intelligence purposes only and any matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
Mnemonic = PPIPL
(P+)

4 **Minor/Remaining DNA profile – Intel profile loaded NCIDD**
This item/sample gave a mixed DNA profile, of which the minor or remaining DNA profile contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes only and any resulting matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
Mnemonic = MDPIL
(P+)

5 **Intel report required for further interpretation**
The results for this item/sample require further explanation which will follow in an intelligence report.
Mnemonic = IRRFI
(PP21 or P+)

This comment should be used when the DNA profile obtained cannot sufficiently be explained by an EXH and an Intelligence report is required to be sent to QPS DRMU in order to explain the interpretations made.

Not Current

4.16 Interim Results (PP21 or P+)

The following comments are to be used when initial results are required to be reported to QPS, however reworking is being carried out on the sample.

1 **Interim result- Part profile obtained- NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Final results are pending.
Mnemonic = INTER1
(P+)

2 **Interim result- Partial profile undergoing rework**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile. Final results are pending.
Mnemonic = INTER2
(P+)

3 **Interim result- Partial profile -Intel NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which contained insufficient information for NCIDD matching according to standard reporting protocols. After further analysis below standard reporting thresholds the profile has been selected for loading to NCIDD for intelligence purposes only. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Final results are pending.
Mnemonic = INTER3
(P+)

4 **Interim result- mixed profile obtained. Rework Reqd**
The interim DNA profile obtained from this sample/item indicated the presence of DNA from two or more contributors. This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
Mnemonic = INTER4
(PP21 or P+)

5 **Interim result- mixed profile - Intel NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile that has been interpreted for intelligence purposes only. This mixed DNA profile indicated the presence of DNA from at least two contributors. An attempt has been made to separate major and minor DNA profiles within this mixed DNA profile in order to load to NCIDD for intelligence purposes only. The major DNA profile has been loaded to NCIDD and further interpretations are required. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. This mixed DNA profile is only reportable by statement in order to clarify interpretation assumptions. Final results are pending.
Mnemonic = INTER5
(P+)

6 **Interim result- no profile obtained- undergoing rework**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.
Mnemonic = INTER6
(PP21 or P+)

Not Current

7 **Interim result- Mixed major comp.- NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Where information was obtained, the major DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.
Mnemonic = INTER7
(P+)

8 **Interim result- Mixed minor comp.- NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Where information was obtained, the minor DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.
Mnemonic = IRMMC
(P+)

9 **Interim- 9 loci, pos. sub-thresh peaks-NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a complete 9 loci DNA profile; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Final results are pending.
Mnemonic = IPTPR
(P+)

10 **Interim result – sample undergoing rework**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. This rework could be due to: instrument failure, requiring the sample to be re-processed; interpretation difficulties, requiring the sample to be re-run to resolve any issues. Final results are pending.
Mnemonic = IRSUR
(PP21 or P+)

11 **Interim Result- incomplete single source. Rework reqd**

Not Current

The interim result obtained from this sample/item was an incomplete single source DNA profile. This is not a final result and the sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
Mnemonic = INTSSR
(PP21)

4.17 Paternity Results (PP21 or P+)

1 **Not excluded as biological father**
The DNA profile obtained from the barcode sent with this exhibit report is not excluded as being a biological father of the DNA profile obtained from the exhibit.
Mnemonic = NEXBF
(PP21 or P+)

This comment is to be used in instances where the questioned father contains all of the obligate paternal alleles. This EXR/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned father barcode in the linked no field.

2 **Excluded as biological father**
The DNA profile obtained from the barcode sent with this exhibit report is excluded as being a biological father of the DNA profile obtained from the exhibit.
Mnemonic = EXBF
(PP21 or P+)

This comment is to be used in instances where the questioned father does not contain all of the obligate paternal alleles and is excluded as being the possible father. This EXR/EXH/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned father barcode in the linked no field.

3 **Consistent with being biological mother**
The DNA profile obtained from this exhibit is consistent with being a biological child of the barcode sent with this exhibit report.
Mnemonic = CWBM
(PP21 or P+)

This comment is to be used in instances where the questioned mother contains alleles that are present in the child's DNA profile. This EXR/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned mother barcode in the linked no field

4 **Not consistent with being biological mother**
The DNA profile obtained from the barcode is not consistent with being a biological mother of the DNA profile obtained from the exhibit.
Mnemonic = NCWBM
(PP21 or P+)

This comment is to be used in instances where the questioned mother does not contain alleles that are present in the child's DNA profile and is excluded as being the possible mother. This EXR/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned mother barcode in the linked no field.

Not Current

5 **Consistent with being child of**
The DNA profile obtained from this exhibit was consistent with being the biological child of the barcode sent with this exhibit report.
Mnemonic = CWBC
(PP21 or P+)

This comment is to be used only in rare instances where a profile obtained from a crime sample could be a biological child of the barcode in the linked no. field.

6 **Not consistent with being child of**
The DNA profile obtained from this exhibit was not consistent with being the biological child of the barcode sent with this exhibit report.
Mnemonic = NCWBC
(PP21 or P+)

This comment is to be used only in rare instances where a profile obtained from a crime sample could not be a biological child of the barcode in the linked no. field.

4.18 Quality control failure Results (PP21 or P+)

1 **Quality control failure – results not reportable**
During the processing of this item/sample, a failure in one of the quality control processes was identified. Investigations into this occurrence were undertaken; however any results for this sample are not reportable.
Mnemonic = QCF
(PP21 or P+)

This comment will be used in instances where a failure in one of the quality control processes has resulted in a DNA profile unable to be reported to QPS.

2 **Quality flag identified, on hold awaiting advice from QPS**
During the processing of this item/sample, QHFSS quality control processes indentified the integrity of this sample may be compromised. Advice is required from QPS to determine whether any results for this sample are reportable.
Mnemonic = QFIH
(PP21 or P+)

This comment will be used in instances where a match is obtained to a QPS elimination sample and advice is required from QPS to determine whether results for this sample can be reported. The barcode of the elimination sample will be entered into the warm link number field.

3 **Quality control failure, refer to QPS**
During the processing of this item/sample, QHFSS quality control processes identified the integrity of this sample is compromised. Results for this sample are not reportable.
Mnemonic = QCFRQ
(PP21 or P+)

Not Current

This comment will be used in instances where a match is obtained to a QPS elimination sample. The barcode of the elimination sample will be entered into the warm link number field. This line is used when advice has been received from QPS that results for this sample cannot be used.

4 **On hold, pending further work**
These results are currently subject to quarantine pending the completion of further quality checks. The outcome of these quality checks will be reported once complete.
Mnemonic = OHPFW
(PP21 or P+)

This comment will be used in instances where a failure in one of the quality control processes has been identified and further investigation is being undertaken to determine if the result can be reported to QPS.

4.19 Environmental Monitoring Final results (PP21 or P+)

Note – Environmental monitoring samples are analysed below the limit of reporting (LOR = 50 RFU for P+, 40 RFU for PP21) for intelligence purposes. Environmental samples will be interpreted using P+ assessment techniques for mixed DNA profiles, and will be interpreted through STRmix^{TM} if further statistical interpretation is required.

Environmental samples that match to QPS samples are reported through the EXH as a match. Environmental samples that match to QHFSS staff samples are reported as for crime scene samples – Quality control failure. If no matches are obtained to any staff databases, a further quality search is performed against the DNA Analysis Database (DAD). Any matches to this are reported via an Intelligence report through the Quality and Projects team, with the EXH line "ENVM – additional quality searches conducted". If no matches are obtained, then the profile is assigned as an unknown male or female with no numerical designation, example UK M or UK F, using the following EXH lines:

1 **ENVM – Full DNA profile**
This environmental sample gave a full DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENFDP
(PP21 or P+)

2 **ENVM –Partial DNA profile**
This environmental sample gave a partial DNA. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained

Not Current

Mnemonic = ENPDP
(PP21 or P+)

3 **ENVM - Partial profile unsuitable for comparison purposes**
This environmental sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENPDPU
(PP21 or P+)

4 **ENVM – No DNA profile**
No DNA profile was obtained from this environmental sample. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENNDP
(PP21 or P+)

5 **ENVM – Major DNA profile**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the major was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.
Mnemonic = ENMDP
(PP21 or P+)

6 **ENVM – Minor DNA profile unsuitable for comparison**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile contained insufficient information for comparison purposes due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENMDPU
(PP21 or P+)

7 **ENVM – Minor DNA profile**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search

Not Current

against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENMIDP
(PP21 or P+)

8 **ENVM- Complex mixture unsuitable for interp or comparison**
This environmental sample gave a complex mixed DNA profile which contained an unknown number of contributors or a limited amount of information. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENCMPU
(PP21 or P+)

9 **ENVM - Complex mixed DNA profile**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles), and as such, no further interpretation can be conducted as this time. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENCMDP
(PP21 or P+)

10 **ENVM additional quality search conducted see Intel report**
Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. If the profile obtained cannot be matched to a QHFSS DNA Analysis staff or QPS staff member; a second Quality assurance process is used. This search capability is restricted within DNA Analysis to the Managing Scientist and the Quality & Projects Senior Scientist and utilises the DNA Analysis Database (DAD). This quality search is only performed to aid QPS in their investigation of any potential contamination events. In this instance, a match was obtained from this additional quality assurance search. Further information is contained within the intelligence report that will accompany this exhibit report.
Mnemonic = ENAQS
(PP21 or P+)

Not Current

5. Amendment History

Version	Date	Author/s	Amendments
1	May 2005	L Ryan	First Issue
2	Jun 2005	L Ryan	Add changes suggested during review
3	Jan 2006	L Ryan	Addition of new EXR/EXH results
4	Feb 2006	L Ryan	Addition of new EXR/EXH results
5	Sep 2006	L Ryan	Grouping like EXR/EXHs and numbering of results Addition of new EXR/EXH results Seminal Fluid Examination EXR/EXH #s: 12,13 Saliva Examination EXR/EXH #: 5 Hair Examination EXR/EXH #: 3 General Examination EXR/EXH #s:4,13,14,15,16,17 Mixed DNA Profile Final EXR/EXH #s:20,21,22,23 Blood Examination EXR/EXH #s: 5,6
6	Nov 2006	P Taylor	Added Blood Examination EXR/EXH# 7
7	21 Feb 2007	P Taylor	Added Saliva Presumptive EXR/EXH# 6,7
8	11 Dec 2007	P Taylor	Removed unused EXR/EXH lines. Added comments for when to use EXR/EXH lines. Added Paternity EXR/EXH lines. New lines – Intelligence EXR/EXH's; Mixed DNA profile EXR/EXH's #13,16; Seminal Fluid Examination EXR/EXH #7; Saliva Examination EXR/EXH #4; and General Examination EXR/EXH's #13,14,15.
9	05 Aug 2008	P Taylor	Added new EXR/EXH lines: 4.1 (7), 4.2 (13), 4.7 (14,15 and 19), 4.12 Quality Control failure EXR/EXH's and 4.13 Interim EXR/EXH's.
10	25 Jan 2010	P Taylor, E Caunt	Complete re-write of comments and explanations, and revision of EXR/EXH lines.
11	23 Sep 2011	P Taylor	Addition of EXH lines to replace FERRO's, ENVM EXH lines, and some other additional EXH lines. Deactivated some EXH lines that were no longer required. Some minor re-writing of expanded comments.
12	30 Nov 2012	P Brisotto, E Caunt	Update with new EXHs for PowerPlex21 and STRmix
13		P Brisotto, E Caunt	Amendments to EXHs and expansion of when to use new EXHs for PP21. Added Appendix relating to requesting new EXHs and LKRs. Removed 2MXUI. Changed 2MXUND to 3MXRUN. Added EXHs for new workflow.
14	28 June 2012	E Caunt R Morgan	Added PP21 EXH lines for designation of remaining components after conditioning two person mixtures and grouping low support and non contribution reporting.

Not Current

6. Appendices

Appendix 1 – Guidelines for creating new EXH and LKR lines

Appendix 1

Guidelines for creating new EXH/LKR lines

- EXH and LKR lines can accommodate 57 characters (inclusive of spaces)
- EXH and LKR mnemonics can be no more than 6 characters (no spaces)
- The follow symbols cannot be used in EXH or LKR lines or expanded comments:
  - single quote '
  - double quote "
  - ampersand &
  - pipe |
  - carrot ^
  - comma ,
  - tilde ~
  - dash – (note: dash has historically been used in EXH/EXR and LKR lines. For these lines, QPS remove the dash, or replace it where appropriate after transfer.)
- > or < symbols can be used, only if a space exists on both sides e.g. LR > 100000

Not Current

EXH lines have expand comments associated with them, and are coded – meaning when the EXH mnemonic transfer across the GSI, at the QPS end the mnemonic expands out to the provided comment associated with the EXH line. AUSLAB contains only the EXH lines and mnemonics. The expanded comments are included by the QPS.

LKR lines do not have expanded comments, but the LKR line and mnemonic are requested from LISS in the same way as EXHs.

New EXH and expanded comments, and LKR lines, are created and reviewed by staff within DNA analysis, and provided to A/Insp Troy O'Malley, S/Sgt Scott McLaren, and the S/Sgt for QPS DNA and Results Management Unit (DRMU) for review.

Once wording has been agreed by both parties, the EXH and LKR lines, along with proposed mnemonics, are entered in a Request for Standard Change form 27593 for LISS (Laboratory Information Systems and Solutions). This request for change needs to be approved by the Senior Director before forwarding to LISS. The EXH and LKR lines plus mnemonic should be provided in a table or attached spreadsheet. Please see Change Project #105 for examples: I:\Change Management\Proposal#105 PowerPlex 21 Reporting and STRmix\LISS requests

The test panels requested are for all EXH or LKR pages: EXH, EXH2, EXH3 or LKR, LKR2, LKR3.
For EXHs, the result/status look-up fields in which the new EXH lines are to be configured are: lines DUM1 to DUM21.
For LKRs, the result/status look-up fields in which the new LKR lines are to be configured are: lines DUML1 to DUML21.

Once LISS has completed the request for change, a spreadsheet of the EXH or LKR lines with the mnemonics and expanded comments is to be emailed to A/Insp Troy O'Malley [redacted] for entry into the Forensic Register. This spreadsheet is versioned, and the current version number can be located G:\ForBiol\AAA Forensic Reporting & Intel\EXH spreadsheets for QPS (versioned)

Note 1: If the expanded comment requires modifying, this does not require LISS involvment. QPS can be contacted to make the change in their system, and this document 23008 be updated to reflect the new expanded comment.

Note 2: If an EXH line is to be changed, the old line should be deactivated and a new line created or both the line and the mnemonic must be changed. If the EXH line is changed and the mnemonic remains the same, all previously reported EXH lines with that mnemonic will be changed to the new line.

Not Current

JH-2

Mnemonic	EXH line	Expanded Comment
1BPPSR	Presumptive blood test pos. Submitted-results pending	This item/sample tested positive to a presumptive test for blood (TMB) and was submitted for DNA testing. Results are pending.
1S9L10	SS DNA profile 9 loci and above LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
1SS20L	Single source 20 loci DNA profile LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It obtained all of the DNA information potentially available. This DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L1	Single source DNA profile < 9 loci LR 100 - 1000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L2	Single source DNA profile < 9 loci LR 1000 - 10 000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L3	Single source DNA profile < 9 loci LR 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L4	Single source DNA profile < 9 loci LR 100 000 - 1 million	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L5	SS DNA profile < 9 loci LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L6	SS DNA profile < 9 loci LR 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L7	SS DNA profile less than 9 loci LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SS9L8	SS DNA profile 9 loci and above LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.

Mnemonic	EXH line	Expanded Comment
1SS9L9	SS DNA profile 9 loci and above LR 1 billion- 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
1SSAKN	Single Source DNA profile - assumed known contributor	This item/sample provided a DNA profile that indicated the presence of one contributor. The associated barcode matches this DNA profile. Based on information provided to the laboratory, it has been assumed that the associated barcode is the donor of this DNA. Given this assumption, no statistical interpretation has been performed.
1SSIND	NCIDD Intel upload - single source partial profile	This item/sample gave an incomplete single source DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes. This incomplete DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be statistically evaluated and reported as a likelihood ratio. Depending on the amount of information in this DNA profile, the strength of the support for inclusion will vary.
1SSINI	NCIDD Intel upload - interim single source profile	This item/sample gave an interim result of an apparent single source DNA profile. This DNA profile has been selected for loading to NCIDD for intelligence purposes, as this sample is currently undergoing further processing. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that the final result may vary. Any reference samples subsequently received will be statistically evaluated against the final DNA profile and reported as a likelihood ratio.
1SSLND	Single source DNA profile < NCIDD matching stringency	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile was below the QHSS stringency for reporting a match on NCIDD, and has therefore not been loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
1SSLOW	Single Source- low support for contribution	This item/sample provided a partial DNA profile which indicated the presence of one contributor. Only limited information has been obtained and this information matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. Statistically, this DNA profile provides low support that the associated barcode sent with this exhibit report is the donor of this DNA. Further information can be provided if required.
1SSNCD	NCIDD upload single source DNA profile	A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.
1SSUND	Single source DNA profile- unsuitable for NCIDD searching	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile contained insufficient information for searching on NCIDD, and is therefore unable to be loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
2MX	Two person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors.
2MX1	2 person mix - support for contribution 100 to 1000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
2MX2	2 person mix - support for contribution 1000 to 10 000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
2MX3	2 person mix, support for contrib 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.

Mnemonic	EXH line	Expanded Comment
2MX4	2 person mix- support for contrib 100 000 to 1 million	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
2MX5	2 person mix - support for contrib 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
2MX6	2 person mix- support for contrib 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
2MX7	2 person mix profile - support for contrib > 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
2MXCI	2 person mixed profile - conditioned on - Intel	This item/sample provided a DNA profile that indicated the presence of two contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
2MXCND	NCIDD upload - conditioned contribution	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The conditioned contribution described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.
2MXCON	2 person mixed profile - conditioned on	This item/sample provided a DNA profile that indicated the presence of two contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.
2MXINC	2 person mixed DNA profile - inconclusive	This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.
2MXIND	NCIDD upload - Intel mixed DNA profile	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
2MXLOW	2 person mix - low support for contribution	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Please contact DNA Analysis if further information is required.
2MXNC	2 person mix - supports non contribution	This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
2MXNCD	NCIDD upload - mixed DNA profile	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.

Mnemonic	EXH line	Expanded Comment
2MXNIR	Mixture contribution loaded to NCIDD - see Intel report	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. A DNA contribution was able to be deconvoluted for loading to NCIDD, and further information about this will follow in an intelligence report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile the, strength of the support for contribution will vary.
2MXR1	2 person mix remaining - support for contrib 100 to 1000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
2MXR2	2 person mix remaining- support for contrib 1000 to 10000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
2MXR3	2 person mix rem - support for contrib 10 000 to 100 000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
2MXR4	2 person mix rem- support for contrib 100000 to 1 million	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
2MXR5	2 person rem- support for contrib 1 million to 1 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
2MXR6	2 person rem - support for contrib 1 billion -100 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
2MXR7	2 person mix rem - support for contribution > 100 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
2MXRCU	2 pers mix remaining consistent with unknown	The mixed DNA profile result for this sample indicated the presence of DNA from two contributors and has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. This remaining contribution is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. This unknown is therefore a possible donor of DNA to the 'remaining' contribution. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.

Mnemonic	EXH line	Expanded Comment
2MXRIN	2 person mixed profile - remaining Intel - NCIDD	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
2MXRL	2 person mix remaining - low support for contrib	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
2MXRLM	Mix Rem DNA contrib < NCIDD matching stringency	The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This remaining contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
2MXRNC	2 person mix remaining - supports non contribution	This item/sample provided a DNA profile that indicated the presence of two contributors. If it is assumed that the barcode sent with the above exhibit report (2 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
2MXRND	NCIDD upload remaining contribution	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. The associated barcode/unknown designation sent with this exhibit report is a possible donor of DNA to the 'remaining contribution’. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
2MXUNM	Mix Remaining DNA contribution indicates male origin	The remaining contribution separated after conditioning the mixed DNA profile indicates male origin
2MXUNS	Mix Rem DNA contrib unsuitable for NCIDD searching	The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin. This remaining contribution is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
3MX	Three person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.
3MX1	3 person mix - support for contribution 100 to 1000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
3MX2	3 person mix - support for contribution 1000 to 10 000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
3MX3	3 person mix - support for contrib 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
3MX4	3 person mix - support for contrib 100 000 to 1 million	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.

Mnemonic	EXH line	Expanded Comment
3MX5	3 person mix - support for contrib 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
3MX6	3 person mix- support for contrib 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
3MX7	3 person mix profile - support for contrib > 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
3MXCI	3 person mixed profile - conditioned on - Intel	This item/sample provided a DNA profile that indicated the presence of three contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
3MXCON	3 person mixed profile - conditioned on	This item/sample provided a DNA profile that indicated the presence of three contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.
3MXINC	3 person mixed DNA profile - inconclusive	This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.
3MXIND	3 pers mixed profile, mix remaining intel NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
3MXLOW	3 person mix - low support for contribution	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
3MXNC	3 person mix - supports non contribution	This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
3MXND	3 person mixed DNA profile not deconvoluted	This item/sample gave a mixed DNA profile which indicated the presence of DNA from three contributors. This mixed DNA profile has been assessed and it is considered that, if the DNA profile were to be deconvoluted, it may provide sufficient information for upload to NCIDD. Deconvolution of this DNA profile has not been performed at this time. Please contact the laboratory if further interpetation is required.
3MXR1	3 person mix remaining - support for contrib 100 to 1000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
3MXR2	3 person mix remaining- support for contrib 1000 to 10000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.

Mnemonic	EXH line	Expanded Comment
3MXR3	3 person mix rem - support for contrib 10 000 to 100 000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
3MXR4	3 person mix rem- support for contrib 100000 to 1 million	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
3MXR5	3 person rem - support for contrib 1 million to 1 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
3MXR6	3 person rem - support for contrib 1 billion-100 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
3MXR7	3 person mix rem - support for contribution > 100 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
3MXRIN	3 per mix, intel cond, remaining intel NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
3MXRL	3 person mix remaining - low support for contrib	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
3MXRNC	3 person mix remaining - supports non contribution	This item/sample provided a DNA profile that indicated the presence of three contributors. If it is assumed that the barcode sent with the above exhibit report (3 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
3MXRND	3 person mixed profile, mixture remaining NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
AINT	All items now tested	All items for this exhibit have now been examined
CMLSNC	Cond mix rem - low supp for contrib or supp non contrib	This item/sample provided a DNA profile that indicated the presence of two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately. When conditioning on the assumed known contributor, then the DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.

Mnemonic	EXH line	Expanded Comment
CMPCE	Complex mixed DNA profile – cannot exclude	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.
CMPU	Complex mixed profile unsuitable for interp or comparison	This item/sample gave a complex Mixed DNA profile with multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.
CMPULN	Complex mixed DNA profile. Unable to load to NCIDD	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. This complex mixed DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.
CWBC	Consistent with being child of	The DNA profile obtained from this exhibit was consistent with being the biological child of the barcode sent with this exhibit report
CWBM	Consistent with being biological mother	The DNA profile obtained from this exhibit is consistent with being a biological child of the barcode sent with this exhibit report.
DIFP	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 DNA Analysis if further information is required.
DPNPTP	9 loci DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
DPPTP	9 loci DNA profile - possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained.
EMDP	Excluded from mixed DNA profile	This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The statistical interpretation shows that some or all of the donors of the reference DNA profiles associated with this case are excluded as having contributed to this mixed DNA profile.
ENAQS	ENVM additional quality search conducted see Intel report	Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. If the profile obtained cannot be matched to a QHFSS DNA Analysis staff or QPS staff member; a second Quality assurance process is used. This search capability is restricted within DNA Analysis to the Managing Scientist and the Quality & Projects Senior Scientist and utilises the DNA Analysis Database (DAD). This quality search is only performed to aid QPS in their investigation of any potential contamination events. In this instance, a match was obtained from this additional quality assurance search. Further information is contained within the intelligence report that will accompany this exhibit report.
ENCMDP	ENVM - Complex mixed DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles), and as such, no further interpretation can be conducted as this time. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
ENCMPU	ENVM- Complex mixture unsuitable for interp or comparison	This environmental sample gave a complex mixed DNA profile which contained an unknown number of contributors or a limited amount of information. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
ENFDP	ENVM - Full DNA profile	This environmental sample gave a full DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained

Mnemonic	EXH line	Expanded Comment
ENMDP	ENVM - Major DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the major was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.
ENMDPU	ENVM – Minor DNA profile unsuitable for comparison	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile contained insufficient information for comparison purposes due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
ENMIDP	ENVM – Minor DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
ENNDP	ENVM - No DNA profile	No DNA profile was obtained from this environmental sample. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
ENPDP	ENVM -Partial DNA profile	This environmental sample gave a partial DNA. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
ENPDPU	ENVM - Partial profile unsuitable for comparison purposes	This environmental sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
ESCD	Entire sample consumed	The entire item/sample was consumed during examination
EXBF	Excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is excluded as being a biological father of the DNA profile obtained from the exhibit.
FUPNPN	9 loci DNA profile. Uploaded to NCIDD	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
FUPROF	9 loci DNA profile	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report.
HLNSA	Hair located. Not suitable for analysis	Hair/s were located on this item/sample. They were observed using microscopy and deemed unsuitable for DNA testing due to no observed cellular material, or possible animal origin.
HLSRP	Hair located. Submitted results pending	Hair/s were located on this item/sample. These hairs have been submitted for DNA testing. Results are pending.
HOIS	Hair located on the outside of an in-tube submission	A hair was located either outside the tube or partially hanging in and out of the tube. It is unclear if this hair was part of the collected item or incorrectly transferred during collection. This hair/hair portion has been stored and will only be analysed if a request is provided.
INTER1	Interim result- Part profile obtained- NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Final results are pending.
INTER2	Interim result- Partial profile undergoing rework	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile. Final results are pending.

Mnemonic	EXH line	Expanded Comment
INTER3	Interim result- Partial profile -Intel NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which contained insufficient information for NCIDD matching according to standard reporting protocols. After further analysis below standard reporting thresholds the profile has been selected for loading to NCIDD for intelligence purposes only. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Final results are pending.
INTER4	Interim result- mixed profile obtained. Rework Reqd	The interim DNA profile obtained from this sample/item indicated the presence of DNA from two or more contributors. This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
INTER5	Interim result- mixed profile - Intel NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile that has been interpreted for intelligence purposes only. This mixed DNA profile indicated the presence of DNA from at least two contributors. An attempt has been made to separate major and minor DNA profiles within this mixed DNA profile in order to load to NCIDD for intelligence purposes only. The major DNA profile has been loaded to NCIDD and further interpretations are required. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. This mixed DNA profile is only reportable by statement in order to clarify interpretation assumptions. Final results are pending.
INTER6	Interim result- no profile obtained- undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.
INTER7	Interim result- Mixed major comp.- NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Where information was obtained, the major DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.
INTSSR	Interim Result- incomplete single source. Rework reqd	The interim result obtained from this sample/item was an incomplete single source DNA profile.This is not a final result and the sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
IPNE	Items Prioritised. Not examined at this time	This item/sample has been prioritised based on case information provided by QPS. Examinations may be conducted in the future.
IPNST	Items prioritised, not submitted at this time	This item/sample has been prioritised and as such samples taken from this exhibit have not been submitted at this time.
IPTPR	Interim- 9 loci, pos.sub-thresh peaks-NCIDD.Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a complete 9 loci DNA profile; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Final results are pending.
IRMMC	Interim result- Mixed minor comp.- NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Where information was obtained, the minor DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.
IRRFI	Intel report required for further information	The results for this item/sample require further explanation which will follow in an intelligence report.
IRSUR	Interim Result. Sample undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. This rework could be due to: instrument failure, requiring the sample to be re-processed; interpretation difficulties, requiring the sample to be re-run to resolve any issues. Final results are pending.

Mnemonic	EXH line	Expanded Comment
ISCB	Incorrect submission of cigarette butt	This cigarette butt was received in a tube. Items provided in a tube are intended to be submitted directly for DNA processing with minimal manual intervention. This sample required further examination as it was received as a whole cigarette butt. Please submit whole cigarette butts in a Crime Scene Sample envelope or as a sub-sample of the filter paper.
LDIS	Labelling discrepancy	There is a labelling discrepancy (Occurrence number or sample description) between the exhibit packaging and the AUSLAB/Forensic Register interface records. This sample can not be processed until the labelling discrepancy is resolved. The discrepancy will be highlighted to the QPS Sample Management Unit for clarification in the first instance, and if unable to be resolved, will be referred to the appropriate QPS officer for resolution. Please ensure all labelling details are correct before submission to the DNA Analysis Laboratory
MDNA1	Mixed DNA profile, complex minor component cannot exclude	This item/sample gave a mixed DNA profile DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to the minor component of this mixed DNA profile.
MDPIL	Minor/Remaining DNA profile - Intel profile loaded NCIDD	This item/sample gave a mixed DNA profile, of which the minor or remaining DNA profile contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes only and any resulting matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
MIES	Sample required manual intervention - excess substrate	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as excess substrate was contained within the tube. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.
MIISB	Multiple items incorrectly submitted under single barcode	Multiple items, or multiple AP positive areas have been submitted under a single barcode identifier. Each item requires its own unique barcode, as the barcode is used for reporting purposes to both the forensic register and the National Criminal Investigation DNA Database. Each item will be allocated a new barcode for processing and reporting purposes.
MINAL	Multiple items - not all tested	This exhibit consisted of multiple items packaged together under one exhibit barcode, of which not all were selected for examination. If more or all of the remaining items are required to be examined, this can be completed upon request.
MIPDNA	Mixed DNA profile conditioned on – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
MIPMAC	Mixed DNA profile. Major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.
MIPMIC	Mixed DNA profile. Minor Component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.
MIPMUN	Mixed DNA profile. Major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
MIPPRO	Mixed profile. Remaining profile after conditioning – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this report. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.

Mnemonic	EXH line	Expanded Comment
MIRIN	Mixture Interp reqd - Intel profile loaded to NCIDD	This item/sample gave a mixed DNA profile that has been interpreted for intelligence purposes only. This interpretation may not be able to be used for evidentiary purposes. This means that we may have lowered our routine interpretational and NCIDD matching guidelines in order to assist with the generation of intelligence information. This intelligence DNA profile has been selected for loading to NCIDD and further explanation of the interpretations made will follow in an intelligence report. It should be noted that the interpretation provided within this intelligence report may not meet the stringent court reporting guidelines and therefore wording within an evidential statement may be different. The Intelligence DNA profile loaded to NCIDD will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It will be outlined in the Intelligence report that this mixed DNA profile may be reported differently in an evidentiary statement.
MISSTL	Sample required manual intervention - swab stick too long	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the swab stick was too long and required shortening to enable downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process. The ideal stick length should be no more than 24mm total length (swab stick plus swab head).
MITRI	Sample reqd manual intervention- tlift rolled incorrectly	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the tapelift was rolled incorrectly, impeding downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.
MLSONC	Mixture - low support for contrib or supports non contrib	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.
MNS	Micro neg for sperm	Spermatozoa were not detected on this item/sample by microscopy.
MPCMU	Mixed profile- complex minor unsuit for interp or compar.	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile is too complex for meaningful interpretation or comparison purposes due to the unknown number of potential contributors and/or the limited amount of information within the minor DNA profile.
MPCO	Mixed DNA profile conditioned on	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”
MPMAIN	Mixed profile, major component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
MPMC3	Mixed profile, minor comp. 3 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
MPMC4	Mixed profile, minor comp. 4 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
MPMC5	Mixed profile, minor comp. 5 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).

Mnemonic	EXH line	Expanded Comment
MPMIIN	Mixed profile, minor component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
MPMINC	Mixed profile, minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been loaded to NCIDD. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
MPMPIM	Mixed profile,minor profile insuff– indicated male origin	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile did not contain sufficient information for comparison purposes other that to say it indicated it was of male origin.
MPMUC	Mixed profile Minor component unsuitable for comparison	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained.
MPNMM	Mixed profile, No major/minor – cannot exclude	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.
MPNMUN	Mixed profile, No major/minor. Unable to load to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. In the absence of reference samples, no further interpretation can be conducted; or comparison with additional reference samples may be possible if forthcoming.
MPPMA	Mixed profile, partial major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
MPPMAN	Mixed DNA profile, partial major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
MPPMI	Mixed profile, partial minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
MPPMIN	Mixed DNA profile, partial minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
MPRO	Mixed profile, complex mixed minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.
MPRP	Mixed DNA profile. Remaining profile after conditioning	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this exhibit report.
MPRPAC	Mixed profile. Remain profile after cond – insuff NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This remaining DNA profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).

Mnemonic	EXH line	Expanded Comment
MPRPC	Mixed profile. Remain profile after cond–unsuitable NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which contained insufficient information for searching on NCIDD, and therefore is unable to be loaded to NCIDD. This remaining DNA profile may contain enough information to compare to other DNA profiles for either inclusion or exclusionary purposes. Where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
NBOS	No barcode on sample	The item/sample provided in a tube was not labelled with a barcode. A barcode is required for the processing of the item and for continuity purposes. A barcode the same as that attached to the packaging has been affixed to the item.
NCWBC	Not consistent with being child of	The DNA profile obtained from this exhibit was not consistent with being the biological child of the barcode sent with this exhibit report.
NCWBM	Not consistent with being biological mother	The DNA profile obtained from the barcode is not consistent with being a biological mother of the DNA profile obtained from the exhibit.
NDNAD	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.
NDPPTP	No DNA profile – possible sub-threshold peaks	A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This could be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
NEXBF	Not excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is not excluded as being a biological father of the DNA profile obtained from the exhibit.
NFEC	No further examinations conducted	This item/sample was tested for the possible presence of biological material and none were detected. No further testing was conducted on this item.
NFWA	No further work able to be conducted on this sample	This item/sample has been assessed and it has been determined that no further processing can be conducted on this sample, due to, but not limited to: no DNA extract left for further testing, current DNA profile improvement processes have already been exhausted.
NHLNE	No hair located. No further examination conducted	The item/sample was examined for the presence of hair and none was located. This could be due to no hair present or item is substance other than hair. No further testing for hair was conducted on this item.
NOPROF	No DNA profile	A DNA profile was not obtained from this item/sample, due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
NRDP	No reportable DNA profile	A DNA profile above QHFSS standard reporting thresholds was not obtained from this sample/item. This may be due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
NWQPS	No further work required as per advice from QPS	QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.
NWQPSR	QPS advised no further work required - results available	QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA testing and results are available, however these have not been interpreted at this stage. QPS can submit a request to QHFSS for an interpretation of the DNA results if required.
OHII	On hold - insufficient information provided for testing	There was insufficient information provided with this submission to determine what type of analysis is required for this item/sample eg, saliva, semen. This sample is to be placed on hold until further information on the testing requirements for this sample is provided.
OHPFW	On hold, pending further work	These results are currently subject to quarantine pending the completion of further quality checks. The outcome of these quality checks will be reported once complete.
PAPNPN	Partial DNA profile. Uploaded to NCIDD	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This partial DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
PAPPRP	Presump. PSA test positive, submitted - results pending	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was submitted for DNA testing. Results are pending.
PBNSC	Presumptive blood test neg. Submitted for cells	This item/sample tested negative to a presumptive test for blood (TMB). This item was submitted for general cell DNA testing.
PBTN	Presumptive blood test neg.	This item/sample tested negative to a presumptive test for blood (TMB).
PD3C	Partial DNA profile, 3 of 18 DNA components	This item/sample gave a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
PD4C	Partial DNA profile, 4 of 18 DNA components	This item/sample gave a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).

Mnemonic	EXH line	Expanded Comment
PD5C	Partial DNA profile, 5 of 18 DNA components	This item/sample gave a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
PDNA	Partial DNA profile	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
PDNAIN	Partial DNA profile. Insufficient for NCIDD matching	This item/sample gave a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
PDNPTP	Partial DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained, which has been selected for loading to NCIDD. This partial DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
PDPTP	Partial DNA profile - possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained.
PIRIN	Partial profile Interp reqd – Intel profile loaded NCIDD	This item/sample gave a partial DNA profile which contained an indication of DNA at a level less than the laboratorys standard reporting threshold. This profile was submitted for further analysis below QHFSS standard reporting thresholds for intelligence purposes. The subsequent profile has been selected for loading to NCIDD for intelligence purposes only and further explanation of the interpretations made will follow in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
PPINPT	Partial profile, insuff NCIDD- pos. sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained. This partial DNA profile was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
PPIPL	Partial profile - Intel profile loaded to NCIDD	This item/sample gave a partial DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. This profile may also have indications of DNA at a level less than the laboratorys standard reporting threshold, therefore the profile may have been submitted for further analysis below standard reporting thresholds for intelligence purposes. The profile has been selected for loading to NCIDD for intelligence purposes only and any matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
PPSANS	Presump. PSA test positive, no sperm found	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. No spermatozoa were detected by microscopy. This item was submitted for DNA testing. Results are pending.
PPSRP	Presump. AP test positive, submitted - results pending	This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Results are pending.
PPUCP	Partial DNA profile unsuitable for comparison purposes	This item/sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information within the DNA profile. This may be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
PREBT	Presumptive blood test positive	This item/sample tested positive to a presumptive test for blood (TMB).
PRNCID	DNA profile removed from NCIDD	The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.
PSNSC	Presump saliva negative. Submitted for cells	This item/sample tested negative to a presumptive test for saliva (Phadebas). This item/sample was submitted for general cell DNA testing.

Mnemonic	EXH line	Expanded Comment
PSPSRP	Presump saliva positive. Submitted-results pending	This item/sample tested positive to a presumptive test for saliva (Phadebas) and was submitted for DNA testing. Results are pending.
PSTI	Possible sub-threshold information	The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.
PSTN	Presump saliva test negative	This item/sample tested negative to a presumptive test for saliva (Phadebas).
PSTP	Presump saliva test positive	This item/sample tested positive to a presumptive test for saliva (Phadebas).
QCF	Quality control failure – results not reportable	During the processing of this item/sample, a failure in one of the quality control processes was identified. Investigations into this occurrence were undertaken; however any results for this sample are not reportable.
QCFRQ	Quality control failure, refer to QPS	During the processing of this item/sample, QHFSS quality control processes identified the integrity of this sample is compromised. Results for this sample are not reportable.
QFIH	Quality flag identified, on hold awaiting advice from QPS	During the processing of this item/sample, QHFSS quality control processes indentified the integrity of this sample may be compromised. Advice is required from QPS to determine whether any results for this sample are reportable.
SAC	Submitted as cells	This item/sample was submitted for general cell DNA testing.
SACPSP	Submitted as cells, Presump saliva test pending	This item/sample was submitted for general cell DNA testing. The item/sample will be tested with the presumptive test for saliva (Phadebas). Results are pending.
SCANM	Suspect check actioned - no match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.
SCII	Suspect check - insufficient information to compare	There was insufficient information in the DNA profile obtained from this item/sample to determine if the nominated suspect could be a potential contributor.
SCLOW	Suspect check - low support for contribution	The DNA profile provides low support for the proposition that the nominated suspect is a possible donor of DNA to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCSC1	Suspect check - support for contribution 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCSC2	Suspect check - support for contribution 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCSC3	Suspect check- support for contribution 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCSC4	Suspect check - support for contrib 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCSC5	Suspect check- support for contrib 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCSC6	Suspect check- support for contrib 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCSC7	Suspect check - support for contribution > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SEMND	Semen not detected	Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. QHFSS recommends QPS to commence further examination on items relating to this case if applicable.
SOHAA	Sample on hold, awaiting advice	This item/sample has been placed on hold and is awaiting additional information from QPS before processing can recommence. This information may relate to, but is not limited to; examination priority, screening requirements.
SPFRU	Sample processed and final results under	This item/sample was processed under the barcode sent with this exhibit report. The final results will be reported under that barcode.
SPP	Sample pooled and processed under	This item/sample was pooled and submitted for DNA testing under the barcode sent with this exhibit report. The final results will be reported under the barcode.
SPPDNA	Micro positive for sperm. Submitted-results pending	Spermatozoa were detected on this item/sample by microscopy. This item/sample was submitted for DNA testing. Results are pending.
SRMI	Sample required manual intervention prior to extraction	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the extraction process.
SRP	Submitted-results pending	This item/sample was submitted for DNA testing. Results are pending.

Mnemonic	EXH line	Expanded Comment
SRPP	Similar result to previous DNA profile	This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. This DNA profile has been assessed and is considered to provide similar information to the DNA profile obtained from the sample barcode sent with this exhibit report and therefore has not been statistically evaluated at this time. Please contact the laboratory if you require a more detailed interpretation of this DNA profile.
SUFP	This sample has undergone further processing	This item/sample has undergone further processing and an improved DNA profile has been obtained.
TRQ	Testing restarted on advice from QPS	QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.
UNSS	Sample unsuitable for analysis	This item/sample is unsuitable for DNA testing due to, but not limited to: excess dirt, or the presence of mould.
NSIP	No statistical interpretation performed	In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.
3MXRUN	3 Person Mix Rem DNA contrib unsuitable for NCIDD	The mixed DNA profile result for this sample indicates three contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The remaining contribution separated after conditioning the mixed DNA profile was unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
EVDEXC	Single evidence sample excluded	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.
SCINMX	Suspect check inconclusive - mixed DNA profile	interpretation relates only to the associated barcode sent with this exhibit report, comparison
MXREMI	Remaining contribution - inconclusive	This item/sample provided a DNA profile that indicated the presence of two or three contributors. When conditioning on the assumed known contributor, the statistical interpretation in relation to the associated barcode is inconclusive.
SUFWC	Sample undergone further work - conditioned	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.
SCSNC	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
SCLNSC	Suspect check - low support or non contrib	One or more of the contributors to this DNA profile has limited information associated with it. All of the profiles from nominated reference barcodes have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of the donors are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.
SCM	Suspect check - match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the DNA components of this full or partial DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.
SCMAJM	Suspect check - major profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial major DNA profile separated from this mixed DNA profile.This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.
SCMINM	Suspect check - minor profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial minor DNA profile separated from this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.
SCCE	Suspect check - cannot exclude	The DNA profile obtained from the nominated reference barcode sent with this exhibit report cannot be excluded as a possible contributor of DNA to this mixed DNA profile. A reference evidence sample should be provided if this information is required in a statement for court. A statistical analysis may not be possible for this interpretation.
IMAJUN	Mixed profile-no major/minor. INTEL Major loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel Major DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.

Mnemonic	EXH line	Expanded Comment
IMINUN	Mixed profile-no major/minor. INTEL Minor loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel minor DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.
IMCOU	INTEL- mix DNA profile conditioned on unknown DNA profile	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. For intelligence purposes only, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix profile remaining after cond on unknown- NCIDD”
IMROU	INTEL - mix profile remaining after cond on unknown- NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. When conditioning on the assumed known contributor for intelligence purposes only, a remaining DNA profile was obtained. This Intel remaining DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only. If the assumption for conditioning no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix DNA profile conditioned on unknown DNA profile”.

JH-3

HealthSupport
Queensland
Forensic and Scientific Services

Procedure for the Release of Results

1 Purpose

To describe the correct format for statements or reports issued from Forensic DNA Analysis.

To document the procedures for issuing reports within Forensic DNA Analysis.

To document workflows leading to the releasing of information via Exhibit Reports to the Queensland Police Service.

2 Scope

This standard operating procedure relates to all statements or reports issued by case analysts to clients.

3 Definitions

DRMU – DNA Results Management Unit (QPS)
EB – Extraction Batch
EXH – Exhibit Report
FSS – Forensic and Scientific Services
GSI – Generic System Interface (interface between AUSLAB and QPS Forensic Register)
LR – Likelihood Ratio
P+ - Profiler® Plus DNA amplification kit
PP21 - PowerPlex® 21 DNA amplification kit
QIS – Quality Information System version 2
QPS – Queensland Police Service
SMU – Sample Management Unit (QPS)
SSLU – Scientific Services Liaison Unit (FSS)
STRmix™ - Software used to assist profile interpretation and Likelihood Ratio generation

4 Actions

4.1 Presumptive Exhibit Reports

The formats of the accepted EXH comments are located in QIS 23008.

A Presumptive EXH should include the following information:

4.1.1 Overall Status

This should reflect the result. This only applies to EXRs, and does not apply to EXHs.

Negative (Forensic Value) – Used for items that are examined but not submitted for testing.
Negative (Not examined) – Used for items that are received but not examined
Not Received at FSS – Used for items that are not received at FSS
Positive (Forensic Value) – Any sample submitted for DNA testing will have this status result.

Not Current

Not Current

4.1.2 Lab Number:

The results are reported under the individual sub-sample. Refer to Appendix 8 for specific guidelines.

4.1.3 Result Status

All result options are available using the F1 lookup function. The results status should reflect any presumptive & confirmatory tests that were conducted and include whether the sample was submitted for DNA testing.

Example 1: If a TMB test was performed that was negative and the swab was submitted as cells but also had a hair attached which was observed under microscopy as not suitable for DNA testing the following lines would be entered:

234967280 Presumptive blood test neg. Submitted as cells.
234967280 Hair located. Not suitable for analysis

Example 2: If different testing was performed on two sub-samples with a positive TMB test recorded for the first which was submitted and both an AP pos and the presence of spermatozoa detected by microscopic examination on the second the following lines would be entered:

234967280 Presumptive blood test pos, submitted – results pending
234967281 Presump sem fluid test pos, submitted – results pending.
234967281 Micro positive for sperm. Submitted – results pending.

NB. Linked No and Warm Link name are not required for presumptive EXHs

4.2 Final Exhibit Reports

The formats of the accepted EXH comments are located in QIS 23008.

4.2.1 Quality Checking:

Final EXHs can only be interpreted and released after the GMID-x batch has been read and Quality Flag checked (and Extraction Batch (EB) checked where appropriate) – refer Appendices 12-13. When flags are raised, Quality Flag checking is usually performed by a Senior Scientist, EB checking is usually performed by a case manager. When flags are not raised, batches can be completed by plate readers or management team members.

For urgent batches (ie. containing urgent (P1) samples), emails are sent by the plate reader or management team members when batches are complete to all case managers alerting them that P1 samples are ready for interpretation.

Incorrect Results

If at statement or Likelihood Ratio calculation stage (ie. when comparing to scene profiles to Evidence Sample profiles) the profile interpretation is not deemed to be consistent with the most current approaches, this reassessment may mean ‘incorrect’ EXH lines will need to be sent to QPS. Refer to QIS 17117. At any stage when an ‘incorrect’ is reviewed in

AUSLAB, an email must accompany the EXH line. The generic QPS email address of [redacted] should be used. See Appendix 5.

If the result change is such that a formerly reported link or LR is reassessed to an interpretation without links or LRs, or a less discriminatory LR, this should be verified by a Team Leader and personally communicated to QPS Senior Sergeant DRMU. Details should be recorded in AUSLAB and advice should be sought on steps forward eg. correction of links, retraction of statement request.

A Final EXH should include the following information (refer to Appendix 4-5):

4.2.2 Lab Number:

The sub-sample no. of the results being reported. This should include the results for all sub-samples that have been entered into the EXH as presumptive EXHs lines. Any further different results should also be added to the EXH. If there are no sub-samples, the EXH of the Item should be entered.

4.2.3 Result/Status:

A description of the result (eg 9 loci, partial, no DNA profile). All result options are available using the F1 lookup function. There may be more than one EXH line which is suitable however the EXH must fully describe the result. For example if there is a major and minor profile an EXH line must be entered for both the major and minor profiles.

Example 1:

234967280	Mixed DNA Profile. Major component uploaded to NCIDD	UKM1
234967280	Mixed profile, minor component insuff for NCIDD matching	UKM2

4.2.4 Linked Number Field:

<u>If the Crime Scene profile matches an Evidence Sample profile</u>: The barcode no. of the evidence sample is added to the Linked No. field.

<u>If the Crime Scene profile does not match an Evidence Sample profile</u>: If there are no matches to evidence sample profiles, then the profile will be 'unknown'. The designations of 'UK' should be used for unknowns with 'F' (female) or 'M' (male) used to provide further information and 'UKP' should be used if the sex of the DNA profile is unable to be determined. '1' should be used to denote the first male, female or person profile obtained.

Example 1: Three different male profiles would each be reported on a different line with UKM1, UKM2 & UKM3 used to distinguish between the contributors.

Example 2: A single (1) unknown male would be reported as UKM1.

NB: If an unknown profile is reported to QPS and an evidence sample is subsequently received that matches the unknown profile, any further unknown profiles continue sequentially eg. If UKM1 matches John SMITH, then the next unknown male in the case is designated UKM2 (it does not replace the UKM1).

Not Current

4.2.5 Warm Link Name:

The name of the evidence sample the profile matches to is entered into this field. This column is not visible to QPS and is useful at case management to determine who has been compared to the crime scene profiles.

4.3 Suspect Checks:

Suspect checks are useful when a profile is insufficient for NCIDD upload and a permanent barcode/profile exists for a suspect. They are also useful with PowerPlex® 21 mixed DNA profiles where profiles may not be deconvoluted for NCIDD but are suitable for comparison to reference samples and LR calculation.

Suspect checks are usually nominated by the QPS through SSLU. This information may be found in the UR notes (this must always contain the barcode).

It is not a necessity that names are entered in the Warm Link field of the EXH for suspect checks.

For PowerPlex® 21 DNA profiles, these are reported in the EXH using an appropriate EXH line (see QIS 23008). This includes the appropriate Likelihood Ratio EXH lines.

For Profiler® Plus DNA profiles, these are only reported in a final EXH if they do not match. For profiles sufficient for NCIDD, the matches are reported via LKRs (QIS 23890 Uploading and Actioning Samples on NCIDD and QIS 22619 Creating and Reviewing Links). For Intelligence Report templates, see QIS 24015 Procedure for Intelligence Reports and Interstate/Interpol Requests.

If there is a suspect check match and the DNA profile is less than the stringency for searching on NCIDD, an Intelligence Report should be issued to QPS DRMU.

For Profiler® Plus interpretations, if the DNA profile is ‘complex’ or ‘no major/minor’ and the suspect check is performed resulting in a ‘cannot exclude’ interpretation, an Intelligence Report should be issued to QPS.

Intelligence samples may be received by Forensic DNA Analysis associated to particular cases. These samples need to be compared to the case. If the crime scene profile is on NCIDD and the Intel sample is ‘Unlimited Purpose’, a match will be reported to QPS DRMU as a cold link. If the Intel sample is ‘Limited Purpose’, the match needs to be reported in an Intelligence Report (Profiler® Plus) or via EXH (PowerPlex® 21). If the Intel sample does not match a crime scene profile, the non-match does not need to be reported in an EXH (Profiler® Plus) but can be reported via EXH for PowerPlex® 21. If the crime scene profile is Single Source and matches someone other than the profile for the Intel sample, then an EXH line is not required.

If an Intelligence sample/suspect check was profiled with Profiler® Plus and the crime scene profiles are all PowerPlex® 21, if the case is high profile, it is preferable to rework the sample to enable a full comparison of the profiles to be reported. Before the rework is ordered, it is important to intuitively assess the crime scene profile to determine if the reference profile is excluded. If clearly excluded, there is no benefit in reworking the sample with PowerPlex® 21. Refer to QIS 17117 for details on billing and reworking.

Not Current

4.4 Interstate/International Requests – Refer to QIS 24015

4.5 Urgent (Priority 1) Requests

4.5.1 Routine Urgent Requests:

The requests for urgent processing will come via Inspector of DNA Results Management Unit (or higher), and are forwarded to the Managing Scientist and Team Leaders. A phonecall may accompany these requests. Details regarding the urgent request (eg. Number of samples, estimated arrival time, status of reference samples) should be forwarded to all Forensic DNA Analysis Management Team staff and Property Point supervisor where appropriate. The case will be allocated by the Reporting Supervising Scientists and all Management staff informed.

Urgent requests are for a 5-day turnaround time (TAT); however, Forensic DNA Analysis will attempt to release results within a 3-day TAT (ie. by 4pm on the third day of processing); however, this is dependant on the types of samples and examinations required, the time of receipt and the availability of other information eg. Item ownership information. The interval is until the time the initial result is reported. If the sample requires a rework, an appropriate EXH line can be used to explain the preliminary result. These reworked samples should be reported as soon as they become available.

If the urgent items are not in the possession of Forensic DNA Analysis, then Property Point staff must be alerted to the likely time of arrival and should communicate with Forensic DNA Analysis staff when the exhibits arrive.

If a reference sample is received for the case, these should have the DNA priority elevated to enable a profile to be obtained before, or soon after the crime scene profile.

NB. Priority '1' is used in AUSLAB for client requested and internally-raised urgent processing. If internally-raised, approval from Supervising Scientist/Team Leader is required.

Not Current

4.5.2 Urgent Result Communication on Fridays (only).

Regarding Priority 1 urgent samples as requested by QPS, if results are likely to be available on Fridays, email DRMU ([redacted] in the morning with the relevant barcodes and expected time of release. Aim to release prior to the 3pm GSI transfer and call DRMU if the results are likely to be released later than 3pm.

When results are reviewed, email DRMU that results have been released and if in the 3pm transfer, alert them whether there are actionable results, or not. Suggested wording is *'the electronic transfer includes actionable results'* or *'the electronic transfer includes non-actionable results'* depending on whether there are results for comparison or not.

4.5.3 Streamlining to Reporting Urgent samples

A streamlining strategy may be employed in consultation with a line manager. It is useful when a large number of urgent samples are being processed at the same time.

If we receive a number of urgent samples for a case, and the results are all indicative of the same unknown profile, select the most suitable and probative profile for interpretation and loading to NCIDD, and any matches will be reported on this sample within the urgent timeframe. Liaise with the QPS to determine if these remaining results can be downgraded to High Priority status. This will enable the reporting scientists to allocate their time to interpreting and reporting other urgent samples. The allocated scientist will ensure the results for all downgraded samples are reported in a timely manner.

A reference sample from the complainant, for example from a sexual assault, as well as ownership of the item is critical for the interpretation of any DNA results obtained. Without these, interpretation of the resulting DNA profiles is limited and may not provide information that can be loaded to NCIDD. If urgent samples are all indicative of the same unknown profile/s, and the reference sample of the complainant has not been received or is still undergoing processing, only the most suitable DNA profile will be chosen for interpretation in order to obtain a DNA profile loadable to NCIDD. This will enable critical information to be sent back to the QPS for the urgent case, and the reporting scientist to allocate their time to interpreting and reporting other urgent P1 samples. The result interpreted in the absence of the reference sample or ownership information will be re-interpreted and reported along with the remaining results once the reference sample is completed.

These strategies will only be implemented on a case by case basis AFTER communication with Inspector DNA Results Management Unit, or S/Sgt DNA Results Management Unit.

4.6 Statements and Certificates

4.6.1 AUSLAB Template

For the layout of a Statement of Witness, refer to Appendix 1.

There is a footer on each page that includes the NATA endorsement, the page number and total number of pages, the case reference number, date, name and signature of Reporting Scientist authorising the statement.

Allows the inclusion of a version of the statement Appendix that lists test methodologies (refer to Appendix 2).

Includes a Justice's Declaration Act (refer to Appendix 3) at the end of the Appendix.

The AUSLAB template is the same as the offline templates available in QIS (refer to QIS 29010).

The AUSLAB template pulls in the case details, including the reference and crime scene sample receipt details, Reporting Scientist details, Defendant and Complainant, Appendix and Justice's Act.

The person who presses F6 on the statement page in AUSLAB will have their details pulled into the statement.

Not Current

NB. Prior to statement release, ensure that all EXHs have ‘Rev-Ack’ in the Peer Review column of the relevant EXH with the exception of ‘low support’ or ‘non-contribution’ EXH lines. If an ‘incorrect’ EXH line was sent to QPS, ensure the status is ‘INR-Ack’ before statement release.

4.6.2 Statement Requirements (AUSLAB Test Code: FBSOW):

Statements will contain the following information (see Appendix 1):

- Declaration & Details of the Reporting Scientist (eg. Name, State)

- Place of Employment and position (eg. Scientist within Forensic DNA Analysis)

- Qualifications held by the Reporting Scientist (eg. B.Sc.)

- ANZFSS Code of Ethics (if applicable)

- Peer review and Date of issue stamp on top left corner. It is ideal to have these dates to be the same, and the same as the dates on the bottom of each page and on the Justice’s Act thus demonstrating the peer review was conducted prior to statement issue. Having a later Date of Issue is acceptable, but not preferable.

- Offence details including Defendant and Complainant details. If there is a deceased involved, the complainant is Regina.

- Details relating to the receipt of items & reference samples including the date of receipt, and the delivery officer (including Australia Post). A list of the barcoded items received.

- Summaries/ Preambles are added by the Reporting Scientist and may include some, all or slight variations of the following depending on case and profile types (see Appendices 9-11):

- The Role of a Forensic Biologist
- Examinations (if performed by another analyst)
- DNA Profiling
- Mixed DNA Profiles
- Blood Stains
- Seminal Stains
- Saliva
- Semen Staining on Items
- Persistence of Semen in the Vagina
- Statistics

- A summary of test results of the Reference Samples, and the type of sample (eg. Blood, Mouth/Buccal, Hair)

- Description and results of each of the Items:

- If Items were examined by QPS, or by QPS and QHFSS, it should be made clear which category the Items fit into.
- Description of the Item including barcode information e.g. 123456789. Receipt sub-numbering e.g. 987654321-002 is optional.
- Condition of the Item (if examined by QHFSS)

Not Current

- Area of staining (if examined by QHFSS)
- Areas submitted for testing (if examined by QHFSS)
- Results obtained eg. Results of comparison to reference DNA profiles and statistical interpretations where appropriate.
- Where relevant, opinions, explanations for opinions and interpretations or summary. A statement of uncertainty where relevant. Reference to other information which may be relevant to the validity or application of the results, e.g. in support of an opinion, explanation or statement of uncertainty.

Note: If a summary of results is required, it should be included at the beginning of the result section of the statement.

Note: It is recommended that the Items are grouped per Receipt. Within each receipt, the similar results are recommended to be grouped together, and then group items examined at QHFSS and QPS, and then to group like results.

- All items received but not tested are listed (listed under each receipt).

- Appendix including information about:

- Accreditation
- Chain of Custody
- DNA Profiling
- Interpreting DNA Profiles
- Use of statistics

- Justices Act 1886 – Signature of Reporting Scientist required. The Justices Act must not be on a page by itself. The number of pages to be written within the Justice's Act should be the same as the number of pages for the whole statement.

Not Current

4.6.3 Subsequent/ Alternative Statements:

4.6.3.1 Further Versions (AUSLAB Test Code: FBSOW):

AUSLAB has the ability for further versions of statements to be produced under the same testcode. This is useful for replacing statements.

4.6.3.2 Addendum Statement (AUSLAB Test Code: FBADDE):

If a subsequent statement is issued (this may be due to additional exhibits being delivered or an additional request for further interpretation), it must be clearly marked as an addendum to the original statement. This test code is also used for pre-AUSLAB cases and other cases that feature manual receipts.

APPVER testcode should be ordered at the same time as FBADDE to enable the Appendix field to be edited and the FBADDE to be used as a standalone statement (on its own barcode). If on a standalone barcode, an FBSOW needs to be ordered as well to enable the original completed date to populate. The date in this FBSOW needs to be in the same format as the way the date is typed into the FBADDE eg. DDMMYY or DD/MM/YYYY.

4.6.3.3 Amended Statement (AUSLAB Test Code: FBAMEN):

If, after the issue of a statement, an error is detected, the original statement shall be withdrawn and, where necessary replaced by one which is clearly indicated as being a replacement statement. This testcode is rarely used since AUSLAB is able to create new versions (see ‘a.’ above).

4.6.3.4 Intelligence Reports (AUSLAB Test Code: FBINTL) (refer to QIS 24015):

If there is information that cannot be included in a statement for evidentiary reasons, an Intelligence Report may be produced. This report type should be approved by a Senior Scientist (or higher), and the Senior Scientist of the Intelligence Team should be notified if work is to involve NCIDD. These reports must go through the same peer review process as required for all results released from the laboratory. The report is written within AUSLAB where the addressee and reviewer’s details can be entered.

Intelligence Reports regarding general casework should be directed to the Senior Sergeant DRMU.

Intelligence Reports written regarding Quality issues, should be directed to the Inspector QPS DNA Results Unit (QPS). These are generally written by the Senior Scientist of Quality and Projects, and reviewed by a Team Leader.

Matches on NCIDD that are below our standard match reporting stringency can be reported to DRMU via Intelligence Reports.

The signed report can be included in the case file, except where it relates to linking information from NCIDD. In these situations, the signed report should be held in the Intelligence Team area.

A scanned PDF of the signed intelligence report should be sent via MS Outlook to DRMU ([redacted] An unsigned PDF (created after validation and saved from AUSLAB when viewed (Shift Insert)) should be sent with the signed copy to DRMU. Upon issuing, the FBIOLR page must be completed. Alternatively, these two PDF files can be sent via email to [redacted] which is managed by SSLU who then send the files on to QPS. SSLU will then complete the FBIOLR page in AUSLAB.

The generic template to be used for offline Intelligence Reports is available in QIS 29011. The FBAR to record the review of the Intelligence Report can be ordered on the same barcode as the FBINTL, as can the FBIOLR testcode to record the release details.

Not Current

4.7 DNA Evidentiary Certificates: AUSLAB Test Code: FBEVC)

4.7.1 Certificate Details:

Refer to Section 95A Evidence Act 1977.

This is a certificate (in an approved form – see Appendix 15) that must be signed by an authorised DNA Analyst.

Current staff who hold appointments (in accordance with Section 133A of the Evidence Act

1977) as DNA Analysts are held with the Managing Scientist. Refer to QIS 25608 for details on the process to undertake to gain approval for a Reporting Scientist to become a DNA Analyst and the process for publishing in the Government Gazette.

It states that any of the following is evidence of the matter:
- Receipt and testing of the item/s
- Stated DNA Profile (specific barcodes should be requested by QPS)
- That the DNA Analyst examined the records relating to the receipt, storage and testing of the item/s in relation to the matter including any test process that was carried out by someone other than the analyst
- Confirms that the records indicate that all quality assurance procedures for receipt, storage and testing for the item/s that were in place in the laboratory at the time of the test were complied with.

If an Evidentiary Certificate is requested, a workflow has been devised to assist the checking involved in order to sign the certificate (see Appendix 14).

A checklist should be used to record the information examined by the DNA Analyst (refer to QIS 30799). There are instructions to complete this checklist recorded in a worksheet tab within the actual checklist file.

If the information gathered to be checked prior to issuing the Evidentiary Certificate is to be considered part of the casefile, then an FBAR page needs to be requested in AUSLAB and the pages should be numbered and the case identifier added.

NB. Appendix v4 cannot be used with FBEVC testcode.

4.8 Civil Casework Processing and Reports

Refer to QIS 10629 for general procedure.

On rare occasions, the laboratory may receive requests for civil work to be conducted. This may be in the situation of a case where a criminal component has been finalised and a civil component is ongoing, or if a profile generated in the laboratory is requested to be compared to DNA profiles generated from other laboratories in, for example, cases of disputed parentage.

Acting upon these requests is at the discretion of the Managing Scientist.

Upon receipt of the request, either the Managing Scientist or Team Leader will confirm arrangements for the work with the requesting party. In confirming this, a written request from the requesting party should be received and timeframes should be negotiated. A cost will be involved and the requesting party should be informed of this.

4.8.1 Negotiation of timeframe

The timeframes should be consistent with the timeframes for criminal work. If the matter had a criminal element that meant the processing was complete at the time of the request, then this should be factored into the negotiated timeframe.

Not Current

4.8.2 Approval process

The Managing Scientist or Team Leader are to complete the form: 20401 Quotation. This may involve clarification from the requesting party for ABN and other official terms and contact points.

Depending on what testing is required, the fee for service will vary. For further advice on costing, HSQ Finance may be consulted.

This Quote is approved by Executive Director FSS or higher.

When an approved Quote is received, this should be emailed to the requesting party before any work commences. Acceptance of the Quote should be saved on the network and all details scanned into AUSLAB.

4.8.3 Report Format

Civil Court reports do not have the same format as Statements of Witness issued for criminal work. Civil work uses the Uniform Civil Procedure Rules 1999 and the format should meet the requirements of these rules.

Some differences to criminal reports include:
- Forensic DNA Analysis is not currently NATA accredited for civil paternity work; therefore, the NATA logo should be removed.
    - A template in AUSLAB does not exist without the NATA logo; therefore, refer to 29008 and ensure all NATA references are removed.
- The Justices Act 1886 should be removed
- Details of testing processes can be detailed in the report by combining the preamble and Appendices used in Criminal matters. Refer to Appendix 19 for an example – NATA references should be removed if the matter is a civil paternity.
- Include the Uniform Civil Procedure Rules 1999 – Sect 428. See Appendix 20.

Not Current

4.8.4 Issue and invoice

When the work is complete, the report should be issued as per Section 4.15.1 below. At this time, the requesting party should be emailed to inform them that the work is complete and that an invoice will be issued.

The Managing Scientist or Team Leader should email [redacted] to ask them to organise issuing the invoice to the requesting party. It is advisable to include the approved quote in this email.

4.9 Other Reports – Crime and Corruption Commission (CCC) or Ethical Standards unit of the QPS.

Due to the confidential nature of these cases, results may not be entered into AUSLAB in either EXH or Statement format (as this information is accessible by QPS and other FSS staff). Barcodes will need to be registered to facilitate analytical processing; a case identifier or SSF may be requested in AUSLAB to facilitate this processing. If a QP number exists, the continued use of the QP number should be checked with the requesting QPS party as it may have security control measures implemented in the QPS system.

Not Current

This report type shall be approved by the Managing Scientist or Team Leader prior to drafting the report, but will generally be Intelligence Reports sent directly to the Inspector of the QPS DNA Management Unit. In rare situations, the requesting party may bypass the Inspector QPS DNA Management Unit and in such cases, may request direct results via Intelligence Report or email.

Clarification from the requesting party will need to be sought if any results are ok to send via the GSI to QPS, or if by other means (above).

Information on authority to upload to NCIDD, and whether Reference Samples will be received should also be sought - QPS will most often make an assessment on this if DNA results are obtained.

This report shall be addressed directly to the Inspector QPS DNA Management Unit, or nominated person and begin with (or equivalent):

> " RE : SSFXXXXX (Complainant Jane Smith)
>
> I am writing to summarise the results of examination conducted in the Forensic DNA Analysis laboratory at Forensic and Scientific Services in relation to the above alleged XXXXXXX incident/s."

This report may include the following statement elements to assist in the understanding of the results:

- Receipt details of reference samples and exhibits
- Preamble (Role of a Forensic Scientist, DNA Profiling and appropriate blood or semen preambles)
- List of Reference Samples (and results)
- Results of testing for exhibits submitted
- Items not examined

The report should end with "This information has been peer-reviewed in accordance with standard laboratory Quality Assurance protocols".

This report must go through the same peer review process as required for all results released from the laboratory. This report shall **NOT** be scanned into AUSLAB. **All results are to be included in the case file only.**

4.10 Statements with coronial samples.

Refer to QIS 17117.

To ensure samples delivered by the Coronial Support Unit (CSU) are pulled through correctly into Statements, the receipted items require an FTAR testcode to be requested (and the delivery officer etc to be recorded), and the Specimen type to be changed to FTAE. If it has correct CRISP association in the registration in AUSLAB, the receipt details should then pull into the Statement of Witness.

4.11 External Testing (Example Low Copy No. or Mitochondrial DNA) in statements

If the results of tests not performed in the laboratory are included in reports, the source of these results shall be clearly and unambiguously identified in the report/statement. This would be a rare event.

If external testing is discussed with the QPS Investigating Officers, these discussions need to be disclosed to the Inspector (or delegate) of QPS DNA Results Management Unit, or the S/Sgt of the QPS Quality Management Unit. Authorisation for external testing must be given and arranged by QPS.

4.12 Offline Statements

If a Statement of Witness needs to be written outside of AUSLAB (eg. when AUSLAB is down, or the testcode is corrupted), the templates are available in QIS. Templates exist for Statements of Witness and Intelligence Reports - see the following documents:

29010 – Statement of Witness template – stamp
29008 – Statement of Witness template – address – no NATA endorsement
29009 – Statement of Witness template – blank – no NATA endorsement
29024 – Use of offline Forensic Reporting templates
29011 – Generic report template

This type of statement may be written in cases where someone other than the Reporting Scientist is requested to write a Statement of Witness. This may be, for example, by the examining scientist, or an analytical scientist. These statements should use the template without the stamp, as the stamp refers to the Reporting Scientist. These statements should be scanned into AUSLAB upon completion.

Alternatively, this particular person may create a barcode in AUSLAB under the same UR number, and request an FBSOW testcode. By pressing F6, their details will pull into the statement.

4.13 Statement/ Report Authorisation

In order to release results to the client in the laboratory (excluding EXHs), QIS 30689 needs to be completed. QIS 26993 describes the overall procedure for releasing results at FSS.

Qualified Forensic DNA Analysis Reporting Scientists are authorised to sign statements and reports given that all policy and procedure requirements have been satisfactorily fulfilled.

All Staff are authorised to sign and initial worksheets, reports etc according to their level of competence.

A staff list with signatures and initials of all staff (QIS 17088) is kept for reference. This is located in the Quality cupboard.

DNA Analysts can sign Evidentiary Certificates. To be authorised as a DNA Analyst, the Director-General of the Department of Health approves a Briefing Note authored by the

Not Current

Managing Scientist, cleared by the Senior Director (FSS) and verified by the Chief Executive (HSQ). The Director- General is permitted to appoint a public service officer as a DNA Analyst according to the requirements of Section 133A of the *Evidence Act 1977*, if satisfied that the officer has the necessary qualifications and acquired competencies. The minimum details considered by the Managing Scientist are relevant qualifications, relevant experience in the field, and competence in Reporting DNA casework. When authorised, the DNA Analyst appointment is published in the Qld Government Gazette. Refer to QIS 25608.

Another scientist with the same or greater level of competence can sign as Peer Reviewer. Relevant training modules apply to the elements of technical reviews.

4.14 Further Documentation Requests (eg. Audit Trails)

Not Current

A written request should be obtained from DPP or QPS detailing what is specifically requested, ideally with item barcodes listed. When information is received by QHFSS via QPS, or the Office of the DPP (ie. another government department), information can be provided directly to the requesting party. When written requests come directly to QHFSS from Defence Legal representatives, it must be referred on to a Senior Scientist or Team Leader and also forwarded on to LALU (Legal Unit) who will ask the Defence Legal team to subpoena the information. It is preferable to avoid this by asking the Defence Legal team to direct their requests through DPP or QPS.

When providing subpoenaed information, the request should come through FSS Correspondence email address: [redacted] who will track its progress to ensure the information is provided by the timeframe stipulated.

If an audit trail is requested and it is subsequently considered part of the casefile, an FBAR page should be requested in AUSLAB and the pages should be numbered and have the case identifier added. If it is not considered part of the casefile, there is no need for page numbering or identifying numbers to be added (refer QIS 17117. Having said this, it is recommended that this occurs as it is helpful if/when it is referred to in court proceedings.

If Standard Operating Procedures and internal reports are provided, it is recommended that these are marked to be used in the matter it was requested for only. A watermark is a suggested way to make this point clear.

The requested information can be saved on disc and password-protected. This can be performed on a computer with Adobe Professional. The Investigating Officer will need to be informed of the password to open the files.

It is recommended that the Reporting Scientist negotiate with the requesting party a suitable timeframe for the release of the information. This timeframe should be verified by a Senior Scientist or Team Leader.

4.15 Release of Reports

4.15.1 Statement of Witness and DNA Evidentiary Certificates

The signed document is copied and stamped as ‘copy’. The copied document is included in the casefile and page numbered. The original is scanned and emailed to SMU by SSLU for uploading directly to QPRIME, and is sent by SSLU or Forensic DNA Analysis Administration Team to the Investigating Officer (or delegate, which could include the DPP). Urgent documents could be faxed where appropriate.

There is only one 'original' statement/certificate that can be issued. This is the document mailed to the requesting party, usually the Investigating Officer. If a QPS or legal party member requests a 'second original', then the copy of the original that is retained in the casefile should be copied and sent to the requesting party. Details of any communications should be recorded in AUSLAB.

4.15.2 Intelligence Reports

The Intelligence Report is sent via MS Outlook to DRMU ([redacted] as a signed PDF file, and an unsigned PDF that is created by AUSLAB post-validation (see section 4.6.3.4)

4.15.3 Coronial and Disaster Victim Identification (DVI) Reports

The originals of these types of reports are hand-delivered to the Coronial Support Unit (QPS). A copy of the report is retained in the casefile (as per Statement of Witness above).

The format/template for DVI Preliminary Reports is in QIS 23955.

4.16 Court Monitoring

Every Reporting Scientist should have their testimony evaluated every 12 months where possible. The evaluation can be performed by another Reporting Scientist, a court official (DPP or Defence) or QPS Officer.

The first page of the Court Testimony Monitoring Evaluation Form (QIS 17047) should be filled out by the assessor. This paperwork should be given to the Reporting Scientist's Line Manager or Team Leader to identify any potential training gaps. The second page should then be filled out by the Line Manager and Reporting Scientist and any plans for further training to be documented. The details of the case number, date, type of court, assessor should be added to QIS in the PD module under the 'Other' tab. This should be sent to the Line Manager for verification. The original paperwork should be kept in the Reporting Scientist's training folder.

If court testimony is infrequent such that an evaluation has not been conducted in a 12 month period, the next court appearance should be assessed. Alternatively, a moot court could be held with the Reporting Scientist and two competent senior staff, ideally the Line Manager and Team Leader.

If there was an unusual court experience, or different questions to ones normally expected, a report of that court appearance should be provided orally at a Forensic Reporting and Intelligence Team meeting. This will allow debriefing from what are sometimes stressful events, the sharing 'real' court questions and current court trends, the refinement of answers through discussions, and the identification of possible areas of improvement for the work unit. It will also help with public speaking, an essential component of court testimony.

Not Current

Refer to FSS Court Testimony and Attendance Requirements (QIS 18034) for more information.

5 Records

All Statements of Witness issued must bear a stamp on the front page that lists the date of issue, the case analyst's signature and the signature of the analyst who performed the technical review of the statement. The stamp is automatically added to statements by AUSLAB.

A copy of the statement issued for any test/examination must be retained in the case file. After the statement has been reviewed, F6 to validate will change the statement to PDF format. The person pressing F6 to validate will have their details auto-populated by AUSLAB. This means the Reporting Scientist needs to perform this function. A time and date stamp will appear in the footer.

Further versions can be created of Statements of Witness, Intelligence Reports and Evidentiary Certificates and can be viewed in AUSLAB prior to printing - Press Shift –Insert on the validated statement page (to view PDF Report Table) and F8 to view HTML Report. The original (validated) statement can also be viewed by pressing F5 on this page, or scrolling to the version you wish to view.

If a mistake is made and another version needs to be created, insert an audit entry to explain that a new version was created to correct an error (or similar wording).

Not Current

6 Associated Documentation

10623 Laboratory report format and content
10629 FSS – Quotation and acceptance of work
16004 AUSLAB Users Manual – Forensic DNA Analysis
17088 Procedure for recording handwriting specimens in Forensic DNA Analysis
17047 Court Testimony Monitoring Evaluation Form
17117 Procedure for Case Management
17137 Procedure for STR fragment analysis using GeneMapper® ID-X software
17142 Examination of Items
18034 FSS Court Testimony and Attendance Requirements
20401 Quotation
22619 Creating and Reviewing Links
23008 Explanations of EXH Results
23602 Environmental Monitoring
23890 Uploading and Actioning Samples on NCIDD
23955 Disaster Victim Identification Preliminary DNA Reports
23968 Forensic DNA Analysis Communications Procedure
24015 Procedure for Intelligence Reports and Interstate/Interpol Requests
25608 Appointment and Cancellation of State Analysts
26993 Procedure for authorising staff to release results
29008 Statement of Witness template – address – no NATA endorsement
29009 Statement of Witness template – blank – no NATA endorsement
29010 Statement of Witness template – stamp
29011 Generic report template
29024 Use of offline Forensic Reporting templates
30799 DNA Evidentiary Certificate Checklist

31389 STR fragment analysis of PowerPlex® 21 profiles using GeneMapper® ID-X software
31523 Use of STRmix™ software

National Association of Testing Authorities (NATA). Forensic Science ISO/IEC 17025 Application Document, July 2015. Refer to NATA website: http://www.nata.com.au

Evidence Act 1977

Supreme Court of Queensland Act 1991: Uniform Civil Procedure Rules 1999.

7 References

Nil

Not Current

8 Amendment History

Version	Date	Author/s	Amendments
	24 Feb 1999	V Ientile	
QIS Edition			
1	8 Oct 2001	V Ientile	
2	23 Jan 2004	L Freney	Changes to references, update appendices
3	11 Mar 2004	V Ientile	No interim unchecked results to be issued
4	10 Aug 2006	M Gardam	Combined with 17158, amended the title and updated statement requirements, included intelligence reports, statement blurbs & Evidential Reports. Added Reference to Communication SOP, Added EXR reporting guidelines.
5	31 May 2007	M Gardam	Sub-numbering is optional when giving a description of the item.
6	April 2008	QIS Migration Project	Headers and Footers changed to new CaSS format. Amended Business references from QHSS to FSS, QHPSS to CaSS and QHPS to Pathology Queensland
7	August 2009	J Howes	Updated Forensic Biology to DNA Analysis, added EXH, added complete preambles, added Evidentiary Certificate workflow, Quality flag checking workflow, updated Statement of Witness and Appendices examples, DNA Analyst list removed, relative frequency paragraph removed from Intel letter example and updated with match probability, EXH table improvements and current lines added to examples.
8	June 2010	J Howes	Added EB checking workflow, added to Quality Flag workflow, moved Quality paragraphs to own Appendix, deleted Pathology and Scientific services logo
9	August 2010	J Howes	Changed FIRMU to DRMU, added some more information to paternity preamble
10	April 2011	J Howes	Changed Appendix 3 to include latest version of Justice's Act, changed HP4/HP5 to 'senior' in Evidentiary Certificate workflow, added some suspect check information.
11	05 April 2012	J Howes	Changed DNA Unit to Sample Mgt Unit, changed 'Evidential Reports' to 'Other Reports', added info to Statement and Intel Report field, changed the number/bullet/paragraph systems to be consistent, added new Appendix version (5), added new preambles, added new Statement of Witness template, add ability to create statement versions, added Offline

Not Current

			statement section, removed Appendices 4 and 5 (covered by 24005), added F6 validation to RECORDS, added Release of Reports section, removed Example 6 (multiple items) from Appendix 9, added Coronial/DVI report release section, add Environmental samples to QFLAG workflow, updated QFLAG and EB checking process, added template for Evidentiary Certificates, updated FBSOW for FBSTAT and workflow, added link to Evidentiary Certificate checklist, added Ethical Standards/CMC information, added Court Monitoring information, added information to Intel report section, added Urgent P1 result communication on Fridays, added FTAs associated to the case (under Suspect Check section).
12	29 Nov 2012	J Howes	Added new HSSA Header, removal of FBSHRT reference that was part of Section 3 and the workflow from Appendix, Linked No. field updated to include use of barcodes for unique profiles, FBEVC added, information on who receives Intel reports added, Intelligence Report section re-organised, added information to negotiate timeframe with requesting party re audit trails, Appendix 6 for statements added to Appendix 2 in this document, added APPVER to workflow for FBADDE and to Section 3, added Appendix 17, added Reference Sample section to Appendices 9-11 to be used where appropriate, Tho1 changed to TH01, Appendix 14 workflow changed to not include AUSLAB matches, added Profiler® Plus for 'cannot exclude' interpretation for suspect check,
13	07 July 2014	J Howes	Reformatted according to Procedures template, added information relating to PowerPlex® 21 and XPLEX, added information from Comments on previous version, re-formatted the Appendices, added 26993 to associated docs, workflow for QFLAGs with PowerPlex® 21, re-ordered Appendices, updated preambles, added Appendix 18 – suggested statement wording, changed HSSA to HSQ, added information to Urgent Processing, changed release of Intel reports to include by Outlook, replaced Appv5 for Appv7 in 9.2, added NATA details, changed Appendix 13 to reflect all carried out in the one spreadsheet, added XPLEX drop down for

Not Current

			Quality Flags to Appendix 13.
14	16 Feb 2016	J Howes	Added to new template and revised numbering, removed Appendix 12 (Quality Paragraphs), added new Appendix 1 screenshot, removed 26874 as associated document, amended rounding examples and added LR less than 10, added 25608 to associated docs and made reference in section 4.7, added macro location to Appendix 14, removed Digital Data Store reference in App 12 and added Environmental sample QFLAG matches details to same Appendix, added info to 4.2.2 regarding QFLAGs, added date of issue details to 4.6.2, added ® and ™ where applicable throughout, added 10629, 20401 and updated NATA details and Uniform Civil Procedure Rules to associated docs, added section 4.8, added Appendices 19 and 20, added information to 4.2.1 regarding incorrects and P1 QFLAG checking, added info to 4.3 regarding LRs for mixtures, added generic QPS DRMU email address, removed 4.2.2 (in previous version), changed wording in 4.2.5, added 'spitting' to App 9 and 10.

Not Current

9 Appendices

1 An example of the layout of the front page of a Statement of Witness

2 Procedural overview and test methodology (Statement Appendices 6 and 7).

3 Example of the Justice's Declaration Act.

4 Completing Exhibit Reports in AUSLAB

5 Review of Exhibit Reports in AUSLAB

6 Creating an Addendum Statement in AUSLAB

7 Creating a Statement with Receipt Details in AUSLAB

8 EXH Reporting (Sub-Sample No. Rules)

9 Complete Casework Preamble – Examinations by QHFSS

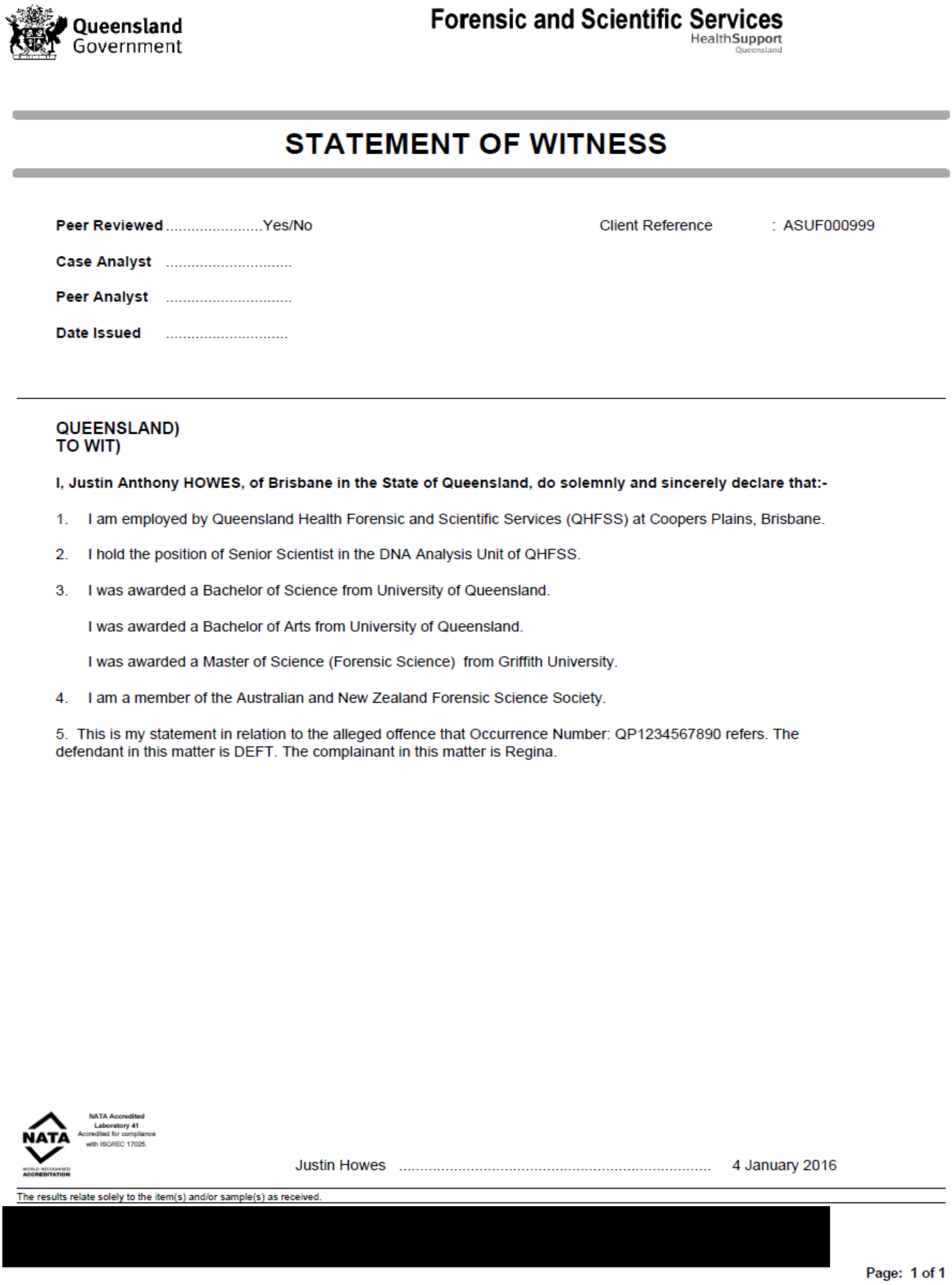
10 Complete Casework Preamble – Examinations by QPS and QHFSS

11 Complete Paternity Preamble

12 Quality Flag Checking Workflow

Not Current

9.1 An example of the layout of the front page of a Statement of Witness



Queensland Government

Forensic and Scientific Services
HealthSupport
Queensland

STATEMENT OF WITNESS

Peer Reviewed ....Yes/No
Client Reference : ASUF000999

Case Analyst ....

Peer Analyst ....

Date Issued ....

QUEENSLAND)
TO WIT)

I, Justin Anthony HOWES, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.
2. I hold the position of Senior Scientist in the DNA Analysis Unit of QHFSS.
3. I was awarded a Bachelor of Science from University of Queensland.

   I was awarded a Bachelor of Arts from University of Queensland.

   I was awarded a Master of Science (Forensic Science) from Griffith University.
4. I am a member of the Australian and New Zealand Forensic Science Society.

5. This is my statement in relation to the alleged offence that Occurrence Number: QP1234567890 refers. The defendant in this matter is DEFT. The complainant in this matter is Regina.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025.

Justin Howes .... 4 January 2016

The results relate solely to the item(s) and/or sample(s) as received.

[redacted]

Page: 1 of 1

9.2 Procedural overview and test methodology (Statement Appendices 6 and 7).

APPENDIX (version 6)

Procedural overview for DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Services Support Agency, for the purposes of conducting DNA analysis.

DNA Analysis operates under the premise that QPS are responsible for item prioritisation, sample selection, selection of screening/sampling methods, anti-contamination procedures and the application of Standard Operating Procedures (SOPs) on work undertaken on the items/samples prior to submission to FSS DNA Analysis. As such, Forensic Biologists may not be able to provide information or opinion on possible biological origin of DNA profiles that may be obtained from these samples.

Some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. This occurs at the discretion of the QPS. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

Chain of Custody

All DNA Analysis case files and exhibits are electronically tracked, monitored and securely stored to ensure that the appropriate chain of custody and continuity measures are maintained. The QPS case number and sample submission information is provided from the QPS via an electronic interface to FSS, and this information is cross-checked against labelling on exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. DNA Analysis forms part of a Health Services Support Agency campus site which has access controlled and monitored by a security team. Records of Visitors to DNA Analysis are retained.

Not Current

Accreditation

DNA Analysis first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998, and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessments (every 3 years) and surveillance visits (18 months).

NATA accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories that demonstrate compliance with the standard have shown that they can competently perform activities and testing within the scope of their accreditation.
The parameters assessed during accreditation include:

- Organisation and management
- Quality management system

- Personnel
- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 standard refer to Standards Australia.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:

http://www.nata.asn.au/publications

Not Current

Technical information relating to DNA profiling at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The testing system used at DNA Analysis looks at 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender of the donor (for details see Table 1). This technique involves the use of a method known as Polymerase Chain Reaction (PCR), used to amplify these specific regions of the DNA to produce numerous copies. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two peaks for each STR, one inherited from their mother and one inherited from their father, unless the same STR is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

<u>DNA profiles assumed to originate from one person (single source)</u>

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together with any other person who has the same reference DNA profile, can be considered as a potential contributor of the DNA.

The evidential significance of such a match is assessed by considering two competing propositions:

Proposition 1: the DNA originated from the person of interest;
Proposition 2: the DNA originated from someone other than and unrelated to the person of interest.

The resultant figure (termed the 'Likelihood Ratio') compares the two opposing propositions. The likelihood ratio describes how likely the DNA profile obtained from the biological material is to have occurred if proposition 1 were true (the DNA originated from the person of interest) rather than if proposition 2 were true (the DNA originated from someone other than and unrelated to the person of interest).

The likelihood ratio is calculated by taking into account the characteristics of the DNA profile and the frequency of occurrence of the individual DNA components that make up the DNA profile. Upon request, an internationally accepted verbal scale to describe the support for one proposition over another can be used to offer some non-numerical explanation for the likelihood ratio (see Table 2).

If less than the 21 regions of DNA are seen in a DNA profile (termed an 'incomplete or partial DNA profile') this will be reflected by a smaller likelihood ratio than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete the DNA profile, the greater the likelihood of obtaining the DNA profile if it came from someone other than, and unrelated to the person of interest.

Not Current

DNA profiles assumed to originate from more than one person (mixed DNA profiles)

In order to assess whether a person could or could not have contributed to a mixed DNA profile, a set of competing propositions (similar to a single source DNA profile) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

The likelihood ratio will not always favour proposition 1 (the DNA originated from the person of interest and an unknown person unrelated to the person of interest). The likelihood ratio could favour proposition 2 (the DNA originated from two unknown people unrelated to the person of interest).

In certain circumstances, if the ownership of an item is established or if the sample was collected from an intimate area, then it may be possible to make the reasonable assumption that the donor of the sample has contributed DNA to the resultant mixed DNA profile. In these cases, a mixed DNA profile can be 'conditioned' on the DNA profile of the known donor, such that the presence of the DNA components corresponding with the donor's reference DNA profile can be factored into the statistical interpretation. This may facilitate a more meaningful statistical analysis of potential second and/or third contributors to the DNA profile. In this situation, the likelihood ratio is based on the following propositions, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then the DNA profile will require additional statistical interpretation.

Datasets Used in Statistical Analyses

Three validated datasets consisting of DNA profiles obtained from individuals of the Australian Caucasian, Aboriginal and South-East Asian populations are used to calculate the likelihood ratio, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are $\theta=0.02$ for the Australian Caucasian dataset, $\theta=0.03$ for South East Asian dataset, and $\theta=0.05$ for the Australian Aboriginal dataset. Unless otherwise specified, the default dataset used in DNA Analysis is the Australian Caucasian dataset. The other datasets are available upon request.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated it allows for any difference the new dataset could make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a ‘ceiling figure’ for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of “150 000 billion times more likely”, would be reported as “more than, or at least 100 billion times more likely”. The actual calculated figure can be provided upon request.

The above listed values for the theta cannot account for close blood relatives. Closely related people, such as siblings, will have a greater chance of sharing similar components within their DNA profiles. However, due to the random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions would be very small. As this relationship becomes more distant, the probability of two relatives having the same DNA profile becomes smaller still. If it is thought that a close blood relative may have been involved, a more meaningful approach would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime stain DNA profile.

Not Current

Standard DNA (STR) profiling system at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

Table 1: PowerPlex® 21 multiplex system, list of loci:

Abbreviated Name	Scientific Name	Chromosomal Name
Amel	AMELOGENIN	Sex (X and Y)
D3	D3S1358	3
D1	D1S1656	1
D6	D6S1043	6
D13	D13S317	13
Penta E	Penta E	15
D16	D16S539	16
D18	D18S51	18
D2	D2S1338	2
CSF	CSF1PO	5
Penta D	Penta D	21
TH01	TH01	11
vWA	HUMVWAFA31/A	12
D21	D21S11	21
D7	D7S820	7
D5	D5S818	5
TPOX	TPOX	2
D8	D8S1179	8
D12	D12S391	12
D19	D19S433	19
FGA	HUMFIBRA	4

Table 2: Verbal scale to describe Likelihood Ratios
(adapted from Evett IW and Weir BS 1998 *Interpreting DNA Evidence*. Sinauer, Sunderland, MA)

RANGE OF VALUE	LEVEL OF SUPPORT
>1 million	Extremely Strong
100 000 – 1 million	Very Strong
10 000 – 100 000	Strong
1000 – 10 000	Moderately Strong
100 – 1000	Moderate
10 – 100	Low Level
1 – 10	Slight
1	Inconclusive

Not Current

APPENDIX (version 7)

Procedural overview for Forensic DNA Analysis, Forensic and Scientific Services (FSS), Health Support Queensland

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by staff within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Support Queensland, for the purposes of conducting DNA analysis.

Forensic DNA Analysis operates under the agreement that QPS are responsible for item prioritisation, sample selection, selection of screening/sampling methods, anti-contamination procedures and the application of Standard Operating Procedures (SOPs) on work undertaken on the items/samples prior to submission to the laboratory. As such, Forensic Biologists may not be able to provide information or opinion on possible biological origin of DNA profiles that may be obtained from these samples.

At the discretion of the QPS, some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

Chain of Custody

All Forensic DNA Analysis case files and exhibits are electronically tracked, monitored and securely stored to ensure that appropriate chain of custody and continuity measures are maintained. The QPS case number and sample submission information is provided from the QPS via an electronic interface to FSS, and this information is cross-checked against labelling on exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site which has access controlled and monitored by a security team. Records of visitors to Forensic DNA Analysis are retained.

Not Current

Accreditation

Forensic DNA Analysis first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998, and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessments (every 3 years) and surveillance visits (18 months).

NATA accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories that demonstrate compliance with the standard have shown that they can competently perform activities and testing within the scope of their accreditation.

The parameters assessed during accreditation include:

- Organisation and management

- Quality management system
- Personnel
- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 standard refer to Standards Australia.
For details of the current ISO/IEC Standard Application Document for accreditation of testing and calibration facilities and Forensic Science ISO/IEC 17025 Application Document, please refer to the NATA website:

http://www.nata.asn.au/publications

Technical information relating to DNA profiling at Forensic DNA Analysis, Forensic and Scientific Services (FSS), Health Support Queensland

Not Current

DNA Profiling

DNA is a complex chemical found in almost all cells of the human body. It carries genetic information which determines the physical and chemical characteristics of a person. Forensic DNA Analysis uses two main systems for the generation of DNA profiling results. In this case the PowerPlex® 21 system was used which examines 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender of the donor (for details see Table 1). The generation of a DNA profile involves a method known as the Polymerase Chain Reaction (PCR), which is used to produce numerous copies of these specific regions of the DNA. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two alleles or peaks for each STR, one inherited from their mother and one inherited from their father, unless the same allele is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

Forensic DNA Analysis uses the STRmix™ software to assist in the interpretation of DNA profiles and calculation of likelihood ratios for DNA profiles generated using the PowerPlex® 21 system. STRmix™ is an expert system developed and validated in Australia and New Zealand.

Not Current

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together with any other person who has the same reference DNA profile, can be considered as a potential contributor of the DNA.

The evidential significance of such a match is assessed by considering two competing propositions:

Proposition 1: the DNA originated from the person of interest;
Proposition 2: the DNA originated from someone other than and unrelated to the person of interest.

The resultant figure (termed the 'Likelihood Ratio') compares the two opposing propositions. The likelihood ratio describes how likely the DNA profile obtained from the biological material is to have occurred if proposition 1 were true (the DNA originated from the person of interest) rather than if proposition 2 were true (the DNA originated from someone other than and unrelated to the person of interest).

The likelihood ratio is calculated by taking into account the characteristics of the DNA profile and the frequency of occurrence of the individual DNA components that make up the DNA profile.

If less than the 21 regions of DNA are seen in a DNA profile the likelihood ratio will be smaller than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete a DNA profile is, the greater the likelihood of obtaining that DNA profile if it came from someone other than, and unrelated to the person of interest.

DNA profiles assumed to originate from more than one person (mixed DNA profiles)

In order to assess whether a person may or may not have contributed to a mixed DNA profile, a set of competing propositions (similar to the single source DNA profile example) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

The likelihood ratio will not always favour proposition 1 (the DNA originated from the person of interest and an unknown person unrelated to the person of interest). The likelihood ratio could favour proposition 2 (the DNA originated from two unknown people unrelated to the person of interest).

In certain circumstances, if the ownership of an item is established or if the sample was collected from an intimate area, then it may be possible to make the reasonable assumption that the donor of the sample has contributed DNA to the resultant mixed DNA profile. In these cases, a mixed DNA profile can be 'conditioned' on the DNA profile of the known donor, such that the presence of the DNA components corresponding with the donor's reference DNA profile can be factored into the statistical interpretation. This may facilitate a more meaningful statistical analysis of potential second and/or third contributors to the DNA profile. In this situation, the likelihood ratio is based on the following propositions, for example:

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When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then the DNA profile will require additional statistical interpretation.

Not Current

Datasets Used in Statistical Analyses

Three validated datasets consisting of DNA profiles obtained from individuals of the Australian Caucasian, Aboriginal and South-East Asian populations are used to calculate the likelihood ratio, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are $\theta=0.02$ for the Australian Caucasian dataset, $\theta=0.03$ for South East Asian dataset, and $\theta=0.05$ for the Australian Aboriginal dataset. In Forensic DNA Analysis likelihood ratios are calculated using all three datasets and the most conservative value is reported.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated, this allowance factors in any difference the new dataset might make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "greater than 100 billion times more likely". The actual calculated figure can be provided upon request.

The above listed values for theta cannot account for close blood relatives. Closely related people, such as siblings, will have a greater chance of sharing similar components within their DNA profiles. However, due to the random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions would be very small. As this relationship becomes more distant, the probability of two relatives having the same DNA profile becomes smaller still. If it is thought that a close blood relative may have been involved, the most meaningful approach to interpretation would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime-scene DNA profile.

Table 1: PowerPlex® 21 system, list of loci

Abbreviated Name	**Scientific Name**	**Chromosomal Name**
Amel	AMELOGENIN	Sex (X and Y)
D3	D3S1358	3
D1	D1S1656	1
D6	D6S1043	6
D13	D13S317	13
Penta E	Penta E	15
D16	D16S539	16
D18	D18S51	18
D2	D2S1338	2
CSF	CSF1PO	5
Penta D	Penta D	21
TH01	TH01	11
vWA	HUMVWAFA31/A	12
D21	D21S11	21
D7	D7S820	7
D5	D5S818	5
TPOX	TPOX	2
D8	D8S1179	8
D12	D12S391	12
D19	D19S433	19
FGA	HUMFIBRA	4

Not Current

9.3 Example of the Justice’s Declaration Act.

JUSTICES ACT 1886

I acknowledge by virtue of Section 110A (6C)(c) of the Justices Act 1886 that::-

(i) This written statement by me dated XXXX, and contained in the pages numbered 1 to _____ is true to the best of my knowledge and belief; and

(ii) I make it knowing that, I would be liable to prosecution for stating anything that I know is false.

____

Signature

Signed at BRISBANE on XXXX.

Not Current

9.4 Completing Exhibit Reports in AUSLAB

Completing Exhibit Reports

AUSLAB Test Code: EXH

Purpose: Exhibit Reports are a summary of results for each item received. The information stored in the exhibit reports is transferred to the QPS Forensic Register once the results have been checked and validated. Exhibit Reports can contain information about examinations performed, screening test results and DNA profile results. Interim results can be entered and sent to the QPS Forensic Register once they have been validated.

To enter Exhibit Report Results:

Main Menu

↓

Patient Enquiry or <F10>
Scan barcode from item in Lab Number field or enter Case No. in UR field e.g. QP12123456789 or access through work list (refer QIS 17117)

↓

If case # entered, select relevant item lab number and select <ENTER>.
<PgDn> to get to Exhibit Report page.

↓

<SF2> to edit page. <Tab> to Overall Status, <F1> for list of options. FBPOS if profile was obtained, FBNEG if no profile was obtained and FBNEG (Not examined) if the item was not examined (note: this only applies to EXRs).

↓

Add name to the Case Scientist field of each relevant 9Plex/XPLEX page

↓

<Tab> to the results table. If sub samples have been taken for DNA analysis, scan the barcode of the section submitted for DNA analysis. Leave empty if no sub samples have been generated. If the entire item was submitted for analysis (in-tube), scan the Item barcode.

↓

<Tab> to the Result/Status field. <F1> for list of options. Choose the most appropriate option. More than one line may be required.

↓

Not Current

If a full profile was obtained and it matched a reference sample taken for the case, enter the reference sample barcode in the Linked No field and enter the name for the sample in the Warm Link Name field.

↓

For Powerplex® 21 profiles: If a mixed DNA profile is obtained, and it cannot be conditioned, each deconvoluted contribution needs to be registered in AUSLAB under its own barcode (refer QIS 17117).

↓

If more than one profile was obtained from a single item or multiple items labelled with one exhibit barcode, enter a line for each profile in the exhibit report table. Enter reference sample barcodes or newly registered barcode (see above) in the Linked No. field for each line (or each profile obtained).

↓

For PowerPlex® 21 profiles and when a whole item is examined: If more than one profile was obtained from multiple items labelled with one exhibit barcode and the profiles are mixed and cannot be conditioned, register a new barcode in AUSLAB for each sub-sample with different results. Under the exhibit, add the EXH line 'Sample processed and Reported Under' EXH, with the new barcode in the Linked No. field. Under the newly registered sub-sample barcode, add the interpretation results. Communicate the new barcodes to DRMU so the information can be added to their system.

↓

<F4> to save entry. Do not validate, Results must be checked and validated by the reviewer. Once results are reviewed and validated, they are transferred to the QPS Forensic Register.

↓

"Pause/Break" key to return to Main Menu

NOTE:

- All mixed DNA profiles that can be separated into major/ minor contributions (for Profiler® Plus), should have the designations filled out under the MIXT testcode for 9Plex/ Profiler® Plus, and on the COMIX page for XPLEX/PowerPlex® 21.

- All mixed DNA profiles that can be ‘conditioned’ should have the designations filled out under the MIXC testcode for 9Plex/ Profiler® Plus, and on the COMIX page for XPLEX/PowerPlex® 21).
- If the interpretation is a conditioned mixture and for intelligence purposes only (eg. conditioned in the absence of a reference sample but using an unknown profile from the same case), this should be made clear in the comments section of the mixture pages.
- If the mixture is major/ minor but the major is mixed and used for POPSTATS purposes, an MIXT testcode should be used and the contributions added to this page. This only applies to 9Plex/ Profiler® Plus profiles.
- If the mixture is major/minor and the major is mixed, and a conditioned interpretation is applied to the major, it may be appropriate to use the MIXC testcode and to record the minor components to the specimen notes (and have these peer reviewed). The comments section can also be used to make it clear what actions have occurred. This should only be relevant for 9Plex/ Profiler® Plus profiles.

Not Current

9.5 Review of Exhibit Reports in AUSLAB

Purpose: An Exhibit report is created for each item as a way of transferring results back to the QPS Forensic Register. Each line of an exhibit report must be reviewed before it can be released and sent to the QPS Forensic Register.

To review an exhibit report:

Main Menu

↓

Patient Enquiry or <F10>
Scan barcode from item in Lab Number field or enter Case No. in UR field e.g. QP12123456789.

↓

If Case No. entered, select relevant item lab number and press <enter>. <PgDn> to find Exhibit Report page.

↓

Check the overall status is correct. Options are FBPOS (Positive forensic value), FBNEG (Negative forensic value) or FBNEG (not examined) (Note: this only applies to EXRs)

↓

Review each line in the results table. If correct, <tab> to corresponding line in the Peer Review Status.
Review each associated 9Plex/Plex21 and enter details in the review fields. Validate these 9Plex/Plex21 pages.

↓

<F2> to edit, enter “REV” or <F1> for options. This will transfer the information to the QPS Forensic Register.
Press <F6> to validate the page to enable ‘V’ to appear on the Shift-F9 screen.

↓

If information needs editing, make changes and get another analyst to review the changes. The reviewer’s login is recorded in the audit trail. For incorrect EXH results, ‘INR’ (Incorrect) can be added to the EXH line and must immediately be accompanied by the correct line and communication to DRMU (email from Senior if incorrect information, email from reviewing scientist if typo or due to the receipt of a reference sample and the method of interpretation changes).

↓

“Pause/Break” key to return to Main Menu

Not Current

9.6 Creating an Addendum Statement in AUSLAB

Purpose: The test code FBADDE creates a statement without the receipt details automatically entered. All statement test codes include the scientist's details, and appendix details. This format is used for cases where an additional statement is being written.

To create an addendum statement:

Main Menu

↓

Patient Enquiry or <F10>. Scan barcode from case file in Lab Number field or enter Case No. in UR field e.g. QP1298765432

↓

If Case No. entered, select lab number with CS screen attached and press <enter>. <Shift>, <F10> to get to registration screen. Select <End> and request FBADDE. <F7>,<F4>,<F4> to save. Testcode APPVER should be ordered at the same time to enable the Appendix field to be edited. FBSOW needs to be ordered on the same barcode to enable original completion date to populate.

↓

<PgDn> to get to Forensic Report page. <Shift>, <F2> to edit.

↓

In the results section, <F2> to go to Word. Select(N) for new version. A suggested font is Courier New (12) font. The statements within AUSLAB are best written using one space after full-stops, rather than two.

↓

Enter the case, receipt details of additional items then the results. Start with "This is an addendum statement and should be read in conjunction with my original statement dated …." or similar.

↓

Once results are complete, <Ctrl T> to save and return to AUSLAB. Enter "Reported Date", e.g. 221003. Enter the appendix version, <F1> will list the current appendix version. The page should be validated (and PDF version created) when the statement has been peer reviewed. The Reporting Scientist should press F6 to validate.

↓

If the FBADDE is a on a standalone barcode, in the ordered FBSOW, add the completed date in the same format as the FBADDE completed date (eg. DD/MM/YY or DDMMYY)

To view statement, <Shift> <Insert>. To print, <Ctrl> <F11> and direct to a printer.

NB. A new barcode should be requested in AUSLAB to record the review and release of the report (FBAR, FBTR and FBIOLR testcodes). The appropriate fields on the Case file Particulars form should be completed.

NB. When an Addendum statement is being written, the Case Status should be changed to REACTIVATED. The status should change to SENT TO PEER, RETURNED FROM PEER and REPORT ISSUED as it progresses through review.

“Pause/Break” key to return to Main Menu

Not Current

9.7 Creating a Statement with Receipt Details in AUSLAB

Purpose: The test code FBSOW creates a statement with the receipt details automatically entered.

To create a statement with receipt details:

Main Menu

↓

Patient Enquiry or <F10>
Scan barcode from case file in Lab Number field or enter Case No. in UR field e.g. QP12123456789 or access through work list.

↓

If Case No. entered, select lab number with CS screen attached and press <enter>. <Shift>, <F10> to get to registration screen. Select <End> and request FBSOW. <F7>,<F4>,<F4> to save. Add Reporting Scientist name to CS field (note: this does not affect the name that will be populated on the statement)

↓

<PgDn> to get to Forensic Statement/Report page. <Shift>, <F2> to edit.

↓

In the results section, <F2> to go to Word. Select(N) for new version. Enter the results. A suggested font is Courier New (12). The statements within AUSLAB are best written using one space after full-stops, rather than two.

↓

Once results are complete, <Ctrl T> to save and return to AUSLAB. Count page numbers and add pages to account for the Appendix (note: Appendix 5 has four pages, Appendix 6 has five pages). To view the statement, <Shift> <Insert> and check other formatting.

↓

Send for Peer Review

↓

Add relevant Appendix, add date, check page numbers.
Reporting Scientist to press F6 and validate (this adds details of this person to the statement, and saves a PDF copy to Auslab).
Statement to be signed by Reporting and Reviewing Scientists and tracked to Admin for issuing.

9.8 EXH Reporting (Sub-Sample No. Rules)

This appendix is for the process of reporting back results via EXHs, to the QPS DRMU for individual items. Note, the examples provided are relevant to Profiler® Plus interpretations and EXH lines. See 23008 Explanations of EXH Results for the complete list of EXHs relevant for Profiler® Plus and PowerPlex® 21 in conjunction with the use of STRmix™

- Since 1 July 2008, the bulk of the examinations have been performed by QPS. After their examinations, samples are received by Forensic DNA Analysis in-tubes. The barcode on the tubes relate to an EXH barcode and as such, the presumptive and final results are reported back on the single barcode.

- Different scenarios have been included in examples given in the following pages. These scenarios relate to reporting of non-in tube cases, and the table format is as per EXH pages (excluding the 'Peer Review' column). For more information, refer to QIS 17142.

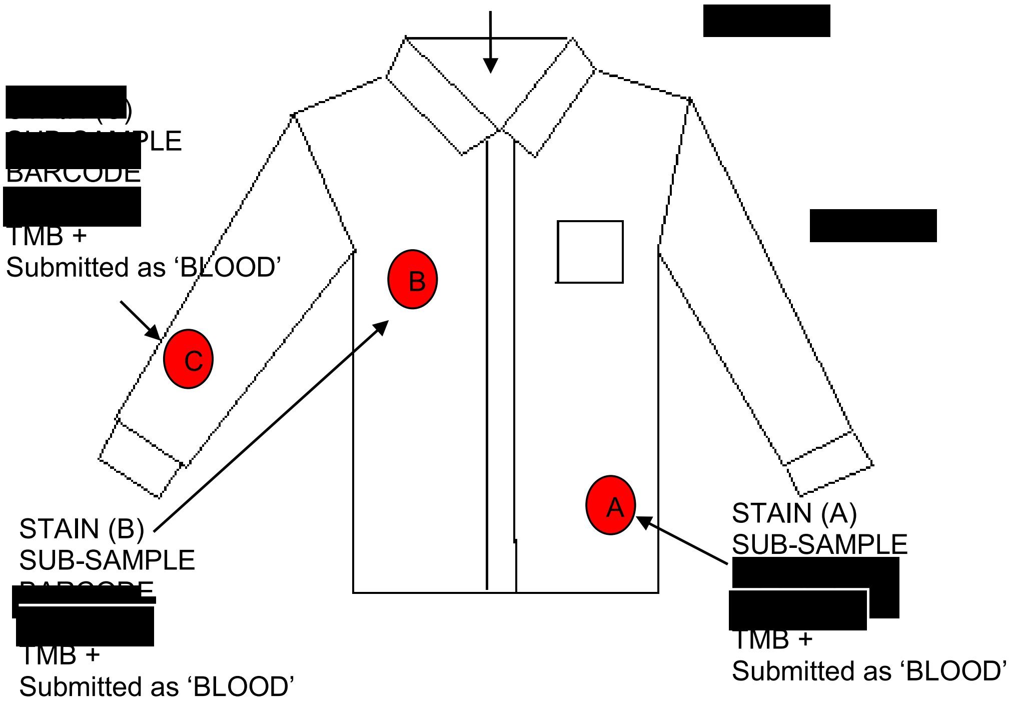
- Examples of different scenarios are depicted below. Some of these examples use Profiler® Plus interpretations (eg. '9Loci DNA profile'):

1. **One whole Item – multiple stains** - same presumptive result and only one type of extraction requested.
2. **One whole Item – multiple stains** - different presumptive results and two types of extractions requested.
3. **One whole Item – multiple stains** - different presumptive results (but with same extraction request) as well as three differing types of extractions requested.
4. **Swabs** – where no sub-sample barcode is required
5. **Cigarette Butts** – where no sub-sample barcode is required
6. **Sexual Assault Investigation Kits** (SAIK) & clothing
7. **Sexual Assault investigation Kits** (SAIK) – negative results.

Not Current

EXAMPLE 1.

T-SHIRT
QPS Barcode 123456789



<u>EXH TEST CODE</u> is **registered under 123456789 (T-SHIRT)**

Only sub-samples are used to report back presumptive tests & final results

Not Cu

<u>PRESUMPTIVE RESULTS</u>

LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Presumptive blood test pos. Submitted – results pending		

Note as all three stains were TMB positive, only one presumptive test result needs to be entered. (Any <u>one</u> of the three sub-samples for the stains can be entered)

<u>FINAL RESULTS</u>

If all three DNA profiles are the same, then only one result needs to be reported back. If this is the case, then use the same sub-sample as used to originally report back the presumptive test results.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Presumptive blood test pos. Submitted – results pending		

[redacted]	9 loci DNA profile	20076738	COOPER

OR

If the sub-sample originally used is not the best profile, you still need to report back on it – but you will also need to add the sub-sample number which does give you the best profile.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Presumptive blood test pos. Submitted – results pending		
[redacted]	Partial DNA profile	20076738	COOPER
[redacted]	9 loci DNA profile	20076738	COOPER

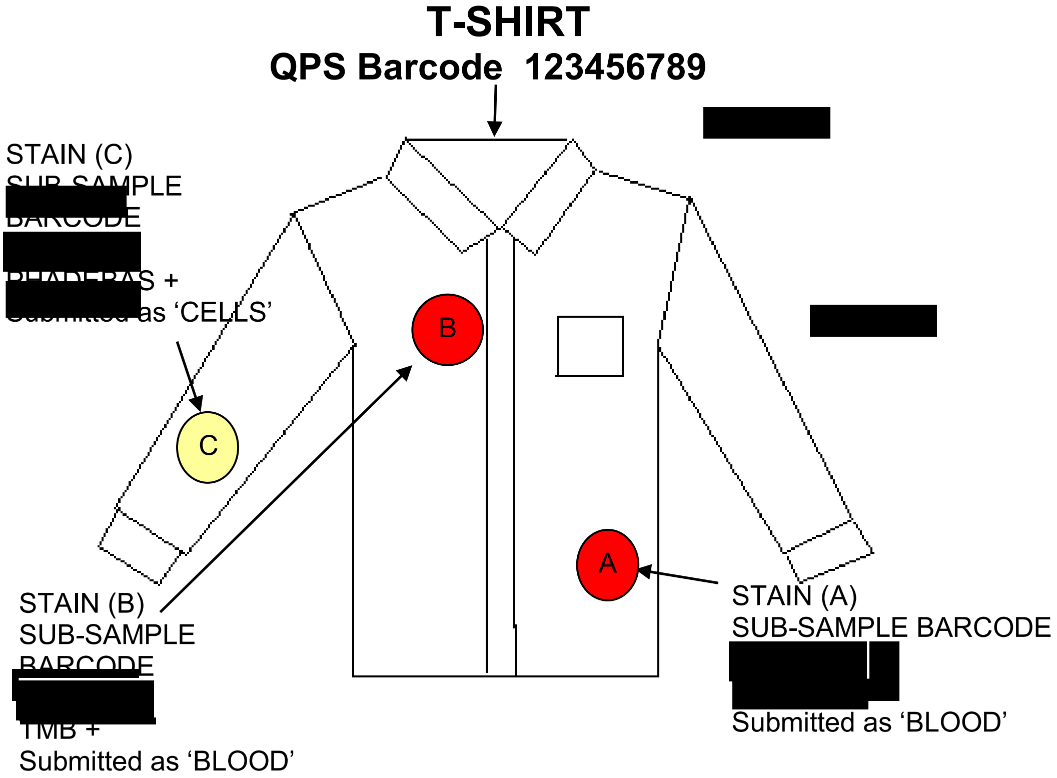
OR

If there are two or three differing DNA profiles resulting from the three stains submitted for analysis, then **report back all <u>differing</u> profiles** using their sub-sample barcodes (as above).

LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Presumptive blood test pos. Submitted – results pending		
[redacted]	9 loci DNA profile	20076738	COOPER
[redacted]	9 loci profile. Uploaded to NCIDD	UKM1	
[redacted]	9 loci profile. Uploaded to NCIDD	UKM2	

Not Current

EXAMPLE 2.



Not Cu

<u>EXH TEST CODE</u> is registered under 123456789 (T-SHIRT)

Only sub-samples are used to report back presumptive tests & final results.

PRESUMPTIVE RESULTS

LAB NO.	**Result/Status**	**Linked No.**	**Warm Linked Name**
[redacted]	Presumptive blood test pos. Submitted – results pending		
[redacted]	Presumptive saliva positive. Submitted – results pending		

Note as two stains were TMB positive, only one TMB+ presumptive test result is to be sent back to QPS DRMU for this item. Any <u>one</u> of the two sub-samples for the TMB+ stains can be entered (as above). A second presumptive result is sent back for the Phadebas + result as well.

FINAL RESULTS

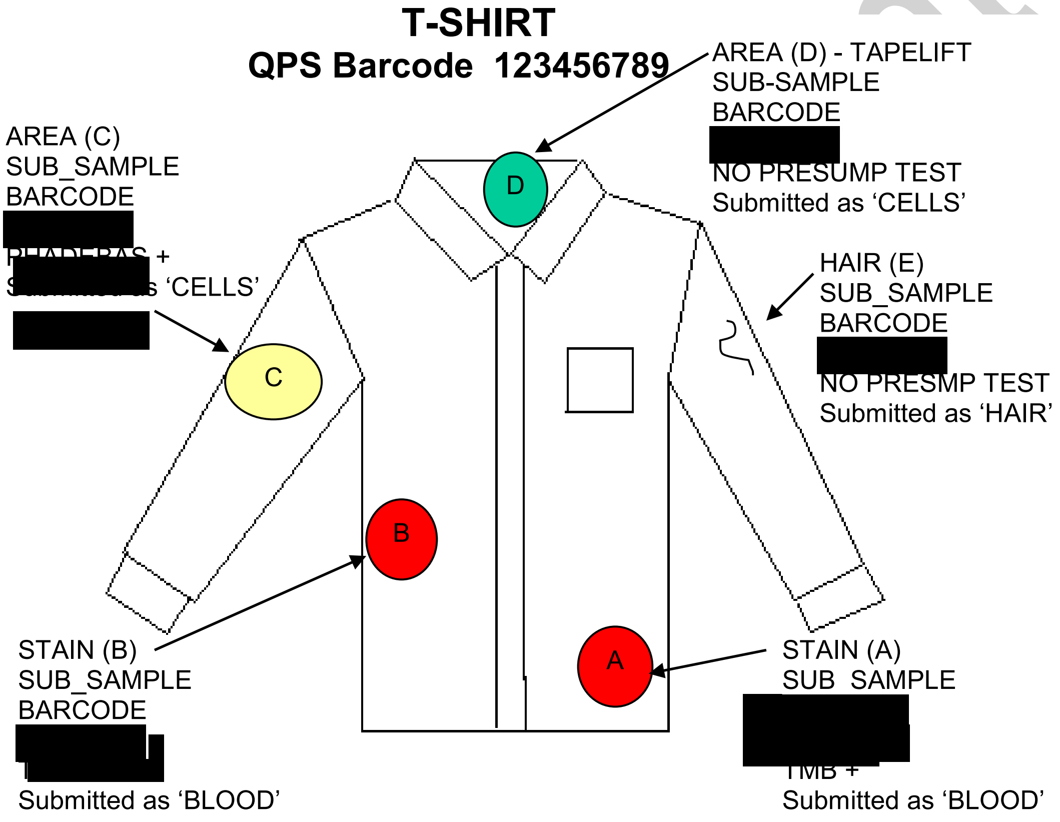
LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Presumptive blood test pos. Submitted – results pending		
[redacted]	Presumptive saliva positive. Submitted – results pending		

[redacted]	9 loci profile. Uploaded to NCIDD	[redacted]	ELLIS
[redacted]	9 loci profile	[redacted]	ELLIS
[redacted]	9 loci profile. Uploaded to NCIDD	[redacted]	JEFFREY

As two presumptive results were sent to DRMU initially, both the final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results. If the profiles differ then both are reported back via their sub-samples.

EXAMPLE 3



<u>EXH TEST CODE</u> is registered under 12345-6789 (T-SHIRT)

<u>PRESUMPTIVE RESULTS</u>

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		

[redacted]	Presumptive saliva positive. Submitted – results pending		
[redacted]	Hair located. Submitted – results pending		

FINAL RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Presumptive blood test pos. Submitted – results pending		
[redacted]	Presumptive saliva positive. Submitted – results pending		
[redacted]	Hair located. Submitted – results pending		
[redacted]	9 loci DNA profile. Uploaded to NCIDD	2021958	GUGIO
[redacted]	Partial DNA profile	2021958	GUGIO
[redacted]	No DNA Profile		
[redacted]	9 loci DNA profile. Uploaded to NCIDD	UKF1	

As three presumptive results were sent to DRMU initially, all three final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

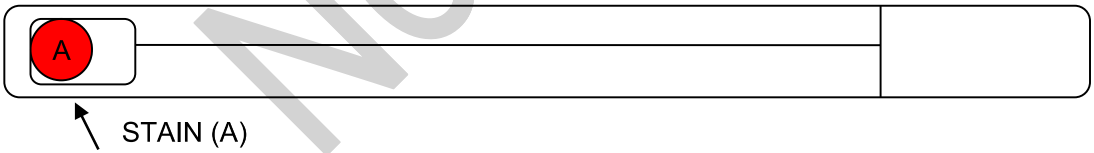
If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results.

If the profiles differ then both are reported back via their sub-samples (as shown above).

Not Current

EXAMPLE 4.

SWAB - QPS BARCODE 123456789



STAIN (A)
NO SUB NUMBER BARCODE GIVEN
TMB +
Submitted as 'BLOOD'

No sub-numbering required for this item as the entire sample is exhausted

PRESUMPTIVE AND FINAL EXH ON SWAB EXH BARCODE

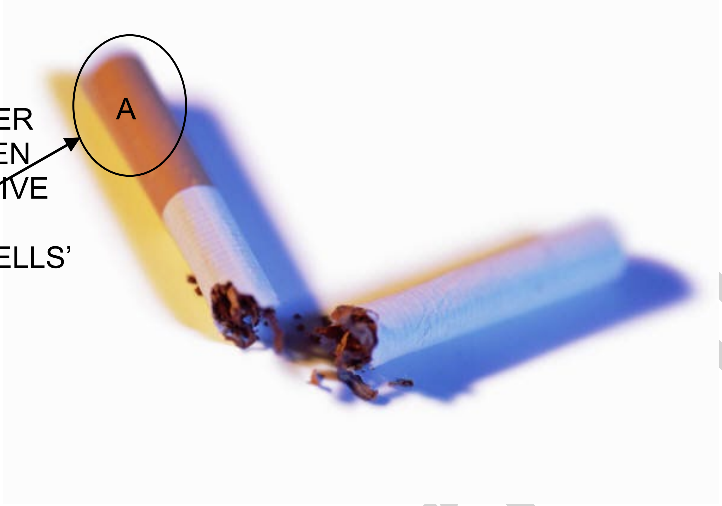
LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Presumptive blood test pos. Submitted – results pending		

[redacted]	9 loci DNA profile. Uploaded to NCIDD	[redacted]	ANDREW

EXAMPLE 5.

CIG BUTT - QPS BARCODE 12345-9999

AREA (A)
NO SUB NUMBER
BARCODE GIVEN
NO PRESUMPTIVE
TEST
Submitted as 'CELLS'



No sub-numbering required for this item

Not Current

PRESUMPTIVE AND FINAL EXH ON CIGERETTE BUTT EXH BARCODE

LAB NO.	Result/Status	Linked No.	Warm Linked Name
[redacted]	Submitted results pending		
[redacted]	9 loci DNA profile. Uploaded to NCIDD	[redacted]	RON

EXAMPLE 6.

SAIK = QPS BARCODE 12345-6789

SAIK CONTAINS FIVE SWABS and TWO CLOTHING ITEMS (NOT BARCODED BY QPS)

A
SUB-BARCODE – [redacted]
MICRO POS FOR SPERMATOZOA
HV SWAB

B
SUB-BARCODE – [redacted]
MICRO POS FOR SPERMATOZOA
LV SWAB

C

SUB-BARCODE – [redacted]

AP NEG MICRO NEGATIVE FOR SPERM

VULVAL SWAB

D

SUB-BARCODE – [redacted]

AP NEG MICRO NEGATIVE FOR SPERM

PERIANAL SWAB

E

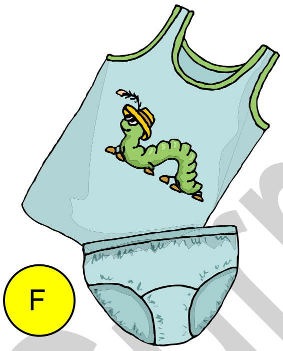
SUB-BARCODE – [redacted]

AP NEG MICRO NEGATIVE FOR SPERM

RECTAL SWAB

TWO CLOTHING ITEMS:

SUB-BAROCDE: [redacted]
ITEM: UNDERPANTS
AP POSITIVE
MICRO POS FOR SPERM



SUB –BARCODE: [redacted]
ITEM: SINGLET TOP
AP NEGATIVE

Not Current

Reporting back on SAIK via EXH registered under barcode 12345-6789.

PRESUMPTIVE RESULTS

	Result/Status	Linked No.	Warm Linked Name
[redacted]	Micro positive for sperm. Submitted results pending		
[redacted]	Semen not detected.		
[redacted]	Micro positive for sperm. Submitted results pending		

Note: only the high vaginal swab is reported back to QPS out of the five swabs submitted in the SAIK. In this example, three swabs share the same positive results and two swabs are negative. The EXH to QPS is reported back on the most probative of all the positive swabs – the high vaginal swab.

There is no need to report back the negative swabs results as these results do not add any information needed by QPS at this stage.

Both items of clothing also have their presumptive results reported back via the same SAIK EXH to QPS. The SAIK and the clothing have their own FBEXAM registered to record the examination details.

When the profile in the Epithelial fraction matches the donor, and is therefore not an unexpected finding, this result is not usually reported in the EXH.

Not Current

FINAL RESULTS

	Result/Status	Linked No.	Warm Linked Name
[redacted]	**Micro positive for sperm. Submitted results pending**		
[redacted]	**Semen not detected.**		
[redacted]	**Micro positive for sperm. Submitted results pending**		
[redacted]	Mixed profile, major component uploaded to NCIDD.	[redacted]	DEVON
[redacted]	Mixed profile, partial minor component.	[redacted]	CHILD
[redacted]	Mixed DNA profile, conditioned on.	[redacted]	CHILD
[redacted]	Mixed DNA profile. Remaining profile after conditioning.	[redacted]	DEVON
[redacted]	Mixed part profile. No major/minor. Unable to load to NCIDD.		

EXAMPLE 7.

SAIK = QPS BARCODE 123456789

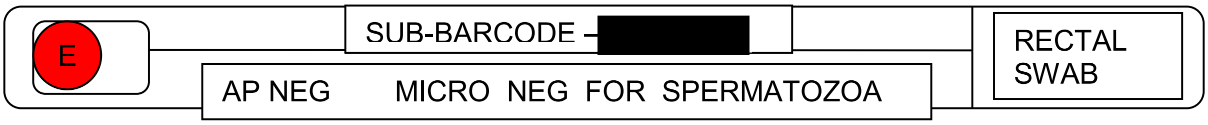
SAIK CONTAINS FIVE SWABS (NOT BARCODED BY QPS)

A
SUB-BARCODE – [redacted]
AP NEG MICRO NEG FOR SPERMATOZOA
HV SWAB

B
SUB-BARCODE – [redacted]
AP NEG MICRO NEG FOR SPERMATOZOA
LV SWAB

C
SUB-BARCODE – [redacted]
AP NEG; MICRO NEG FOR SPERM; SUBMIT FOR CELLS
VULVAL SWAB

D
SUB-BARCODE – [redacted]
AP NEG MICRO NEG FOR SPERMATOZOA
PERIANAL SWAB



PRESUMPTIVE RESULTS

	Result/Status	**Linked No.**	**Warm Linked Name**
[redacted]	Semen not detected.		
[redacted]	Submitted as cells		

In this example, the five swabs were all negative for AP and microscopy, and the EXH has the parent barcode as the barcode entered to summarise that the whole item did not have semen detected. The two items of clothing are also reported back as negative to QPS. However, even though the vulval swab was also negative to all presumptive testing, it will still be submitted for a 'cell' extraction. DNA analysis is requested for the vulval swab as a last ditch effort, given both the SAIK and clothing are negative for all testing performed.

If QPS request an item for specific testing (eg blood) and the whole item was negative (eg Presump blood test neg), then the EXH will use the item/parent barcode to report back the results.

FINAL RESULTS

	Result/Status	**Linked No.**	**Warm Linked Name**
[redacted]	**Semen not detected.**		
[redacted]	**Submitted as cells**		
[redacted]	No DNA profile		

Not Current

9.9 Complete Casework Preamble – Examinations by QHFSS

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biology

As a forensic biologist, it is my role to report on the examination of items submitted in relation to this case for the presence of possible biological material. If identified, a sample of the biological material is analysed in an attempt to obtain a DNA profile. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were performed in accordance with the SOPs of this laboratory.

Forensic DNA Analysis case files and any samples remaining are available for independent examination and / or testing upon request.

As a representative of the laboratory, I am only able to comment on the processes performed within Forensic DNA Analysis.

DNA Profiling

Please refer to the Appendix for an overview of DNA profiling.

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex®21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex®21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Not Current

Mixed DNA profiles *(Profiler® Plus only)*

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as 'conditioning').

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so complex or incomplete that it may not be possible to draw any conclusions as to whether a person may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered by a swab, tape lift or excision depending upon the nature of the surface in question, and the sample can then be subjected to DNA profiling.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

Not Current

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains are located in the laboratory by means of their visual appearance and the use of a presumptive chemical test (Tetramethylbenzidine – TMB). A positive result with this test is a good indication that blood may be present, however it does not provide proof as other substances are known to give the same result.

Semen Stains

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular fractions. This separation is not always completely effective, and a mixing of fractions can occur. This is often referred to as cellular carryover.

The current practice within Forensic DNA Analysis is for epithelial fractions from intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be stored indefinitely, and can be sent for DNA profiling at a future date if required.

Not Current

Semen staining on items

The presence of semen on an item is normally the result of either direct ejaculation or contact with an item wet with semen. Any semen which may have been transferred / deposited can subsequently be lost by actions such as washing.

Persistence of semen in the vagina

The presence of semen in the vagina is normally the result of vaginal intercourse with internal ejaculation. The likelihood of detecting semen on a vaginal swab depends upon a number of factors such as:
- the effectiveness of the sampling process;
- the delay between deposition of the semen and sampling during the medical examination;
- the biochemical conditions within the vagina.

The greater the delay between deposition and sampling, the less chance there is of finding semen. Semen is likely to be found on vaginal swabs if they were taken 1-2 days after the act of vaginal intercourse. Semen is sometimes found on swabs taken between 2-7 days afterwards, but it is unlikely to be detected after 7 days. This is due to a number of factors which can include the following:
- drainage of semen from the vagina;
- loss of semen by bathing or washing (especially on external sites);
- degradation of the spermatozoa.

Saliva

A presumptive chemical test (Phadebas) may be used to detect the possible presence of saliva. This test exploits the enzyme activity of a constituent of saliva called amylase. Amylase is usually present at a relatively high concentration in saliva, though this can vary considerably between individuals. Amylase may also be detected in other body fluids such as sweat, vaginal fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva may also be transferred by actions such as spitting. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

XX. The results of the scientific examinations conducted in this laboratory are as follows:

Not Current

9.10 Complete Casework Preamble – Examinations by QPS and QHFSS

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biologist

As a forensic biologist, it is my role to:

1. Report on the examination of items submitted in relation to a case for the presence of possible biological material. If identified, a sample of the biological material is analysed in an attempt to obtain a DNA profile.

2. Report on the DNA profiles obtained from samples submitted by the Queensland Police Service (QPS) in relation to a case.

Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations and DNA Profiling *(PowerPlex® 21 only)*

Please refer to the Appendix for an overview of DNA profiling.

Forensic DNA Analysis case files and any samples remaining are available for independent examination and / or testing upon request.

As a representative of the laboratory, I am only able to comment on the processes performed within Forensic DNA Analysis.

Examinations *(Profiler® Plus only)*

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the QPS. Sub-samples from these items were forwarded to Queensland Health Forensic and Scientific Services (QHFSS) for the purposes of conducting DNA analysis.

Samples submitted to QHFSS for DNA analysis may include swabs, tape-lifts or small sections of material cut from an exhibit. Individual samples are typically submitted within small plastic tubes and are referred to as 'in-tube' samples.

It is my understanding that the QPS are responsible for item prioritisation, sample selection, selection of screening / sampling methods, application of anti-contamination and standard operating procedures (SOPs) on work undertaken on the items / samples prior to submission to QHFSS. As such, forensic biologists may not be able to provide information or opinion on the possible biological origin of any DNA profiles that may be obtained from these samples.

At the discretion of the QPS, some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the case file.

Forensic DNA Analysis case files and any samples remaining are available for independent examination and / or testing upon request.

Not Current

As a representative of the laboratory, I am only able to comment on the processes performed within Forensic DNA Analysis.

DNA Profiling ***(Profiler® Plus only)***

Please refer to the Appendix for an overview of DNA profiling.

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex®21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex®21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Mixed DNA profiles (*Profiler® Plus only)*

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as ‘conditioning’).

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Not Current

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so complex or incomplete that it may not be possible to draw any conclusions as to whether a person may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Not Current

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered by a swab, tape lift or excision depending upon the nature of the surface in question, and the sample can then be subjected to DNA profiling.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains are located in the laboratory by means of their visual appearance and the use of a presumptive chemical test (Tetramethylbenzidine – TMB). A positive result with this test is a good indication that blood may be present, however it does not provide proof as other substances are known to give the same result.

Semen Stains

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular fractions. This separation is not always completely effective, and a mixing of fractions can occur. This is often referred to as cellular carryover.

The current practice within Forensic DNA Analysis is for epithelial fractions from intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be stored indefinitely, and can be sent for DNA profiling at a future date if required.

Semen staining on items

The presence of semen on an item is normally the result of either direct ejaculation or contact with an item wet with semen. Any semen which may have been transferred / deposited can subsequently be lost by actions such as washing.

Persistence of semen in the vagina

The presence of semen in the vagina is normally the result of vaginal intercourse with internal ejaculation. The likelihood of detecting semen on a vaginal swab depends upon a number of factors such as:
- the effectiveness of the sampling process;
- the delay between deposition of the semen and sampling during the medical examination;
- the biochemical conditions within the vagina.

The greater the delay between deposition and sampling, the less chance there is of finding semen. Semen is likely to be found on vaginal swabs if they were taken 1-2 days after the act of vaginal intercourse. Semen is sometimes found on swabs taken between 2-7 days afterwards, but it is unlikely to be detected after 7 days. This is due to a number of factors which can include the following:
- drainage of semen from the vagina;
- loss of semen by bathing or washing (especially on external sites);
- degradation of the spermatozoa.

Not Current

Saliva

A presumptive chemical test (Phadebas) may be used to detect the possible presence of saliva. This test exploits the enzyme activity of a constituent of saliva called amylase. Amylase is usually present at a relatively high concentration in saliva, though this can vary considerably between individuals. Amylase may also be detected in other body fluids such as sweat, vaginal fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva may also be transferred by actions such as spitting. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

XX. The results of the scientific examinations conducted in this laboratory are as follows:

Not Current

9.11 Complete Paternity Preamble

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biology

As a Forensic Biologist, it is my role to report on the examination of items submitted in relation to this case for the presence of possible biological material. If identified, a sample of the biological material is analysed in an attempt to obtain a DNA profile. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were carried out in accordance with Standard Operating Procedures.

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The DNA system used at Queensland Health looks at 10 regions of DNA, 9 of which contain Short Tandem Repeats (STRs). The tenth region gives an indication as to the gender of the donor.

Or, if PowerPlex® 21 was used for all samples:

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The DNA system used at Queensland Health looks at 21 regions of DNA, 20 of which contain Short Tandem Repeats (STRs). The twenty-first region gives an indication as to the gender of the donor.

Two DNA components (alleles) are detected at each region of DNA tested. This total of 18 alleles *(or 40 alleles),* plus gender information, comprises an individual's DNA profile. Of the two alleles detected at each of the regions tested, one is inherited from an individual's biological mother, and the other component is inherited from an individual's biological father.

Reference Samples (NB, Remove if all samples profiled with PowerPlex® 21).

One or more reference sample/s provided for this case have been profiled using the PowerPlex®21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex®21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Parentage testing and Statistical calculations:

In a disputed paternity matter, DNA profiles are obtained from the foetus/child, the biological mother and the putative father(s). Based on the assumption that the mother is indeed the biological mother of the foetus/child, it is possible to determine which DNA components within the DNA profile of the child could have originated from her. The remaining DNA components within the DNA profile of the foetus/child must have originated from the biological father, and are called *obligate paternal alleles*.

If the DNA profile of a putative father **does not** contain the obligate paternal alleles in at least two of the DNA regions tested, then that person is **excluded** as a potential biological father of the foetus/child.

If the DNA profile of a putative father **does** contain the obligate paternal alleles at each of the DNA regions tested, then that person is **not excluded** as a potential biological father of the foetus/child. This means that this putative father could indeed be the biological father.

Statistical analysis is then conducted to aid in the understanding of the strength of the evidence. The Paternity Index (PI) is a likelihood of two probabilities conditional upon different competing hypotheses;

1. The alleged father contributed the obligate paternal alleles observed in the DNA profile of the foetus/child

2. Another man chosen at random contributed the obligate paternal alleles observed in the DNA profile of the foetus/child.

The PI reflects how many times more likely it is to see the evidence (ie. Set of alleles) under the first hypothesis compared to the second hypothesis. The generally accepted minimum standard for an inclusion of paternity is a PI of 200 or greater (NATA Paternity Testing Technical Advisory Group, 2004).

(Adapted from Butler, J.M. (2005) Chapter 23, *Kinship and Parentage Testing in* Forensic DNA Typing, Biology, Technology, and Genetics of STR Markers, 2 Ed. Elsevier Academic Press: Burlington, MA 01803, USA.)

XX. The results of the scientific examinations conducted in this laboratory are as follows:

Reference Samples

nn: XX - mother
nn: XY - suspect
nn: CC - child

DNA profiles were obtained from these reference samples. These DNA profiles were different to each other.

Not Current

Information was observed within the DNA profile of CC, supporting the assumption that XX is indeed the biological mother of CC.

The DNA profile obtained from the reference sample from XY was compared to the DNA profiles obtained from the reference samples of XX and CC in order to assist in the determination of the possible paternity of CC.

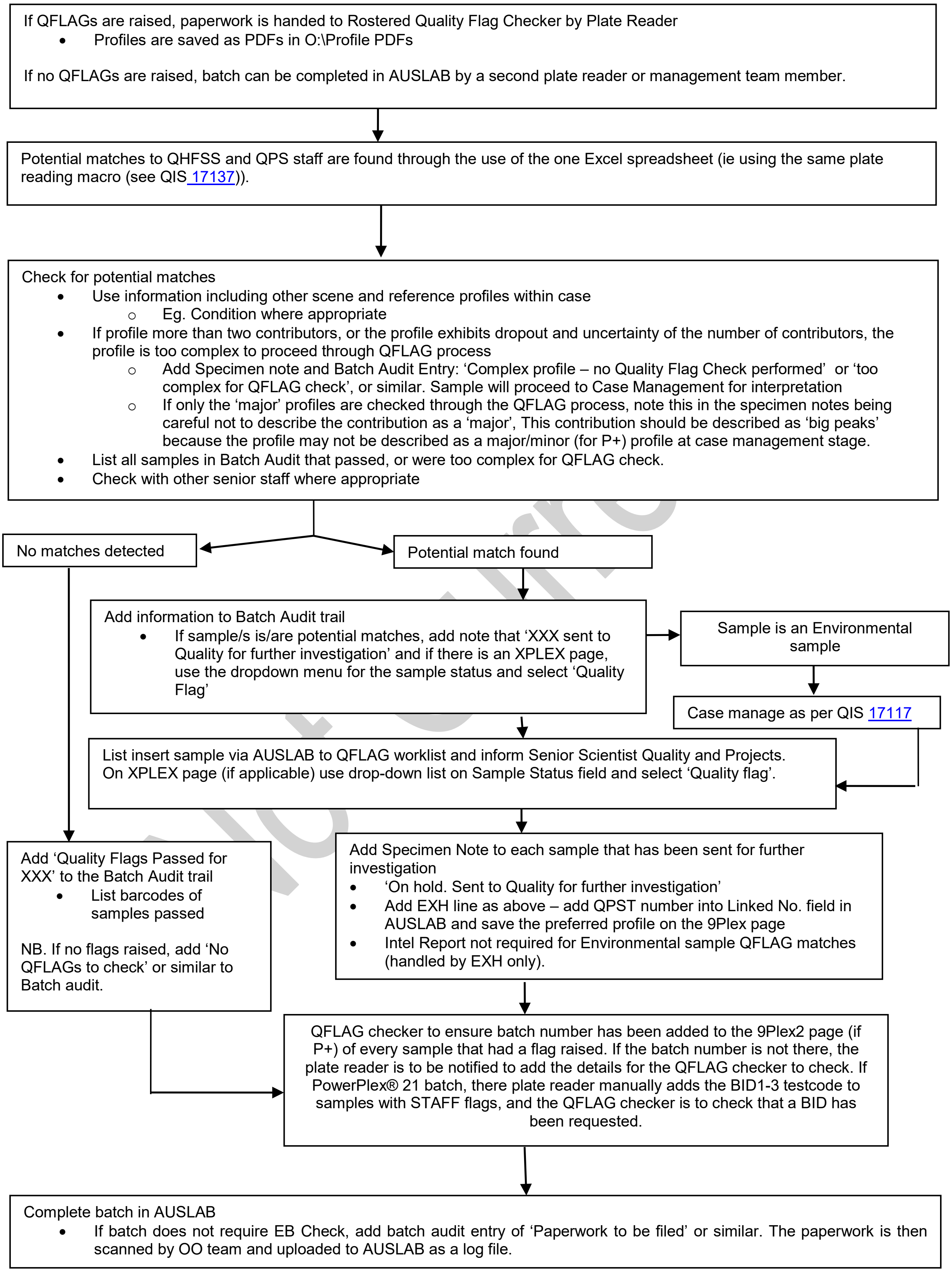
XY possesses all of the obligate paternal alleles. In my opinion, it is possible that XY is the biological father of CC given that XX is the natural mother. The following statistical weighting has been calculated in support of this opinion:

The DNA profile from CC is n times more likely to have occurred if CC was the offspring of XX and XY rather than if CC was the offspring of XX and a random man unrelated to XY <population data set>.

Not Current

Not Current

9.12 Quality Flag Checking Workflow



If QFLAGs are raised, paperwork is handed to Rostered Quality Flag Checker by Plate Reader
- Profiles are saved as PDFs in O:\Profile PDFs

If no QFLAGs are raised, batch can be completed in AUSLAB by a second plate reader or management team member.

Potential matches to QHFSS and QPS staff are found through the use of the one Excel spreadsheet (ie using the same plate reading macro (see QIS 17137)).

Check for potential matches
- Use information including other scene and reference profiles within case
    - Eg. Condition where appropriate
- If profile more than two contributors, or the profile exhibits dropout and uncertainty of the number of contributors, the profile is too complex to proceed through QFLAG process
    - Add Specimen note and Batch Audit Entry: 'Complex profile – no Quality Flag Check performed' or 'too complex for QFLAG check', or similar. Sample will proceed to Case Management for interpretation
    - If only the 'major' profiles are checked through the QFLAG process, note this in the specimen notes being careful not to describe the contribution as a 'major', This contribution should be described as 'big peaks' because the profile may not be described as a major/minor (for P+) profile at case management stage.
- List all samples in Batch Audit that passed, or were too complex for QFLAG check.
- Check with other senior staff where appropriate

No matches detected

Potential match found

Add information to Batch Audit trail
- If sample/s is/are potential matches, add note that 'XXX sent to Quality for further investigation' and if there is an XPLEX page, use the dropdown menu for the sample status and select 'Quality Flag'

Sample is an Environmental sample

Case manage as per QIS 17117

List insert sample via AUSLAB to QFLAG worklist and inform Senior Scientist Quality and Projects. On XPLEX page (if applicable) use drop-down list on Sample Status field and select 'Quality flag'.

Add 'Quality Flags Passed for XXX' to the Batch Audit trail
- List barcodes of samples passed

NB. If no flags raised, add 'No QFLAGs to check' or similar to Batch audit.

Add Specimen Note to each sample that has been sent for further investigation
- 'On hold. Sent to Quality for further investigation'
- Add EXH line as above – add QPST number into Linked No. field in AUSLAB and save the preferred profile on the 9Plex page
- Intel Report not required for Environmental sample QFLAG matches (handled by EXH only).

QFLAG checker to ensure batch number has been added to the 9Plex2 page (if P+) of every sample that had a flag raised. If the batch number is not there, the plate reader is to be notified to add the details for the QFLAG checker to check. If PowerPlex® 21 batch, there plate reader manually adds the BID1-3 testcode to samples with STAFF flags, and the QFLAG checker is to check that a BID has been requested.

Complete batch in AUSLAB
- If batch does not require EB Check, add batch audit entry of 'Paperwork to be filed' or similar. The paperwork is then scanned by OO team and uploaded to AUSLAB as a log file.

Not Current

Notes on the Quality Flag Checking Process:

- Quality Flag Checking is to detect gross contamination that could have occurred at collection or during processing of the sample.
    - This includes single-source profiles, distinct major or minor profiles, or remaining contributions if the mixed profile has been conditioned.

- Due to the complexity of some DNA profiles, profiles that indicate at least three contributors (and therefore an unknown number of contributors) are generally not suitable for Quality Flag checking for the following reasons:
    - The number of contributors is not known and the often partial nature adds complexity.
    - At most, a person may not be able to be excluded as a potential contributor and this interpretation may not be useful to the client as we cannot evaluate the significance of a possible inclusion by adding statistical weight for Profiler Plus profiles.
    - For PowerPlex® 21 profiles, a STRmix™ evaluation is possible, yet the LR value obtained requires a subjective assessment for QPS to determine likelihood of contributing DNA to the mixture. Caution should be exercised and this can be done by searching and reporting gross contaminations.

- When profiles of at least three contributors are obtained, the Quality Flag Checker should note in the Batch Audit and the Specimen Notes:
    - ‘Complex profile – no Quality Flag check performed’ or similar wording
    - The profile will then proceed to case management for interpretation with case context.

- It may be possible for the higher RFU peaks (if demonstrating a pattern as such across the profile) to be QFLAG checked.
    - If the peaks pass, write in the Batch Audit and Specimen Notes: ‘Big peaks passed QFLAGs. Small peaks too complex for QFLAG checking’ or similar wording
    - Refrain from using ‘Major/Minor’ terminology because the Case Manager may interpret the profile not to be a major/minor profile (vis. PowerPlex® 21 profiles).

- The macro that is applied to detect potential Quality Flags has a stringency of 13 alleles. This means, crime scene profiles with less than 13 alleles detected will not go through the macro and therefore will not be Quality Flag checked.

- If a profile with less than 13 alleles is obtained, this may be checked by the Quality Team as a separate comparison to the QFLAG process. List insert the sample to BQUAL worklist in AUSALB and provide instructions in the Specimen Notes.

- If there are more than 6 alleles at a locus for P+ DNA profiles, there is too much information to be exported from GMID-x and the profile will need further quality checking at case management stage.
    - If the profile is determined to be ‘complex unsuitable’, then the profile would have been too complex for QFLAG checking.
    - If the profile is ‘suitable’ for comparison (eg. ‘complex cannot exclude’), then a further assessment is made:
        - If there is a ‘major’ within the first six alleles, then this would have gone through the QFLAG check process – no further work is required.
        - If there are ‘major’ peaks outside the first six alleles and therefore not captured in the table, this this contribution will need a separate comparison outside the QFLAG process through the Quality Team. List insert the sample to BQUAL and provide instructions in the Specimen Notes in AUSLAB.

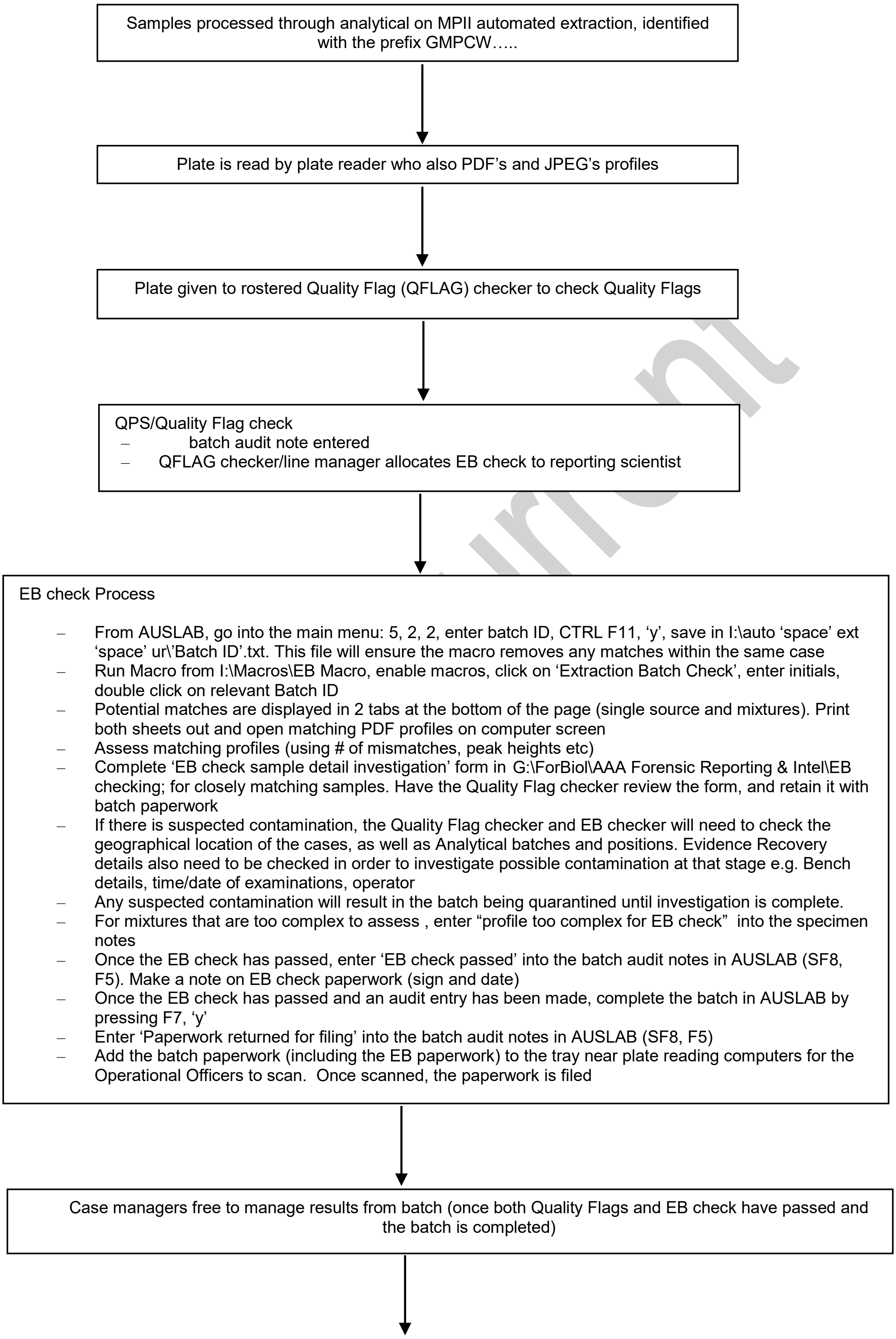
- If an EB check is required to check for cross-sample contamination in locked batches (eg. GMPCW…):

  - Write ‘Paperwork given to EB Checker/checking team’ or similar, and deliver paperwork to Senior Scientist on the rotation that includes EB Check, or delegate.
  - If batch does not require EB Check, add batch audit entry of ‘Paperwork to be filed’ or similar. The paperwork is then scanned by OO team and uploaded to AUSLAB as a log file.

- Once comments from both Quality Flag checker and EB checker have been entered and no remaining flags are to be investigated, the person performing the last of the above tasks is to complete the batch (F7in AUSLAB on batch).

Not Current

9.13 Extraction Batch Checking Workflow (EB Checking)



Samples processed through analytical on MPII automated extraction, identified with the prefix GMPCW…..

Plate is read by plate reader who also PDF's and JPEG's profiles

Plate given to rostered Quality Flag (QFLAG) checker to check Quality Flags

QPS/Quality Flag check
- batch audit note entered
- QFLAG checker/line manager allocates EB check to reporting scientist

EB check Process

- From AUSLAB, go into the main menu: 5, 2, 2, enter batch ID, CTRL F11, 'y', save in I:\auto 'space' ext 'space' ur\'Batch ID'.txt. This file will ensure the macro removes any matches within the same case
- Run Macro from I:\Macros\EB Macro, enable macros, click on 'Extraction Batch Check', enter initials, double click on relevant Batch ID
- Potential matches are displayed in 2 tabs at the bottom of the page (single source and mixtures). Print both sheets out and open matching PDF profiles on computer screen
- Assess matching profiles (using # of mismatches, peak heights etc)
- Complete 'EB check sample detail investigation' form in G:\ForBiol\AAA Forensic Reporting & Intel\EB checking; for closely matching samples. Have the Quality Flag checker review the form, and retain it with batch paperwork
- If there is suspected contamination, the Quality Flag checker and EB checker will need to check the geographical location of the cases, as well as Analytical batches and positions. Evidence Recovery details also need to be checked in order to investigate possible contamination at that stage e.g. Bench details, time/date of examinations, operator
- Any suspected contamination will result in the batch being quarantined until investigation is complete.
- For mixtures that are too complex to assess , enter "profile too complex for EB check" into the specimen notes
- Once the EB check has passed, enter 'EB check passed' into the batch audit notes in AUSLAB (SF8, F5). Make a note on EB check paperwork (sign and date)
- Once the EB check has passed and an audit entry has been made, complete the batch in AUSLAB by pressing F7, 'y'
- Enter 'Paperwork returned for filing' into the batch audit notes in AUSLAB (SF8, F5)
- Add the batch paperwork (including the EB paperwork) to the tray near plate reading computers for the Operational Officers to scan. Once scanned, the paperwork is filed

Case managers free to manage results from batch (once both Quality Flags and EB check have passed and the batch is completed)

Case managers to manage rework results (>6 alleles) and perform EB check on samples that were originally extracted on the MPII automated platforms

- access EB Macro
- enter details into fields (sample ID, profile obtained, reader comments) in 'Update and Check from Rework' section
- click on 'Update and check'
- find the original GMPCW 9PLEX batch
- assess updated profile against matches
- if sample passed, enter specimen note 'EB check for rework performed – passed'
- If EB check not completed, enter a specimen note indicating the reason
- file rework EB check paperwork in date order in the blue folder next to the printer

EB Macro Notes:

- The Extraction Batch macro is performed before results are case managed and released to the QPS. It allows for the detection of contamination between samples that we extracted on the same automated MPII extraction batch. These batches are identified by GMPCW…..
- It compares profiles from different cases that have greater than 6 alleles against each other.
- Matches are assessed by the reporting scientist, considering both samples as the potentially contaminating and contaminated profiles.
- The EB macro divides and displays any potential matches into single source and mixtures, in two separate tabs.
- The profile highlighted in white is the profile that the profiles underneath have matched to.
- The macro displays matching loci in different colours: green indicates that there are at least 2 matching alleles, yellow indicates 1 matching allele, light orange indicates a mismatch at the entire loci, and bright orange indicates a mismatch at Amelogenin.
- The EB check can be performed at any desk. The profile highlighted in white is to be printed off, and the profiles matching to it can be displayed on the computer screen so that comparisons can be made.
- Once samples have been reworked, the reworked result needs to be checked against the batch the sample was originally extracted on. If the 9plex result is used as the reported profile; or the rework result is the same, similar, has less information or is too complex, a rework EB check is not necessary. This is assessed by the case manager, and a specimen note added with the reason the EB check was not performed.

Not Current

9.14 General DNA Evidentiary Certificate Workflow

Receive written request and clarify which samples are required to be included.

↓

Ensure that there is adequate time to complete audit trails and issue certificate at least 10 days before court date – negotiate with IO/DPP if required.
Timeframes approx. 4 weeks for Evidentiary Certificate alone, 6 weeks if requested at the same time as a statement.

↓

Create Evidentiary checklist using:
QIS 30799: DNA Evidentiary Certificate Checklist
Follow instructions on Worksheet entitled: 'Instructions'
The minimum requirement is to check the electronic records of samples and batches in AUSLAB.

↓

Work through each sample and the relevant batches, looking at audit trail in AUSLAB to see if any issues have been raised. eg sample removed has not transferred yet, pos control is partial profile, failure of batch due to controls not working/OQI.
If you have examined the records relating to the receipt, storage and testing of the things covered by the Evidentiary Certificate, by 'checking' the boxes, you are confirming that the Quality Assurance Procedures relevant to the above at the time of testing were complied with.

If in examining the records, something needs to be addressed, notify your Senior Scientist and/or Team Leader to co-ordinate a possible investigation.

↓

Check storage audit trail for each sample, noting that there should be two final locations for most samples – one for spin basket and one for final amplified product. Ensure that throughout the audit trail, sample has been added and removed from particular location as it works its way through the process.

↓

As a minimum, AUSLAB audit trails can be checked for departures from the standard operating procedure. If required, the batch paperwork is scanned into the batches as 'log' files and can be checked by the following:

enter into batch □ Shift F6 ('Files') □ scroll to 'Log' □ Export file to location to be retrieved □

↓

If the paperwork is not complete, get original paperwork correction signed and dated or whatever is required. If this staff member is on holidays, or no longer working in department, get their Senior to sign and date on their behalf.

↓

Not Current

Print out checklist and add to front of file with associated documentation including written request for certificate.

↓

Create Evidentiary Certificate by requesting testcode in AUSLAB: FBEVC.
This code has information and formatting based on the template in Appendix 17.

↓

See Appendix 16 for Evidentiary Certificate Workflow in AUSLAB

↓

Create cumulative results table. This will become the last page of certificate documentation. Macros can assist in the table creation: I:\Macros\s95A Table 9PLEX and s95A Table PP21

↓

Have Evidentiary Certificate Peer Reviewed - only Administrative Review is required to check transcription of samples to certificate, and to cross check with written request. Reviewer to use checklist to check the correct batches are listed according to the Specimen Audits of each sample,

↓

Issue, and copy for the case file. Keep checklist and other paperwork (if gathered) within casefile and have the casefile page numbered and case identifier added.

9.15 DNA Evidentiary Certificate (and Appendix v5)

Section 95A
Evidence Act 1977
Form 3 Version 2

DNA EVIDENTIARY CERTIFICATE

I, name, state

1. I am a DNA Analyst employed by Queensland Health Scientific Services

2. I am a Scientist in the DNA Analysis Unit.

3. My qualifications are: fill in

4. I hold appointment as a DNA Analyst under the Evidence Act 1977.

5. Appendix 1 to this certificate sets out the procedures and methodology used by Queensland Health Scientific Services in DNA testing. These procedures are carried out in accordance with the requirements of the National Association of Testing Authorities (NATA).

6. On the DD day of MM, YYYY, insert delivery officer delivered a number of items to Queensland Health Scientific Services, which were then received and registered under laboratory number: 123456789.

7. These things were:

8. On the …

10. On (or between) the date of initial receipt and the statement date, these things, namely insert specified items here
Reference samples:

Items

were tested by me (and other laboratory staff):

11. I have examined the laboratory's records relating to the receipt, storage and testing of the things referred to in paragraph 10 (including where the testing process was done by someone other than me) and confirm that the records indicate that all quality assurance procedures for the receipt, storage and testing of the things that were in place in the laboratory at the time of the testing were complied with.

12. The results of the testing of the things referred to in paragraph 10 are as follows:
Refer to attached table of results.

Not Current

Signed ____

Name **Your Name**

DNA Analyst ____

Date ____

Notes:

A. A party intending to rely on this DNA Evidentiary Certificate must give a copy to each other party in the proceeding at least 10 business days before the hearing day
B. The DNA Analyst giving the certificate will be called to give evidence at the hearing where the certificate is to be used.
C. Any party may request from the Chief Executive of the Department of Health a copy of the laboratory's records relating to the receipt, storage and testing of any things referred to in this certificate.
D. If any party intends to challenge any matter stated in this certificate that party must give written notice of the matter to be challenged (in form 4) to the Chief Executive of the Department of Health and each other party at least 3 business days before the hearing.

Not Current

APPENDIX 1

Procedural overview for the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

Accreditation
The DNA Analysis Unit first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998, and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessments (every 3 years) and surveillance visits (18 months).

NATA Accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories that demonstrate compliance with the standard have shown that they can competently perform activities and testing within the scope of their accreditation.
The parameters assessed during accreditation include:

- Organisation and management
- Quality management system
- Personnel
- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 standard refer to Standards Australia.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:
http://www.nata.asn.au/publications

Chain of Custody
All DNA Analysis Unit case files and exhibits are electronically tracked, monitored and securely stored to ensure that the appropriate chain of custody and continuity measures are maintained. The Queensland Police Service (QPS) case number and sample submission information is provided by the QPS via an electronic interface to QHFSS, and this information is cross-checked against labelling on exhibit packaging. The packaging and labelling of any exhibit is checked and recorded before the sample is sent for DNA analysis.

Entry into the DNA Analysis Unit is restricted to authorised persons only, via electronically encoded swipe access cards. The DNA Analysis Unit forms part of a Queensland Health campus site which has access controlled and monitored by a security team. Records of Visitors to the DNA Analysis Unit are retained.

Technical information relating to DNA profiling at the DNA Analysis Unit of Queensland Health Forensic and Scientific Services (QHFSS)

Not Current

DNA (STR) Profiling
STR (Short Tandem Repeat) profiling is the standard technique currently in use for forensic DNA analysis. Deoxyribonucleic acid (DNA) is a complex chemical found in almost all cells of the body. It carries genetic information which governs a person's physical and biochemical characteristics. Half of a persons DNA is inherited from their mother, and half from their father. A person's DNA is the same in almost all cell types in their body, so that DNA recovered from someone's blood will normally be the same as DNA from their hair roots, saliva or skin cells.

Except for identical twins, each person's total DNA is unique to themselves, although current DNA (STR) profiling techniques do not allow the analysis of the whole of someone's DNA. Instead, specific regions (loci) of the DNA are tested which contain short sequences of DNA (STRs) repeated a number of times end to end. The number of times a particular STR is repeated at each locus (region of DNA) will tend to vary between people, and it is these differences which allow DNA from different people to be compared.

A method known as the Polymerase Chain Reaction (PCR) is used to amplify specific STR regions of the DNA to produce many copies of the original DNA template. In this way, minute amounts of DNA isolated from small or degraded samples can be greatly increased to potentially yield a sufficient quantity of DNA to obtain a DNA profile.

The DNA Analysis Unit currently uses a DNA profiling system called Profiler® Plus which tests nine regions (loci) of DNA containing STRs, and a tenth region which provides an indication of the gender of the DNA source. Another DNA profiling system called COfiler®, although not routinely used at QHFSS, is available if required. The COfiler® system includes two of the regions included in Profiler® Plus, with four additional STR loci. For a list of the loci included in these DNA profiling systems, please refer to Tables 1 and 2 below.

Interpreting DNA Profiles
The individual components of a DNA profile can be represented in a graphical form as a series of peaks, which are measured and given a numerical designation by comparing them against standard sizing DNA components, processed alongside each sample.

If less than the ten regions of DNA tested are present in a DNA profile, this is referred to as a partial or incomplete DNA profile. When more than one person has contributed to a DNA profile, this is referred to as a mixed DNA profile.

A DNA profile obtained from biological material such as blood, semen, saliva or hair can be visually compared with a DNA profile obtained from a reference sample from a person. If each of the individual components within the two DNA profiles have the same corresponding numerical designations, the DNA profiles are said to match each other. If the DNA profiles match then that person, together with anyone else who has the same DNA profile, can be considered as a potential source of the biological material.

If any of the components of the two DNA profiles are different when compared, then the two DNA profiles do not match and the person can normally be excluded as a possible source of the biological material.

The term match does not impart increased significance to the result it describes. Although it may be considered highly unlikely that two unrelated people happen to have matching full DNA profiles, without testing every person in the population we cannot know exactly how many people may share matching DNA profiles.

The Use of Queensland Caucasian Data

The evidential significance of obtaining a match can be evaluated by estimating how common or rare the DNA profile is within a specific population. This can be calculated by estimating the frequency of occurrence of each component in the DNA profile and using a mathematical formula to multiply these frequencies together.

No assumptions are made as to the ethnic origin of any DNA obtained from alleged crime scenes. The DNA Analysis Unit routinely uses Queensland Caucasian data, taken from the largest sub-population in Queensland, for statistical calculations. Calculations using Queensland Aboriginal and Asian data can be provided upon request.

It is laboratory policy to use the Queensland Caucasian data unless the alleged incident occurred off the Queensland mainland, in which case figures from the Queensland Caucasian and Queensland Aboriginal data would both be quoted.

The statistical figure applied to DNA profiles will depend on how closely related people are. The closer the biological relationship (eg. siblings), the greater the chance that the people in question may have DNA profiles which share matching DNA components. However, due to the random nature by which DNA from each parent is combined in their offspring, the probability that two siblings would share the same components at all regions tested is very small. As the relationship becomes more distant, the probability of two relatives having matching DNA profile becomes smaller still. If it is proposed that a relative should be considered as an alternative source of DNA, the best course of action would be to obtain a reference DNA sample from the relative in question, for DNA profiling and comparison.

Validity of the Caucasian Data

The population frequency data used for statistical interpretations in the laboratory have been validated for use by external Forensic Statisticians Dr Simon J WALSH and Dr John S BUCKLETON. The report of their findings is held in the laboratory and is available upon request.

Not Current

DNA (STR) profiling systems available at the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

Table 1: Profiler® Plus multiplex system, list of loci:

Abbreviated Name	Scientific Name	Chromosomal Name
D3	D3S1358	3
vWA	HUMVWFA31/A	12
FGA	HUMFIBRA	4
Amel	AMELOGENIN	Sex X and Y
D8	D8S1179	8
D21	D21S11	21
D18	D18S51	18
D5	D5S818	5
D13	D13S317	13
D7	D7S820	7

Table 2: COfiler® multiplex system, list of loci:

Abbreviated Name	Scientific Name	Chromosomal Name
D3	D3S1358	3
D16	D16S539	16
TH01	TH01	11
TPOX	TPOX	2
CSF	CSF	5
D7	D7S820	7
Amel	AMELOGENIN	Sex X and Y

Not Current

9.16 DNA Evidentiary Certificate Workflow in AUSLAB

Order **FBEVC**

↓

Go to **all relevant receipt pages** (that contain the samples specified to be included in the certificate) and type into **Old Receipt** field: Yes
F6 this page

↓

Go to **FTAR pages** that need to be pulled in and type into **Operation** field: Yes
F6 this page

If the reference sample has been registered on a CA number (coronial case), the reference sample requires some registration changes:

- change **SPECIMEN type** to **FTAE** (Evidence) in Shft F10
- Request FTAR testcode and fill in appropriate areas and associate the QP number to this reference sample

↓

Add dates (receipt to statement date)
- can be 230412, 23042012, 23 April 2012, 23/04/12 and will all come out as 23 April 2012

↓

Items section to keep blank – this section serves no purpose and does not affect the end product

↓

Samples section: Edit to open WORD document and type in the relevant/requested barcodes and descriptions

↓

Add relevant Appendix

↓

Total number of pages is to **include the DNA table** (therefore, Shift Insert to view with App and add the pages for the DNA table).

↓

F6 to bring in your details

NB.
- As for Statements of Witness, Coronial cases registered under CA#'s will not associate to this test code.

9.17 Suggested PowerPlex® 21 (and STRmix™) statement wording

<u>NOTE 1:</u>
When wording your statements it is important to remember that the comparison is being performed by STRmix™ and therefore the conclusions are based on statistical interpretation. Intuitive checking is performed only to ensure that STRmix™ is giving an appropriate interpretation. Therefore statements such as 'Mr X cannot be excluded as having contributed to this profile and therefore I have considered the following propositions' are not appropriate under this model. Your statement should refer only to your assumptions and the statistical interpretation.

<u>NOTE 2:</u>
A link between the profile obtained and the assumption of number of contributors is recommended.

This could be written <u>for mixtures</u> in the following ways:

- *The mixed DNA profile(s) obtained from this sample indicates the presence of DNA from three contributors. As such, an assumption of three contributors has been made for statistical analysis.*

  <u>Or</u>

- *A mixed DNA profile has been obtained from this sample. Based on the information within this DNA profile, an assumption of three contributors has been made for statistical analysis.*

This could be written <u>for single source</u> in the following ways:

- *The DNA profile(s) obtained from this sample indicates the presence of DNA from a single contributor. As such, this DNA profile matches the reference DNA profile of XY.*

  <u>Or</u>

- *The DNA profile(s) obtained from this sample matches the DNA profile of XY.*

<u>NOTE 3:</u>
Rounding of LRs should be in the following conservative format:
- *if the LR = 157 232, round to LR = 150 thousand.*
- *If the LR = 129, round to LR = 120*
- *If the LR =72, no rounding performed..*
- *If the LR = 2.3, round to LR = 2*
- *If the LR favours Hd and = 157 232, round to 160 thousand*
- *If the LR favours Hd and = 129, round to 130*
- *If the LR favours Hd and =72, no rounding performed.*
- *If the LR favours Hd and = 2.3, round to LR = 3*

<u>Example wording</u>

Unknowns	**123456789** **123456789**	**Swab (A), near rear door** **Swab (D), floor in foyer near charge counter**

Not Current

The DNA profiles obtained from these samples *[match each other and]* do not match the reference DNA profiles associated with this matter. Each of these DNA profiles indicated male gender.

Single Source

123456789 Swab (E), floor in charge area

The DNA profile(s) obtained from this sample indicates the presence of DNA from a single contributor. As such, this DNA profile matches the reference DNA profile of XY.

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if the DNA originated from Mr X, rather than if the DNA originated from someone other than Mr X.

OR

The DNA profile obtained from this sample matches the DNA profile of Mr X.

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if Mr X had contributed DNA rather than if he had not.

Non-conditioned Mixture

123456789 Swab (B), floor near cells

The mixed DNA profile(s) obtained from this sample indicates the presence of DNA from three contributors. As such, an assumption of three contributors has been made for statistical analysis.

The reference DNA profiles of John, Sam and Carol have been compared with this mixed DNA profile separately, in order to assess whether or not any of them may have contributed DNA. Based on statistical analyses, the results are as follows:

In favour of <u>contribution</u>:

John - It is estimated that the mixed DNA profile obtained is approximately 4 times more likely to have occurred if he <u>has contributed</u> DNA rather than if he has not.

In favour of <u>non-contribution</u>:

Carol – It is estimated that the mixed DNA profile obtained is approximately 100,000 times more likely to have occurred if she <u>has not contributed</u> DNA rather than if she has contributed DNA.

<u>Inconclusive</u>:

Sam – It is estimated that the mixed DNA profile obtained is <u>equally likely</u> if he has contributed DNA rather than if he has not.

Conditioned Mixture

Conditioned Mixture

The mixed DNA profile(s) obtained from this sample indicates the presence of DNA from X contributors, one of whom could be Carol. Since this sample is said to have been collected from

Not Current

Carol, it would not be unexpected to find DNA which could have come from her. In order to interpret this mixed DNA profile an assumption of DNA from X contributors, one of whom is Carol, has been made.

The reference DNA profile of John has been compared to this mixed DNA profile, to assess whether or not he may have contributed DNA along with Carol.

Based on statistical analysis it is estimated that:

In favour of contribution:

John - It is estimated that the mixed DNA profile obtained is approximately 4 times more likely to have occurred if he has contributed DNA *[along with Carol]* rather than if he has not.

In favour of non-contribution:

John - It is estimated that the mixed DNA profile obtained is approximately 4 times more likely to have occurred if he has not contributed DNA rather than if he has contributed DNA.

Inconclusive:

John - It is estimated that the mixed DNA profile obtained is equally likely to have occurred if he has contributed DNA rather than if he has not.

Excluded:

Based on the assumption of X contributors and the presence of DNA from Carol, the following reference samples are excluded as potential contributors to the mixed DNA profile obtained: John et al

Not Current

Not unexpected findings

Rectal swab
Anterior lower gum swab

The DNA profiles obtained from these samples *[match each other and also]* match the reference DNA profile of Carol. As these samples are said to have been taken from Carol, the finding of DNA which could have come from her is not unexpected, and therefore no statistical analysis has been performed.

Insufficient DNA

123456789 Graph 21; swab; pop bottle

This sample contained insufficient DNA to be suitable for analysis and was not tested further.

No DNA Detected

123456789 Graph 9; swab; cot
123456789 Graph 2; swab; flyscreen

DNA was not detected in these samples and therefore they were not tested further.

Complex – no STRmix

123456789 Graph 11; swab; right thong
123456789 Item 6; tapelift; back of hand

The complex mixed DNA profiles obtained from these samples indicate the presence of DNA from more than three contributors and are therefore unsuitable for statistical analysis.

Complex – unsuitable

123456789 Graph 5

Due to the complex nature of this DNA profile, including uncertainty as to the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation.

Not Current

9.18 QFLAG workflow for Quality Team (when a possible match is identified)

Preparing QFLAG Intel Report:

1. Print QFLAG profile and associated "Matching" profile (i.e. QPSTF profile) for visual assessment/evaluation.
2. Using the report template prepare an appropriate Intel report (refer to I:\Quality & Projects\Intelligence reports or Intel report folder - for examples)
3. Complete EXH: Add case manager, save preferred profile, add EXH (eg. QFIH) with QPSTF laboratory number (if applicable) in Link# Field
4. Add "Refer to Specimen Note" in 9PLEX/XPLEX comment, and add specimen note to indicate possible quality issue.
5. Register new barcode AUSLAB [1], [1] FULL Reception Entry with the sample UR number as the QFLAG EXH barcode
a.Specimen type=Case
b. Add FBINTL, FBAR and FBIOLR test codes
6. Enter into newly registered barcode (ensure Microsoft Word is NOT open)
a. On INTEL report page [F2] in word document section to create new word document [E]. (for subsequent drafts save a new version "N")
b. Paste in word draft of document (ensure at least one carriage return between each paragraph. [Ctl][T] to upload to word file back into AUSLAB
c. Add contact QPS Name and Address (as per previous INTEL reports) and Name of Forensic DNA Analysis peer reviewer and position. DO NOT ADD date of report or date of review until after it has been checked – draft version.
d. Check Intel report using [Shft][Ins]
e. [F6] to validate
f. Print a copy [Shft F11] and provide to reviewer (with profiles).

Review and sending of QFLAG Intel report:

When draft is approved by the reviewer:
1. Add date of report and date of peer review and [F6] to validate. *This creates a PDF of the report – viewable by [Ctl][Ins]. (If further edits are required after review dates are added, delete review dates, edit document then re-add review dates and validates, this creates a new PDF Intel report)
2. Reviewer to validate QFIH EXH, 9PLEX/XPLEX and complete FBAR
3. Print Intel report, and have it signed by quality and reviewer.
4. Completed and signed PDF Intel report to be and scanned and emailed to QPS (by QPS email account only)
5. Add specimen note "Quality Flags noted with sample to QPS Elimination sample. Intel report regarding Quality flags sent to [Insert QPS Staff Name] for action"
6. Complete FBIOLR page with:
a. Posted to: [Insert email recipient]
b. Of: [DNA Management Section]
c. QHSS Officer Posting: [Insert email sender]
d. Date of Posting: [Insert date of sending]
e. [F6] to validate

QPS reply to QFLAG Intel reports:

Not Current

QPS will email back with investigation findings, following actions required:
1. Specimen note detailing QPS investigation findings (eg. “Email received from XXXXXXX, contamination event confirmed – refer to scanned email”)
2. Scan QPS email response to AUSLAB under the relevant barcode
3. Add UR Note if applicable: “Quality Flags noted for XXXXXX refer to specimen notes”
4. If applicable add an additional EXH line (eg. Quality Control failure, refer to QPS) and request the reviewer to validate the additional EXH line.

9.19 Example of combined preamble and Appendix for Civil casework report

XX The following information is provided to assist in the understanding of the contents of this statement.

DNA Profiling
DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The testing system used at DNA Analysis looks at 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The remaining region gives an indication as to the gender of the donor. This technique involves the use of a method known as Polymerase Chain Reaction (PCR), used to amplify these specific regions of the DNA to produce numerous copies. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two peaks for each STR, one inherited from their mother and one inherited from their father, unless the same STR is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Not Current

Touch DNA / Transfer of DNA
When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered by a swab, tape lift or excision depending upon the nature of the surface in question, and the sample can then be subjected to DNA profiling.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to FSS for the purposes of conducting DNA analysis.

DNA Analysis operates under the premise that QPS are responsible for item prioritisation, sample selection, selection of screening/sampling methods, anti-contamination procedures and the application of Standard Operating Procedures (SOPs) on work undertaken on the items/samples prior to submission to FSS DNA Analysis. As such, Forensic Biologists may not be able to provide information or opinion on possible biological origin of DNA profiles that may be obtained from these samples.

Some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. This occurs at the discretion of the QPS. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

Analytical Techniques

In order to perform the DNA profiling process, DNA must first be isolated from the sub-sample obtained during examination. This is achieved by separating the cell containing the DNA from the substrate (eg, swab, tape lift, fabric, etc) by performing a number of washes and agitative steps. The cell is then broken open to release the DNA. During this step the DNA is separated from the cellular debris. This phase is termed ‘DNA Extraction’.

The next phase is known as ‘Quantitation’ and is used to assess the amount of DNA within the sample. This information is then used to optimise the next stage called ‘Amplification’. Amplification is a process designed to make many copies of the targeted DNA regions within the extracted DNA of a specific sample. This procedure is based on the laboratory technique called the ‘Polymerase Chain Reaction’ (PCR) and can be thought of as a DNA photocopier.

The amplified DNA is then separated based on the size of the targeted DNA fragments during a process called ‘Capillary Electrophoresis’. This information is then analysed during a data analysis process aimed at labelling the individual fragments according to the relative size.

The result of the above processes is a DNA profile which displays as peaks on a graph which are assessed by a reporting scientist.

Reporting DNA Analyst

It is the role of a reporting scientist to interpret the results obtained from the above processes and includes assessment of possible reworking strategies, if required, to gain further information from a sample. The DNA results are then able to be compared to reference DNA

Not Current

profiles associated to the case, and statistical analysis evaluating the strength of the evidence can be performed.

Statistical Analysis of DNA profiles

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together with any other person who has the same reference DNA profile, can be considered as a potential contributor of the DNA.

The evidential significance of such a match is assessed by considering two competing propositions:

Proposition 1: the DNA originated from the person of interest;
Proposition 2: the DNA originated from someone other than and unrelated to the person of interest.

The resultant figure (termed the 'Likelihood Ratio') compares the two opposing propositions. The likelihood ratio describes how likely the DNA profile obtained from the biological material is to have occurred if proposition 1 were true (the DNA originated from the person of interest) rather than if proposition 2 were true (the DNA originated from someone other than and unrelated to the person of interest).

The likelihood ratio is calculated by taking into account the characteristics of the DNA profile and the frequency of occurrence of the individual DNA components that make up the DNA profile.

If less than the 21 regions of DNA are seen in a DNA profile (termed an 'incomplete or partial DNA profile') this will be reflected by a smaller likelihood ratio than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete the DNA profile, the greater the likelihood of obtaining the DNA profile if it came from someone other than, and unrelated to the person of interest.

DNA profiles assumed to originate from more than one person (mixed DNA profiles)

In order to assess whether a person could or could not have contributed to a mixed DNA profile, a set of competing propositions (similar to a single source DNA profile) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

The likelihood ratio will not always favour proposition 1 (the DNA originated from the person of interest and an unknown person unrelated to the person of interest). The likelihood ratio could

Not Current

favour proposition 2 (the DNA originated from two unknown people unrelated to the person of interest).

In certain circumstances, if the ownership of an item is established or if the sample was collected from an intimate area, then it may be possible to make the reasonable assumption that the donor of the sample has contributed DNA to the resultant mixed DNA profile. In these cases, a mixed DNA profile can be 'conditioned' on the DNA profile of the known donor, such that the presence of the DNA components corresponding with the donor's reference DNA profile can be factored into the statistical interpretation. This may facilitate a more meaningful statistical analysis of potential second and/or third contributors to the DNA profile. In this situation, the likelihood ratio is based on the following propositions, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then the DNA profile will require additional statistical interpretation.

Datasets Used in Statistical Analyses

Three validated datasets consisting of DNA profiles obtained from individuals of the Australian Caucasian, Aboriginal and South-East Asian populations are used to calculate the likelihood ratio, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for South East Asian dataset, and θ=0.05 for the Australian Aboriginal dataset. Unless otherwise specified, the default dataset used in DNA Analysis is the Australian Caucasian dataset. The other datasets are available upon request.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated it allows for any difference the new dataset could make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "more than, or at least 100 billion times more likely". The actual calculated figure can be provided upon request.

The above listed values for the theta cannot account for close blood relatives. Closely related people, such as siblings, will have a greater chance of sharing similar components within their DNA profiles. However, due to the random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions would be very small. As this relationship becomes more distant, the probability of two relatives having the same DNA profile becomes smaller still. If it is thought that a close blood relative may have been

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involved, a more meaningful approach would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime stain DNA profile.

Quality

All testing completed by the Forensic DNA Analysis laboratory is conducted under a strict quality framework to ensure the utmost reliability and integrity of all results released. This is achieved by establishing and maintaining the following quality measures, to name a few:

- Use of Standard Operating Procedures (SOPs)
- Intensive training schedule for staff associated to individual processes to ensure that only competent staff are conducting the tasks
- Maintenance of continuity throughout the processes with the use of electronic batch /audit records and tracking of each exhibit/sample
- Review of all work and results prior to release
- Use of control and blank samples with every analytical processes
- Internal validation of all techniques utilised within the Forensic DNA laboratory
- Establishment and maintenance of staff and QPS DNA elimination databases
- Environmental monitoring and cleaning of the individual laboratory spaces
- Use of Personal Protective Equipment (PPE) throughout sample processing
- Restricted access to the laboratory including specific areas within the laboratory

Chain of Custody

All Forensic DNA Analysis case files and exhibits are electronically tracked, monitored and securely stored to ensure that the appropriate chain of custody and continuity measures are maintained. The QPS case number and sample submission information is provided from the QPS via an electronic interface to FSS, and this information is cross-checked against labelling on exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site which has access controlled and monitored by a security team. Records of Visitors to Forensic DNA Analysis are retained.

Accreditation

Forensic DNA Analysis first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998, and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessments (every 3 years) and surveillance visits (18 months).

NATA accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories that demonstrate compliance with the standard have shown that they can competently perform activities and testing within the scope of their accreditation.

The parameters assessed during accreditation include:

- Organisation and management
- Quality management system
- Personnel

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- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 standard refer to Standards Australia.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:

http://www.nata.asn.au/publications

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9.20 Uniform Civil Procedure Rules 1999 – Sect 428

Uniform Civil Procedure Rules 1999 – Sect 428

In accordance with the Uniform Civil Procedure Rules 1999 – Sect 428, I confirm that:

(a) the factual matters stated in the report are, as far as the expert knows, true; and

(b) the expert has made all enquiries considered appropriate; and

(c) the opinions stated in the report are genuinely held by the expert; and

(d) the report contains reference to all matters the expert considers significant; and

(e) the expert understands the expert’s duty to the court and has complied with the duty.

……………………………………………..

XXXXX

Signed at BRISBANE on DD Month YYYY

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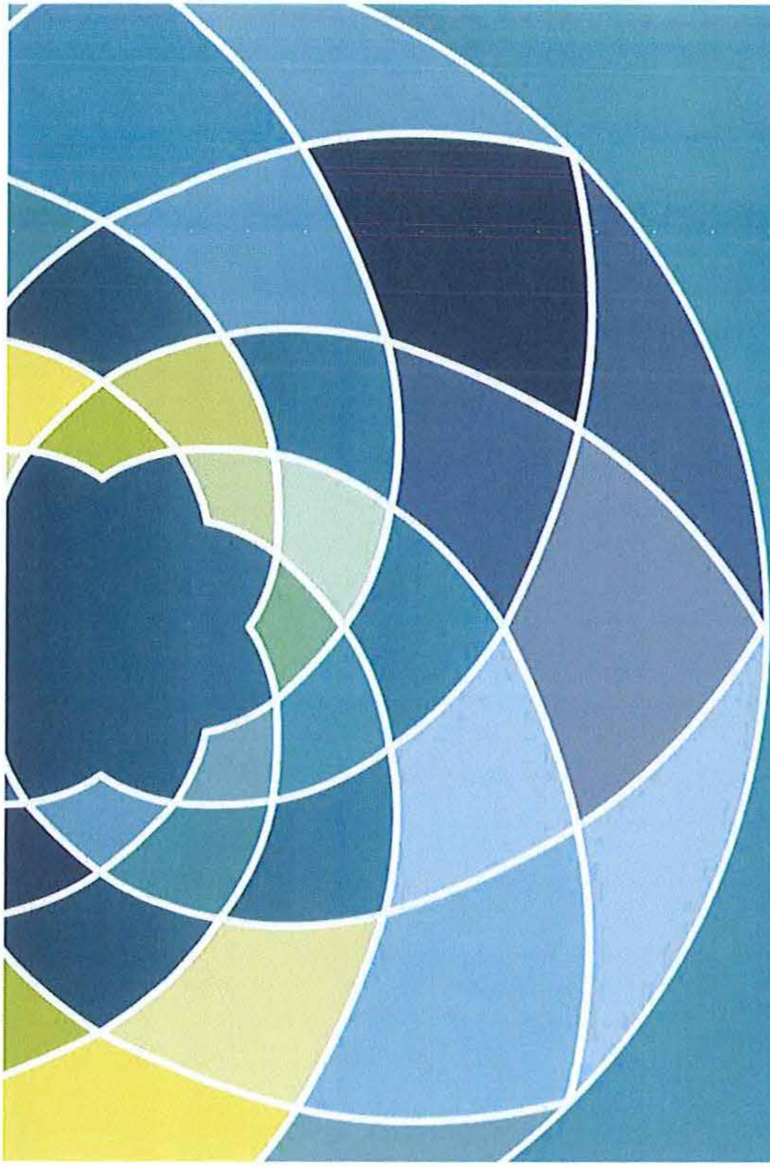

HealthSupport
Queensland

Validation of Quantifiler® Trio

Pierre Acedo, Megan Mathieson, Luke Ryan and Cathie Allen
September 2015

Great state. Great opportunity.

Queensland Government

Validation of Quantifiler® Trio for Casework and Reference Samples Published by the State of Queensland (Queensland Health), September 2015.

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Contents

1. Abstract

Life Technologies Quantifiler® Trio is an improved DNA quantification kit designed to simultaneously quantify the total amount of amplifiable human DNA and human male DNA in a sample. It uses multiple copy target loci for improved detection sensitivity.

The validation of Quantifiler® Trio was undertaken to assess the capabilities of the kit in determining the quantities of human DNA and/or male DNA, the quantities of human male and female DNA in mixture samples and DNA quality, with respect to the levels of degradation and inhibition. Additionally, the Promega Genomic Male DNA G147A standards were also tested to assess whether its performance in conjunction with Quantifiler® Trio is comparable or superior to Life Technologies standards included in the kits.

A total of seven experiments were performed in the validation of Quantifiler® Trio, and was used to quantify the following samples:

- DNA from three Standard Reference Material® 2372 DNA components (SRM) supplied by the National Institute of Standards and Technology (NIST) (Components A, B and C)
- Male and Female samples
- Male and Female mixture samples
- Samples containing known inhibiting substances
- Degraded samples

Overall, the validation has shown that Quantifiler® Trio (using Life Technology standards) is a sensitive DNA quantification kit that is able to accurately detect DNA quantity, low levels of male DNA in mixture samples, as well as accurately measure inhibition and degradation. During this validation the manufacturer modified the formulation of the internal positive control (IPC). Further testing was performed and the modification of the IPC did not affect the performance of the kit and the overall quality of the results. The Quantifiler® Trio DNA Quantification kit is recommended to be routinely used in the laboratory within DNA Analysis to quantify casework and reference samples.

2. Introduction

Forensic DNA Analysis currently uses Life Technology Quantifiler® Human DNA Quantification Kit (Quantifiler® Human) for the quantification of DNA extracts from casework and reference samples. The Quantifiler® Trio DNA Quantification Kit (Quantifiler® Trio) is an updated quantification kit which is designed to simultaneously quantify the total amount of human DNA and human male DNA.

Quantifiler® Trio provides DNA quantification results for three DNA targets:

- Short Autosomal Target (SAT) – whole human DNA quantification, previously included in Quantifiler® Human.

- Large Autosomal Target (LAT) – whole human DNA quantification, not included in Quantifiler® Human.
- Y Target – male DNA quantification, not included in Quantifiler® Human.

The manufacturer reports that Quantifiler® Trio has a number of benefits when compared to Quantifiler® Human:

1. Quantifiler® Human uses a single copy loci for the human target, therefore the quantification of low level DNA samples could be affected by stochastic effects and give false negative quantification results. Quantifiler® Trio uses multiple copy target loci to overcome stochastic effects and to provide increased sensitivity when compared to Quantifiler® Human [1].
2. Quantifiler® Trio uses the ratio of quantification results for the SAT and LAT to give an estimate of degradation in a sample, expressed as the Degradation Index (DI). The use of DI is based on degradation preferentially affecting molecular weight loci [3], which results in higher quantification results for the SAT than the LAT. DI results may be able to be used to guide sample workflows which may streamline processing [4].
3. Quantifiler® Trio also includes a Y Target, not included in Quantifiler® Human. This provides a quantification concentration for male DNA in a sample, including in mixtures of male and female DNA, which in the future will enable the identification of samples suitable for testing with Y-STR analysis.
4. The new HID Real-Time PCR Analysis Software, used for Quantifiler® Trio analyses, uses an IPCCT flag to identify samples which may be inhibited [1].
5. The recent modification from a super-coiled IPC to a linearised IPC within the Quantifiler® Trio kit improves the overall stability of the kit by maintaining the IPCCt over extended long-term storage[8].

National Institute of Standards and Technology (NIST) human DNA quantitation standards were used throughout this project as a standard of known DNA concentration. In particular the NIST sets were used to assess the accuracy of Life Technologies and Promega quantification standards.

3. Resources

The following resources were used for this validation.

3.1 Reagents

- FTA negative controls (Forensic DNA Analysis, QLD, AU)
- 5 % v/v Hypo 10 bleach (elite Chemicals Pty. Ltd.,Lytton, QLD, AU)
- 5 % v/v Trigene II (CEVA DEIVET Pty. Ltd., Seven Hills, NSW, AU)
- Proteinase K (20mg/mL) (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Dithiothreitol (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Trigene (Medichem International, Kent, GB)
- Ethanol (Recochem Incorporated, Wynnum, QLD,AU)
- Bleach (Ionics Australasia Pty Ltd., Lytton, QLD, AU)

- Amphyl (Rickitt Benckiser Inc. Parsippany, NJ, US)
- Sarcosyl (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Nanopure water (Forensic DNA Analysis, Brisbane, QLD, AU)
- Positive extraction controls (Forensic DNA Analysis, Brisbane, QLD, AU)
- TNE (Forensic DNA Analysis, Brisbane, QLD, AU)
- TE-4 (Forensic DNA Analysis, Brisbane, QLD, AU)
- Hi-Di™ Formamide (Applied Biosystems®, Foster City, CA, US)
- 3130 POP-4™ Polymer (Applied Biosystems®, Foster City, CA, US)
- Running Buffer (Applied Biosystems®, Foster City, CA, US)
- Promega PowerPlex® 21 system (Promega Corp., Madison, WI, US)
- Promega CC5 Internal Lane Standard 500 (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 5 Dye Matrix Standard (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 21 Allelic Ladder Mix (Promega Corp., Madison, WI, US)
- 2800M Control DNA, 10ng/µl (Promega Corp., Madison, WI, US)
- Water amplification grade (Promega Corp., Madison, WI, US)
- Anode buffer container (ABC) (Applied Biosystems®, Foster City, CA, US)
- Cathode buffer container (CBC) (Applied Biosystems®, Foster City, CA, US)
- Conditioning reagent (Applied Biosystems®, Foster City, CA, US)
- HID 5-DYE Installation Standard (Applied Biosystems®, Foster City, CA, USA)
- Quantifiler® Trio DNA Quantification Kit (Applied Biosystems®, Foster City, CA, USA)
- Quantifiler® Human DNA Quantification Kit (Applied Biosystems®, Foster City, CA, USA)

3.2 Materials

- 96-well PCR micro-plates (Axygen Scientific Inc., Union City, CA, US)
- 96-well plate Septa mats (Axygen Scientific Inc., Union City, CA, US)
- Sterile 2 mL screw-cap tubes (Axygen Scientific Inc., Union City, CA, US)
- Sterile 1.5mL screw-cap tubes (Axygen Scientific Inc., Union City, CA, US)
- Sterile 5 mL screw-cap tubes (Axygen Scientific Inc., Union City, CA, US)
- ART Filtered 1000, 300 & 20p pipette tips (Molecular BioProducts Inc., San Diego, CA, US)
- One Touch filtered 10 µL and 200 µL pipette tips (Quantum Scientific Lab Advantage, Murrarie, QLD, AU)
- F1-ClipTip pipette tips 10 µL (Thermo Fisher Scientific Inc, Waltham, MA, US)
- Rediwipes (Cello Paper Pty. Ltd., Fairfield, NSW, AU)
- Adhesive film (QIAGEN, Hilden, DE)
- Sterile conductive filtered Roborack 25µL disposable tips (PerkinElmer, Downers Grove, IL, USA)
- Sterile conductive filtered Roborack 175µL disposable tips (PerkinElmer, Downers Grove, IL, USA)
- MicroAmp® Optical 96- well Reaction plate (Applied Biosystems®, Foster City, CA, USA)
- Septa cathode buffer container 3500xL series (Applied Biosystems®, Foster City, CA, USA)

3.3 Equipment

- BSD Duet 600 Series II (BSD Robotics, AU)
- LaboGene Scanspeed 1248 Centrifuge (Labgear, Lynge, Denmark)
- Hot-block (Ratek Instruments Pty. Ltd., Boronia, VIC, AU)
- Biological safety cabinets class II (Labsystems)
- Refrigerators and freezers (Westinghouse Pty. Ltd., AU)
- FTA® collection kits (Whatman)
- GeneMapper-IDX ver.1.1.1 (Applied Biosystems®, Foster City, CA, USA)
- AB 7500 Real Time PCR System (Applied Biosystems®, Foster City, CA, US)
- GeneAmp PCR system 9700 (Applied Biosystems®, Foster City, CA, USA)
- ABI 3130xl Genetic Analyzer (Applied Biosystems®, Foster City, CA, USA)
- STORstar instrument (Process Analysis & Automation, Hampshire, GB)
- MultiPROBE II PLUS HT EX with Gripper Integration Platform (PerkinElmer, Downers Grove, IL, US)
- Thermomixer (Eppendorf AG, Hamburg, DE)
- MixMate (Eppendorf AG, Hamburg, DE)
- Vortex (Ratek Instruments Pty Ltd, Melbourne, VIC, AU)
- Micro centrifuge (Tomy, Tokyo, JP)
- Pipettes (Eppendorf, Hamburg, DE and Thermo Fisher Scientific (Finnpipette), Waltham, MA, US)

4. Methods

4.1 Quantification Standards

4.1.1 Creation of Quantifiler Trio Standard Sets

Ten Quantifiler® Trio Standard Sets were prepared by diluting five sets of Quantifiler THP DNA Standard in Quantifiler THP DNA Dilution Buffer that are included within the kit. These were prepared manually by serial dilution to create 50, 5, 0.5, 0.05 and 0.005 ng/µL dilutions. These standard sets were used within one week of preparation for Experiment 1 and 2, with the most stable standard further utilised in Experiment 3, 4, 5 and 6.

4.1.2 Creation of Promega Standard Sets

Ten Promega Standard Sets were prepared by diluting five sets of Promega Genomic Male DNA G147A with TE-4 buffer and glycogen. These were prepared manually by serial dilution to create 50, 5, 0.5, 0.05 and 0.005 ng/µL dilutions. These standard sets were used within one week of preparation for Experiment 1 and 2.

4.2 Samples

4.2.1 Creation of NIST Samples - Set A, B and C

NIST sets A, B and C were prepared manually by serial dilution to create 5, 1, 0.5, 0.1, 0.01, 0.001 and 0.0001 ng/µL dilutions. These were prepared by diluting NIST Standard Reference Material® 2372 Components A, B and C with TE-4 buffer.

4.2.2 Creation of Male and Female Samples

Five male and five female Reference FTA buccal samples which have been submitted by Queensland Police Service for routine testing were selected and extracted using the DNA IQ™ Casework Pro Kit for Maxwell®16 according to QIS 29344 "DNA IQ™ Extraction using the Maxwell®16".

The extracted samples were pooled according to QIS 24012 "Miscellaneous Analytical Section Tasks".

Quantification reactions of the male and female extracts were performed as per section 4.3.1.

Serial dilutions of the extracts were performed using TE-4 buffer to create 0.09, 0.07, 0.05, 0.03, 0.01, 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002 and 0.001 ng/µL dilutions.

Two sets of male:female mixtures were prepared from one male and one female extracts as above. Each set with the following male:female ratios: 4000:1, 2000:1, 1500:1, 1000:1, 100:1, 20:1, 10:1, 5:1 ,1:1, 1:5, 1:10, 1:20, 1:100, 1:1000, 1:1500, 1:2000 and 1:4000.

4.2.3 Inhibitor Samples

Humic Acid

Five Humic Acid samples with concentrations 1% (w/v) (14.74 x 10^7 ng/ µL), 5% (w/v) (73.7 x 10^6 ng/µL), 10% (w/v) (17.74 x 10^8 ng/µL), 15% (w/v) (22.11 x 10^8 ng/µL) and 20% (w/v) (29.48 x 10^8 ng/µL) were prepared by adding stock Humic Acid with nano pure water and male DNA samples utilised in Experiment 3.

After reviewing the results of Experiment 5, the concentration of Humic Acid was determined to be significantly above what is likely to be found in normal casework samples. Therefore five additional Humic Acid samples were prepared. From a 90 ng/uL stock solution of Humic Acid, five samples with concentrations 20 ng/µL, 30 ng/µL, 40 ng/µL, 60 ng/µL and 80 ng/µL were prepared.

Hematin

From a 1000µM stock solution of Hematin, five Hematin samples with concentrations 50 µM, 75 µM, 100 µM, 125 µM and 150 µM were prepared by diluting stock Hematin with nano pure water and male DNA samples utilised in Experiment 3.

Ethanol

Five Ethanol samples with concentrations 1% (v/v), 5% (v/v), 10% (v/v), 15% (v/v) and 20% (v/v) were prepared by diluting stock 70% ethanol with nano pure water and male DNA samples utilised in Experiment 3. 70% ethanol is routinely used for decontamination in the laboratory.

Trigene Advance

Five Trigene Advance samples with concentrations 1% (v/v), 5% (v/v), 10% (v/v), 15% (v/v) and 20% (v/v) were prepared by diluting 5% Trigene Advance with nanopure water and male DNA samples utilised in Experiment 3. 5% Trigene Advance is routinely used for decontamination in the laboratory.

Seminal Fluid

Five Semen samples with concentrations 1% (v/v), 5% (v/v), 10% (v/v), 15% (v/v) and 20% (v/v) were prepared from a Semen stock solution with nano pure water and male DNA samples utilised in Experiment 3. The Semen stock solution is the laboratory's in-house semen positive control prepared as a 1/30 dilution.

Table 1 displays the concentrations of the various inhibitors described above.

Table 1: Samples prepared for Inhibition Experiment.

Sample	DNA Input (in quant reaction)	Inhibitor Concentration (in extract)
Control	0.2 ng	0
Humic Acid-1	0.2 ng	20 ng/µL
Humic Acid-2	0.2 ng	30 ng/µL
Humic Acid-3	0.2 ng	40 ng/µL
Humic Acid-4	0.2 ng	60 ng/µL
Humic Acid-5	0.2 ng	80 ng/µL
Hematin-1	0.2 ng	50 µM
Hematin-2	0.2 ng	75 µM
Hematin-3	0.2 ng	100 µM
Hematin-4	0.2 ng	125 µM
Hematin-5	0.2 ng	150 µM
Ethanol-1	0.2 ng	1% (v/v)
Ethanol-2	0.2 ng	5% (v/v)
Ethanol-3	0.2 ng	10% (v/v)

Ethanol-4	0.2 ng	15% (v/v)
Ethanol-5	0.2 ng	20% (v/v)
Trigene Advance-1	0.2 ng	1% (v/v)
Trigene Advance-2	0.2 ng	5% (v/v)
Trigene Advance-3	0.2 ng	10% (v/v)
Trigene Advance-4	0.2 ng	15% (v/v)
Trigene Advance-5	0.2 ng	20% (v/v)
Semen-1	0.2 ng	1% (v/v)
Semen-2	0.2 ng	5% (v/v)
Semen-3	0.2 ng	10% (v/v)
Semen-4	0.2 ng	15% (v/v)
Semen-5	0.2 ng	20% (v/v)

4.3 Quantification

4.3.1 Quantifiler® Human Kit

Quantification reactions were performed using the Quantifiler® Human DNA Quantification Kit. The set up was performed by manual methods and using the MultiPROBE II plus HT EX platform according to QIS 19977 “Quantification of Extracted DNA using the Quantifiler® Human DNA Quantitation Kit”.

4.3.2 Quantifiler® Trio Kit

Quantification reactions were performed using the Quantifiler® Trio DNA Quantification Kit according to the manufacturer’s manual [1]. The reaction set ups were prepared by manual methods and using the MultiPROBE II plus HT EX platform according to QIS 19977 “Quantification of Extracted DNA using the Quantifiler® Human DNA Quantitation Kit”, incorporating a customised program.

All quantification data were analysed using the HID Real-Time PCR Analysis Software v1.2 according to the manufacturer’s manual.

4.4 DNA Amplification

All amplification set ups were prepared manually according to QIS 31511 “Amplification of Extracted DNA using the PowerPlex®21 System”.

Table 2 lists the PCR cycling conditions utilised in this validation.

Table 2: PCR cycling conditions for PowerPlex®21 System.

PowerPlex® 21 Kit	**Standard**
GeneAmp 9700 mode	Max
	30 cycles
Activation	96°C for 1 minute
Cycling	94°C for 10 seconds
	59°C for 1 minute
	72°C for 30 seconds
Extension	60°C for 10 minutes
	4°C Soak

4.5 DNA Fragment Analysis

Plates for DNA fragment analysis were prepared and the PCR fragments separated by capillary electrophoresis (CE) according to QIS 15998 “Procedure for the Use and Maintenance of the AB 3130xl Genetic Analysers”.

Table 3 outlines the 3130xl Genetic Analyser running conditions.

Table 3: 3130xl CE protocol conditions.

Injection time	**Injection voltage**	**Run time**
5s	**3kV**	**1500s**

4.6 Profile Interpretation

All samples were CE quality checked as per QIS 17130 “CE Quality Check” and interpreted according to QIS 31389 “STR fragment analysis of PowerPlex®21 profiles using Genemapper® ID-X software.”

5. Experimental Design

5.1 Experiment 1: Assessment of Quantification Standards

The NIST sets A, B and C (see section 4.2.1) were quantified using the Quantifiler® Trio Kit according to section 4.3.2. The Slope, Y-intercept and the R2 value were also calculated for each of the standard sets.

The NIST sets were quantified in duplicate and the results calculated from each of the ten Life Technologies (LT) Quantifiler Trio standard sets, referred to as LT1 – LT10 (see Section 4.1.1). The results were also calculated using each of the ten Promega (PR) standards sets, referred to as PR1 – PR10 (see Section 4.1.2). A total of four quantification plates including reagent blanks were manually prepared as shown in Figure 1 – Figure 4. All plates were run and analysed on 7500A.

The average short autosomal target (SAT) and the Ct values were calculated for each NIST sample, comparing the results between the LT standard sets and the PR standard sets. The average inaccuracy percentages were also calculated and the results compared between both manufacturers using the Equation 1.

Equation 1:

% Inaccuracy = [(SAT result – expected concentration) / expected concentration x 100]

	1	2	3	4	5	6	7	8	9	10	11	12
A	LT 1-1 50 ng/µL	LT 1-1 50 ng/µL	PR 1-1 50 ng/µL	PR 1-1 50 ng/µL	LT 2-1 50 ng/µL	LT 2-1 50 ng/µL	PR 2-1 50 ng/µL	PR 2-1 50 ng/µL	LT 3-1 50 ng/µL	LT 3-1 50 ng/µL	NIST A 0.0001 ng/µL	NIST A 0.0001 ng/µL
B	LT 1-2 5.000 ng/µL	LT 1-2 5.000 ng/µL	PR 1-2 5.000 ng/µL	PR 1-2 5.000 ng/µL	LT 2-2 5.000 ng/µL	LT 2-2 5.000 ng/µL	PR 2-2 5.000 ng/µL	PR 2-2 5.000 ng/µL	LT 3-2 5.000 ng/µL	LT 3-2 5.000 ng/µL	NIST B 0.0001 ng/µL	NIST B 0.0001 ng/µL
C	LT 1-3 0.500 ng/µL	LT 1-3 0.500 ng/µL	PR 1-3 0.500 ng/µL	PR 1-3 0.500 ng/µL	LT 2-3 0.500 ng/µL	LT 2-3 0.500 ng/µL	PR 2-3 0.500 ng/µL	PR 2-3 0.500 ng/µL	LT 3-3 0.500 ng/µL	LT 3-3 0.500 ng/µL	NIST C 0.0001 ng/µL	NIST C 0.0001 ng/µL
D	LT 1-4 0.050 ng/µL	LT 1-4 0.050 ng/µL	PR 1-4 0.050 ng/µL	PR 1-4 0.050 ng/µL	LT 2-4 0.050 ng/µL	LT 2-4 0.050 ng/µL	PR 2-4 0.050 ng/µL	PR 2-4 0.050 ng/µL	LT 3-4 0.050 ng/µL	LT 3-4 0.050 ng/µL	Reagent Blank	Reagent Blank
E	LT 1-5 0.005 ng/µL	LT 1-5 0.005 ng/µL	PR 1-5 0.005 ng/µL	PR 1-5 0.005 ng/µL	LT 2-5 0.005 ng/µL	LT 2-5 0.005 ng/µL	PR 2-5 0.005 ng/µL	PR 2-5 0.005 ng/µL	LT 3-5 0.005 ng/µL	LT 3-5 0.005 ng/µL	Reagent Blank	Reagent Blank
F	NIST A 5 ng/µL	NIST A 5 ng/µL	NIST A 1 ng/µL	NIST A 1 ng/µL	NIST A 0.5 ng/µL	NIST A 0.5 ng/µL	NIST A 0.1 ng/µL	NIST A 0.1 ng/µL	NIST A 0.01 ng/µL	NIST A 0.01 ng/µL	NIST A 0.001 ng/µL	NIST A 0.001 ng/µL
G	NIST B 5 ng/µL	NIST B 5 ng/µL	NIST B 1 ng/µL	NIST B 1 ng/µL	NIST B 0.5 ng/µL	NIST B 0.5 ng/µL	NIST B 0.1 ng/µL	NIST B 0.1 ng/µL	NIST B 0.01 ng/µL	NIST B 0.01 ng/µL	NIST B 0.001 ng/µL	NIST B 0.001 ng/µL
H	NIST C 5 ng/µL	NIST C 5 ng/µL	NIST C 1 ng/µL	NIST C 1 ng/µL	NIST C 0.5 ng/µL	NIST C 0.5 ng/µL	NIST C 0.1 ng/µL	NIST C 0.1 ng/µL	NIST C 0.01 ng/µL	NIST C 0.01 ng/µL	NIST C 0.001 ng/µL	NIST C 0.001 ng/µL

Figure 1: Plate map of LT1 – LT3 and PR1 – PR2 standards sets and NIST samples quantified using Quantifiler Trio reaction mix for Experiment 1 prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

	1	2	3	4	5	6	7	8	9	10	11	12
A	PR 3-1 50 ng/µL	PR 3-1 50 ng/µL	LT 4-1 50 ng/µL	LT 4-1 50 ng/µL	PR 4-1 50 ng/µL	PR 4-1 50 ng/µL	LT 5-1 50 ng/µL	LT 5-1 50 ng/µL	PR 5-1 50 ng/µL	PR 5-1 50 ng/µL	NIST A 0.0001 ng/µL	NIST A 0.0001 ng/µL
B	PR 3-2 5.000 ng/µL	PR 3-2 5.000 ng/µL	LT 4-2 5.000 ng/µL	LT 4-2 5.000 ng/µL	PR 4-2 5.000 ng/µL	PR 4-2 5.000 ng/µL	LT 5-2 5.000 ng/µL	LT 5-2 5.000 ng/µL	PR 5-2 5.000 ng/µL	PR 5-2 5.000 ng/µL	NIST B 0.0001 ng/µL	NIST B 0.0001 ng/µL
C	PR 3-3 0.500 ng/µL	PR 3-3 0.500 ng/µL	LT 4-3 0.500 ng/µL	LT 4-3 0.500 ng/µL	PR 4-3 0.500 ng/µL	PR 4-3 0.500 ng/µL	LT 5-3 0.500 ng/µL	LT 5-3 0.500 ng/µL	PR 5-3 0.500 ng/µL	PR 5-3 0.500 ng/µL	NIST C 0.0001 ng/µL	NIST C 0.0001 ng/µL
D	PR 3-4 0.050 ng/µL	PR 3-4 0.050 ng/µL	LT 4-4 0.050 ng/µL	LT 4-4 0.050 ng/µL	PR 4-4 0.050 ng/µL	PR 4-4 0.050 ng/µL	LT 5-4 0.050 ng/µL	LT 5-4 0.050 ng/µL	PR 5-4 0.050 ng/µL	PR 5-4 0.050 ng/µL	Reagent Blank	Reagent Blank
E	PR 3-5 0.005 ng/µL	PR 3-5 0.005 ng/µL	LT 4-5 0.005 ng/µL	LT 4-5 0.005 ng/µL	PR 4-5 0.005 ng/µL	PR 4-5 0.005 ng/µL	LT 5-5 0.005 ng/µL	LT 5-5 0.005 ng/µL	PR 5-5 0.005 ng/µL	PR 5-5 0.005 ng/µL	Reagent Blank	Reagent Blank
F	NIST A 5 ng/µL	NIST A 5 ng/µL	NIST A 1 ng/µL	NIST A 1 ng/µL	NIST A 0.5 ng/µL	NIST A 0.5 ng/µL	NIST A 0.1 ng/µL	NIST A 0.1 ng/µL	NIST A 0.01 ng/µL	NIST A 0.01 ng/µL	NIST A 0.001 ng/µL	NIST A 0.001 ng/µL
G	NIST B 5 ng/µL	NIST B 5 ng/µL	NIST B 1 ng/µL	NIST B 1 ng/µL	NIST B 0.5 ng/µL	NIST B 0.5 ng/µL	NIST B 0.1 ng/µL	NIST B 0.1 ng/µL	NIST B 0.01 ng/µL	NIST B 0.01 ng/µL	NIST B 0.001 ng/µL	NIST B 0.001 ng/µL
H	NIST C 5 ng/µL	NIST C 5 ng/µL	NIST C 1 ng/µL	NIST C 1 ng/µL	NIST C 0.5 ng/µL	NIST C 0.5 ng/µL	NIST C 0.1 ng/µL	NIST C 0.1 ng/µL	NIST C 0.01 ng/µL	NIST C 0.01 ng/µL	NIST C 0.001 ng/µL	NIST C 0.001 ng/µL

Figure 2: Plate map of LT4 – LT5 and PR3 – PR5 standards sets and NIST samples quantified using Quantifiler Trio reaction mix for Experiment 1 prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

	1	2	3	4	5	6	7	8	9	10	11	12
A	LT 6-1 50 ng/µL	LT 6-1 50 ng/µL	PR 6-1 50 ng/µL	PR 6-1 50 ng/µL	LT 7-1 50 ng/µL	LT 7-1 50 ng/µL	PR 7-1 50 ng/µL	PR 7-1 50 ng/µL	LT 8-1 50 ng/µL	LT 8-1 50 ng/µL	NIST A 0.0001 ng/µL	NIST A 0.0001 ng/µL
B	LT 6-2 5.000 ng/µL	LT 6-2 5.000 ng/µL	PR 6-2 5.000 ng/µL	PR 6-2 5.000 ng/µL	LT 7-2 5.000 ng/µL	LT 7-2 5.000 ng/µL	PR 7-2 5.000 ng/µL	PR 7-2 5.000 ng/µL	LT 8-2 5.000 ng/µL	LT 8-2 5.000 ng/µL	NIST B 0.0001 ng/µL	NIST B 0.0001 ng/µL
C	LT 6-3 0.500 ng/µL	LT 6-3 0.500 ng/µL	PR 6-3 0.500 ng/µL	PR 6-3 0.500 ng/µL	LT 7-3 0.500 ng/µL	LT 7-3 0.500 ng/µL	PR 7-3 0.500 ng/µL	PR 7-3 0.500 ng/µL	LT 8-3 0.500 ng/µL	LT 8-3 0.500 ng/µL	NIST C 0.0001 ng/µL	NIST C 0.0001 ng/µL
D	LT 6-4 0.050 ng/µL	LT 6-4 0.050 ng/µL	PR 6-4 0.050 ng/µL	PR 6-4 0.050 ng/µL	LT 7-4 0.050 ng/µL	LT 7-4 0.050 ng/µL	PR 7-4 0.050 ng/µL	PR 7-4 0.050 ng/µL	LT 8-4 0.050 ng/µL	LT 8-4 0.050 ng/µL	Reagent Blank	Reagent Blank
E	LT 6-5 0.005 ng/µL	LT 6-5 0.005 ng/µL	PR 6-5 0.005 ng/µL	PR 6-5 0.005 ng/µL	LT 7-5 0.005 ng/µL	LT 7-5 0.005 ng/µL	PR 7-5 0.005 ng/µL	PR 7-5 0.005 ng/µL	LT 8-5 0.005 ng/µL	LT 8-5 0.005 ng/µL	Reagent Blank	Reagent Blank
F	NIST A 5 ng/µL	NIST A 5 ng/µL	NIST A 1 ng/µL	NIST A 1 ng/µL	NIST A 0.5 ng/µL	NIST A 0.5 ng/µL	NIST A 0.1 ng/µL	NIST A 0.1 ng/µL	NIST A 0.01 ng/µL	NIST A 0.01 ng/µL	NIST A 0.001 ng/µL	NIST A 0.001 ng/µL
G	NIST B 5 ng/µL	NIST B 5 ng/µL	NIST B 1 ng/µL	NIST B 1 ng/µL	NIST B 0.5 ng/µL	NIST B 0.5 ng/µL	NIST B 0.1 ng/µL	NIST B 0.1 ng/µL	NIST B 0.01 ng/µL	NIST B 0.01 ng/µL	NIST B 0.001 ng/µL	NIST B 0.001 ng/µL
H	NIST C 5 ng/µL	NIST C 5 ng/µL	NIST C 1 ng/µL	NIST C 1 ng/µL	NIST C 0.5 ng/µL	NIST C 0.5 ng/µL	NIST C 0.1 ng/µL	NIST C 0.1 ng/µL	NIST C 0.01 ng/µL	NIST C 0.01 ng/µL	NIST C 0.001 ng/µL	NIST C 0.001 ng/µL

Figure 3: Plate map of LT6 – LT8 and PR6 – PR7 standards sets and NIST samples quantified using Quantifiler Trio reaction mix for Experiment 1 prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

	1	2	3	4	5	6	7	8	9	10	11	12
A	PR 8-1 50 ng/µL	PR 8-1 50 ng/µL	LT 9-1 50 ng/µL	LT 9-1 50 ng/µL	PR 9-1 50 ng/µL	PR 9-1 50 ng/µL	LT 10-1 50 ng/µL	LT 10-1 50 ng/µL	PR 10-1 50 ng/µL	PR 10-1 50 ng/µL	NIST A 0.0001 ng/µL	NIST A 0.0001 ng/µL
B	PR 8-2 5.000 ng/µL	PR 8-2 5.000 ng/µL	LT 9-2 5.000 ng/µL	LT 9-2 5.000 ng/µL	PR 9-2 5.000 ng/µL	PR 9-2 5.000 ng/µL	LT 10-2 5.000 ng/µL	LT 10-2 5.000 ng/µL	PR 10-2 5.000 ng/µL	PR 10-2 5.000 ng/µL	NIST B 0.0001 ng/µL	NIST B 0.0001 ng/µL
C	PR 8-3 0.500 ng/µL	PR 8-3 0.500 ng/µL	LT 9-3 0.500 ng/µL	LT 9-3 0.500 ng/µL	PR 9-3 0.500 ng/µL	PR 9-3 0.500 ng/µL	LT 10-3 0.500 ng/µL	LT 10-3 0.500 ng/µL	PR 10-3 0.500 ng/µL	PR 10-3 0.500 ng/µL	NIST C 0.0001 ng/µL	NIST C 0.0001 ng/µL
D	PR 8-4 0.050 ng/µL	PR 8-4 0.050 ng/µL	LT 9-4 0.050 ng/µL	LT 9-4 0.050 ng/µL	PR 9-4 0.050 ng/µL	PR 9-4 0.050 ng/µL	LT 10-4 0.050 ng/µL	LT 10-4 0.050 ng/µL	PR 10-4 0.050 ng/µL	PR 10-4 0.050 ng/µL	Reagent Blank	Reagent Blank
E	PR 8-5 0.005 ng/µL	PR 8-5 0.005 ng/µL	LT 9-5 0.005 ng/µL	LT 9-5 0.005 ng/µL	PR 9-5 0.005 ng/µL	PR 9-5 0.005 ng/µL	LT 10-5 0.005 ng/µL	LT 10-5 0.005 ng/µL	PR 10-5 0.005 ng/µL	PR 10-5 0.005 ng/µL	Reagent Blank	Reagent Blank
F	NIST A 5 ng/µL	NIST A 5 ng/µL	NIST A 1 ng/µL	NIST A 1 ng/µL	NIST A 0.5 ng/µL	NIST A 0.5 ng/µL	NIST A 0.1 ng/µL	NIST A 0.1 ng/µL	NIST A 0.01 ng/µL	NIST A 0.01 ng/µL	NIST A 0.001 ng/µL	NIST A 0.001 ng/µL
G	NIST B 5 ng/µL	NIST B 5 ng/µL	NIST B 1 ng/µL	NIST B 1 ng/µL	NIST B 0.5 ng/µL	NIST B 0.5 ng/µL	NIST B 0.1 ng/µL	NIST B 0.1 ng/µL	NIST B 0.01 ng/µL	NIST B 0.01 ng/µL	NIST B 0.001 ng/µL	NIST B 0.001 ng/µL
H	NIST C 5 ng/µL	NIST C 5 ng/µL	NIST C 1 ng/µL	NIST C 1 ng/µL	NIST C 0.5 ng/µL	NIST C 0.5 ng/µL	NIST C 0.1 ng/µL	NIST C 0.1 ng/µL	NIST C 0.01 ng/µL	NIST C 0.01 ng/µL	NIST C 0.001 ng/µL	NIST C 0.001 ng/µL

Figure 4: Plate map of LT9 – LT10 and PR8 – PR10 standards sets and NIST samples quantified using Quantifiler Trio reaction mix for Experiment 1 prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

5.2 Experiment 2 – Standard Stability Assessment

The five most accurate and stable standard sets from both LT and PR were chosen from Experiment 1 to be utilised in Experiment 2.

The NIST sets A, B and C (see section 4.2.1) were quantified using the Quantifiler® Trio Kit according to section 4.3.2 and the results were obtained from each of the standard curves generated.

The NIST sets were quantified in duplicate and the results calculated from the five LT standard sets, referred to as LT2, LT4, LT5, LT7 and LT9. The results of the NIST sets were also calculated from each of the five PR standard sets, referred to as PR1, PR2, PR4, PR6 and PR7. Utilising a customised WinPrep program, a total of two quantification plates were prepared - including four reagent blanks - using the MultiPROBE II plus HT EX as shown in Figure 5 and 6. The plates were run and analysed on 7500 A, with the Slope, Y-intercept and R2 value calculated for each standard set. The accepted slope ranges according to the Quantifiler® Trio DNA Quantification Kit User Guide [1] are as follows:

- SAT -3.0 to -3.6
- LAT -3.1 to -3.7
- Y-target -3.0 to -3.6

The plates were re-prepped and run each week for a total of 6 weeks to test the stability of the standards over time.

The slope of each standard curve from each standard set was compared to the acceptable slope ranges.

The average SAT, long autosomal target (LAT) and Y-target values were also calculated for each NIST sample each week. The data was combined to calculate an overall average, producing a percentage change each week at each concentration for both standards.

From the standard curve and NIST results the stability of each of the standard sets was assessed and determined.

	1	2	3	4	5	6	7	8	9	10	11	12
A	LT 2 50 ng/µL	LT 2 50 ng/µL	LT 4 50 ng/µL	LT 4 50 ng/µL	LT 5 50 ng/µL	LT 5 50 ng/µL	LT 7 50 ng/µL	LT 7 50 ng/µL	LT 9 50 ng/µL	LT 9 50 ng/µL	NIST A 0.0001 ng/µL	NIST A 0.0001 ng/µL
B	LT 2 5.000 ng/µL	LT 2 5.000 ng/µL	LT 4 5.000 ng/µL	LT 4 5.000 ng/µL	LT 5 5.000 ng/µL	LT 5 5.000 ng/µL	LT 7 5.000 ng/µL	LT 7 5.000 ng/µL	LT 9 5.000 ng/µL	LT 9 5.000 ng/µL	NIST B 0.0001 ng/µL	NIST B 0.0001 ng/µL
C	LT 2 0.500 ng/µL	LT 2 0.500 ng/µL	LT 4 0.500 ng/µL	LT 4 0.500 ng/µL	LT 5 0.500 ng/µL	LT 5 0.500 ng/µL	LT 7 0.500 ng/µL	LT 7 0.500 ng/µL	LT 9 0.500 ng/µL	LT 9 0.500 ng/µL	NIST C 0.0001 ng/µL	NIST C 0.0001 ng/µL
D	LT 2 0.050 ng/µL	LT 2 0.050 ng/µL	LT 4 0.050 ng/µL	LT 4 0.050 ng/µL	LT 5 0.050 ng/µL	LT 5 0.050 ng/µL	LT 7 0.050 ng/µL	LT 7 0.050 ng/µL	LT 9 0.050 ng/µL	LT 9 0.050 ng/µL	Reagent Blank	Reagent Blank
E	LT 2 0.005 ng/µL	LT 2 0.005 ng/µL	LT 4 0.005 ng/µL	LT 4 0.005 ng/µL	LT 5 0.005 ng/µL	LT 5 0.005 ng/µL	LT 7 0.005 ng/µL	LT 7 0.005 ng/µL	LT 9 0.005 ng/µL	LT 9 0.005 ng/µL	Reagent Blank	Reagent Blank
F	NIST A 5 ng/µL	NIST A 5 ng/µL	NIST A 1 ng/µL	NIST A 1 ng/µL	NIST A 0.5 ng/µL	NIST A 0.5 ng/µL	NIST A 0.1 ng/µL	NIST A 0.1 ng/µL	NIST A 0.01 ng/µL	NIST A 0.01 ng/µL	NIST A 0.001 ng/µL	NIST A 0.001 ng/µL
G	NIST B 5 ng/µL	NIST B 5 ng/µL	NIST B 1 ng/µL	NIST B 1 ng/µL	NIST B 0.5 ng/µL	NIST B 0.5 ng/µL	NIST B 0.1 ng/µL	NIST B 0.1 ng/µL	NIST B 0.01 ng/µL	NIST B 0.01 ng/µL	NIST B 0.001 ng/µL	NIST B 0.001 ng/µL
H	NIST C 5 ng/µL	NIST C 5 ng/µL	NIST C 1 ng/µL	NIST C 1 ng/µL	NIST C 0.5 ng/µL	NIST C 0.5 ng/µL	NIST C 0.1 ng/µL	NIST C 0.1 ng/µL	NIST C 0.01 ng/µL	NIST C 0.01 ng/µL	NIST C 0.001 ng/µL	NIST C 0.001 ng/µL

Figure 5: Plate map of LT2, LT4, LT5, LT7, LT9 standards sets and NIST samples quantified using Quantifiler Trio for Experiment 2 prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

	1	2	3	4	5	6	7	8	9	10	11	12
A	PR 1 50 ng/μL	PR 1 50 ng/μL	PR 2 50 ng/μL	PR 2 50 ng/μL	PR 4 50 ng/μL	PR 4 50 ng/μL	PR 6 50 ng/μL	PR 6 50 ng/μL	PR 7 50 ng/μL	PR 7 50 ng/μL	NIST A 0.0001 ng/μL	NIST A 0.0001 ng/μL
B	PR 1 5.000 ng/μL	PR 1 5.000 ng/μL	PR 2 5.000 ng/μL	PR 2 5.000 ng/μL	PR 4 5.000 ng/μL	PR 4 5.000 ng/μL	PR 6 5.000 ng/μL	PR 6 5.000 ng/μL	PR 7 5.000 ng/μL	PR 7 5.000 ng/μL	NIST B 0.0001 ng/μL	NIST B 0.0001 ng/μL
C	PR 1 0.500 ng/μL	PR 1 0.500 ng/μL	PR 2 0.500 ng/μL	PR 2 0.500 ng/μL	PR 4 0.500 ng/μL	PR 4 0.500 ng/μL	PR 6 0.500 ng/μL	PR 6 0.500 ng/μL	PR 7 0.500 ng/μL	PR 7 0.500 ng/μL	NIST C 0.0001 ng/μL	NIST C 0.0001 ng/μL
D	PR 1 0.050 ng/μL	PR 1 0.050 ng/μL	PR 2 0.050 ng/μL	PR 2 0.050 ng/μL	PR 4 0.050 ng/μL	PR 4 0.050 ng/μL	PR 6 0.050 ng/μL	PR 6 0.050 ng/μL	PR 7 0.050 ng/μL	PR 7 0.050 ng/μL	Reagent Blank	Reagent Blank
E	PR 1 0.005 ng/μL	PR 1 0.005 ng/μL	PR 2 0.005 ng/μL	PR 2 0.005 ng/μL	PR 4 0.005 ng/μL	PR 4 0.005 ng/μL	PR 6 0.005 ng/μL	PR 6 0.005 ng/μL	PR 7 0.005 ng/μL	PR 7 0.005 ng/μL	Reagent Blank	Reagent Blank
F	NIST A 5 ng/μL	NIST A 5 ng/μL	NIST A 1 ng/μL	NIST A 1 ng/μL	NIST A 0.5 ng/μL	NIST A 0.5 ng/μL	NIST A 0.1 ng/μL	NIST A 0.1 ng/μL	NIST A 0.01 ng/μL	NIST A 0.01 ng/μL	NIST A 0.001 ng/μL	NIST A 0.001 ng/μL
G	NIST B 5 ng/μL	NIST B 5 ng/μL	NIST B 1 ng/μL	NIST B 1 ng/μL	NIST B 0.5 ng/μL	NIST B 0.5 ng/μL	NIST B 0.1 ng/μL	NIST B 0.1 ng/μL	NIST B 0.01 ng/μL	NIST B 0.01 ng/μL	NIST B 0.001 ng/μL	NIST B 0.001 ng/μL
H	NIST C 5 ng/μL	NIST C 5 ng/μL	NIST C 1 ng/μL	NIST C 1 ng/μL	NIST C 0.5 ng/μL	NIST C 0.5 ng/μL	NIST C 0.1 ng/μL	NIST C 0.1 ng/μL	NIST C 0.01 ng/μL	NIST C 0.01 ng/μL	NIST C 0.001 ng/μL	NIST C 0.001 ng/μL

Figure 6: Plate map of PR1, PR2, PR4, PR6, PR7 standards sets and NIST samples quantified using Quantifiler Trio for Experiment 2 prepared in a 96-well plate. The concentration of each in ng/μl is shown. "Reagent Blank" denotes a well containing master mix only.

5.3 Experiment 3 – Sensitivity (LOD) and Mixture Studies

5.3.1 Experiment 3a – Single Source Sensitivity (LOD)

Five male (M1-M5) and five female (F1-F5) reference FTA samples were selected, extracted in duplicate and pooled after extraction (see section 4.2.2). The samples were quantified in duplicate using Quantifiler® Human DNA Quantification Kit (see section 4.3.1).

Based on the Quantifiler® Human results, serial dilutions were calculated and prepared with TE-4 buffer producing samples ranging in concentrations from 0.09 ng/μL to 1pg/μL (see section 4.2.2).

All male and female samples were quantified in duplicate using the Quantifiler® Trio Kit according to section 4.3.2 and the results were obtained using the LT2 standard set utilised in Experiment 1 and 2.

A total of four quantification plates were prepared manually and are shown in Figure 7 - 10 below, including two reagent blanks on each plate. All plates were run and analysed on 7500A.

The average SAT, LAT, Y-target and the Ct values were calculated for each male and female sample to determine the Quantifiler® Trio Kit's level of detection (LOD).

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	M 1-7 0.008 ng/µL	M 1-1 0.09 ng/µL	M 1-9 0.006 ng/µL	M 2-3 0.05 ng/µL	M 2-11 0.004 ng/µL	M 2-5 0.01 ng/µL	M 2-13 0.002 ng/µL	M 3-7 0.008 ng/µL	M 3-1 0.09 ng/µL	M 3-9 0.006 ng/µL
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	M 1-8 0.007 ng/µL	M 1-2 0.07 ng/µL	M 1-10 0.005 ng/µL	M 2-4 0.03 ng/µL	M 2-12 0.003 ng/µL	M 2-6 0.009 ng/µL	M 2-14 0.001 ng/µL	M 3-8 0.007 ng/µL	M 3-2 0.07 ng/µL	M 3-10 0.005 ng/µL
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	M 1-9 0.006 ng/µL	M 1-3 0.05 ng/µL	M 1-11 0.004 ng/µL	M 2-5 0.01 ng/µL	M 2-13 0.002 ng/µL	M 2-7 0.008 ng/µL	M 3-1 0.09 ng/µL	M 3-9 0.006 ng/µL	M 3-3 0.05 ng/µL	M 3-11 0.004 ng/µL
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL	M 1-10 0.005 ng/µL	M 1-4 0.03 ng/µL	M 1-12 0.003 ng/µL	M 2-6 0.009 ng/µL	M 2-14 0.001 ng/µL	M 2-8 0.007 ng/µL	M 3-2 0.07 ng/µL	M 3-10 0.005 ng/µL	M 3-4 0.03 ng/µL	M 3-12 0.003 ng/µL
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL	M 1-11 0.004 ng/µL	M 1-5 0.01 ng/µL	M 1-13 0.002 ng/µL	M 2-7 0.008 ng/µL	M 2-1 0.09 ng/µL	M 2-9 0.006 ng/µL	M 3-3 0.05 ng/µL	M 3-11 0.004 ng/µL	M 3-5 0.01 ng/µL	M 3-13 0.002 ng/µL
F	M 1-1 0.09 ng/µL	M 1-4 0.03 ng/µL	M 1-12 0.003 ng/µL	M 1-6 0.009 ng/µL	M 1-14 0.001 ng/µL	M 2-8 0.007 ng/µL	M 2-2 0.07 ng/µL	M 2-10 0.005 ng/µL	M 3-4 0.03 ng/µL	M 3-12 0.003 ng/µL	M 3-6 0.009 ng/µL	M 3-14 0.001 ng/µL
G	M 1-2 0.07 ng/µL	M 1-5 0.01 ng/µL	M 1-13 0.002 ng/µL	M 1-7 0.008 ng/µL	M 2-1 0.09 ng/µL	M 2-9 0.006 ng/µL	M 2-3 0.05 ng/µL	M 2-11 0.004 ng/µL	M 3-5 0.01 ng/µL	M 3-13 0.002 ng/µL	M 3-7 0.008 ng/µL	Reagent Blank
H	M 1-3 0.05 ng/µL	M 1-6 0.009 ng/µL	M 1-14 0.001 ng/µL	M 1-8 0.007 ng/µL	M 2-2 0.07 ng/µL	M 2-10 0.005 ng/µL	M 2-4 0.03 ng/µL	M 2-12 0.003 ng/µL	M 3-6 0.009 ng/µL	M 3-14 0.001 ng/µL	M 3-8 0.007 ng/µL	Reagent Blank

Figure 7: Plate map of M1 – M3 samples quantified using Quantifiler Trio reaction mix for Experiment 3a prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	M 4-7 0.008 ng/µL	M 4-1 0.09 ng/µL	M 4-9 0.006 ng/µL	M 5-3 0.05 ng/µL	M 5-11 0.004 ng/µL	M 5-5 0.01 ng/µL	M 5-13 0.002 ng/µL	F 1-7 0.008 ng/µL	F 1-1 0.09 ng/µL	F 1-9 0.006 ng/µL
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	M 4-8 0.007 ng/µL	M 4-2 0.07 ng/µL	M 4-10 0.005 ng/µL	M 5-4 0.03 ng/µL	M 5-12 0.003 ng/µL	M 5-6 0.009 ng/µL	M 5-14 0.001 ng/µL	F 1-8 0.007 ng/µL	F 1-2 0.07 ng/µL	F 1-10 0.005 ng/µL
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	M 4-9 0.006 ng/µL	M 4-3 0.05 ng/µL	M 4-11 0.004 ng/µL	M 5-5 0.01 ng/µL	M 5-13 0.002 ng/µL	M 5-7 0.008 ng/µL	F 1-1 0.09 ng/µL	F 1-9 0.006 ng/µL	F 1-3 0.05 ng/µL	F 1-11 0.004 ng/µL
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL	M 4-10 0.005 ng/µL	M 4-4 0.03 ng/µL	M 4-12 0.003 ng/µL	M 5-6 0.009 ng/µL	M 5-14 0.001 ng/µL	M 5-8 0.007 ng/µL	F 1-2 0.07 ng/µL	F 1-10 0.005 ng/µL	F 1-4 0.03 ng/µL	F 1-12 0.003 ng/µL
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL	M 4-11 0.004 ng/µL	M 4-5 0.01 ng/µL	M 4-13 0.002 ng/µL	M 5-7 0.008 ng/µL	M 5-1 0.09 ng/µL	M 5-9 0.006 ng/µL	F 1-3 0.05 ng/µL	F 1-11 0.004 ng/µL	F 1-5 0.01 ng/µL	F 1-13 0.002 ng/µL
F	M 4-1 0.09 ng/µL	M 4-4 0.03 ng/µL	M 4-12 0.003 ng/µL	M 4-6 0.009 ng/µL	M 4-14 0.001 ng/µL	M 5-8 0.007 ng/µL	M 5-2 0.07 ng/µL	M 5-10 0.005 ng/µL	F 1-4 0.03 ng/µL	F 1-12 0.003 ng/µL	F 1-6 0.009 ng/µL	F 1-14 0.001 ng/µL
G	M 4-2 0.07 ng/µL	M 4-5 0.01 ng/µL	M 4-13 0.002 ng/µL	M 4-7 0.008 ng/µL	M 5-1 0.09 ng/µL	M 5-9 0.006 ng/µL	M 5-3 0.05 ng/µL	M 5-11 0.004 ng/µL	F 1-5 0.01 ng/µL	F 1-13 0.002 ng/µL	F 1-7 0.008 ng/µL	Reagent Blank
H	M 4-3 0.05 ng/µL	M 4-6 0.009 ng/µL	M 4-14 0.001 ng/µL	M 4-8 0.007 ng/µL	M 5-2 0.07 ng/µL	M 5-10 0.005 ng/µL	M 5-4 0.03 ng/µL	M 5-12 0.003 ng/µL	F 1-6 0.009 ng/µL	F 1-14 0.001 ng/µL	F 1-8 0.007 ng/µL	Reagent Blank

Figure 8: Plate map of M4, M5 and F1 samples quantified using Quantifiler Trio reaction mix for Experiment 3a prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	F 2-7 0.008 ng/µL	F 2-1 0.09 ng/µL	F 2-9 0.006 ng/µL	F 3-3 0.05 ng/µL	F 3-11 0.004 ng/µL	F 3-5 0.01 ng/µL	F 3-13 0.002 ng/µL	F 4-7 0.008 ng/µL	F 4-1 0.09 ng/µL	F 4-9 0.006 ng/µL
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	F 2-8 0.007 ng/µL	F 2-2 0.07 ng/µL	F 2-10 0.005 ng/µL	F 3-4 0.03 ng/µL	F 3-12 0.003 ng/µL	F 3-6 0.009 ng/µL	F 3-14 0.001 ng/µL	F 4-8 0.007 ng/µL	F 4-2 0.07 ng/µL	F 4-10 0.005 ng/µL
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	F 2-9 0.006 ng/µL	F 2-3 0.05 ng/µL	F 2-11 0.004 ng/µL	F 3-5 0.01 ng/µL	F 3-13 0.002 ng/µL	F 3-7 0.008 ng/µL	F 4-1 0.09 ng/µL	F 4-9 0.006 ng/µL	F 4-3 0.05 ng/µL	F 4-11 0.004 ng/µL
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL	F 2-10 0.005 ng/µL	F 2-4 0.03 ng/µL	F 2-12 0.003 ng/µL	F 3-6 0.009 ng/µL	F 3-14 0.001 ng/µL	F 3-8 0.007 ng/µL	F 4-2 0.07 ng/µL	F 4-10 0.005 ng/µL	F 4-4 0.03 ng/µL	F 4-12 0.003 ng/µL
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL	F 2-11 0.004 ng/µL	F 2-5 0.01 ng/µL	F 2-13 0.002 ng/µL	F 3-7 0.008 ng/µL	F 3-1 0.09 ng/µL	F 3-9 0.006 ng/µL	F 4-3 0.05 ng/µL	F 4-11 0.004 ng/µL	F 4-5 0.01 ng/µL	F 4-13 0.002 ng/µL
F	F 2-1 0.09 ng/µL	F 2-4 0.03 ng/µL	F 2-12 0.003 ng/µL	F 2-6 0.009 ng/µL	F 2-14 0.001 ng/µL	F 3-8 0.007 ng/µL	F 3-2 0.07 ng/µL	F 3-10 0.005 ng/µL	F 4-4 0.03 ng/µL	F 4-12 0.003 ng/µL	F 4-6 0.009 ng/µL	F 4-14 0.001 ng/µL
G	F 2-2 0.07 ng/µL	F 2-5 0.01 ng/µL	F 2-13 0.002 ng/µL	F 2-7 0.008 ng/µL	F 3-1 0.09 ng/µL	F 3-9 0.006 ng/µL	F 3-3 0.05 ng/µL	F 3-11 0.004 ng/µL	F 4-5 0.01 ng/µL	F 4-13 0.002 ng/µL	F 4-7 0.008 ng/µL	Reagent Blank
H	F 2-3 0.05 ng/µL	F 2-6 0.009 ng/µL	F 2-14 0.001 ng/µL	F 2-8 0.007 ng/µL	F 3-2 0.07 ng/µL	F 3-10 0.005 ng/µL	F 3-4 0.03 ng/µL	F 3-12 0.003 ng/µL	F 4-6 0.009 ng/µL	F 4-14 0.001 ng/µL	F 4-8 0.007 ng/µL	Reagent Blank

Figure 9: Plate map of F2 - F4 samples quantified using Quantifiler Trio reaction mix for Experiment 3a prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	F 5-7 0.008 ng/µL	F 5-1 0.09 ng/µL	F 5-9 0.006 ng/µL							
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	F 5-8 0.007 ng/µL	F 5-2 0.07 ng/µL	F 5-10 0.005 ng/µL							
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	F 5-9 0.006 ng/µL	F 5-3 0.05 ng/µL	F 5-11 0.004 ng/µL							
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL	F 5-10 0.005 ng/µL	F 5-4 0.03 ng/µL	F 5-12 0.003 ng/µL							
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL	F 5-11 0.004 ng/µL	F 5-5 0.01 ng/µL	F 5-13 0.002 ng/µL							
F	F 5-1 0.09 ng/µL	F 5-4 0.03 ng/µL	F 5-12 0.003 ng/µL	F 5-6 0.009 ng/µL	F 5-14 0.001 ng/µL							
G	F 5-2 0.07 ng/µL	F 5-5 0.01 ng/µL	F 5-13 0.002 ng/µL	F 5-7 0.008 ng/µL	Reagent Blank							
H	F 5-3 0.05 ng/µL	F 5-6 0.009 ng/µL	F 5-14 0.001 ng/µL	F 5-8 0.007 ng/µL	Reagent Blank							

Figure 10: Plate map of F5 samples quantified using Quantifiler Trio reaction mix for Experiment 3a prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

5.3.2 Experiment 3b – Mixture Studies and Sensitivity

One male (M1) and one female (F1) reference FTA sample already extracted and quantified using the Quantifiler® Human kit from Experiment 3a were selected and utilised in Experiment 3b. Serial dilutions of both samples were performed with TE-4 buffer to generate concentrations of 0.1, 0.01, 0.001, 0.0001 and 0.00001 ng/µL. These were then used to prepare all the mixture samples required.

Two sets of male:female mixtures (M1:F1 and M2:F2) were prepared according to the ratios listed in section 4.2.2.

Each mixture sample was quantified in duplicate using the Quantifiler® Trio Kit according to section 4.3.2 and the results were obtained using the LT2 standard set utilised in Experiments 1 and 2.

The quantification plate was prepared manually, run and analysed on 7500A as shown in Figure 11.

The average SAT, LAT, Y-target, and Ct of the male:female ratios were all calculated to determine the kit's ability to detect the male component in mixture samples - especially at very low concentrations.

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 4 0.050 ng/µL	MF3 (M1:F1)	MF7 (M1:F1)	MF11 (M1:F1)	MF15 (M1:F1)	MF2 (M2:F2)	MF6 (M2:F2)	MF10 (M2:F2)	MF14 (M2:F2)		
B	STD 2 5.000 ng/µL	STD 5 0.005 ng/µL	MF4 (M1:F1)	MF8 (M1:F1)	MF12 (M1:F1)	MF16 (M1:F1)	MF3 (M2:F2)	MF7 (M2:F2)	MF11 (M2:F2)	MF15 (M2:F2)		
C	STD 3 0.500 ng/µL	Reagent Blank	MF4 (M1:F1)	MF8 (M1:F1)	MF12 (M1:F1)	MF16 (M1:F1)	MF3 (M2:F2)	MF7 (M2:F2)	MF11 (M2:F2)	MF15 (M2:F2)		
D	STD 4 0.050 ng/µL	MF1 (M1:F1)	MF5 (M1:F1)	MF9 (M1:F1)	MF13 (M1:F1)	MF17 (M1:F1)	MF4 (M2:F2)	MF8 (M2:F2)	MF12 (M2:F2)	MF16 (M2:F2)		
E	STD 5 0.005 ng/µL	MF1 (M1:F1)	MF5 (M1:F1)	MF9 (M1:F1)	MF13 (M1:F1)	MF17 (M1:F1)	MF4 (M2:F2)	MF8 (M2:F2)	MF12 (M2:F2)	MF16 (M2:F2)		
F	STD 1 50 ng/µL	MF2 (M1:F1)	MF6 (M1:F1)	MF10 (M1:F1)	MF14 (M1:F1)	MF1 (M2:F2)	MF5 (M2:F2)	MF9 (M2:F2)	MF13 (M2:F2)	MF17 (M2:F2)		
G	STD 2 5.000 ng/µL	MF2 (M1:F1)	MF6 (M1:F1)	MF10 (M1:F1)	MF14 (M1:F1)	MF1 (M2:F2)	MF5 (M2:F2)	MF9 (M2:F2)	MF13 (M2:F2)	MF17 (M2:F2)		
H	STD 3 0.500 ng/µL	MF3 (M1:F1)	MF7 (M1:F1)	MF11 (M1:F1)	MF15 (M1:F1)	MF2 (M2:F2)	MF6 (M2:F2)	MF10 (M2:F2)	MF14 (M2:F2)	Reagent Blank		

Figure 11: Plate map of MF1-14 samples quantified using Quantifiler Trio reaction mix for Experiment 3b prepared in a 96-well plate. "Reagent Blank" denotes a well containing master mix only.

5.4 Experiment 4 – Repeatability and Reproducibility

5.4.1 Experiment 4a - Repeatability

Plate 2 from Experiment 3a (section 5.3.1, Figure 8) was prepared manually and quantified using the Quantifiler® Trio Kit according to section 4.3.2. This was performed twice (Plate A and Plate B) by the same operator on the same day. The results were obtained using the LT2 standard set utilised in Experiment 1 and 2. The Slope, Y-intercept and the R2 value were calculated for each plate.

Plate A and Plate B were run and analysed on 7500A as shown in Figure 12.

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	M 4-7 0.008 ng/µL	M 4-1 0.09 ng/µL	M 4-9 0.006 ng/µL	M 5-3 0.05 ng/µL	M 5-11 0.004 ng/µL	M 5-5 0.01 ng/µL	M 5-13 0.002 ng/µL	F 1-7 0.008 ng/µL	F 1-1 0.09 ng/µL	F 1-9 0.006 ng/µL
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	M 4-8 0.007 ng/µL	M 4-2 0.07 ng/µL	M 4-10 0.005 ng/µL	M 5-4 0.03 ng/µL	M 5-12 0.003 ng/µL	M 5-6 0.009 ng/µL	M 5-14 0.001 ng/µL	F 1-8 0.007 ng/µL	F 1-2 0.07 ng/µL	F 1-10 0.005 ng/µL
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	M 4-9 0.006 ng/µL	M 4-3 0.05 ng/µL	M 4-11 0.004 ng/µL	M 5-5 0.01 ng/µL	M 5-13 0.002 ng/µL	M 5-7 0.008 ng/µL	F 1-1 0.09 ng/µL	F 1-9 0.006 ng/µL	F 1-3 0.05 ng/µL	F 1-11 0.004 ng/µL
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL	M 4-10 0.005 ng/µL	M 4-4 0.03 ng/µL	M 4-12 0.003 ng/µL	M 5-6 0.009 ng/µL	M 5-14 0.001 ng/µL	M 5-8 0.007 ng/µL	F 1-2 0.07 ng/µL	F 1-10 0.005 ng/µL	F 1-4 0.03 ng/µL	F 1-12 0.003 ng/µL
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL	M 4-11 0.004 ng/µL	M 4-5 0.01 ng/µL	M 4-13 0.002 ng/µL	M 5-7 0.008 ng/µL	M 5-1 0.09 ng/µL	M 5-9 0.006 ng/µL	F 1-3 0.05 ng/µL	F 1-11 0.004 ng/µL	F 1-5 0.01 ng/µL	F 1-13 0.002 ng/µL
F	M 4-1 0.09 ng/µL	M 4-4 0.03 ng/µL	M 4-12 0.003 ng/µL	M 4-6 0.009 ng/µL	M 4-14 0.001 ng/µL	M 5-8 0.007 ng/µL	M 5-2 0.07 ng/µL	M 5-10 0.005 ng/µL	F 1-4 0.03 ng/µL	F 1-12 0.003 ng/µL	F 1-6 0.009 ng/µL	F 1-14 0.001 ng/µL
G	M 4-2 0.07 ng/µL	M 4-5 0.01 ng/µL	M 4-13 0.002 ng/µL	M 4-7 0.008 ng/µL	M 5-1 0.09 ng/µL	M 5-9 0.006 ng/µL	M 5-3 0.05 ng/µL	M 5-11 0.004 ng/µL	F 1-5 0.01 ng/µL	F 1-13 0.002 ng/µL	F 1-7 0.008 ng/µL	Reagent Blank
H	M 4-3 0.05 ng/µL	M 4-6 0.009 ng/µL	M 4-14 0.001 ng/µL	M 4-8 0.007 ng/µL	M 5-2 0.07 ng/µL	M 5-10 0.005 ng/µL	M 5-4 0.03 ng/µL	M 5-12 0.003 ng/µL	F 1-6 0.009 ng/µL	F 1-14 0.001 ng/µL	F 1-8 0.007 ng/µL	Reagent Blank

Figure 12: Plate map of M1-M3 (Plate A & Plate B) samples quantified using Quantifiler Trio reaction mix for Experiment 4a prepared in a 96-well plate. The concentration of each in ng/µl is shown. "Reagent Blank" denotes a well containing master mix only.

The SAT, LAT, Y-target and Ct values were calculated for each sample and a Student's t-test was performed to compare the results from Plate A and Plate B.

The standard curve results were also calculated and compared between Plate A and Plate B.

From the Student's t-test scores and the standard curve results the repeatability for Quantifiler® Trio was assessed - assessing whether Quantifiler® Trio produces the same results when one sample set is processed in duplicate by one user, under the same conditions.

5.4.2 Experiment 4b - Reproducibility

Plate 2 from Experiment 3a (section 5.3.1, Figure 8) was prepared manually and quantified using the Quantifiler® Trio Kit according to section 4.3.2. This was performed by a second operator the following day after Experiment 4a (Plate C).

The results were obtained using the LT2 standard set utilised in Experiment 1 and 2. The Slope, Y-intercept and the R2 value was calculated for Plate C.

Plate C was run and analysed on 7500A as shown in Figure 12 in section 5.4.1.

The SAT, LAT, Y- target and the Ct values were calculated and a Student's t-test was performed comparing the results between the following:
Plate C from day 2 to Plate A from day 1
Plate C from day 2 to Plate B from day 1

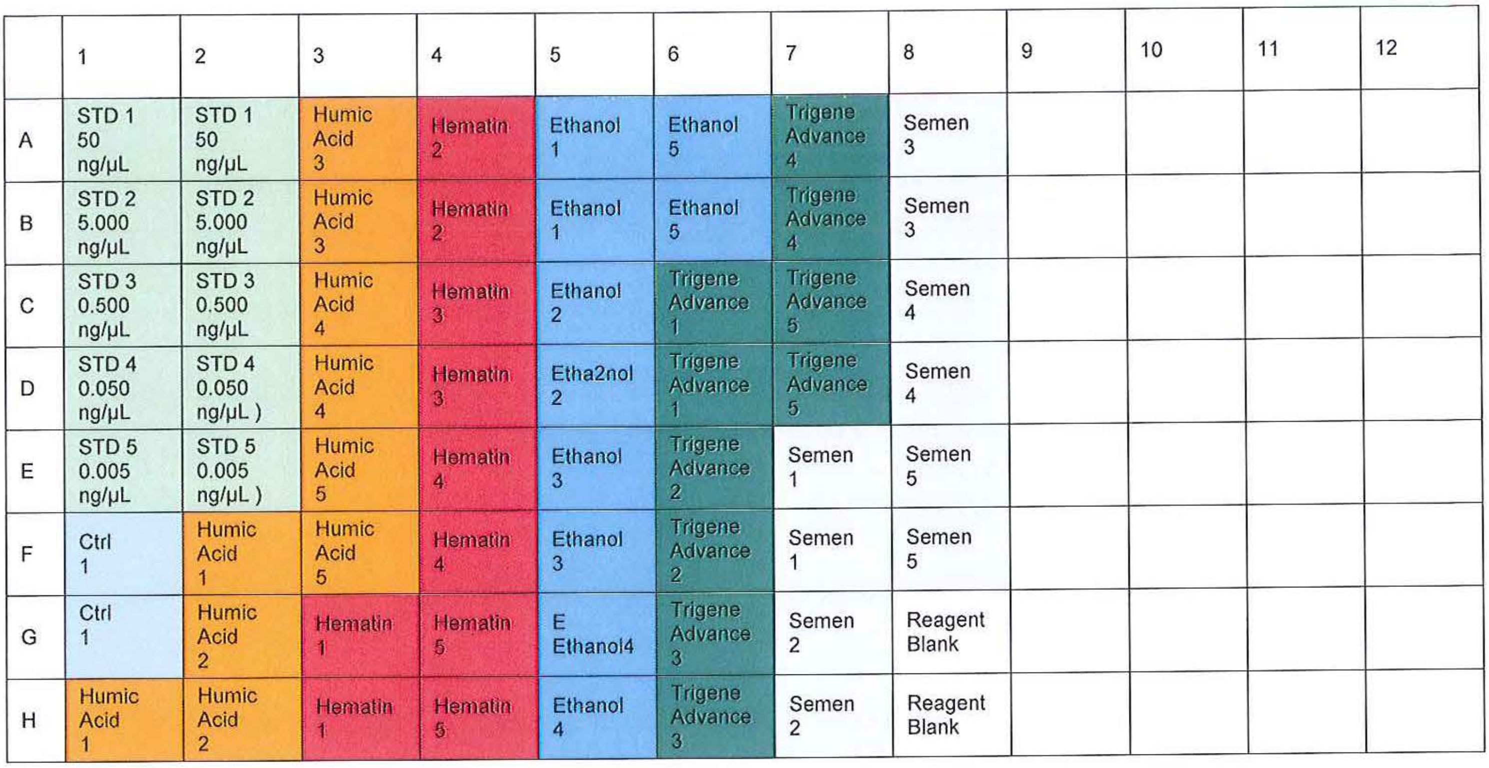
The standard curve results was also calculated and compared between the three plates as above.

From the Student's t-test scores and the standard curve results the reproducibility for Quantifiler® Trio was assessed – assessing whether Quantifiler® Trio produces the same results when one sample set is processed by different operators under same conditions.

5.5 Experiment 5 - Inhibition

A total of 26 samples were prepared with a consistent level of input DNA of 0.1 ng/µL with a range of inhibitor concentrations. These included a control sample with no inhibitor, five humic acid samples, five hematin samples, five ethanol samples, five trigene advance samples and five seminal fluid samples (see section 4.2.3).

All samples were quantified in duplicate using the Quantifiler® Trio Kit according to section 4.3.2 and the results were obtained using the LT2 standard set utilised in Experiment 1 and 2. The quantification plate was prepared manually and was run and analysed on 7500A including two reagent blanks as shown in Figure 13.



	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	Humic Acid 3	Hematin 2	Ethanol 1	Ethanol 5	Trigene Advance 4	Semen 3				
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	Humic Acid 3	Hematin 2	Ethanol 1	Ethanol 5	Trigene Advance 4	Semen 3				
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	Humic Acid 4	Hematin 3	Ethanol 2	Trigene Advance 1	Trigene Advance 5	Semen 4				
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL)	Humic Acid 4	Hematin 3	Etha2nol 2	Trigene Advance 1	Trigene Advance 5	Semen 4				
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL)	Humic Acid 5	Hematin 4	Ethanol 3	Trigene Advance 2	Semen 1	Semen 5				
F	Ctrl 1	Humic Acid 1	Humic Acid 5	Hematin 4	Ethanol 3	Trigene Advance 2	Semen 1	Semen 5				
G	Ctrl 1	Humic Acid 2	Hematin 1	Hematin 5	E Ethanol4	Trigene Advance 3	Semen 2	Reagent Blank				
H	Humic Acid 1	Humic Acid 2	Hematin 1	Hematin 5	Ethanol 4	Trigene Advance 3	Semen 2	Reagent Blank				

Figure 13: Plate map of inhibitor samples quantified using Quantifiler Trio reaction mix for Experiment 5 prepared in a 96-well plate. "Reagent Blank" denotes a well containing master mix only.

The average SAT, LAT, internal positive control Ct value (IPCCt) and the IPCCt flag were calculated to assess whether the IPCCt and IPCCt flag accurately indicate inhibition.

Excluding the samples with Trigene Advance, all samples were amplified using the PowerPlex®21 Amplification kit. The amplification reaction volumes were calculated using the Quantifiler® Trio results and the PP21 Full SV1 calculation v3 macro – a macro routinely used in the laboratory to calculate amplification volumes based on the quantification results.

The amplification plate was prepared manually and run on the GeneAmp® PCR system 9700 (see section 4.4) as shown in Figure 14.

	1	2	3	4	5	6	7	8	9	10	11	12
A	Pos Ctrl	LADDER 1	Ethanol 3	LADDER 2								
B	Neg Ctrl	Hematin 1	Ethanol 4									
C	Control Nil	Hematin 2	Ethanol 5									
D	Humic Acid 1	Hematin 3	Semen 1									
E	Humic Acid 2	Hematin 4	Semen 2									
F	Humic Acid 3	Hematin 5	Semen 3									
G	Humic Acid 4	Ethanol 1	Semen 4									
H	Humic Acid 5	Ethanol 2	Semen 5									

Figure 14: Plate map of the inhibitor samples amplified using PowerPlex21 reaction mix for Experiment 5 prepared in a 96-well plate.

DNA fragment analysis and profile interpretation were performed according to section 4.5 and 4.6 to determine the number of alleles and to assess how PCR inhibitors affect Quantifiler® Trio.

5.6 Experiment 6 - Degradation

5.6.1 Experiment 6a – Degradation Protocol

26 extracted in-house blood positive controls were selected and pooled to provide enough extract required for this experiment. Thirteen 90μL aliquots of the pooled blood positive control extract were pipetted into a 96-well PCR micro-plate and exposed to ultraviolet (UV) light in the biohazard safety cabinet in room 3194. The UV exposure times for each aliquot are listed below in Table 18.

Table 4: UV Exposure times for Experiment 6a.

Sample (aliquot)	UV Exposure
1	Nil
2	10 minutes
3	10 minutes
4	1 hour
5	1 hour

6	5 hours
7	5 hours
8	8 hours
9	8 hours
10	15 hours
11	15 hours
12	24 hours
13	24 hours

Each aliquot was then transferred into a NUNC tube and stored after UV exposure as per laboratory procedures. All samples were quantified using the Quantifiler® Human Kit using the Promega standard set currently used in the laboratory for routine analysis (see section 4.3.1). The quantification plate was prepared manually, run and analysed on 7500A.

The quantification value, Ct value and the IPCCt was calculated and the effect of UV was assessed.

All samples were amplified using the PowerPlex®21 Amplification kit and run on the GeneAmp® PCR system 9700 (see section 4.4).

DNA fragment analysis and profile interpretation were performed according to sections 4.5 and 4.6 to determine the number of alleles in the DNA profiles.

From the quantification results and the number of alleles present in the DNA profiles, the method of degrading samples by UV radiation was assessed.

5.6.2 Experiment 6b – Degradation Index Proof of Concept

The same thirteen samples utilised in Experiment 6a were also used in Experiment 6b. All samples were quantified using the Quantifiler® Trio kit using the LT2 standard set utilised in Experiment 1 and 2. The quantification plate was prepared manually and run on 7500A including a reagent blank as shown in Figure 15.

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	UV 5 Hours #2									
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	UV 8 Hours #1									
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	UV 8 Hours #2									
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL)	UV 15 Hours #1									
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL)	UV 15 Hours #2									
F	UV Nil	UV 1 Hour #1	UV 24 Hours #1									
G	UV 10 Min #1	UV 1 Hour #2	UV 24 Hours #2									
H	UV 10 Min #2	UV 5 Hours #1	Reagent Blank									

Figure 15: Plate map of the UV samples quantified using Quantifiler Trio kit reaction mix for Experiment 6b prepared in a 96-well plate. "Reagent Blank" denotes a well containing master mix only.

The SAT, LAT, Ct value, IPCCt and the Degradation Index (DI) were calculated for all samples and the effect of UV was assessed. The DI was also assessed to determine whether it is a reliable indicator of the level of degradation.

5.6.3 Experiment 6c – Degradation Index Threshold

An additional 19 extracted in-house blood positive controls were selected and pooled with the stock prepared in Experiment 6a. Thirty four 90µL aliquots of extract were pipetted into a 96-well PCR micro-plate and exposed to UV light in the biohazard safety cabinet in room 3194. The UV exposure times for each aliquot are listed in Table 5.

Table 5: UV Exposure times for Experiment 6c.

Sample	UV Exposure
1	Nil
2	5 Minutes
3	5 Minutes
4	5 Minutes
5	10 Minutes
6	10 Minutes
7	10 Minutes
8	20 Minutes
9	20 Minutes
10	20 Minutes
11	30 Minutes
12	30 Minutes
13	30 Minutes
14	40 Minutes
15	40 Minutes
16	40 Minutes
17	50 Minutes
18	50 Minutes
19	50 Minutes
20	1 Hour
21	1 Hour
22	1 Hour
23	2 Hours
24	2 Hours
25	2 Hours
26	4 Hours
27	4 Hours
28	4 Hours
29	8 Hours
30	8 Hours
31	8 Hours
32	24 Hours
33	24 Hours
34	24 Hours

Each aliquot was then transferred into a NUNC tube and stored after UV exposure as per laboratory procedures. All samples were quantified using the Quantifiler® Trio kit using the LT2 standard set utilised in Experiment 1 and 2. The quantification plate was prepared manually and run on 7500A including a reagent blank as shown in Figure 16.

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 1 50 ng/µL	UV 10 Mins #3	UV 40 Mins #2	UV 2 Hours #1	UV 8 Hours #3						
B	STD 2 5.000 ng/µL	STD 2 5.000 ng/µL	UV 20 Mins #1	UV 40 Mins #3	UV 2 Hours #2	UV 24 Hours #1						
C	STD 3 0.500 ng/µL	STD 3 0.500 ng/µL	UV 20 Mins #2	UV 50 Mins #1	UV 2 Hours #3	UV 24 Hours #2						
D	STD 4 0.050 ng/µL	STD 4 0.050 ng/µL)	UV 20 Mins #3	UV 50 Mins #2	UV 4 Hours #1	UV 24 Hours #3						
E	STD 5 0.005 ng/µL	STD 5 0.005 ng/µL)	UV 30 Mins #1	UV 50 Mins #3	UV 4 Hours #2	Reagent Blank						
F	UV Nil	UV 5 Min #3	UV 30 Mins #2	UV 1 Hour #1	UV 4 Hours #3							
G	UV 5 Mins #1	UV 10 Mins #1	UV 30 Mins #3	UV 1 Hour #2	UV 8 Hours #1							
H	UV 5 Mins #2	UV 10 Mins #2	UV 40 Mins #1	UV 1 Hour #3	UV 8 Hours #2							

Figure 16: Plate map of the UV samples quantified using Quantifiler Trio kit reaction mix for Experiment 6c prepared in a 96-well plate. "Reagent Blank" denotes a well containing master mix only.

The average SAT, LAT, Ct value, IPCCt and the Degradation Index were calculated for all samples and the effect of UV was assessed.

All samples were amplified using the PowerPlex®21 Amplification kit and run on the GeneAmp® PCR system 9700 (see section 4.4).

DNA fragment analysis and profile interpretation were performed according to sections 4.5 and 4.6 to determine the number of alleles in the DNA profiles.

From the quantification and the DNA profile results, the DI threshold was investigated in order to determine which samples are too degraded to give useful DNA profiles.

5.7 Experiment 7 – Quantifiler® Trio Kit New Formulation (IPC modification)

Plate 1 from Experiment 3a (Figure 7 - Section 5.3.1) and the inhibition plate from Experiment 5 (Figure 13 – Section 5.5) were used to test the recently modified Quantifiler® Trio Kit. The samples on Plate 1 and the inhibition plate were re-quantified with the new formulation kit using one standard set freshly prepared as per Section 4.1.1. The quantification plates were prepared manually and run on 7500A including reagent blanks.

From Plate 1 the SAT, LAT, Y-target and Ct values were calculated and a Student's t-test was performed comparing the results to the original plate run in Experiment 3a.

From the inhibition plate the average SAT, Ct values, IPCCt and the IPCCt flag were calculated and a Student's t-test was performed comparing the results to the original plate run in Experiment 5.

The standard curve results were also calculated and a comparison was performed between the modified kit and the original kit.

6. Results and Discussion

6.1 Experiment 1 – Assessment of Quantification Standards

The Quantifiler® Trio Kit was used to quantify NIST components A, B and C in duplicate to assess the accuracy of Life Technologies (LT) and Promega (PR) quantification standards. The results of the SAT, LAT and Y standard curve were calculated – recording the slope, Y-intercept, R2 and the efficiency percentage. The average SAT quantification results were compared to the expected NIST concentrations and the average percentage inaccuracies were calculated.

All four reagent blanks on each plate yielded an undetermined result.

From the ten PR standard sets, six standard curves performed within the Quantifiler® Trio slope ranges for SAT, LAT and Y. Four standard curves failed, these were PR set 5, 8, 9 and 10. These standard curves failed due to the standard curve slope values falling outside Quantifiler® Trio slope ranges for SAT, LAT and Y. In comparison, all ten LT standard curves results performed within the recommended Quantifiler® Trio slope ranges.

The performances of the standard curves were also compared between both manufacturers by calculating the average efficiency percentages. The LT standards showed an average efficiency percentage of 103.58%, compared to PR's 118.83%. Alternatively, this shows that the LT standards have a percentage inaccuracy of 3.58% compared to 18.83% from the PR standards. Therefore, the LT standards appear to be more efficient and stable – showing less variability in the standard curve results compared to the PR standards.

The overall accuracy of the standard sets from each manufacturer was also evident in the measurement of NIST sets A, B and C. The average percentage inaccuracies were calculated at each concentration and are displayed below in Figure 17 to Figure 22.

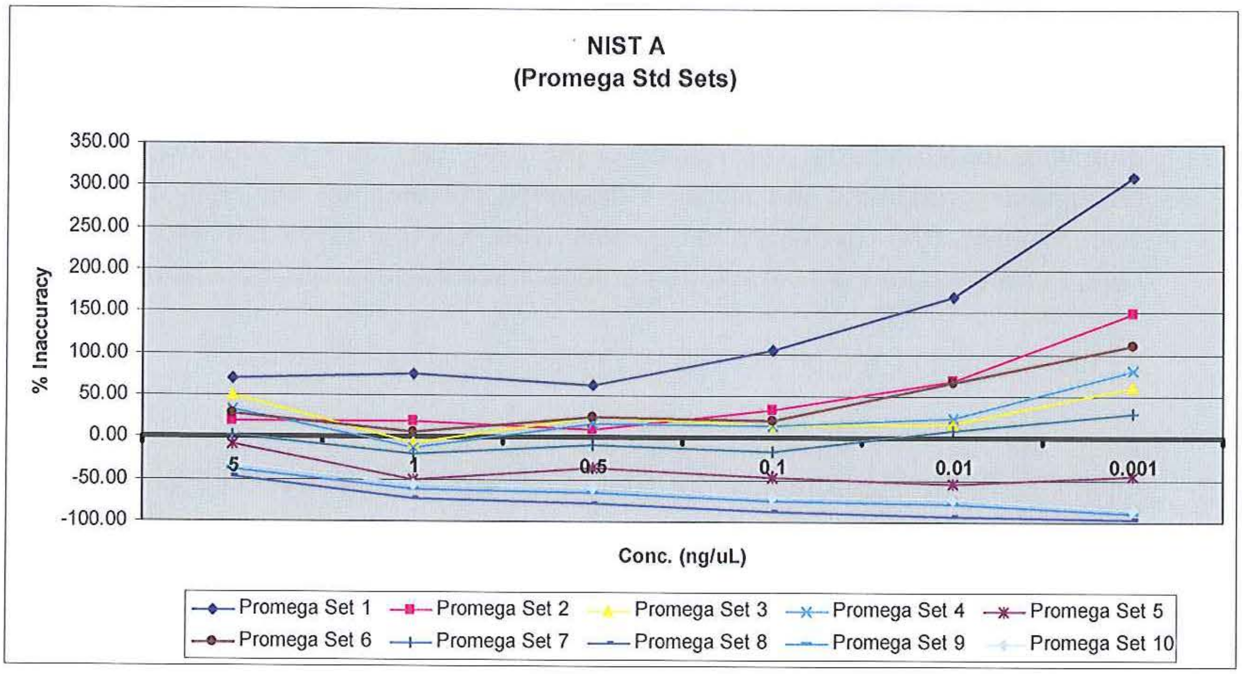


Figure 17: Percentage inaccuracy graph of the 10 PR standard sets measuring NIST Set A.

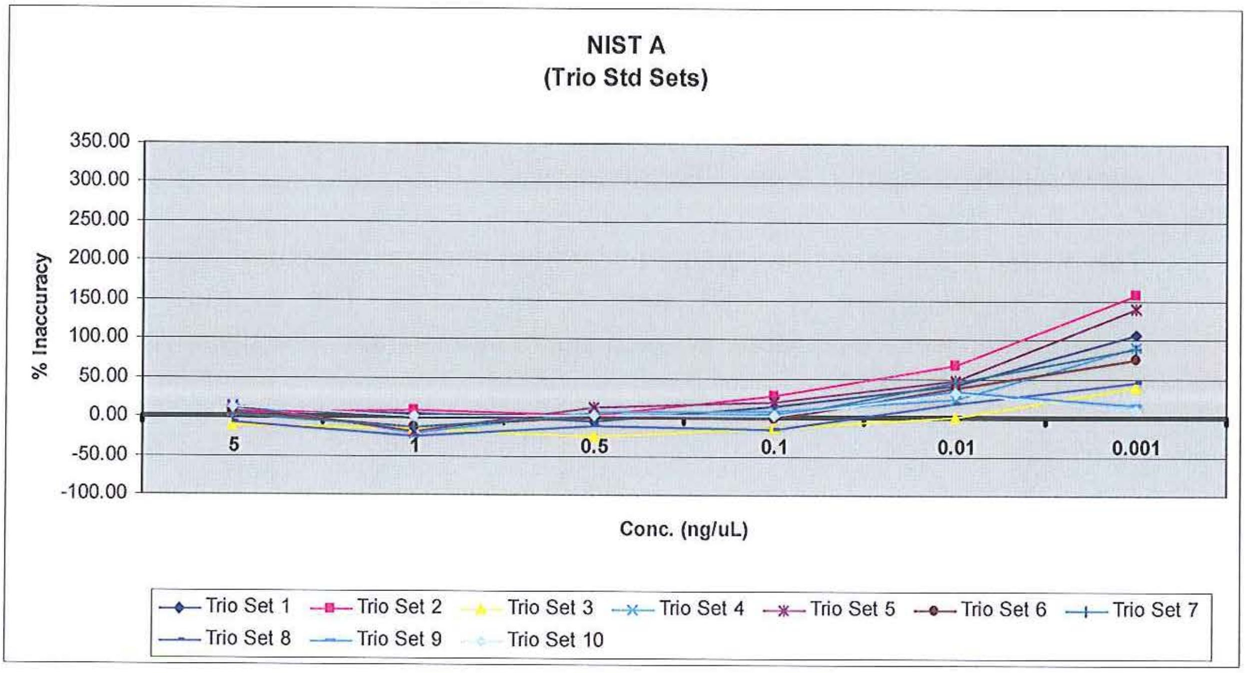


Figure 17: Percentage inaccuracy graph of the 10 LT standard sets measuring NIST Set A.

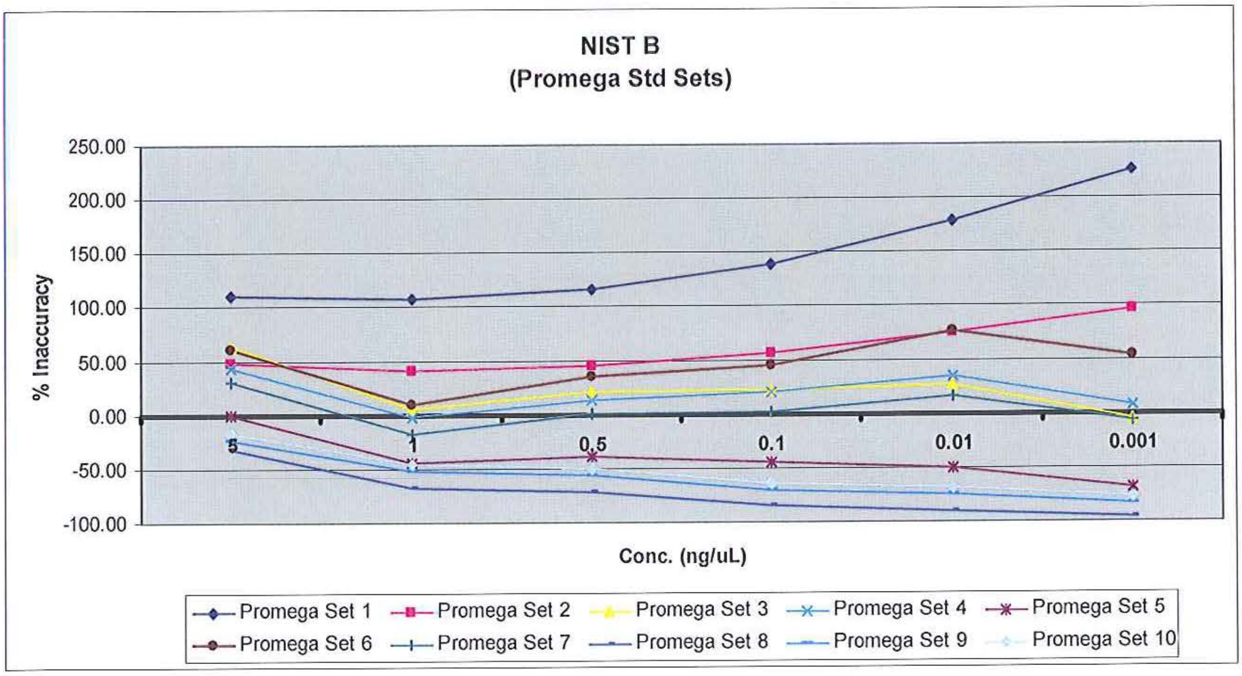


Figure 18: Percentage inaccuracy graph of the 10 PR standard sets measuring NIST Set B.

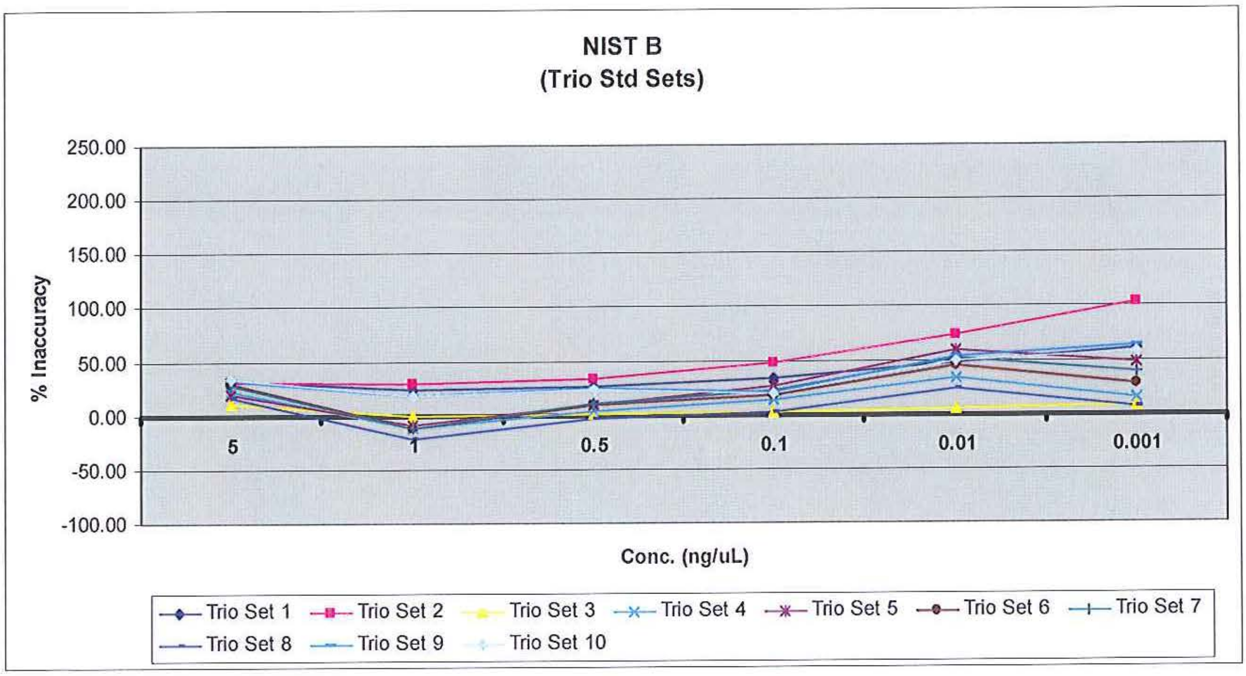


Figure 19: Percentage inaccuracy graph of the 10 LT standard sets measuring NIST Set B.

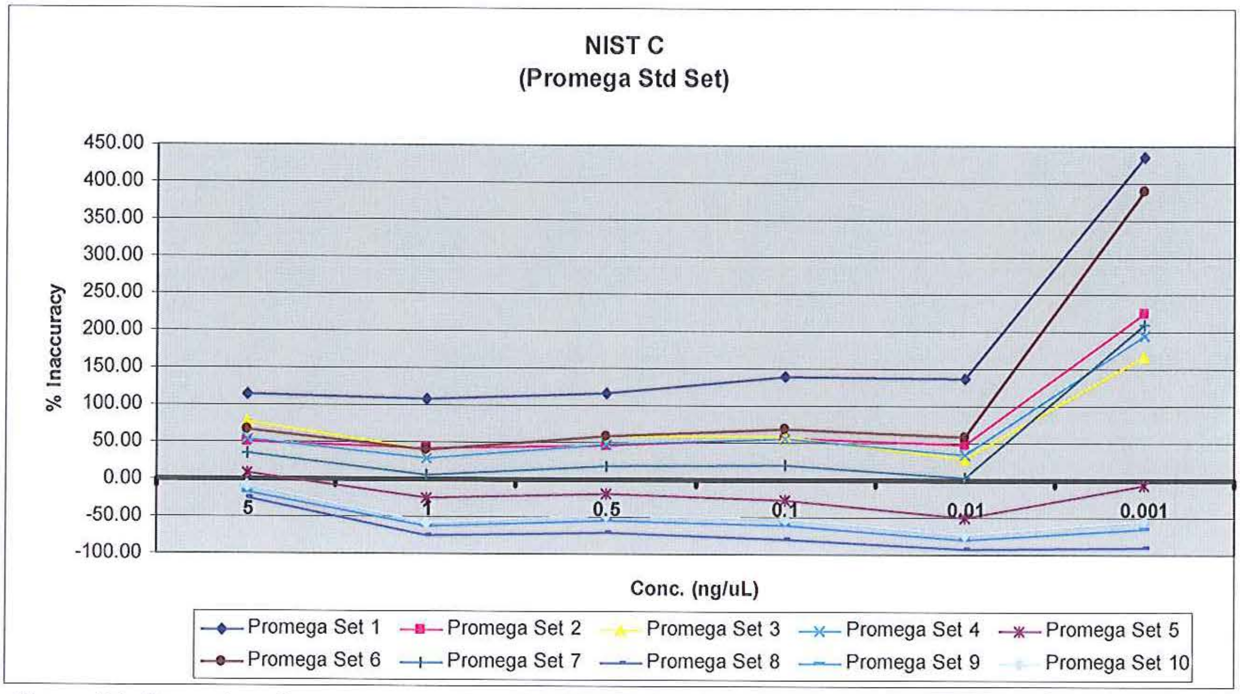


Figure 21: Percentage inaccuracy graph of the 10 PR standard sets measuring NIST Set C.

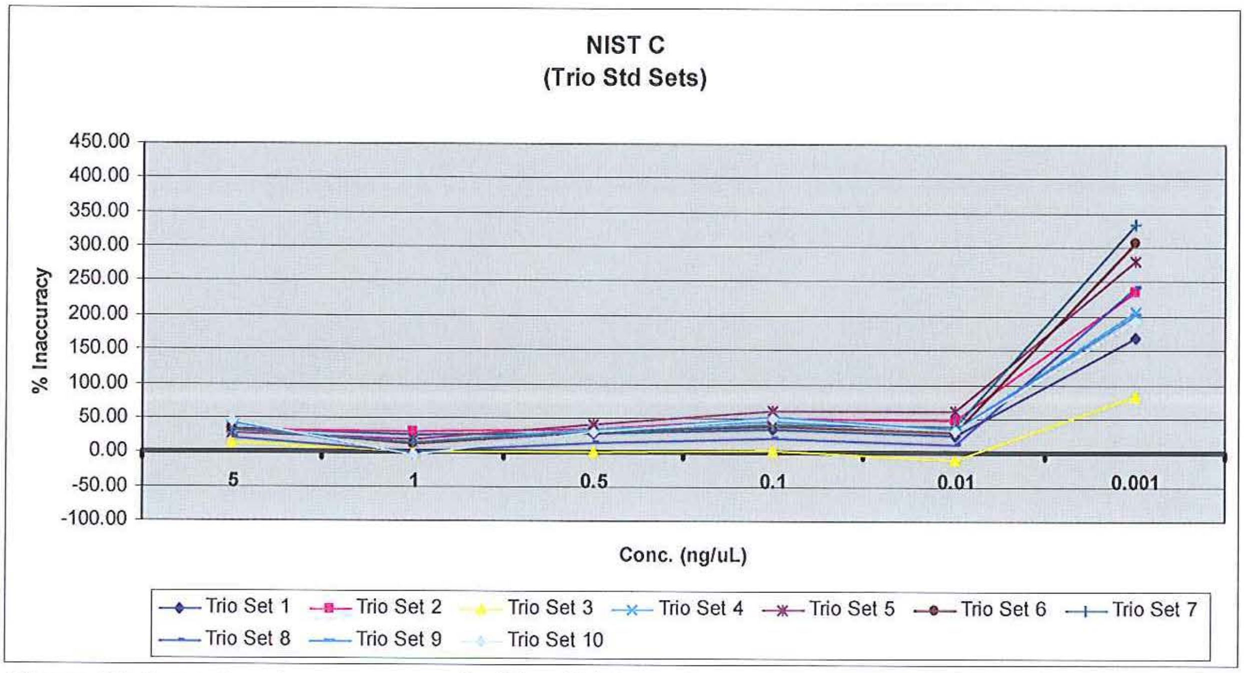


Figure 22: Percentage inaccuracy graph of the 10 LT standard sets measuring NIST set C.

The percentage inaccuracies at the lowest concentration (0.0001ng/µL) were excluded from the results as high levels of inaccuracy and variation was observed from all standard sets. It is accepted concentrations below 5pg/µL produce significant variability [1] therefore the results were not unexpected.

The graphs clearly show the LT standard sets were consistently more accurate than the PR standard sets when measuring all the NIST sets. They also showed lower percentage inaccuracies whilst displaying less variation at each concentration. Based on these results the LT standards were used for experiments 3-7.

It is possible to compare the accuracy of the Quantifiler® Trio kit to the Quantifiler® Human kit currently used routinely within Forensic DNA Analysis. The results in Experiment 2 (section 6.2) in Proposal #147 - Testing of Updated Quantifiler® Human DNA Quantification Kit showed that the percentage inaccuracy of Quantifiler® Human averaged across NIST standards A, B and C was -15.48%. The results of this experiment showed that the percent inaccuracy for Quantifiler® Trio averaged across NIST standards A, B and C was 3.58%. Therefore, based on these results, Quantifiler® Trio is more accurate than Quantifiler® Human.

6.2 Experiment 2 – Standard Stability Assessment

From the standard curve results in Experiment 1, the five most efficient standard sets from both LT and PR were selected and utilised in this experiment. These were the standard sets from each manufacturer that showed standard curve efficiency percentages closest to 100%. Quantifiler® Trio was used to quantify NIST A, B and C in duplicate using LT standard sets 2, 4, 5, 7 and 9 and PR sets 1, 2, 4, 6 and 7. The standard curve results were calculated for each standard set and an overall quantification average was calculated for the five LT standard sets combined and the five PR standard sets combined. The overall results at each concentration each week were then compared to the results in week one to calculate a percentage change.

All five LT standard curves passed each week over the total six weeks – all results falling within the acceptable ranges (see section 5.2). In comparison, PR standard set 7 failed in week one, the same set again failed in week three and PR set 4 failed in week six. Furthermore, multiple PR standard curves gave results which were close to falling outside the acceptable ranges from week two onwards. This demonstrates that the LT standards are more stable over time displaying less variation in the standard curve results.

Figures 23 and 24 show the efficiency percentages of the standard curves (SAT, LAT and Y-targets) for the entire six week period for LT and PR.

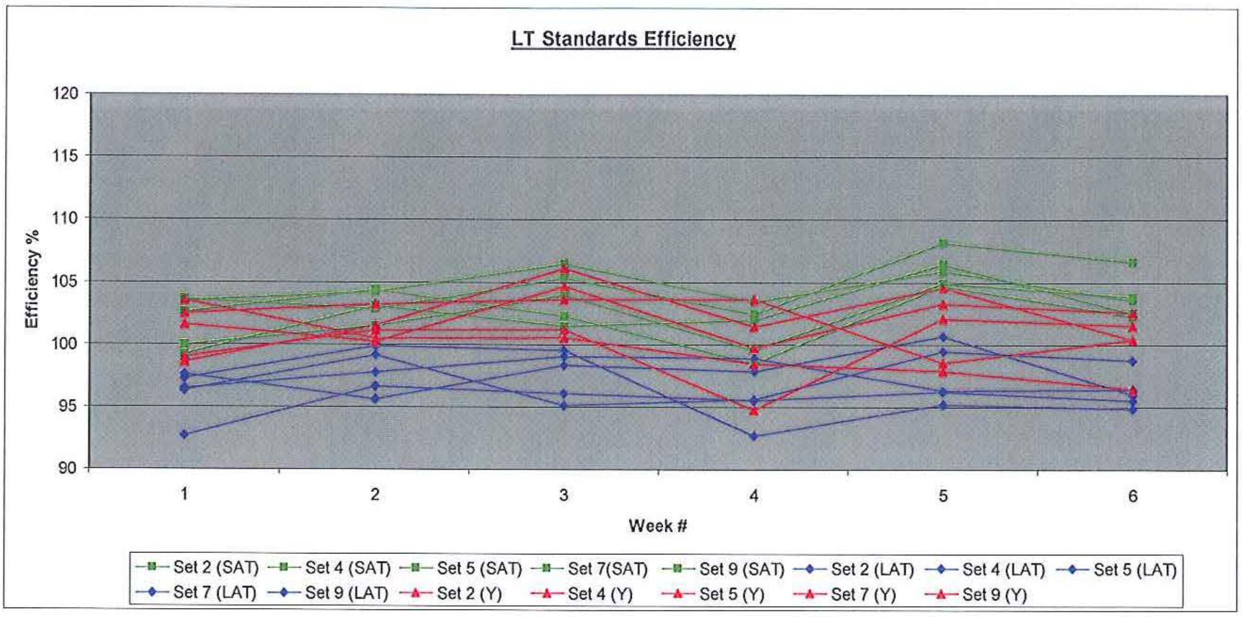


Figure 20: LT Standard Sets efficiency % over 6 weeks.

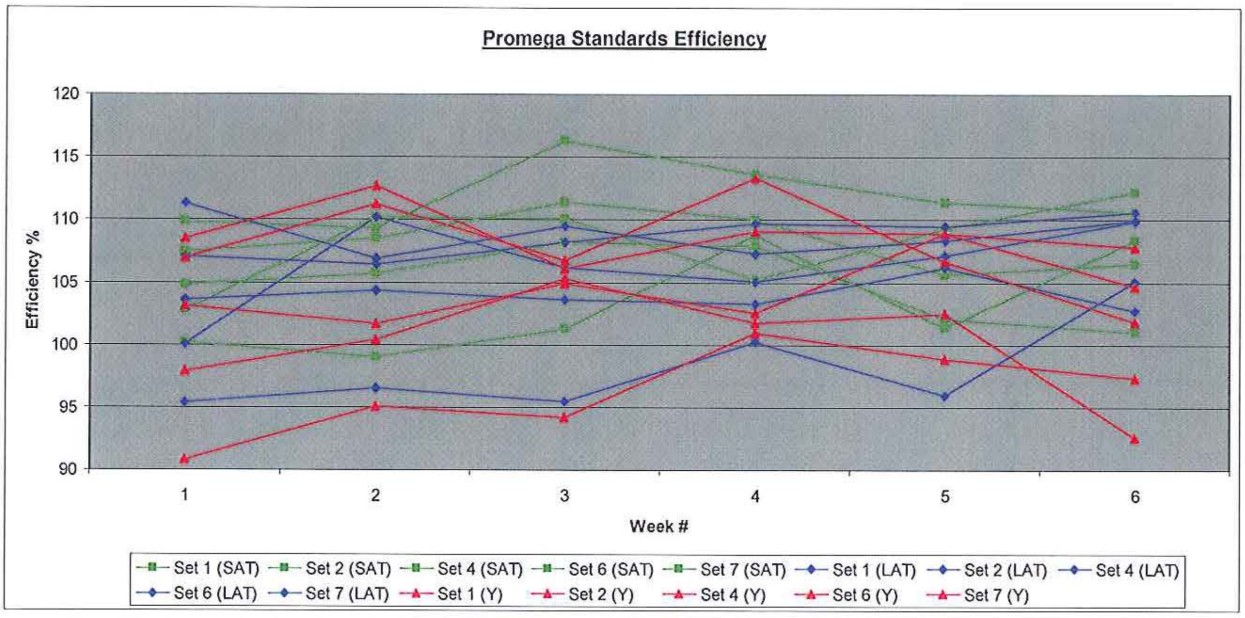


Figure 21: PR Standard Sets efficiency % over 6 weeks.

The graphs above show that the LT standards curves were more efficient and more stable – showing less variation - over the six week period compared to the PR standard curves. The LT standards showed an average efficiency percentage of 100.46%, compared to PR's 105.30%. Alternatively, this showed the LT standards have a percentage inaccuracy of 0.46% compared to 5.30% from the PR standards.

The average quantification results of the NIST components combined at each concentration, each week were calculated for the LT and PR standard sets. The percentage change from week two to week six was then calculated by comparing the results back to the results in week one. This showed the change in the results each week - showing the stability of the standards from when it was initially prepared (in week one). Figure 25 below shows the percentage change of both LT and PR standard sets each week at each concentration.

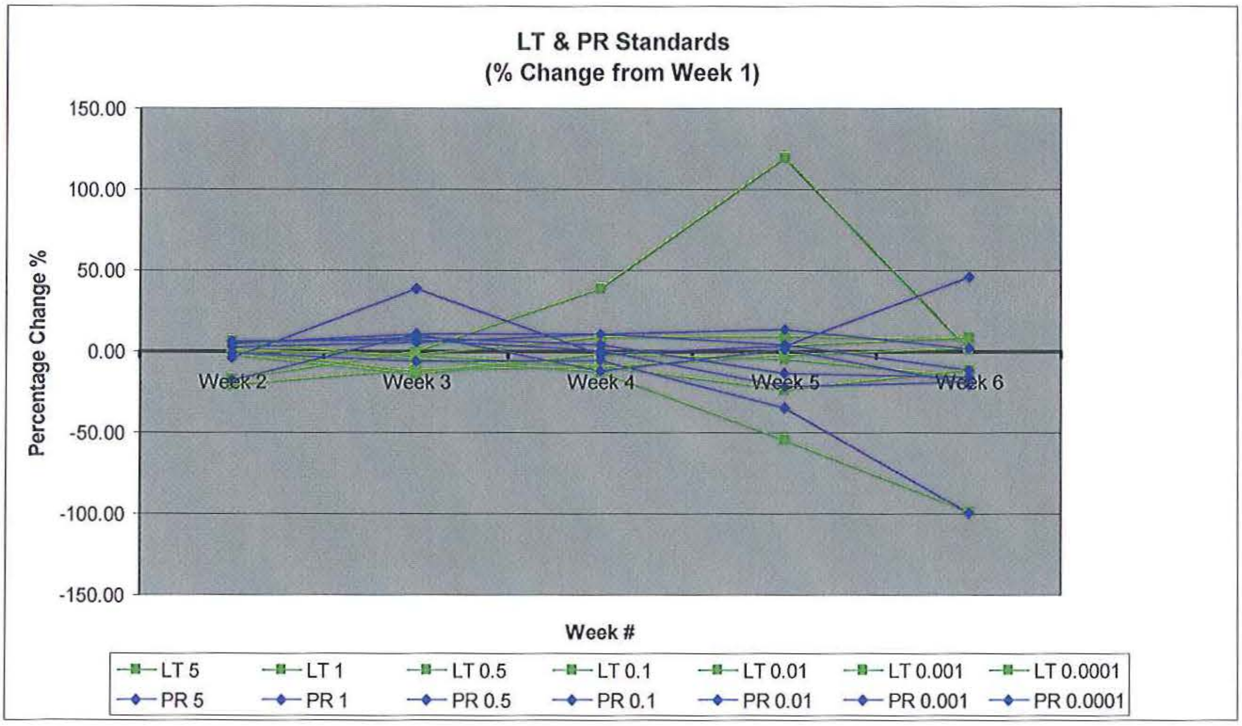


Figure 22: Percentage change of LT & PR Standard sets form week 1.

Overall, the percentage change of both LT and PR from week two appears to be similar. The outliers observed at week three, week four and week five are generated from the results at 0.0001ng/µL. As mentioned, concentrations below 5pg/µL produce significant variation in quantification results and therefore these outliers are not unexpected. However, when the entire data from 0.0001ng/µL were excluded, both LT and PR standards appear to be stable (both showing low percentage change) up until week five as shown in Figure 26 below.

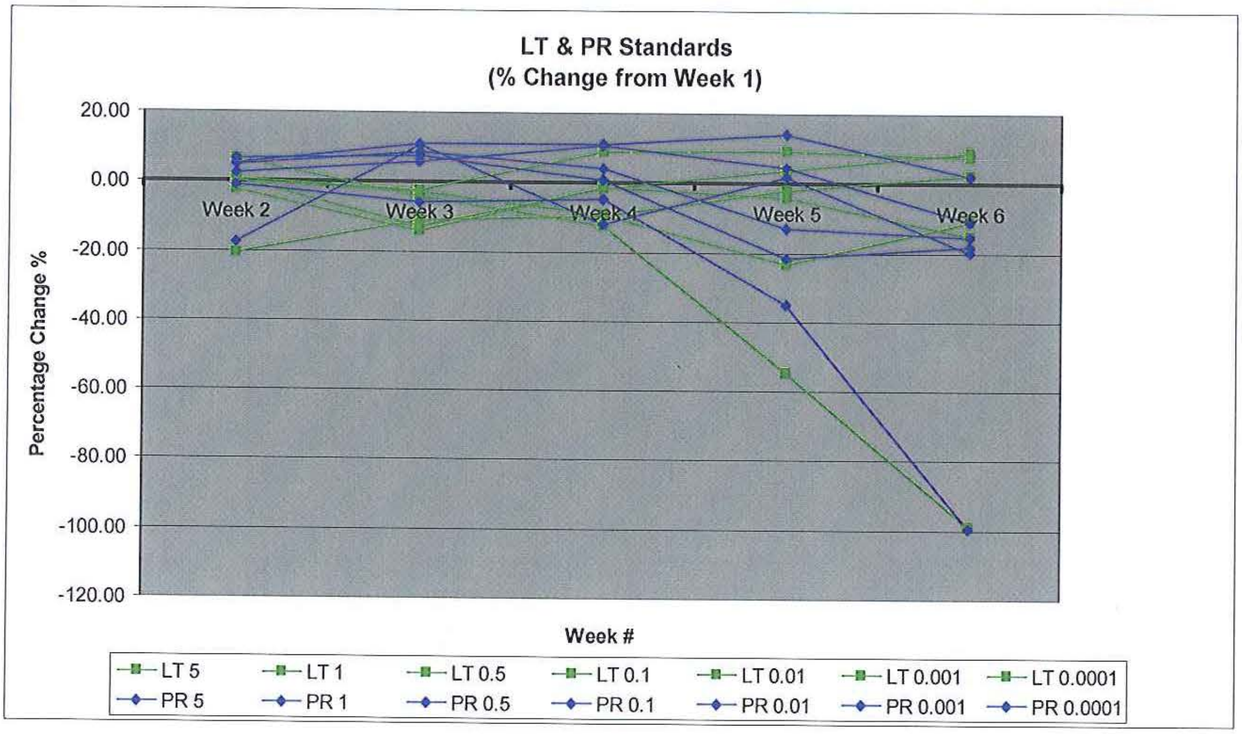


Figure 23: Percentage change of LT & PR Standard sets from week 1 (outliers removed).

Both standards show less that a 21 % change in the quantification results each week until week five. From the fifth week both LT and PR standards start showing higher percentage changes and variability and therefore maybe becoming unstable at this period of time.

Overall, both standard sets behaved similarly over the observed six week period, exhibiting signs of instability from week five. Based on the results of this experiment, it is recommended the Life Technologies quantification standard once prepared, are used for a period up to 4 weeks.

6.3 Experiment 3a – Single Source Sensitivity (LOD)

Five male and five female samples were serially diluted to obtain a range of concentrations from 0.09ng/μL to 1 pg/μL. These samples were quantified in duplicate with the Quantifiler® Trio kit using LT standard Set 2 – which was the most accurate and stable standard set observed in Experiment 1 and 2. The limit of detection (LOD) was assessed in this experiment.

Table 6 below shows the expected and the average SAT, LAT and Y-target results of each target for the male samples. The SAT, LAT and Y-target results for the male samples all gave quantification results down to 1 pg/μL.

Table 6: Average male quantification results for single source sensitivity

Male			
DNA Concentration (ng/µL)	**Average SAT**	**Average LAT**	**Average Y Target**
0.09	0.16118	0.21884	0.18307
0.07	0.10541	0.14707	0.12782
0.05	0.08821	0.11241	0.09839
0.03	0.06041	0.07942	0.07091
0.01	0.02045	0.02415	0.02213
0.009	0.01820	0.02374	0.01924
0.008	0.01547	0.02070	0.01802
0.007	0.01347	0.01804	0.01466
0.006	0.01199	0.01469	0.01450
0.005	0.00861	0.01068	0.00954
0.004	0.00725	0.00866	0.00769
0.003	0.00506	0.00660	0.00520
0.002	0.00357	0.00449	0.00434
0.001	0.00257	0.00274	0.00307

Table 7 shows the expected and the average SAT, LAT and Y-target results of the SAT and LAT target for the female samples. The SAT and LAT results for the female samples all gave quantification results down to 1 pg/µL. A small quantification value was observed for the Y-target in one replicate of one female sample (0.004 ng/µL), resulting in a small average quantification value. No quantification result was observed in the other sample replicate at that concentration. This may likely be a very small contamination event of a male component, or may be an example of cross reactivity.

Table 7: Average female quantification results for single source sensitivity

Female			
DNA Concentration (ng/µL)	**Average SAT**	**Average LAT**	**Average Y Target**
0.09	0.13408	0.17968	0
0.07	0.07626	0.10859	0
0.05	0.05708	0.07710	0
0.03	0.03742	0.04886	0
0.01	0.01652	0.02408	0
0.009	0.01420	0.01990	0
0.008	0.01107	0.01433	0
0.007	0.00922	0.01396	0
0.006	0.00782	0.01109	0
0.005	0.00697	0.00912	0
0.004	0.00446	0.00572	0.00011
0.003	0.00386	0.00511	0

0.002	0.00220	0.00311	0
0.001	0.00225	0.00234	0

Table 8 shows the expected and the average SAT and LAT of each target for male and female samples combined.

Table 8: Combined average male & female quantification results for single source sensitivity

Male and Female Combined		
DNA Concentration (ng/µL)	**Average SAT**	**Average LAT**
0.09	0.148	0.199
0.07	0.091	0.128
0.05	0.073	0.095
0.03	0.049	0.064
0.01	0.018	0.024
0.009	0.016	0.022
0.008	0.013	0.018
0.007	0.011	0.016
0.006	0.010	0.013
0.005	0.008	0.010
0.004	0.006	0.007
0.003	0.004	0.006
0.002	0.003	0.004
0.001	0.002	0.003

The SAT and LAT results in Tables 6, 7 and 8 show that Quantifiler® Trio detected DNA in each male and female sample down to concentrations of 1 pg/µL. The Y-target results show that Quantifiler® Trio detected DNA in each male sample down to concentrations of 1 pg/µL.

The results of Experiment 1 further support the findings of this experiment that Quantifiler® Trio can reliably detect DNA down to concentrations of 1 pg/µL.

The results of Experiments 1 and 2 have however shown inaccuracy at low DNA concentrations (i.e. nearing 1 pg/µL). This is not unexpected given the manufacturer has reported that Quantifiler® Trio has single source sensitivity only down to 5 pg/µL [1].

The results from this Experiments 1 and 2 support setting the Quantifiler® Trio LOD at 1 pg/µL. The Quantifiler® Trio LOD is lower than the LOD for Quantifiler® Human (0.00214 ng/µL as per QIS 19977).

6.4 Experiment 3b – Mixture Studies and Sensitivity

Male sample one and female sample three prepared in Experiment 3a were utilised in this experiment. From these two stock samples, two sets of male:female mixture sets were prepared (see Section 4.2.2). These mixture samples were quantified in duplicate with the Quantifiler$^{®}$ Trio using LT standard Set 2 – which was the most accurate and stable standard set observed in Experiments 1 and 2. The sensitivity of Quantifiler$^{®}$ Trio for mixture samples and detecting the male components in low concentrations was assessed.

Table 9 displays the standard curve results from LT standards Set 2. The standard curve result was within the acceptable ranges for Quantifiler$^{®}$ Trio (showing efficiency percentages close to 100%) and the reagent blank yielded an undetermined result.

Table 9: Standard Curve results for STA, LAT and Y-Target.

Trio Std Set 2	
Small Autosomal	
Slope	-3.248
Y-Intercept	27.416
R2 value	0.999
Eff%	103.185
Large Autosomal	
Slope	-3.39
Y-Intercept	25.638
R2 value	0.999
Eff%	97.232
Y Target	
Slope	-3.432
Y-Intercept	27.012
R2 value	0.995
Eff%	95.599

Table 10 shows the average SAT results, the expected concentration and the percentage inaccuracy.

Table 10: Average SAT results from mixture samples.

			SAT		
Sample	**Male:Female Ratio**	**Expected Total Conc. (ng.µL)**	**Ct**	**Quant value**	**% inacc.**
MF1	4000:1	0.025075	32.02205	0.03820	52.33
MF2	2000:1	0.01675	32.62618	0.02526	50.80
MF3	1500:1	0.01250875	32.70058	0.02506	100.31
MF4	1000:1	0.05005	30.72410	0.09605	91.90
MF5	100:1	0.0505	30.78113	0.09496	88.03
MF6	20:1	0.0175	32.44180	0.02849	62.78
MF7	10:1	0.055	31.04209	0.07651	39.12
MF8	5:1	0.04	31.59037	0.05193	29.82
MF9	1:1	0.1	29.82469	0.18145	81.45
MF10	1:5	0.04	31.31025	0.06362	59.04
MF11	1:10	0.055	31.53057	0.05418	-1.50
MF12	1:20	0.0175	32.79605	0.02222	26.98
MF13	1:100	0.0505	30.98511	0.07963	57.69
MF14	1:1000	0.05005	31.58307	0.05243	4.75
MF15	1:1500	0.01250875	32.59609	0.02599	107.74
MF16	1:2000	0.01675	32.45841	0.03023	80.47
MF17	1:4000	0.025075	31.84974	0.04327	72.56

Figure 27 shows the average quantification results for the SAT were higher than expected for each of the mixture samples which explains the percentage inaccuracies shown in Table 11 and 12.

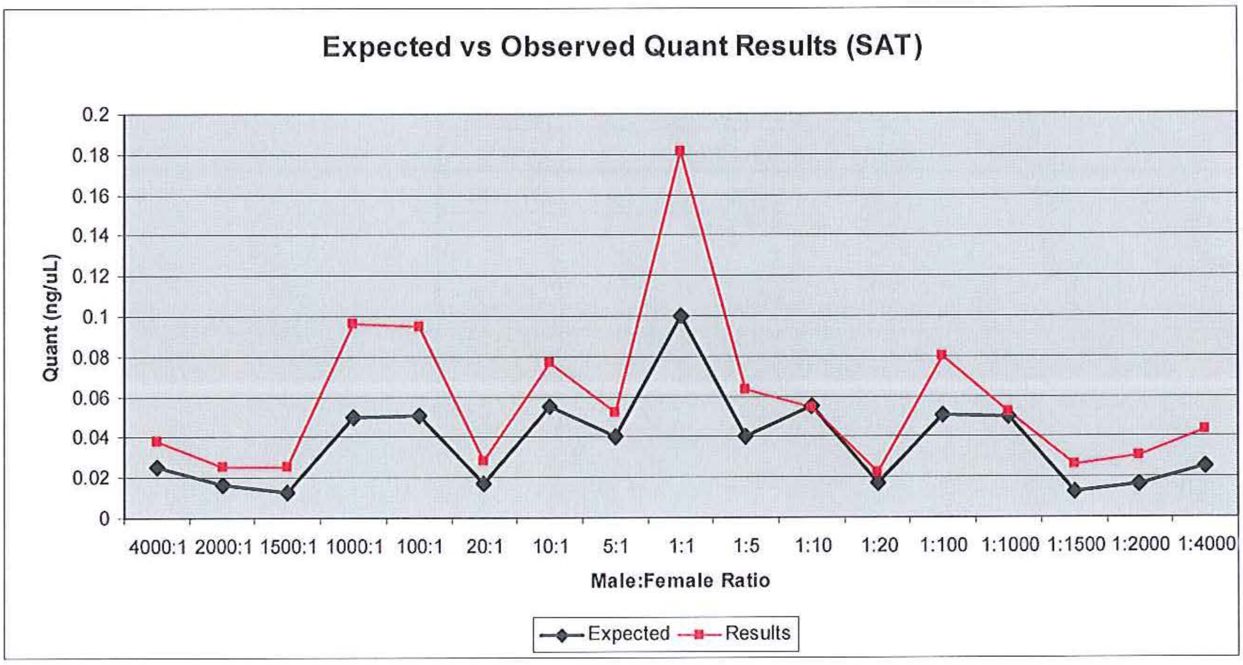


Figure 24: The expected and observed SAT results.

Table 11 shows the average Y-target results, the expected male concentration and the inaccuracy percentage. The levels of inaccuracy for the Y-target results for most of the mixture ratios were higher compared to the SAT results in Experiment 1.

Table 11: Average Y-target results from mixture samples.

			SAT		
Sample	**Male:Female Ratio**	**Expected Total Conc. (ng.µL)**	**Ct**	**Quant value**	**% inacc.**
MF1	4000:1	0.0250675	31.61387	0.04594	83.27
MF2	2000:1	0.0166667	31.92395	0.03765	125.88
MF3	1500:1	0.0124213	32.31022	0.03025	143.52
MF4	1000:1	0.0500000	30.46812	0.09867	97.33
MF5	100:1	0.0500000	30.07393	0.12911	158.23
MF6	20:1	0.0166667	32.11263	0.03269	96.13
MF7	10:1	0.0500000	30.66069	0.08659	73.18
MF8	5:1	0.0333333	31.21141	0.05985	79.54
MF9	1:1	0.0500000	30.24774	0.11441	128.81
MF10	1:5	0.0066667	33.42494	0.01377	106.59
MF11	1:10	0.0050000	33.78366	0.01065	113.10
MF12	1:20	0.0008333	37.57111	0.00109	31.32
MF13	1:100	0.0005000	37.37260	0.00110	120.81
MF14	1:1000	0.0000500	38.11446	0.00058	1064.82
MF15	1:1500	0.0000088	undetermined	undetermined	n/a
MF16	1:2000	0.0000833	38.40884	0.00057	588.33
MF17	1:4000	0.0000075	undetermined	undetermined	n/a

Table 12 shows the average SAT, LAT, Y-target value and the Male:Female Ratio results. The male:female ratios were calculated and only sample MF10 (1:5) and MF12 (1:20) gave accurate male:female ratios. Although a ratio result was obtained from sample MF16 at 1:2000, the accuracy was low – showing a male:female ratio of only 1:51.698. Additionally, no ratio values were produced for samples MF15 (1:1500) and MF17 (1:4000).

Table 12: Average Quantifiler Trio results including the Male:Female Ratio.

		SAT		LAT		Y-Target		
Sample	**Male:Female Ratio**	**Ct**	**Quant value**	**Ct**	**Quant value**	**Ct**	**Quant value**	**Male:Female Ratio**
MF1	4000:1	32.02205	0.03820	30.30657	0.04230	31.61387	0.04594	n/a
MF2	2000:1	32.62618	0.02526	30.93408	0.02750	31.92395	0.03765	n/a
MF3	1500:1	32.70058	0.02506	30.66698	0.03370	32.31022	0.03025	n/a
MF4	1000:1	30.72410	0.09605	28.64207	0.13011	30.46812	0.09867	n/a
MF5	100:1	30.78113	0.09496	28.63181	0.13391	30.07393	0.12911	n/a
MF6	20:1	32.44180	0.02849	30.60663	0.03434	32.11263	0.03269	n/a
MF7	10:1	31.04209	0.07651	29.26893	0.08496	30.66069	0.08659	n/a
MF8	5:1	31.59037	0.05193	29.22619	0.08758	31.21141	0.05985	n/a
MF9	1:1	29.82469	0.18145	27.50811	0.28126	30.24774	0.11441	n/a
MF10	1:5	31.31025	0.06362	29.46560	0.07499	33.42494	0.01377	1:3.619
MF11	1:10	31.53057	0.05418	29.22449	0.08774	33.78366	0.01065	1:4.085
MF12	1:20	32.79605	0.02222	30.97661	0.02689	37.57111	0.00109	1:19.306
MF13	1:100	30.98511	0.07963	28.57373	0.13643	37.37260	0.00110	1:71.129
MF14	1:1000	31.58307	0.05243	29.58046	0.06889	38.11446	0.00058	1:89.019
MF15	1:1500	32.59609	0.02599	30.89240	0.03023	undetermined	undetermined	n/a
MF16	1:2000	32.45841	0.03023	30.54290	0.03966	38.40884	0.00057	1:51.698
MF17	1:4000	31.84974	0.04327	29.50445	0.07252	undetermined	undetermined	n/a

The main aim of this experiment was to test the Y-Target sensitivity, i.e. the ability for Quantifiler® Trio to detect low levels of male DNA in mixtures with high levels of female DNA. The significant limitation of this experiment, particularly for the MF12 – MF17, was the low level of male input DNA in the mixture samples, which was below the LOD for Quantifiler® Trio (i.e. 0.001ng/µL as per Experiment 3a, or 0.005 ng/µL as recommended by the manufacturer [1]). To effectively test the Y-Target sensitivity, the mixtures needed to be prepared using a highly concentrated female sample, which would enable the addition of an amount of male DNA above the Quantifiler® Trio LOD. This experiment was limited by the fact that routine FTA reference samples were used to prepare mixtures, and that a highly concentrated female sample was not available. Further testing of Quantifiler® Trio is recommended, using a highly concentrated female sample so that the Y-Target sensitivity can be more thoroughly investigated.

Although the accuracy was low and limited conclusions can be obtained from the results, the experiment did show that the Quantifiler® Trio can detect a male component in a mixture sample with a male:female ratio down to 1:89. As previously stated, it is recommended that prior to implementation further investigation of the Y-target sensitivity is conducted for mixtures with low levels of male DNA, ensuring that male input DNA is above the Quantifiler® Trio LOD.

6.5 Experiment 4a - Repeatability

The samples used in Experiment 3a were also utilised in this experiment. The samples were quantified in duplicate with Quantifiler® Trio using LT standard Set 2 – which was the most accurate and stable standard set observed in Experiments 1 and 2. The samples were prepared as per Plate 1 in Experiment 3a and was prepared and run twice by the same operator on the same day (Plates A and B). A Student's t-test was performed between the results of both plates at each concentration to test the repeatability of the kit. The standard curve results from the two plates were also compared. Table 13 shows the standard curve results.

Table 13: Standard curve results from Plate 1 and Plate 2 on Day 1.

Plate A		**Plate B**	
Trio Std Set 2		**Trio Std Set 2**	
Small Autosomal		*Small Autosomal*	
Slope	-3.275	**Slope**	-3.274
Y-Intercept	27.639	**Y-Intercept**	27.559
R2 value	0.999	**R2 value**	0.999
Eff%	101.983	**Eff%**	102.057
Large Autosomal		*Large Autosomal*	
Slope	-3.441	**Slope**	-3.422
Y-Intercept	25.609	**Y-Intercept**	25.654
R2 value	0.999	**R2 value**	0.999
Eff%	95.245	**Eff%**	96.006
Y Target		*Y Target*	
Slope	-3.297	**Slope**	-3.205
Y-Intercept	26.96	**Y-Intercept**	26.858
R2 value	0.995	**R2 value**	0.999
Eff%	101.059	**Eff%**	105.122

The standard curve results from both plates were accepted according to the Quantifiler® Trio ranges and the reagent blanks yielded an undetermined result.

Table 14: Student's *t*-test scores between Plate A and Plate B at each concentrations.

DNA Concentration (ng/µL)	**Repeatability - Student's *t*-test scores (Plate A vs Plate B)**
0.09	0.68661
0.07	0.97921
0.05	0.39456
0.03	0.21046
0.01	n/a
0.009	0.84092
0.008	0.15763
0.007	0.86225
0.006	0.97404
0.005	0.55770
0.004	0.59461
0.003	0.94205
0.002	0.13090
0.001	0.01226

The 0.01ng/uL DNA sample was omitted from the results (showing n/a in the table above) as the DNA extract was exhausted during the experiment.

The Student's t-test scores in Table 14 show that no significant differences were observed except for the results at 0.001ng/uL. The low t-test score at 0.001ng/uL is not unexpected given that the results of Experiments 1 and 2 have shown significant inaccuracy very low concentrations.

Overall, Quantifiler® Trio produces the same results when one sample set is processed in duplicate by one user, under the same conditions – i.e. the results are repeatable.

6.6 Experiment 4b - Reproducibility

The samples used in Experiment 4a were also utilised in this experiment. The samples were quantified in duplicate with the Quantifiler® Trio using LT standard Set 2 – which was the most accurate and stable standard set observed in Experiments 1 and 2. A third preparation of the plate used in Experiment 4a was prepared and run once by a different operator on the day following Experiment 4a (Plate C). A Student's t-test score was calculated to compare the results between the reproducibility plate (i.e. Plate C), and the two plates run for the repeatability experiment (i.e. Plates A and B). The standard curve results were also compared to the results in Experiment 4a. Table 15 below shows the standard curve results.

Table 15: Standard curve results of Plate C.

Plate C	
Trio Std Set 2	
Small Autosomal	
Slope	-3.149
Y-Intercept	27.9
R2 value	0.999
Eff%	107.779
Large Autosomal	
Slope	-3.359
Y-Intercept	25.84
R2 value	0.999
Eff%	98.484
Y Target	
Slope	-3.208
Y-Intercept	27.12
R2 value	0.998
Eff%	104.998

The standard curve results from this experiment were accepted according to the Quantifiler® Trio ranges and the reagent blanks yielded an undetermined result. Therefore, no difference was observed in the standard curve results in Experiment 4a and 4b.

From Table 16 below, the 0.01ng/uL sample was omitted from the results (n/a in the table) as the DNA extract was exhausted during the experiment.

Table 16: Student's *t*-test scores between Plate C & Plate A and Plate C & Plate B at each concentration.

DNA Concentration (ng/µL)	Reproducibility - Student's *t*-test scores (Plate C vs Plate A)	Reproducibility - Student's *t*-test scores (Plate C vs Plate B)
0.09	0.51022	0.33511
0.07	0.47368	0.44903
0.05	0.96020	0.36927
0.03	0.28338	0.69796
0.01	n/a	n/a
0.009	0.40860	0.54476
0.008	0.42745	0.53824
0.007	0.49104	0.56289
0.006	0.87782	0.90678
0.005	0.50371	0.96399
0.004	0.18382	0.48788
0.003	0.78928	0.72049
0.002	0.99693	0.11119
0.001	0.00787	0.74229

The Student's t-test scores in Table 16 shows no significant differences between the results of Plate C on day two and Plate A on day one except at 0.001ng/uL. As discussed in Experiment 4a, the low t-test score at 0.001ng/uL is due to the low accuracy and the high variability at that DNA concentration level, therefore the t-test score of 0.00787 ($p \geq 0.05$) is not unexpected.

No significant differences in the results were also seen between the results of Plate C on day two and Plate B on day one. Even at the lowest DNA concentration, the t-test score shows no significant difference between the runs.

Therefore, Quantifiler® Trio produces the same results when one sample set is processed by different operators under the same conditions – i.e. the results are reproducible.

6.7 Experiment 5 - Inhibition

Five types of known DNA inhibitor substances were tested in this experiment to assess how these inhibitors affect Quantifiler® Trio and to determine whether the IPCCt results and IPCCt flag accurately indicate inhibition.

The samples were quantified in duplicate with Quantifiler® Trio using LT standard Set 2 – which was the most accurate and stable standard set observed in Experiment 1 and 2. All inhibitor samples excluding the Trigene Advance were amplified using the PowerPlex®21 Amplification kit.

The standard curve results, IPCCt, IPCCt flag, SAT values and the allele counts were calculated and averaged for each inhibitor sample. Table 17 below shows the standard curve results. The standard curve results from this experiment were within acceptable ranges for Quantifiler® Trio and the reagent blanks yielded undetermined results.

Table 17: Standard curve results.

Trio Standard (Set 2)	
Small Autosomal	
Slope	-3.242
Y-Intercept	27.531
R2 value	0.999
Eff%	103.469
Large Autosomal	
Slope	-3.375
Y-Intercept	25.668
R2 value	0.999
Eff%	97.824
Y Target	
Slope	-3.451
Y-Intercept	27.049
R2 value	0.994
Eff%	94.882

Table 18 shows the quantification results of the inhibitor samples. The control sample containing no inhibitors showed quantification results, full allele calls in the DNA profile and displayed no IPCCt flag.

Only two out of the five inhibitors appear to have affected DNA quantification and DNA amplification. Humic acid at each concentration showed complete inhibition and the three highest concentration of Trigene Advance also showed complete inhibition. As it is known that Trigene Advance adversely affects the capillary arrays in the genetic analysers [9], DNA profiles were not generated for these samples.

Hematin, Ethanol and Semen did not appear to have any effect – resulting in quantification values and full allele calls in the DNA profiles. It should be noted that the samples spiked with semen gave mixed DNA profiles, with full allelic representation from the in-house blood positive control and the semen donor (even though un-extracted semen was used).

After a review of the Humic Acid results, the five concentrations that were initially prepared were deemed too concentrated and did not simulate the concentrations that may occur in routine crime scene samples. As a result, full inhibition at all concentrations was observed as mentioned above. Therefore, the concentrations of the Humic Acid added to the DNA samples were reduced (see Section 4.2.3). The Humic Acid repeat results are shown in Table 19.

Table 18: Quantification results table of inhibitor samples.

Sample	IPCCT Flag	IPC Ct Value (Mean)	Ct Value - SAT (Mean)	Quant Value - SAT (Mean)	# Alleles (Total 42)
Control	no	27.7882	29.6944	0.2154	42
Humic Acid-1	yes	undetermined	n/a	n/a	0
Humic Acid-2	yes	undetermined	n/a	n/a	0
Humic Acid-3	yes	undetermined	n/a	n/a	0
Humic Acid-4	yes	36.7674	n/a	n/a	0
Humic Acid-5	yes	undetermined	n/a	n/a	0
Hematin-1	no	27.8708	30.3048	0.1394	42
Hematin-2	no	26.7139	30.636	0.1102	42
Hematin-3	no	27.4044	30.4392	0.1271	42
Hematin-4	no	27.0259	30.4591	0.1249	42
Hematin-5	no	27.9048	30.6087	0.1123	42
Ethanol-1	no	27.481	30.0746	0.1647	42
Ethanol-2	no	26.8181	30.2016	0.15	42
Ethanol-3	no	26.8561	29.9629	0.1778	42
Ethanol-4	no	27.3737	29.8653	0.1909	42
Ethanol-5	no	27.6428	29.9955	0.1751	42
Trigene Advance-1	no	26.5418	30.5517	0.1174	n/a (affects capillary)
Trigene Advance-2	no	28.5102	n/a	n/a	n/a (affects capillary)
Trigene Advance-3	yes	undetermined	n/a	n/a	n/a (affects capillary)
Trigene Advance-4	yes	undetermined	n/a	n/a	n/a (affects capillary)
Trigene Advance-5	yes	undetermined	n/a	n/a	n/a (affects capillary)
Semen-1	no	27.2567	29.8234	0.1962	42
Semen-2	no	27.2507	29.222	0.3018	42
Semen-3	no	26.0779	29.2576	0.2974	42
Semen-4	no	26.8895	29.0098	0.35	42
Semen-5	no	26.4272	28.0948	0.7451	42

Table 19 shows the results from a repeat of the five humic acid inhibitor samples.

Table 19: Humic Acid repeat quantification results.

Sample	IPCCT Flag	IPC Ct Value (Mean)	Ct Value - SAT (Mean)	Quant Value - SAT (Mean)	# Alleles (Total 42)
Control	no	27.0704	30.1641	0.2059	42
Humic Acid-1	no	26.7641	29.804	0.267	42
Humic Acid-2	no	27.6209	29.6318	0.3019	42
Humic Acid-3	no	27.539	30.2767	0.1899	42
Humic Acid-4	no	27.5001	29.9775	0.2357	42
Humic Acid-5	no	26.3479	29.9446	0.2413	42

From the repeat results, at lower concentrations the Humic Acid samples did not affect DNA quantification and amplification at any concentration, resulting in quantification results and also displaying full allele calls in the DNA profile.

The samples that did show inhibition were accurately flagged by the IPCCt value and the IPCCt Flag within the HID Real-Time PCR Analysis Software. According to the manufacturer an IPCCt flag should be observed on samples with an undetermined IPCCt value or a value two units above the baseline (i.e. 27.53 in this experiment) [1]. As shown in Table 19, this was observed as all undetermined samples and IPCCt values two units above the baseline of 27.53 was identified by the software via the IPCCt flag.

Based on the results from this experiment, the IPCCt result and the IPCCt Flag from Quantifiler® Trio accurately determines inhibited samples and the kit also appears not to be affected by some known inhibitory substances such as Humic Acid, Hematin, Ethanol and Semen at the concentrations tested. Quantifiler® Trio was inhibited by Trigene Advance, however this is not unexpected given that Trigene Advance is a cleaning agent, designed to break down DNA.

6.8 Experiment 6a – Degradation Protocol

Extracted in-house blood positive controls were exposed to UV in duplicate at increasing exposure times to develop a viable mechanism for degrading samples from low to high levels. A total of thirteen samples were quantified using the Quantifiler® Human kit using a Promega standard set currently used in the laboratory for routine analysis. A control sample which wasn't subjected to UV was also included. All samples were then amplified using the PowerPlex®21 Amplification kit.

The effect of UV on the quantification results and the DNA profiles were assessed. Table 20 shows the standard curve results obtained for the PR standard set used. The standard curve results from this experiment were accepted according to the laboratory's current thresholds and the reagent blank yielded an undetermined result.

Table 20: Quantifiler Human standard curve results.

Promega Stds.	
Slope	-3.1058
Y-Intercept	27.778151
R2 value	0.995598

Table 21 shows the Quantifiler® Human quantification results (Ct value, quant value, IPCCt) and the total number of alleles for each UV exposure time. From the quantification results, increasing the UV exposure times resulted in the consistent decrease in the DNA quantification values. In addition, the allele calls in the DNA profiles also showed a consistent decrease. Therefore, UV exposure was shown to work and is an efficient method in degrading DNA samples.

Table 21: Quantifiler Human results and allele numbers.

		HUMAN			
Sample	**UV Exposure**	**Ct Value**	**Quant Value**	**IPCCT**	**# Allele (Total 42)**
1	Nil	27.73	1.03000	28.04	42
2	10 minutes	28.29	0.68300	27.91	35
3	10 minutes	28.28	0.68800	27.83	37
4	1 hour	30.41	0.14200	27.88	19
5	1 hour	30.35	0.14800	27.78	19
6	5 hours	33.95	0.01030	28.00	4
7	5 hours	34.81	0.00546	28.11	7
8	8 hours	35.35	0.00364	28.25	4
9	8 hours	36.36	0.00172	28.15	4
10	15 hours	undetermined	undetermined	28.07	0
11	15 hours	undetermined	undetermined	28.00	0
12	24 hours	undetermined	undetermined	27.88	0
13	24 hours	undetermined	undetermined	27.94	0

6.9 Experiment 6b – Degradation Index Proof of Concept

The same thirteen samples used in Experiment 6a were also utilised in this experiment. All samples were quantified using Quantifiler® Trio using the LT standard Set 2 – which was the most accurate and stable standard set observed in Experiments 1 and 2.

The effect of UV on the quantification results was assessed as well as whether the degradation index (DI) was a reliable measure of degradation and if a DI threshold could be established. Table 22 below shows the standard curve results. The standard curve results from this experiment were within acceptable ranges for Quantifiler® Trio (showing efficiency percentages close to 100%) and the reagent blank yielded an undetermined result.

Table 22: Quantifiler Trio standard curve results.

Trio Standard (Set 2)	
Small Autosomal	
Slope	-3.136
Y-Intercept	27.729
R2 value	0.997
Eff%	108.376
Large Autosomal	
Slope	-3.377
Y-Intercept	25.794
R2 value	0.996
Eff%	97.756
Y Target	
Slope	-3.188

Y-Intercept	27.055
R2 value	0.998
Eff%	105.905

Table 23 shows the Quantifiler® Trio quantification results (IPCCt, SAT, LAT, Ct and the DI). From the results, as the UV exposure time increased the SAT and LAT quantification results decreased. The LAT concentration results decreased more rapidly than the SAT results, which is as expected. A DI value of 6.5288 and 8.2193 was observed at 10 minutes of UV, and at 1 hour of UV exposure the DI had increased to 119.5277 and 162.5102. At 5 hours of UV exposure, an SAT concentration was calculated, however the LAT result was undetermined, therefore a DI could not be calculated. At UV exposure times greater than 5 hours, both the SAT and LAT results were undetermined therefore no DI was calculated.

Table 23: Quantifiler Trio quantification results.

Sample	**UV Exposure**	**IPCCT**	**Ct Value (SAT)**	**Quant Value (SAT)**	**Ct Value (LAT)**	**Quant Value (LAT)**	**Degradation Index**
1	Nil	28.58	26.80	1.9786	24.20	2.9638	n/a
2	10 min	27.46	28.41	0.6064	29.28	0.0929	6.5288
3	10 min	27.74	28.62	0.5209	29.84	0.0634	8.2193
4	1 hour	27.44	32.11	0.0402	37.52	0.0003	119.5277
5	1 hour	27.46	31.95	0.0451	37.80	0.0003	162.5102
6	5 hours	27.17	38.49	0.0004	Undetermined	Undetermined	n/a
7	5 hours	27.47	38.00	0.0005	Undetermined	Undetermined	n/a
8	8 hours	27.35	Undetermined	Undetermined	Undetermined	Undetermined	n/a
9	8 hours	27.29	Undetermined	Undetermined	Undetermined	Undetermined	n/a
10	15 hours	26.78	Undetermined	Undetermined	Undetermined	Undetermined	n/a
11	15 hours	27.34	Undetermined	Undetermined	Undetermined	Undetermined	n/a
12	24 hours	25.21	Undetermined	Undetermined	Undetermined	Undetermined	n/a
13	24 hours	26.35	Undetermined	Undetermined	Undetermined	Undetermined	n/a

The quantification results in this experiment including the total number of alleles calculated in Experiment 6a shows that the DI value is a reliable measure of degradation. The small DI scores observed at 10 minutes of UV exposure coincides with a drop in the total number of alleles from a full 42 to 36 alleles on average. At 1 hour of UV, the large DI score correlated with a further reduction in alleles obtained (i.e. 19 alleles, less than half compared to a full DNA profile). Lastly, samples with undetermined SAT/LAT values or DI values that are unable to be calculated, show significantly lower allele totals of 4 or less .

This experiment has shown the Quantifiler® Trio DI is a reliable measure of inhibition (i.e. as the level of inhibition increases, the DI also increases and the number of alleles obtained from amplification decreases). Further, a DI threshold may be able to be determined, beyond which useful DNA profiles are not likely to be obtained, and therefore sample processing would cease.

6.10 Experiment 6c – Degradation Index Threshold

Eleven extracted in-house blood positive control samples were exposed to increasing UV exposure times in triplicate (including one control sample that was not exposed to UV). A total of 34 samples were quantified using Quantifiler® Trio kit using the LT standard Set 2 – which was the most accurate and stable standard set observed in Experiment 1 and 2. All samples were then amplified using the PowerPlex®21 Amplification kit.

The effect of UV on the quantification results and the DNA profiles was assessed and a DI threshold (a set value above which samples are too degraded to give useful DNA profiles) was explored. Table 24 shows the standard curve results. The standard curve results from this experiment were within acceptable ranges for Quantifiler® Trio (showing efficiency percentages close to 100%) and the reagent blank yielded an undetermined result.

Table 24: Quantifiler Trio standard curve results.

Trio Standard (Set 2)	
Small Autosomal	
Slope	-3.014
Y-Intercept	27.583
R2 value	0.999
Eff%	114.66
Large Autosomal	
Slope	-3.23
Y-Intercept	25.524
R2 value	0.999
Eff%	103.971
Y Target	
Slope	-3.164
Y-Intercept	26.811
R2 value	0.998
Eff%	107.031

Table 25 shows the average Quantifiler® Trio quantification results (IPCCt, SAT, LAT, Ct, DI and the total number of alleles).

Table 25: Average Quantifiler Trio quantification results.

Sample	UV Exposure	Average IPCCT	Average Ct Value (SAT)	Average Quant Value (SAT)	Average Ct Value (LAT)	Average Quant Value (LAT)	Degradation Index	Average #Allele (Total 42)
1	Nil	28.24	26.6378	2.0580	24.1924	2.5834	0.7966	42.00
2	5 min	27.49	28.5263	0.4871	28.0807	0.1619	3.0153	42.00
3	10 min	26.62	29.3653	0.2609	30.7718	0.0240	10.8882	36.33
4	20 min	27.16	29.8703	0.1743	32.1978	0.0086	20.3921	35.33
5	30 min	27.35	31.0887	0.0687	35.3250	0.0009	75.3547	24.33
6	40 min	27.35	31.3946	0.0544	35.1298	0.0011	53.0365	26.00
7	50 min	27.25	31.7351	0.0420	37.6957	0.0002	250.4552	23.00
8	1 hour	27.23	32.2540	0.0282	39.0460	0.0001	444.4416	21.33
9	2 hours	27.26	33.8743	0.0084	39.6577	0.0000	194.4811	18.33
10	4 hours	27.09	39.3915	0.0001	undetermined	undetermined	n/a	4.00
11	8 hours	27.12	undetermined	undetermined	undetermined	undetermined	n/a	1.67
12	24 hours	26.75	undetermined	undetermined	undetermined	undetermined	n/a	0.00

Table 26 shows the average peak heights of the smallest and largest fragment in each DNA profile. This is additional data was added to compliment the results of the total number of alleles.

Table 26: Degradation index and amplification results.

Sample	UV Exposure	Degradation Index	Average # Allele (Total 42)	Ave. Pk Height (smallest fragment - THO1)	Ave. Pk Height (largest fragment - PENTA D)
1	Nil	0.7966	42.00	2426.00	1694.00
2	5 min	3.0153	42.00	1457.00	108.33
3	10 min	10.8882	36.33	1999.67	65.00
4	20 min	20.3921	35.33	2500.33	26.00
5	30 min	75.3547	24.33	3035.67	80.67
6	40 min	53.0365	26.00	4775.50	47.00
7	50 min	250.4552	23.00	4143.67	62.00
8	1 hour	444.4416	21.33	4051.33	59.33
9	2 hours	194.4811	18.33	2097.67	88.33
10	4 hours	n/a	4.00	79.33	395.67
11	8 hours	n/a	1.67	59.00	69.00
12	24 hours	n/a	0.00	n/a	n/a

One replicate of the 40 minute UV exposure sample was excluded from the results as an outlier because it had a higher quantification result than the other 2 replicates (approximately twice), and may not have been properly exposed to the UV.

According to Life Technologies [1], a DI of 1-10 is considered slightly to moderately degraded and a DI above 10 is considered significant degradation. However from the results shown in Table 26, the samples which were considered by the manufacturer as significantly degraded were still able to generate DNA profiles that with useful numbers of alleles. Samples showing a DI value of 20.3921 on average were still able to recover approximately 35 alleles. However, DI values beyond this value begin to show significant decreases in the total number of alleles in the DNA profile.

In addition to allele count, the imbalance between the peak heights of the smallest locus and the largest locus was examined (see Table 26). Even at a DI of 10, the peak height imbalance between the smallest and largest locus is significant (i.e. 1999.67 – 65.00 RFU). Interpretation of samples with this level of imbalance may be difficult.

This experiment has shown the DI can be used to predict the level of degradation in a sample. Samples with a DI greater than 10, may still give informative numbers of alleles, but these samples may have significant peak height imbalance from smallest to largest loci, which may make interpretation difficult. Further investigation is required to determine whether a DI threshold can be established for sample processing to cease due to low chances of obtaining useful DNA profiles.

It is recommended that once implemented and in routine use, data mining is conducted so a larger data set can be used to determine if a DI threshold can be established.

6.11 Experiment 7 – Quantifiler® Trio Kit New Formulation (IPC modification)

Life Technologies Quantifiler® Trio has been recently modified to improve the stability of the kit long term. The IPC structure has been changed from a super-coiled structure to a linearised form and according to the manufacturer the modification only ensures a more stable IPCCt over extended long-term storage and does not change the kit's overall performance [8].

As the original Quantifiler® Trio kit was used throughout this validation, a test of the modified kit was performed to determine any differences in the resulting standard curve results and quantification values.

Plate 1 from Experiment 3a was re-prepared using the modified kit and a Student's t-test was then performed between the results in this experiment and original results from Experiment 3a. The standard curve results from the original and the modified kit are shown below in Table 27.

Table 27: Sensitivity Plate standard curve results (Original vs Modified Kit)

	Old Formulation	**New Formulation**
Small Autosomal		
Slope	-3.244	-3.05
Y-Intercept	27.598	29.257
R2 value	0.998	0.997
Eff%	103.345	112.776
Large Autosomal		
Slope	-3.444	-3.364
Y-Intercept	25.78	25.972
R2 value	0.999	1
Eff%	95.161	98.29
Y Target		
Slope	-3.418	-3.253
Y-Intercept	27.146	27.741
R2 value	0.991	0.996
Eff%	96.122	102.941

Although the SAT slope result was slightly higher from the modified kit, both standard curve results were within acceptable ranges for Quantifiler® Trio and the reagent blanks yielded undetermined results.

A Student's t-test score of 0.580 ($p \geq 0.05$) was calculated, resulting in no significant difference in the overall quantification results between the original and the modified kit.

The inhibition plate in Experiment 5 was also re-prepared using the modified kit. A Student's t-test and a comparison of the IPCCt flags on both set of results were performed. The standard curve results from the original and the modified kit are shown in Table 28.

Table 28: Inhibition Plate standard curve results (Original vs Modified Kit)

	Old Formulation	**New Formulation**
Small Autosomal		
Slope	-3.242	-3.023
Y-Intercept	27.531	28.785
R2 value	0.999	0.995
Eff%	103.469	114.178
Large Autosomal		
Slope	-3.375	-3.341
Y-Intercept	25.668	25.844
R2 value	0.999	0.999
Eff%	97.824	99.223
Y Target		
Slope	-3.451	-3.212
Y-Intercept	27.049	27.573
R2 value	0.994	0.993
Eff%	94.882	104.797

Although the SAT slope results were again slightly higher for the modified kit, both standard curve results were within acceptable ranges for Quantifiler® Trio and the reagent blanks yielded undetermined results.

A Student's t-test score of 0.763 ($p \geq 0.05$) was calculated, again resulting in no significant difference in the average quantification results between the original and the modified kit. Additionally, the samples that did show inhibition were also accurately flagged by the IPCCt value and the IPCCt Flag.

Based on this experiment, the overall quantification results using the modified Quantifiler® Trio kit were consistent with the original results.

6.12 Quantifiler® Trio Standard Curve Results - Acceptable Ranges

Based on all the standard curve results throughout this validation, as well as the manufacturer's recommended ranges, the acceptable range for the Slope, Y-target, R2 value are as follows:

SAT

- Slope = -3.0 to -3.6
- Y-intercept = 26.49482 to 27.39453 (1SD), 26.04497 to 27.84438 (2SD), 25.59512 to 28.29423 (3SD)
- R2 = ≥0.98

LAT

- Slope = -3.1 to -3.7
- Y-intercept = 24.47537 to 25.6442 (1SD), 23.89096 to 26.22861 (2SD), 23.30654 to 26.81302 (3SD)
- R2 = ≥0.98

Y-Target

- Slope = -3.0 to -3.6
- Y-intercept = 26.08669 to 26.81522 (1SD), 25.72243 to 27.17948 (2SD), 25.35817 to 27.54375 (3SD)
- R2 = ≥0.98

The acceptable ranges listed will be utilised once the Quantifiler® Trio kit is implemented and further assessment of the Y-intercept ranges will be conducted after the kit has been in routine use in the laboratory for a period of time – this is to determine whether the majority of the Y-intercept values fall within 1 SD, 2 SD or 3 SD ranges.

7. Conclusions

This validation study has shown that Quantifiler® Trio is a suitable test for determining the concentration of DNA in a sample by measurement of the SAT. Quantifiler® Trio has a LOD of 0.001ng/µL, which is more sensitive than the Quantifiler® Human kit currently in use. Quantifiler® Trio also gives repeatable and reproducible results.

The Life Technologies quantification standard, included in the Quantifiler® Trio kit, is more accurate than the Promega standard currently used for the Quantifiler® Human kit. The Life Technologies standard is stable for a period of five weeks. Implementation of the Life Technologies standard should improve the accuracy of quantification results in Forensic DNA Analysis.

The Y-Target can be used to detect male DNA in mixtures of male and female DNA, however the sample selection limitations in this study meant this could not be tested beyond a mixture ratio of 1:89 (M:F). Further testing is recommended, in conjunction with the validation/implementation of Y-Filer® Plus, so that mixtures with male components less than 1:89 (M:F) can be tested (n.b. male components in these mixtures must be above the Quantifiler® Trio LOD).

The IPCCt result and IPCCt flag can be used to determine whether the Quantifiler® Trio quantification reaction has been affected by inhibitors present in a sample. Further, the Quantifiler® Trio reaction appears not to be affected by known PCR inhibitors including Humic Acid, Hematin, Ethanol and Semen. Trigene Advance was shown to inhibit the reaction, but this is not unexpected given that Trigene Advance is a cleaning agent designed to break down DNA.

The SAT and LAT quantification results can be used together to determine a DI which is a measure of DNA degradation. Further post-implementation studies are required, drawing on a larger data set, to determine if a DI threshold can be set, above which sample processing would cease due to the low likelihood of obtaining useful results.

Finally, the new modified Quantifiler® Trio kit (which includes a modified IPCCT) showed no change in performance and quality when compared to the previous version of the kit.

8. Recommendations

1. Quantifiler® Trio is implemented as a replacement for the Quantifiler® Human DNA quantification kit.
2. The acceptable ranges for the standard curve results (section 6.12) will be used once Quantifiler® Trio is implemented with continuous monitoring of the Y-intercept values over time.
3. Quantifiler® Trio is implemented initially using AUSLAB, without any modifications to the AUSLAB quantification results page/s. This requires the development of an Excel macro to convert the Quantifiler® Trio results file into an AUSLAB compatible format.
4. The Life Technologies quantification standard is implemented, and once prepared, used for a period up to 5 weeks and continued to be monitored.
5. The Quantifiler® Trio LOD for sample workflow is set at 0.001 ng/µL
6. Current auto-microcon business rules are retained (as per QIS 24012)
7. Further study be conducted into the Y-Target sensitivity (LOD), specifically mixtures with proportions of male contributions less than 1:89 (M:F) where the male component concentration is above the Quantifiler® Trio LOD.
8. The IPCCt flag is used to identify samples which are inhibited and direct these samples automatically to a Nucleospin cleanup.
9. Further study be conducted into whether a DI threshold can be set, above which sample processing would be ceased due to the low likelihood of obtaining useful DNA results.
10. Using the Standard Curve Result's Efficiency Percentage to monitor and indicate when to change standard sets.
11. Before Quantifiler® Trio is used in conjunction with Yfiler® Plus, the potential cross reactivity of the Quantifiler® Trio Y-target with highly concentrated

female DNA must be further investigated. It is recommended that the following experiments be conducted:

- Data mine all female reference samples quantified with Quantifiler® Trio post implementation to identify any cross Y-target cross reactivity; and
- Include an experiment in the future Yfiler® Plus validation/implementation project, whereby highly concentrated female reference samples are quantified with Quantifiler® Trio to investigate possible cross reactivity with the Y-target.

9. References

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JH-5

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Project Report #185

Validation of two QuantStudio™ 5 Real-Time PCR Systems

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Queensland
Government

Document Details

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Document sign off

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Contents

Abstract

The purpose of this project was to validate both QuantStudio™ 5 (QS5) instruments for the analysis of Quantifiler® Trio (Quant Trio) DNA quantification reactions. Both QS5-A and QS5-B were validated separately using the experiments outlined below.

The following experiments were performed on both QS5-A and QS5-B:

- Sensitivity and Limit of Detection
- Comparison of QS5 and 7500
- Y-Intercept Thresholds

Repeatability and reproducibility was performed on QS5-A only.

The results of this verification found that both QS5-A and QS5-B instruments are suitable to perform DNA quantification using the Quantifiler® Trio quantification kit, and can replace the two 7500 instruments that are currently in use.

Introduction

Forensic DNA Analysis has two 7500 Real-Time PCR instruments (7500s) which are used to analyse Quantifiler® Trio DNA quantification reactions. Both 7500s are at the end of life and are being replaced under the Health Technology Equipment Replacement Program (HTER). The HTER process identified the QuantStudio™ 5 Real-Time PCR System (QS5) as the most suitable replacement for the 7500s. Two QS5s were purchased.

Both QS5s were validated for the analysis of Quantifiler® Trio DNA quantification reactions by the manufacturer. The QS5s were delivered with pre-installed protocols for the Quantifiler® Trio kit.

Validation of the two QS5s were performed separately (except for repeatability and reproducibility), QS5-A followed by QS5-B. Both QS5s will be implemented concurrently and replace the two 7500s. The validation experiments for both QS5s were the same.

Resources

All reagents, materials and equipment used in this project were as specified in the approved in-house document Project Proposal #185 – Validation of QuantStudio™ Real-Time PCR Systems (June 2017) [4]. This document will be referred to as the Experimental Design. The following QIS documents are referenced throughout this report:

- Operation and Maintenance of the Microlab STARlet and LabElite Integrated I.D.Capper. QIS 34050. [5]
- Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit. QIS 33407. [6]

Methods

The methods for each experiment in this verification were as per the Experimental Design unless otherwise specified.

Sample Selection

NIST standards were used for this validation. NIST Standard sets A, B and C were used to create serial dilutions using TE-4 buffer with final concentrations as per the Experimental Design. NIST Standards A, B, and C, are derived from a single male donor, multiple female donors, and multiple male and female donors, respectively [3].

Experiment 3 will utilise twelve previously extracted Collaborative Testing Service (CTS) samples with volumes greater than 70 µL.

Experiments and Results

Experiment 1: Sensitivity, Limit of Detection and Inaccuracy

Purpose

Quantifiler® Trio has been shown to have a single source sensitivity down to concentrations of 0.005 ng/µL[1]. The validation of Quantifiler® Trio on the 7500s determined the Limit of Detection (LOD) to be 0.001 ng/µL[2]. Serial dilutions of NIST standards were used to determine the LOD for Quantifiler® Trio on the QS5 instruments. Percent change (inaccuracy) was calculated from the expected and observed result. This was performed for each of the quantification targets: SAT, LAT and Y-Target for both QS5 instruments and 7500-A.

Results

Two plates of NIST standards A, B, and C serial dilution duplicates were prepared each for the 7500-A and both QS5s as outlined in Tables 1 and 2 below. Dilutions ranged from 5 – 0.0001 ng/µL.

Table 1: NIST Standards Serial Dilutions – Platemap 1 of 2

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 5 0.005 ng/µL	NIST C 5.0 ng/µL	NIST B 0.5 ng/µL	NIST A 0.1 ng/µL	NIST C 0.09 ng/µL	NIST B 0.05 ng/µL	NIST A 0.03 ng/µL	NIST C 0.01 ng/µL	NIST B 0.008 ng/µL	NIST A 0.007 ng/µL	NIST C 0.006 ng/µL
B	STD 1 50 ng/µL	STD 5 0.005 ng/µL	NIST A 1.0 ng/µL	NIST C 0.5 ng/µL	NIST B 0.1 ng/µL	NIST A 0.07 ng/µL	NIST C 0.05 ng/µL	NIST B 0.03 ng/µL	NIST A 0.009 ng/µL	NIST C 0.008 ng/µL	NIST B 0.007 ng/µL	NIST A 0.005 ng/µL
C	STD 2 5.000 ng/µL	Reagent Blank	NIST B 1.0 ng/µL	NIST A 0.5 ng/µL	NIST C 0.1 ng/µL	NIST B 0.07 ng/µL	NIST A 0.05 ng/µL	NIST C 0.03 ng/µL	NIST B 0.009 ng/µL	NIST A 0.008 ng/µL	NIST C 0.007 ng/µL	NIST B 0.005 ng/µL
D	STD 2 5.000 ng/µL	NIST A 5.0 ng/µL	NIST C 1.0 ng/µL	NIST B 0.5 ng/µL	NIST A 0.09 ng/µL	NIST C 0.07 ng/µL	NIST B 0.05 ng/µL	NIST A 0.01 ng/µL	NIST C 0.009 ng/µL	NIST B 0.008 ng/µL	NIST A 0.006 ng/µL	NIST C 0.005 ng/µL
E	STD 3 0.500 ng/µL	NIST B 5.0 ng/µL	NIST A 1.0 ng/µL	NIST C 0.5 ng/µL	NIST B 0.09 ng/µL	NIST A 0.07 ng/µL	NIST C 0.05 ng/µL	NIST B 0.01 ng/µL	NIST A 0.009 ng/µL	NIST C 0.008 ng/µL	NIST B 0.006 ng/µL	NIST A 0.005 ng/µL
F	STD 3 0.500 ng/µL	NIST C 5.0 ng/µL	NIST B 1.0 ng/µL	NIST A 0.1 ng/µL	NIST C 0.09 ng/µL	NIST B 0.07 ng/µL	NIST A 0.03 ng/µL	NIST C 0.01 ng/µL	NIST B 0.009 ng/µL	NIST A 0.007 ng/µL	NIST C 0.006 ng/µL	NIST B 0.005 ng/µL
G	STD 4 0.050 ng/µL	NIST A 5.0 ng/µL	NIST C 1.0 ng/µL	NIST B 0.1 ng/µL	NIST A 0.09 ng/µL	NIST C 0.07 ng/µL	NIST B 0.03 ng/µL	NIST A 0.01 ng/µL	NIST C 0.009 ng/µL	NIST B 0.007 ng/µL	NIST A 0.006 ng/µL	NIST C 0.005 ng/µL
H	STD 4 0.050 ng/µL	NIST B 5.0 ng/µL	NIST A 0.5 ng/µL	NIST C 0.1 ng/µL	NIST B 0.09 ng/µL	NIST A 0.05 ng/µL	NIST C 0.03 ng/µL	NIST B 0.01 ng/µL	NIST A 0.008 ng/µL	NIST C 0.007 ng/µL	NIST B 0.006 ng/µL	Reagent Blank

Plates were prepared as per Operation and Maintenance of the Microlab STARlet and LabElite Integrated I.D.Capper (QIS 34050) [5] and Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit (QIS 33407) [6] for 7500-A and both QS5s.

Combined results for NIST A, B and C were used to determine the LOD for the SAT and LAT. Results from only NIST A were used to determine the LOD for the Y-Target.

Table 2: NIST Standards Serial Dilutions – Platemap 2 of 2

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 5 0.005 ng/µL	NIST C 0.004 ng/µL	NIST B 0.002 ng/µL	NIST A 0.001 ng/µL	NIST C 0.0001 ng/µL						
B	STD 1 50 ng/µL	STD 5 0.005 ng/µL	NIST A 0.003 ng/µL	NIST C 0.002 ng/µL	NIST B 0.001 ng/µL							
C	STD 2 5.000 ng/µL	Reagent Blank	NIST B 0.003 ng/µL	NIST A 0.002 ng/µL	NIST C 0.001 ng/µL							
D	STD 2 5.000 ng/µL	NIST A 0.004 ng/µL	NIST C 0.003 ng/µL	NIST B 0.002 ng/µL	NIST A 0.0001 ng/µL							
E	STD 3 0.500 ng/µL	NIST B 0.004 ng/µL	NIST A 0.003 ng/µL	NIST C 0.002 ng/µL	NIST B 0.0001 ng/µL							
F	STD 3 0.500 ng/µL	NIST C 0.004 ng/µL	NIST B 0.003 ng/µL	NIST A 0.001 ng/µL	NIST C 0.0001 ng/µL							
G	STD 4 0.050 ng/µL	NIST A 0.004 ng/µL	NIST C 0.003 ng/µL	NIST B 0.001 ng/µL	NIST A 0.0001 ng/µL							
H	STD 4 0.050 ng/µL	NIST B 0.004 ng/µL	NIST A 0.002 ng/µL	NIST C 0.001 ng/µL	NIST B 0.0001 ng/µL							

Table 3 outlines the expected and the average quantification values and % inaccuracy for each serial dilution obtained from the 7500-A and QS5 instruments. The SAT, LAT and Y-Target results for both instrument types all gave quantification results down to 0.0001 ng/µL. Figure 1 displays the % inaccuracy for both SAT replicate values obtained for the 7500, QS5A and QS5B (Figures 2-4 shows % inaccuracy for NIST A, B and C respectively).

The % inaccuracy for SAT and LAT for the 7500-A was markedly higher (>180%) at 0.0001 ng/µL than for QS5-A (<70%) and QS5-B (<117%), which supports the recommendation of previous studies [2] that the LOD for Quantifiler® Trio on the 7500s should be set at 0.001 ng/µL. The data indicates that both QS5s are more accurate than 7500-A at the lowest dilution concentration tested (0.0001 ng/µL) for SAT and LAT, although it should be noted that the inaccuracy % for all instruments fluctuates across the range of dilutions tested (Figures 1-7).

Y-Target % inaccuracy appeared to increase with decreasing concentration for all instruments with QS5-B registering the greatest inaccuracy reading for the data set at 0.0001 ng/µL which was produced by a single outlying quantification value (0.00056 ng/µL) as the replicate failed to produce a value from which an average could be calculated.

Table 3: Average quantification results and % inaccuracy

	7500-A						QS5-A						QS5-B					
Concentration (ng/µL)	**SAT Average (ng/µL)**	**SAT % Inacc.**	**LAT Average (ng/µL)**	**LAT % Inacc.**	**Y-Target Average (ng/µL)**	**Y-Target % Inacc.**	**SAT Average (ng/µL)**	**SAT % Inacc.**	**LAT Average (ng/µL)**	**LAT % Inacc.**	**Y-Target Average (ng/µL)**	**Y-Target % Inacc.**	**SAT Average (ng/µL)**	**SAT % Inacc.**	**LAT Average (ng/µL)**	**LAT % Inacc.**	**Y-Target Average (ng/µL)**	**Y-Target % Inacc.**
5	5.23438	4.7	5.65350	13.1	7.69158	53.8	5.93264	18.7	6.55684	31.1	7.69477	53.9	5.64724	12.9	6.12456	22.5	7.92748	58.5
1	0.83839	-16.2	1.00262	0.3	1.29179	29.2	0.92602	-7.4	1.15516	15.5	1.29869	29.9	0.68532	-31.5	0.81726	-18.3	0.84837	-15.2
0.5	0.40486	-19.0	0.47043	-5.9	0.53297	6.6	0.40410	-19.2	0.55648	11.3	0.53550	7.1	0.36752	-26.5	0.45626	-8.7	0.37763	-24.5
0.1	0.08333	-16.7	0.10740	7.4	0.12445	24.5	0.09544	-4.6	0.12827	28.3	0.13520	35.2	0.08792	-12.1	0.10440	4.4	0.10567	5.7
0.09	0.07025	-21.9	0.09250	2.8	0.11651	29.5	0.07659	-14.9	0.11041	22.7	0.11979	33.1	0.06873	-23.6	0.08394	-6.7	0.09569	6.3
0.07	0.05418	-22.6	0.07967	13.8	0.10983	56.9	0.07768	11.0	0.10107	44.4	0.13110	87.3	0.05848	-16.5	0.07519	7.4	0.06782	-3.1
0.05	0.03357	-32.9	0.04646	-7.1	0.05238	4.8	0.04542	-9.2	0.05750	15.0	0.05022	0.4	0.03041	-39.2	0.03950	-21.0	0.03315	-33.7
0.03	0.01906	-36.5	0.02510	-16.3	0.02913	-2.9	0.02372	-20.9	0.03104	3.5	0.03598	19.9	0.01678	-44.1	0.02045	-31.8	0.02557	-14.8
0.01	0.00898	-10.2	0.01146	14.6	0.01457	45.7	0.01172	17.2	0.01321	32.1	0.01511	51.1	0.00942	-5.8	0.00957	-4.3	0.01337	33.7
0.009	0.00815	-9.4	0.01009	12.1	0.01543	71.4	0.01008	12.0	0.01152	27.9	0.01234	37.1	0.00724	-19.5	0.00791	-12.1	0.00974	8.3
0.008	0.00768	-4.0	0.00922	15.2	0.01249	56.2	0.01025	28.1	0.01051	31.3	0.01435	79.3	0.00744	-7.0	0.00897	12.1	0.01147	43.3
0.007	0.00684	-2.3	0.00769	9.9	0.01013	44.7	0.00958	36.9	0.00939	34.1	0.00703	0.5	0.00563	-19.6	0.00602	-13.9	0.00863	23.3
0.006	0.00597	-0.6	0.00681	13.5	0.00658	9.6	0.00638	6.4	0.00730	21.6	0.00939	56.6	0.00390	-35.1	0.00417	-30.5	0.00534	-11.0
0.005	0.00582	16.4	0.00487	-2.5	0.00806	61.3	0.00735	47.0	0.00611	22.2	0.00964	92.8	0.00444	-11.2	0.00445	-11.1	0.00507	1.5
0.004	0.00397	-0.7	0.00431	7.7	0.00313	-21.8	0.00421	5.2	0.00382	-4.6	0.00328	-18.0	0.00315	-21.1	0.00281	-29.7	0.00146	-63.5
0.003	0.00299	-0.4	0.00317	5.6	0.00339	13.0	0.00340	13.4	0.00286	-4.7	0.00518	72.7	0.00177	-41.0	0.00155	-48.2	0.00185	-38.4
0.002	0.00215	7.6	0.00267	33.6	0.00291	45.5	0.00246	22.8	0.00202	1.2	0.00223	11.4	0.00108	-46.1	0.00063	-68.4	0.00093	-53.5
0.001	0.00103	3.1	0.00096	-4.0	0.00166	65.6	0.00155	55.0	0.00095	-4.7	0.00197	96.9	0.00081	-19.3	0.00057	-43.1	0.00084	-16.5
0.0001	0.00028	181.6	0.00030	198.0	0.00019	92.9	0.00015	47.0	0.00017	67.6	0.00019	90.8	0.00015	52.3	0.00022	116.2	0.00056	461.2

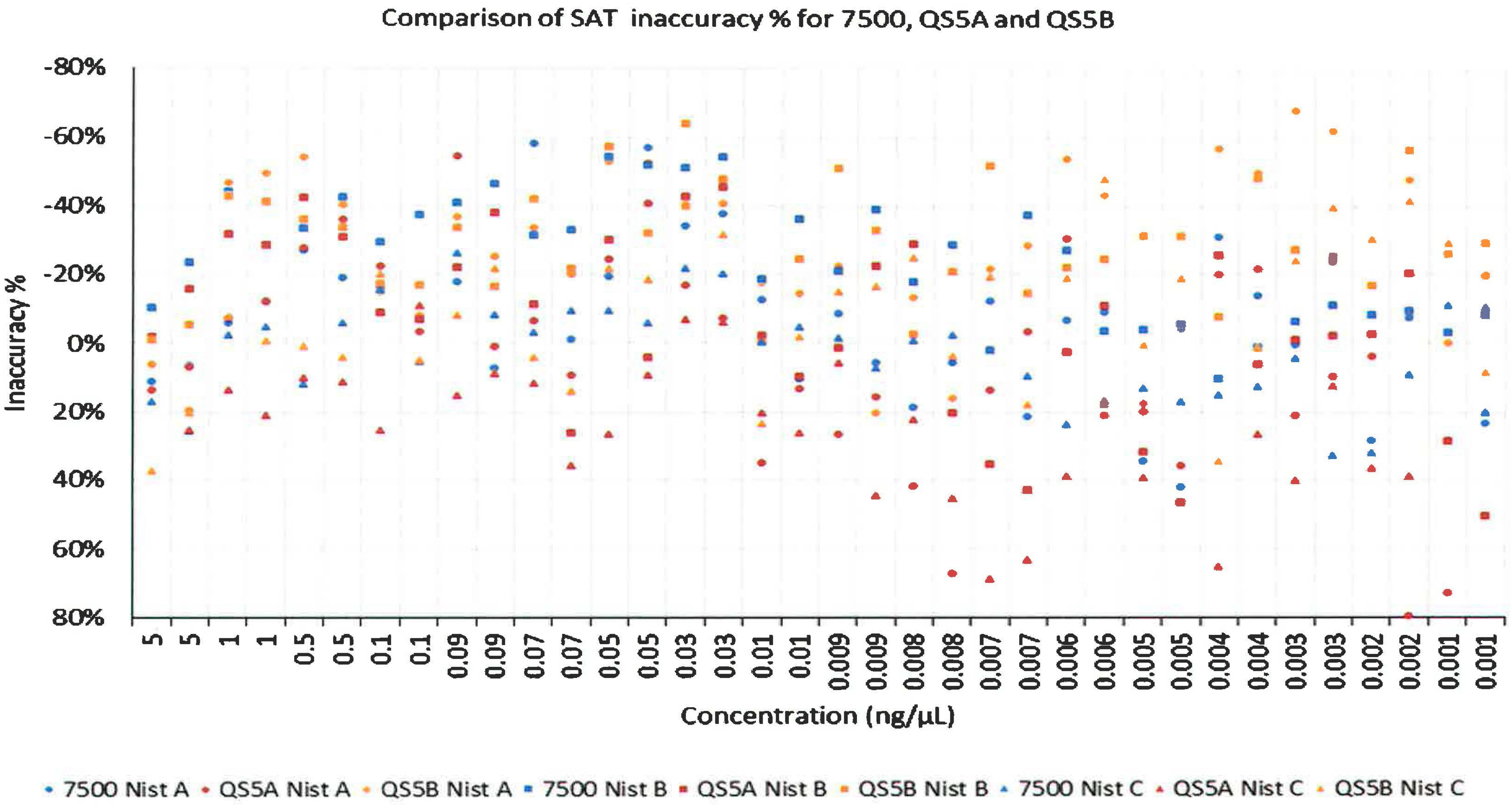

Figure 1: Comparison of SAT inaccuracy percentage for 7500, QS5A and QS5B

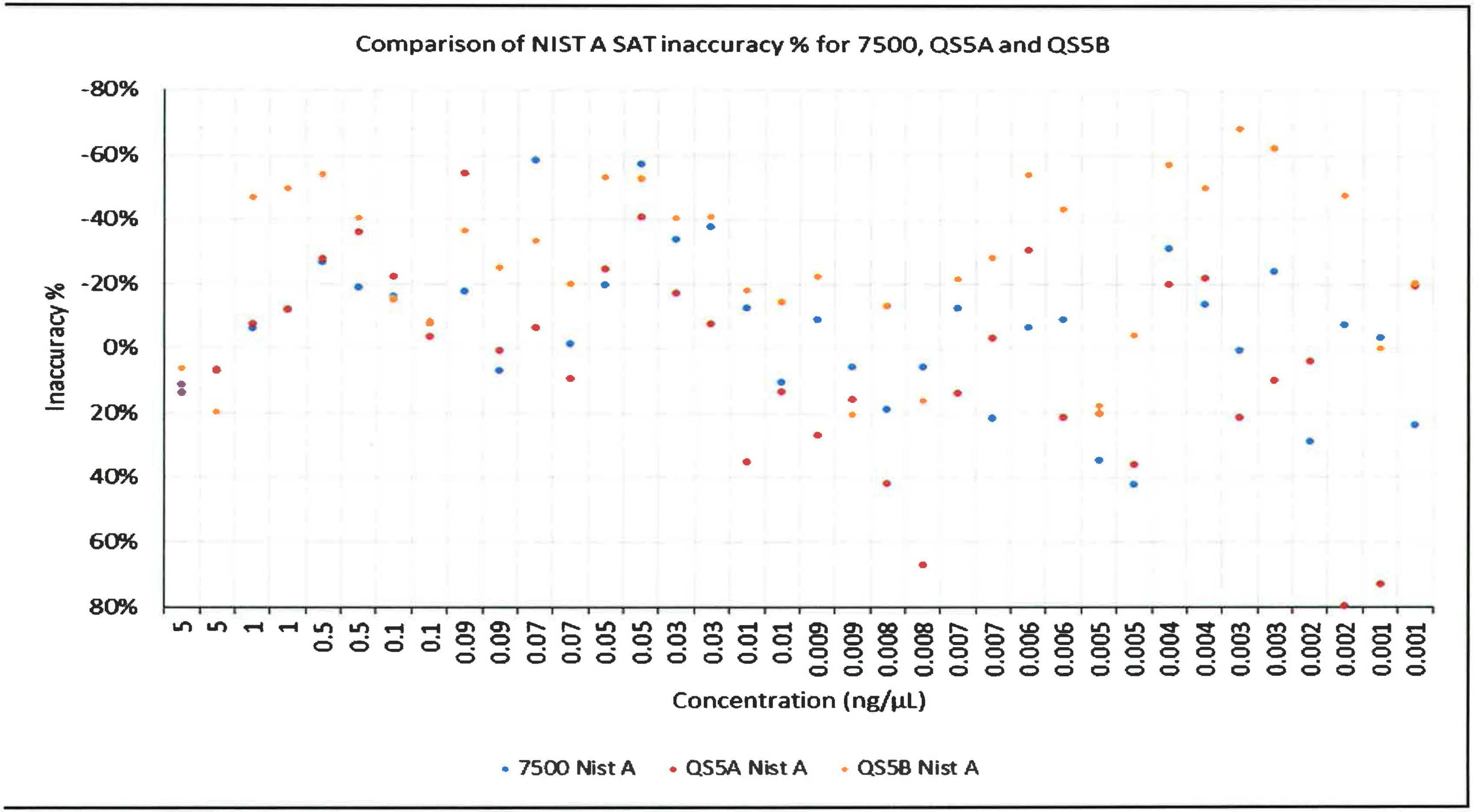

Figure 2: Comparison of NIST A SAT inaccuracy percentage for 7500, QS5A and QS5B

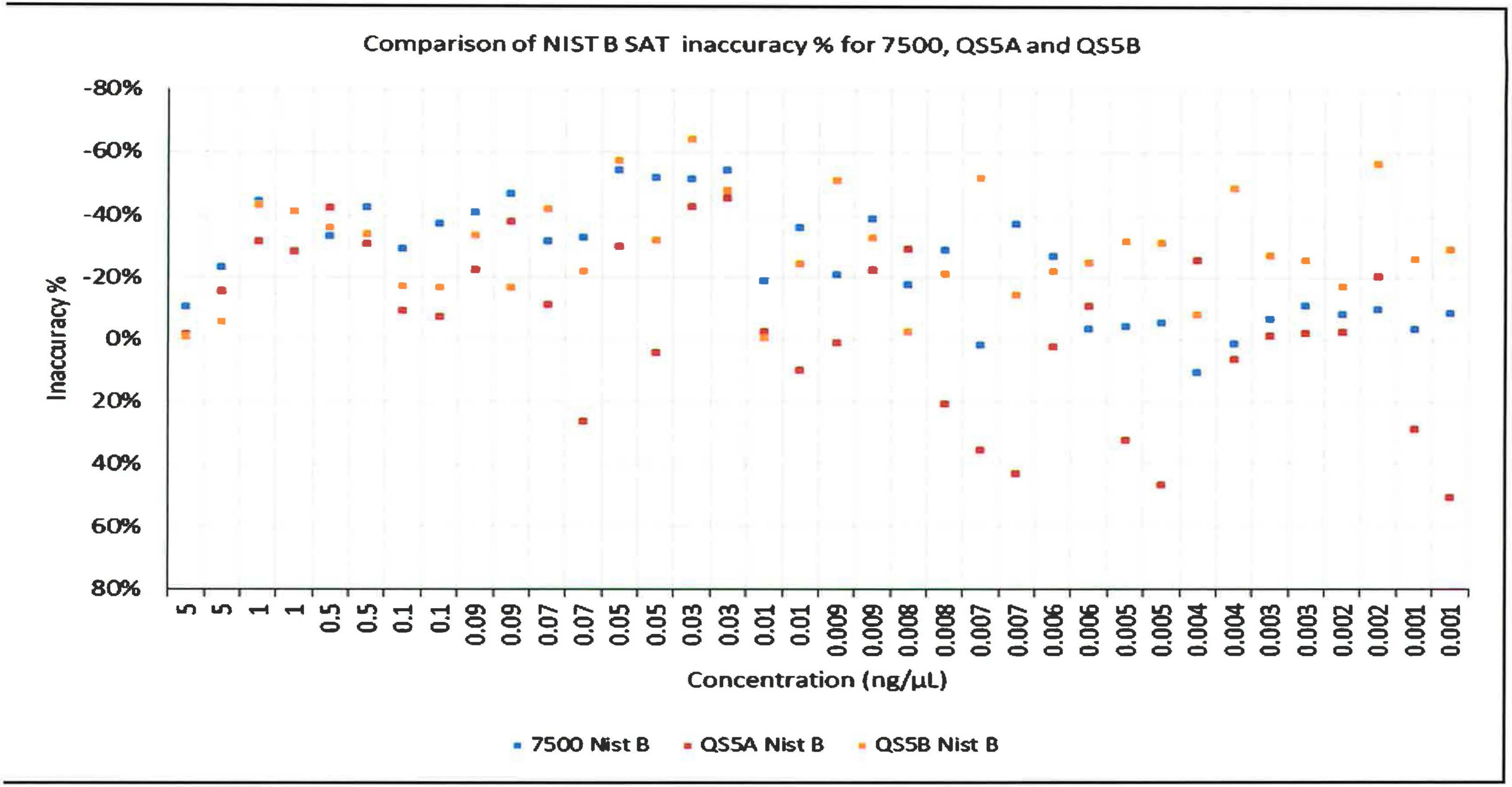

Figure 3: Comparison of NIST B SAT inaccuracy percentage for 7500, QS5A and QS5B

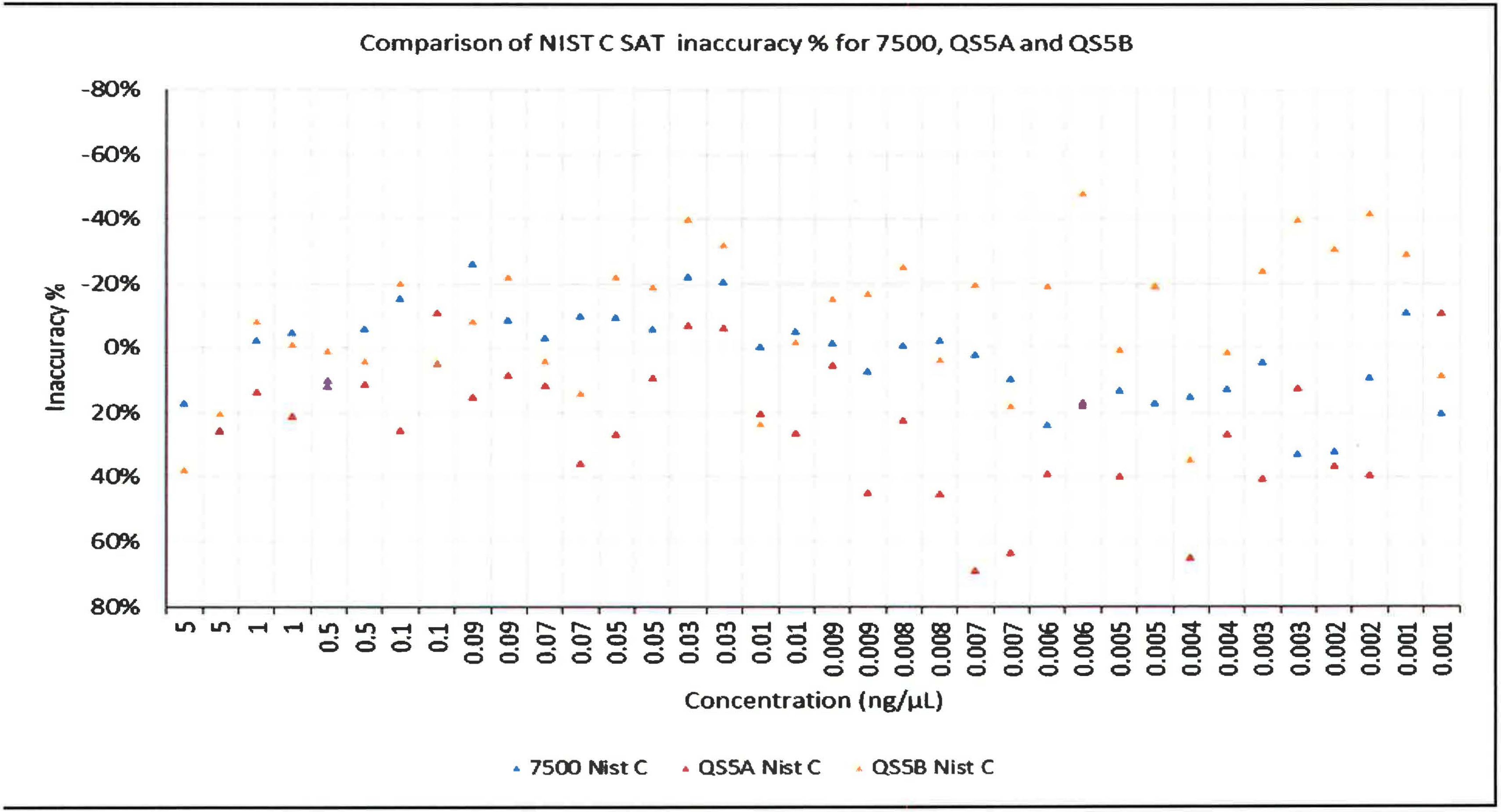

Figure 4: Comparison of NIST C SAT inaccuracy percentage for 7500, QS5A and QS5B

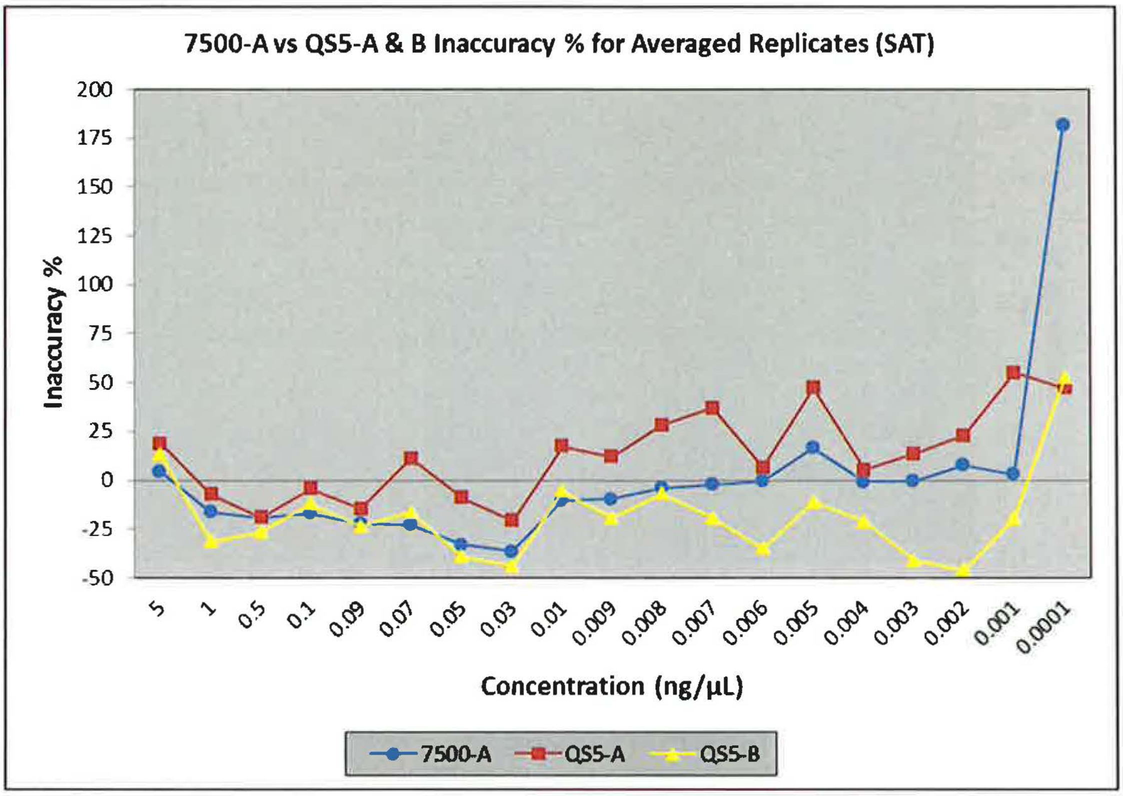

Figure 5: Percent inaccuracy for SAT

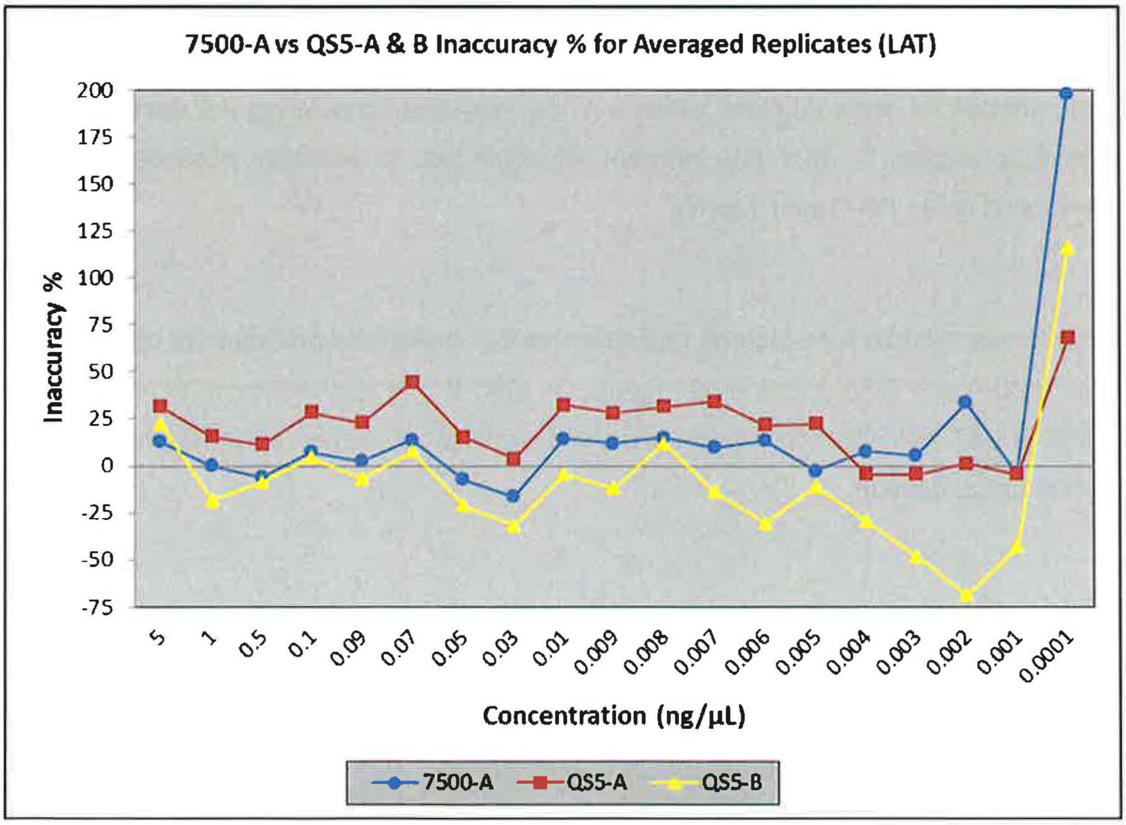

Figure 6: Percent inaccuracy for LAT

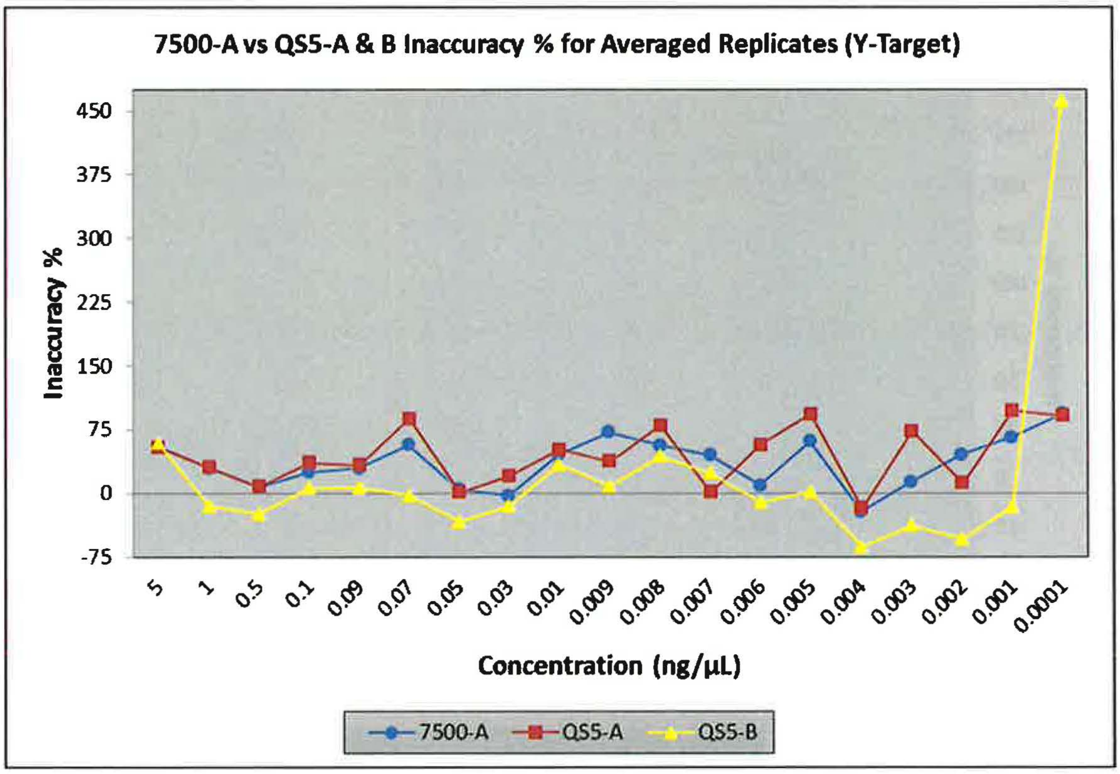

Figure 7: Percent inaccuracy for Y-Target

Discussion

The percent inaccuracy for 7500-A and the QS5s for all quantification targets (SAT, LAT and Y-Target) were similar for most dilutions, although the difference in inaccuracy was greater for some dilutions which is to be expected considering the observations of previous studies [2], and the inherent variation that is routinely observed between replicates using the Quant Trio kit.

The lowest dilution for which all replicates gave a quantification result for all targets on the 7500-A and QS5-A was 0.001 ng/µL. On QS5-B one replicate each of NIST A SAT, NIST B LAT and NIST C Y-target showed quantification values of undetermined at the 0.001 ng/µL dilution.

At the 0.0001 ng/µL dilution, 8/16 replicates gave an undetermined result for the 7500-A compared to 6/16 replicates for QS5-A and 11/16 for QS5-B (data not shown). This suggests the LOD for the QS5s are comparable to the 7500-A.

The large disparity between the 7500-A and the QS5s observed for SAT and LAT at 0.0001 ng/µL (Figures 5 & 6) supports the recommendations of previous studies [2] that the LOD for Quant Trio on the 7500s should be set at 0.001 ng/µL. This suggests the QS5s may be more accurate than the 7500-A at concentrations between 0.001 ng/µL and 0.0001 ng/µL.

Acceptance Criteria

The results indicate the LOD for Quant Trio on the QS5s is as good or better than the 7500A. Considering all the results, it is recommended the LOD for Quant Trio on the QS5 for SAT, LAT and Y-Target be set at 0.001 ng/µL.

Experiment 2: Comparison of QS5s and 7500

Purpose

To compare the performance of the two instrument types, the Student *t*-test (two-tailed distribution, paired) was performed to determine if there was a significant difference in quantification results across the entire dilution series. Student *t*-tests were performed separately for SAT, LAT and Y-Targets specific to each of the NIST standards using both replicates for each instrument. Only NIST A and C were used for Y-Target results. The two QS5s were compared to 7500-A using separate *t*-tests.

Results

The *t*-test results indicate that there is no significant difference between the quantification values between 7500-A and the QS5 instruments at quantification targets SAT, LAT and Y-Target as shown in Table 4.

Table 4: Student's *t*-test P-values for comparison of QS5-A and QS5-B with 7500-A

Standard	Instruments compared	SAT	LAT	Y-Target
NIST A	QS5-A & 7500-A	0.70050	0.06813	0.42519
	QS5-B & 7500-A	0.44247	0.77529	0.19765
NIST B	QS5-A & 7500-A	0.05212	0.06054	N/A
	QS5-B & 7500-A	0.19258	0.15191	
NIST C	QS5-A & 7500-A	0.23834	0.09180	0.39582
	QS5-B & 7500-A	0.52538	0.45386	0.32165

Note: P-values < 0.05 indicate a significant difference between results produced by the two instruments.

Discussion

The results indicate the difference between quantification values for 7500-A and the QS5s are not significant for the SAT, LAT and Y-Targets for both the QS5s. The difference in LAT values for the QS5-A comparison was observed to be higher than for QS5-B, however the opposite trend was evident for the Y-Target comparison, where the QS5-B comparison showed a greater difference. The difference between SAT values showed no specific trend with QS5-A showing a greater difference than QS5-B for NIST B and C, but not for A.

As the LAT region component of the Quant Trio kit is designed to provide only an approximate estimation of the level of degradation for samples, it is expected quantification values for this target would vary over time and with freeze/thaw cycles since the target is more than twice the size of the SAT and Y-Targets [1]. The LAT and degradation index is currently not used by Forensic DNA Analysis.

Acceptance Criteria

The comparison of the QS5s and 7500-A quantification results using student *t*-tests indicates there is no significant difference in the ability to quantify SAT, LAT and Y-Targets, therefore both the QS5 instruments are comparable to 7500-A for these parameters and should be accepted.

Experiment 3a: Repeatability

Purpose

To assess whether the QS5-A produced the same results when a set of twelve CTS samples was processed in replicates of seven by one operator under the same conditions. The SAT results from the repeatability plate (Table 5) were compiled using a scatter plot, and the comparability of results was assessed qualitatively.

Table 5: CTS Sample Platemap for Repeatability

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 5 0.005 ng/µL	CTS 1	CTS 2	CTS 4	CTS 5	CTS 6	CTS 7	CTS 8	CTS 9	CTS 10	CTS 12
B	STD 1 50 ng/µL	STD 5 0.005 ng/µL	CTS 1	CTS 3	CTS 4	CTS 5	CTS 6	CTS 7	CTS 8	CTS 9	CTS 11	CTS 12
C	STD 2 5.000 ng/µL	Reagent Blank	CTS 2	CTS 3	CTS 4	CTS 5	CTS 6	CTS 7	CTS 8	CTS 10	CTS 11	CTS 12
D	STD 2 5.000 ng/µL	CTS 1	CTS 2	CTS 3	CTS 4	CTS 5	CTS 6	CTS 7	CTS 9	CTS 10	CTS 11	CTS 12
E	STD 3 0.500 ng/µL	CTS 1	CTS 2	CTS 3	CTS 4	CTS 5	CTS 6	CTS 8	CTS 9	CTS 10	CTS 11	CTS 12
F	STD 3 0.500 ng/µL	CTS 1	CTS 2	CTS 3	CTS 4	CTS 5	CTS 7	CTS 8	CTS 9	CTS 10	CTS 11	CTS 12
G	STD 4 0.050 ng/µL	CTS 1	CTS 2	CTS 3	CTS 4	CTS 6	CTS 7	CTS 8	CTS 9	CTS 10	CTS 11	CTS 12
H	STD 4 0.050 ng/µL	CTS 1	CTS 2	CTS 3	CTS 5	CTS 6	CTS 7	CTS 8	CTS 9	CTS 10	CTS 11	Reagent Blank

Results

The quantification results for the twelve CTS sample replicates are displayed in a scatter plot (Figure 8). It is evident from these results the repeatability of measured quantification values between each of the seven replicates is qualitatively comparable for all twelve samples.

A clear trend is apparent in the variability between replicates for each sample, with extracts of a higher concentration displaying a greater spread of quantification values than extracts with concentrations below 2 ng/µL.

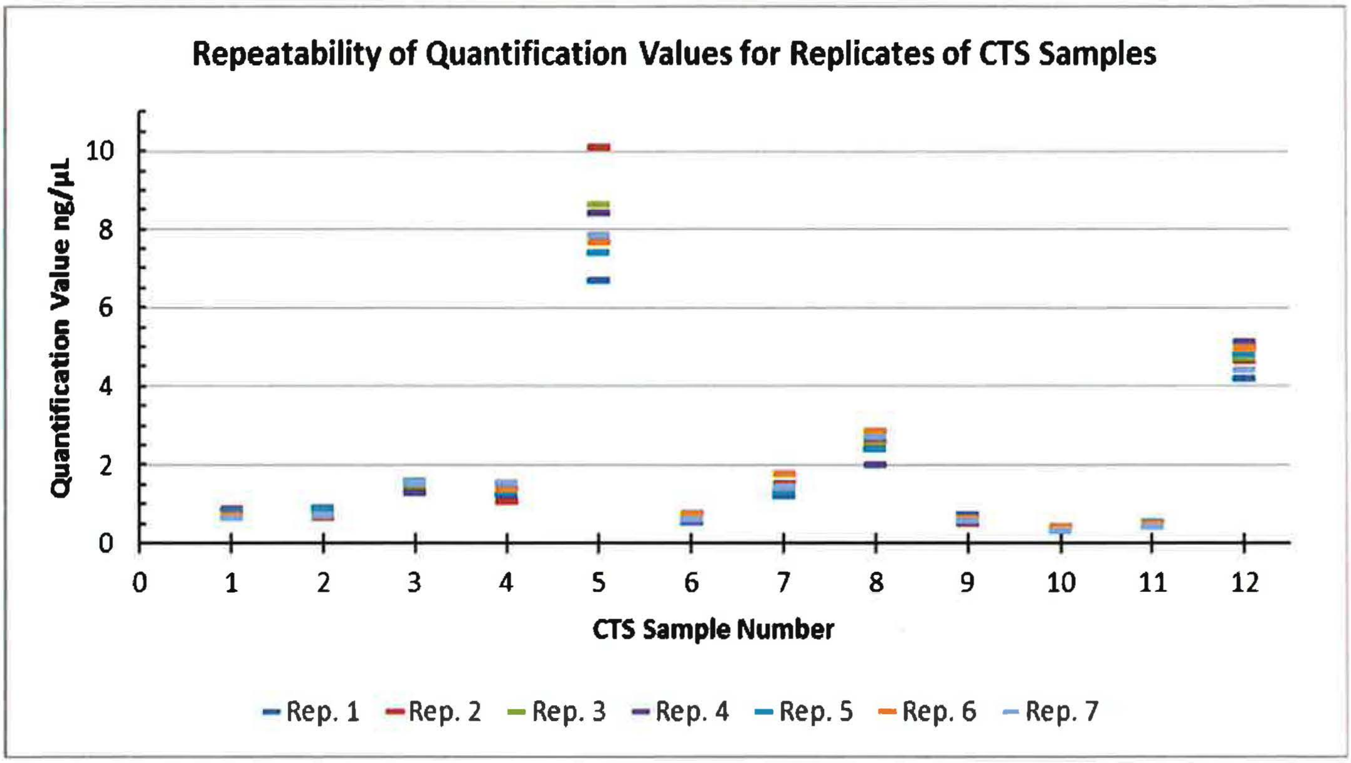

Figure 8: Repeatability of Quantification Values for Replicates of CTS Samples

Discussion

The variability observed between replicates for each CTS sample provides evidence that a degree of variation is present in the Quantifiler Trio system's ability to produce repeatable results. This is particularly evident for CTS sample 5, which had the highest measured concentrations for each of the replicates.

Variation among replicates is seen to reduce dramatically as the quantification values decrease below 2 ng/µL, with CTS sample 10 displaying the lowest variation. This observation is to be expected as variations in amplification efficiency are more likely to occur in samples with higher concentrations, which is further exacerbated by the exponential increase of amplicons during PCR ultimately leading to a wider range of replicate variability.

Variability in quantification result repeatability using Quantifiler Trio has also been documented in previous studies [2], and as in the current study the values for each replicate of a specific samples were comparable.

Acceptance Criteria

Repeatability across all CTS samples were shown to be comparable between the seven replicates. These findings indicate the QS5 has produced results that are comparable to the original Quantifiler® Trio validation using the 7500 instrument [2], which also showed comparably similar results between replicates. Therefore the QS5 should be accepted.

Experiment 3b: Reproducibility

Purpose

To assess whether the QS5 reproduces the same quantification results by different operators on 5 different days, the results from the twelve CTS samples were compiled on a scatter plot together with the minimum and maximum values recorded for each sample in experiment 3a (Repeatability).

Table 6: CTS Sample Platemap for Reproducibility

	1	2	3	4	5	6	7	8	9	10	11	12
A	STD 1 50 ng/µL	STD 5 0.005 ng/µL	CTS 6									
B	STD 1 50 ng/µL	STD 5 0.005 ng/µL	CTS 7									
C	STD 2 5.000 ng/µL	Reagent Blank	CTS 8									
D	STD 2 5.000 ng/µL	CTS 1	CTS 9									
E	STD 3 0.500 ng/µL	CTS 2	CTS 10									
F	STD 3 0.500 ng/µL	CTS 3	CTS 11									
G	STD 4 0.050 ng/µL	CTS 4	CTS 12									
H	STD 4 0.050 ng/µL	CTS 5	Reagent Blank									

Results

The quantification results for the twelve CTS samples reproduced over five days are displayed in a scatter plot (Figure 9). The majority of values are close to or within the maximum/minimum values recorded in the repeatability experiment, however as expected, some of the reproducibility results are above or below these earlier observed upper and lower values.

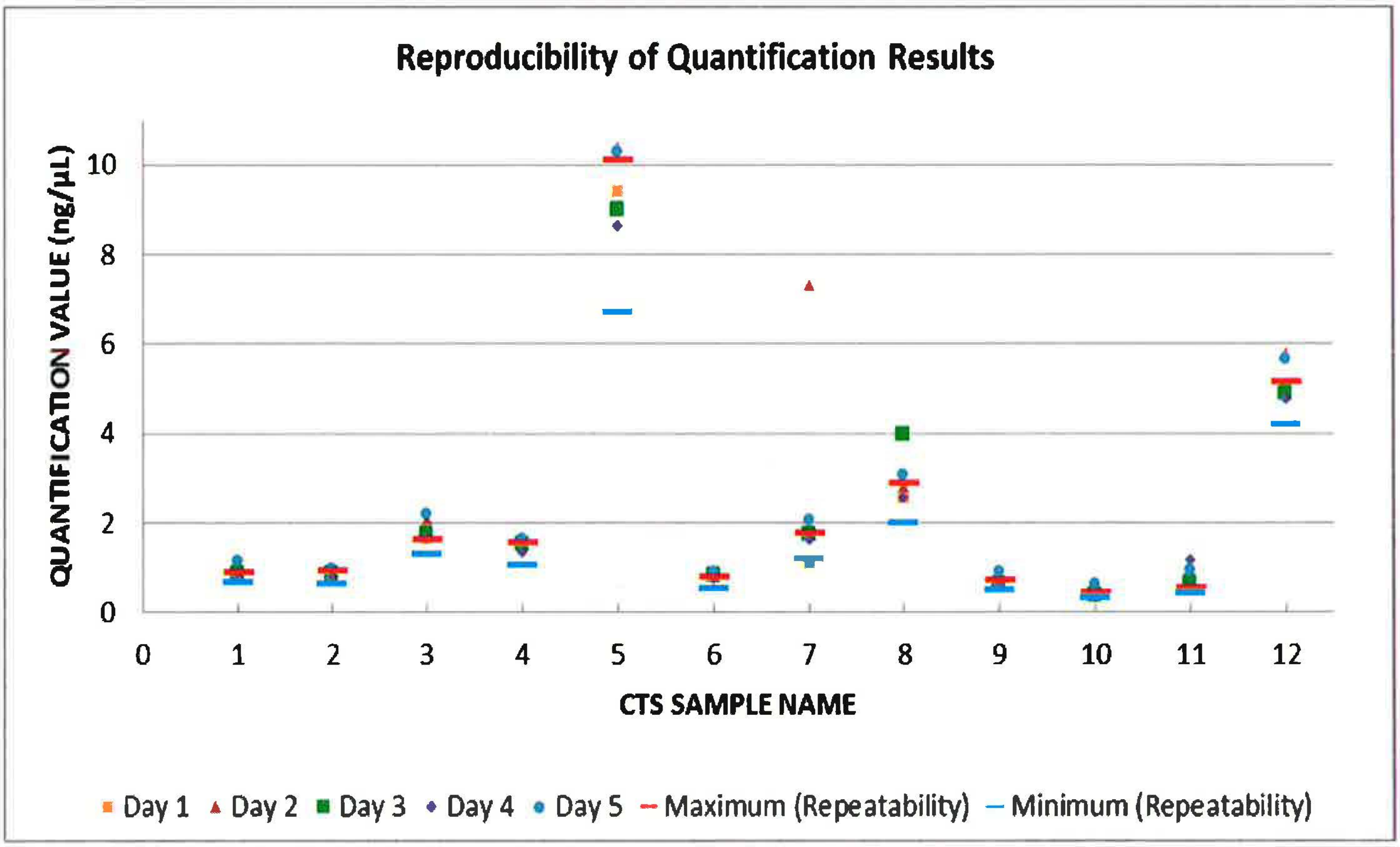

Figure 9: Reproducibility of Quantification Values for CTS Samples over 5 days

The quantification result for sample seven reproduced on day two resulted in a value that was dramatically higher than all other recorded quantification values for this sample. It is relevant to note here that a singular, aberrant, result was observed in experiments that were conducted as part of an earlier version of this report (data not shown).

Discussion

As for experiment 3a (repeatability), the variability between reproduced results for each of the twelve CTS samples supports the premise that a degree of variation is present in the Quantifiler Trio system's ability to generate reproducible results. As previously discussed in Experiment 3a, the degree of this variation appears to correlate with concentration as observed for samples 5, 8 & 12, which had the three highest concentrations. Furthermore, samples that provide overestimated quantification results would likely produce partial or No Signal Detected Profiles during the Profile Data Analysis stage which would either be re-quantified or re-amplified at a higher template input to provide an uncompromised result.

Overall, the data shows that for a range of samples, the QS5 reproduces comparable results regardless of which personnel are operating the PCR setup and QS5 instruments, or on which day the assay and analysis was performed.

The unexpected high quantification value for sample seven on day two could not be attributed to any one source, and may be the result of a range of factors including the Quantification PCR variations, pipetting variation and QS5 detection anomalies. Standard operating procedures within Forensic DNA Analysis requires samples that produce quantification values >5 ng/µL to be diluted which effectively eliminates the chance of overloading subsequent amplification reactions.

Acceptance Criteria

Reproducibility of quantification values across the twelve CTS samples were shown to be qualitatively comparable despite the presence of some outlying data points. It is expected to observe some of the five reproducibility values that fall outside the minimum/maximum value range (obtained in experiment 3a) since only seven replicates were performed in experiment 3a to establish this range. Replicate numbers were limited to seven by the number of sample wells in the 96 well plate.

These findings indicate that the QS5 has produced results that are comparable to the original Quantifiler® Trio validation using the 7500 instrument [2], which showed that the same results can be produced for one sample set by different operators under the same conditions – i.e the results are reproducible and the QS5 should be accepted.

Experiment 4: Y-Intercept Thresholds

Purpose

To determine the Y-Intercept thresholds for the SAT, LAT and Y-Targets, the values from eleven plates run on the QS5s (Plate 1 (QS5-A & B), Plate 2 (QS5-A & B), QS5-B standards only, repeatability QS5-A, and five reproducibility plates QS5-A) were used. The current ranges [5] will be used for the implementation of the two QS5 instruments with Quantifiler® Trio if the calculated Y-intercept values fall within these ranges.

Results

The average Y-intercept values taken from the thirteen plates ran on the QS5s +/- 3 x standard deviations was calculated and compared to the current Y-Intercept thresholds [5] as shown in Table 7.

Table 7: Y-Intercept ranges calculated for QS5 compared to current ranges.

	QS5 Y-Int. Range	Current Y-Int. Range
LAT	23.85 – 25.63	24.28 – 26.30
SAT	25.83 – 27.73	26.36 – 28.63
Y-Target	24.68 – 26.81	25.51 – 28.11

The QS5 Y-Intercept upper ranges for SAT, LAT and Y-Target are all within the current ranges, and below the current upper ranges. However the calculated QS5 lower ranges all fall outside (below) the current ranges outlined in the Quantification SOP [5]. It is important to note that only one of the eleven QS5 plates had Y-Intercept ranges that fell outside of the current ranges, therefore this one plate contributed greatly to shift the newly calculated ranges out of the current ranges.

Discussion

The newly calculated Y-Intercept ranges for QS5 are considerably narrower than the current ranges, which is in part due to the relatively small number of plates used to calculate them. It is important to consider that calculated thresholds are instrument and kit specific so variation is to be expected. As more plates are processed after implementation, the cumulative data will be used to recalculate these ranges over time.

Acceptance Criteria

Since the newly calculated QS5 Y-Intercept ranges are relatively narrow and fall under the current upper ranges but below the lower ranges, the QS5 implementation will utilise the current ranges until more data is available to allow recalculation for QS5.

Conclusion

The results of experiment 1 showed the LOD for QS5 is similar to that of 7500 and possibly even more sensitive although more studies are required to confirm this. These findings support the recommendations of the original Quantifiler® Trio validation that the LOD be set to 0.001 ng/µL.

Independently comparing the results of both QS5 instruments to those produced by 7500-A showed no significant differences in SAT, LAT and Y-Target quantification results demonstrating comparability between 7500 and QS5.

The QS5 instrument showed qualitative comparability in repeatability results across all CTS samples demonstrating comparability to the 7500 instrument which also produced repeatable results in the original Quantifiler® Trio validation.

The QS5 instrument was also able to demonstrate comparable results reproduced by different operators on different days for the selected CTS samples. These results are comparable to the findings for the original Quantifiler® Trio validation using the 7500.

The Y-intercept ranges calculated from the values obtained from all eleven QS5 plates produced in this study all fall below the upper ranges that are currently in use, however these new ranges also fall below the lower current ranges. Given the ranges calculated for QS5 are considerably narrower than current ranges, it is recommended that the current ranges be used for QS5 implementation, and the thresholds revised every 2 weeks for the first 3 months once the data set is expanded.

Recommendations

1. QuantStudio™ 5 Real-Time PCR systems A and B be implemented for DNA quantification using the Quantifiler® Trio DNA quantification kit, and thus replacing the two 7500 Real-Time PCR systems.
2. Y-Intercept data for SAT, LAT and Y-Targets are to be collated and used to recalculate/monitor ranges over time after implementation of the QS5s (not greater than 6 months.

References

[1] Thermo Fisher Scientific, Quantifiler® HP and Trio DNA Quantification Kits UserGuide, Publication Number 4485354, Revision A. Publication Number 4485354, Revision A ed2014.

[2] Validation of Quantifiler® Trio. P. Acedo, M. Mathieson, L. Ryan, C. Allen. September 2015. Forensic DNA Analysis.

[3] Certificate of Analysis – Standard Reference Material® 2372 Human DNA Quantitation Standard. National Institute of Standards & Technology.

[4] Project Proposal #185 – Validation of the QuantStudio™ Real-Time PCR Systems (June 2017).

[5] Operation and Maintenance of the Microlab STARlet and LabElite Integrated I.D.Capper. QIS 34050.

[6] Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit. QIS 33407.

JH-6

applied biosystems

Quantifiler™ HP and Trio DNA Quantification Kits

USER GUIDE

for use with:
Quantifiler™ HP DNA Quantification Kit (Cat. No. 4482911)
Quantifiler™ Trio DNA Quantification Kit (Cat. No. 4482910)

Publication Number 4485354
Revision G

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Contents

About this guide

IMPORTANT! Before using this product, read and understand the information in the "Safety" appendix in this document.

Revision history

Revision	Date	Description
A	January 2014	New document.
B	March 2014	• Add Chapter 6, Experiments and Results. • Change the storage time for DNA quantification standards to 2 weeks. • Add statement regarding the statistical significance between using the manual and automatic baseline methods. • Minor adjustments to the text supporting the changes mentioned above.
C	August 2014	• Change the quantity of tubes of Quantifiler THP DNA Dilution Buffer included in the kit from 1 to 2. • Change the typical slope ranges on page 44. • Add a paragraph about DNA ratios on page 53. • Change Figure 32 on Page 83.
D	July 2015	Add Appendix C, Degraded sample studies: GlobalFiler™ STR Kit and HID-Ion AmpliSeq™ Identity and Ancestry Panel.
E	October 2015	• Add information on minimizing bubbles to Prepare the Reactions. • Add Examine the multicomponent plot to check for noise to Interpretation of Results.
F	December 2016	Add information about Quantifiler™ Automation Enhancer.
G	April 2017	Minor edits.

Purpose

The *Quantifiler™ HP and Trio DNA Quantification Kits User Guide* provides information about Thermo Fisher Scientific instruments, chemistries, and software associated with the Quantifiler™ HP and Trio DNA Quantification Kits.

1

Overview

Product overview

Purpose

This document describes the Quantifiler™ HP DNA Quantification Kit (Cat. No. 4482911) and Quantifiler™ Trio DNA Quantification Kit (Cat. No. 4482910). The Quantifiler™ HP Kit is designed to quantify the total amount of amplifiable human DNA in a sample. The Quantifiler™ Trio Kit is designed to simultaneously quantify the total amount of amplifiable human DNA and human male DNA in a sample. As with our Quantifiler™ Duo, Human, and Y Human Male DNA Quantification Kits, these kits use TaqMan® quantitative real-time PCR technology. The results obtained using the kits can aid in determining:

- If the sample contains sufficient human DNA and/or human male DNA to proceed with short tandem repeat (STR) analysis.
- The amount of sample to use in STR analysis applications.
- For the Quantifiler™ Trio Kit only, the relative quantities of human male and female DNA in a sample that can assist in the selection of the applicable STR chemistry.
- The DNA quality, with respect to both the DNA degradation level and the inhibition level. This metric is useful for determining if the STR loci with larger amplicon sizes will likely be recovered in the STR profile.

  Highly degraded samples that cannot be recovered by STR can be analyzed with HID-Ion AmpliSeq™ Panels and the Ion Personal Genome™ (PGM™) System (see "Degraded sample studies: GlobalFiler™ STR kit and HID-Ion AmpliSeq™ Identity and Ancestry Panel" on page 103).
- If PCR inhibitors are present in a sample that may require additional purification before proceeding to STR analysis.

Product description

The Quantifiler™ HP and Trio DNA Quantification Kits use multiple-copy target loci for improved detection sensitivity. The human-specific target loci (Small Autosomal, Large Autosomal, and Y-chromosome targets) each consist of multiple copies dispersed on various autosomal chromosomes (Small Autosomal and Large Autosomal), or multiple copies on the Y-chromosome.

To maximize the consistency of quantification results, genomic targets were selected with conserved primer- and probe-binding sites within individual genomes and also with minimal copy number variability between different individuals and population groups. As a result, the detection sensitivity of the Quantifiler™ HP and Trio assays is improved over Quantifiler™ Duo, Human, and Y Human Male DNA Quantification Kit assays. The primary quantification targets (Small Autosomal and Y) consist of relatively short amplicons (75 to 80 bases) to improve the detection of degraded DNA samples. In addition, the Quantifiler™ HP and Trio Kits each contain a Large Autosomal target with a longer amplicon (>200 bases) to aid in determining if a DNA sample is degraded.

Assay chemistry has been optimized for more efficient multiplexing, faster PCR cycle times (1 hour), and better inhibitor tolerance. The overall performance improvements allow the Quantifiler™ HP and Trio Kits to better match the enhanced performance of newer STR kits that are designed to accommodate more challenging samples, for example, the Identifiler™ Plus, NGM SElect™ or the GlobalFiler™ PCR Amplification Kits. (STR kits are For Forensic or Paternity Use Only.)

Quantifiler™ HP DNA Quantification Kit contains all the necessary reagents for the amplification, detection and quantification of two human-specific DNA targets. Quantifiler™ Trio DNA Quantification Kit contains all the necessary reagents for the amplification, detection and quantification of two human-specific DNA targets and a human male-specific DNA target.

The reagents are designed and optimized for use with the Applied Biosystems™ 7500 Real-Time PCR System for Human Identification, which includes:

- **HID Real-Time PCR Analysis Software v1.2**– Designed specifically to assist human identification laboratories performing DNA quantitation, by simplifying assay setup, streamlining data review, dilution and reaction setup for downstream STR analysis.
- **7500 Instrument** – Real-time PCR instrument. For more information, see "7500 Real-Time PCR System for Human Identification" on page 95.

IMPORTANT! The 7500 Fast Real-Time PCR System is not supported for use with the Quantifiler™ HP and Trio DNA Quantification Kits.

Chemistry overview

Assay overview

The Quantifiler™ HP assay combines three 5′ nuclease assays:

- Two separate target-specific human assays; one with a short PCR amplicon and one with a long PCR amplicon
- An internal PCR control (IPC) assay

The Quantifiler™ Trio assay combines four 5′ nuclease assays:

- Two separate target-specific human assays; one with a short PCR amplicon and one with a long PCR amplicon
- A target-specific human male DNA assay
- An internal PCR control (IPC) assay

Target-specific assay components

Each target consists of PCR primers and dye-labeled TaqMan® probes (with non-fluorescent quenchers) for the amplification of multicopy genomic loci. Table 1 provides information about the targets of PCR amplification in the Quantifiler™ HP and Trio DNA Quantification Kits.

Table 1 Quantifiler™ HP and Trio DNA Quantification Kit targets

Target	Amplicon length	Ploidy	Copy Number	Dye/Quencher
Human Target, small autosomal	80 bases	Diploid	multicopy	VIC™ dye with MGB quencher
Human Target, large autosomal	214 bases	Diploid	multicopy	ABY™ dye with QSY™ quencher
Human Male Target†	75 bases	Haploid	multicopy	FAM™ dye with MGB quencher
Internal PCR Control	130 bases	NA	Synthetic IPC template is included in the primer mix	JUN™ dye with QSY™ quencher

† Contained in the Quantifiler™ Trio DNA Quantification Kit only

The Quantifiler™ HP and Trio assay targets serve the following functions in the multiplex system:

- **Small Autosomal (SA) Target:** The SA target is the primary quantification target for total human genomic DNA. Its smaller amplicon size (80 bp) is aligned with the sizes of typical "mini" STR loci and makes it better able to detect degraded DNA samples.
- **Large Autosomal (LA) Target:** The LA target is used mainly as an indicator of DNA degradation, by comparing the ratio of its quantification result with that of the SA target.
- **Y chromosome Target** (not present in the Quantifiler™ HP Kit assay): The Y target allows the quantification of a sample's human male genomic DNA component, and is particularly useful in assessing mixture samples of male and female genomic DNAs.

Internal PCR Control system components

The internal PCR control (IPC) system consists of:

- IPC template DNA (a synthetic sequence not found in nature)
- Primers for amplifying the 130 base IPC template DNA
- TaqMan® probe dye-quencher—JUN™ dye with QSY™ quencher

The IPC present in each sample contains a synthetic DNA template, and provides positive confirmation that all assay components are functioning as expected. This internal control is particularly useful to confirm the validity of negative results. It is also useful to identify samples that contain PCR inhibitors.

About the probes

The TaqMan® MGB probes contain:

- A reporter dye (FAM™ or VIC™ dye) linked to the 5′ end of the probe
- A minor groove binder (MGB) at the 3′ end of the probe

  This modification increases the melting temperature (T_m) without increasing probe length (Afonina et al., 1997; Kutyavin et al., 1997), to allow for the design of shorter probes.
- A nonfluorescent quencher (NFQ) at the 3′ end of the probe

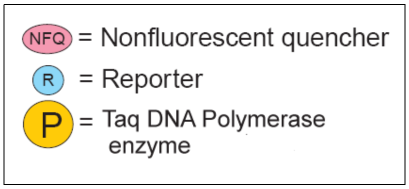
The TaqMan® QSY™ probes contain:

- A reporter dye (ABY™ or JUN™ dye) linked to the 5′ end of the probe
- A nonfluorescent quencher (QSY™) at the 3′ end of the probe

5′ Nuclease assay process

The 5′ nuclease assay process (Figure 1 through Figure 5) takes place during PCR amplification. This process occurs in every cycle, and it does not interfere with the exponential accumulation of product.

Figure 1 Legend for 5′ nuclease assay process



During PCR, the TaqMan® probe anneals specifically to a complementary sequence between the forward and reverse primer sites (Figure 2).

With both the reporter dye and quencher bound, see Figure 2 and Figure 3, the proximity of the reporter dye to the quencher results in suppression of the reporter fluorescence primarily by Förster-type energy transfer (Förster, 1948; Lakowicz, 1983).

Figure 2 Polymerization

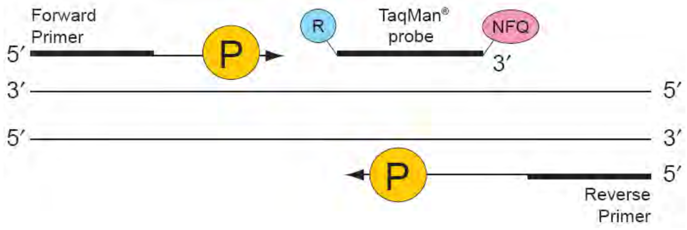
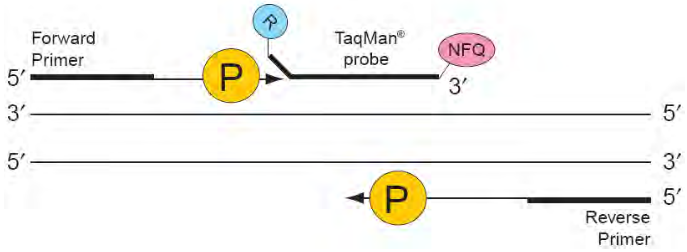
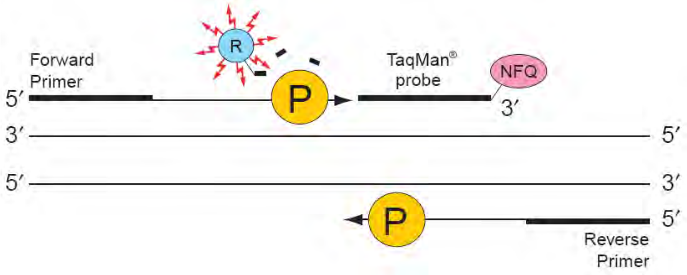


Figure 3 Strand displacement



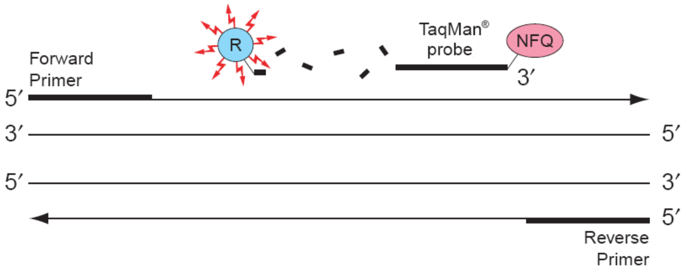
Taq DNA polymerase enzyme cleaves only probes that are hybridized to the target (Figure 4). Cleavage separates the reporter dye from the quencher, resulting in increased fluorescence by the reporter. This increase in fluorescence signal occurs only if the target sequence is complementary to the probe and is amplified during PCR. Because of these requirements, nonspecific amplification is not detected.

Figure 4 Cleavage



Polymerization of the strand continues, but because the 3′ end of the probe is blocked, there is no extension of the probe during PCR (Figure 5).

Figure 5 Completion of polymerization



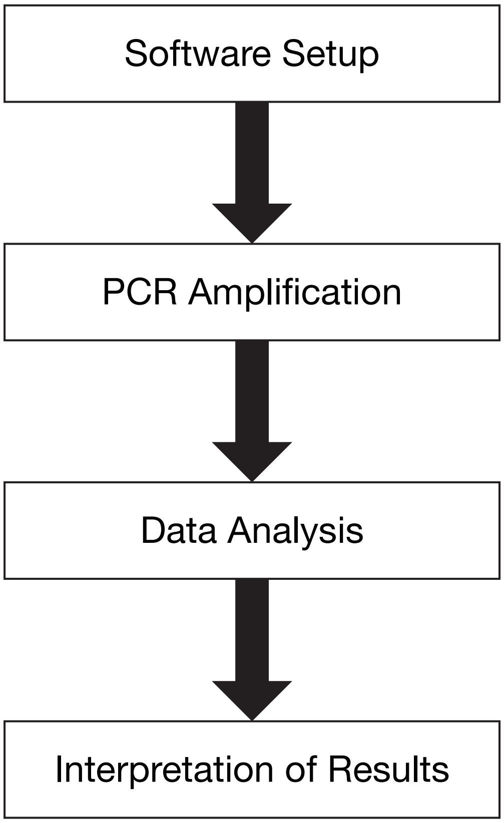
Normalization of reporter signals

During a run, the software displays cycle-by-cycle changes in normalized reporter signal (ΔR_n). The software normalizes each reporter signal by dividing it by the fluorescent signal of the passive reference dye. Because the passive reference is one component of the PCR master mix, it is present at the same concentration in all wells of the reaction plate. By normalizing the reporter signal using the passive reference, the software can account for minor variations in signal caused by pipetting inaccuracies and make better well-to-well comparisons of the reporter signal.

Human DNA standard

The human DNA used to generate the DNA quantification standards dilution series consists of pooled human male genomic DNA. As such, the performance of the Quantifiler™ HP and Quantifiler™ Trio assays are optimized for use with this DNA standard. The use of an alternate DNA standard may result in the reporting of different concentration values for the unknown samples. Use of an alternate DNA standard is not recommended.

Quantifiler™ Kits workflow



Materials and equipment

Kit contents and storage

The Quantifiler™ HP and Trio DNA Quantification Kits contain materials sufficient to perform 400 reactions at a 20-µL reaction volume.

Table 2 Quantifiler™ HP DNA Quantification Kit (Cat. No. 4482911)°C

Reagent	Contents	Quantity	Storage†
Quantifiler™ THP PCR Reaction Mix	dNTPs, buffer, enzyme, Mustang Purple™ Passive Reference Standard, and stabilizers	4 tubes, 1 mL/tube	–25°C to –15°C upon receipt 2°C to 8°C after initial use Store protected from light
Quantifiler™ HP Primer Mix	Target-specific primers, ABY™, JUN™, and VIC™ dye-labeled probes, and Internal PCR Control (IPC) template	4 tubes, 0.8 mL/tube	–25°C to –15°C upon receipt 2°C to 8°C after initial use Store protected from light
Quantifiler™ THP DNA Dilution Buffer	Genomic DNA Standard dilution buffer	2 tubes, 1.8 mL/tube	–25°C to –15°C upon receipt 2°C to 8°C after initial use
Quantifiler™ THP DNA Standard	Genomic DNA Standard formulated at 100 ng/mL to generate standard curves	1 tube, 0.12 mL	–25°C to –15°C upon receipt 2°C to 8°C after initial use

† See reagent labels for expiration dates

Table 3 Quantifiler™ Trio DNA Quantification Kit (Cat. No. 4482910)

Reagent	Contents	Quantity	Storage†
Quantifiler™ THP PCR Reaction Mix	dNTPs, buffer, enzyme, Mustang Purple™ Passive Reference Standard, and stabilizers	4 tubes, 1 mL/tube	–25°C to –15°C upon receipt 2°C to 8°C after initial use Store protected from light
Quantifiler™ Trio Primer Mix	Target-specific primers, ABY™, JUN™, VIC™, and FAM™ dye-labeled probes, and Internal PCR Control (IPC) template	4 tubes, 0.8 mL/tube	–25°C to –15°C upon receipt 2°C to 8°C after initial use Store protected from light
Quantifiler™ THP DNA Dilution Buffer	Genomic DNA Standard dilution buffer	2 tubes, 1.8 mL/tube	–25°C to –15°C upon receipt 2°C to 8°C after initial use
Quantifiler™ THP DNA Standard	Genomic DNA Standard formulated at 100 ng/µL to generate standard curves	1 tube, 0.12 mL	–25°C to –15°C upon receipt 2°C to 8°C after initial use

† See reagent labels for expiration dates

Additional storage guideline for primer mix and PCR reaction mix

Keep Primer Mix and PCR Reaction Mix protected from direct exposure to light. Excessive exposure to light may affect the fluorescent probes and/or the passive reference dye.

Equipment and materials not included

Table 4 and Table 5 list required and optional equipment and materials not supplied with the Quantifiler™ HP and Trio DNA Quantification Kits. Unless otherwise noted, some of the items are available from major laboratory suppliers (MLS).

Table 4 Equipment not included

Equipment	Source
7500 Real-Time PCR Instrument	Contact your local Thermo Fisher sales representative
Tabletop centrifuge with 96-well plate adapters (optional)	MLS

Table 5 User-supplied materials

Material	Source
Applied Biosystems™ Non-Stick RNase-free Microfuge Tubes, 1.5 mL	Thermo Fisher (Cat. No. AM12450)
Pipettors and pipette tips	MLS
High-Throughput Setup	
MicroAmp™ Optical 96-Well Reaction Plate with Barcode	Thermo Fisher (Cat. No. 4306737)
MicroAmp™ Optical Adhesive Film	Thermo Fisher (Cat. No. 4311971)
MicroAmp™ Splash Free 96-Well Base	Thermo Fisher (Cat. No. 4312063)
Quantifiler™ Automation Enhancer	Please contact HID Sales and Support for assistance with this product.
Mid-to-Low-Throughput Setup	
MicroAmp™ Optical 8-Tube Strip (8 tubes/strip, 125 strips)	Thermo Fisher (Cat. No. 4316567)
MicroAmp™ 96-Well Tray/Retainer Set	Thermo Fisher (Cat. No. 403081)
MicroAmp™ Optical 8-Cap Strip (8 tubes/strip, 125 strips)	Thermo Fisher (Cat. No. 4323032)

2

Setup the software

Start the 7500 Real-Time PCR System

Start the computer

1. Press the power button on the computer.
2. In the Enter User name field of the login window, type your name or the user name associated with the computer, if applicable.
3. If required, type your password in the Password field.

Power on the instrument

Note: Wait for the computer to finish starting up before powering on the 7500 instrument.

Press the power button on the lower right front of the 7500 instrument.

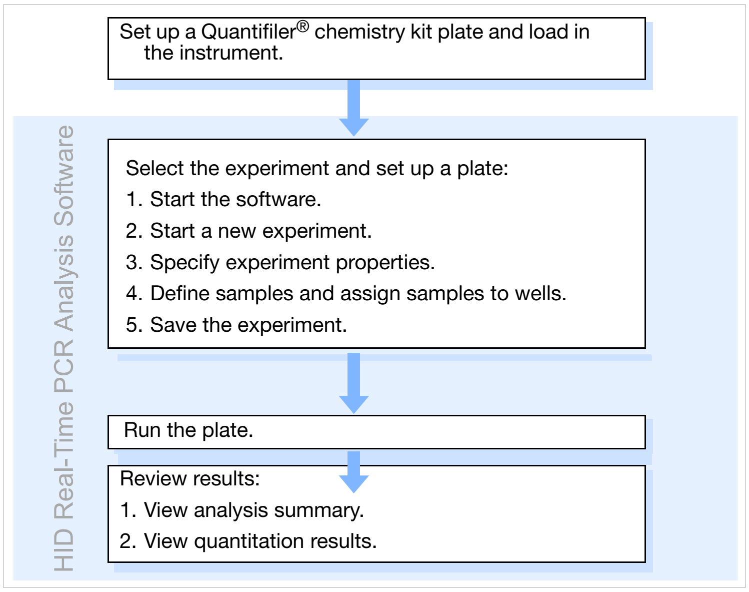
- The indicator lights on the lower left of the front panel cycle through a power on sequence.
- When the green power indicator is lit (not flashing), communication is established between the computer and the instrument.

If the green power-on indicator is flashing or the red error indicator is lit, see the *Applied Biosystems™ 7500/7500 Fast Real-Time PCR Systems System Maintenance* (Pub. No. 4387777).

Start the HID Real-Time PCR Analysis Software

1. Select **Start ▸ Programs ▸ Applied Biosystems ▸ HID Real-Time PCR Analysis Software ▸ HID Real-Time PCR Analysis Software v1.2**.
2. Login using your user name or guest.

Workflow


Set up a Quantifiler® chemistry kit plate and load in the instrument.
HID Real-Time PCR Analysis Software
Select the experiment and set up a plate:
1. Start the software.
2. Start a new experiment.
3. Specify experiment properties.
4. Define samples and assign samples to wells.
5. Save the experiment.
Run the plate.
Review results:
1. View analysis summary.
2. View quantitation results.

The software includes additional functionality to simplify Quantifiler™ assay setup, and streamline data review and downstream STR reaction setup. For information, see *HID Real-Time PCR Analysis Software v1.2 Getting Started Guide* (Pub. No. MAN0009819).

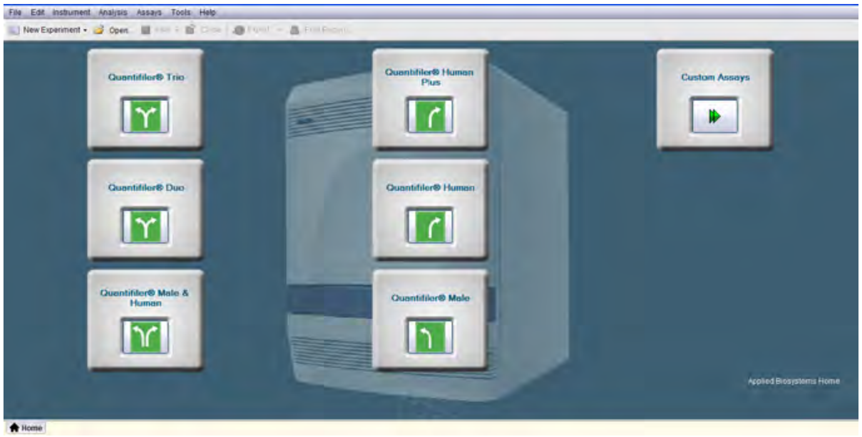
Calibrate the instrument

Before running samples using the Quantifiler™ HP and Trio DNA Quantification Kits for the first time, ensure that the instrument has been calibrated as described in "Calibrate the instrument" on page 100.

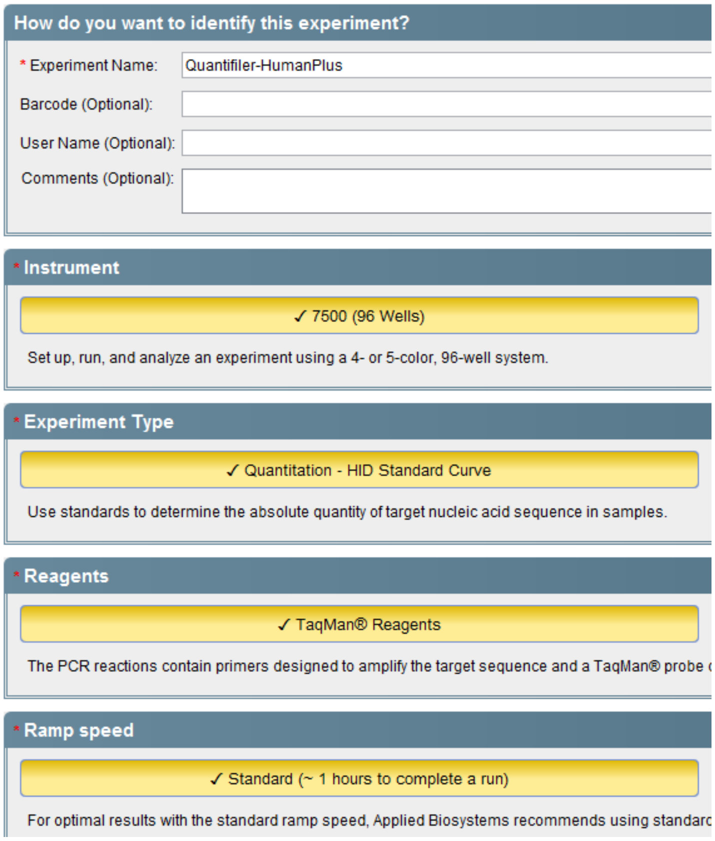
Create an experiment

This section contains brief procedures. For more information, see *HID Real-Time PCR Analysis Software v1.2 Getting Started Guide* (Pub. No. MAN0009819).

1. In the Home screen, click the icon for your application.



2. In the Experiment Properties screen, enter a name for the experiment. All other settings on this screen are automatically set for your application or are optional.



How do you want to identify this experiment?

* Experiment Name: Quantifiler-HumanPlus

Barcode (Optional):

User Name (Optional):

Comments (Optional):

*** Instrument**

✓ 7500 (96 Wells)

Set up, run, and analyze an experiment using a 4- or 5-color, 96-well system.

*** Experiment Type**

✓ Quantitation - HID Standard Curve

Use standards to determine the absolute quantity of target nucleic acid sequence in samples.

*** Reagents**

✓ TaqMan® Reagents

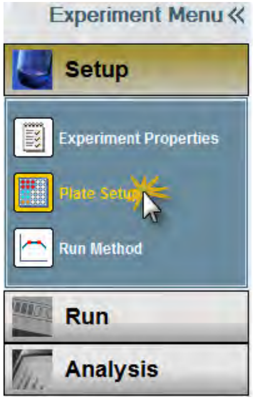
The PCR reactions contain primers designed to amplify the target sequence and a TaqMan® probe

*** Ramp speed**

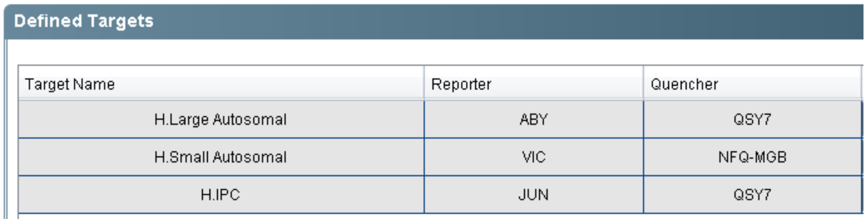
✓ Standard (~ 1 hours to complete a run)

For optimal results with the standard ramp speed, Applied Biosystems recommends using standar

3. In the left navigational panel, click **Setup** ▸ **Plate Setup**. Targets are automatically specified for your application.

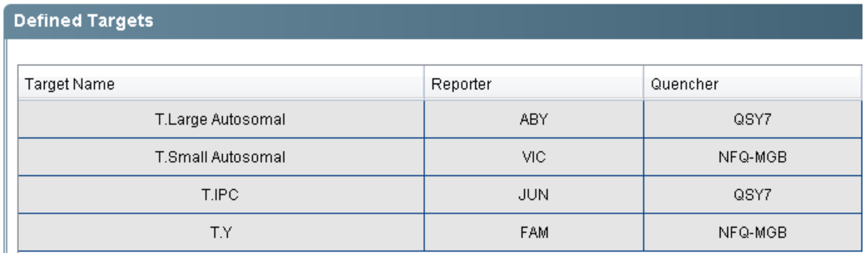


Quantifiler™ HP targets:



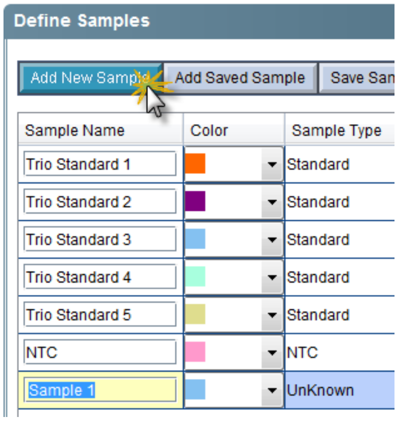
Target Name	Reporter	Quencher
H.Large Autosomal	ABY	QSY7
H.Small Autosomal	VIC	NFQ-MGB
H.IPC	JUN	QSY7

Quantifiler™ Trio targets:



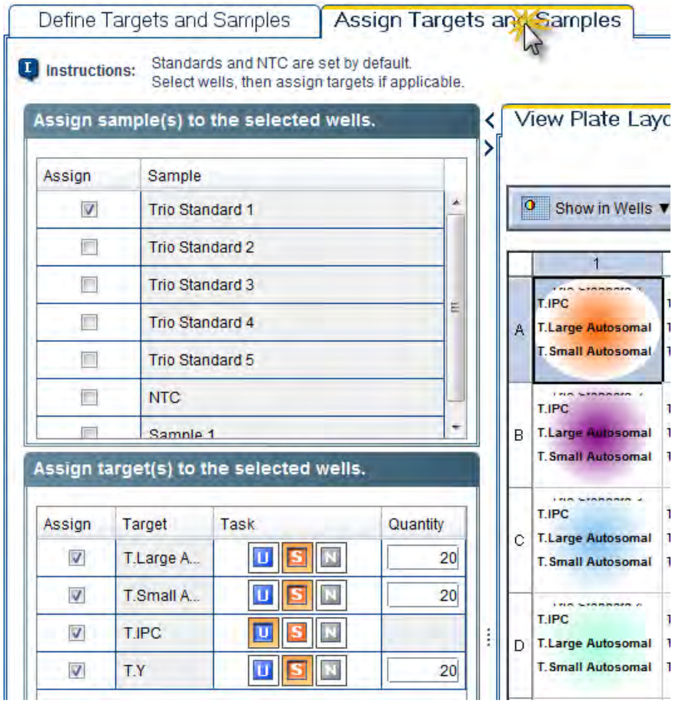
Target Name	Reporter	Quencher
T.Large Autosomal	ABY	QSY7
T.Small Autosomal	VIC	NFQ-MGB
T.IPC	JUN	QSY7
T.Y	FAM	NFQ-MGB

4. Define samples: Click **Add New Sample**, then type the name for the sample. Repeat for remaining samples.



Sample Name	Color	Sample Type
Trio Standard 1	🟧	Standard
Trio Standard 2	🟪	Standard
Trio Standard 3	🟦	Standard
Trio Standard 4	🟩	Standard
Trio Standard 5	🟨	Standard
NTC	🟥	NTC
Sample 1	🟦	UnKnown

5. Click **Assign Targets and Samples**. Targets are automatically assigned, and the standard quantities are automatically specified. The figure below is the standard setup for the Quantifiler™ Trio assay. The Quantifiler™ HP assay has the same setup, except the Y Target is not available for selection.



Instructions: Standards and NTC are set by default.
Select wells, then assign targets if applicable.

Assign sample(s) to the selected wells.

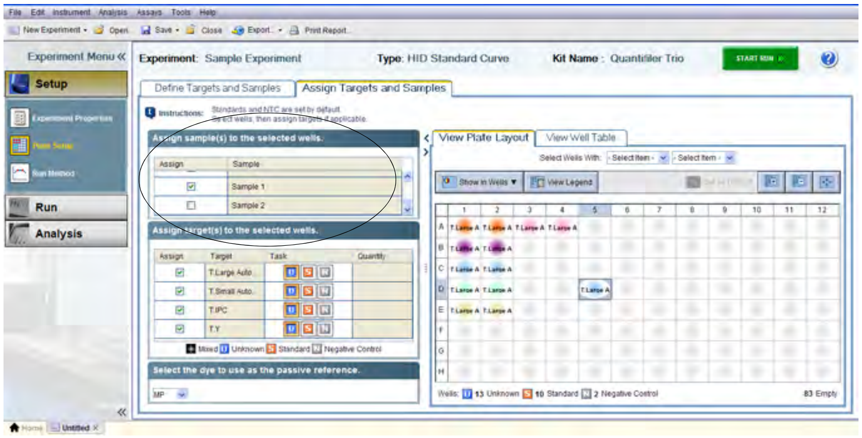
Assign	Sample
☑	Trio Standard 1
☐	Trio Standard 2
☐	Trio Standard 3
☐	Trio Standard 4
☐	Trio Standard 5
☐	NTC
☐	Sample 1

Assign target(s) to the selected wells.

Assign	Target	Task	Quantity
☑	T.Large A...	U [✓ S] N	20
☑	T.Small A...	U [✓ S] N	20
☑	T.IPC	[✓ U] S N	
☑	T.Y	U [✓ S] N	20

6. Assign the samples to the plate wells:
   a. To select well(s):
      - **Single well**—Click the well
      - **Row of wells**—Click a letter on the side of the layout
      - **Column of wells**—Click a number at the top of a column
      - **More than one well, row, or column**—Drag the pointer over the wells, letters, or columns to select

b. In the Assign sample(s) to wells section to the left of the plate layout, locate the desired sample and select the checkbox in the Assign column next to the sample name. The target for each sample is set by default.


File Edit Instrument Analysis Assays Tools Help
New Experiment Open Save Close Export... Print Report...
Experiment Menu «
Setup
Experiment Properties
Plate Setup
Run Method
Run
Analysis
Define Targets and Samples
Assign Targets and Samples
View Plate Layout
View Well Table
Assign
Sample
Target
Task
Quantity
START RUN

Experiment: Sample Experiment Type: HID Standard Curve Kit Name : Quantifiler Trio

Assign sample(s) to the selected wells.

Assign	Sample
☑	Sample 1
☐	Sample 2

Assign target(s) to the selected wells.

Assign	Target
☑	T.Large Auto
☑	T.Small Auto
☑	T.IPC
☑	T.Y

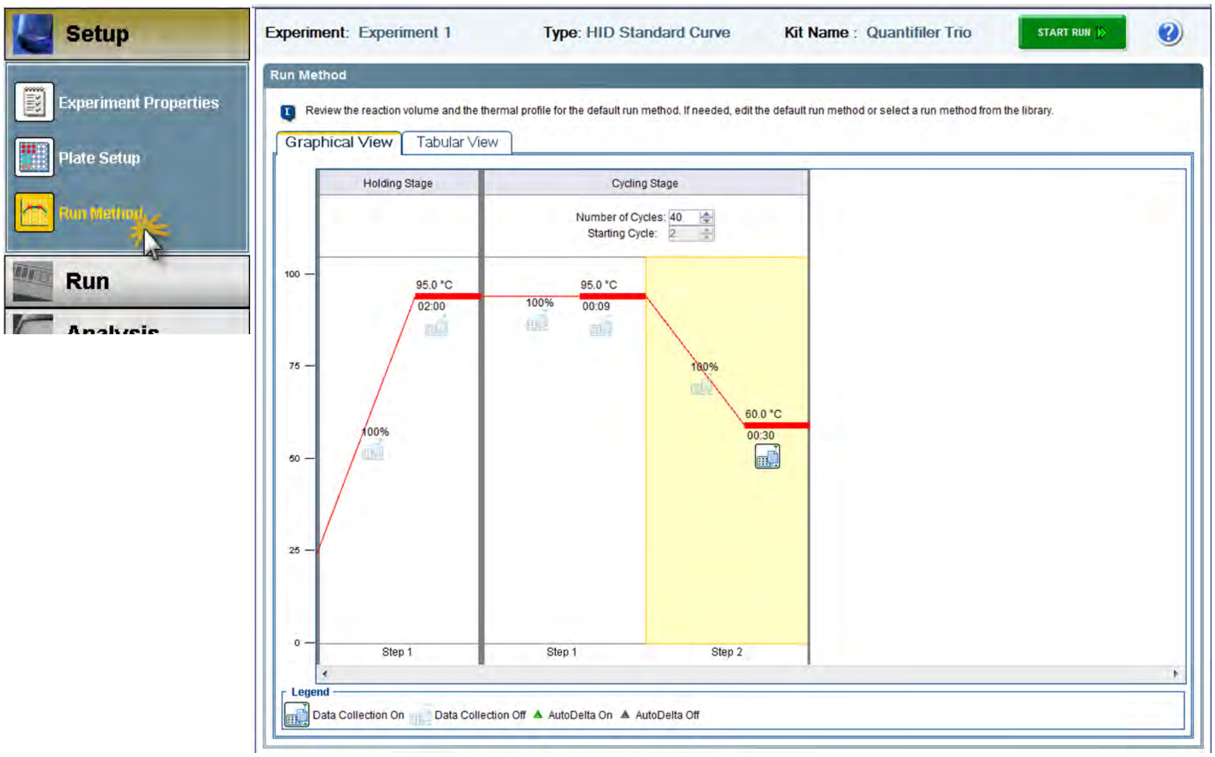
Select the dye to use as the passive reference.

Wells: 13 Unknown 10 Standard 2 Negative Control 83 Empty

c. Repeat steps a and b for the remaining samples.

7. To change the well a sample is assigned to, click the well, deselect the sample in the Assign Samples section, click the new well, then select the sample in the Assign Samples section.

8. In the left navigational panel, click **Setup ▸ Run Method** to view the parameters. The parameters are automatically specified.



Experiment: Experiment 1 Type: HID Standard Curve Kit Name : Quantifiler Trio

Run Method

Review the reaction volume and the thermal profile for the default run method. If needed, edit the default run method or select a run method from the library.

Number of Cycles: 40
Starting Cycle: 2

9. Click **Save**.

Save an experiment template

Template settings

In addition to assay settings, templates can contain:

- Assay-specific detectors
- Well assignments for quantification standards, with targets, tasks, and quantity
- Well assignments for unknown samples, with targets and tasks
- Instrument settings: reaction volume settings and 9600 Emulation setting

Create and use a template

1. Select **File ▸ New Experiment**, then select the application for the template.
2. Specify settings and plate layout as needed.
3. Select **Save ▸ Save As Template**. Templates are saved as.edt files. The default location is C:\Applied Biosystems\7500\Experiments.
4. Click **Open**, then navigate to the template of interest.

3

PCR amplification

Prepare the DNA quantification standards

Required materials

The required materials include:

- Pipettors
- Pipette tips
- Low-bind microfuge tubes
- Quantifiler™ THP DNA Standard
- Quantifiler™ THP DNA Dilution Buffer

Note: You can store the diluted DNA quantification standards for up to 2 weeks at 2°C to 8°C. Longer term storage is not recommended. Store diluted DNA standards in low-bind tubes (for example, Applied Biosystems™ Non-Stick RNase-free Microfuge Tubes, 1.5 mL, Cat. No. AM12450).

Guidelines for calculating the standards dilution series

The standards dilution series example shown in Table 6 on page 28 is suitable for general use.

Note: We recommend:

- Ten-fold dilution series with 5 concentration points as described in Table 6. You can add an optional 100 ng/μL standard point if needed. However, you may see an increase in the IPC C_T for the 100 ng/μL standard. For more information, see "Use the Internal PCR Control system" on page 47.
- Minimum input volume of 10 μL DNA for dilutions (to ensure accuracy of manual pipetting).

Standards dilution series example

Table 6 shows an example of one standards dilution series with the concentrations ranging from 50 ng/μL (Std. 1) to 0.005 ng/μL, or 5 pg/μL (Std. 5). When 2.0 μL of a sample at the lowest concentration (5 pg/μL) is loaded in a reaction, the well contains approximately 1.5 diploid human genome equivalents.

Table 6 Standards dilution series example

Standard	Concentration (ng/µL)	Example volumes	Dilution factor
Std. 1	50.000	10 µL [100 ng/µL stock] + 10 µL Quantifiler™ THP DNA dilution buffer	25
Std. 2	5.000	10 µL [Std. 1] + 90 µL Quantifiler™ THP DNA dilution buffer	105
Std. 3	0.500	10 µL [Std. 2] + 90 µL Quantifiler™ THP DNA dilution buffer	105
Std. 4	0.050	10 µL [Std. 3] + 90 µL Quantifiler™ THP DNA dilution buffer	105
Std. 5	0.005	10 µL [Std. 4] + 90 µL Quantifiler™ THP DNA dilution buffer	105

Note: To ensure manual pipetting accuracy, pipet a minimum volume of 10 µL.

Preparation guidelines

While preparing the standards, keep in mind that:

- DNA quantification standards are critical for accurate analysis of run data
- The quality of pipettors and tips, use of low-binding DNA tubes for dilutions, and the care used in measuring and mixing dilutions affect accuracy

Prepare the DNA quantification standards

When using Quantifiler™ THP DNA Dilution Buffer, you can store the prepared DNA quantification standards in low-binding tubes for up to 2 weeks at 2°C to 8°C.

To prepare the DNA quantification standards dilution series:

1. Label five microcentrifuge tubes: Std. 1, Std. 2, Std. 3, and so on.
2. Dispense the required amount of diluent (Quantifiler™ THP DNA Dilution Buffer) to each tube (refer to Table 6 for volumes).
3. Prepare Std. 1:
    a. Vortex the Quantifiler™ THP DNA Standard 3 to 5 seconds.
    b. Using a new pipette tip, add the appropriate volume of Quantifiler™ THP DNA Standard for your dilution series to the tube for Std. 1.
    c. Mix the dilution thoroughly.
4. Prepare Std. 2 through 5:
    a. Using a new pipette tip, add the appropriate volume of the prepared standard to the tube for the next standard (refer to Table 6 for volumes).
    b. Mix the standard thoroughly.
    c. Repeat steps a and b for each subsequent standard until you complete the dilution series.

Prepare the reactions

Required materials

- Quantifiler™ HP or Quantifiler™ Trio Primer Mix
- Quantifiler™ THP PCR Reaction Mix
- 1.5-mL or 2.0-mL low-binding DNA tubes (depending on reaction volume needed)
- 96-well optical reaction plate *or* optical 8-tube strip
- Extracted DNA samples
- DNA quantification standards dilutions series
- Optical adhesive cover *or* optical 8-cap strip

Importance of minimizing bubbles

Bubbles in reaction wells can cause noise in the fluorescence signal and can affect results. When dispensing reagents and samples, use the following techniques to avoid introducing bubbles:

Manual setup:

- Place the pipette tip against the side of the well above the surface of the master mix, then dispense sample.
- Place the pipette tip below the surface of the master mix, then dispense sample *only until the first stop of the pipette*. Place the pipette tip against the side of the well above the surface of the liquid to dispense remaining sample in the tip.

Automated high throughput setup:

Quantifiler™ Automation Enhancer can assist with preventing bubbles from being introduced during robotic mixing and pipetting procedures.

To use, add 1 µL of Quantifiler™ Automation Enhancer to 1 mL of Quantifiler™ PCR Reaction Mix (1:1000 dilution) in the Quantifiler™ HP or Trio kit. Follow the standard kit setup for the PCR reactions and 7500 instrument. Contact HID Sales and Support for assistance ordering Quantifiler™ Automation Enhancer.

Prepare the reactions

While preparing the reactions, keep the 96-well optical reaction plate or optical 8-tube strip in its base and do not place it directly on the bench top to protect it from scratches and particulate matter.

Note: When processing samples using harsh chemicals from differential extraction procedures, it may be necessary (depending on the protocol used and the specific properties of the resulting lysate solution) to add additional wash steps with $T_{10}E_{0.1}$ buffer prior to quantification with the Quantifiler™ HP and Trio Kit assays.

To prepare the reactions:

1. Calculate the volume of each component needed to prepare the reactions, using the appropriate table below.

   For the Quantifiler™ HP DNA Quantification Kit:

Component	Volume per reaction (µL)
Quantifiler™ HP Primer Mix	8
Quantifiler™ THP PCR Reaction Mix	10

   For the Quantifiler™ Trio DNA Quantification Kit:

Component	Volume per reaction (µL)
Quantifiler™ Trio Primer Mix	8
Quantifiler™ THP PCR Reaction Mix	10

   Note: Include additional reactions in your calculations to provide excess volume for the loss that occurs during reagent transfers.

2. Prepare the reagents:
   - Thaw the Quantifiler™ HP or Quantifiler™ Trio Primer Mix completely, then vortex 3 to 5 seconds and centrifuge briefly before opening the tube.
   - Gently vortex the Quantifiler™ THP PCR Reaction Mix before using.

3. Pipet the required volumes of components into an appropriately sized polypropylene tube.

4. Vortex the PCR mix 3 to 5 seconds, then centrifuge briefly.

5. Dispense 18 µL of the PCR mix into each reaction well or tube.

6. Add 2 µL of sample, standard, or control to the applicable wells or tubes.

   Note: We recommend running duplicates of each sample of the DNA quantification standards for each reaction plate.

7. Seal the reaction plate with the Optical Adhesive Cover, or the strip tube with the optical 8-cap strip.

8. Remove bubbles: While the plate is inside the base, tap the base on the benchtop to bring the bubbles to the liquid surface. Lift the plate, then inspect each well for bubbles; tap each well with a marker, pen, or gloved fingertip.

   IMPORTANT! This step is critical to avoid noise in the fluorescence signal that bubbles can cause.

9. Centrifuge the plate at 3,000 rpm for about 20 seconds in a tabletop centrifuge with plate holders to remove any bubbles.

   Note: If a tabletop centrifuge with 96-well plate adapters is not available, visually inspect the plate for bubbles, and lightly tap the plate to remove bubbles in wells.

Run the reactions

Before you run the reactions

Before you run the reactions, make sure that you have:

- Powered on the computer, 7500 Real-Time PCR instrument, and software. For setup procedures, see page 19.
- Create an experiment for the run. See page 20.

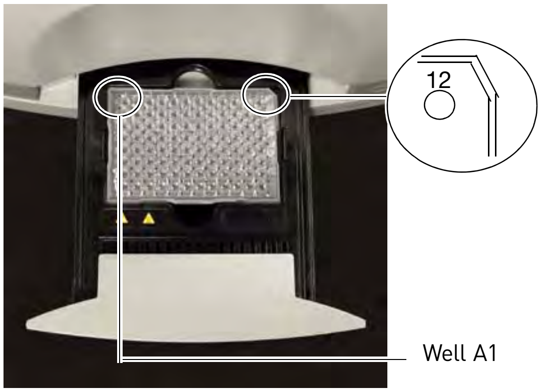
Run the plate on the 7500 Real-Time PCR instrument

To run the plate on the 7500 Real-Time PCR instrument:

1. Press the tray door to open it.

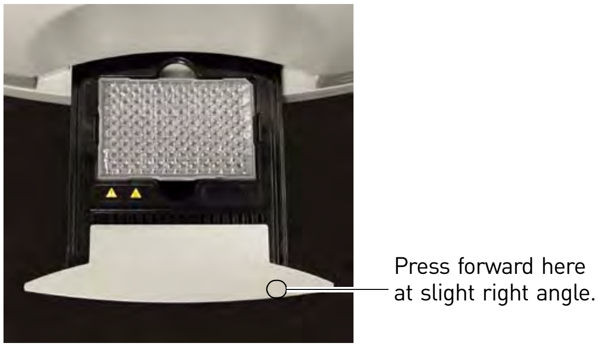
2. Load the plate into the plate holder in the instrument. Ensure that the plate is correctly aligned in the holder.

3. Load the 96-well optical plate with the notched A12 position at the top-right of the tray.



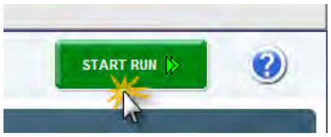
4. Close the tray door.

5. Apply pressure to the right side of the tray and at an angle to close the tray door.



6. In the HID Real-Time PCR Analysis Software, open the experiment that you set up for the run.

7. Click **Start Run**.



4

Data analysis and results

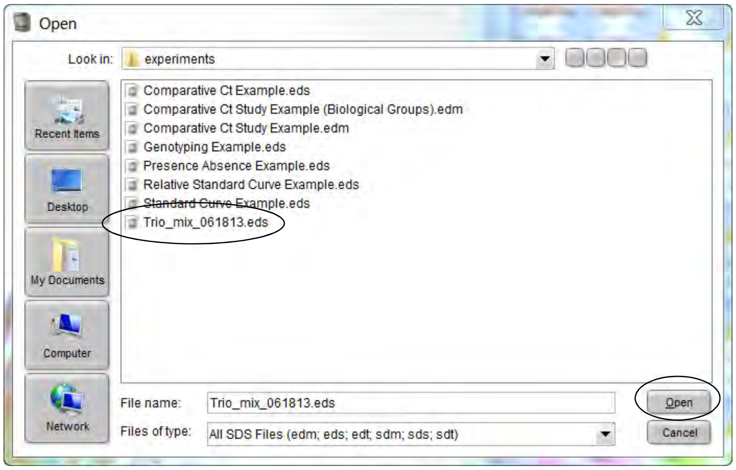
Analyze the experiment

Analyze a run after it is complete and reanalyze after you make any changes to the experiment, such as sample names.

To analyze an experiment:

1. To open the experiment for analysis:
   - Navigate to the folder where the run file is stored, and double-click the run file.

     or
   - Launch the software from the shortcut on your desktop:
     – Double-click the HID Real-Time PCR Analysis Software icon,
     – Click **File** ▸ **Open**,
     – Then navigate to the run file and click **Open** (or double-click the run file).



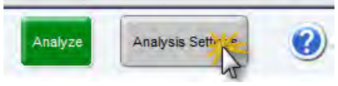
Look in: experiments

File name: Trio_mix_061813.eds

Files of type: All SDS Files (edm; eds; edt; sdm; sds; sdt)

Open
Recent Items
Desktop
My Documents
Computer
Network
Comparative Ct Example.eds
Comparative Ct Study Example (Biological Groups).edm
Comparative Ct Study Example.edm
Genotyping Example.eds
Presence Absence Example.eds
Relative Standard Curve Example.eds
Standard Curve Example.eds
Trio_mix_061813.eds
Open
Cancel

2. Verify the analysis settings:
   a. Click **Analysis Settings** in the upper-right corner of the window.



   b. Click the $\mathbf{C_T}$ **Settings** tab.

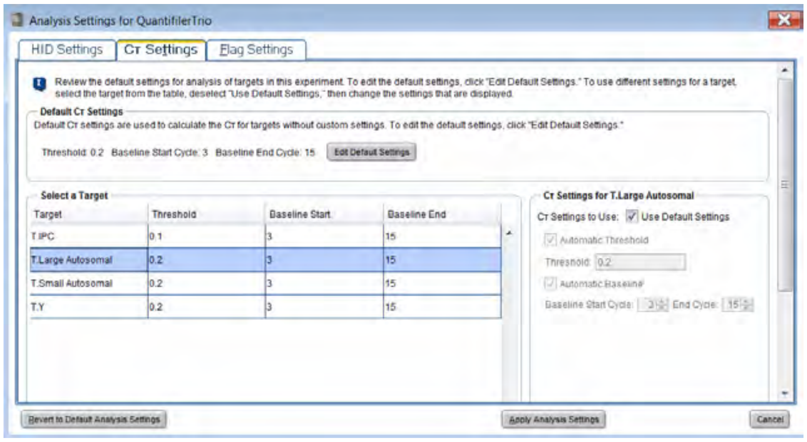
c. Verify that the settings are as shown below, then:

- If the analysis settings are correct, click **Apply Analysis Settings**.

  or

- If the analysis settings differ from those shown below, change them to match the settings, then click **Apply Analysis Settings**.

Large, small, and Y target threshold and baseline settings:



Analysis Settings for QuantifilerTrio

Review the default settings for analysis of targets in this experiment. To edit the default settings, click "Edit Default Settings." To use different settings for a target, select the target from the table, deselect "Use Default Settings," then change the settings that are displayed.

Default C_T Settings

Default C_T settings are used to calculate the C_T for targets without custom settings. To edit the default settings, click "Edit Default Settings."

Threshold: 0.2 Baseline Start Cycle: 3 Baseline End Cycle: 15

Select a Target

Target	Threshold	Baseline Start	Baseline End
T.IPC	0.1	3	15
T.Large Autosomal	0.2	3	15
T.Small Autosomal	0.2	3	15
T.Y	0.2	3	15

C_T Settings for T.Large Autosomal

C_T Settings to Use: ☑ Use Default Settings

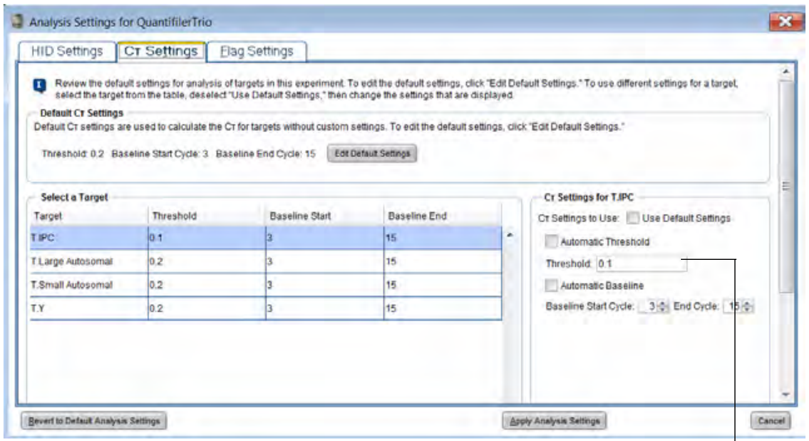
☑ Automatic Threshold

Threshold: 0.2

☑ Automatic Baseline

Baseline Start Cycle: 3 End Cycle: 15

IPC target threshold and baseline settings:



Analysis Settings for QuantifilerTrio

Review the default settings for analysis of targets in this experiment. To edit the default settings, click "Edit Default Settings." To use different settings for a target, select the target from the table, deselect "Use Default Settings," then change the settings that are displayed.

Default C_T Settings

Default C_T settings are used to calculate the C_T for targets without custom settings. To edit the default settings, click "Edit Default Settings."

Threshold: 0.2 Baseline Start Cycle: 3 Baseline End Cycle: 15

Select a Target

Target	Threshold	Baseline Start	Baseline End
T.IPC	0.1	3	15
T.Large Autosomal	0.2	3	15
T.Small Autosomal	0.2	3	15
T.Y	0.2	3	15

C_T Settings for T.IPC

C_T Settings to Use: ☐ Use Default Settings

☐ Automatic Threshold

Threshold: 0.1

☐ Automatic Baseline

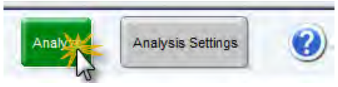
Baseline Start Cycle: 3 End Cycle: 15

For IPC threshold, 0.1
(see the note below)

Note: Quantifiler™ HP and Trio Kits have been validated using the Manual Baseline method. Studies were also performed applying the Automatic Baseline method and the Manual Baseline method to evaluate potential differences between the methods for concentrations from 5 – 0.005 ng/µL. No statistically significant differences were observed within this range for C_T values generated using the Automatic Baseline and Manual analysis methods.

A value of 0.1 was used for the IPC Threshold during the developmental validation studies. Before using alternative baseline methods, (e.g. automatic) or thresholds, perform the appropriate internal validation studies.

3. Click **Analyze**.



View results

Overview

Viewing the results of data analysis can involve one or more of the following:

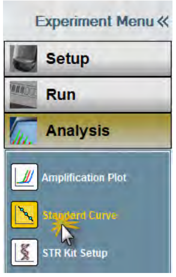
- View the standard curve (page 35)
- View the amplification plot (page 36)
- Export the results (page 38)

View the standard curve

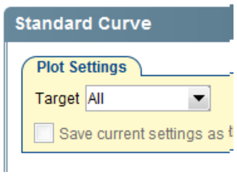
For information about interpreting and troubleshooting the standard curve, see "Examine the standard curve" on page 43 and "Troubleshoot the standard curve" on page 46.

To view the standard curve:

1. In the left navigational panel, click **Analysis ▸ Standard Curve**.



2. In the Target drop-down list, select **All**.

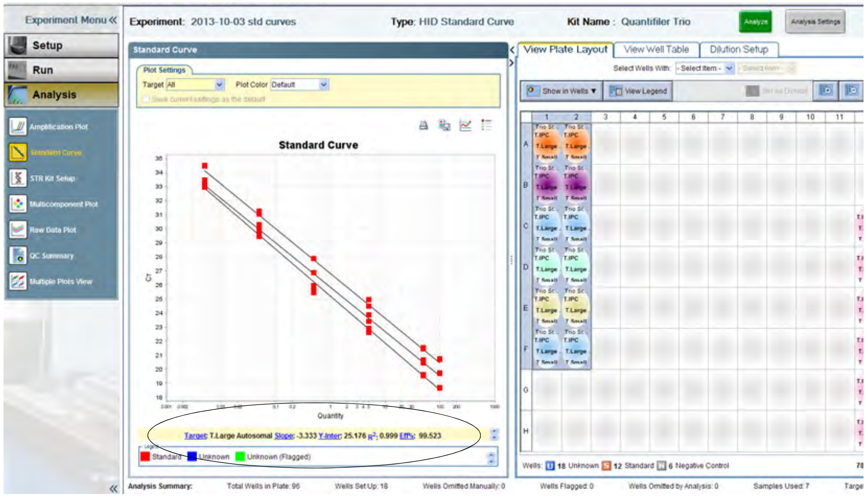


Target All

☐ Save current settings as t

3. View the C_T values for the quantification standard reactions and the calculated regression line, slope, y-intercept, and R^2 values.

Note: The figure below shows an example of standard curve plots. The gap between the Small Autosomal, Large Autosomal, and Male C_T values may vary depending on the relative slopes of the targets and the instrument.


Experiment: 2013-10-03 std curves
Type: HID Standard Curve
Kit Name : Quantifiler Trio

Plot Settings: Target All, Plot Color Default

Target: T.Large Autosomal Slope: -3.333 Y-Inter: 25.176 R^2: 0.999 Eff%: 99.523

Wells: 18 Unknown 12 Standard 6 Negative Control

Analysis Summary: Total Wells in Plate: 96 Wells Set Up: 18 Wells Omitted Manually: 0 Wells Flagged: 0 Wells Omitted by Analysis: 0 Samples Used: 7

Amplification plot results

The amplification plot can display one of the following:

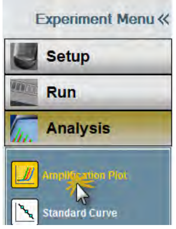
- C_T versus well position view
- Plot of normalized reporter signal (R_n) versus cycle (linear view)

For more information about the amplification plot, see "Real-time data analysis" on page 97 or the *7300/7500/7500 Fast Real-Time PCR System Absolute Quantification Getting Started Guide* (Pub. No. 4378658).

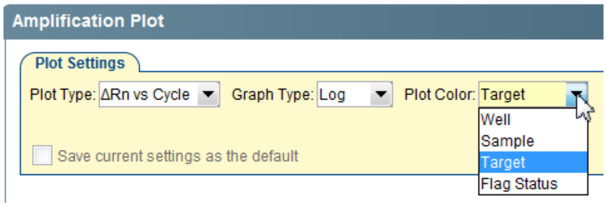
View the amplification plot

To view the amplification plot:

1. In the left navigational panel, click **Analysis ▸ Amplification Plot**.



2. Select a plot color in the drop-down list:
   - Well
   - Sample
   - Target
   - Flag Status

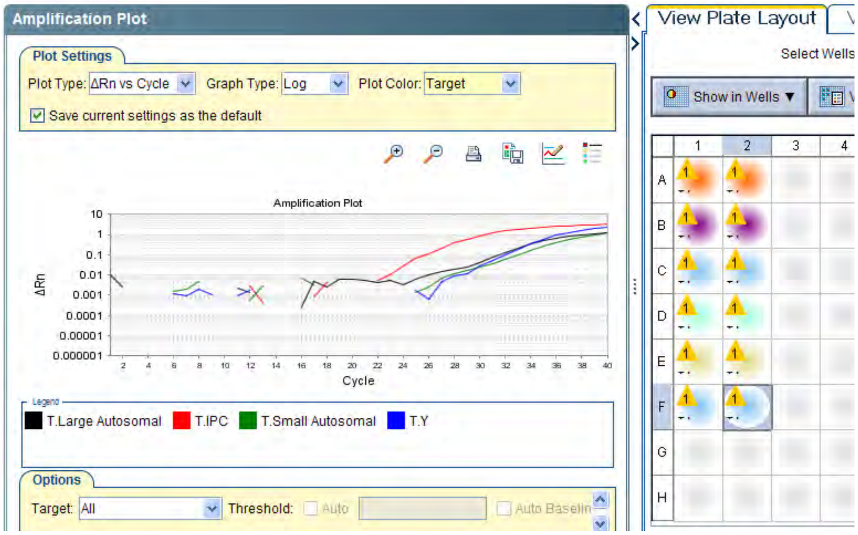

Plot Settings: Plot Type: ΔRn vs Cycle, Graph Type: Log, Plot Color: Target

3. Select the target(s) to view in drop-down list located under the amplification plots.
   - Select **All** to view all targets simultaneously

     or
   - Select a single target from the appropriate column in the table:

Quantifiler™ HP targets	Quantifiler™ Trio targets
H.IPC	T.IPC
H.Large Autosomal	T.Large Autosomal
H.Small Autosomal	T.Small Autosomal
—	T.Y

4. Select the applicable sample(s) in the Plate layout. The example below displays all targets for a single sample using target plot colors.



Amplification Plot

Plot Settings

Plot Type: ΔRn vs Cycle

Graph Type: Log

Plot Color: Target

☑ Save current settings as the default

Legend: ■ T.Large Autosomal 🟥 T.IPC 🟩 T.Small Autosomal 🟦 T.Y

Options

Target: All

Threshold: ☐ Auto

☐ Auto Baselin

5. If a single target was selected in step 3, repeat steps 3 and 4 for the remaining targets.

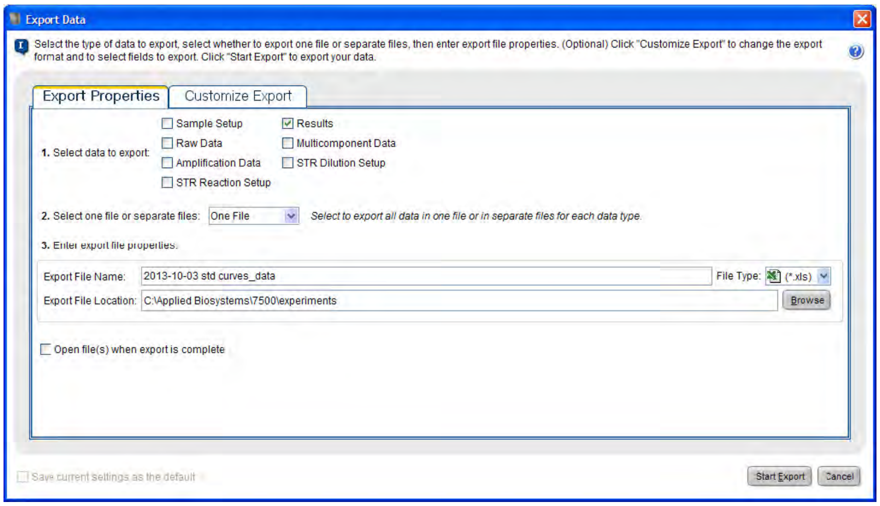
For troubleshooting information, see “Troubleshoot amplification plots” on page 51.

Export the results

You can export numeric data into text files, which can then be imported into spreadsheet applications such as Microsoft™ Excel™ software.

To export the results:

1. In the Experiment Menu, click **Analysis**. Click any Analysis screen, then click either **View Plate Layout** or **View Well Table**.
2. Select the wells to export.
3. Complete the Export dialog box and export the data:
    a. In the toolbar, click **Export**.



Select the type of data to export, select whether to export one file or separate files, then enter export file properties. (Optional) Click "Customize Export" to change the export format and to select fields to export. Click "Start Export" to export your data.

1. Select data to export: ☐ Sample Setup ☑ Results ☐ Raw Data ☐ Multicomponent Data ☐ Amplification Data ☐ STR Dilution Setup ☐ STR Reaction Setup

2. Select one file or separate files: One File

Select to export all data in one file or in separate files for each data type.

3. Enter export file properties.

Export File Name: 2013-10-03 std curves_data

File Type: (*.xls)

Export File Location: C:\Applied Biosystems\7500\experiments

☐ Open file(s) when export is complete

☐ Save current settings as the default

    b. Select **Results** as the type of data to export.
    c. Select **Separate Files** or **One File** in the drop-down list.
    d. Enter a file name and export location.
    e. Click **Start Export** to export the data to the file(s) that you selected.

4. When the export is complete, click:
    - **Export More Data**—to export different types of data for the same samples

      or
    - **Close Export Tool**
5. For more information about exporting data, see the *7300/7500/7500 Fast Real-Time PCR System Absolute Quantification Getting Started Guide* (Pub. No. 4378658).

5

Interpretation of results

Typical plots obtained with the Quantifiler™ HP and Trio assays

The figures below are examples of typical male, female, and no template control (NTC) amplification plots for the Quantifiler™ Trio assay. The Quantifiler™ HP assay amplification plots are similar, but do not include the Human Male Target (T.Y.).

Figure 6 Typical male amplification plot (horizontal blue line=C_T threshold for small autosomal, large autosomal and male targets; horizontal red line=C_T threshold for IPC)

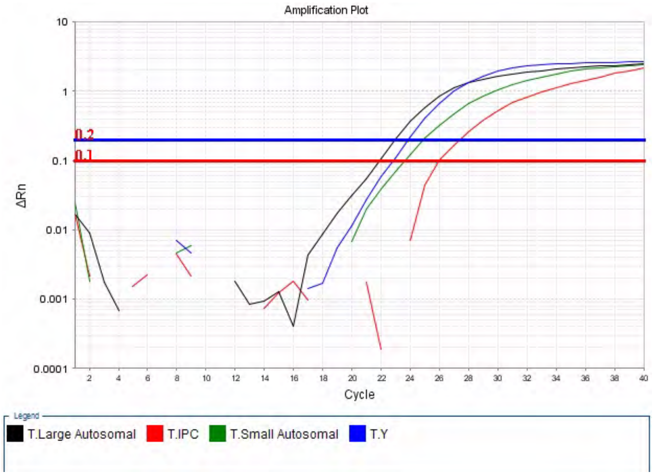


Figure 7 Typical female amplification plot (horizontal blue line=C_T threshold for small autosomal, large autosomal and male targets; horizontal red line=C_T threshold for IPC)

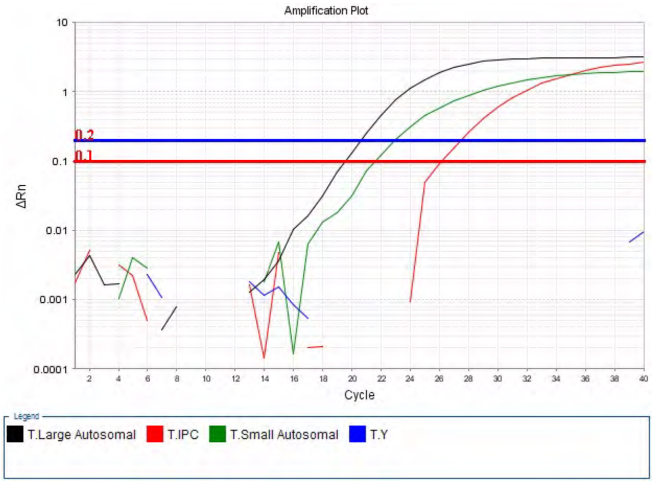
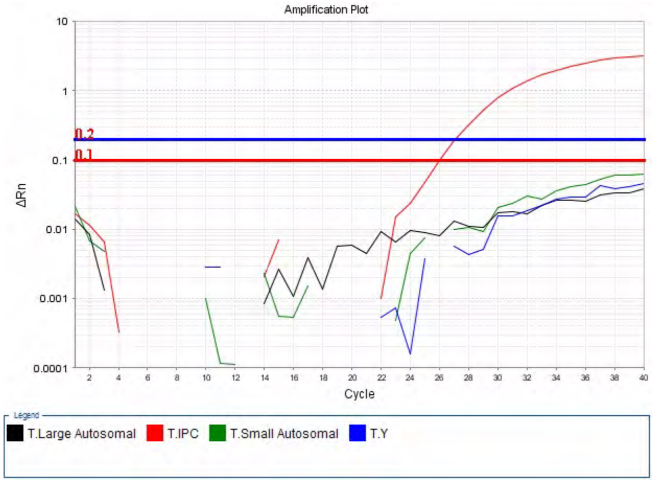


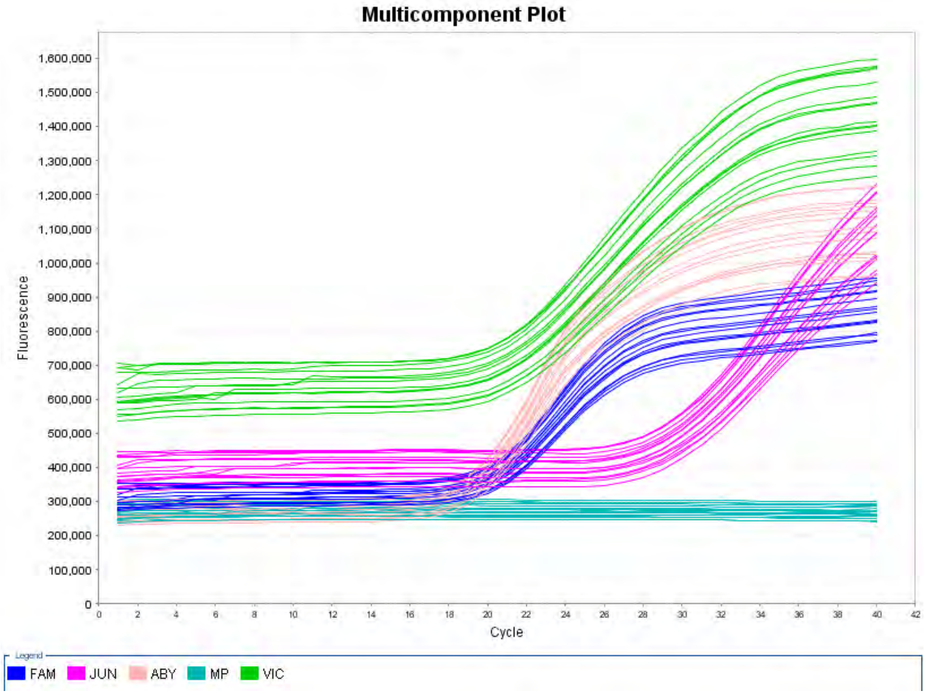
Figure 8 Typical no template control (NTC) amplification plot (horizontal blue line=C_T threshold for small autosomal, large autosomal and male targets; horizontal red line=C_T threshold for IPC)



Examine the multicomponent plot to check for noise

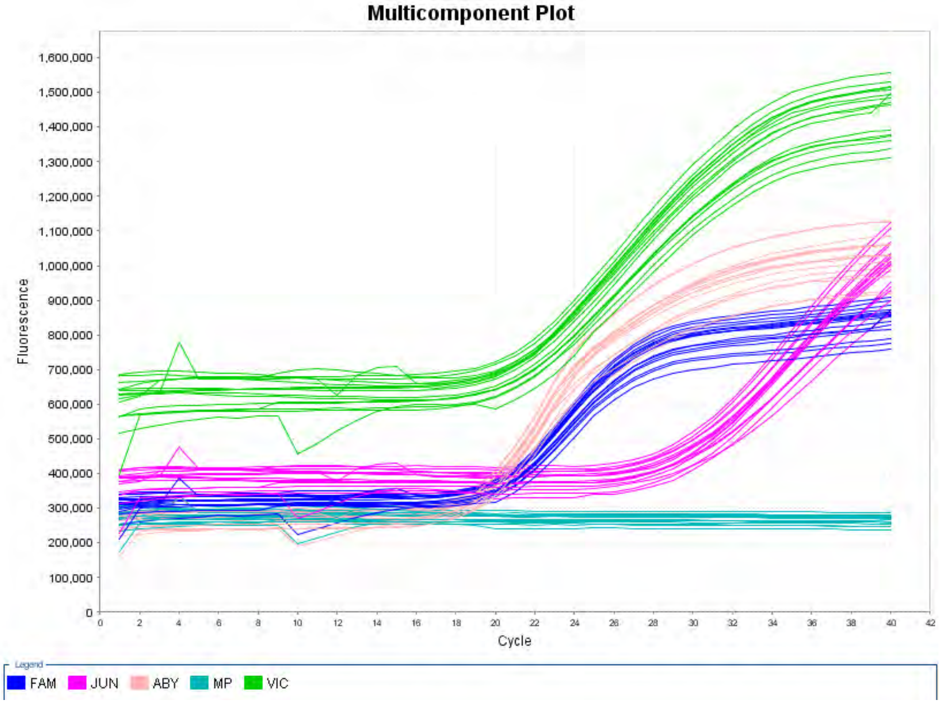
The multicomponent plot displays the fluorescence data for each target in the quantification assay plotted against cycle number. Samples in a normal multicomponent plot generally demonstrate a flat line for at least the first 15–20 cycles, before exponential growth of the PCR product can be detected. If using the default settings for the Quantifiler™ Trio kit, the flat line between cycles 3–15 is used to calculate the baseline for the sample.

Figure 9 Typical Quantifiler™ Trio kit multicomponent plot; small autosomal target = VIC™ dye, large autosomal target = ABY™ dye, male target = FAM™ dye, IPC = JUN™ dye, passive reference = Mustang Purple™ (MP) dye



Samples with an abnormal multicomponent plot may exhibit short or long dips or rises in the fluorescence readings. When this noise occurs between cycles 3–15, it may affect the baseline calculation for the sample, which can in turn affect the C_T value calculated for the DNA targets.

Figure 10 Multicomponent plot with noise between cycles 3-15

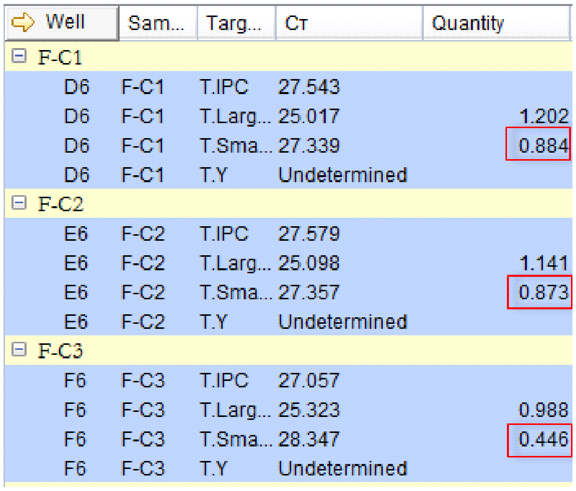


Impact of fluorescence noise on quantification and STR results

Fluorescence noise may alter the C_T value calculated for the DNA targets, but this effect is difficult to observe unless multiple replicates of a sample have been quantified. In our observations, results for the small autosomal target are the most susceptible to the effects of fluorescent noise.

In the following example, three replicates of sample F–C have been quantified. The first two replicates had small autosomal target concentrations of 0.884 ng/µL and 0.873 ng/µL, but the third replicate had a small autosomal target concentration of 0.446 ng/µL.

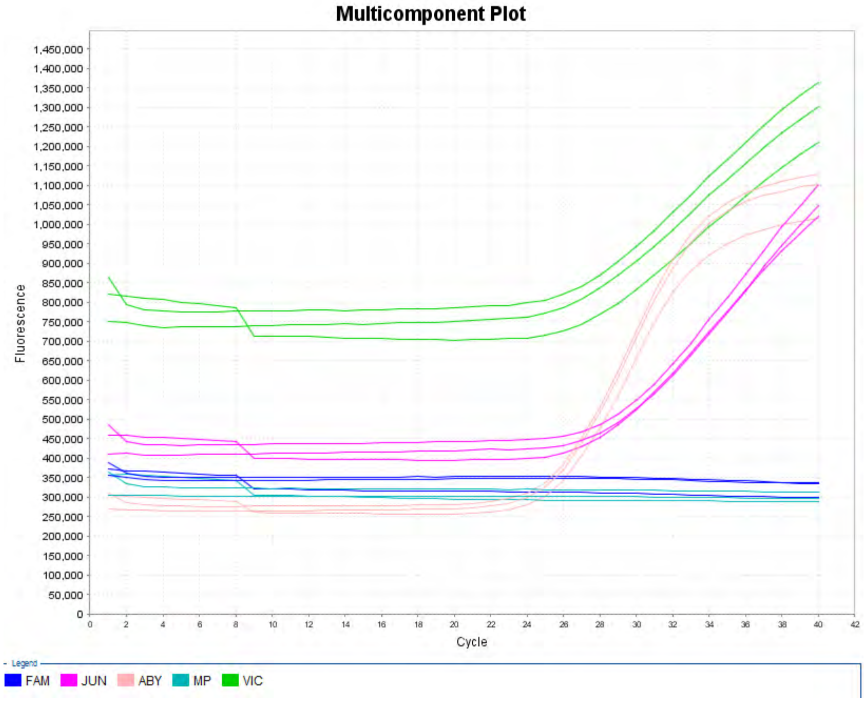
Figure 11 C_T results for F-C example data



Well	Sam...	Targ...	C_T	Quantity
⊟ F-C1				
D6	F-C1	T.IPC	27.543	
D6	F-C1	T.Larg...	25.017	1.202
D6	F-C1	T.Sma...	27.339	0.884
D6	F-C1	T.Y	Undetermined	
⊟ F-C2				
E6	F-C2	T.IPC	27.579	
E6	F-C2	T.Larg...	25.098	1.141
E6	F-C2	T.Sma...	27.357	0.873
E6	F-C2	T.Y	Undetermined	
⊟ F-C3				
F6	F-C3	T.IPC	27.057	
F6	F-C3	T.Larg...	25.323	0.988
F6	F-C3	T.Sma...	28.347	0.446
F6	F-C3	T.Y	Undetermined	

The multicomponent plot for these samples shows a dip in fluorescence between cycle 8 and cycle 9 that corresponds to F06, the well that contains the outlier replicate.

Figure 12 Multicomponent plot for F-C example data



If an inaccurate quantification result (caused by fluorescence noise) is used to determine DNA input volume for STR amplification, STR results may be inaccurate.

In the F-C example above, sample concentration is ~0.88 ng/µL. If the third replicate was not identified as an outlier, approximately 2.2 µL of DNA might be added to an STR reaction to target an input of 1 ng, resulting in almost double the intended target being added to the reaction (1.94 ng).

Examine the standard curve

Examine the standard curve results to evaluate the quality of the results from the quantification standard reactions.

About standard curve results

The standard curve is a graph of the C_T of quantification standard reactions plotted against the starting quantity of the standards. The software calculates the regression line by calculating the best fit with the quantification standard data points. The regression line formula has the form:

$$C_T = m\,[\log (Qty)] + b$$

where **m** is the slope, **b** is the y-intercept, and **Qty** is the starting DNA quantity. The values associated with the regression analysis can be interpreted as follows:

- **R^2 value –** Measure of the closeness of fit between the standard curve regression line and the individual C_T data points of quantification standard reactions. A value of 1.00 indicates a perfect fit between the regression line and the data points.
- Regression coefficients:
  - **Slope –** Indicates the PCR amplification efficiency for the assay. A slope of –3.3 indicates 100% amplification efficiency.
  - **Y-intercept –** Indicates the expected C_T value for a sample with Qty = 1 (for example, 1 ng/µL).

Linearity

The standard curve for the Quantifiler™ HP and Trio Kits is linear from 5 pg/µL to 100 ng/µL.

The kits can detect DNA concentrations lower than <5pg/µL, however, the CV (Coefficient of Variation) values may be higher than those observed for the 5 pg/µL to 100 ng/µL range.

R^2 Value

An R^2 value ≥0.99 indicates a close fit between the standard curve regression line and the individual C_T data points of quantification standard reaction

If the R^2 value is <0.98 check the following:

- Quantity values entered for quantification standards in the Plate Setup - Assign Targets to the Selected Wells during experiment setup
- Making of serial dilutions of quantification standards
- Loading of reactions for quantification standards
- Failure of reactions containing quantification standards

Slope

A slope close to –3.3 indicates optimal, 100% PCR amplification efficiency.

Table 7 Range and average of standard-curve slope values

Quantifiler™ HP/Trio targets	Typical slope (range)	Average slope
Small Autosomal (SA)	–3.0 to –3.6	–3.3
Large Autosomal (LA)	–3.1 to –3.7	–3.4
Y Target (Y)	–3.0 to –3.6	–3.3

The slope values listed in Table 7 on page 44 represent the typical range of slope values observed during the development and validation of the Quantifiler™ HP and Trio DNA Quantification Kits. Some deviations from this range may be observed due to instrument performance. If the slope varies beyond the typical range indicated in Table 7, check the following:

- Assay setup
- Software setup
- Reagents
- Instrument

Y-intercept

As with Quantifiler™ Duo, Human, and Y Human Male DNA Quantification Kit assays, you may observe some variation in the Y-intercept value with the Quantifiler™ HP and Trio DNA Quantification Kit assays, therefore we cannot provide a meaningful Y-intercept specification that will apply to all laboratories over time. We suggest that your lab monitor Y-intercept over time. In addition to variations that can be caused by pipetting of standards or minor lot-to-lot variations in the kits, Y-intercept can also be affected by:

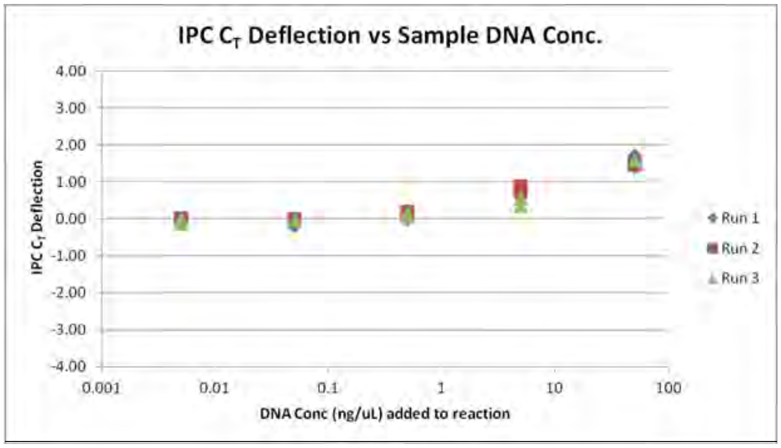
- Target-to-target variation: The Y-intercept for the large autosomal target is typically lower than the Y-intercept for the small autosomal target or the Y target. This is because of the higher copy number of the large autosomal target relative to the copy number of the small autosomal and Y targets.
- Instrument-to-instrument variation: Differences between 7500 instruments result in small differences in Y-intercept values for each of the targets. Minor differences do not affect assay performance or quantification accuracy.

IPC C_T

To assess C_T values for the Internal PCR Control (IPC), view the JUN™ dye signal in the amplification plots for the quantification standards. Typical reactions are expected to show relatively consistent IPC amplification for standards with concentrations ≤5 ng/µL. With higher concentrations of human genomic DNA, competition between the human and/or male-specific and IPC PCR reactions may suppress IPC amplification. We have observed IPC C_T values begin to increase at concentrations >5 ng/µL, and a greater magnitude of increase at concentrations >50 ng/µL. Figure 13 below displays an example of how the IPC C_T values may deflect upwards with increasing DNA concentrations.

Note: This is only an example and the magnitude of deflection may vary and laboratory to laboratory this effect may differ in magnitude.

Figure 13 Example of impact of increasing sample DNA concentration on IPC C_T deflection



Troubleshoot the standard curve

The following table provides common errors that can result from incorrect quantities or task(s) not being set properly.

Table 8 Troubleshooting the standard curve

Observation	Possible cause	Recommended action
Slope for the standard curve is outside the typical range *or* R^2 value is significantly less than 0.98	When defining quantification values for the standards, an incorrect quantity was applied.	1. From the analysis section, move the cursor over the well and verify that the quantity is correct. 2. Update with the correct values and reanalyze, if necessary.
At each concentration, the standard curves for all targets are not shown	For the standard curve samples, the task was set to unknown for one of the targets in the assay.	1. From the analysis section, move the cursor over the well and verify that the task is set to "S" for all of the standard curve samples. 2. Update and reanalyze, if necessary.
Slope value for standard is outside the expected range (see "Slope" on page 44)	Standards have not been properly stored, or are older than 2 weeks.	Prepare fresh standards.
A failed standard is incorporated into the standard curve.	Standard DNA not loaded in well.	Exclude failed standard from standard curve analysis. (Select **Plate Setup ▸ Define Samples and Targets**, then change the Sample Type from Standard to Unknown), then reanalyze.

Use the Internal PCR Control system

Purpose

Use the Internal PCR Control (IPC) system to distinguish between true negative sample results and reactions affected by:

- The presence of PCR inhibitors
- Assay setup
- A chemistry or instrument failure

Note: The IPC in the Quantifiler™ HP and Trio DNA Quantification Kits have been developed with increased inhibitor tolerance to better correlate with our more recently introduced STR kits, such as Identifiler™ Plus, NGM SElect™ and GlobalFiler™ PCR Amplification Kits. (STR kits are For Forensic or Paternity Use Only.)

Components

The following components of the IPC system are present in the Quantifiler™ HP and Trio Primer mixes:

- Synthetic DNA template
- Primers that hybridize specifically to the synthetic DNA template
- Probe labeled with JUN™ dye

Interpret IPC results

Positive amplification occurs when the C_T value for the target is <40. Because samples contain unknown amounts of DNA and inhibitors, a large range of C_T values is possible. The IPC system template DNA is present at a consistent concentration across all reactions on a plate. Therefore, the IPC (JUN™ dye) C_T should be relatively constant in typical reactions. However, the presence of PCR inhibitors and/or higher concentrations of DNA can increase the IPC C_T relative to the average IPC C_T of the quantification standards on the same plate.

In the amplification plot window of the HID Real-Time PCR Analysis Software, observe amplification of the assay targets, then use Table 10 to interpret the IPC results.

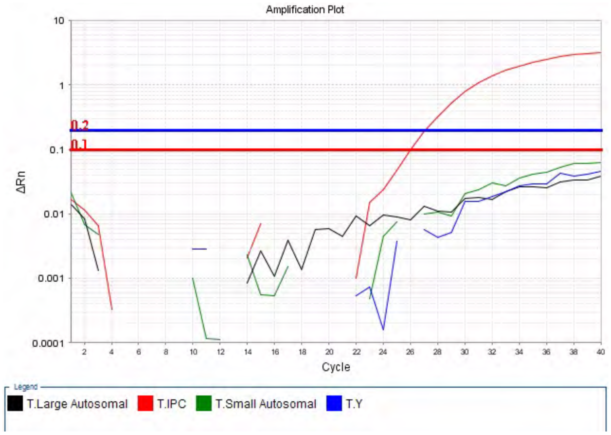
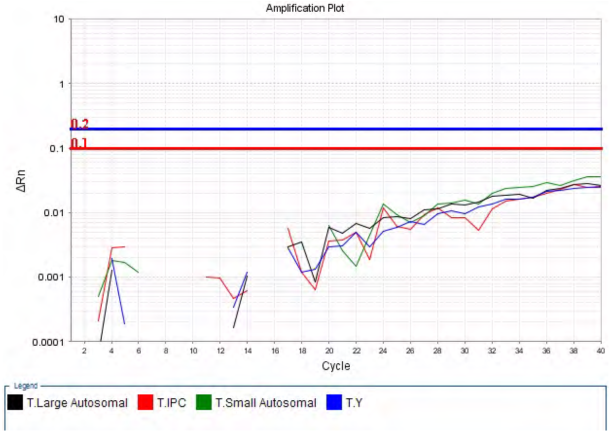
IMPORTANT! Perform validation studies to determine the IPC interpretation guidelines appropriate for your sample types, sample concentrations, and protocols.

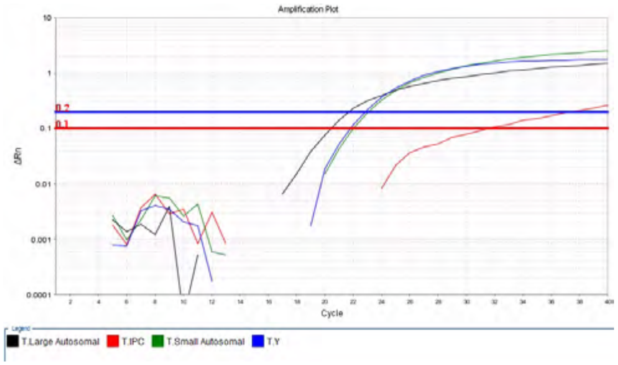
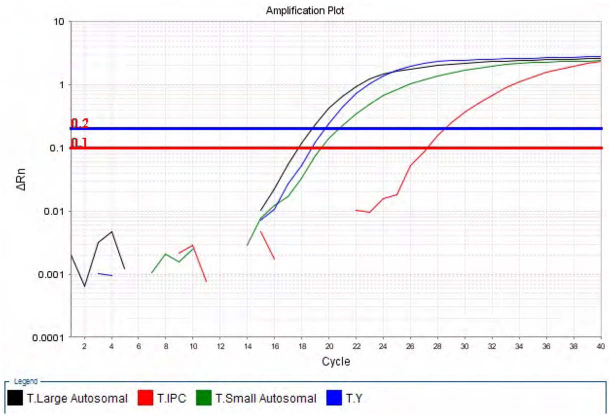
Table 9 Quantifiler™ HP and Trio DNA Quantification Kit targets

Target	Dye/quencher
Human Target, small autosomal	VIC™ dye with MGB quencher
Human Target, large autosomal	ABY™ dye with QSY™ quencher
Human Male Target†	FAM™ dye with MGB quencher
Internal PCR Control	JUN™ dye with QSY™ quencher

† Contained in the Quantifiler™ Trio DNA Quantification Kit only

Table 10 Interpreting IPC amplification results

Quantifiler™ HP and Trio Human (VIC™ and ABY™ dyes) and/or Quantifiler™ Trio Male (FAM™ Dye)	Quantifiler™ HP and Trio IPC (JUN™ Dye)	Interpretation
No amplification 	Amplification	Negative result - no human DNA detected
No amplification 	No amplification	Invalid result, perhaps caused by severe PCR inhibition, improper formulation of reagents, or failure of critical assay components

Quantifiler™ HP and Trio Human (VIC™ and ABY™ dyes) and/or Quantifiler™ Trio Male (FAM™ Dye)	Quantifiler™ HP and Trio IPC (JUN™ Dye)	Interpretation
Amplification  Note: Suppressed amplification (high C_T value and low ΔR_n value) of the human and/or male-specific targets can also occur due to PCR inhibition. This is often more pronounced in the large autosomal target that is more susceptible to inhibitory effects.	No amplification or amplification appears significantly reduced relative to the average IPC C_T value for quantification standards.	Possible Inhibitor present
Amplification, Quantity >5 ng/µL The example below is a sample free of PCR inhibitors with 100 ng/µL DNA. It illustrates that it is possible to see increased IPC C_T with no inhibition. Note: The IPC C_T shown below is 1.11 higher than the average IPC C_T value for the quantification standards from 50 ng/µL to 0.005 ng/µL (5 standards, 2 replicates each). For additional information, see also Figure 13 on page 45.  	Amplification appears reduced relative to the average IPC C_T value for the quantification standards.	High sample concentration may contribute to suppression of IPC amplification. This may occur independently or in combination with the effect of PCR inhibitors, yielding inconclusive IPC results.

Negative results

No human DNA is detected when:

- No signal for the Small Autosomal, Large Autosomal and Y targets (VIC™, ABY™ and FAM™ dyes, respectively) is detected, indicating that the human and/or male-specific targets did not amplify.
- The IPC target (JUN™ dye) amplifies and amplification does not appear reduced relative to the average IPC C_T value for quantification standards.

Complete amplification failure

Undetected results for all assay targets, including human and male-specific targets and the IPC target, indicates a complete failure of PCR amplification for the reaction. This could be caused by conditions such as incorrect thermal cycling or incorrect formulation of PCR reagent mix (which would affect multiple reactions or possibly the entire plate), or by severe PCR inhibition affecting individual samples. This type of result is invalid, and the samples should be prepared again to confirm the result or new samples should be extracted.

PCR inhibition

No amplification or weak amplification of the IPC may indicate PCR inhibition (partial or complete) in the sample. In addition, suppressed amplification (high C_T value and low ΔR_n value) of the human and/or male-specific targets can occur due to PCR inhibition. This is typically more pronounced in the large autosomal target than the small autosomal target since the large autosomal target is more susceptible to inhibitory effects.

IPC results inconclusive

With increasing concentrations of human genomic DNA (>5 ng/µL), competition between the human and/or male-specific and IPC PCR reactions may suppress IPC amplification for that sample. This can occur independently or in combination with the effect of PCR inhibitors, yielding inconclusive results. However, samples with high DNA concentration will be diluted during STR reaction setup to meet the optimal target input amount of DNA in the STR reaction. Therefore, the effect of most inhibitors, if present in the sample, on next generation STR kit performance is likely to be minimized.

Evaluate IPC amplification

If the IPC amplification for certain samples appears reduced relative to IPC amplification for quantification standards or is completely suppressed, it may be caused by:

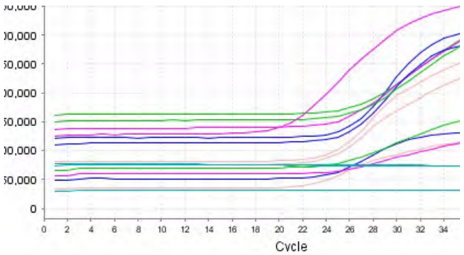
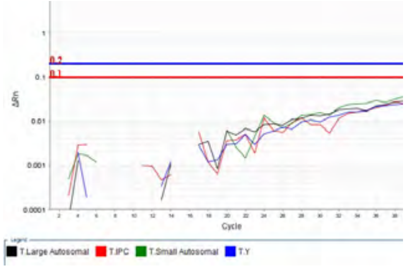
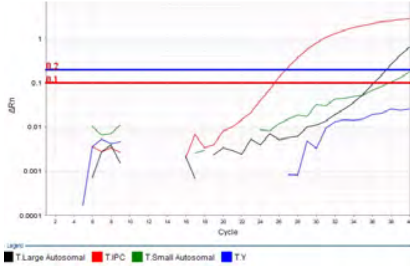
- Presence of PCR inhibitors
- Higher concentrations of DNA (for example, >5 ng/uL)

The IPC results can help you determine the next step:

- Proceed directly to an STR analysis of the sample
- Dilute the sample before adding it to the STR reaction
- Perform additional cleanup of the sample to remove potential inhibitors and requantify the sample if necessary
- Select a next generation STR kit for improved performance with inhibited samples

Troubleshoot amplification plots

Table 11 Troubleshooting amplification plots

Observation	Possible cause	Recommended action
ΔR_n and C_T values inconsistent with replicates 	Incorrect volume of Quantifiler™ THP PCR Reaction Mix added to some reactions.	1. Select the multicomponent plot. Wells with incorrect volume of Quantifiler™ THP PCR Reaction Mix should generate significantly less fluorescence compared to unaffected wells. 2. Verify that the correct volume of reaction mix was added to the plate by comparing the volume of the affected well(s) to the surrounding wells.
High C_T value and low ΔR_n value 	High levels of PCR inhibition resulting in no amplification of the human and male targets.	Consider diluting the sample before adding to STR reaction. If inhibition is still present, repurify the sample and rerun.
Unpredictable pattern of positive/undetected results from assay targets, with very high C_T values (for example, >37) 	Stochastic effects with very low-concentration samples may cause wide variations in C_T results among replicates, or result in unpredictable patterns of positive/undetected results with assay targets.	Perform validation studies to determine analysis guidelines for samples with extremely low concentrations of DNA that are close to or below the detection threshold for standard STR assays.

Assess quantity

Purpose

After viewing the results and assessing the quality of the results, determine whether sufficient DNA is present to proceed with a short tandem repeat (STR) assay.

Note: The primary quantification value is from the small autosomal target. Use this value for determination of STR input amount.

Assay sensitivity

The Quantifiler™ HP and Trio DNA Quantification Kits can reproducibly quantify 5 pg/µL of human genomic DNA in a sample. When 2.0 µL of a sample at the lowest concentration standard (5 pg/µL) is loaded in a reaction, the well contains approximately 1.5 diploid human genome equivalents.

Stochastic effects

The Quantifiler™ HP and Trio DNA Quantification Kits can detect DNA concentrations <5 pg/µL; however, at concentrations <5 pg/µL, stochastic effects, or the statistical effect of random sampling of alleles present at a very low copy number, can produce significant variability in assay results. When using samples containing DNA in this concentration range, you can perform replicate analysis to confirm true absence of DNA.

If insufficient DNA is present

If the results from Quantifiler™ HP or Trio DNA Quantification Kit reactions indicate that insufficient DNA is present to perform an STR assay, some options available to improve STR kit performance are:

- Re-extract the DNA, then repeat the test with the Quantifiler™ HP or Trio DNA Quantification Kits before performing STR analysis.
- Concentrate the sample, then repeat the test with the Quantifiler™ HP or Trio DNA Quantification Kits before performing STR analysis.
- Use an STR assay which allows for higher volume of DNA input, for example, GlobalFiler™ PCR Amplification Kit.

Calculate male:female DNA ratio

Forensic DNA samples may contain mixtures of DNA from multiple individuals. In DNA mixtures of male and female individuals, it may be useful to calculate the ratio of total autosomal DNA to the male-specific Y-chromosome DNA.

Note: The ratio is automatically calculated in the HID Real-Time PCR Analysis Software v1.2.

The Quantifiler™ Trio DNA Quantification Kit assesses the quantity of human and male DNA in biological samples. The quantity of human DNA in this calculation is based on the quantity value for the small autosomal target. From these values, one can calculate the ratio of male and female DNA using the following equation:

> Male DNA:Female DNA Ratio = Quantity of Male DNA/Quantity of Male DNA : (Quantity of Human DNA - Quantity of Male DNA)/Quantity Male DNA

All quantities in the above equation are ng/µL.

For example, assuming:

Male DNA concentration = 2 ng/μL
Human DNA concentration = 8 ng/μL then the Male DNA:Female DNA ratio is:

2/2: (8-2)/2 = 1:3

This ratio helps determine the extent of the mixture and is useful in determining whether to proceed with autosomal STR or Y-STR analysis.

As the ratio of female DNA increases relative to male DNA, the ability to detect the minor male component may be limited with autosomal STR analysis. In these instances Y-STR analysis may be considered. Based on each laboratory's protocols, detection instrumentation and analysis thresholds, internal validation studies should be performed to determine M:F ratio thresholds to indicate when Y-STR analysis should be considered. In house experiments have shown that the Quantifiler™ Trio assay can accurately quantify 20 pg/μL male DNA in >1,000-fold excess female DNA.

Determine Quality Index

Quality Index

You can use two results from the HID Real-Time PCR Software to determine the Quality Index for a sample:

- Degradation Index
- IPCC_T flag

Degradation Index

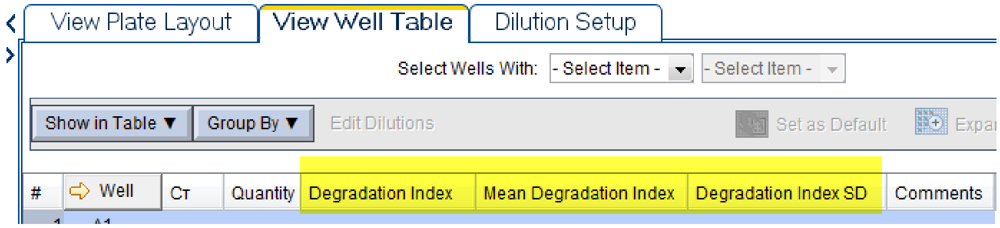
"Degradation Index" refers to the data observed when a sample displays a decrease in measured amount for large DNA fragments compared to small DNA fragments. The Degradation Index is for use as a general indicator of whether large DNA fragments may perform more poorly relative to small DNA fragment in STR reactions.

The Degradation Index is automatically calculated by the HID Real-Time PCR Software using the following formula:

$$\frac{\text{Small autosomal target DNA conc. (ng/}\mu\text{L)}}{\text{Large autosomal target DNA conc. (ng/}\mu\text{L)}}$$

The Degradation Index value is displayed in the Well Table view in any of the analysis screens (you may have to scroll to the right to display it.) The mean and standard deviation for replicates are also displayed in the Well Table view.

Note: When the quantity for the small or large autosomal target is undetermined, the Degradation Index is not calculated and the Degradation Index field in the Well Table will be empty. When the large autosomal target is undetermined, this can be an indication of significant degradation and/or inhibition affecting the sample. See Determining the Quality Index on the following page for more information.



The Degradation Index can be affected by:

- Degree of degradation of the large autosomal target DNA
- Presence of PCR inhibitors

  PCR inhibitors (particularly target-specific inhibitors) act in many ways to disrupt amplification. PCR inhibitors that negatively affect the large autosomal target in comparison to the small autosomal target cause less efficient amplification and higher C_T values for the large autosomal target. Evaluate Degradation Index in conjunction with the IPC C_T as described below.

IPC C_T flag

The IPC C_T flag is triggered for an unknown sample that has an IPC C_T of:

- Undetermined
- Greater than the average of the IPC C_T values for all the standards plus the threshold you set in the software HID Settings

For example if you set the IPCT C_T Variance to 2.0 and the average IPC C_T for the standards is 29, the IPC C_T flag is triggered for samples with a $C_T \geq 31$.

The IPC C_T flag is displayed in Analysis QC Summary screen and the Plate View or Well Table view in any of the analysis screens.

When the IPC C_T flag is triggered this typically indicates the presence of PCR inhibitors in sufficient concentration to significantly impact downstream performance with next generation STR kits. See the "Interpret IPC results" on page 47 for more information.

IMPORTANT! Perform validation studies to determine an IPC C_T threshold appropriate for your laboratory's sample types and protocols.

Determining the Quality Index

To determine the Quality Index, evaluate the Degradation Index in conjuction with the IPC C_T to assess the potential presence of PCR inhibitors and degradation that may have an impact on downstream sample processing.

IPCCT flag triggered?	Degradation Index	Quality Index interpretation†
No	<1	Typically indicates that DNA is not degraded or inhibited.
	1 to 10	Typically indicates that DNA is slightly to moderately degraded. PCR inhibition is also possible, however not enough to significantly suppress IPC amplification.
	>10 or blank (no value)	Typically indicates that DNA is significantly degraded. PCR inhibition is also possible, however not enough to significantly suppress IPC amplification. Highly degraded samples that cannot be recovered by STR can be analyzed with HID-Ion AmpliSeq™ Panels and the Ion Personal Genome™ (PGM™) System (see "Degraded sample studies: GlobalFiler™ STR kit and HID-Ion AmpliSeq™ Identity and Ancestry Panel" on page 103).
Yes	<1	Although theroretically possible, this result is unlikely because PCR inhibitors in sufficient concentration to trigger the IPCCT flag typically would affect the large autosomal target as well.
	>1 or blank (no value)	Typically indicates that the DNA is affected by degradation and/or PCR inhibition.

† These are general guidelines that may not apply to all samples depending on the inhibitors present, the varying quantity of contributor DNA in mixed samples and the STR kit used. (STR kits are For Forensic or Paternity Use Only.)

IMPORTANT! Perform validation studies to determine interpretation guidelines for the Quality Index for your laboratory.

The Quality Index results can help you determine next steps, including:

- Proceed directly to an STR analysis of the sample
- Dilute the sample before adding to the STR reaction
- Perform additional cleanup of the sample to remove potential inhibitors and requantify the sample if necessary
- Use one of the next generation STR kits for improved performance with inhibited samples
- Use an STR assay that includes a high number of miniSTR loci, such as the GlobalFiler™ and MiniFiler™ PCR Amplification Kits (or a combination of those kits), for increased data recovery from degraded samples
- Use an HID-Ion AmpliSeq™ Panels and the Ion Personal Genome™ (PGM™) System for samples that cannot be recovered by STR (see "Degraded sample studies: GlobalFiler™ STR kit and HID-Ion AmpliSeq™ Identity and Ancestry Panel" on page 103).

Assess sensitivity and results

About assay sensitivity

Real-time PCR assays are extremely sensitive, and detection of C_T values >35 may indicate the presence of exceedingly low quantities of DNA. It is possible to detect C_T values <40 for extraction blank and negative control samples while performing a real-time PCR reaction with the Quantifiler™ Kits.

Detection of such a low quantity of DNA can vary from amplification to amplification based on stochastic effects. Such levels may be considered background signal and may vary from laboratory to laboratory, and may not produce detectable product when the STR Kits are used. (STR kits are For Forensic or Paternity Use Only.)

The Quantifiler™ HP and Trio DNA Quantification Kit reagents undergo rigorous quality control to help ensure that the reagents are free of extraneous DNA. However, due to the extreme sensitivity of the test, background DNA from the environment can be detected on rare occasions.

Each laboratory should take standard precautions to minimize contamination in its own facility. Each laboratory should also establish a C_T value above which a positive result represents background signal only.

Evaluating the strengths and limitations of any test is common practice in forensic laboratories. We recommend applying a similar approach when validating the Quantifiler™ HP and Trio DNA Quantification Kits.

Negative control samples, DNA contamination, and spectral artifacts

Due to the extremely high sensitivity of the Quantifiler™ HP and Trio DNA Quantification Kit assays, you may occasionally observe amplification in:

- Negative Control (no template control or NTC) samples caused by contamination of assay reagents or consumables
- Case samples containing minute amounts of DNA below the detection limit for the assay

It is possible to obtain sporadic signal in any of the genomic targets. However, detection of signal may be more likely for the large autosomal target. In these samples, amplification is most likely caused by the high copy number of the large autosomal target (which leads to a higher probability of amplification). Samples with a C_T >38 for the large autosomal target and no amplification for the small autosomal and Y targets typically contain extremely small quantities (a fraction of 1 genome equivalent) of DNA. Amplification of only the large autosomal target may not indicate the presence of DNA quantity sufficient for STR analysis.

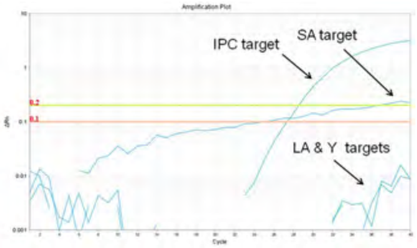
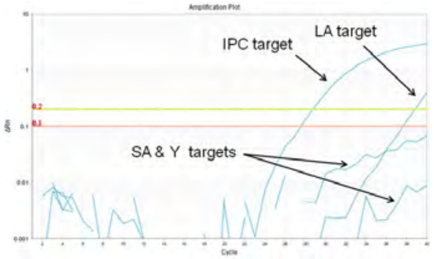
IMPORTANT! Perform validation studies to determine the minimum C_T value for each of the assay targets that correlate to a DNA quantity that will yield an interpretable STR result.

See Table 12 on page 57 for information to help you distinguish between a real DNA signal due to the contamination of assay reagents or consumables and an apparent positive result due to spectral artifacts that can (very rarely) generate a fluorescence signal that crosses the ΔR_n threshold. Such artifacts may be the result of anomalous baseline signals, and can often be eliminated by changing the baseline window setting.

Note: The HID Real-Time PCR Analysis Software uses a specialized multicomponenting algorithm that provides precise deconvolution of multiple dye signals in each well. This algorithm helps ensure minimal crosstalk when using multiple fluorophores for multiplex assays. However, a residual spectral overlap may be observed if the instrument is in need of calibration.

Assess apparent positive results in Negative Control Samples

Table 12 Troubleshooting apparent positive results in Negative Control Samples

Observation	Possible cause	Recommended action
Amplification plot for the SA target (VIC dye channel) shows a very gradual increase in ΔR_n with abnormal appearance (compared to IPC amplification plot), eventually crossing the 0.2 threshold to register as a positive. 	If the HID v1.2 software Analysis Settings are set to automatic baseline, spurious fluorescence signals in early cycles may cause an artifact that falsely elevates the ΔR_n signal.	If Analysis Settings are set to use automatic baseline, change them to manual baseline as follows: 1. In **HID Real-Time PCR Analysis Software**, select **Analysis ▸ Analysis Settings**. 2. Click the **C_T Settings** tab. 3. Select the **Use Default Settings** to apply the Manual Baseline method: Manual C_T = 0.2, Baseline Start Cycle = 3, and Baseline End Cycle =15. 4. Click **Apply Analysis Settings**. 5. In main Analysis window, click **Analyze**.
C_T value <40 is observed for one or more genomic targets in an NTC reaction, normally expected to be negative for all genomic detectors. 	Contamination of reagents or consumables (assay plate, pipette tips, etc.) with human genomic DNA or amplified PCR products.	Ensure that stringent contamination controls and laboratory cleanliness protocols are in place. Always wear clean disposable gloves when handling assay consumables and ensure that reagent tubes and consumable boxes are opened using appropriate safeguards.

Prevent PCR contamination

Laboratory practices to minimize false positives

PCR assays require special laboratory practices to avoid false positive amplifications, as detailed in Table 12. The high sensitivity of these assays may result in the amplification of a single DNA molecule.

To minimize false positives due to the presence of amplified material in your work area, follow these recommended laboratory practices:

- When possible, maintain separate work areas, dedicated equipment and supplies for:
  - Sample preparation
  - PCR setup
  - PCR amplification
  - Analysis of PCR products
- Wear a clean lab coat (not previously worn while handling amplified PCR products or during sample preparation) and clean gloves when preparing samples for PCR amplification.
- Change gloves whenever you suspect they are contaminated and before entering or leaving the work area.
- Establish procedures for handling new, unopened and partially used packages of sample tubes and reaction plates to prevent interaction between clean and used packaging.
- Use positive-displacement pipettes or aerosol-resistant pipette tips.
- Never bring amplified PCR products into the PCR setup area.
- Open and close all sample tubes and reaction plates carefully.
- Try not to splash or spray PCR samples.
- When pipetting from a kit component tube, hold the cap of the tube in your gloved hand, or be sure to set it down on a clean, decontaminated surface.
- Keep reactions and components sealed when possible.
- Do not open sealed reaction tubes or plates after amplification.
- Clean work areas periodically with freshly diluted 10% bleach or other cleaning solution known to destroy DNA. If using bleach, rinse the areas with DI water to ensure the work areas do not contain residual bleach after cleaning.

6

Experiments and results

Overview

About this chapter

This chapter provides results of the validation experiments performed using the Quantifiler™ HP and Trio DNA Quantification Kits.

Importance of validation

The Scientific Working Group on DNA Analysis Methods (SWGDAM) provides guidelines intended to "assist laboratories in establishing reliable methods for DNA analysis and identifying limitations of the procedures." The Quantifiler™ HP and Trio assays are not genotyping methods themselves, but they are an important part of extraction based STR genotyping workflows. It is therefore important to understand the characteristics and limitations of the quantification kits to inform their use in obtaining more effective genotyping results.

Developmental validation experiments

Experiments to evaluate the performance of the Quantifiler™ HP and Trio DNA Quantification Kits were performed at Thermo Fisher Scientific according to the Validation Guidelines for DNA Analysis Methods, approved by the SWGDAM membership in November, 2012. The guidelines define Developmental Validation as "the acquisition of test data and determination of conditions and limitations of a new or novel DNA methodology for use on forensic, database, known or casework reference samples."

The experiments focus on kit performance parameters relevant to the intended use of the kits as DNA quantification assays and as a part of a forensic DNA genotyping procedure. Each laboratory using the Quantifiler™ HP and Trio DNA Quantification Kits should perform appropriate internal validation studies, as recommended in the guidelines document.

Characteristics of loci in the Quantifiler™ HP and Trio kits

Mapping

The Quantifiler™ HP and Trio assays share common sets of primers and TaqMan® fluorescent probes to amplify and detect two autosomal, multiple-copy target loci, known as the Small Autosomal (SA) and Large Autosomal (LA) targets. Additionally, the Quantifiler™ Trio DNA Quantification Kit (but not the Quantifiler™ HP kit) contains a primer/probe set designed to detect a multiple-copy human male-specific target locus (Y) located on the Y chromosome. All assay targets are multiple-copy, meaning that each target-specific primer/probe set amplifies several-fold more copies relative to the single-copy target loci used in earlier kits like the Quantifiler™ Duo DNA Quantification Kit. The use of multiple-copy target loci provides much greater detection sensitivity than kits using single-copy assay targets.

Locus name	Amplicon size (bp)	Chromosomal location(s)	Probe dye/ quencher
Small Autosomal (SA)	80	Multiple copies on multiple autosomes	VIC™ dye with MGB quencher
Large Autosomal (LA)	214	Multiple copies on multiple autosomes	ABY™ dye with QSY™ quencher
Y Chromosome (Y)	75	Multiple copies on the Y chromosome	FAM™ dye with MGB quencher

During the initial screening and selection process for quantification assay target loci, candidate assay targets were assessed for factors such as genomic copy number, copy number variability (CNV) between individuals, and specificity for human DNA.

Given that the use of multicopy targets was necessary to obtain adequate sensitivity for sub-picogram amounts of DNA, candidate multicopy targets needed to have relatively stable copy numbers (i.e. low CNV) between individuals to provide consistent quantification results. The screening process made use of published literature on multi-genomic studies (Sudman, P.H., et al. 2010), in silico analyses of potential primer and probe sequences, and studies with hundreds of human genomic DNA samples from multiple populations.

Detection

The Quantifiler™ HP and Trio Kits use the TaqMan® assay process for quantitative, real-time PCR amplification of assay targets. A general overview of the principles of this process is provided in Chapter 1. The kits use a system of reporter dyes, quenchers, and a passive reference dye (Mustang Purple™) that were designed for optimal multiplexing capability on the Applied Biosystems™ 7500 Real-Time PCR System. This allows simultaneous quantification of the three genomic targets (SA, LA, and Y), plus an additional Internal Positive Control (IPC) target in each reaction.

Species specificity study

Because forensic samples may be wholly comprised of, or contaminated with, non-human DNA, species specificity measurements of the Quantifiler™ HP and Trio Kit assay primers and probes are crucial. For this study, we used the Quantifiler™ Trio assay. Results can be extrapolated to represent the expected results for the Quantifiler™ HP Kit, which uses the same primers and probes (with the exception of the Y target), master mix, and amplification conditions.

Experiment

Cross-reactivity was examined using DNA from common farm animals, domestic animals, microorganisms, and higher primates. The DNA samples from non-human biological species were obtained commercially or purified in the laboratory from whole blood animal samples. For some of these samples, the sex of the donor was unknown before analysis. The microorganism pool contains the following: (*Candida albicans*, *Staphylococcus aureus*, *Escherichia coli*, *Neisseria gonorrhoeae*, *Bacillus subtilis*, and *Lactobacillus rhamnosus* (equivalent to 10^5 copies). Species DNA sample concentrations used were:

- Non-primates EXCEPT Cat: 10 ng total DNA per reaction
- Cat: 2 ng total DNA per reaction
- Primates: Total per reaction: Cynomolgous 5 ng, human female 7.5 ng, gorilla 4 ng, male human 10 ng, orangutan 4 ng

Results

Figure 14 and Figure 15 show C_T results for each replicate.

Figure 14 Species specificity for common animals and microorganisms

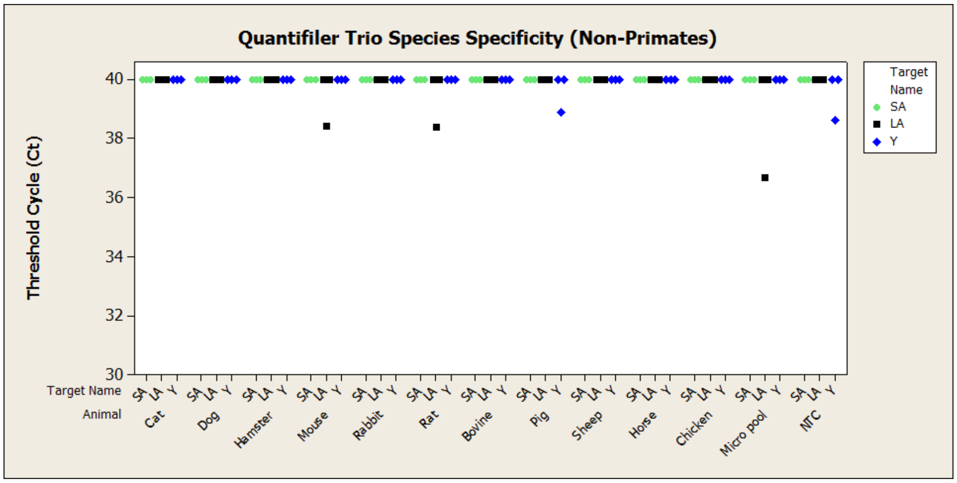
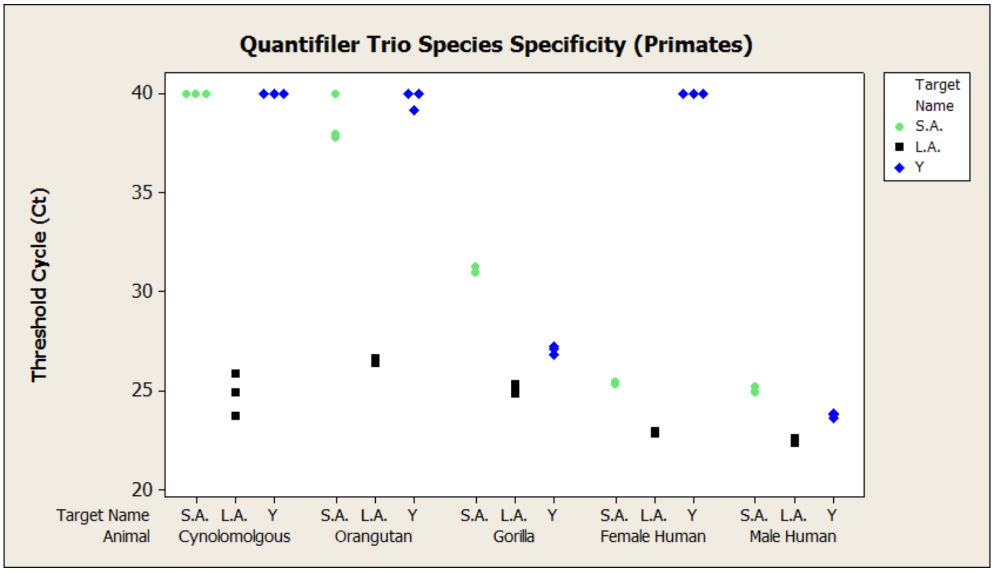


Figure 15 Species specificity for higher primates (undetected samples represented by C_T of 40)



In general, the common farm and domestic animals as well as the microorganism pool targets did not show cross-reactivity. An occasional single target signal was detected, but not confirmed by a signal in the remaining targets or in subsequent replicates. For example, the single replicate result obtained for the LA target of the microorganism pool can be considered an outlier due to the lack of reproducibility in other replicates or other targets of the same replicate (i.e. LA or Y targets).

Note: Multicopy targets are utilized in the Quantifiler™ HP and Trio kits, and are highly sensitive compared to single-copy based systems.

For the higher primates, some expected cross reactivity was observed with the three genomic targets for the gorilla sample and the LA target for Cynomolgous and Orangutan.

Dynamic range (sensitivity) study

Experiments

The dynamic range of the Quantifiler™ Trio assay was tested using serial dilutions of purified human male or female genomic DNA to obtain concentrations ranging from 5 pg/µL to 120 ng/µL in $T_{10}E_{0.1}$ buffer.

- The male DNA sample was quantified in triplicate using the Quantifiler™ Trio and the Quantifiler™ HP DNA Quantification Kits.
- The female DNA sample was quantified in triplicate using the Quantifiler™ HP DNA Quantification Kit.

Quantification assays were performed in parallel with the GlobalFiler™ kit STR assay for each DNA dilution (three replicate reactions with each kit per dilution). For the GlobalFiler™ kit assay, samples were amplified with 29 PCR cycles on an Applied Biosystems™ Veriti™ thermal cycler. The STR reactions were analyzed on an Applied Biosystems™ 3500xL Genetic Analyzer. Electropherograms were analyzed with

GeneMapper™ *ID-X* Software v1.4 with a peak amplitude threshold of 175 RFUs. Sample DNA input volumes for Quantifiler™ HP and Trio assays were 2 µL in 20-µL reactions, and for the GlobalFiler™ kit STR assay, 15 µL (the maximum possible sample volume) in 25-µL reactions.

Results for male DNA sample

The quantities of DNA obtained from the Quantifiler™ Trio DNA Quantification Kit were very similar to the expected quantities, as shown in Table 13 and Table 14. A linear relationship between expected quantity and actual concentration was observed for DNA dilutions within the supported quantification range of the assay, from 5 pg/µL to 100 ng/µL. The DNA concentrations measured with the Quantifiler™ HP DNA Quantification Kit were comparable to those measured with the Quantifiler™ Trio DNA Quantification Kit as shown in Figure 16 and Figure 17.

Table 13 Dynamic range of male samples using the Quantifiler™ Trio DNA Quantification Kit and the GlobalFiler™ kit

Sample number	**Expected quantity (ng/µL)**	**Quantifiler™ Trio DNA Quantification Kit**			**GlobalFiler™ kit**
		Avg measured quantity of SA target (ng/µL)	**Avg measured quantity of Y target (ng/µL)**	**Avg measured quantity of LA target (ng/µL)**	**Avg% of alleles recovered (15 µL DNA input)**
1	120	123 ± 24	111 ± 13	128 ± 15	100
2	100	99 ± 16	87 ± 13	103 ± 15	100
3	80	84 ± 15	74 ± 8	88 ± 9	100
4	60	64 ± 11	55 ± 8	67 ± 8	100
5	40	46 ± 7	39 ± 4	46 ± 7	100
6	20	22 ± 2	18 ± 1	22 ± 3	100
7	10	9.9 ± 1.5	9 ± 0.7	10 ± 0.9	100
8	5	4.6 ± 0.96	4.3 ± 0.6	5.2 ± 0.9	100
9	1	0.69 ± 0.26	0.8 ± 0.16	1 ± 0.19	100
10	0.5	0.39 ± 0.044	0.39 ± 0.04	0.52 ± 0.05	100
11	0.10	0.08 ± 0.007	0.07 ± 0.004	0.1 ± 0.01	100
12	0.05	0.04 ± 0.005	0.04 ± 0.005	0.05 ± 0.007	100
13	0.03	0.03 ± 0.005	0.02 ± 0.007	0.02 ± 0.006	100
14	0.01	0.009 ± 0.003	0.01 ± 0.002	0.01 ± 0.001	100
15	0.01	0.005 ± 0.001	0.004 ± 0.001	0.006 ± 0.002	88
16	0.003	0.002 ± 0.001	0.002 ± 0.001	0.002 ± 0.0004	82
17	0.0016	0.0008 ± 0.001	0.001 ± 0.00032	0.001 ± 0.001	20
18	0.0008	0.0006 ± 0.001	0.00002 ± 0.00004	0.001 ± 0.0003	4
19	0.0004	0.0002 ± 0.001	0.0002 ± 0.0002	0.00009 ± 0.0002	2
20	0.0002	0.0002 ± 0.001	0.0001 ± 0.0002	0.00013 ± 0.0002	0
21	0.0001	0.0001 ± 0.001	0.001 ± 0.0003	0.001 ± 0.0003	0
22	0.00005	0.0002 ± 0.001	0.00009 ± 0.0002	0.00009 ± 0.0002	0
NTC	0	–	–	–	–

Table 14 Sensitivity of lower-concentration male samples using the Quantifiler™ HP and Trio DNA Quantification Kits and the GlobalFiler™ kit

Sample	Expected quantity (ng/µL)	Quantifiler™ Trio kit number of samples with C_T<40			Quantifiler™ HP kit number of samples with C_T<40		Ave% alleles recovered; GlobalFiler™ kit (15 µL DNA input)
		SA target (N=3)	LA target (N=3)	Y target (N=3)	SA target (N=3)	LA target (N=3)	
16	0.003	3	3	3	3	3	82
17	0.0016	3	3	3	3	3	20
18	0.0008	3	3	3	3	3	4
19	0.0004	2	1	1	3	3	2
20	0.0002	2	2	2	0	1	0
21	0.0001	1	2	2	1	0	0
22	0.00005	2	0	0	0	2	0

Note: Input volumes for the GlobalFiler™ kit amplifications were based on the quantification value of the SA target in the Quantifiler™ Trio assay. For the GlobalFiler™ kit assay, 15 µL DNA extract input volume and 29 PCR cycles were used.

Figure 16 shows the quantification results for higher DNA concentrations using the Quantifiler™ Trio DNA Quantification Kit and the Quantifiler™ HP DNA Quantification Kit.

Figure 16 Dynamic range of male samples using the Quantifiler™ Trio DNA Quantification Kit and Quantifiler™ HP DNA Quantification Kit (DNA concentrations >30 ng/µL)

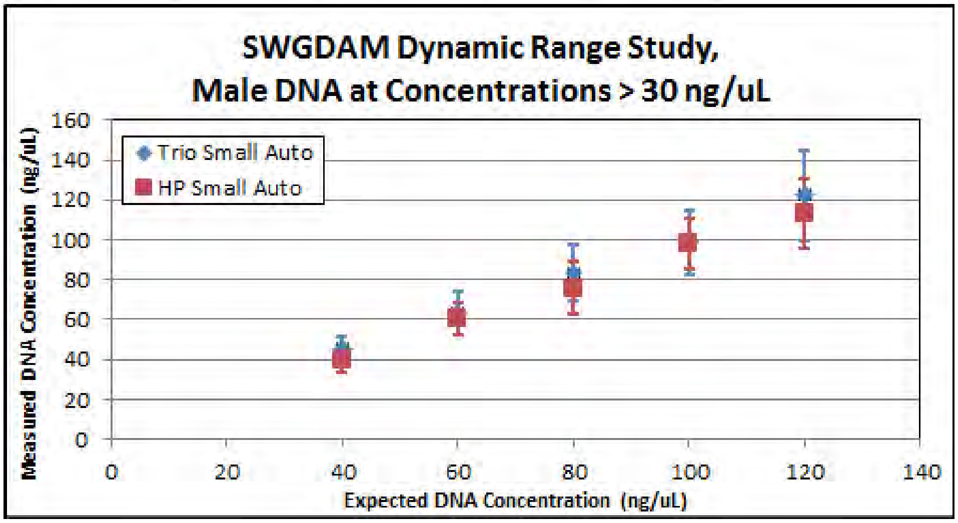
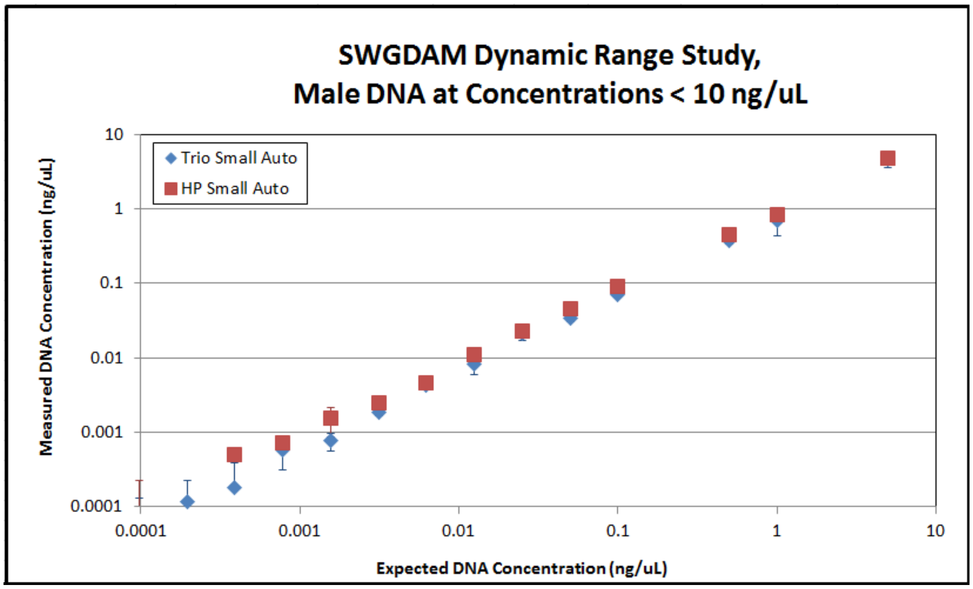


Figure 17 shows the quantification results for low DNA concentrations using the Quantifiler™ Trio DNA Quantification Kit and Quantifiler™ HP DNA Quantification Kit.

Figure 17 Dynamic range of male samples using Quantifiler™ Trio DNA Quantification Kit and Quantifiler™ HP DNA Quantification Kit (DNA concentrations <10 ng/µL)

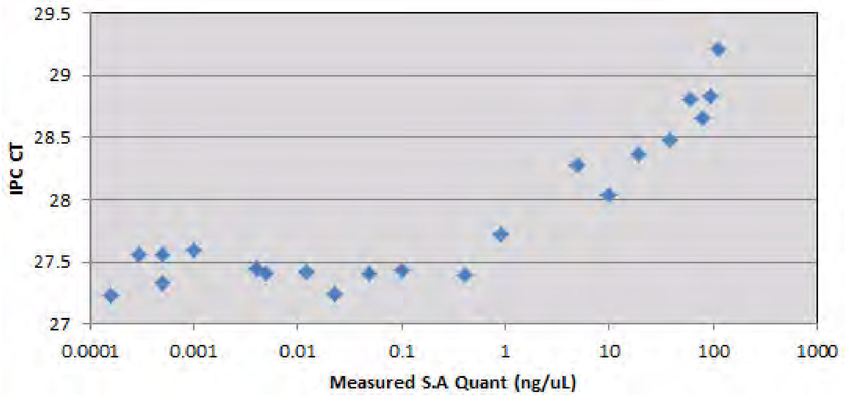


IPC C_T shift at higher concentrations

Figure 18 shows the IPC C_T shift in response to increasing DNA concentrations using the Quantifiler™ Trio DNA Quantification Kit.

Due to competition among targets, some deflection of the IPC C_T is expected for higher concentration samples. We observed IPC C_T values begin to increase at concentrations >5 ng/µL, and a greater magnitude of increase at concentrations >50 ng/µL. Figure 18 displays an example of how the IPC C_T values may deflect upwards with increasing DNA concentrations.

Figure 18 Dynamic range of male samples using Quantifiler™ Trio DNA Quantification Kit: IPC C_T shift



IMPORTANT! Figure 18 is an example only. The magnitude of deflection may vary for different samples and concentrations. Perform validation studies to determine the IPC interpretation guidelines appropriate for your sample types, sample concentrations, and protocols.

Results for female DNA sample

The quantities of DNA obtained from the Quantifiler™ HP DNA Quantification Kit were very similar to the expected quantities as shown in Table 15 and Table 16. A linear relationship between expected quantity and actual concentration was observed for DNA dilutions within the supported quantification range of the assay from 5 pg/µL to 100 ng/µL.

Table 15 Dynamic range of female samples using the Quantifiler™ HP DNA Quantification Kit and the GlobalFiler™ kit

Sample	Expected quantity (ng/µL)	Avg measured quantity SA target (ng/µL)	Avg measured quantity LA target (ng/µL)	% Alleles recovered; GlobalFiler™ kit (15 µL of DNA input)
1	120	111 ± 15	141 ± 13	100
2	100	95 ± 11	124 ± 8	100
3	80	79 ± 11	103 ± 11	100
4	60	59 ± 7	79 ± 9	100
5	40	38 ± 4	53 ± 4	100
6	20	19 ± 3	26 ± 4	100
7	10	10 ± 2	13 ± 2	100
8	5	5 ± 1	6 ± 1	100
9	1	1 ± 0.2	1 ± 0.2	100
10	0.5	0.4 ± 0.05	0.6 ± 0.05	100
11	0.10	0.1 ± 0.02	0.1 ± 0.01	100
12	0.05	0.05 ± 0.01	0.06 ± 0.01	100
13	0.03	0.02 ± 0.003	0.03 ± 0.003	100
14	0.01	0.01 ± 0.002	0.01 ± 0.004	100
15	0.01	0.005 ± 0.0005	0.007 ± 0.001	99
16	0.003	0.004 ± 0.002	0.005 ± 0.003	78
17	0.0016	0.001 ± 0.0004	0.002 ± 0.00003	24
18	0.0008	0.001 ± 0.0004	0.001 ± 0002	7
19	0.0004	0.0005 ± 0.0001	0.0004 ± 0.0002	2.7
20	0.0002	0.0002 ± 0.0002	0.0006 ± 0.0003	2.7
21	0.0001	0.0001 ± 0.0001	0.0001 ± 0.0001	0
22	0.00005	0.0001 ± 0.0001	0 ± 0.0001	0
NTC	0	0	0	

Table 16 Sensitivity of lower-concentration female samples using the Quantifiler™ HP DNA Quantification Kit

Sample	Expected quantity (ng/µL)	Positive replicates for SA target	Positive replicates for LA target	% Alleles recovered with GlobalFiler™ kit
18	0.0008	3	3	7
19	0.0004	3	3	2.7
20	0.0002	2	3	2.7
21	0.0001	1	2	0
22	0.00005	1	1	0

Stability study: PCR inhibitor

Experiment

Forensic casework samples may sometimes contain exogenous substances that can interfere with DNA amplification, possibly affecting the results of quantification assays or STR analysis assays. Studies were performed with the Quantifiler™ HP and Trio assays to test the effects of two inhibitors, humic acid and hematin, which represent naturally occurring substances associated with soil and decomposed blood, respectively. Samples were prepared with a constant level of human genomic DNA (0.1 ng/µL) and a range of concentrations of either hematin (Hem) or humic acid (HA) PCR inhibitors, to produce effects ranging from mild to complete inhibition of PCR. Corresponding STR analysis was performed on all samples with the Identifiler™ Plus and GlobalFiler™ kits to correlate the quantification assays results to the STR kit results.

Table 17 Sample preparation for PCR inhibition experiment

Sample	DNA content		Inhibitor concentration		
	In quant reactions (ng total)	In STR reactions (ng total)	In sample	In quant reaction	In STR reaction
Control	0.2	1.0	0	0	0
Hem-A	0.2	1.0	250 µM	25 µM	100 µM
Hem-B	0.2	1.0	500 µM	50 µM	200 µM
Hem-C	0.2	1.0	750 µM	75 µM	300 µM
Hem-D	0.2	1.0	1000 µM	100 µM	400 µM
Hem-E	0.2	1.0	1250 µM	125 µM	500 µM
HA-A	0.2	1.0	200 ng/µL	20 ng/µL	80 ng/µL
HA-B	0.2	1.0	300 ng/µL	30 ng/µL	120 ng/µL
HA-C	0.2	1.0	400 ng/µL	40 ng/µL	160 ng/µL
HA-D	0.2	1.0	600 ng/µL	60 ng/µL	240 ng/µL
HA-E	0.2	1.0	800 ng/µL	80 ng/µL	320 ng/µL

Quantifiler™ HP and Trio assays were set up with 2 µL of samples in 20 µL (total volume) reactions (total target amount = 0.2 ng), while STR reactions (Identifiler™ Plus and GlobalFiler™ kits) were set up with 10 µL of sample in 25 µL reactions (total target amount = 1.0 ng) and run for 28 and 29 cycles respectively. The total amount of DNA in reactions targeted 0.2 ng in Quantifiler™ HP and Trio assays and 1.0 ng total per reaction in STR assays. Because sample volumes comprised a different proportion of total reaction volumes in quantification assays vs. STR assays, the STR assays always contained ~4X higher inhibitor concentration for the same sample.

IPC C_T flag

An IPC C_T threshold setting of 2 C_T units was used in the HID Flag Settings of the HID Real-Time PCR Analysis Software v1.2. Therefore, an IPC C_T flag is displayed if a sample's IPC C_T is more than 2 C_T units above the baseline. The baseline is calculated automatically by the software as the mean IPC C_T for all quantification standards on the plate. The IPC C_T flag indicates reactions that fail to amplify with normal efficiency, which could be the result of a general system failure (for example, an instrument problem or improperly formulated PCR reactions) or, as is shown in the results for this experiment, the presence of PCR inhibitors that impair PCR amplification.

The IPC C_T flag is a useful indicator of potentially challenging samples that could result in partial or complete failure of subsequent STR analysis, and which might require additional measures such as re-purification, dilution, and/or the use of a more robust, next-generation STR kit such as the GlobalFiler™ kit.

Results

Quantification results for each assay target and IPC C_T results are shown for all replicate reactions in Table 18.

Table 18 Results of Quantifiler™ HP and Trio Assay results with inhibited test samples

Sample	Quantifiler™ Trio kit results (ng/µL)					Quantifiler™ HP kit results (ng/µL)			
	SA	LA	Y	IPC C_T	IPC C_T flag?	SA	LA	IPC C_T	IPC C_T flag?
Ctrl	0.10	0.12	0.08	27.71	N	0.11	0.12	27.66	N
Ctrl	0.10	0.10	0.08	27.41	N	0.10	0.12	27.37	N
Ctrl	0.07	0.09	0.06	27.67	N	0.07	0.10	27.56	N
HA-A	0.11	0.08	0.09	27.93	N	0.16	0.08	27.77	N
HA-A	0.10	0.07	0.09	27.72	N	0.10	0.08	27.37	N
HA-A	0.10	0.06	0.07	27.82	N	0.09	0.09	27.52	N
HA-B	0.12	0.02	0.09	28.18	N	0.11	0.05	28.07	N
HA-B	0.10	0.04	0.08	27.78	N	0.10	0.06	27.82	N
HA-B	0.11	0.04	0.08	27.60	N	0.08	0.06	27.96	N
HA-C	0.13	†	0.07	30.48	Y	0.12	†	31.10	Y
HA-C	0.11	†	0.07	28.77	N	0.09	†	28.64	N
HA-C	0.11	†	0.07	28.50	N	0.10	0.00	28.37	N
HA-D	0.02	†	†	†	Y	0.02	†	†	Y
HA-D	0.11	†	0.03	†	Y	0.09	†	†	Y
HA-D	0.11	†	0.03	†	Y	0.10	†	†	Y
HA-E	†	†	†	†	Y	†	†	†	Y
HA-E	†	†	†	†	Y	†	†	†	Y
HA-E	0.01	†	†	†	Y	†	†	†	Y
Hem-A	0.06	0.06	0.07	27.96	N	0.06	0.08	27.93	N
Hem-A	0.06	0.07	0.06	27.83	N	0.03	0.06	27.81	N
Hem-A	0.06	0.08	0.06	27.67	N	0.05	0.09	27.47	N
Hem-B	0.08	0.00	0.08	28.63	N	0.09	0.00	28.42	N
Hem-B	0.08	0.01	0.08	28.40	N	0.06	0.03	28.31	N
Hem-B	0.05	0.04	0.05	28.29	N	0.05	0.05	28.17	N
Hem-C	0.06	†	0.02	†	Y	0.07	†	†	Y

Sample	Quantifiler™ Trio kit results (ng/µL)					Quantifiler™ HP kit results (ng/µL)			
	SA	LA	Y	IPC C_T	IPC C_T flag?	SA	LA	IPC C_T	IPC C_T flag?
Hem-C	0.07	†	0.05	37.32	Y	0.07	†	31.27	Y
Hem-C	0.06	†	0.07	28.74	N	0.05	†	28.97	N
Hem-D	0.00	†	†	†	Y	0.00	†	†	Y
Hem-D	0.02	†	0.00	†	Y	0.03	†	†	Y
Hem-D	0.04	†	0.01	†	Y	0.04	†	†	Y
Hem-E	†	†	†	†	Y	†	†	†	Y
Hem-E	†	†	†	†	Y	†	†	†	Y
Hem-E	†	†	†	†	Y	0.00	†	†	Y

† Undetermined

Note: Data shows that the LA target may be impacted by the increasing inhibitor amounts before the SA target and before the IPC C_T flag is triggered. Slightly elevated Degradation Index (DI) values may be caused by degradation and/or inhibition. Refer to the "Determine Quality Index" on page 5-53 for additional information.

The inhibited sample series was analyzed in parallel with the Identifiler™ Plus and GlobalFiler™ kits, to correlate the results of quantification assays with STR results. Samples were added at 10 µL to STR kit reactions to give final reaction volumes of 25 µL. We used amplification conditions as specified in the user guide for the kit; 28 cycles for Identifiler™ Plus Kit reactions and 29 cycles for GlobalFiler™ kit reactions. The results of STR assays were assessed by allele recovery compared to the known genotype for the 007 DNA.

Figure 19 through Figure 22 show Identifiler™ Plus and GlobalFiler™ kit STR assay results with the inhibited sample series. Electrophoresis was performed on the Applied Biosystems™ 3500xL Genetic Analyzer. Allele peaks were included in resulting genotype profiles if they were higher than the peak amplitude threshold of 175 RFU.

Figure 19 Humic acid sample series with the Identifiler™ Plus kit

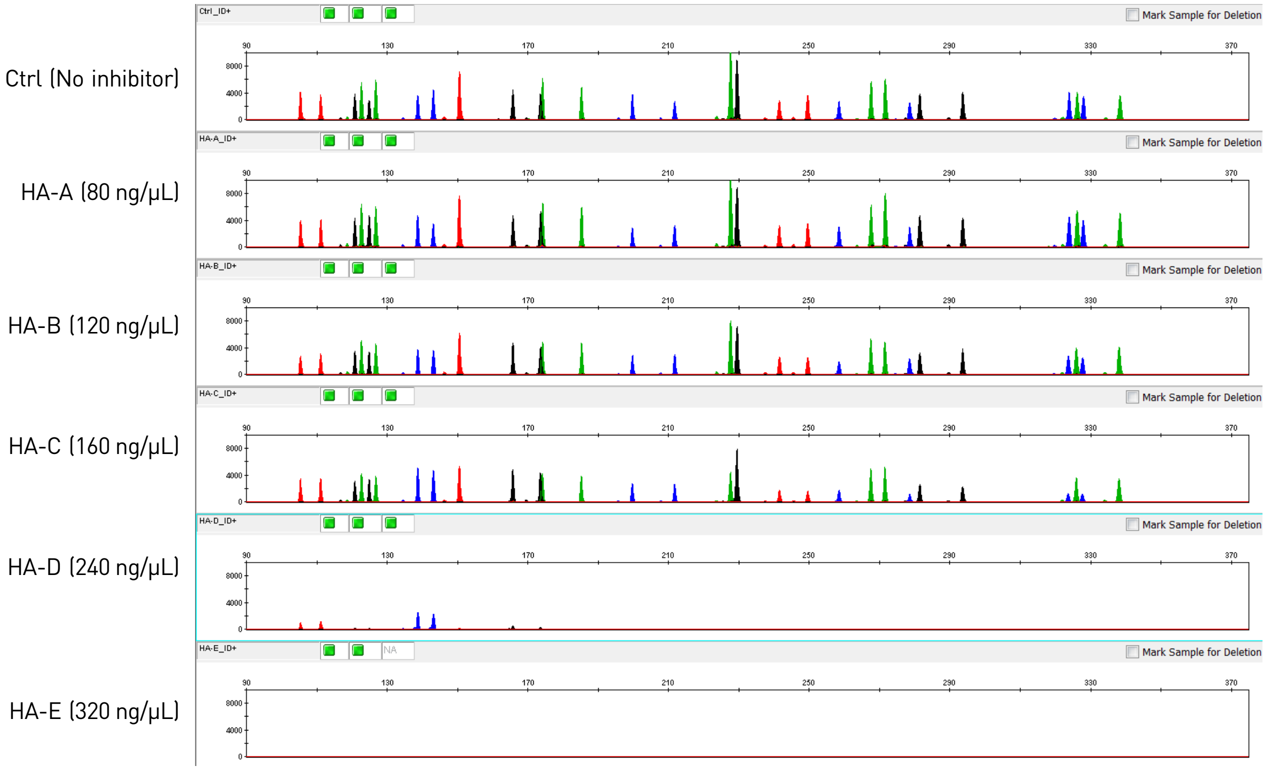


Figure 20 Humic acid sample series with the GlobalFiler™ kit

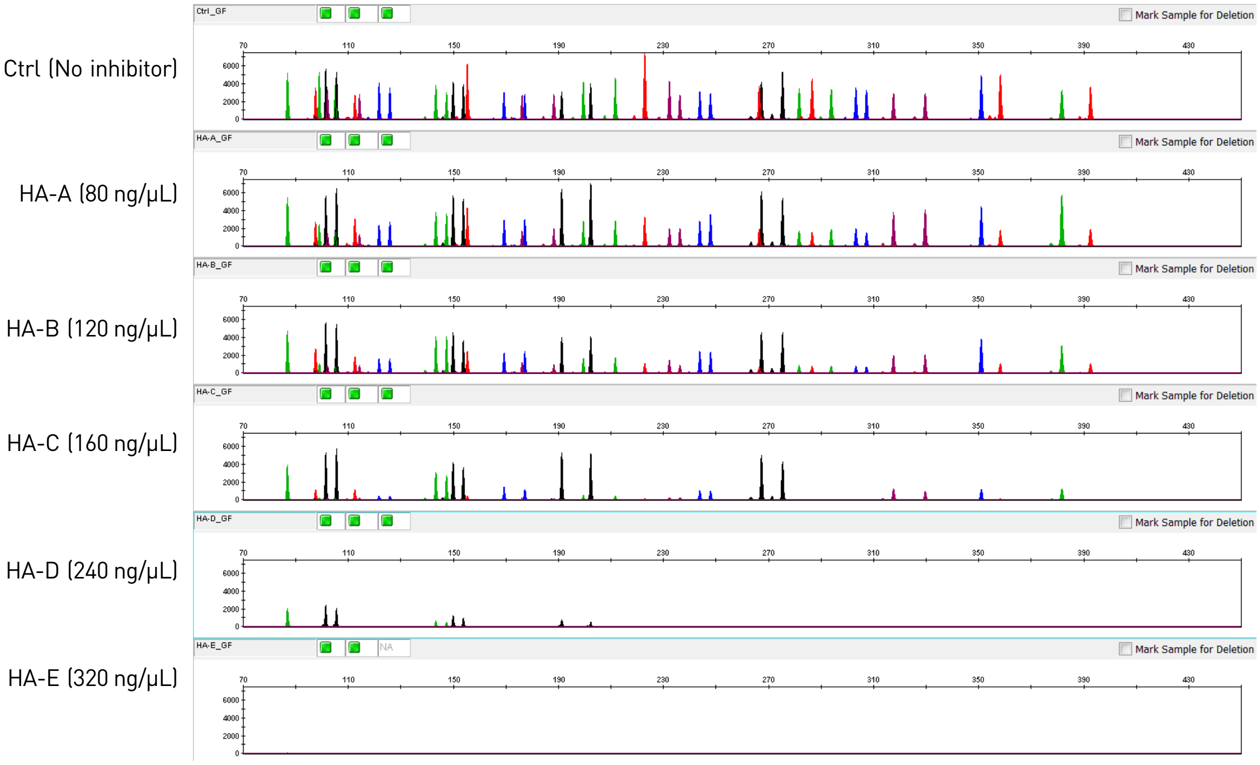


Figure 21 Hematin sample series with the Identifiler™ Plus kit

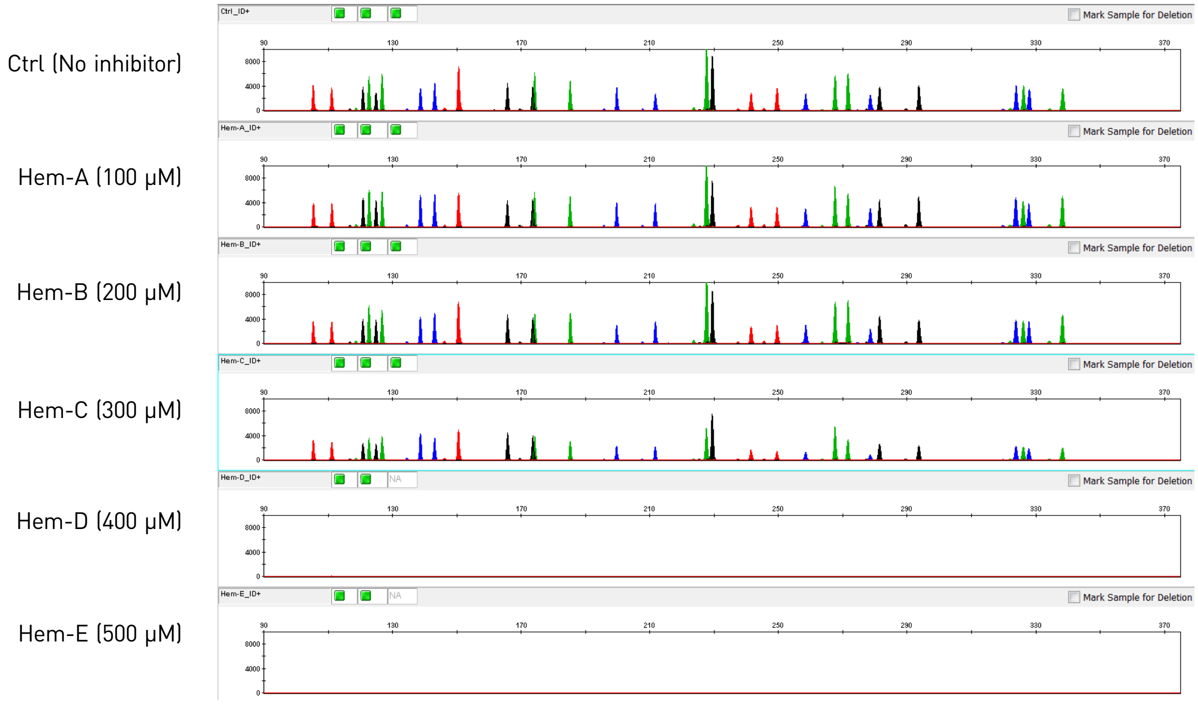
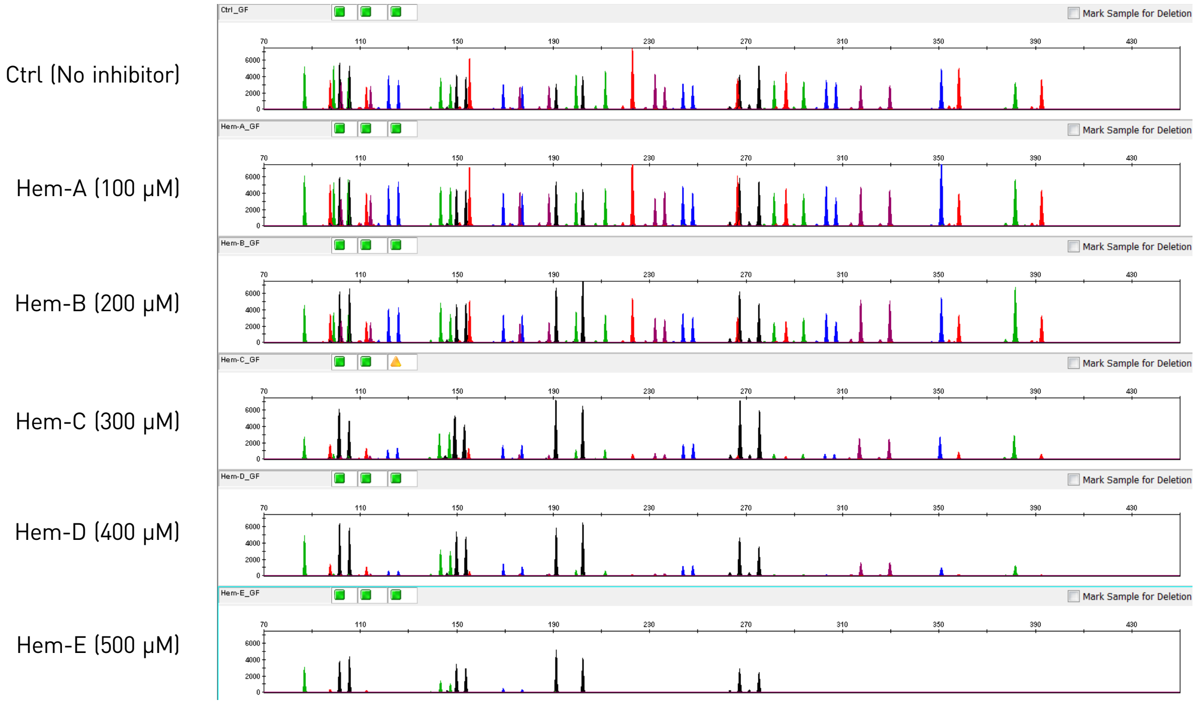


Figure 22 Hematin sample series with the GlobalFiler™ kit



Example electropherograms above showed the typical progression of increasing inhibitor concentrations. Lower levels of inhibitor compounds had only minor effects on allele peak heights, and full STR profiles were obtained. Higher inhibitor concentrations showed more marked effects, such as “ski-slope effect,” where larger alleles tended to have lower peak heights than smaller alleles (e.g. HA-C or Hem-C sample profiles, above), or the partial or complete failure of alleles to amplify at all (e.g. HA-E or Hem-E sample profiles).

IPC C_T, IPC C_T flag, and STR allele recovery

The IPC C_T and IPC C_T flag can be useful indicators of potentially problematic samples that may contain a significant level of PCR inhibitors and therefore may result in reduced allele recovery or complete amplification failure during subsequent STR analysis. Table 19 lists IPC C_T results, IPC C_T flag state (IPC C_T flag threshold of 2 was used) for inhibited samples, and the corresponding allele counts of Identifiler™ Plus and GlobalFiler™ kit STR assays. The results demonstrate that the IPC C_T results >2 C_T above the average C_T of the quantification standards was a strong predictor of subsequent reduced allele detection efficiency in the STR assays, resulting in partial or blank profiles.

Table 19 IPC C_T, IPC C_T flag, and STR allele recovery

Sample	Quantifiler™ Trio kit		Quantifiler™ HP kit		Identifiler™ Plus kit STR results			GlobalFiler™ kit STR results		
	IPC C_T	IPC C_T flag?	IPC C_T	IPC C_T flag?	Allele count	Allele recovery (%)	Avg% ICB‡	Allele count	Allele recovery (%)	Avg% ICB†
Ctrl	27.71	N	27.66	N	29	100	48	43	100	61
Ctrl	27.41	N	27.37	N	29	100	49	43	100	63
Ctrl	27.67	N	27.56	N	29	100	48	43	100	61
HA-A	27.93	N	27.77	N	29	100	45	43	100	37
HA-A	27.72	N	27.37	N	29	100	52	43	100	55
HA-A	27.82	N	27.52	N	29	100	44	43	100	57
HA-B	28.18	N	28.07	N	29	100	38	26	60	‡
HA-B	27.78	N	27.82	N	29	100	49	43	100	37
HA-B	27.60	N	27.96	N	29	100	45	43	100	39
HA-C	30.48	Y	31.10	Y	20	69	‡	21	49	‡
HA-C	28.77	N	28.64	N	29	100	34	29	67	‡
HA-C	28.50	N	28.37	N	29	100	37	43	100	26
HA-D	§	Y	§	Y	0	0	‡	0	0	‡
HA-D	§	Y	§	Y	6	21	‡	9	21	‡
HA-D	§	Y	§	Y	9	31	‡	15	35	‡
HA-E	§	Y	§	Y	0	0	‡	0	0	‡
HA-E	§	Y	§	Y	0	0	‡	0	0	‡
HA-E	§	Y	§	Y	0	0	‡	1	2	‡
Hem-A	27.96	N	27.93	N	29	100	52	43	100	62
Hem-A	27.83	N	27.81	N	29	100	67	43	100	69

Sample	Quantifiler™ Trio kit		Quantifiler™ HP kit		Identifiler™ Plus kit STR results			GlobalFiler™ kit STR results		
	IPC C_T	IPC C_T flag?	IPC C_T	IPC C_T flag?	Allele count	Allele recovery (%)	Avg% ICB‡	Allele count	Allele recovery (%)	Avg% ICB†
Hem-A	27.67	N	27.47	N	29	100	52	43	100	67
Hem-B	28.63	N	28.42	N	29	100	52	43	100	61
Hem-B	28.40	N	28.31	N	29	100	47	43	100	62
Hem-B	28.29	N	28.17	N	29	100	46	43	100	62
Hem-C	§	Y	§	Y	18	62	‡	43	100	30
Hem-C	37.32	Y	31.27	Y	29	100	32	43	100	61
Hem-C	28.74	N	28.97	N	28	97	16	43	100	42
Hem-D	§	Y	§	Y	0	0	‡	33	77	‡
Hem-D	§	Y	§	Y	0	0	‡	33	77	‡
Hem-D	§	Y	§	Y	11	38	‡	43	100	34
Hem-E	§	Y	§	Y	0	0	‡	0	0	‡
Hem-E	§	Y	§	Y	0	0	‡	15	35	‡
Hem-E	§	Y	§	Y	0	0	‡	16	37	‡

† Intra Color Balance (ICB) for each dye was calculated as the peak height of the lowest locus compared to the peak heights obtained for the highest locus. for each dye color. Peak height data for each locus is calculated by averaging the peak heights of heterozygotes or dividing the homozygote peak height value by half. The ICB value for each dye set was then used to calculate the Average Percent ICB for all dye sets. Low ICB values, i.e "ski slope effect," represents a typical consequence of more severe PCR inhibition in STR assays.

‡ ICB not calculated due to one or more alleles falling below the 175 RFU threshold used for this study.

§ Undetermined

Results demonstrated that samples that *did not* trigger the IPC C_T flag mostly gave full profiles with subsequent STR analysis using either the Identifiler™ Plus or GlobalFiler™ kits. In contrast, samples that *did* trigger the IPC C_T flag produced significantly reduced allele counts with the STR kits (only 21% and 42% of a full profile were detected for IPC C_T-flagged samples, on average, with the Identifiler™ Plus and GlobalFiler™ kits, respectively).

Stability study: Degraded DNA

Degradation Index

Various environmental factors to which forensic DNA samples may be exposed, such as heat, radiation (sunlight) or microbes, may cause DNA molecules to fragment. DNA degradation typically reduces the average size of DNA fragments in a sample. With increasing degradation, fragment size continues to decrease. Larger fragments may be disproportionately reduced in concentration or eliminated.

The Quantifiler™ HP and Trio kit assays were designed to quantify two different autosomal multicopy target loci with different amplicon sizes. With increasing degradation, longer-amplicon targets tend to decrease disproportionately relative to shorter amplicon targets. Therefore, the HID Real-Time PCR Analysis Software v1.2 Degradation Index (DI), which is the ratio of quantification results between the Small Autosomal (SA, 80 bp) and Large Autosomal (LA, 214 bp) assay targets, may indicate potential DNA degradation of samples. The Degradation Index, evaluated in conjunction with the IPC C_T result, can provide useful guidance for downstream STR genotyping strategies, such as the use of STRs with smaller, “mini” amplicon sizes that are more likely to amplify and provide genotype information from degraded samples. Refer to “Determine Quality Index” on page 5-53 for additional information.

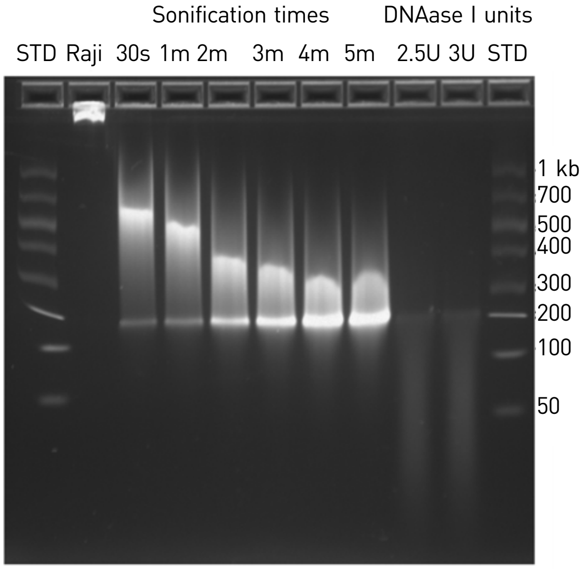
Experiment

To evaluate the Degradation Index feature of the kits and software, two separate sample sets of purified human male genomic DNA were mechanically sheared with a sonicator to break up longer DNA strands in a random manner, and then the sheared DNA was digested with varying amounts of DNase I enzyme and different incubation times to generate samples with varying levels of degradation.

Two sample series were tested: a higher overall concentration series made with “PB001” human male DNA purified from peripheral blood cells, and a lower overall concentration series using a commercial preparation of “Raji” cell-line DNA. The PB001 series consisted of an undegraded Control sample, plus “Low,” “Medium” and “High” degraded fractions. The Raji DNA series consisted of a Control sample, and samples designated as “3 u,” “4 u,” “5 u” and “6 u,” (“u” refers to the amount of DNase added during the degradation treatment) with progressively higher levels of DNA degradation.

Figure 23 shows the agarose gel analysis of fractions generated during the preparation of the degraded Raji human cell-line DNA series. Raji DNA is seen in its intact state (lane 2), following sonication treatment for different times (lanes 3–8), and after sonication followed by digestion with different amounts of DNase enzyme (lanes 9–10). More extensive exposure to degradation-inducing treatments can be seen to systematically reduce the average size of DNA fragments, as indicated by the downward shift in the smears of DNA on the gel.

Figure 23 Quantifiler™ HP and Trio assays of degraded DNA fractions



Triplicate Quantifiler™ HP and Trio reactions were performed for each sample according to the procedure in this guide. STR analysis was also performed on the degraded DNA samples using the GlobalFiler™ kit (29 cycles). Sample volumes added to GlobalFiler™ kit reactions varied according to the small autosomal DNA concentrations measured by the Quantifiler™ Trio Kit assay, up to 10 µL, resulting in variable total nanogram amounts. *In some instances, additional volume of DNA added to the GlobalFiler reaction (up to 15 µL) may improve DNA recovery.*

Quantification and STR results

Table 20 shows the concentration and Degradation Index (DI) results of Quantifiler™ HP and Trio assays, with corresponding GlobalFiler™ kit STR assay results.

Table 20 Concentration, Degradation Index (DI), and STR results

Sample	Quantifiler™ Trio kit (ng/µL)				Quantifiler™ HP kit (ng/µL)‡			GlobalFiler™ kit STR analysis		
	SA	**LA**	**Y**	**DI**	**SA**	**LA**	**DI**	**Total DNA/ reaction (ng)**	**Allele count**	**Avg pk ht**
PB001 Ctrl	10.057	13.566	9.767	0.74	12.519	17.812	0.70	1.00	43	6308
PB001 Ctrl	9.629	13.376	9.869	0.72	10.214	15.764	0.65	1.00	43	6286
PB001 Ctrl	7.377	11.543	8.691	0.64	10.175	15.291	0.67	1.00	43	7572
PB001 Low	1.415	0.474	1.407	2.98	1.659	0.652	2.54	1.00	20	946
PB001 Low	1.165	0.439	1.195	2.65	1.548	0.552	2.81	1.00	33	1104
PB001 Low	1.074	0.419	1.133	2.56	1.284	0.509	2.52	1.00	37	1125
PB001 Med	0.445	0.013	0.342	34.69	0.446	0.022	20.19	1.00	15	1617
PB001 Med	0.310	0.012	0.258	25.60	0.370	0.018	20.51	1.00	18	2057
PB001 Med	0.271	0.010	0.221	26.56	0.343	0.014	23.97	1.00	16	2727
PB001 High	0.050	†	0.024	‡	0.081	0.0001	646.10	0.46	7	1100
PB001 High	0.046	†	0.026	‡	0.064	0.0001	526.18	0.46	8	1699
PB001 High	0.044	†	0.029	‡	0.079	0.0002	512.63	0.46	9	1603
Raji 0 u	0.024	0.048	0.032	0.49	0.036	0.055	0.65	0.23	41	1271
Raji 0 u	0.024	0.045	0.027	0.52	0.029	0.053	0.55	0.23	40	1899
Raji 0 u	0.023	0.041	0.028	0.55	0.024	0.043	0.57	0.23	40	1656
Raji 3 u	0.018	0.007	0.023	2.49	0.022	0.010	2.15	0.15	26	442
Raji 3 u	0.014	0.007	0.018	1.94	0.016	0.008	2.07	0.15	36	614
Raji 3 u	0.013	0.007	0.017	2.00	0.018	0.008	2.23	0.15	34	518
Raji 4 u	0.013	0.002	0.013	6.12	0.017	0.005	3.36	0.11	14	384
Raji 4 u	0.010	0.002	0.011	4.39	0.014	0.003	4.62	0.11	19	366
Raji 4 u	0.008	0.002	0.011	4.43	0.012	0.002	4.95	0.11	15	513
Raji 5 u	0.010	0.0013	0.011	7.50	0.015	0.0043	3.43	0.09	16	308
Raji 5 u	0.010	0.0013	0.009	7.73	0.013	0.0030	4.42	0.09	19	456
Raji 5 u	0.009	0.0008	0.009	11.08	0.013	0.0017	7.52	0.09	21	435
Raji 6 u	0.004	0.0009	0.004	4.88	0.007	0.0005	13.80	0.04	5	236
Raji 6 u	0.003	0.0003	0.003	9.91	0.005	0.0003	19.03	0.04	5	333
Raji 6 u	0.003	0.0003	0.002	10.18	0.005	0.0003	17.02	0.04	7	383

† Undetermined

‡ When the quantity for the SA or LA target is undetermined, the Degradation Index is not calculated and the Degradation Index field in the Well Table is empty. When the LA target is undetermined, this can be an indication of significant degradation and/or inhibition affecting the sample.

The average IPC C_T for the above degraded DNA samples was 27.77 indicating, as expected, no significant PCR inhibition. For the highest-concentration sample (PB001 Control), its higher DNA concentration (mean QuantSA = 9.0 ng/µL) caused a detectable shift in IPC C_T (mean IPC C_T = 28.79), but not significant enough to trigger the IPC C_T flag.

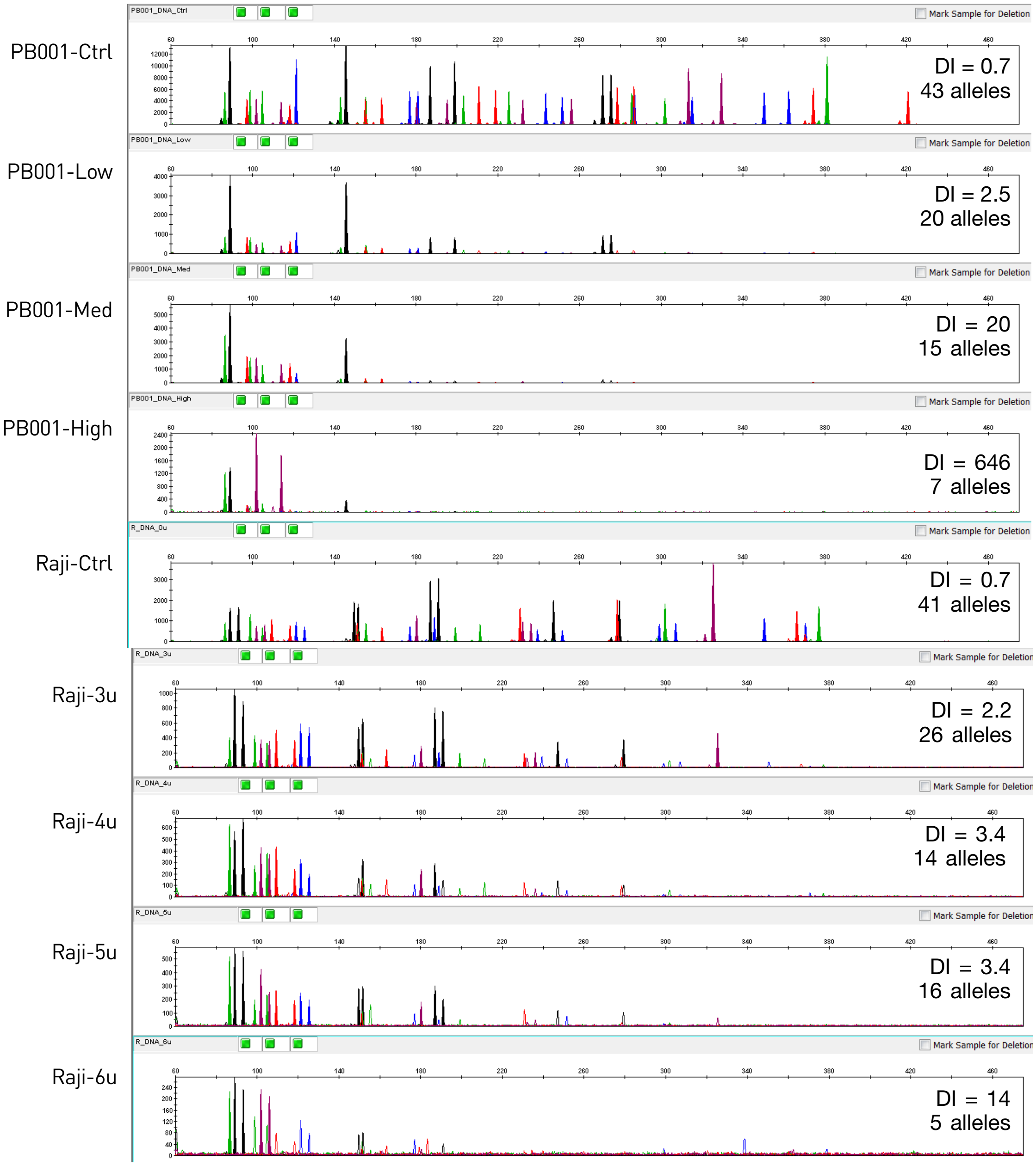
Note: Samples, including pristine samples, may have a DI value <1.0. This condition is not abnormal, and is simply the consequence of LA target quantification results being slightly higher than that of the SA target. Use the SA target quantification value to estimate target DNA concentration for downstream STR applications. The quantification value for the LA target is provided as an indicator of DNA degradation only. The software compares the LA quantification result with that of the SA target to determine the Degradation Index value.

Degradation Index results

The Degradation Index (DI) was automatically calculated from the quantification results by the HID Real Time PCR Software v1.2 (HID v1.2). DI is a unit-less measurement calculated simply as the SA quantification result divided by the LA quantification result for each sample. In more degraded samples, the LA quantification result decreases disproportionately relative to the SA quantification result, so that the DI ratio increases with increasing levels of DNA degradation. In this experiment, for example, the Quantifiler™ HP assay DI ranged from <1 in the PB001 Control sample to an average of 562 in the PB001 most-degraded "High" sample. For the Quantifiler™ Trio assay, the LA target gave undetected (i.e. completely negative) quantification results for the PB001 High sample, so that the DI was not calculated. In either case, the DI result indicated that the PB001 "High" fraction was highly degraded.

GlobalFiler™ kit electropherogram results confirmed the degradation state of samples, as shown below. Degraded DNA profiles displayed the typical incidence of "ski slope effect," which is the manifestation of larger DNA fragments becoming disproportionately depleted in more highly degraded samples, so that shorter-amplicon STR loci produced higher allele peak heights than longer-amplicon loci. In the most highly degraded samples, no higher molecular weight allele peaks were detected. Allele counts show that the expected recovery of genotype information from degraded samples is influenced not just by the DI, but also by the total amount of DNA added to STR assay reactions. Comparing the PB001 "High" (mean DI = 562) and Raji DNA "6 u" (mean DI = 17) fractions, similar allele counts were obtained despite the wide difference in the DNA degradation level between the samples. This was likely because the more highly degraded PB001 fraction contained a much higher concentration of DNA, allowing more DNA to be added to STR assay PCRs.

Figure 24 GlobalFiler™ Kit results for degraded DNA samples



Note: Electrophoresis was performed on the Applied Biosystems™ 3500xL Genetic Analyzer and data was evaluated using a 175 RFU peak amplitude threshold. DI values shown above are from the Quantifiler™ HP kit results.

Repeatability study

Experiment

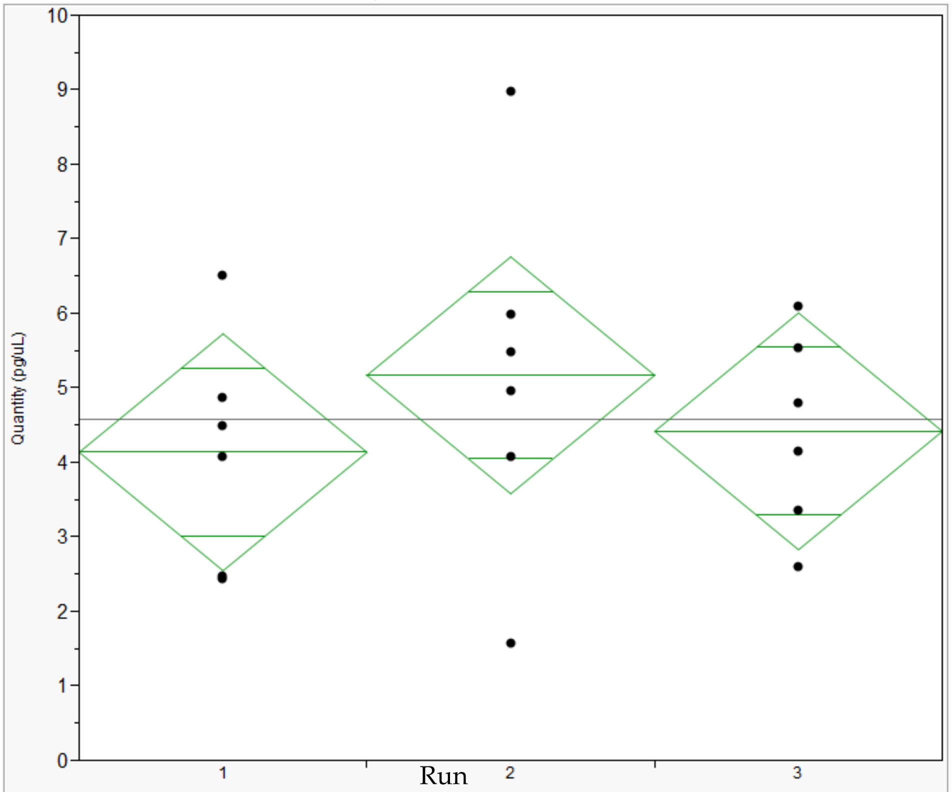
Repeatability analysis was performed to assess the variation of the quantification results obtained due to run-to-run variability. Runs were conducted on one instrument by a single operator using a single lot of reagents, and a single 007 human male genomic DNA from a commercial supplier.

The DNA sample was diluted to 500, 50, and 5 pg/µL. All dilutions were made in $T_{10}E_{0.1}$ Buffer. All samples and dilutions were tested with six replicates per sample per plate using the Quantifiler™ Trio DNA Quantification Kit. Four replicate instrument runs were performed. For each sample reaction the C_T values were obtained and the DNA quantities calculated.

Results

Figure 25 shows the run-to-run variability for a sample containing approximately 5 pg/µL male DNA. Results for the Y target are shown. The mean diamonds are used to demonstrate the range of values typically seen in the quantification assay. The mean line across the middle of each diamond represents the mean for all samples tested. Overlap marks appear as lines above and below the group mean. Overlap marks are computed as group mean ± (√2)/2 * CI/2. The top and bottom of each diamond represent the 95% confidence interval for each group.

Figure 25 Run-to-run variability for the Y target with sample containing 5 pg/µL DNA. The results of the Analysis of Variance (ANOVA) statistical test showed no statistically significant differences for the SA, LA, and Y target data points in the three runs.



Reproducibility study

Experiment

The reproducibility study assessed the variability of quantification results across multiple runs on two different 7500 Real-Time PCR instruments. Runs were conducted by one operator using a single lot of reagents.

Two human genomic DNA preparations were used; human male cell-line 007 DNA obtained from a commercial vendor, and human female 3408 DNA, purified in-house from a preparation of peripheral blood cells. Based on Quantifiler™ Trio kit quantifications of higher-concentration stock solutions, each DNA was diluted to approximately 5 ng/µL, then three 10-fold serial dilutions were prepared at ~ 5, 0.5, 0.05, and 0.005 ng/µL (designated as dilutions A, B, C, and D, respectively). Each run consisted of a duplicate quantification standards (50, 5, 0.5, 0.05, and 0.005 ng/µL) reactions, and 4 replicates of each dilution sample. Each plate was run using the recommended reaction volumes and thermal cycling conditions on either of two 7500 instruments. Three replicate runs were performed on each of the two 7500s.

Results

Figure 26 through Figure 29 show quantification results for each Quantifiler™ Trio kit assay target for the 4 dilutions of 007 DNA. The run numbers in the graphs correspond to the following instruments or conditions: 7500 instrument 1 (Runs 1, 3, and 5); 7500 instrument 2 (Runs 2, 4, and 6).

Figure 26 007 Dilution A (5 ng/µL sample)

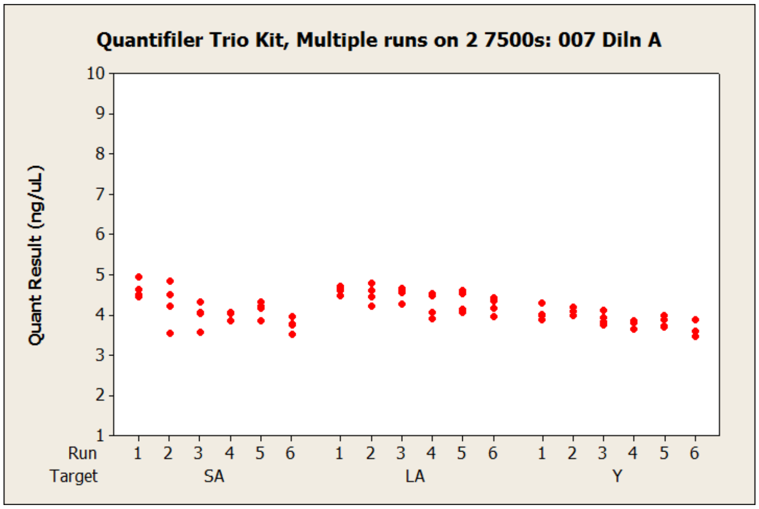


Figure 27 007 Dilution B (0.5 ng/µL sample)

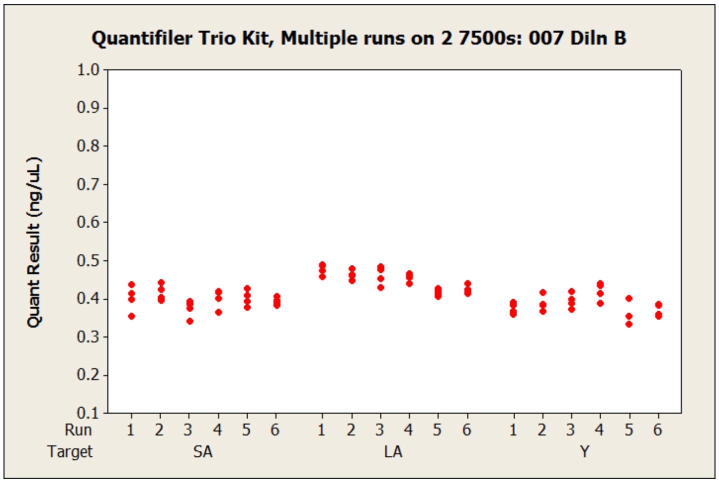


Figure 28 007 Dilution C (0.05 ng/µL sample)

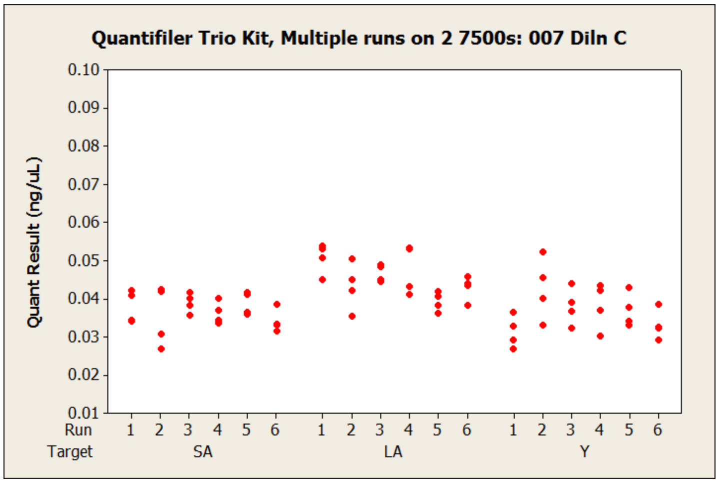
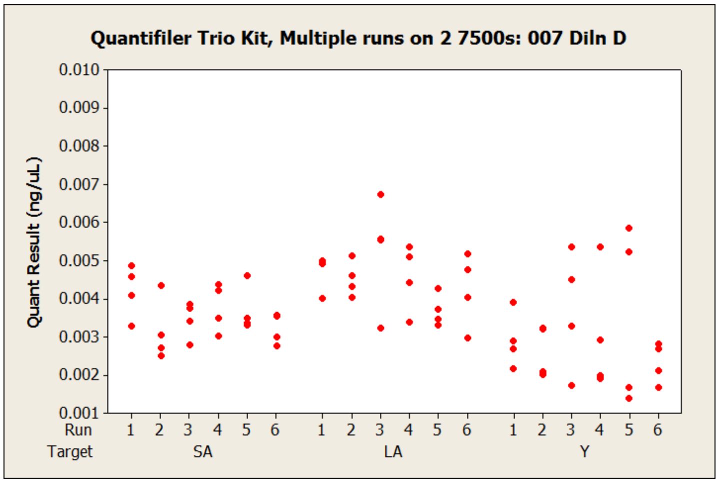


Figure 29 007 Dilution D (0.005 ng/µL sample)



Between runs and across instruments, the quantification results were relatively consistent and no apparent unexpected trends were observed. The data points from replicate reactions at different DNA dilution levels provide a graphic representation of stochastic effects that caused a dramatic increase in the variability of results at the lowest-concentration dilutions. The typical stochastic effects became visually apparent in Dilution C, and increased dramatically in Dilution D.

Table 21 shows the mean quantification results and average within-run variability for different dilution levels over 6 standard runs performed on both 7500 instruments, expressed as the Coefficient of Variation (Standard Deviation ÷ Mean, in percent). Stochastic effects were again apparent as an increase in the CV% for lower-concentration dilutions. This was most apparent for the Y target at the lowest-concentration dilution of male 007 DNA, and is likely to be a consequence of the Y chromosome targets having fewer total copies than the autosomal targets, thereby further increasing the impact of stochastic amplification on CV for the Y target compared to the autosomal target.

Table 21 Mean quantification and variability of two dilutions of DNA

Sample	Mean Quant (ng/µL)			Quant CV%		
	SA	LA	Y	SA	LA	Y
3408 (fem) A (5 ng/µL)	4.799	4.965	†	7.10	4.62	†
3408 (fem) B (.5 ng/µL)	0.464	0.502	†	5.82	2.17	†
3408 (fem) C (.05 ng/µL)	0.044	0.050	†	5.60	6.99	†
3408 (fem) D (.005 ng/µL)	0.004	0.005	†	16.03	18.72	†
007 (male) A (5 ng/µL)	4.130	4.410	3.881	6.25	4.93	3.78
007 (male) B (.5 ng/µL)	0.398	0.449	0.386	5.65	3.10	5.56
007 (male) C (.05 ng/µL)	0.037	0.045	0.037	10.75	9.15	14.14
007 (male) D (.005 ng/µL)	0.004	0.005	0.003	17.02	16.94	39.22

† Undetermined

Statistical analysis of the reproducibility runs data was performed to determine if runs performed on different 7500 instruments produced equivalent results. Figure 30 through Figure 33 are plots for the 3408 Dilution C sample, and 007 Dilution A sample, grouped by 7500 instrument and analyzed by the Student's t-test. The overlapping circles on the right panel of each graph indicate that there was no significant difference between instruments.

Figure 30 3408 Dilution C (0.05 ng/µL sample). Blue, green, red, and black data points represent data from different reproducibility runs.

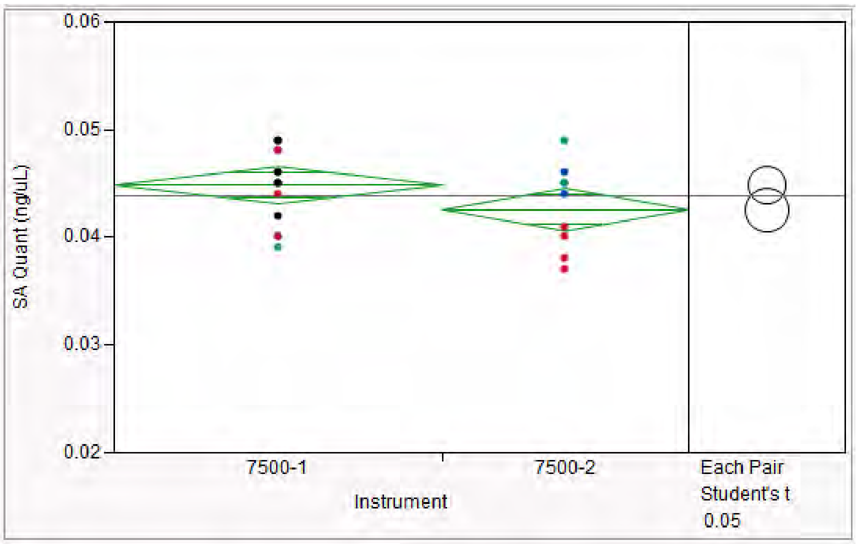
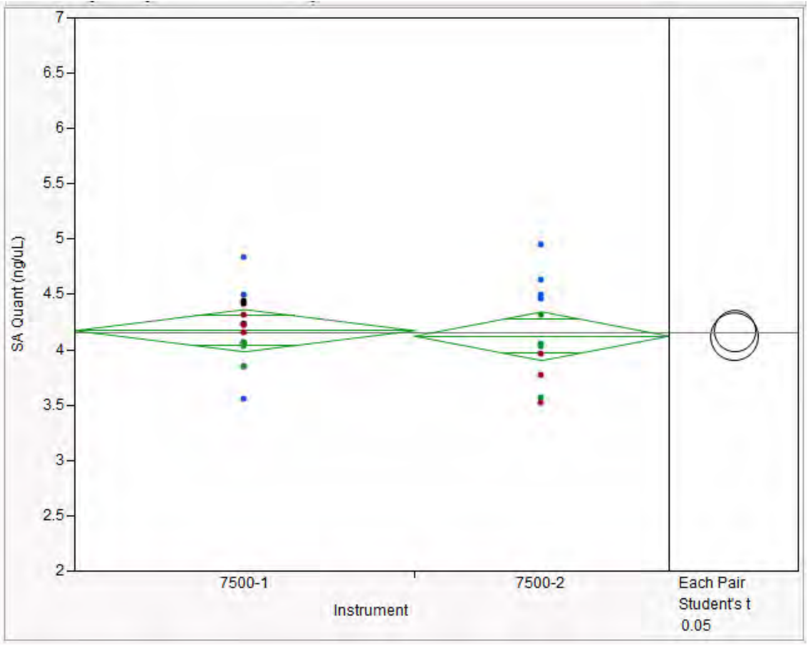


Figure 31 007 Dilution A (5 ng/µL sample). Blue, green, red, and black data points represent data from different reproducibility runs.



Stability of DNA standard dilution series

To determine the acceptable storage time for the DNA standard dilution series, a stability study was run. First, a DNA standard dilutions series (50 ng/µL – 5 pg/µL) was made with 50 µL volume for each sample in low-bind tubes.

Note: Previous troubleshooting work with our Quantifiler™ Duo, Human, and Y Human Male DNA Quantification Kits have demonstrated the effectiveness of using low binding tubes for DNA standard preparation to avoid sample stability issues with lower template dilutions. Use low-bind tubes such as Applied Biosystems™ Non-Stick RNase-free Microfuge Tubes (Cat. No. AM12450) for this purpose.

The DNA standard dilution series, stored in low-bind tubes at 2 to 8°C, was analyzed on multiple days across a 17-day period. In addition, a control sample with an approximate DNA concentration of 7 ng/µL was also analyzed on each plate in triplicate.

Figure 32 Effect of storage on DNA standard stability, slope

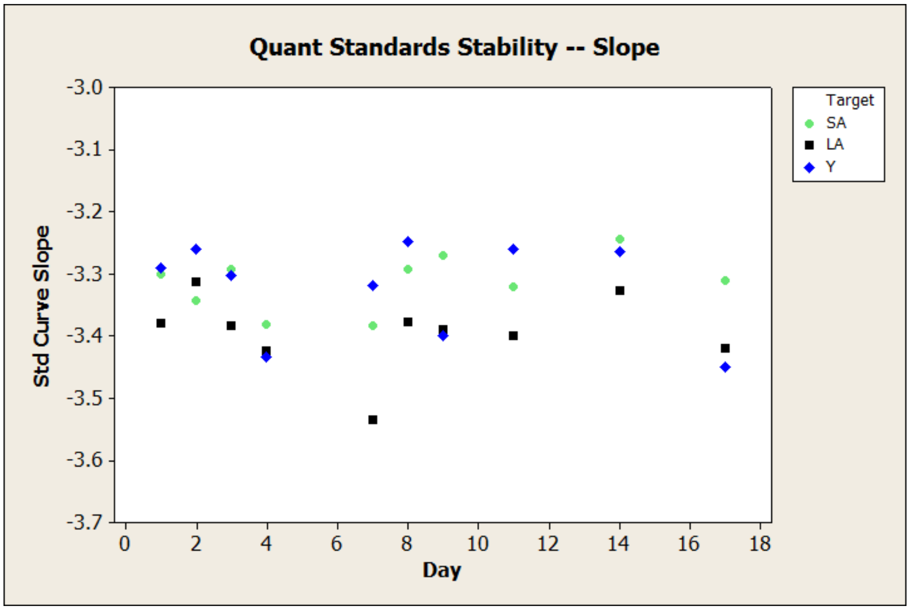
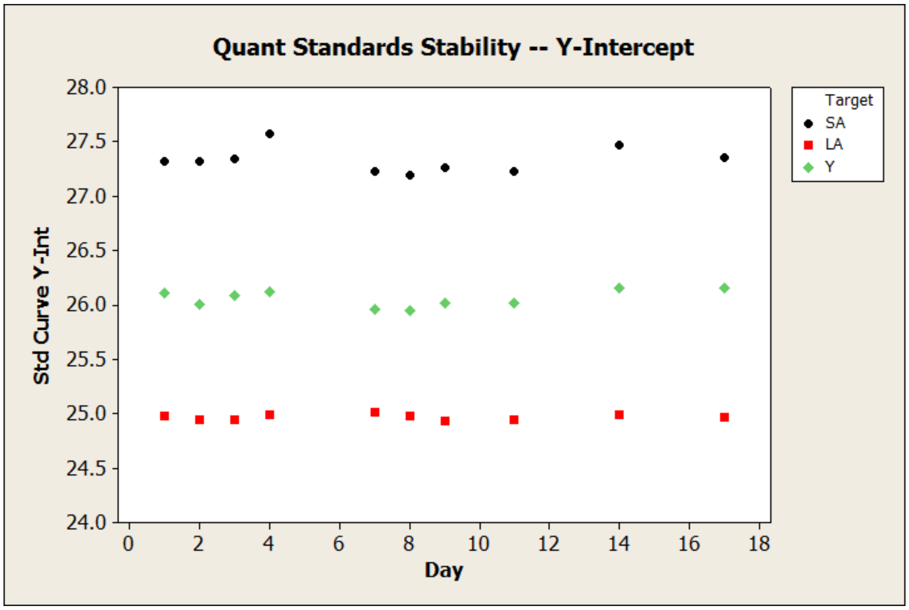


Figure 33 Effect of storage on DNA standard stability, Y-intercept



Across a 17-day period, the slope values for the genomic targets remained within the acceptable range. Based on the results of these validation studies and additional development studies, we recommend storing the prepared DNA standards in low-bind tubes at 2 to 8°C for up to 2 weeks.

Casework-type sample study

Experiment

Testing was performed to demonstrate the efficacy of the Quantifiler™ Trio kit using a subset of samples typically encountered in forensic laboratories. The Quantifiler™ Trio assay was used to quantify single-source human genomic DNA in a variety of simulated casework samples prepared by different extraction/purification methods commonly used in testing laboratories. Quantification results were then used to determine sample input amounts for subsequent STR genotyping with the GlobalFiler™ kit, and resulting profiles were assessed.

Quantifiler™ Trio kit and GlobalFiler™ kit analyses were performed in single reactions, with the quantification results from the Quantifiler™ Trio assay used to determine input quantities for GlobalFiler™ kit reactions.

Results

Table 22 lists sample information, concentration, Degradation Index (DI), and IPC CT results of Quantifiler™ HP and Trio assays, with corresponding GlobalFiler™ kit STR assay results (29 cycles).

Figure 34 and Figure 35 show the electropherograms for the samples tested.

Table 22 Results of Quantifiler™ Trio Kit using typical forensic samples

Sample	Sample info		Quantifiler™ Trio results					GlobalFiler™ kit STR results		
	Description	**Prep method**	**SA (ng/µL)[†]**	**LA (ng/µL)**	**Y (ng/µL)**	**IPC C_T[‡]**	**DI**	**DNA per reaction (ng)**	**Allele count[§]**	**Average peak ht**
1	Blood on cloth	PCI	0.106	0.066	0.122	27.61	1.6	1.00	43	3361
2	Cigarette filter	PCI	0.138	0.021	0.134	27.51	6.5	1.00	31	1713
3	Blood on cloth	PCI	0.202	0.125	0.226	27.64	1.6	1.00	43	3613
4	Saliva on envelope	PCI	0.525	0.595	[††]	27.76	0.9	1.00	39	5285
5	Semen on cotton	PF-Man	0.072	0.111	0.069	27.56	0.6	0.72	44	6418
6	Blood stain on denim	PF-Man	0.227	0.521	0.253	28.48	0.4	1.00	43	5505
7	Semen on cotton	PF-Man	0.076	0.137	0.084	27.53	0.6	0.76	44	6862
8	Epithelial cell/cotton	PF-Man	0.153	0.141	0.138	27.42	1.1	1.00	39	4165
9	1:50 diluted blood	PF-AM	0.020	0.028	0.020	27.58	0.73	0.20	43	1346
10	Chewing gum	EZ1	0.074	0.091	[††]	27.80	0.8	0.74	39	6445
11	Chewing gum	EZ1	0.088	0.091	[††]	27.38	1.0	0.88	39	5898
12	Buccal swab	DNA IQ	0.099	0.090	0.101	27.45	1.1	0.99	41	6250
13	Buccal swab	DNA IQ	0.193	0.231	[††]	27.55	0.8	1.00	39	5794
14	Buccal swab	DNA IQ	0.028	0.019	0.020	27.31	1.5	0.28	41	1338
15	Buccal swab	PF-Man	0.426	0.404	0.409	27.64	1.1	1.00	41	6202
16	Blood on denim	PF-Man	0.428	0.834	0.331	29.81	0.5	1.00	41	6197

[†] Prep method codes: PCI (Phenol: Chloroform: Isoamyl organic extraction); PF-Man (PrepFiler™ manual extraction); PF-AM (PrepFiler™ on the AutoMate Express™ instrument); EZ1™ (Qiagen™ robotic platform); DNA IQ (Promega DNA IQ™ Kit).

[‡] The average IPC C_T for standard dilution series was 27.61. The average IPC C_T for samples 1–16 was 27.75.

[§] Donor reference DNA genotypes were not available, so total allele counts were not known.

[††] Undetermined

Figure 34 Casework-type sample profiles with the GlobalFiler™ kit (Part 1)

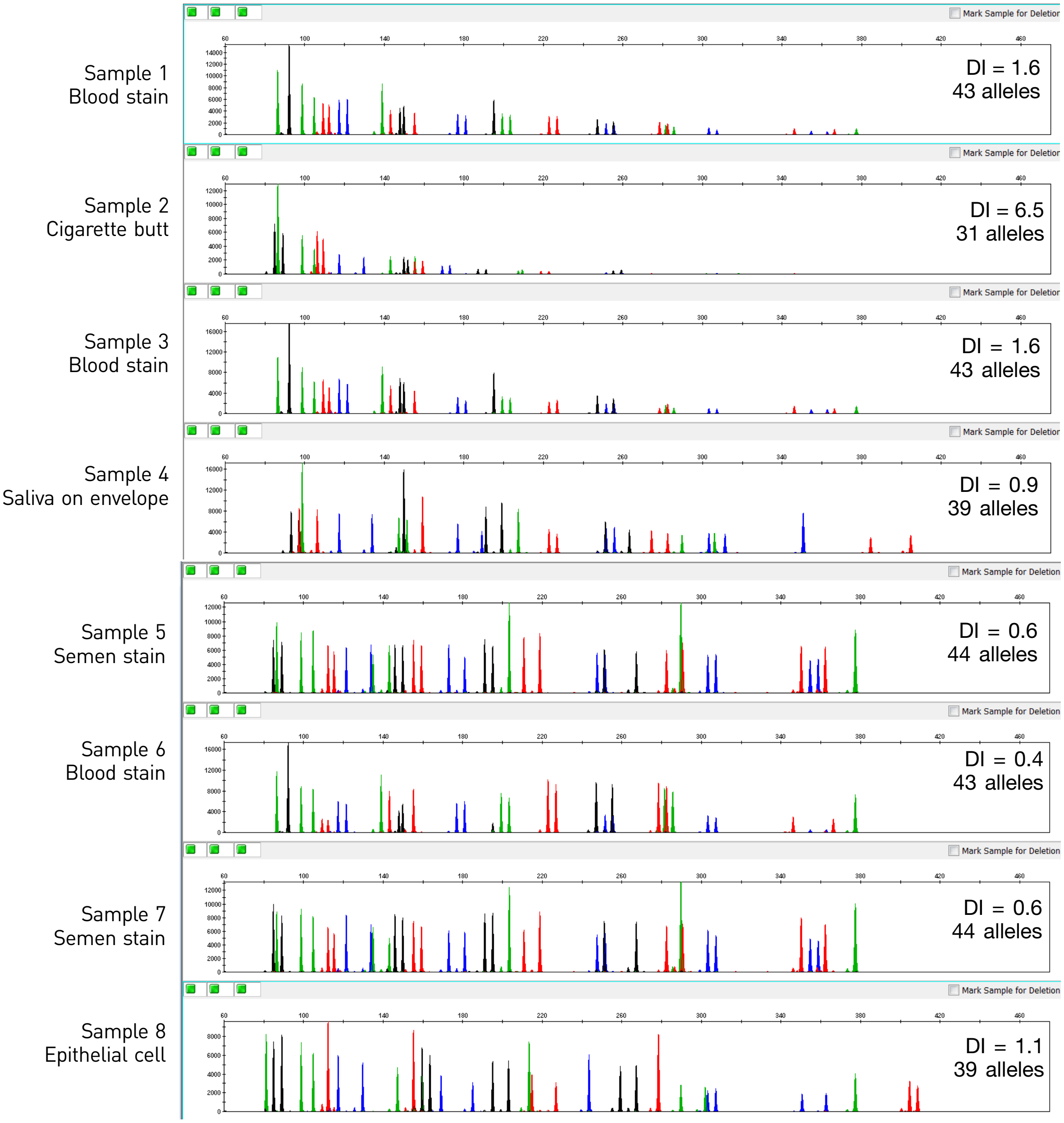
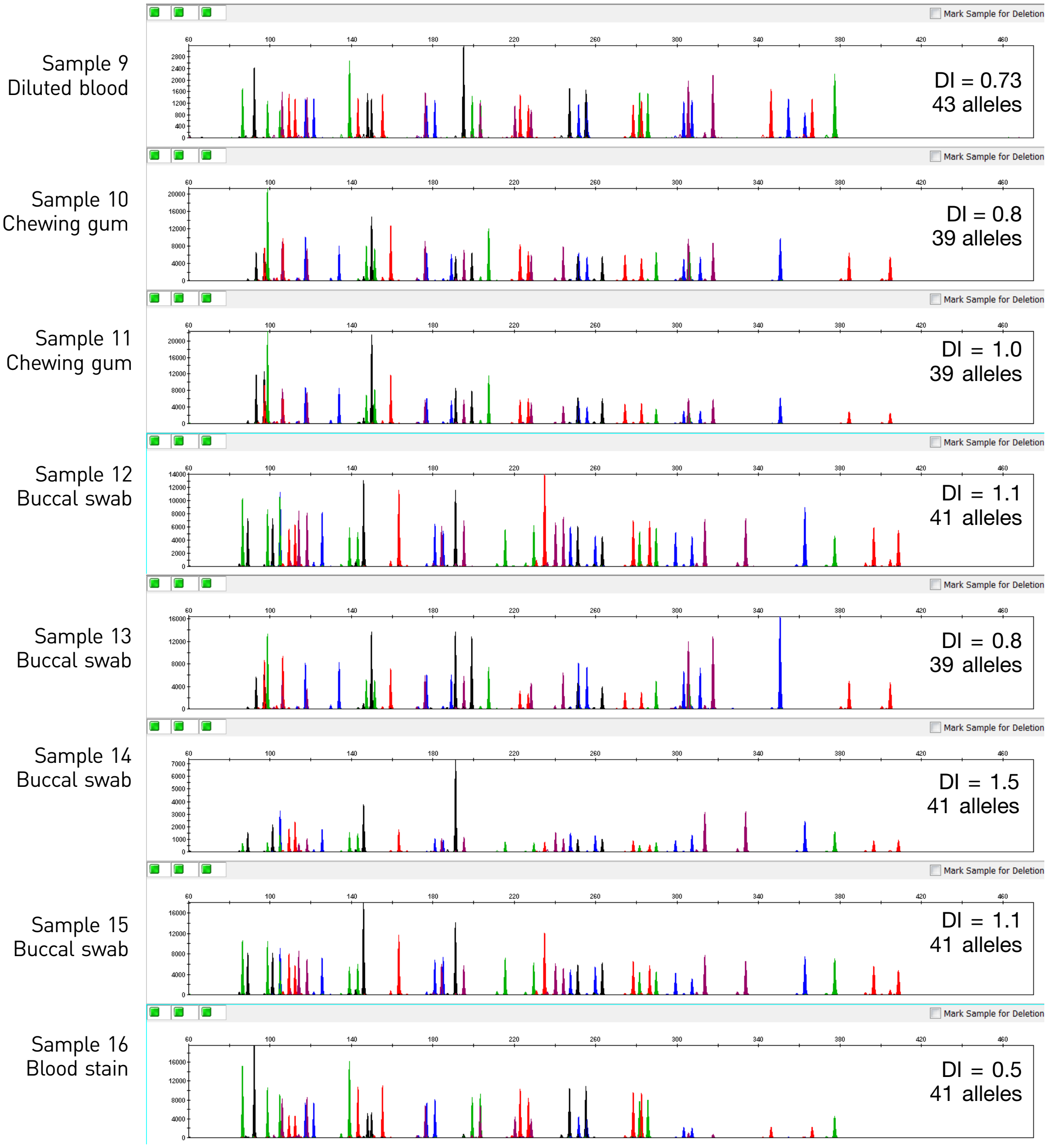


Figure 35 Casework-type sample profiles with the GlobalFiler™ kit (Part 2)



For most samples where a full 1.0 ng of sample DNA was added to the GlobalFiler™ kit reaction, the profile average peak height was over 5,000 RFU on the 3500xL genetic analyzer, and full or nearly-full profiles were obtained (i.e. the relatively high quality of electropherogram results and absence of any autosomal loci with null genotypes made it likely that profiles were complete).

Samples 1–4 which were extracted using the phenol:chloroform method, may have suffered from DNA degradation and overall loss of quality during approximately three years of storage prior to sample extraction. They exhibited reduced average peak heights largely due to varying degrees of ski-slope effect. Sample 2 (cigarette butt) was particularly notable with a moderate Degradation Index (6.5) and significant ski-slope effect leading to reduced peak heights and allele dropout.

Another notable was Sample 16 (blood stain on denim), in which 1.0 ng of DNA (contained in 3.7 µL of sample) was added to the GlobalFiler™ kit STR reaction. No alleles were detected for the TPOX locus using a 175 RFU peak amplitude threshold. While ski slope effect did not appear to be severe for this sample, some higher-molecular-weight alleles at other loci had reduced peak height (<1,000 RFU) as well. The IPC C_T for Sample 16 was shifted higher by 1.6 units relative to the IPC C_T baseline for quantification standard reactions. This may indicate that this sample was affected by some degree of PCR inhibition which could be confirmed by comparing its IPC C_T results against those of other reactions with similar concentrations in the run.

In general, results of this sample set indicated that samples in which the Quantifiler™ Trio Degradation Index (DI) was approximately 1.0 or less and no significant IPC C_T shift would exhibit little or no ski-slope effect and provide mostly full STR profiles. For this data set, samples with DI of approximately 1.5 and no significant shift in IPC C_T, may exhibit significant ski-slope effect but still provide full profiles (Samples 1, 3, and 14), indicating mild degradation. As the DI increases above 1.5 with minimal IPC C_T shift, significant enough degradation may be present to cause allele dropout (Sample 2, cigarette butt DI of 6.5).

Population study

Experiment

As mentioned previously, bioinformatics information and previous locus screening indicated that, for the targets selected, copy number variation (CNV) was expected to be relatively low for the LA, SA, and Y targets. To test this further, human DNA from four racial population groups was analyzed to verify low CNV across individuals and populations.

Whole blood samples, provided by the Interstate Blood Bank (Memphis, Tennessee) and Boca Biolistics (Coconut Creek, Florida), were collected from randomly selected individuals of different population groups in the United States. Ethnicities of sample donors are listed in Table 23. The samples used here are archived DNA samples which were previously extracted from the whole blood samples using a 6100 Nucleic Acid PrepStation method.

Table 23 Population samples for copy number consistency study

Population	Male samples	Female samples
Caucasian	53	28
African-American	64	14
Hispanic	46	34
Asian	31	42
Total	194	118

Results for SA and Y targets

For the male DNA samples, the average ratio of the quantification values for the SA target/Y target is 1.08 ± 0.18. ANOVA analysis (analysis of variance) confirmed no significant difference across populations for this ratio (p-value = 0.27). As shown in Figure 36, for the vast majority of male samples, the ratio of the SA target/Y target is between 0.75–1.5. This indicates a low expected incidence of CNV across populations for these multicopy targets. In our population study, 98% of all samples tested for the ratio of SA target/Y target fell within this range.

Figure 36 Quantification values for the SA target/ Y target

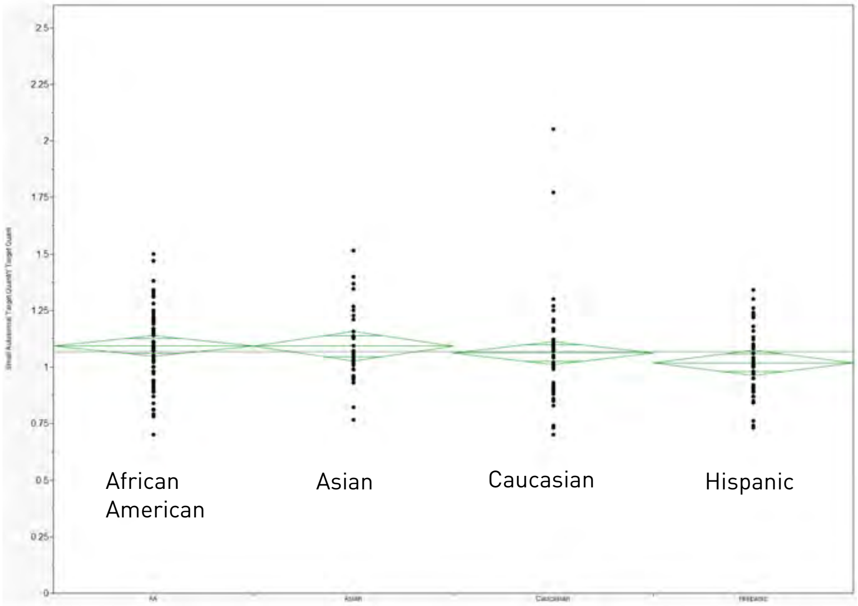
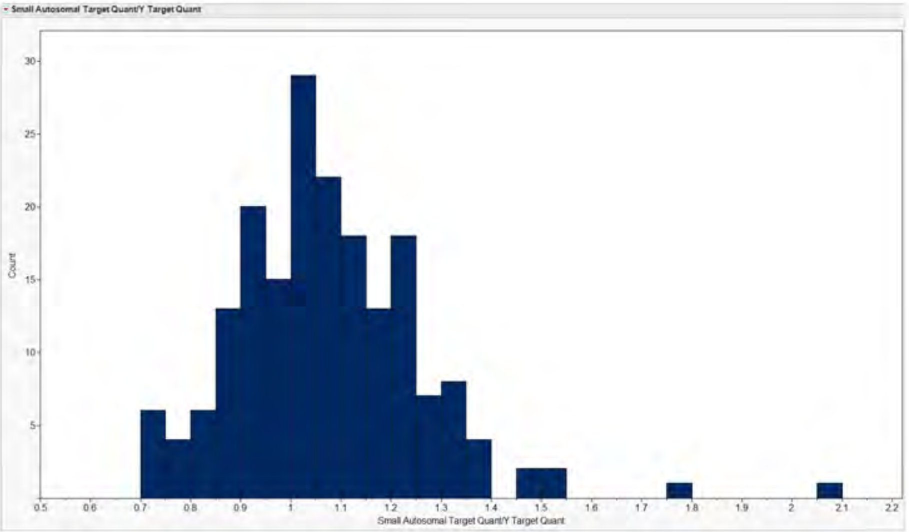


Figure 36 shows the quantification values for the SA target/ Y target, separated by populations. The mean diamonds are used to demonstrate the range of values typically seen in the quant assay. The mean line across the middle of each diamond represents the mean for all samples tested. Overlap marks appear as lines above and below the group mean. Overlap marks are computed as group mean ± (√2)/2 * CI/2. The top and bottom of each diamond represent the 95% confidence interval for each group.

Note: Samples, including pristine samples, may have a DI value <1.0. Use the SA target quantification value to estimate target DNA concentration for downstream STR applications. The quantification value for the LA target is provided *only* to allow determination of the DI.

Figure 37 Histogram for quantification values for the SA target/ Y target



Results for SA and LA targets

For all samples, the average ratio of the quantification values for the SA target/LA target (Degradation Index, DI) is 0.75 ± 0.14; the theoretical ideal DI is 1.0. For each population, the lowest DI values observed with pristine DNA were 0.51–0.57.

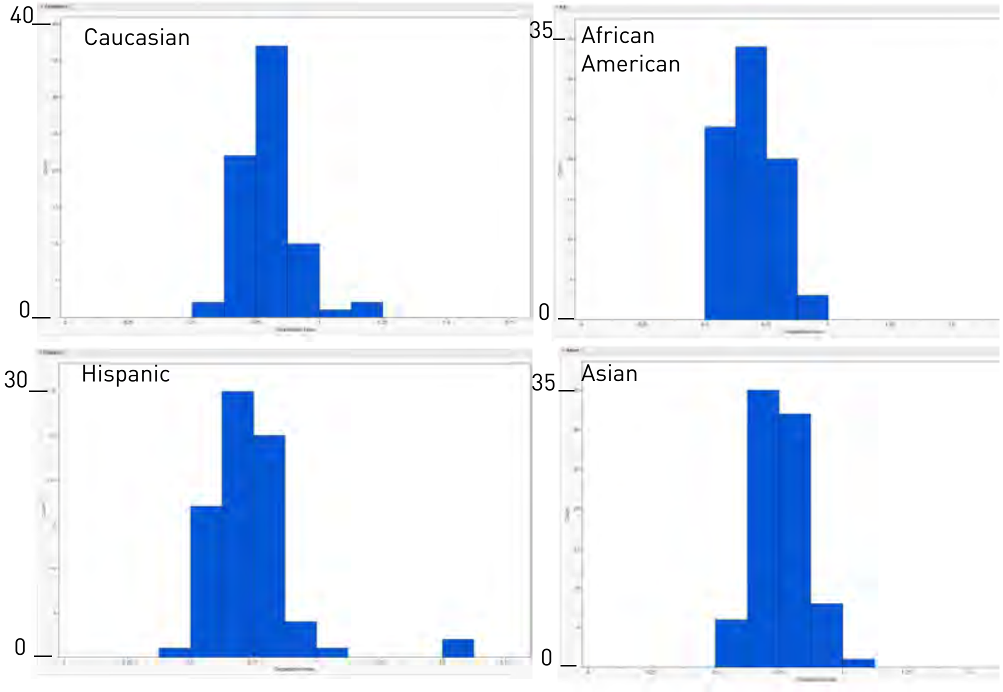
Note: Samples, including pristine samples, may have a DI value <1.0. Use the SA target quantification value to estimate target DNA concentration for downstream STR applications. The quantification value for the LA target is provided *only* to allow determination of the DI.

When analyzing the distribution of DI values from each population group, we found that the data was not normally distributed for any of these population groups, therefore, ANOVA analysis was not possible. Instead, the distribution of data for each population was compared using the metrics shown in Table 24. Analysis of these metrics and visual inspection of the histograms for each population in Figure 38 demonstrate copy number consistency across populations.

Table 24 Statistics calculated for the SA target and LA target ratio from the population study

Statistic	Caucasian	African American	Hispanic	Asian	All four populations
Mean	0.82	0.68	0.73	0.75	0.75
Standard Deviation	0.18	0.09	0.16	0.10	0.14
0% Quartile (Minimum)	0.51	0.50	0.47	0.56	0.47
25% Quartile	0.73	0.61	0.63	0.68	0.66
50% Quartile (Median)	0.80	0.68	0.72	0.75	0.74
75% Quartile	0.85	0.76	0.79	0.82	0.81
100% Quartile (Maximum)	2.07	0.92	1.50	1.06	2.07

Figure 38 SA target/LA target (Degradation Index) for four population groups. The x-axis is "Degradation Index" from 0 to 1.75. The y-axis is "Count."



Mixture study

Experiment

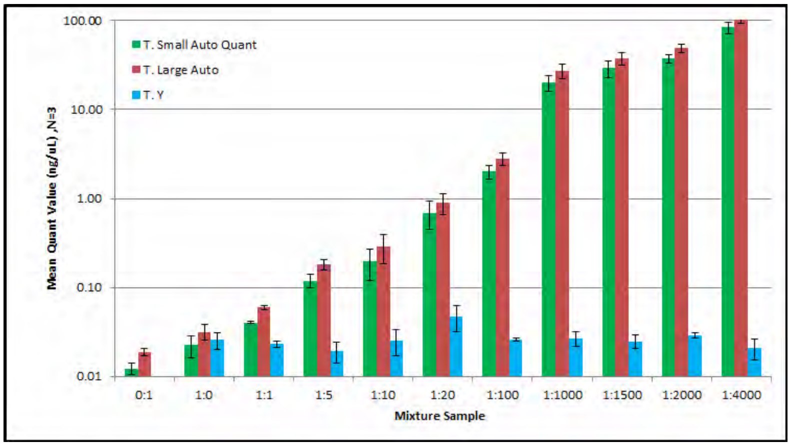
The mixture studies were designed to simulate circumstances where a small component of a single-source male DNA is present with increasing amounts of single-source female DNA.

Mixture samples containing 20 pg/µL of human male DNA and varying amounts of female DNA were prepared. The ratio of male and female DNA in these samples was approximately 1:0, 1:1, 1:5, 1:10, 1:20, 1:100, 1:1000, 1:1,500, 1:2000, 1:4000, and 0:1. The mixture samples were processed for quantification in triplicate using the Quantifiler™ Trio DNA Quantification Kit.

Results

Figure 39 shows the mixture study quantification results; the quantification values for the two autosomal genomic targets and the Y target.

Figure 39 Mixture study: quantification results



As shown in Figure 39, the measured quantification values correlate well with the expected values for all ratios tested. The male DNA concentration stayed consistent across the entire mixture range at approximately 20 pg/µL. For the 1:4000 mixture sample, quantification values measured 84 ng/µL for the SA target which is consistent with the expected 80 ng/µL value.

Contamination study

Experiment

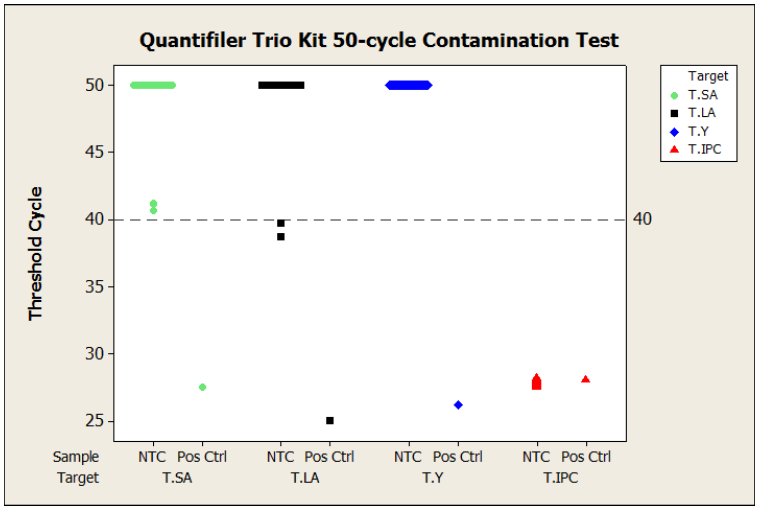
Analysis of non-template control (NTC) samples was performed using the Quantifiler™ HP and Trio kits to determine the level of background signal commonly observed and to evaluate the expected level of signal for the various targets and reagents in the assays.

For this study, we used the conditions specified in this guide, but extended the number of PCR cycles from 40 to 50 in the PCR amplification step to stress test the performance of the system. A 96-well plate was set up for each assay with 47 NTCs and one positive control sample (at a concentration of approximately 1 ng/µL).

Results

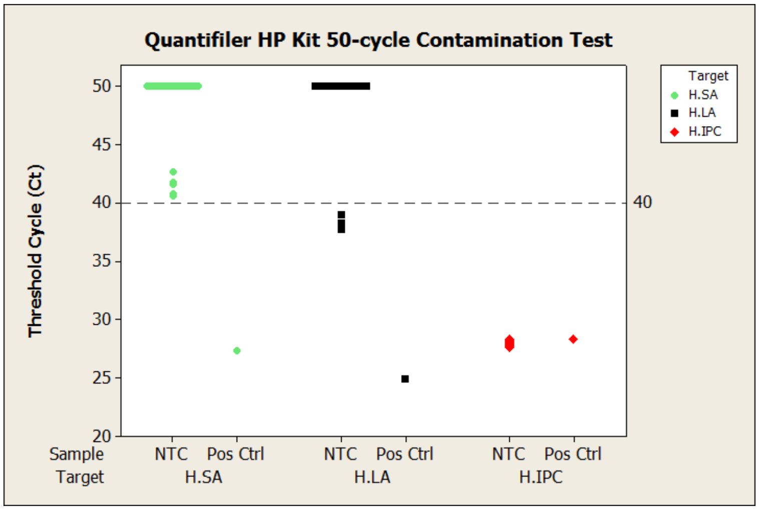
Figure 40 and Figure 41 show the contamination study results.

Figure 40 Quantifiler™ Trio results for NTC and positive control data for the contamination study



For the Quantifiler™ Trio assay, 2 of the 47 replicates exhibited LA target C_T values less than 40. The LA C_T values for these two samples were 38.7 and 39.8. For the SA target and Y target, no $C_T$values $C_T$values <40 were observed. The C_T values for the IPC signal (JUN™ dye) fell within a range of variation of 0.7 C_T. The positive control sample provided the expected C_T values.

Figure 41 Quantifiler™ HP results for the NTC and positive control data for the contamination study



For the Quantifiler™ HP assay, 3 of the 47 replicates had LA target C_T values less than 40. The LA C_T values for these three samples were 37.8, 38.2 and 39. For the SA target and Y target, no C_T values <40 were observed. As with the Quantifiler™ Trio assay run, the C_T values for the IPC signal (JUN™ dye) fell within a range of variation of 0.7 C_T. The positive control sample provided the expected $C_T$values.

The Quantifiler™ HP and Trio assays are highly sensitive as shown here. From this data, where 96% of the samples produced no signal <40 C_T for any of the three targets, users can conclude that the reagents used were free of detectable human DNA. The spurious signal obtained in the outlier samples are possibly the result of ambient DNA specific to those amplification wells or sporadic signal from the LA target. However, presence of human DNA was not confirmed with the SA target because no samples with a C_T <40 were observed.

With both The Quantifiler™ HP and Trio assays, sporadic signal is more likely to be observed with the LA target than the SA target. The LA target has a higher copy number than the SA target or Y target, which may contribute to the sporadic signal observation. If you observe a signal in one target, check the results of the other targets to determine whether the signal is caused by a reliably detectable level of DNA.

Perform the appropriate validation studies to determine the C_T threshold that will reliably produce an interpretable STR result for your workflow.

IMPORTANT! Before using the highly sensitive Quantifiler™ HP and Trio kits, assess the cleanliness of your environment. Use stringent contamination controls and laboratory cleanliness protocols to minimize contamination.

A

Safety

⚠ **WARNING! GENERAL SAFETY.** Using this product in a manner not specified in the user documentation may result in personal injury or damage to the instrument or device. Ensure that anyone using this product has received instructions in general safety practices for laboratories and the safety information provided in this document.

- Before using an instrument or device, read and understand the safety information provided in the user documentation provided by the manufacturer of the instrument or device.
- Before handling chemicals, read and understand all applicable Safety Data Sheets (SDSs) and use appropriate personal protective equipment (gloves, gowns, eye protection, etc.). To obtain SDSs, see the "Documentation and Support" section in this document.

Chemical safety

⚠ **WARNING! GENERAL CHEMICAL HANDLING.** To minimize hazards, ensure laboratory personnel read and practice the general safety guidelines for chemical usage, storage, and waste provided below, and consult the relevant SDS for specific precautions and instructions:

- Read and understand the Safety Data Sheets (SDSs) provided by the chemical manufacturer before you store, handle, or work with any chemicals or hazardous materials. To obtain SDSs, see the "Documentation and Support" section in this document.
- Minimize contact with chemicals. Wear appropriate personal protective equipment when handling chemicals (for example, safety glasses, gloves, or protective clothing).
- Minimize the inhalation of chemicals. Do not leave chemical containers open. Use only with adequate ventilation (for example, fume hood).
- Check regularly for chemical leaks or spills. If a leak or spill occurs, follow the manufacturer's cleanup procedures as recommended in the SDS.
- Handle chemical wastes in a fume hood.
- Ensure use of primary and secondary waste containers. (A primary waste container holds the immediate waste. A secondary container contains spills or leaks from the primary container. Both containers must be compatible with the waste material and meet federal, state, and local requirements for container storage.)
- After emptying a waste container, seal it with the cap provided.
- Characterize (by analysis if necessary) the waste generated by the particular applications, reagents, and substrates used in your laboratory.
- Ensure that the waste is stored, transferred, transported, and disposed of according to all local, state/provincial, and/or national regulations.
- **IMPORTANT!** Radioactive or biohazardous materials may require special handling, and disposal limitations may apply.

B

7500 Real-Time PCR System for Human Identification

7500 Real-Time PCR System for Human Identification overview

Description

The 7500 Real-Time PCR System for Human Identification provides an advanced, validated solution for casework, databasing, and paternity applications.

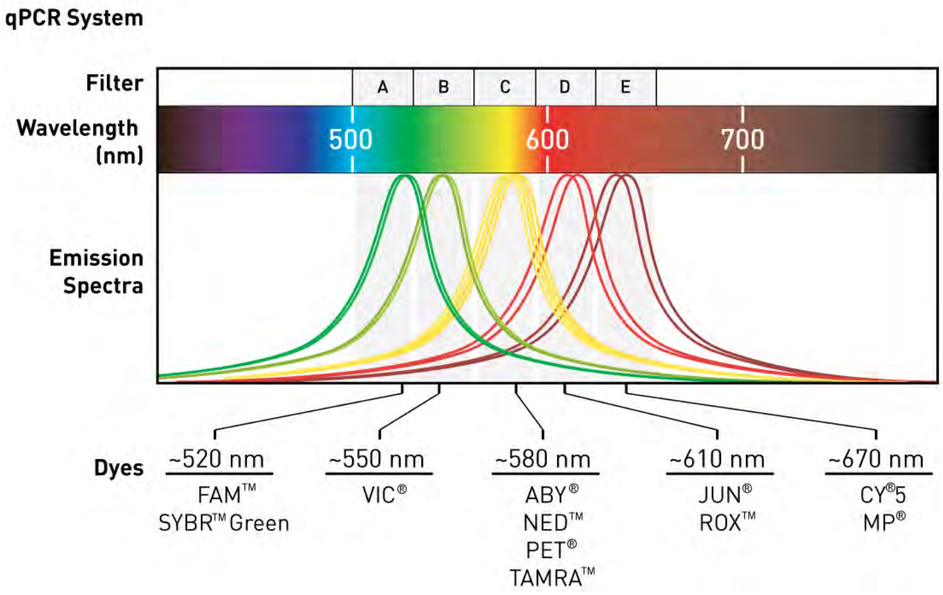
The 7500 instrument is controlled by the HID Real-Time PCR Analysis Software v1.2 .

The 7500 instrument is calibrated with several dyes including, FAM™, SYBR™ Green, VIC™, ABY™, TAMRA™, NED™, CY™3, ROX™, Texas Red™, CY™5, JUN™, and Mustang Purple™ (MP).

The 7500 system uses the data obtained from the pure-dye calibration to distinguish the individual contribution of each dye in the collective fluorescence, as gathered by the instrument during a run. After each run, the instrument software receives raw spectra-signal data for each reading. To make sense of the raw data, the software determines the contribution of each fluorescent dye used in the sample by comparing the raw spectra data to a set of pure dye standards contained in the pure spectra file. When an experiment is saved after analysis, the software stores the pure spectra information with the collected fluorescent data for that experiment.

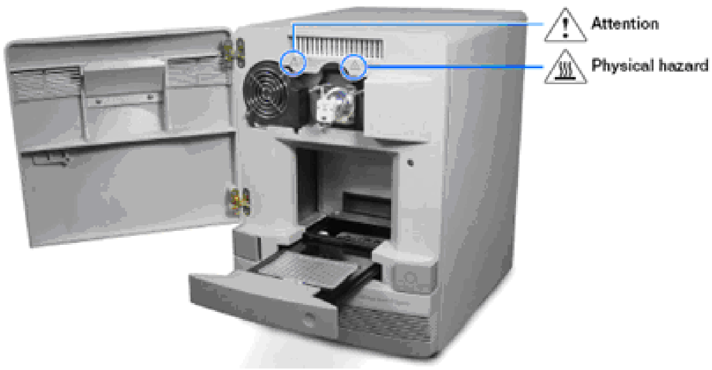
Figure 42 shows the emission spectrum for each dye, and the filters and wavelengths at which each dye is read.

Figure 42 Example of an emission spectrum



During a run

1. A tungsten-halogen lamp directs light to each well on the reaction plate. The light excites the fluorescent dyes in each well of the plate.
2. The CCD camera detects the fluorescence emission.
3. The software obtains the fluorescence emission data from the CCD camera and applies data analysis algorithms.



For more information

For more information on the 7500 Real-Time PCR System, see: *Applied Biosystems™ 7500/7500 Fast Real-Time PCR Systems System Maintenance* (Pub. No. 4387777).

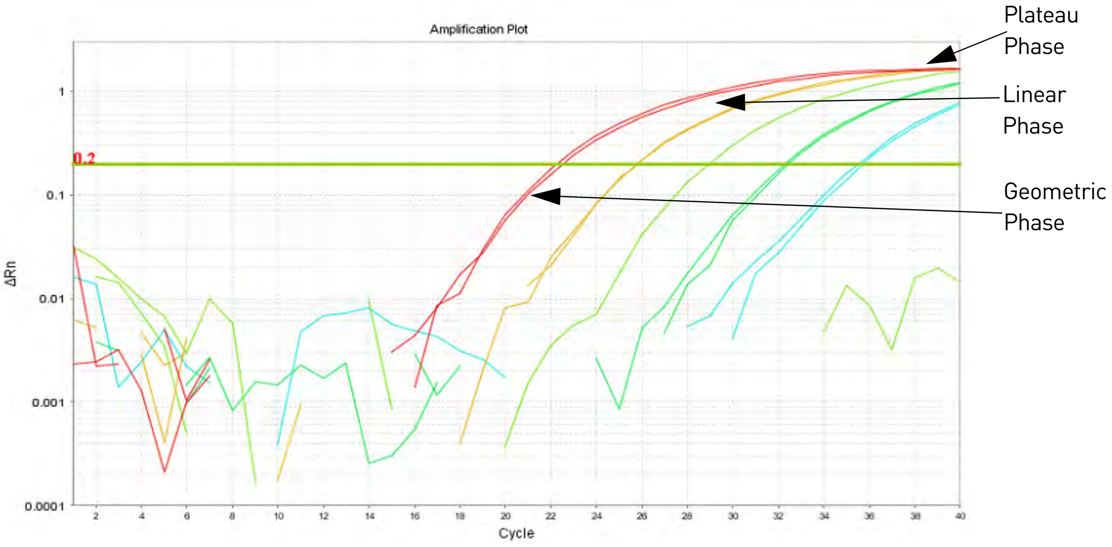
Real-time data analysis

The 7500 Real-Time PCR instrument can be used to determine the relative quantity of a target nucleic acid sequence in a sample by analyzing the cycle-to-cycle change in fluorescent signal as a result of amplification (Figure 43).

Amplification plot example

When using TaqMan® probes with the 7500 Real-Time PCR instrument, the fluorescence signal (or normalized reporter, R_n) increases as the amount of specific amplified product increases. Figure 43 shows the amplification of PCR product in a plot of R_n vs. cycle number during PCR. This amplification plot contains three distinct phases that characterize the progression of the PCR.

Figure 43 Phases of PCR amplification



Phases of amplification

Phase 1: Geometric (exponential)

Upon detection, the signal increases in direct proportion to the increase of PCR product. As PCR product continues to increase, the ratio of Taq DNA polymerase enzyme to PCR product decreases.

During the geometric phase, amplification is characterized by a high and constant efficiency. Amplification occurs between the first detectable rise in fluorescence and the beginning of the linear phase. During the geometric phase, a plot of DNA concentration versus cycle number on a log scale should approximate a straight line with a slope. Typically, the real-time PCR system is sufficiently sensitive to detect at least 3 cycles in the geometric phase, assuming reasonably optimized PCR conditions.

Phase 2: Linear

During the linear phase, the slope of the amplification plot decreases steadily. At this point, one or more components of the PCR has decreased below a critical concentration, and the amplification efficiency begins to decrease. This phase is termed linear because amplification approximates an arithmetic progression, rather than a geometric increase. Because amplification efficiency is continually decreasing during the linear phase, the amplification curves exhibit low precision.

Phase 3: Plateau

The amplification plot achieves the plateau phase when the PCR stops, the R_n signal remains relatively constant, and the template concentration reaches a plateau at about 10–7 M (Martens and Naes, 1989).

Relationship of amplified PCR product to initial template concentration

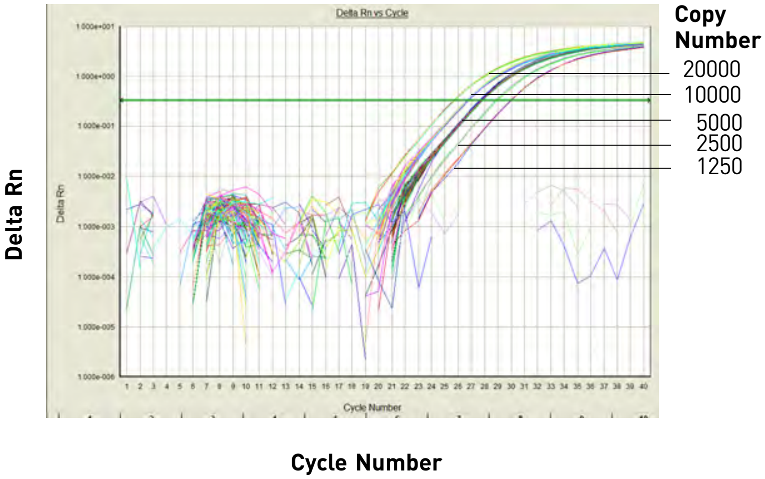
Because of the progressive cleavage of TaqMan® fluorescent probes during the PCR, as the concentration of amplified product increases in a sample, so does the R_n value. The following equation describes the relationship of amplified PCR product to initial template during the geometric phase:

$$N_c = N(1+E)^c$$

where N_c is the concentration of amplified product at any cycle, N is the initial concentration of target template, E is the efficiency of the system, and c is the cycle number.

For example, with the dilutions of RNase P target in the TaqMan® RNase P Instrument Verification Plate, the ratio of template concentration to detectable signal is preserved in the geometric phase for all dilutions (Figure 44). As the rate of amplification approaches a plateau, the amount of product is no longer proportional to the initial number of template copies.

Figure 44 Amplification plot from a real-time run of an RNase P Instrument Verification Plate



About the threshold

The HID Real-Time PCR Analysis Software uses a threshold setting to define the level of detectable fluorescence. Based on the number of cycles required to reach the threshold, the software can compare test samples quantitatively: A sample with a higher starting template copy number reaches the threshold earlier than a sample with a lower starting template copy number.

About the threshold cycle

The threshold cycle (C_T) for a specified amplification plot occurs when the fluorescent signal increases beyond the value of the threshold setting. The C_T value depends on:

- Starting template copy number
- Efficiency of DNA amplification by the PCR system

How C_T values are determined

To determine the C_T value, the HID Real-Time PCR Analysis Software uses the R_n values collected from a predefined range of PCR cycles called the baseline (the default baseline occurs between cycles 3 and 15 on the 7500 Real-Time PCR instrument):

1. The software generates a baseline-subtracted amplification plot of ΔR_n versus cycle number.
2. An algorithm defines the cycle where the ΔR_n value crosses the threshold setting as the threshold cycle (C_T).

Relationship of threshold cycles to initial template amount

The following equation describes the exponential amplification of the PCR:

$$X_n = X_m(1 + E_X)^{n-m}$$

where:

X_n = number of target molecules at cycle n (so that n > m)

X_m = number of target molecules at cycle m

E_X = efficiency of target amplification (between 0 and 1)

n – m = number of cycles elapsed between cycle m and cycle n

Our amplicons are designed and optimized to yield optimum amplification efficiencies. Therefore $E_X = 1$ so that:

$$\begin{aligned} X_n &= X_m(1+1)^{n-m} \\ &= X_m(2)^{n-m} \end{aligned}$$

To define the significance in amplified product of one thermal cycle, set n – m = 1 so that:

$$\begin{aligned} X_n &= X_m(2)^{1} \\ &= 2X_m \end{aligned}$$

Therefore, each cycle in the PCR reaction corresponds to a two-fold increase in product. Likewise, a difference in C_T values of 1 equates to a two-fold difference in initial template amount.

Calibrate the instrument

If you upgraded your instrument from:

Software Version	Perform
HID Real-Time PCR Analysis Software PCR v1.1	All calibration is carried over from 1.1. Perform Custom Dye calibration to calibrate ABY™, JUN™ and Mustang Purple™ (MP) dyes
SDS Software v1.2.3	Perform all calibrations and run the RNase P plate

Required materials

Table 25 lists the materials needed to perform the instrument calibration.

Table 25 User-supplied materials

Material	Cat. No.	Needed for calibration of upgrade from Software Version
7500 Real Time PCR Systems Spectral Calibration Kit I	4349180	SDS 1.2.3
TaqMan™ RNase P Instrument Verification Plate	4350584	SDS 1.2.3
96-Well Spectral Calibration Plate with ABY™ Dye	4461591	HID 1.1 and SDS 1.2.3
96-Well Spectral Calibration Plate with JUN™ Dye	4461593	
96-Well Spectral Calibration Plate with Mustang Purple™ Dye	4461599	

Calibration procedure

Below is an outline of the calibration procedure. Refer to *Applied Biosystems™ 7500/ 7500 Fast Real-Time PCR Systems System Maintenance* (Pub. No. 4387777) for complete instructions.

Perform:

- Regions of Interest (ROI) calibration
- Background Calibration
- Optical Calibration
- Dye Calibration of all system dyes and the new ABY™, JUN™ and Mustang Purple™ (MP) dyes
  - For the new dyes ABY™, JUN™ and Mustang Purple™, follow the custom dye procedure
  - Use 60°C as the default temperature
- RNase P Instrument Verification Plate run

New dye spectra

Figure 45 through Figure 47 show the calibration spectra for ABY™, JUN® and Mustang Purple™ (MP) dyes.

Figure 45 ABY™ dye spectra

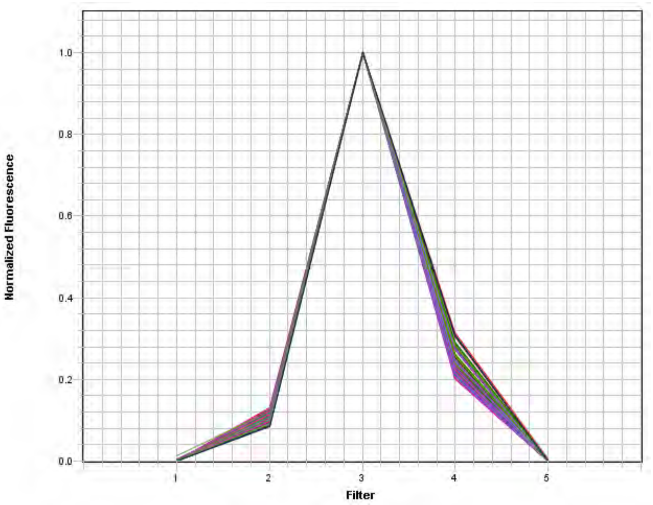


Figure 46 JUN™ dye spectra

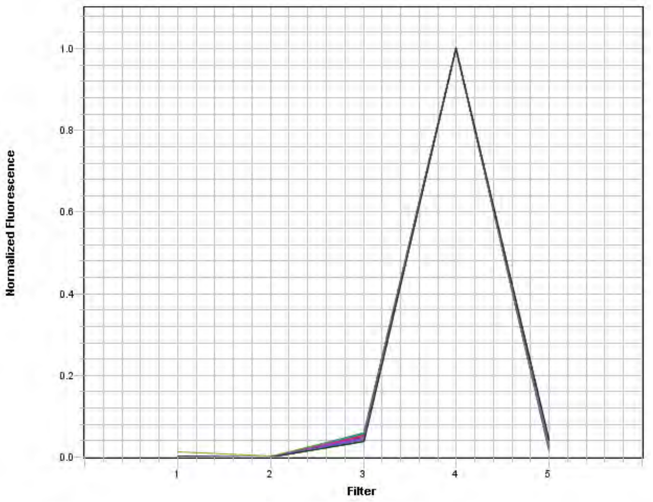
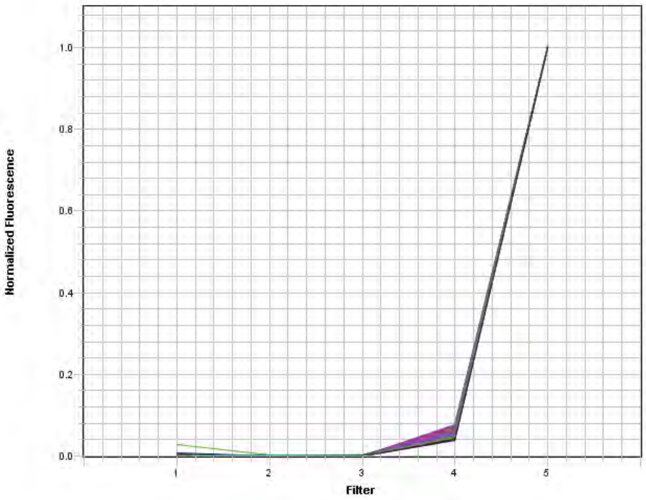


Figure 47 Mustang Purple™ (MP) dye spectra



C

Degraded sample studies: GlobalFiler™ STR kit and HID-Ion AmpliSeq™ Identity and Ancestry Panel

This section provides examples of degraded samples with lower Degradation Indices as determined by the HID Real-Time PCR Software that yield incomplete STR profiles. It compares the results and Degradation Indices for sample data generated using the GlobalFiler™ STR kit by capillary electrophoresis (CE) with data obtained with the HID-Ion AmpliSeq™ Identity Panel on the Ion Personal Genome Machine™ System (PGM™). It also shows examples of the additional information provided by the HID-Ion AmpliSeq™ Identity and Ancestry Panel that complement CE STR results.

After performing internal validation studies to correlate Degradation Index with incomplete profile generation by STR, you may choose to analyze degraded samples with Degradation Indices below your laboratory-determined threshold with HID-Ion AmpliSeq™ Identity and Ancestry Panels.

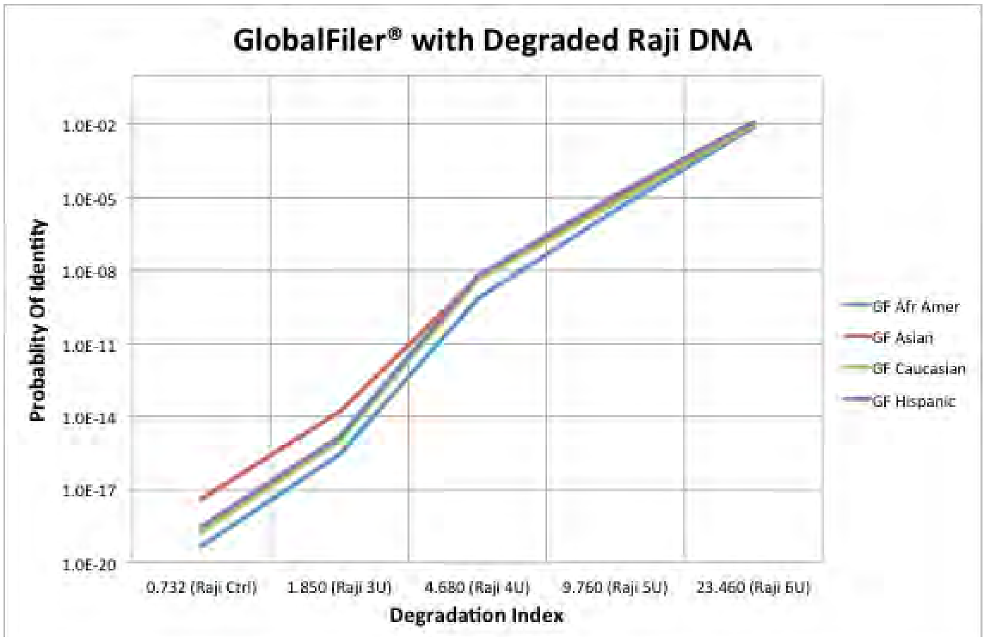
Data in this section was produced using products that have been internally tested but that have not been validated under SWGDAM guidelines. Perform internal validation studies to determine the appropriate procedures for your laboratory.

Probability of Identity in STR analysis of degraded samples

"Quantification and STR results" on page 75 includes a study that shows the relationship between degradation index and the number of alleles identified.

Figure 48 illustrates the relationship between degradation index and the Probability of Identity (PI) derived from the alleles identified in an artificially degraded Raji DNA sample (quantified with the Quantifiler™ Trio DNA Quantification Kit and analyzed with the GlobalFiler™ PCR Amplification Kit; PI values obtained from GlobalFiler™ PCR Amplification Kit (Pub. No. 4477604 Rev. C).

Figure 48 Probability of Identity vs degradation index in STR analysis of one sample; results may differ with more samples



As the degradation index increases, the number of alleles identified decreases and may yield incomplete profiles.

Probability of Identity in HID-Ion AmpliSeq™ Identity Panel analysis (autosomal SNPs) of degraded samples

The HID-Ion AmpliSeq™ Identity and Ancestry Panel is a high multiplex system consisting of 90 Autosomal and 34 upper Y-Clade SNPs chosen by Dr. Kenneth Kidd from Yale University and the SNPforID Consortium[1], [2], [3]. This panel provides probabilities from 1×10^{-31} to 6×10^{-35}.

Figure 49 shows the correlation of the Probability of Identity (PI) obtained with STR analysis and the PI of the same artificially degraded Raji DNA sample (quantified with the Quantifiler™ Trio DNA Quantification Kit and analyzed with the HID-Ion AmpliSeq™ Identity Panel; PI values obtained from 1000 Genomes http://www.1000genomes.org/) obtained with HID-Ion AmpliSeq™ Identity Panel analysis.

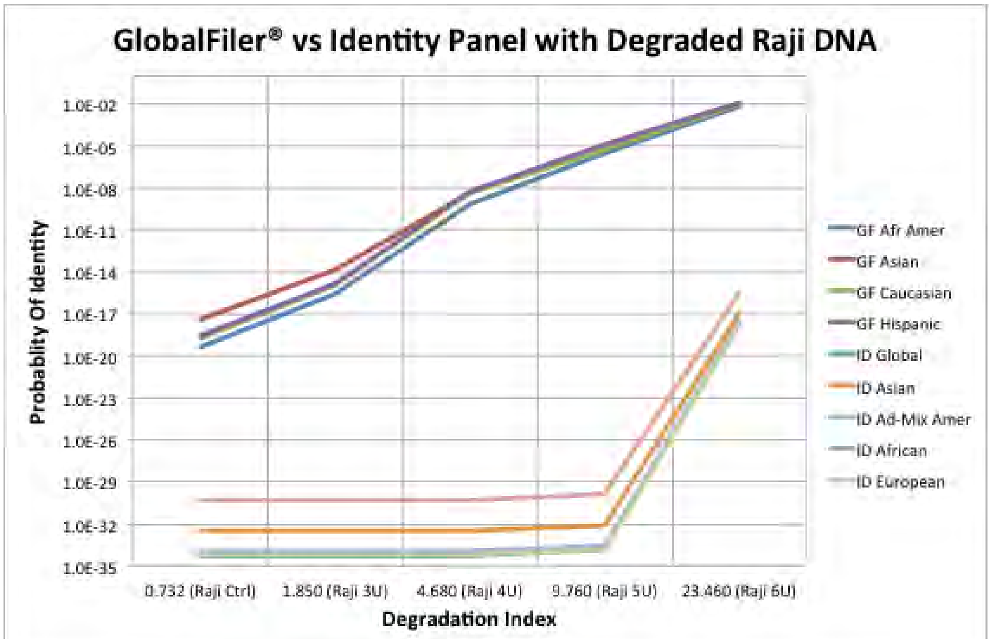
---

[1] Pakstis, A. J., Speed, W. C., Fang, R., Hyland, F. C., Furtado, M. R., Kidd, J. R., & Kidd, K. K. (2010). SNPs for a universal individual identification panel. Human Genetics, 127(3), 315-324.

[2] Phillips, C., Fang, R., Ballard, D., Fondevila, M., Harrison, C., Hyland, F., et al. (2007). Evaluation of the Genplex SNP typing system and a 49plex forensic marker panel. Forensic Science International: Genetics, 1(2), 180-185.

[3] Karafet, T. M., Mendez, F. L., Meilerman, M. B., Underhill, P. A., Zegura, S. L., & Hammer, M. F. (2008). New binary polymorphisms reshape and increase resolution of the human Y chromosomal haplogroup tree. Genome Research, 18(5), 830-838.

Figure 49 Probability of Identity vs degradation index in HID-Ion AmpliSeq™ Identity Panel; results may differ depending on sample type and integrity



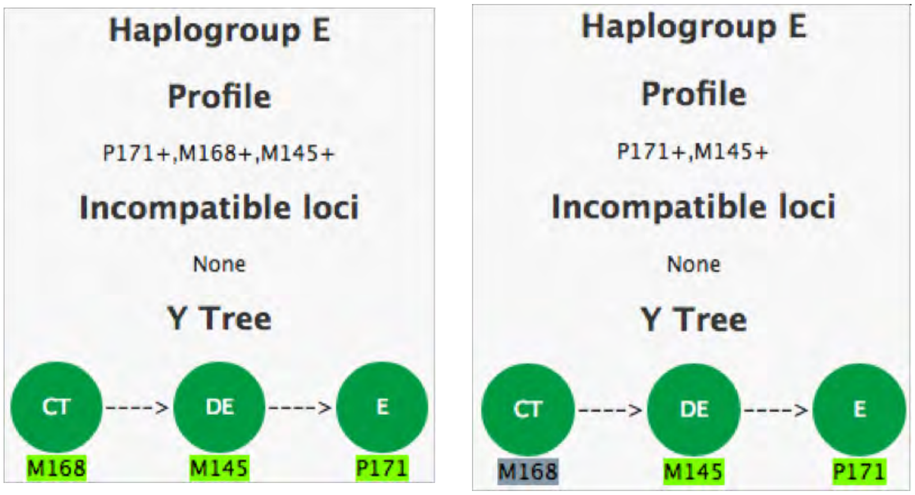
Additional Y SNP and ancestry information provided by HID-Ion AmpliSeq™ Identity and Ancestry Panel analysis

Y haplo type information

Figure 50 shows Y haplogroup results for the same degraded Raji DNA.

Results shown are for example purposes. Results will vary depending on sample.

Figure 50 Y haplogroup of Raji DNA 0 U no degradation (left) and 6 U degradation (right)


Haplogroup E

Profile

P171+,M168+,M145+

Incompatible loci

None

Y Tree

Haplogroup E

Profile

P171+,M145+

Incompatible loci

None

Y Tree

Ancestry information

The HID-Ion AmpliSeq™ Ancestry Panel includes 165 autosomal markers chosen by Dr. Kenneth Kidd from Yale University[1] and Michael Seldin from University of California, Davis[2]. The panel provides additional information useful in analyzing degraded samples.

Figure 51 and Figure 52 show the similarity of the ancestral profiles of the samples used to perform the degradation index studies described in Table 20 on page 75.

Note: Because of the sensitivity and configuration of the panel (no redundant SNPs), the degradation of any critical SNPs may generate a Low Confidence result, even though the ancestry results are similar.

Figure 51 Biogeographical Ancestry of PB001 Ctrl

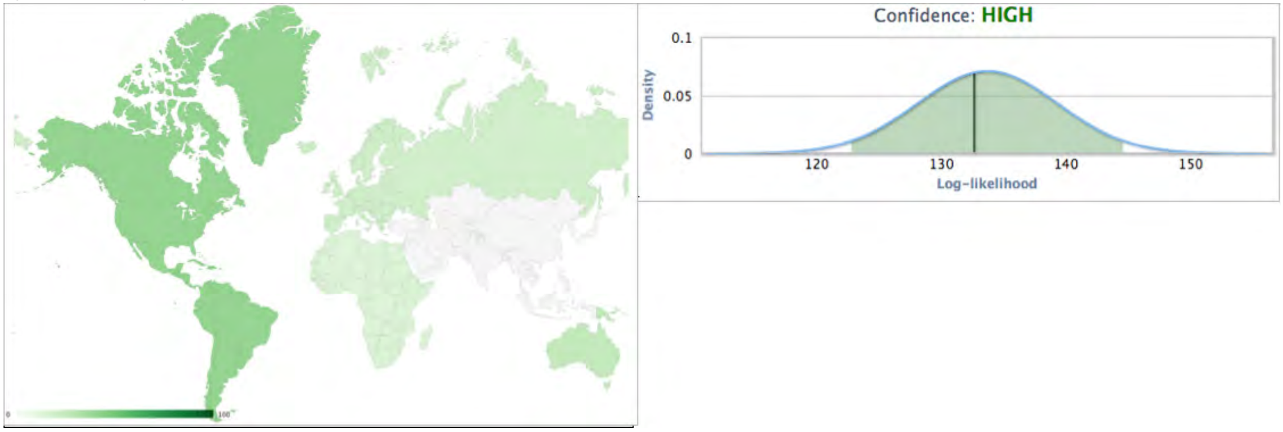
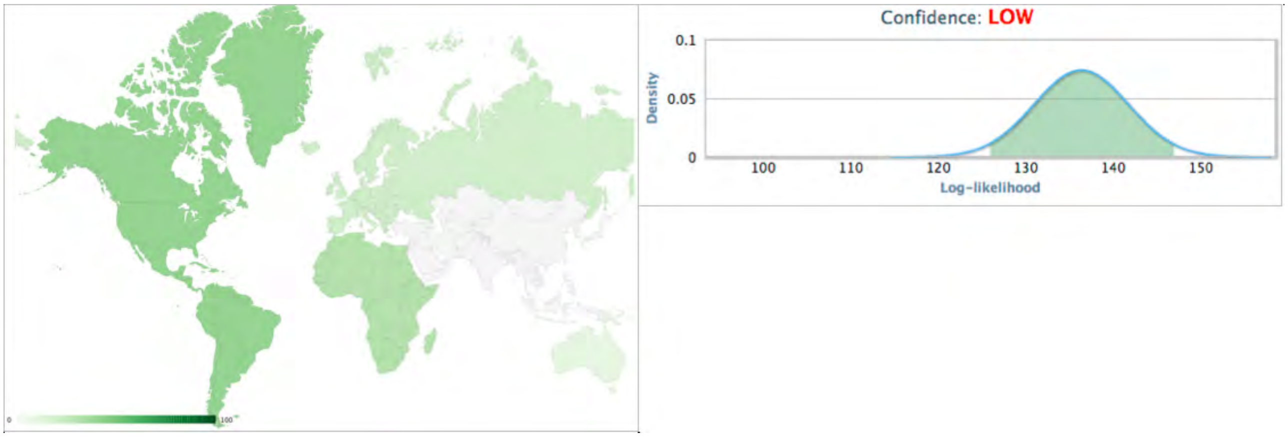


Figure 52 Biogeographical Ancestry of PB001 High



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1 Kidd et. al. Poster: Better SNPs for Better Forensics: Ancestry, Phenotype, and Family Identification. Shown at National Institute of Justice annual meeting, Arlington VA, June 2012.

2 Kosoy R, Nassir R, Tian C, et al. (2009) Ancestry informative marker sets for determining continental origin and admixture proportions in common populations in America. Hum Mutat 30(1) 69-78.

Documentation and support

Related documentation

Document title	Pub. No.
Applied Biosystems™ *7500/7500 Fast Real-Time PCR Systems System Maintenance*	4387777
7300/7500/7500 Fast Real-Time PCR System Absolute Quantification Getting Started Guide	4378658
HID Real-Time PCR Analysis Software v1.2 Getting Started Guide	MAN0009819
Quantifiler™ HP DNA Quantification Kit Product Insert	4485355
Quantifiler™ Trio DNA Quantification Kit Product Insert	4485357

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- **Outside North America –** Contact your local support office.

For the latest services and support information for all locations, go to:

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- Search through frequently asked questions (FAQs)
- Submit a question directly to Technical Support
- Search for user documents, SDSs, vector maps and sequences, application notes, formulations, handbooks, certificates of analysis, citations, and other product support documents
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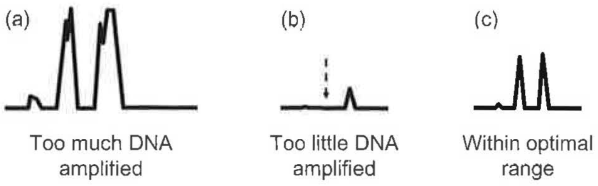

FIGURE 3.1 Illustration of STR typing results at a single heterozygous locus for a single source sample with (a) too much DNA template showing off-scale, split peaks, (b) too little DNA template where the arrow points to allele dropout due to stochastic effects, or (c) just the right amount so that two allele peaks are balanced and on-scale.

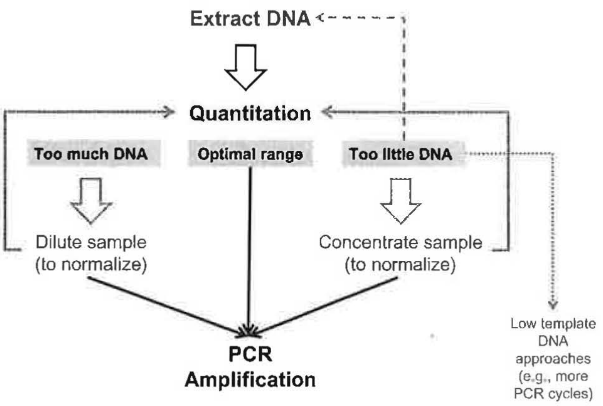
Extract DNA
Quantitation
Too much DNA
Optimal range
Too little DNA
Dilute sample (to normalize)
Concentrate sample (to normalize)
PCR Amplification
Low template DNA approaches (e.g., more PCR cycles)

FIGURE 3.2 Flow chart illustrating role of DNA quantitation following DNA extraction. If the sample contains a DNA quantity within the optimal range, then an analyst would proceed with PCR amplification. With too much DNA, a sample could be diluted and either re-checked for DNA quantity or sent directly to the PCR amplification step. When DNA results below the optimal range are observed, the sample could be concentrated, re-extracted or treated with low template DNA approaches depending on laboratory policy and amount of available sample.

If the amount of DNA in a sample is outside of the target range for creating a "just right" DNA profile, then the DNA amount must be adjusted prior to putting it into the PCR reaction. The process of achieving a DNA concentration that fits the optimal window for analysis is called *normalization*. This involves diluting the sample down to the desired range or concentrating it by removing excess fluid. Figure 3.2 illustrates that if too little DNA is detected during the quantitation step then re-extraction or increased PCR cycles (provided the laboratory has a validated protocol, see Chapter 11) may be attempted.

Evaluation of human DNA quantity in a sample can be used to screen for samples that should be sent forward through the DNA testing process. When having to wade through a large number of samples, a sample screening process based on the amount of human DNA present can be very helpful and cost-effective. DNA quantitation that is performed well can save time during the data review process as data signal will be on-scale. By not having to repeat the testing process for an off-scale DNA result, the often-limited biological evidence will not have to be further consumed to try and obtain a better quality result.

TABLE 3.1 Quality Assessments Possible with Appropriate Quantitative PCR (qPCR) Assays.

Quality Assessment	How Assessed	Possible PCR Solutions
PCR inhibitor	IPC cycle threshold	PCR kit with improved buffer (Ch. 5)
Male-to-total DNA ratio is low	Dual Y and human qPCR	Y-STRs (Ch. 13)
Very low human genomic DNA	Multi-copy probe target can help; mtDNA can help	Increased cycles (Ch. 11); mtDNA (Ch. 14)
Degraded DNA	Different size qPCR targets	miniSTRs (Ch. 10); mtDNA (Ch. 14)
Non-human DNA	Species test (e.g., cyt b)	Use appropriate non-human DNA primers (Ch. 16)

In addition, DNA quantitation can serve as a gateway to potential DNA testing options. For example, if an assay can assess the relative levels of total genomic DNA compared to male DNA, then depending on the DNA quantitation results either autosomal STRs or Y-STRs may be attempted as a the first course of action with the evidentiary sample (Table 3.1).

DNA Quantities Used

PCR amplification is dependent on the quantity of template DNA molecules added to the reaction. Based on the amount of DNA determined to be in a sample with a quantitation method, the extracted DNA for each sample is adjusted to a level that will work optimally in the PCR amplification reaction. As mentioned above, commercial STR typing kits work best with an input DNA template of around 1 ng.

A quantity of 1 ng of human genomic DNA corresponds to approximately 303 copies of each locus that will be amplified (D.N.A. Box 3.1). There are approximately 6 pg (one millionth of one millionth of a gram or 10^{-12} grams) of genomic DNA in each cell containing a single diploid copy of the human genome. Thus, a range of typical DNA quantities from 0.1 ng to 25 ng would involve approximately 30 to 8330 copies of every nuclear DNA sequence to be examined.

Attempts to correlate the measured DNA quantity to PCR performance are complicated by the fact that target regions for the qPCR and STR assays are not the same. As more human genomes are being sequenced, we are learning that the differences between people can be greater than previously thought (e.g., copy number variation for large chromosomal regions).

DNA QUANTITATION METHODS

A number of DNA quantitation tests have been used over the years to estimate the amount of total DNA or human DNA present in a sample (Nicklas & Buel 2003, Barbisin & Shewale 2010). These DNA quantitation tests, which will be discussed briefly below, include UV absorbance, yield gels, slot blot, PicoGreen, end-point PCR, and real-time quantitative PCR. Early assays were "home-brew" (i.e., prepared by the laboratory performing the test)

D.N.A. BOX 3.1

CALCULATION OF DNA QUANTITIES IN GENOMIC DNA

1. Relative molecular mass of a DNA base pair = 618 g/mol
   A = 313 g/mol; T = 304 g/mol; A-T base pairs = 617 g/mol
   G = 329 g/mol; C = 289 g/mol; G-C base pairs = 618 g/mol
2. Relative molecular mass of DNA = 1.98×10^{12} g/mol
   There are 3.2 billion base pairs in a haploid cell ($\approx 3.2 \times 10^9$ bp).
   ($\approx 3.2 \times 10^9$ bp) × (618 g/mol/bp) = 1.98×10^{12} g/mol
3. Quantity of DNA in a haploid cell = 3 picograms
   1 mole = 6.02×10^{23} molecules
   (1.98×10^{12} g/mol) × (1 mole/6.02×10^{23} molecules)
   $= 3.3 \times 10^{-12}$ g = 3.3 picograms (pg)
   A diploid human cell contains ≈6.6 pg genomic DNA.
4. One ng of human DNA comes from ≈152 diploid cells.
   1 ng genomic DNA (1000 pg)/6.6 pg/cell = ≈303 copies of each locus
   (2 per 152 diploid genomes)

while most forensic DNA quantitation is now performed using commercial kits from suppliers like Applied Biosystems or Promega Corporation.

UV Absorbance and Yield Gels

Early methods for DNA quantitation typically involved either measurement of absorbance at a wavelength of 260 nm or fluorescence after staining a yield gel with ethidium bromide. Unfortunately, because these approaches are not very sensitive, they consume valuable and often irreplaceable forensic specimens. In addition, absorbance measurements are not specific for DNA, and contaminating proteins or phenol left over from the extraction procedure can give falsely high signals. To overcome these problems, several methods have been developed for DNA quantitation purposes. These include the slot blot procedure and fluorescence-based microtiter plate assays as well as so-called "real-time" or "quantitative PCR" approaches.

Slot Blot

The most commonly used method in forensic labs during the late 1990s and beginning years of the twenty-first century for genomic DNA quantitation was the so-called "slot blot" procedure. This test was specific for human and other primate DNA due to a 40 base pair probe that bound to a region on chromosome 17 called D17Z1. The slot blot assay was

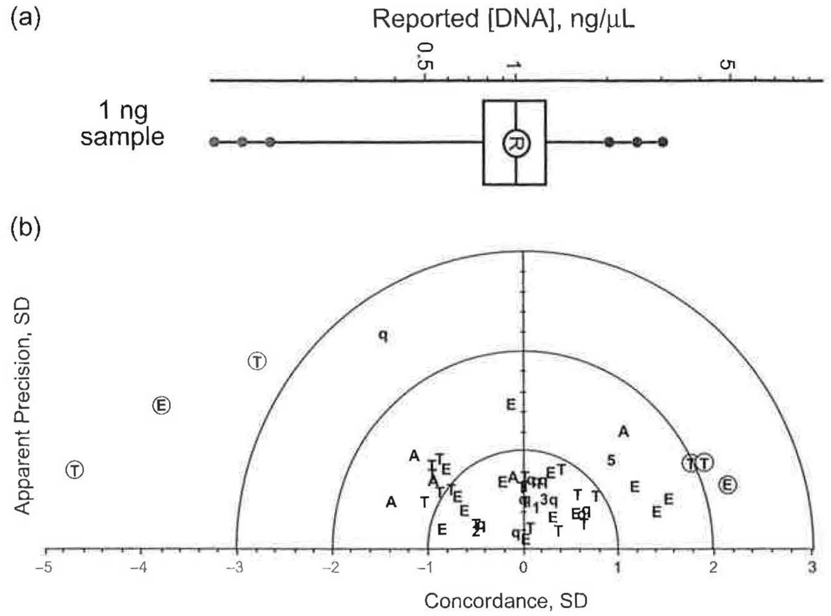

FIGURE 3.6 (a) Range of DNA concentrations reported for a 1 ng DNA sample supplied to 74 laboratories in an interlaboratory study (Kline et al. 2003). Overall the median value was very close to the expected 1 ng level with 50% falling in the boxed region. However, laboratories returned values ranging from 0.1 ng to 3 ng. (b) A target plot examining concordance and apparent precision for the various laboratory methods used. Legend: A = ACES kit; q = Quantiblot with unreported visualization method; E = Quantiblot with chemiluminescent detection; T = Quantiblot with colorimetric detection; 1, 2, 3, 4, and 5 represent methods used by only one lab.

this degree of imprecision may seem large, recall that a factor of two corresponds to one exponential-phase PCR amplification cycle; quantitation results are usually sufficiently valid to estimate DNA template amounts that will enable optimal PCR amplification.

In the NIST Quantitation Study 2004 (QS04), a total of 60 data sets from 287 submitted involved qPCR (Kline et al. 2005). Of the 60 qPCR data sets, 37 came from Quantifiler (Figure 3.7). Overall the Quantifiler assay performed well with the median value from participants coming close to the expected value (center of the target plot in Figure 3.7). However, outliers did exist emphasizing the need for care in pipetting and conducting qPCR assays.

Correlation of DNA Quantity and STR Amplification

In spite of the sensitivity of qPCR, some studies have shown that STR typing results can be obtained even when a "zero" quantitative value is observed (Cupples et al. 2009). Stochastic variation with low amounts of DNA is the reason for such observations (see Chapter 4). While there is DNA present in such samples, the qPCR result is very low or zero due to the PCR primers failing to find sufficient target to amplify. How then can qPCR

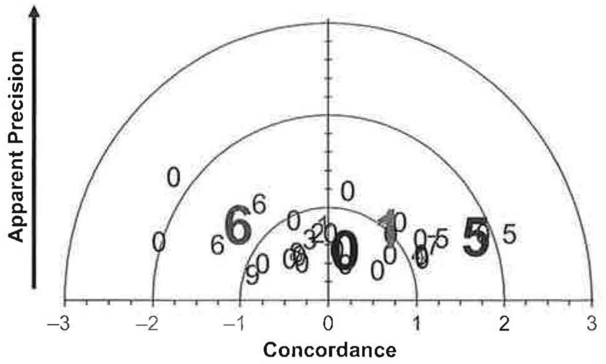

FIGURE 3.7 Target plot comparing interlaboratory results from 60 data sets involving 8 different samples using 10 different qPCR methods (Kline et al. 2005). Larger characters in bold font represent the median performance for all results submitted for a particular method. Note that specific methods may exhibit a bias relative to other assays. 0 = Quantifiler, which represented 37 of the 60 data sets (see Table 1 in Kline et al. 2005 for full description of qPCR assay codes).

results be an appropriate gatekeeper about whether or not a DNA sample should be processed further?

It is important that several things be kept in mind. First, just as with STR typing results from low amounts of DNA, stochastic variation can limit the reliability of qPCR results due to allele dropout. And, as with low template DNA testing (see Chapter 11), replicate qPCR testing is a possible solution to strengthen confidence in the result (D.N.A. Box 3.3).

Second, remember that there are different volumes of input DNA being used. Many qPCR assays require 2 µL of input DNA while STR typing PCR reactions can take 10 µL or more of input DNA. Thus, because five times as much DNA extraction volume can be included in the STR amplification reaction, more input DNA can be included giving rise to a result when the qPCR value was "zero."

Third, the PCR buffers between the qPCR and STR reactions may be different. If the STR amplification buffer contains a different polymerase or materials to enable overcoming PCR inhibition, then results may not be equivalent and the qPCR assay may not provide a true measure of STR typing performance. Furthermore, the different input volumes going into the qPCR versus STR amplification reactions could lead to different concentrations for PCR inhibitors coming from casework samples so that the qPCR or STR amplifications fail at a different rate.

Fourth, pipetting accuracy may be a factor. Pipetting 2 µL is generally less accurate than is pipetting 10 µL. A mis-pipetting of the DNA sample going into the qPCR assay could make a result appear lower than it really is. Reduction of volume to save money with qPCR assays (Westring et al. 2007) could exacerbate pipetting accuracy issues as well as effectively concentrate PCR inhibitors.

Finally, it is important that the qPCR result is appropriately correlated with STR typing performance. Internal validation (see Chapter 7) is crucial in developing appropriate interpretation of results. Variation in different lots of qPCR kit calibrants have led to problems in

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How a murder and a bombing cleaned up DNA profiling

BY **ANDY EXTANCE** | 18 JULY 2022

The UK pioneered a forensic process to identify suspects from tiny amounts of DNA, but occasional flaws had big consequences. Andy Extance pieces together the whole story for the first time

In 2002, 10 years after the notorious unsolved murder of Rachel Nickell, Andrew McDonald entered a small briefing room in Abingdon, UK. There, in the offices of Forensic Alliance, Metropolitan Police Detective Chief Inspector Richard Brooks shared details about how the 23-year-old was killed while walking with her two-year-old son and dog on Wimbledon Common in London on July 15, 1992. She was sexually assaulted and died with 49 stab wounds.

After Brooks had spoken, a reporting scientist from the UK Forensic Science Service (FSS) London laboratory handed a file to McDonald, DNA lead at Cellmark Forensic Services in Abingdon. ‘I distinctly remember him saying “Good luck, you won’t find anything”,’ McDonald tells *Chemistry World*.

McDonald was part of a Forensic Alliance team assembled by company founder Angela Gallop

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When we got the results back, we had an indication of something at a much lower level from another individual

McDonald was looking at results from a DNA profiling method known as a low copy number (LCN) test. The FSS had started devising LCN testing in 1998 to deal with cases where there was very little DNA material available, then applied it to the Nickell case. DNA profiling relies on the polymerase chain reaction (PCR) method, best known to the public today for helping detect Covid-19. PCR copies DNA in forensic samples, boosting it to measurable levels. LCN tests push this amplification to its limits, and McDonald had seen that this sometimes stopped the test from working properly.

In the test sample which returned no result, there was much more material than expected. The FSS scientists had not realised this because, to avoid using more than needed, the FSS scientists had not measured the quantity. With so much sample, it was far likelier to contain substances that could inhibit the polymerase enzyme central to the PCR method and stop it working.

McDonald re-ran the same test at Cellmark, but using a smaller sample, thinking nothing would happen. 'When we got the results back, we had now a really strong profile matching Rachel Nickell – with an indication of something at a much lower level from another individual, possibly a male individual,' McDonald says.

That finding was pivotal for the Rachel Nickell case and for DNA profiling in general. The FSS reported potential issues, after which the UK's forensic science regulator commissioned a review

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genetic material. Such methods start by extracting DNA from an evidence sample, explains John Butler, research scientist and DNA forensics expert at the National Institute of Standards and Technology (NIST) in Maryland, US. That might involve washing the sample in solvents like phenol, chloroform, or methanol, though in the 1990s UK forensic scientists often extracted DNA with a resin called Chelex 100. After extraction, scientists use many rounds of PCR to amplify DNA at very specific locations, known as short tandem repeat markers, or STRs, Butler adds.

STRs are hyper-variable sequences in our genomes ‘that differentiate you and me, and we believe just about everybody we’ve ever sampled’, explains Adrian Linacre, from Flinders University in Adelaide, Australia. ‘Every one of your cells has essentially the same DNA profile. The regions we look at have no effect on what you look like. They are non-coding bits of DNA that happen to show a repetitive nature that have a four base pair repeat, something like AATG, AATG, AATG. And that repetitive nature is very useful for us.’

There are half a million repeated sequences, Linacre adds, but most of them just repeat two bases. The very first DNA profiling techniques used just four locations with four-base STRs, with LCN originally looking at 10 STR locations. ‘The more [locations] we look at the less likely it is that two people by chance will share that DNA,’ says Linacre.

Using primer molecules PCR can target these locations, with each PCR cycle doubling the amount of STR DNA. The most-used DNA profiling method in the UK in the early 2000s, called SGM Plus, used 28–30 cycles of PCR doubling. Scientists can then separate STRs by electrophoresis, labelling each with coloured fluorescent molecules. An automated analyser can then record the intensity of fluorescence, showing each STR as a peak on a software plot.

It becomes so sensitive that it will actually detect a single copy of DNA

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calculating the chance that they originated from the same individual.

Building on such techniques, an FSS team led by Peter Gill published its first paper on the LCN technique in 2000. Previously, the lower limit on the amount of DNA it was possible to profile with had been around 250 picograms. The FSS team showed that LCN could identify people using less than 100pg of DNA, by amplifying it with 34 PCR cycles. ‘It becomes so sensitive that it will actually detect a single copy of DNA,’ says Gill, who now leads the forensic genetics research group at Oslo University Hospital in Norway.

Getting the suspect on tape

From 2003 onwards, McDonald, Gallop and their colleagues gradually worked on the evidence from the Rachel Nickell case. But after discovering the important clue of male DNA in the original extract, they were running out of material. So, they revisited other forensic evidence, specifically ‘tapings’ from around Rachel Nickell’s vagina. Examiners had attached sticky tape, removed it again to collect debris, and stored it so the sticky side was protected, McDonald recalls. He and his colleagues were then able to swab the tape again, extracting enough DNA to repeat their earlier feat with standard SGM Plus 28-cycle profiling. They found Nickell’s DNA and around five STR sequences that didn’t match her, but this was not enough to identify a suspect.

Comparing the 12 STR sequences against the police’s ‘persons of interest’ list gave only one match

To improve on this, McDonald did trial experiments on other samples, changing the electrophoresis technique to make it 10 times more sensitive. Purifying the post-PCR mixture to remove unwanted salts and enzymes gave a total 15-fold increase in peak height. Applying this to the product of PCR from Nickell’s body taping using a profiling technique covering more STR locations identified 12 sequences from a different person. ‘That gave us enough to make a

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DNA.

That prompted the team to look for more evidence among Napper's possessions linking him to the Nickell murder, Gallop says. 'One of the shoes that Robert Napper had could have left the footwear mark at the scene,' she notes. 'The paint flakes that we found in the hair combings from Rachel's son could have come from the toolbox that he kept his tools in.' Gallop also reveals that near the start of the investigation, a key member of her team reported to the police similarities with the Green Chain rapes. This series of 70 brutal attacks in London ended the same year that Napper went into Broadmoor, and he admitted to some of them in 1995.

LCN on trial

Together the evidence was overwhelming, convincing the police to charge Napper, who changed his plea from not guilty to guilty during the trial. In December 2008, he was convicted of Nickell's manslaughter and sentenced to indefinite incarceration in Broadmoor. Yet the fact that LCN had missed Napper's DNA in the first place was worrying. 'We had demonstrated that there was a flaw with the FSS LCN technique as it was being employed at the time,' McDonald explains. 'Not quantifying the sample was missing potentially critical results. Alarm bells were ringing for good reason in the criminal justice system.'

In 2006 the FSS told the police and Home Office that LCN could 'fail to identify a DNA profile from genetic material in a sample that should reveal a profile or mixture of profiles'. That helped spur the Home Office to appoint a forensic regulator to oversee forensic provision in England and Wales, recalls Linacre. The first regulator commissioned a review into the LCN technique led by Brian Caddy from the University of Strathclyde, where Linacre also worked at the time. Caddy himself was not a forensic geneticist, so he recruited Linacre, who had previously used LCN in criminal case work and Graham Taylor, head of genomic services at Cancer Research UK.

In late 2006 and early 2007 the FSS also started a secret 'backtracking operation' for samples that had produced no result, known as Operation Cube. Huw Turk, currently scientific lead at Cellmark, was one of three FSS scientists that went through the affected LCN tests, reported as over 5000 samples affecting 2180 cases by the *Evening Standard*. 'We went back to those samples, and re-

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The trial for someone accused of the 1998 Omagh bombing also put low copy number DNA testing in the dock

Then, in December 2007, LCN issues entered headline news stories. Sean Hoey was being tried on 58 charges including the murders of 29 people in the 1998 Omagh bombing in Northern Ireland. The trial was conducted by a judge sitting in the case without a jury, due to fears that paramilitary organisations might intimidate jurors. Forensic scientists working on the case used LCN to produce a profile of Hoey, making the method a focus for the defence team. The judge, Mr Justice Weir, had therefore called the technique’s inventor, Peter Gill, to give evidence in Belfast crown court in January 2007. ‘It was the worst experience I’ve ever had,’ Gill recalls.

It might have been enough that the defence in the case put up a scientist of whom a judge in a different case wrote, ‘it is impossible to understand how [the defence expert] had sufficient expertise to be able to give evidence’. Yet the judge also questioned Gill proactively and

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as allelic drop-out. It arises because, with so little starting DNA, the two copies of an allele might not be amplified equally. The primer DNA strands used to tell the polymerase enzyme which sequences to amplify might not bind their target. If the primer doesn't bind at one STR location, it would look like the person from whom a DNA sample originates received the same genotype from both parents. In this case, one of their alleles has dropped out.

Source: © 2012 Elsevier Inc

With very low amounts of DNA, allele drop-out (where one copy of an allele is not amplified) or drop-in (an extra allele appears from contamination) can occur

'If an allele disappears, it obviously reduces the strength of the evidence, and you have to factor

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honest and said 'It's not reproducible'. And immediately the judge did not like that type of concept.'

The evidence wasn't being collected in the way that it should have been

'That's probably the part where he started shouting at me,' Gill says. 'We don't deal with the definitive. In fact, no scientist does. But the judge did not understand that. He wanted definitive answers.'

Another issue in the Omagh bombing case was better founded, because the technique is so sensitive it easily picks up contamination. That could be one or two extra alleles from highly degraded DNA from dust, for example, known as allelic drop-in. Or it might be contamination with multiple alleles from an uninvolved person. With LCN only just beginning to be developed when the Omagh bombing happened, the forensic scientists and police involved hadn't considered this. They had stored evidence together in bags with holes in. 'I remember being asked, "Is it possible that DNA can go from one item of evidence to another?",' Gill says. 'To which my answer was yes. The evidence wasn't being collected in the way that it should have been.'

So, in his final December 2007 verdict, Mr Justice Weir ultimately cleared Hoey of all charges and said that he was not satisfied that the LCN method was well enough validated. Shortly following that judgment, the police suspended use of the LCN method, pending results of the Caddy review.

After four months of interviews, in April 2008, Caddy, Linacre and Taylor made 21 recommendations on the use of LCN in forensics. The headline conclusion was that it was a safe method to use. 'In cases where you could not otherwise generate a DNA profile using 28 cycles under current technology, but you could under 34 cycles, then the process is fit for purpose and should go ahead,' is Linacre's summary.

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recommendation focussed on minimising contamination, including a national standard for 'DNA clean' crime scene recovery kits, and sterile consumables in forensic labs.

Gallop highlights that such problems went beyond the UK. In Germany, DNA profiling consistently identified the same woman as a suspect in cases nationwide, who turned out to be a worker in a factory making cotton swabs. In general, Gallop adds, the Caddy review 'really was very helpful' in stressing the need for proper forensics training for people working on cases and for test validation and standardisation.

For Turk, the most important lesson concerning inhibition in the Nickell case was the need to quantify the DNA. 'From that point onwards, we would have a much better idea if there was any DNA present [and] if it was at risk of inhibition,' he explains.

> ***A laboratory won't spend a lot of time trying to work out why a sample hasn't worked***

Technology has also progressed rapidly since the Caddy review to mitigate other problems with profiling low amounts of DNA, adds NIST's Butler. 'The biggest change has been the development of probabilistic genotyping software to assign the chances of there being allele drop-out or allele drop-in information,' he says.

In Oslo, Gill continues to work in this area, developing software packages to help implement mathematical concepts he has introduced. He warns that inhibition is always possible, however, and still happens. He also notes that people still don't always quantify their DNA samples because of how tests are funded, especially in Europe. Tests still might not work thanks to inhibition, but given their financial constraints, forensic scientists might not go back to look at why. 'A laboratory won't spend a lot of time trying to work out why a sample hasn't worked, unless it's a really important case,' he says.

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Andy Extance is a science writer based in Exeter, UK

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[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
710213215	TRUE	0.006	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.003	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution
[redacted]	TRUE	0.003	Auto		Submitted-results pending. QPS advised no further work required - results available
[redacted]	TRUE	0.002	Auto	FAIL	Submitted as cells, Presump saliva test pending presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.007	Auto		Submitted-results pending.
[redacted]	TRUE	0.003	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.003	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		ENVM - Complex mixed DNA profile
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Presump. PSA test positive, no sperm found
[redacted]					Two person mixed DNA profile
[redacted]					2 person mixed profile - conditioned on
[redacted]					2 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.008	Auto		Micro positive for sperm. Submitted-Results pending
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.007	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.008	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted for cells. Presumptive saliva test pending.
[redacted]	TRUE	0.009	Auto		Presump Saliva test negative
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending.
[redacted]	TRUE	0.003	Auto		Submitted-results pending.
[redacted]	TRUE	0.004	Auto		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.007	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.009	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.008	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.006	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.008	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]	TRUE	0.008	Auto		Mixture-low support for contrib or supports non contrib
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.009	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.009	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.007	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.007	Auto	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		Submitted-results pending. Two person mixed DNA profile
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	SUCCESS	Presump. PSA test positive, no sperm found SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD
[redacted]	TRUE	0.006	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.008	Auto	FAIL	Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix remaining - supports non contribution Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	TRUE	0.007	Auto		Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.004	Auto	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.003	Auto	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Submitted as cells Single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 2 person mix - supports non contribution
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto		Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.009	Auto	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted as cells, Presump saliva test pending presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion
[redacted]	TRUE	0.009	Auto		Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix - low support for contribution 3 person mixed DNA - inconclusive
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Two person mixed DNA profile
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	SUCCESS	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mixed DNA - inconclusive Excluded from mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution Excluded from mixed DNA profile
[redacted]	TRUE	0.006	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending.
[redacted]	TRUE	0.007	Auto		Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.009	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. Quality control failure - results not reportable
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

[redacted]	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 100 000 to 1 million 2 person mix - supports non contribution Single evidence sample excluded
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.007	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.007	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.009	Auto		
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.009	Auto		Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.008	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending.
[redacted]	TRUE	0.005	Auto		Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.009	Auto		Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.008	Auto		Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.005	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Three person mixed DNA profile No statistical interpretation performed Sample undergone further work - conditioned 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - low support for contrib Single evidence sample excluded
[redacted]	TRUE	0.006	Auto	FAIL	presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.007	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS
[redacted]	TRUE	0.008	Auto		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.006	Auto	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.009	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.007	Auto		Submitted as cells, Presump saliva test pending presump Saliva test positive Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	RUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto		Submitted-results pending. No DNA profile Possible sub-threshold information
[redacted]	RUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.009	Auto	FAIL	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 Person Mix Rem contrib unsuitable for NCIDD
[redacted]	RUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.007	Auto		Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	RUE	0.008	Auto		Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	RUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto		
[redacted]	RUE	0.003	Auto	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	RUE	0.002	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.006	Auto		
[redacted]	RUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.005	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.007	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.005	Auto		
[redacted]	RUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto		
[redacted]	RUE	0.002	Auto		
[redacted]	RUE	0.005	Auto		Submitted-results pending. Single Source DNA profile - assumed known contributor
[redacted]	RUE	0.003	Auto		
[redacted]	RUE	0.006	Auto		
[redacted]	RUE	0.005	Auto		
[redacted]	RUE	0.004	Auto		
[redacted]	RUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.005	Auto		
[redacted]	RUE	0.005	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.002	Auto		Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.006	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.002	Auto		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.008	Auto		Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem - support for contrib 1 billion -100 billion
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.005	Auto	FAIL	Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mix remaining DNA contribution unsuitable for NCIDD Cond mix rem-low supp for contrib or supp non contrib
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.005	Auto	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Two person mixed DNA profile Single evidence sample excluded Single evidence sample excluded
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.003	Auto		Submitted-results pending.
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	SUCCESS	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Semen not detected Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Semen not detected Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending.
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Possible sub-threshold information 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.008	Auto		Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Micro neg for sperm
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile DNA profile removed from NCIDD
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Two person mixed DNA profile
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.002	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.009	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	SUCCESS	Micro positive for sperm. Submitted-Results pending Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. Micro neg for sperm
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. Presump Saliva test negative Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.007	Auto	SUCCESS	Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Presumptive blood test pos. Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.009	Auto		Submitted-results pending. Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.008	Auto		Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending. Sample processed and final results under
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Sample processed and final results under
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto		Submitted as cells, Presump saliva test pending presump Saliva test positive
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.009	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		
[redacted]	TRUE	0.006	Auto	FAIL	Submitted as cells, Presump saliva test pending presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.008	Auto	SUCCESS	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.009	Auto	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Micro positive for sperm. Submitted-Results pending No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.007	Auto		Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted-results pending. Micro positive for sperm. Submitted-Results pending No DNA profile
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		Submitted-results pending. Two person mixed DNA profile
[redacted]	TRUE	0.007	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.004	Auto	SUCCESS	Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending. No DNA detected
[redacted]	TRUE	0.003	Auto		Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.007	Auto		Presumptive blood test pos. Submitted-results pending. Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution Excluded from mixed DNA profile
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.006	Auto		Two person mixed DNA profile 2 person mixed profile - conditioned on
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.002	Auto		Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.006	Auto		Submitted-results pending.
[redacted]	TRUE	0.005	Auto	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.007	Auto		Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded 2 person mix remaining consistent with unknown Possible sub-threshold information 2 person mix rem - support for contribution > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.009	Auto	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.008	Auto		Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution 3 person mix rem - support for contrib 10 000 to 100 000 3 person mix remaining - low support for contrib
[redacted]	TRUE	0.004	Auto		Micro positive for sperm. Submitted-Results pending
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.003	Auto	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		ENVM -Partial DNA profile
[redacted]	TRUE	0.002	Auto		ENVM -Partial DNA profile
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.005	Auto	SUCCESS	Submitted-results pending. Micro neg for sperm Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion DNA profile removed from NCIDD
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.005	Auto		Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.009	Auto		Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending.
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.007	Auto		presump Saliva test positive
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.004	Auto	FAIL	Presumptive blood test pos. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		
[redacted]	TRUE	0.002	Auto		
[redacted]	TRUE	0.002	Auto		Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Presumptive blood test pos. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted as cells Single source DNA profile
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto		Hair located. Submitted-results pending
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.002	Auto	FAIL	Presumptive blood test pos. Submitted-results pending. Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending.
[redacted]	TRUE	0.008	Auto		Hair located. Submitted-results pending Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending. Sample processed and final results under
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto		Submitted-results pending.
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.002	Auto		Submitted-results pending. Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.009	Auto		
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Presumptive blood test pos. Submitted-results pending. Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		Submitted-results pending. Micro neg for sperm
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.003	Auto	FAIL	Single source DNA profile- unsuitable for NCIDD searching
[redacted]	TRUE	0.005	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.003	Auto	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto		Submitted-results pending.
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.008	Auto		Submitted-results pending.
[redacted]	TRUE	0.005	Auto		Submitted-results pending.
[redacted]	TRUE	0.004	Auto		Submitted-results pending.
[redacted]	TRUE	0.002	Auto		Submitted-results pending.
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.009	Auto		
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.007	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.008	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.003	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		Submitted-results pending.
[redacted]	TRUE	0.008	Auto	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.004	Auto		
[redacted]	TRUE	0.005	Auto	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.006	Auto		
[redacted]	TRUE	0.007	Auto		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.002	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.001	Manual		Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.029	Manual	FAIL	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual	FAIL	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Presump. PSA test positive, no sperm found Single source DNA profile < NCIDD matching stringency Single Source DNA profile - assumed known contributor

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.038	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix - supports non contribution
[redacted]	TRUE	0	Manual	FAIL	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.03	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.03	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	SUCCESS	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	TRUE	0.029	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	3E-04	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	TRUE	4E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.026	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 3 person mix profile - support for contrib > 100 billion

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.032	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual		Two person mixed DNA profile 2 person mixed profile - conditioned on
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile Single evidence sample excluded
[redacted]	TRUE	0.017	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution 3 person mix - support for contrib 10 000 - 100 000 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 2 person mix rem - support for contrib 10 000 to 100 000 2 person mix remaining - supports non contribution 2 person mix remaining - supports non contribution 3 person mix rem - support for contrib 10 000 to 100 000 3 person mix remaining - supports non contribution 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	3E-04	Manual		Submitted-results pending. No DNA detected
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.032	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.03	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution
[redacted]	TRUE	0.035	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.033	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	TRUE	0.014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual		Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.024	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.01	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.027	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual		Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	TRUE	0.011	Manual	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.033	Manual	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.002	Manual		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Single source DNA profile SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.028	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.027	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.015	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.017	Manual		Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.015	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Two person mixed DNA profile Single evidence sample excluded This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	7E-04	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	2E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.014	Manual		Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Possible sub-threshold information
[redacted]	TRUE	0	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	SUCCESS	Submitted as cells Single source DNA profile NCIDD upload single source DNA profile Single Source DNA profile - assumed known contributor DNA profile removed from NCIDD
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	TRUE	2E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	3E-04	Manual		ENVM - No DNA profile
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	TRUE	0.009	Manual		
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.018	Manual		
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix rem - support for contribution > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.024	Manual	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.017	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.027	Manual		Semen not detected Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.032	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.02	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD Intel upload - single source partial profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.031	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.074	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.024	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.01	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - supports non contribution
[redacted]	TRUE	0.018	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - supports non contribution
[redacted]	TRUE	0.011	Manual		Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile Suspect check - supports non contribution
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.024	Manual	FAIL	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.009	Manual		
[redacted]	TRUE	0.022	Manual		Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.032	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
					Submitted-results pending.
					Three person mixed DNA profile
					3 person mix profile - support for contrib > 100 billion
					3 person mix - low support for contribution
[redacted]					Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.014	Manual		3 person mix - low support for contribution
[redacted]					Semen not detected
[redacted]					Submitted as cells
[redacted]	TRUE	0.037	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Single source DNA profile
[redacted]					NCIDD upload single source DNA profile
[redacted]					Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.017	Manual	SUCCESS	DNA profile removed from NCIDD
[redacted]	TRUE	0.009	Manual		
[redacted]	TRUE	0.015	Manual		
[redacted]	TRUE	0.016	Manual		
[redacted]					Submitted-results pending.
[redacted]					Single source DNA profile
[redacted]	TRUE	0.011	Manual	SUCCESS	NCIDD upload single source DNA profile
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		
[redacted]					Submitted for cells. Presumptive saliva test pending.
[redacted]					presump Saliva test positive
[redacted]					Three person mixed DNA profile
[redacted]	TRUE	0.01	Manual		3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.022	Manual		
[redacted]	TRUE	0.02	Manual		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.022	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.022	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]	TRUE	0.025	Manual		No statistical interpretation performed
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.015	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Two person mixed DNA profile
[redacted]	TRUE	0.026	Manual		2 person mix profile - support for contrib > 100 billion
[redacted]					Presump. PSA test positive, no sperm found
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual		No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.025	Manual		Submitted-results pending.
[redacted]					Submitted-results pending.
[redacted]					Two person mixed DNA profile
[redacted]	TRUE	0.022	Manual		No statistical interpretation performed
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	8E-04	Manual		
[redacted]					Micro positive for sperm. Submitted-Results pending
[redacted]					No DNA detected
[redacted]					This sample has undergone further processing
[redacted]	TRUE	7E-04	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	2E-04	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Two person mixed DNA profile
[redacted]					2 person mix profile - support for contrib > 100 billion
[redacted]					2 person mix profile - support for contrib > 100 billion
[redacted]					Excluded from mixed DNA profile
[redacted]	TRUE	0.021	Manual		2 person mix profile - support for contrib > 100 billion
[redacted]					Submitted as cells
[redacted]	TRUE	0.017	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]					3 person mixed profile - conditioned on
[redacted]	TRUE	0.029	Manual		Cond mix rem-low supp for contrib or supp non contrib
[redacted]	TRUE	0.002	Manual		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.019	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.035	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	RUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.014	Manual		Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million Mixture-low support for contrib or supports non contrib Excluded from mixed DNA profile
[redacted]	RUE	0.029	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.028	Manual		Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	RUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.027	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.061	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	RUE	0.01	Manual		
[redacted]	RUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.001	Manual	FAIL	Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.011	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	RUE	0.029	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	RUE	0.016	Manual		2 person mix remaining - supports non contribution Submitted as cells Two person mixed DNA profile 2 person mix - supports non contribution Sample undergone further work - conditioned Two person mixed DNA profile 2 person mixed profile - conditioned on
[redacted]	RUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.016	Manual	FAIL	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	RUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	RUE	0.013	Manual		Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	RUE	0.029	Manual		Presumptive blood test pos. Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	RUE	0.024	Manual		Submitted-results pending. Two person mixed DNA profile
[redacted]	RUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	RUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.002	Manual	FAIL	Submitted-results pending. Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.002	Manual		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
					Submitted-results pending.
[redacted]	TRUE	0.014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]					Submitted-results pending.
[redacted]					Interim result - sample undergoing rework
[redacted]					Quality flag identified, on hold awaiting advice from QPS
[redacted]	TRUE	0.016	Manual		Quality control failure, refer to QPS
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.019	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual		No DNA profile - possible sub-threshold peaks
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.015	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.023	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		
[redacted]	TRUE	0.024	Manual		
[redacted]					Micro positive for sperm. Submitted-Results pending
[redacted]	TRUE	0.015	Manual		QPS advised no further work required - results available
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.012	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.027	Manual		Possible sub-threshold information
[redacted]					Submitted-results pending.
[redacted]					No DNA detected
[redacted]					This sample has undergone further processing
[redacted]	TRUE	0	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					No DNA detected
[redacted]					This sample has undergone further processing
[redacted]	TRUE	0	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Hair located. Submitted-results pending
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted as cells
[redacted]	TRUE	0.028	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Three person mixed DNA profile
[redacted]					No statistical interpretation performed
[redacted]					Sample undergone further work - conditioned
[redacted]					Three person mixed DNA profile
[redacted]					3 person mixed profile - conditioned on
[redacted]	TRUE	0.023	Manual		3 person mix remaining - supports non contribution
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.015	Manual		Two person mixed DNA profile
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]					No statistical interpretation performed
[redacted]					Single evidence sample excluded
[redacted]	TRUE	0.011	Manual		3 person mix profile - support for contrib > 100 billion
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.014	Manual		Three person mixed DNA profile
[redacted]					Submitted-results pending.
[redacted]					No DNA profile
[redacted]	TRUE	0.002	Manual		Possible sub-threshold information
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.013	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]	TRUE	0.02	Manual		Single evidence sample excluded
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.015	Manual		Two person mixed DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.002	Manual		Submitted as cells Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	SUCCESS	Submitted as cells Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.014	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual		
[redacted]	TRUE	0.033	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile DNA profile removed from NCIDD
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.033	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.033	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted as cells, Presump saliva test pending Presump Saliva test negative Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.029	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion Submitted as cells, Presump saliva test pending presump Saliva test positive
[redacted]	TRUE	0.013	Manual	SUCCESS	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	TRUE	0.013	Manual		
[redacted]	TRUE	0.018	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD
[redacted]	TRUE	8E-04	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	TRUE	3E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]					Submitted-results pending.
	TRUE	0.01	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
	TRUE	0.012	Manual		
	TRUE	0.012	Manual		
	TRUE	4E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
					Submitted-results pending.
	TRUE	0.009	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.019	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
					Single source DNA profile
					NCIDD upload single source DNA profile
					Possible sub-threshold information
					Complex mixed profile unsuitable for interp or comparison
	TRUE	0.009	Manual	SUCCESS	DNA profile removed from NCIDD
					Submitted-results pending.
	TRUE	0.012	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.022	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.053	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted as cells, Presump saliva test pending
					presump Saliva test positive
	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
	TRUE	0.016	Manual		Submitted-results pending.
					Submitted-results pending.
	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.002	Manual		No DNA profile - possible sub-threshold peaks
					Submitted-results pending.
	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
	TRUE	0.009	Manual		
					Submitted-results pending.
					Three person mixed DNA profile
					3 person mixed profile - conditioned on
	TRUE	0.015	Manual		3 person mix remaining - supports non contribution
					Submitted-results pending.
	TRUE	0.001	Manual		No DNA profile
					Submitted-results pending.
	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.002	Manual		No DNA profile
					Submitted-results pending.
	TRUE	0.001	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
					Submitted-results pending.
	TRUE	0.001	Manual		No DNA profile - possible sub-threshold peaks
					Semen not detected
					Submitted as cells
	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.01	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
	TRUE	0.025	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
	TRUE	2E-04	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
					Submitted-results pending.
					Three person mixed DNA profile
	TRUE	0.021	Manual		No statistical interpretation performed
					Submitted-results pending.
	TRUE	0.028	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted as cells
					Three person mixed DNA profile
					3 person mixed profile - conditioned on
	TRUE	0.014	Manual		3 person rem- support for contrib 1 billion-100 billion
					Submitted-results pending.
					Three person mixed DNA profile
					Excluded from mixed DNA profile
					3 person mix profile - support for contrib > 100 billion
	TRUE	0.02	Manual		3 person mix - support for contribution 100 to 1000
	TRUE	0.023	Manual		
	TRUE	0.025	Manual		
					Submitted-results pending.
					Three person mixed DNA profile
					3 person mixed profile - conditioned on
					3 person mix profile - support for contrib > 100 billion
	TRUE	0.012	Manual		3 person mix rem - support for contribution > 100 billion

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.002	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.012	Manual	SUCCESS	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual		
[redacted]	TRUE	0.017	Manual		
[redacted]	TRUE	0.032	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.018	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		
[redacted]	TRUE	0.013	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.032	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.026	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0.035	Manual		Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.017	Manual	SUCCESS	Submitted-results pending. Single source DNA profile Possible sub-threshold information This sample has undergone further processing Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.04	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.011	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion
[redacted]	TRUE	0.009	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.03	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Possible sub-threshold information
[redacted]	TRUE	0.009	Manual		Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.032	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.024	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.025	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.04	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.022	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Submitted-results pending.
[redacted]	TRUE	0.038	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.032	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	TRUE	0.009	Manual		
[redacted]	TRUE	0.022	Manual		This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 10 000 - 100 000 Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.024	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual		No DNA profile
[redacted]					Submitted-results pending.
[redacted]					No DNA profile
[redacted]	TRUE	0.002	Manual		Possible sub-threshold information
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]					3 person mix profile - support for contrib > 100 billion
[redacted]					3 person mix - support for contrib 1 million - 1 billion
[redacted]	TRUE	0.032	Manual		Excluded from mixed DNA profile
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.027	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.018	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Two person mixed DNA profile
[redacted]					2 person mix profile - support for contrib > 100 billion
[redacted]					2 person mix- support for contrib 1 billion - 100 billion
[redacted]	TRUE	0.02	Manual		2 person mix profile - support for contrib > 100 billion
[redacted]					Submitted-results pending.
[redacted]					Two person mixed DNA profile
[redacted]					2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.01	Manual		Excluded from mixed DNA profile
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.091	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.023	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.01	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]					3 person mixed profile - conditioned on
[redacted]	TRUE	0.021	Manual		Excluded from mixed DNA profile
[redacted]					Submitted-results pending.
[redacted]					Two person mixed DNA profile
[redacted]					2 person mixed profile - conditioned on
[redacted]	TRUE	0.022	Manual	FAIL	Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	6E-04	Manual		ENVM -Partial DNA profile
[redacted]	TRUE	9E-04	Manual		ENVM -Partial DNA profile
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]					Three person mixed DNA profile
[redacted]					3 person mixed profile - conditioned on
[redacted]	TRUE	0.019	Manual		3 person mix remaining - supports non contribution
[redacted]	TRUE	0	Manual		
[redacted]					
[redacted]					Micro positive for sperm. Submitted-Results pending
[redacted]					SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.01	Manual	SUCCESS	NCIDD upload single source DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile Possible sub-threshold information
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.015	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.033	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 1 million - 1 billion 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.01	Manual	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.035	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0	Manual		ENVM -Partial DNA profile
[redacted]	TRUE	0	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0	Manual		ENVM - No DNA profile
[redacted]	TRUE	2E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.011	Manual	FAIL	Labelling discrepancy Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.02	Manual	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.018	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.002	Manual		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	4E-04	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0.032	Manual	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.027	Manual		Semen not detected Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	TRUE	0.013	Manual	FAIL	Sample on hold - awaiting advice Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual		
[redacted]	TRUE	0.009	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile
[redacted]	TRUE	0.01	Manual		SS DNA profile 9 loci and above LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.013	Manual		
[redacted]	TRUE	0.011	Manual		
[redacted]	TRUE	0.024	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	TRUE	0.014	Manual		Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile Mix Rem DNA contrib < NCIDD matching Stringency
[redacted]	TRUE	0.001	Manual		Submitted-results pending.
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.032	Manual		Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix- support for contrib 1 billion - 100 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.023	Manual		Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000 3 person mix - support for contribution 100 to 1000 3 person mix - low support for contribution
[redacted]	TRUE	0.029	Manual		
[redacted]	TRUE	0.027	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.024	Manual		Submitted-results pending. Intel report required for further interpretation

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual		Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.011	Manual		
[redacted]	TRUE	0.01	Manual		Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem - support for contrib 1 billion -100 billion
[redacted]	TRUE	0.019	Manual		Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Semen not detected Submitted as cells Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual		Submitted-results pending. No DNA detected
[redacted]	TRUE	0.015	Manual		
[redacted]	TRUE	0.011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile
[redacted]	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Possible sub-threshold information
[redacted]	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Possible sub-threshold information
[redacted]	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution
[redacted]	TRUE	0.035	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.011	Manual	SUCCESS	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile
[redacted]	TRUE	0.03	Manual		Submitted as cells Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	SUCCESS	Hair located. Submitted-results pending Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual		
[redacted]	TRUE	0.029	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - low support for contribution
[redacted]	TRUE	0.002	Manual	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile DNA profile removed from NCIDD
[redacted]	TRUE	0.032	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Single evidence sample excluded 3 person mix - support for contribution 100 to 1000
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.033	Manual	FAIL	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 Person Mix Rem contrib unsuitable for NCIDD 3 person mix remaining - low support for contrib
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	5E-04	Manual		ENVM -Partial DNA profile
[redacted]	TRUE	3E-04	Manual		ENVM -Partial DNA profile
[redacted]	TRUE	0.001	Manual		ENVM -Partial DNA profile
[redacted]	TRUE	0	Manual		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.015	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.025	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual		Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual		Single evidence sample excluded Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.024	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual		
[redacted]	TRUE	0.014	Manual		Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion
[redacted]	TRUE	0.002	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.058	Manual		Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000 3 person mix - supports non contribution

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.014	Manual	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	SUCCESS	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual		Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted-results pending.
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded 3 Person Mix Rem contrib unsuitable for NCIDD
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Two person mixed DNA profile Suspect check inconclusive - mixed DNA profile Suspect check - supports non contribution
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.022	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.029	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.03	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.029	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.009	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]					Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]					This sample has undergone further processing
[redacted]	TRUE	0.013	Manual	FAIL	Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.017	Manual		Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual		Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.029	Manual		Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.009	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual		
[redacted]	TRUE	0.018	Manual		
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.013	Manual		
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile Suspect Check Actioned - No Match
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0	Manual		ENVM - No DNA profile
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	2E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	7E-04	Manual		ENVM - No DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	2E-04	Manual		
[redacted]	TRUE	2E-04	Manual		
[redacted]	TRUE	0	Manual		
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	RUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.018	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	RUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.01	Manual		
[redacted]	RUE	0.01	Manual		Hair located. Submitted-results pending Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	RUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.001	Manual		
[redacted]	RUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.012	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	RUE	0.014	Manual		Submitted-results pending. Single source DNA profile Possible sub-threshold information Single Source DNA profile - assumed known contributor
[redacted]	RUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.001	Manual		
[redacted]	RUE	0.002	Manual		
[redacted]	RUE	0.014	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	RUE	0.001	Manual		
[redacted]	RUE	0.015	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	RUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.024	Manual		Submitted-results pending.
[redacted]	RUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.001	Manual		
[redacted]	RUE	0.001	Manual		
[redacted]	RUE	0.001	Manual		
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0	Manual		Submitted-results pending. No DNA detected
[redacted]	RUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.024	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.002	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]	RUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	RUE	0.024	Manual		Submitted-results pending. Three person mixed DNA profile Cond mix rem-low supp for contrib or supp non contrib 3 person mixed profile - conditioned on
[redacted]	RUE	0.032	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 3 person mix remaining - supports non contribution

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
					Single source DNA profile
					NCIDD upload single source DNA profile
[redacted]	TRUE	0.014	Manual	SUCCESS	Possible sub-threshold information
					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.002	Manual		
					Submitted-results pending.
					Micro neg for sperm
					Two person mixed DNA profile
					2 person mixed profile - conditioned on
[redacted]	TRUE	0.01	Manual	FAIL	Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	TRUE	0.018	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
					Submitted-results pending.
[redacted]	TRUE	0.024	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.032	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.026	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.027	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.027	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.01	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.017	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted as cells
					Three person mixed DNA profile
					3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.014	Manual		Excluded from mixed DNA profile
					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
					Submitted as cells, Presump saliva test pending
					Presump Saliva test negative
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	5E-04	Manual		
					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.013	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	2E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	3E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
					Submitted-results pending.
[redacted]	TRUE	0.024	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.013	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Hair located. Submitted-results pending
[redacted]	TRUE	0.002	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual		
					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted as cells
					Three person mixed DNA profile
					3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.031	Manual		3 person mix - support for contrib 1 million - 1 billion
					Micro positive for sperm. Submitted-Results pending
[redacted]	TRUE	0.011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
					Submitted-results pending.
[redacted]	TRUE	0.029	Manual		Three person mixed DNA profile

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.025	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.024	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 100 to 1000 3 person mix - supports non contribution
[redacted]	TRUE	0.03	Manual		Submitted as cells Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Submitted-results pending.
[redacted]	TRUE	0.021	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.002	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.027	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.014	Manual	SUCCESS	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	TRUE	0.029	Manual		
[redacted]	TRUE	0.021	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.047	Manual		Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded 2 person mix profile - support for contrib > 100 billion This sample has undergone further processing Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.03	Manual		Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.017	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual		Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.027	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.03	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual		Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile Possible sub-threshold information
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.031	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000
[redacted]	TRUE	0.009	Manual		Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	2E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	5E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Submitted-results pending.
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.019	Manual		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.029	Manual		Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Submitted-results pending.
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.039	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual		Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Single evidence sample excluded 3 person mix - supports non contribution
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix- support for contrib 1 billion - 100 billion 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.016	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Excluded from mixed DNA profile
[redacted]	TRUE	0.002	Manual		Hair located. Submitted-results pending Interim result - sample undergoing rework Two person mixed DNA profile 2 person mix - supports non contribution 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.031	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Single Source DNA profile - assumed known contributor
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.016	Manual	FAIL	Semen not detected Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.03	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.023	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on Remaining contribution - inconclusive

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.032	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 Single evidence sample excluded 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual		
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Two person mixed DNA profile
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution
[redacted]	TRUE	0.001	Manual	FAIL	Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million
[redacted]	TRUE	0.036	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		
[redacted]	TRUE	0.031	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	TRUE	0.027	Manual		Submitted-results pending.
[redacted]	TRUE	0.01	Manual		
[redacted]	TRUE	0.023	Manual		
[redacted]	TRUE	0.018	Manual		Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	7E-04	Manual		ENVM -Partial DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.024	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted-results pending. Micro neg for sperm Semen not detected Single source DNA profile Single source DNA profile < 9 loci LR 1000 - 10 000
[redacted]	TRUE	0.014	Manual	SUCCESS	Submitted-results pending. Two person mixed DNA profile Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.022	Manual		
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.002	Manual		Micro positive for sperm. Submitted-Results pending
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		
[redacted]	TRUE	0.009	Manual	FAIL	Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib
[redacted]	TRUE	0.011	Manual	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.002	Manual		Submitted-results pending. No DNA detected
[redacted]	TRUE	0.009	Manual		Submitted-results pending.
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual		Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Single evidence sample excluded
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.013	Manual		Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 100 000 to 1 million
[redacted]	TRUE	0.033	Manual		Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 3 person mix - support for contribution 100 to 1000
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.03	Manual		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.03	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted-results pending. No DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual		Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.013	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	2E-04	Manual		ENVM - No DNA profile
[redacted]	TRUE	4E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.021	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	TRUE	0.019	Manual		Submitted-results pending.
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.031	Manual	SUCCESS	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	TRUE	0.031	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual		Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.031	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.033	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution
[redacted]	TRUE	0.01	Manual		Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	TRUE	0.028	Manual		presump Saliva test positive Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - support for contrib 100 to 1000
[redacted]	TRUE	0.031	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.023	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual		Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.014	Manual	SUCCESS	Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile NCIDD upload - mixed DNA profile Excluded from mixed DNA profile
[redacted]	TRUE	0.011	Manual		
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.009	Manual		Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion 3 person mix - support for contribution 100 to 1000
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution
[redacted]	TRUE	0.016	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.017	Manual		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.002	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib 3 person mix remaining - supports non contribution
[redacted]	TRUE	0.01	Manual		
[redacted]	TRUE	0.017	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		
[redacted]	TRUE	0.024	Manual		Submitted-results pending. Single source DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual		Submitted-results pending.
[redacted]	TRUE	0.015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Micro positive for sperm. Submitted-Results pending Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual		Submitted-results pending. Semen not detected No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.009	Manual		Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 3 person mix - supports non contribution
[redacted]	TRUE	0.017	Manual		
[redacted]	TRUE	0.023	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution
[redacted]	TRUE	0.028	Manual		
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual		Submitted-results pending. Two person mixed DNA profile
[redacted]	TRUE	0.03	Manual		
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.037	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.02	Manual		Submitted-results pending.
[redacted]	TRUE	0.019	Manual		Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	TRUE	0.001	Manual	FAIL	Presumptive blood test pos. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.002	Manual		No DNA profile
[redacted]					Submitted-results pending.
[redacted]					Two person mixed DNA profile
[redacted]					2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.014	Manual		2 person mix - low support for contribution
[redacted]					Submitted-results pending.
[redacted]					Two person mixed DNA profile
[redacted]					2 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.022	Manual		2 person mix - low support for contribution
[redacted]	TRUE	0.015	Manual		Submitted-results pending.
[redacted]	TRUE	0.031	Manual		Submitted-results pending.
[redacted]	TRUE	0.002	Manual		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.02	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.024	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual		No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.002	Manual		
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect check - low support for contribution
[redacted]					Micro positive for sperm. Submitted-Results pending
[redacted]					Interim result- mixed profile obtained. Rework Reqd
[redacted]					Two person mixed DNA profile
[redacted]					2 person mixed profile - conditioned on
[redacted]					Excluded from mixed DNA profile
[redacted]					Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect Check Actioned - No Match
[redacted]	TRUE	0.019	Manual	FAIL	Suspect Check Actioned - No Match
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect check - supports non contribution
[redacted]					Three person mixed DNA profile
[redacted]					3 person mixed profile - conditioned on
[redacted]					Suspect check- support for contribution 10 000 to 100 000
[redacted]					Mixture-low support for contrib or supports non contrib
[redacted]					Suspect check - supports non contribution
[redacted]	TRUE	0.031	Manual		Suspect check - supports non contribution
[redacted]	TRUE	0.031	Manual		
[redacted]					Submitted-results pending.
[redacted]					Presump. PSA test positive, no sperm found
[redacted]	TRUE	5E-04	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	2E-04	Manual		
[redacted]	TRUE	3E-04	Manual		
[redacted]					Interim result- mixed profile obtained. Rework Reqd
[redacted]					Three person mixed DNA profile
[redacted]					3 person mixed profile - conditioned on
[redacted]					3 person mix remaining - supports non contribution
[redacted]					3 person mix remaining - supports non contribution
[redacted]					Single evidence sample excluded
[redacted]					Suspect check - support for contrib 100 000 - 1 million
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect Check Actioned - No Match
[redacted]					Suspect check - supports non contribution
[redacted]					Suspect check - supports non contribution
[redacted]	TRUE	0.024	Manual		Suspect Check Actioned - No Match
[redacted]	TRUE	0.001	Manual		Micro positive for sperm. Submitted-Results pending
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual		No DNA profile - possible sub-threshold peaks
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual		
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.001	Manual		No DNA profile - possible sub-threshold peaks
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.01	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]					Submitted-results pending.
[redacted]	TRUE	0.015	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	TRUE	0.01	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.009	Manual		Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib
[redacted]	TRUE	0.014	Manual		Submitted-results pending.
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	SUCCESS	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	TRUE	0.017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.02	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.015	Manual		Submitted-results pending. Three person mixed DNA profile
[redacted]	TRUE	0.027	Manual		Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - low support or non contrib Suspect check - low support or non contrib
[redacted]	TRUE	0.002	Manual		Submitted-results pending. Micro neg for sperm
[redacted]	TRUE	0.002	Manual		Micro positive for sperm. Submitted-Results pending
[redacted]	TRUE	0.013	Manual	SUCCESS	Submitted-results pending. Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	TRUE	0.013	Manual	FAIL	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.03	Manual		Submitted-results pending.
[redacted]	TRUE	0.001	Manual		Submitted-results pending. Sample processed and final results under
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.011	Manual		
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.013	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	TRUE	7E-04	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	TRUE	0.036	Manual		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	9E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	6E-04	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	TRUE	0.028	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.028	Manual		
[redacted]	TRUE	0.01	Manual		
[redacted]	TRUE	0.016	Manual		
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.017	Manual		Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 1 million - 1 billion Excluded from mixed DNA profile
[redacted]	TRUE	0.02	Manual		Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted-results pending.
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		Submitted-results pending.
[redacted]	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.002	Manual		
[redacted]	TRUE	0.045	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	TRUE	0.002	Manual	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.001	Manual		
[redacted]	TRUE	0.031	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.022	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.035	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.025	Manual	FAIL	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mixture-low support for contrib or supports non contrib Single evidence sample excluded This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.026	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.009	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	TRUE	0.029	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.018	Manual		Submitted-results pending. Micro neg for sperm
[redacted]	TRUE	0.016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.01	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	TRUE	0.021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Submitted-results pending.
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	FALSE	0	n/a		Submitted as cells
[redacted]	FALSE	0	n/a		Submitted-results pending. QPS advised no further work required - results available
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	ENVM - Partial profile unsuitable for comparison purposes
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Three person mixed DNA profile 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	FALSE	0	n/a		Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. DNA insufficient for further processing This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	SUCCESS	Submitted-results pending. Interim result - sample undergoing rework Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix- support for contrib 1 billion - 100 billion 3 person mix - supports non contribution 3 person mix - supports non contribution This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		Submitted-results pending. Interim result- Partial profile undergoing rework Single source DNA profile SS DNA profile 9 loci and above LR > 100 billion
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	SUCCESS	Submitted as cells Single source DNA profile NCIDD Intel upload - single source partial profile This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Hair located. Submitted-results pending No DNA detected This sample has undergone further processing No DNA profile
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Submitted as cells No DNA detected This sample has undergone further processing No DNA profile - possible sub-threshold peaks
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Submitted-results pending. No DNA profile - possible sub-threshold peaks

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		Submitted-results pending. 9 loci DNA profile- NCIDD- possible sub-threshold peaks 9 loci DNA profile- NCIDD- possible sub-threshold peaks This sample has undergone further processing Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion DNA profile removed from NCIDD
[redacted]	FALSE	0	n/a	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		Partial DNA profile
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[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		

Barcode	HasQuant	Quant	Auto/Manu	EXHinterp	EXH
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
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[redacted]	FALSE	0	n/a		
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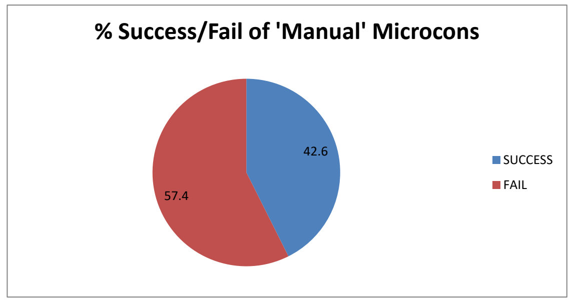
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		
[redacted]	FALSE	0	n/a		

MANUAL MICROCON CHARTS

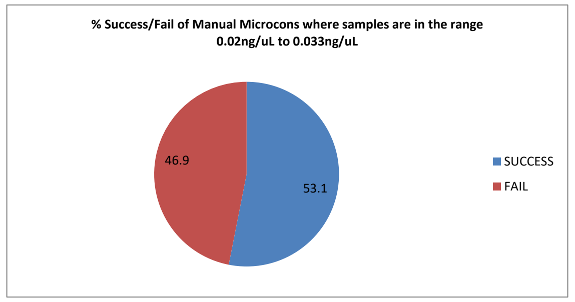
n=752 samples = all samples

	%Success/Fail
SUCCESS	42.6
FAIL	57.4



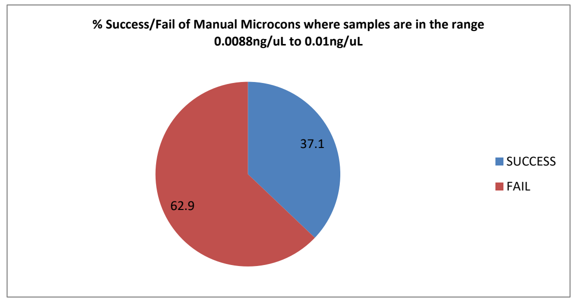
n=226 = 0.02ng/uL < SAMPLES > 0.033ng/uL

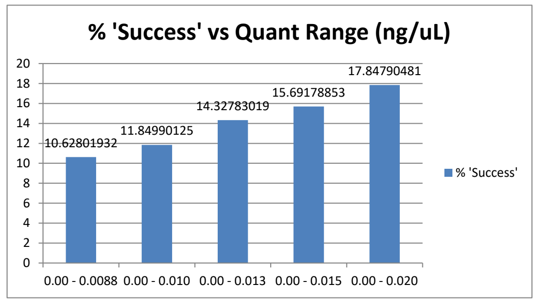
	% Success/Fail
SUCCESS	53.1
FAIL	46.9

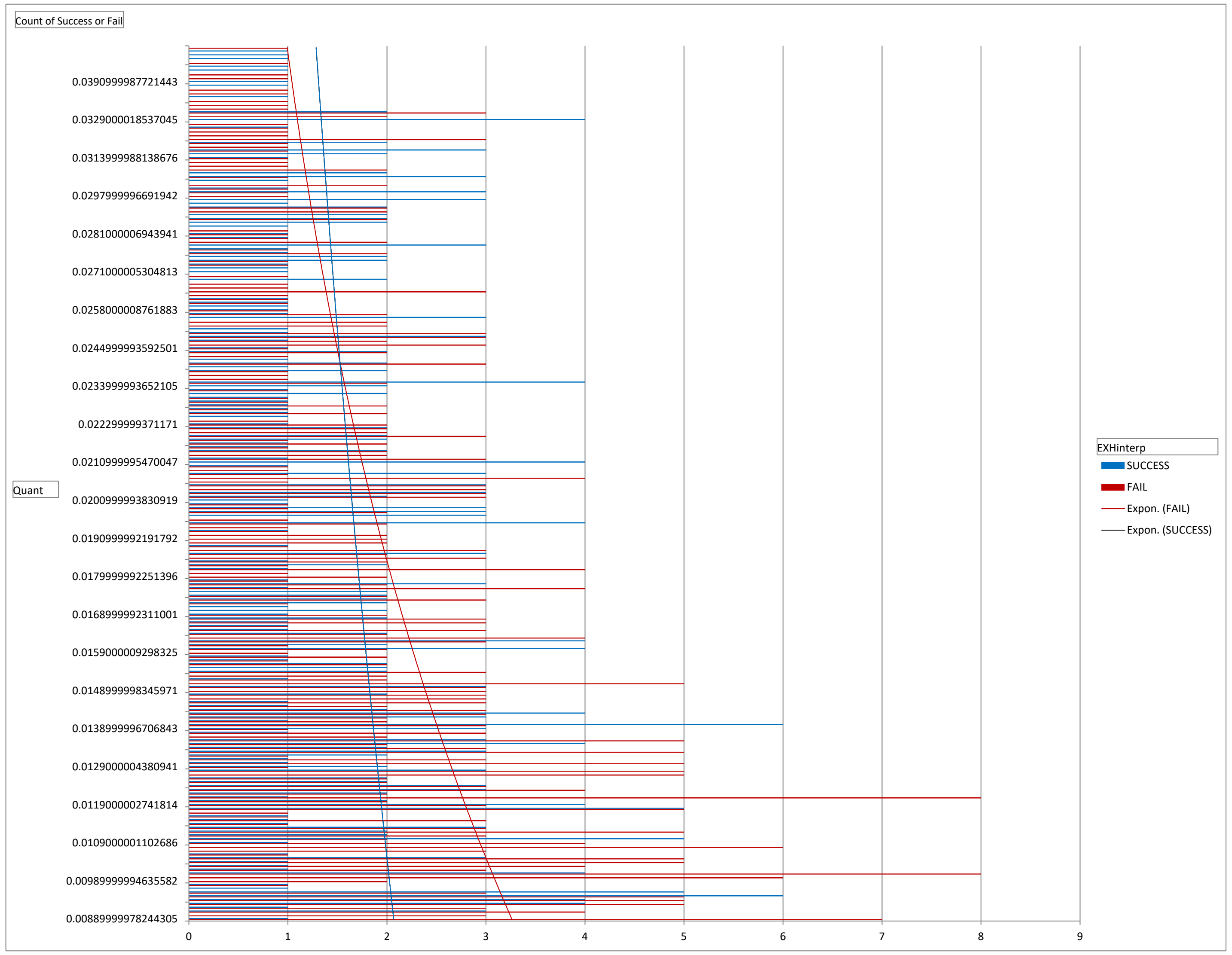


n = 70 = 0.0088ng/uL < Samples> 0.01ng/uL

	% Success/Fail
SUCCESS	37.1
FAIL	62.9





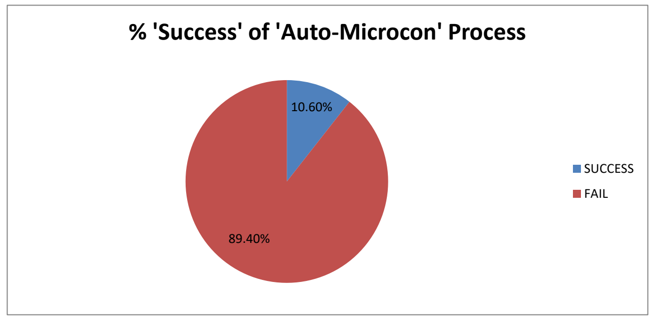


Quant (ng/uL)	No. samples	No. samples 'success'	% 'Success'
0.00 - 0.0088	1449	154	10.62801932
0.00 - 0.010	1519	180	11.84990125
0.00 - 0.013	1696	243	14.32783019
0.00 - 0.015	1778	279	15.69178853
0.00 - 0.020	1933	345	17.84790481

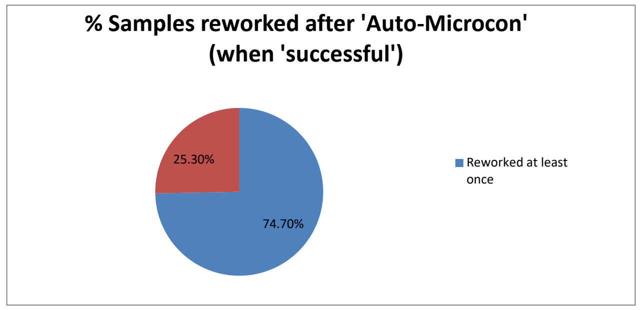
AUTO-MICROCON CHARTS

Difference ('fold') between pre and post MCONC Quants when SUCCESS
 - removed 2 data points as outliers: 34 fold, 22 fold

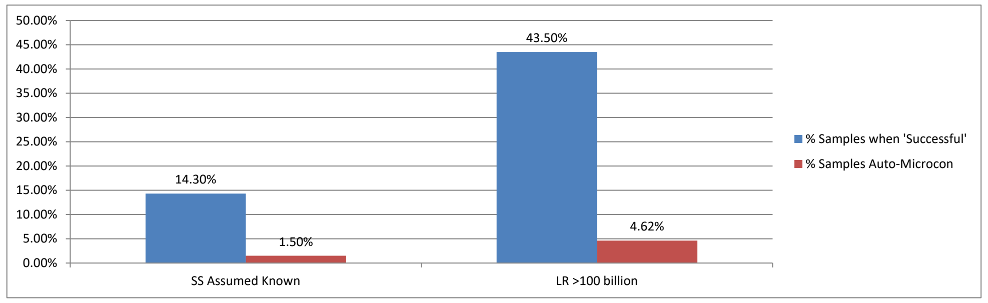
		% Success
SUCCESS	154	10.60%
FAIL	1295	89.40%



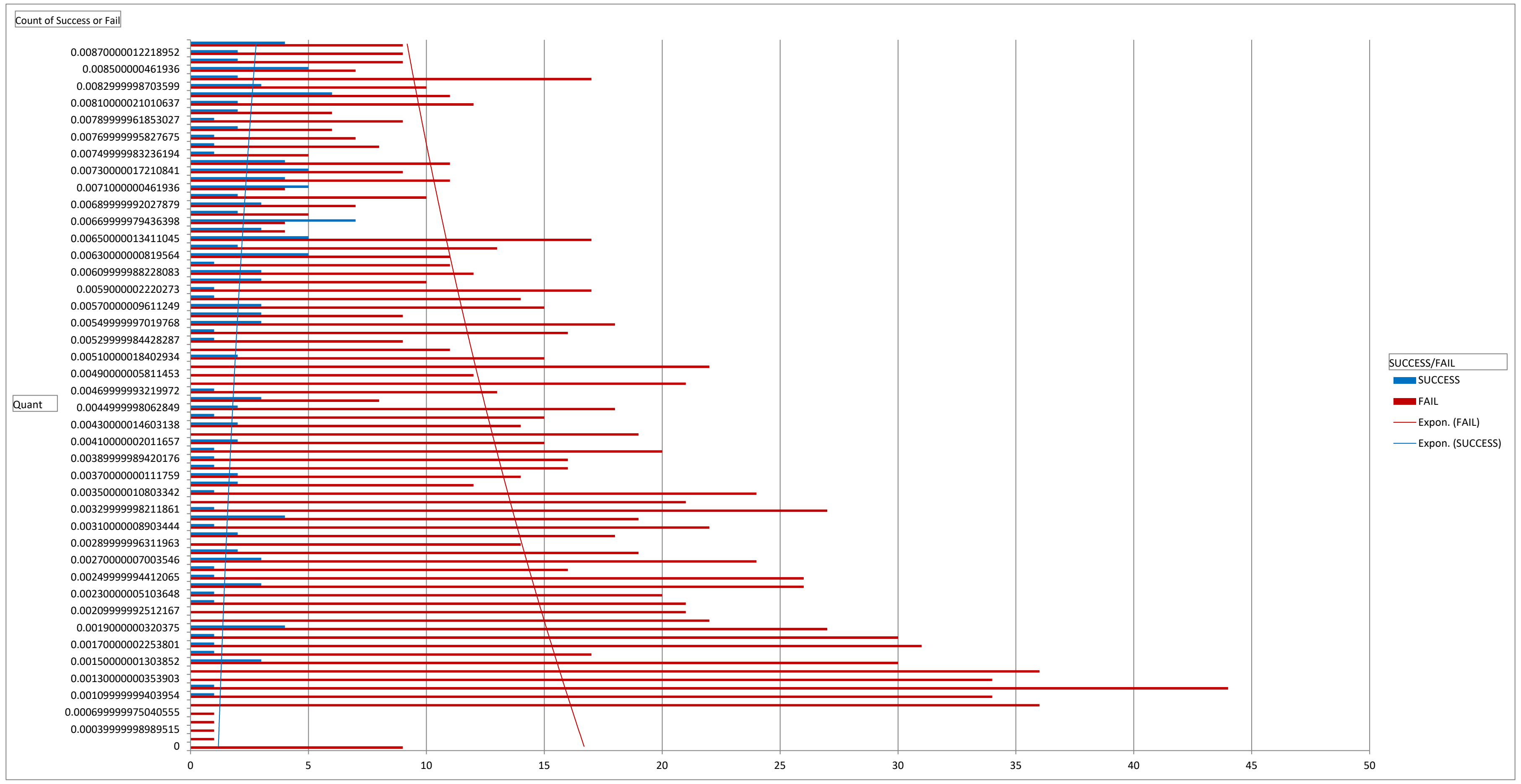
rework after MCONC when SUCCESS	count	%
Reworked at least once	115	74.70%
Not Reworked	39	25.30%



	% Samples when 'Successful'	% Samples Auto-Microcon
SS Assumed Known	14.30%	1.50%
LR >100 billion	43.50%	4.62%

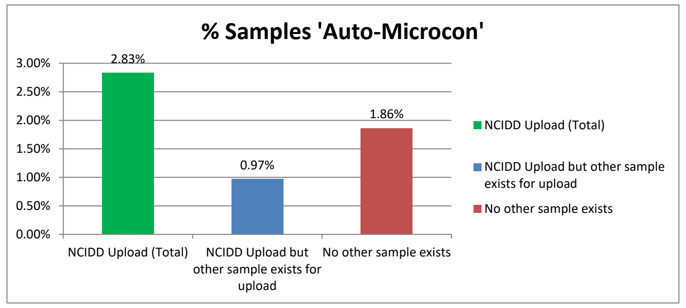


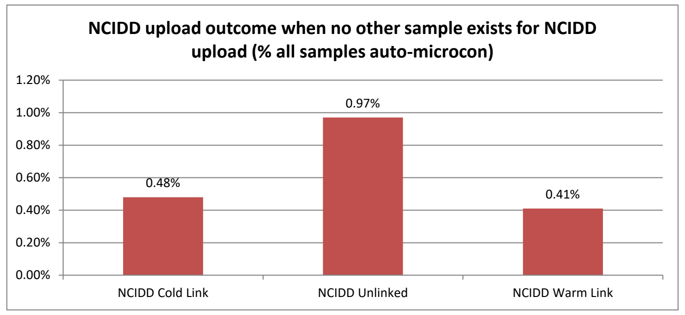
Original Quant vs No. samples and Success/Fail



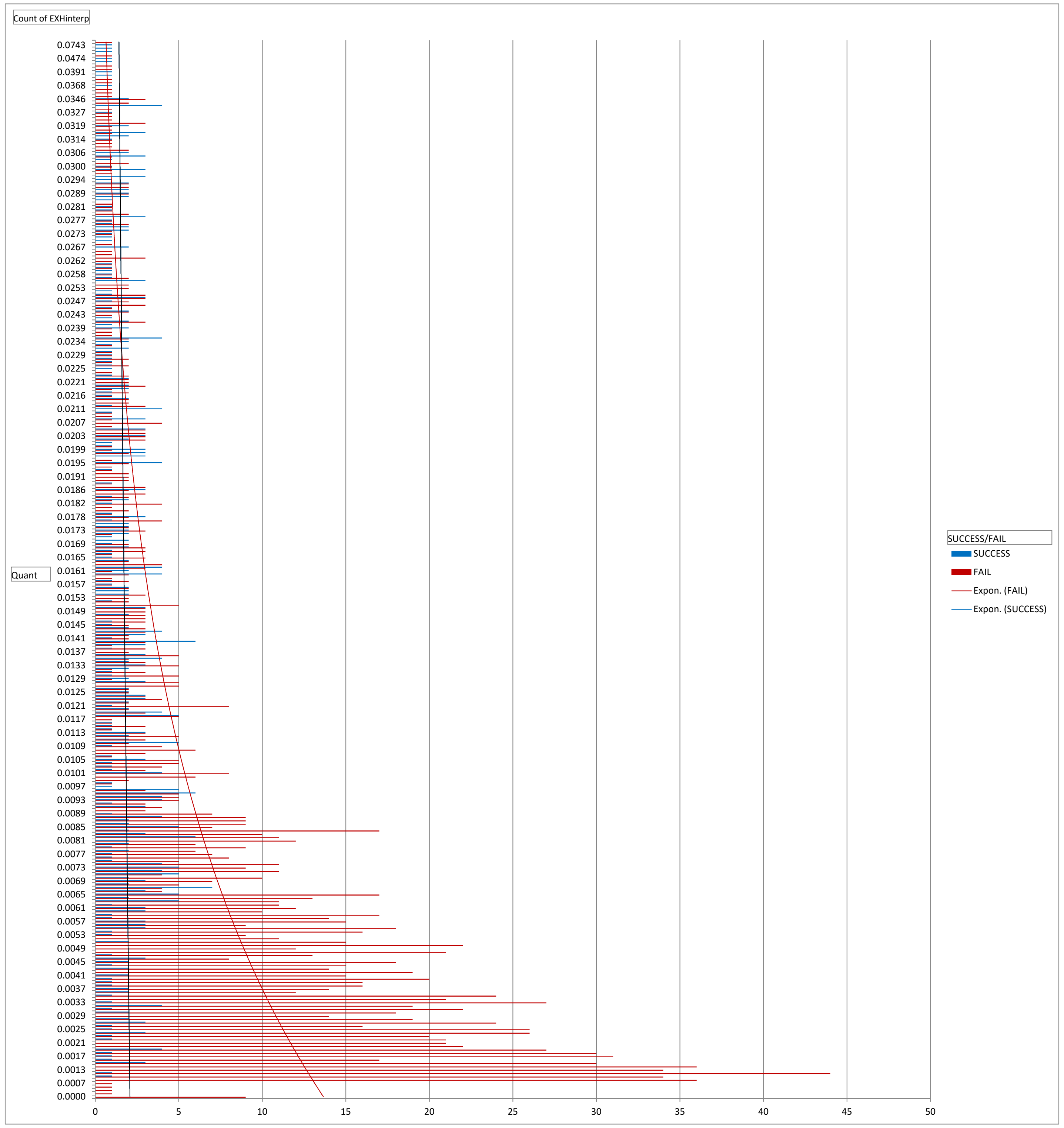
	Number of samples	% Samples 'Auto-Microcon'
NCIDD Upload (Total)	41	2.83%
NCIDD Upload but other sample exists for upload	14	0.97%
No other sample exists	27	1.86%

	Number of samples (where no other sample could be uploaded)	% Samples 'Auto-Microcon'
NCIDD Cold Link	7	0.48%
NCIDD Unlinked	14	0.97%
NCIDD Warm Link	6	0.41%

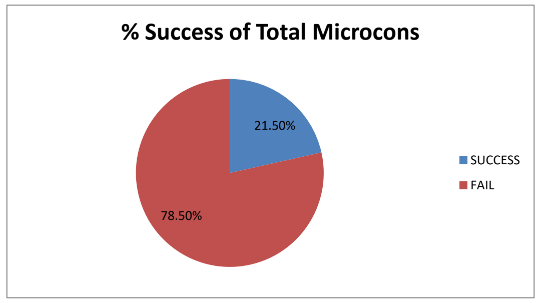




COMBINED / TOTAL DATA



		% Success
SUCCESS	474	21.50%
FAIL	1727	78.50%


% Success of Total Microcons

709939723	0.0023	SUCCESS	y		3356.52	34.57	
Barcode	Quant	EXHinterp	XAMP1	XAMP2		INTERP for NCIDD upload - was there another sample that could have been uploaded?	Link - warm (w), cold (c), unlinked (u)
[redacted]	0.0074	SUCCESS	y			n	u
[redacted]	0.0046	SUCCESS	y			n	u
[redacted]	0.0032	SUCCESS	n			n	w
[redacted]	0.0032	SUCCESS	y			n	c
[redacted]	0.0038	SUCCESS	y			n	c
[redacted]	0.0068	SUCCESS	y			n	c
[redacted]	0.0063	SUCCESS	y			n	u
[redacted]	0.0072	SUCCESS	y			n	c
[redacted]	0.0067	SUCCESS	y			n	w
[redacted]	0.0019	SUCCESS	y			n	u
[redacted]	0.0067	SUCCESS	y			n	c
[redacted]	0.0051	SUCCESS	n			n	u
[redacted]	0.0086	SUCCESS	y	y		n	u
[redacted]	0.0019	SUCCESS	y			n	c
[redacted]	0.0088	SUCCESS	y			n	w
[redacted]	0.0063	SUCCESS	n			n	w
[redacted]	0.0065	SUCCESS	y			n	u
[redacted]	0.0067	SUCCESS	y			n	u
[redacted]	0.0069	SUCCESS	y			n	u
[redacted]	0.0055	SUCCESS	y	2154.55	22.55	n	u
[redacted]	0.0088	SUCCESS	y			n	w
[redacted]	0.0056	SUCCESS	y			n	c
[redacted]	0.0051	SUCCESS	y			n	u
[redacted]	0.0041	SUCCESS	y			n	u
[redacted]	0.0028	SUCCESS	y			n	u

[redacted]	.0043	SUCCESS	y	n	u	
[redacted]	.0082	SUCCESS	y	n	w	
[redacted]	.0055	SUCCESS	n	n/a	n/a	removed from NCIDD
[redacted]	.0085	SUCCESS	y	y	c	
[redacted]	.0066	SUCCESS	n	y	w	
[redacted]	.0015	SUCCESS	y	y	w	
[redacted]	.0056	SUCCESS	y	y	c	
[redacted]	.0082	SUCCESS	y	y	w	
[redacted]	.0039	SUCCESS	y	y	w	
[redacted]	.0072	SUCCESS	y	y	w	
[redacted]	.0024	SUCCESS	y	y	w	
[redacted]	.0064	SUCCESS	y	y	w	
[redacted]	.0063	SUCCESS	y	y	c	
[redacted]	.0068	SUCCESS	y	y	u	
[redacted]	.0067	SUCCESS	y	y	c	
[redacted]	.0035	SUCCESS	y	y	w	
[redacted]	.0057	SUCCESS	y	y	u	
[redacted]	.0016	FAIL				
[redacted]	.0047	SUCCESS	y			
[redacted]	.0048	FAIL				
[redacted]	.0072	FAIL				
[redacted]	.0026	FAIL				
[redacted]	.0012	FAIL				
[redacted]	0	FAIL				
[redacted]	.0031	FAIL				
[redacted]	.0086	SUCCESS	y			
[redacted]	.0063	FAIL				
[redacted]	0.004	FAIL				

[redacted]	0.001	FAIL	
[redacted]	0.0046	FAIL	
[redacted]	0.0047	FAIL	
[redacted]	0.0039	FAIL	
[redacted]	0.0054	SUCCESS	y
[redacted]	0.0025	FAIL	
[redacted]	0.0017	FAIL	
[redacted]	0.0018	FAIL	
[redacted]	0.0028	FAIL	
[redacted]	0.0034	FAIL	
[redacted]	0.0012	FAIL	
[redacted]	0.0014	FAIL	
[redacted]	0.0043	FAIL	
[redacted]	0.0042	FAIL	
[redacted]	0.0031	FAIL	
[redacted]	0.0021	FAIL	
[redacted]	0.0026	FAIL	
[redacted]	0.0043	SUCCESS	y
[redacted]	0.0037	SUCCESS	y
[redacted]	0.0074	SUCCESS	y
[redacted]	0.0041	FAIL	
[redacted]	0.0082	FAIL	
[redacted]	0.0041	FAIL	
[redacted]	0	FAIL	
[redacted]	0.0052	FAIL	
[redacted]	0.0058	FAIL	
[redacted]	0.0015	FAIL	
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[redacted]	0.0054	FAIL	
[redacted]	0.006	FAIL	
[redacted]	0.0042	FAIL	
[redacted]	0.0018	FAIL	
[redacted]	0.005	FAIL	
[redacted]	0.005	FAIL	
[redacted]	0.0035	FAIL	
[redacted]	0.0012	SUCCESS	n
[redacted]	0.0057	FAIL	
[redacted]	0.0062	SUCCESS	n
[redacted]	0.0022	FAIL	

[redacted]	0.0074	FAIL		
[redacted]	0.0021	FAIL		
[redacted]	0.0082	FAIL		
[redacted]	0.006	FAIL		
[redacted]	0.0086	FAIL		
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[redacted]	0.0063	FAIL		
[redacted]	0.0017	SUCCESS	y	
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[redacted]	0.0044	SUCCESS	y	
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[redacted]	0.0007	FAIL		
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[redacted]	0.0068	FAIL		
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[redacted]	0.0088	FAIL		
[redacted]	0.0064	SUCCESS	y	y
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[redacted]	0.0083	SUCCESS	y	
[redacted]	0.0084	FAIL		
[redacted]	0.007	FAIL		
[redacted]	0.0022	FAIL		
[redacted]	0.0019	FAIL		
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[redacted]	0.0032	SUCCESS	y	

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[redacted]	0.0019	SUCCESS	n		
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[redacted]	0.0048	FAIL	

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[redacted]	0.0058	FAIL		
[redacted]	0.0046	SUCCESS	y	
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[redacted]	0.0065	SUCCESS	y	
[redacted]	0.0086	FAIL		
[redacted]	0.0076	SUCCESS	n	
[redacted]	0.0015	FAIL		

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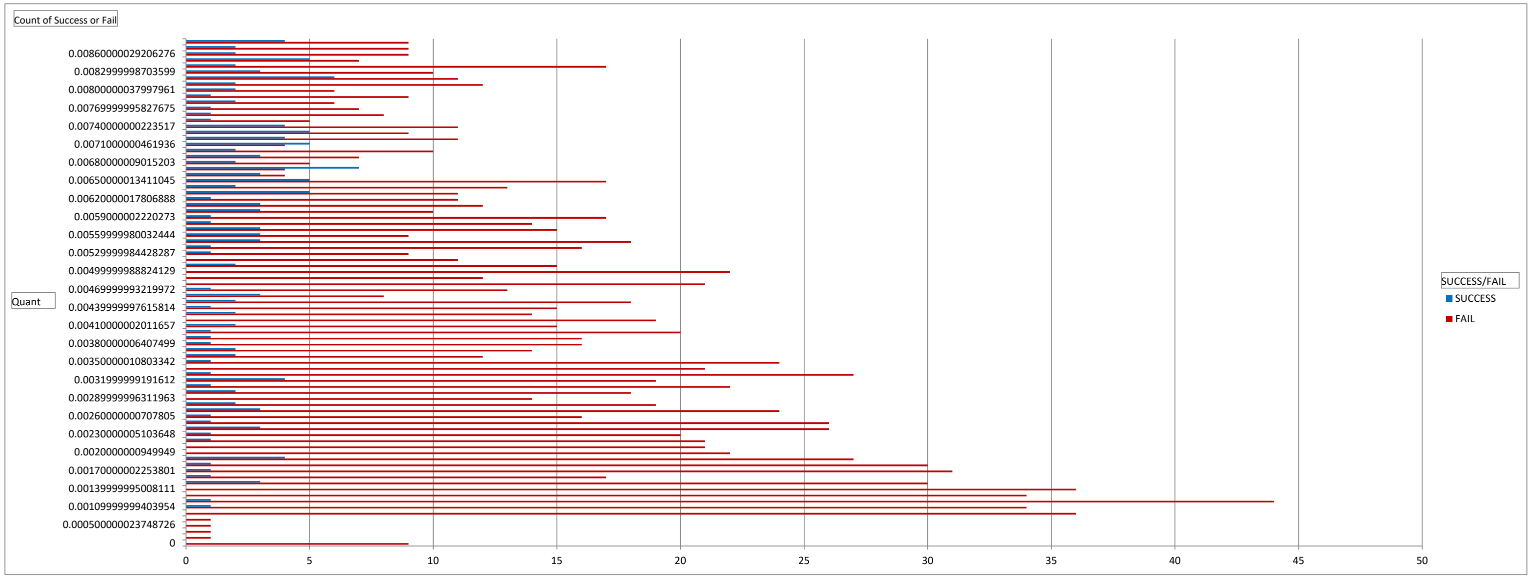
0.0022	FAIL	
0.0056	SUCCESS	n
0.008	SUCCESS	Y
0.0049	FAIL	
0.0045	FAIL	
0.0048	FAIL	
0.0012	FAIL	
0.0011	FAIL	
0.0077	FAIL	
0.0073	FAIL	
0.0013	FAIL	
0.0021	FAIL	
0.0044	FAIL	
0.0048	FAIL	
0.0064	FAIL	
0.0031	FAIL	
0.0013	FAIL	
0.0012	FAIL	
0.004	FAIL	

Count of Success or	Column Labels		
Row Labels	**FAIL**	**SUC**	**Grand Total**
0	9		9
0.0003	1		1
0.0004	1		1
0.0005	1		1
0.0007	1		1
0.001	36		36
0.0011	34	1	35
0.0012	44	1	45
0.0013	34		34
0.0014	36		36
0.0015	30	3	33
0.0016	17	1	18
0.0017	31	1	32
0.0018	30	1	31
0.0019	27	4	31
0.002	22		22
0.0021	21		21
0.0022	21	1	22
0.0023	20	1	21
0.0024	26	3	29
0.0025	26	1	27
0.0026	16	1	17
0.0027	24	3	27
0.0028	19	2	21
0.0029	14		14
0.003	18	2	20
0.0031	22	1	23
0.0032	19	4	23
0.0033	27	1	28
0.0034	21		21
0.0035	24	1	25
0.0036	12	2	14
0.0037	14	2	16
0.0038	16	1	17
0.0039	16	1	17
0.004	20	1	21
0.0041	15	2	17
0.0042	19		19
0.0043	14	2	16
0.0044	15	1	16
0.0045	18	2	20
0.0046	8	3	11
0.0047	13	1	14
0.0048	21		21
0.0049	12		12
0.005	22		22
0.0051	15	2	17
0.0052	11		11
0.0053	9	1	10
0.0054	16	1	17
0.0055	18	3	21
0.0056	9	3	12
0.0057	15	3	18
0.0058	14	1	15
0.0059	17	1	18
0.006	10	3	13
0.0061	12	3	15
0.0062	11	1	12
0.0063	11	5	16
0.0064	13	2	15
0.0065	17	5	22
0.0066	4	3	7
0.0067	4	7	11
0.0068	5	2	7
0.0069	7	3	10
0.007	10	2	12
0.0071	4	5	9
0.0072	11	4	15
0.0073	9	5	14
0.0074	11	4	15
0.0075	5	1	6
0.0076	8	1	9
0.0077	7	1	8
0.0078	6	2	8
0.0079	9	1	10
0.008	6	2	8
0.0081	12	2	14
0.0082	11	6	17
0.0083	10	3	13
0.0084	17	2	19
0.0085	7	5	12
0.0086	9	2	11
0.0087	9	2	11
0.0088	9	4	13
Grand Total	**1295**	**154**	**1449**



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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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Barcode	Quant	EXHinterp	SUCCESS/FAIL
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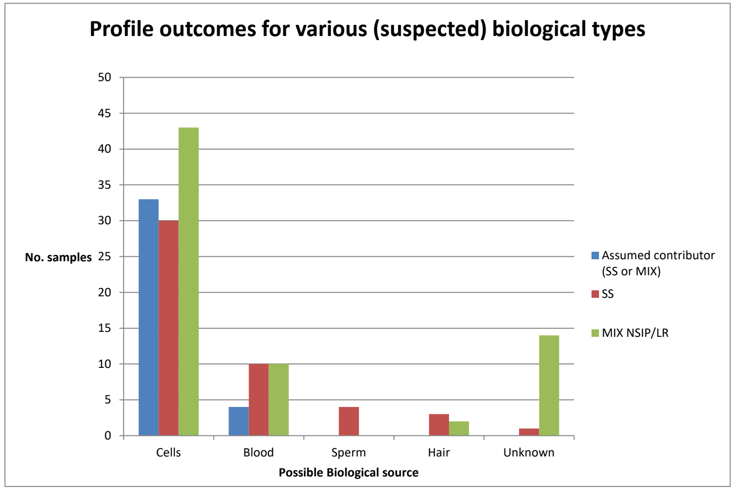
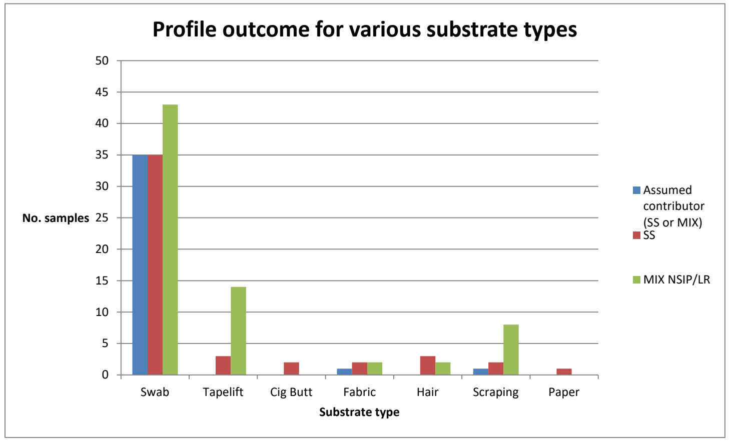
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1

Barcode	Quant	EXHinterp	Sample type	Sampled Substrate type	? Possible biological type	Profile type	
[redacted]	0.0011	SUCCESS	swab	LVS SFRAC	Cells	SS AKC	
[redacted]	0.0012	SUCCESS	swab	Anal/Rectal SFRAC	Cells	SS AKC	
[redacted]	0.0015	SUCCESS	swab	PM Body SFRAC	Cells	SS AKC	
[redacted]	0.0015	SUCCESS	swab	Shoe stain	Blood	SS AKC	
[redacted]	0.0015	SUCCESS	swab	Perianal	Cells	SS AKC	
[redacted]	0.0016	SUCCESS	swab	Unknown	Cells	MIX NSIP/LR	2p or 3 p mix, suitable for LRs only if obtained
[redacted]	0.0017	SUCCESS	swab	Anal/Rectal SFRAC	Cells	SS AKC	
[redacted]	0.0018	SUCCESS	hair	drop sheet	hair	MIX NSIP/LR	
[redacted]	0.0019	SUCCESS	swab	endocervical SFRAC	Cells	SS AKC	
[redacted]	0.0019	SUCCESS	swab	penis	Cells	SS AKC	
[redacted]	0.0019	SUCCESS	hair	drop sheet	hair	SS	Ownership not known; contribution can't be assumed; matches profile elsewhere eg. UK; profile for NCIDD
[redacted]	0.0019	SUCCESS	swab	Wall stain	Blood	SS	
[redacted]	0.0022	SUCCESS	swab	LVS SFRAC	Cells	SS AKC	
[redacted]	0.0023	SUCCESS	tapelift	Bag handles	Cells	MIX NSIP/LR	
[redacted]	0.0024	SUCCESS	swab	penis	Cells	MIX AKC	Where conditioned and nothing remaining (s/thresh)
[redacted]	0.0024	SUCCESS	swab	Nail scrapings	Cells	MIX AKC	
[redacted]	0.0024	SUCCESS	tapelift	wipe SFRAC	Unknown	MIX NSIP/LR	
[redacted]	0.0025	SUCCESS	swab	buccal/oral SFRAC	Cells	SS AKC	
[redacted]	0.0026	SUCCESS	swab	penis SFRAC	Cells	SS AKC	Most likely in absence of reference profile, and given other samples in case.
[redacted]	0.0027	SUCCESS	swab	buccal/oral SFRAC	Cells	SS AKC	
[redacted]	0.0027	SUCCESS	swab	vulval SFRAC	Unknown	MIX NSIP/LR	
[redacted]	0.0027	SUCCESS	swab	Cervical SFRAC	Cells	SS AKC	
[redacted]	0.0028	SUCCESS	hair	drop sheet	hair	MIX NSIP/LR	
[redacted]	0.0028	SUCCESS	swab	Glasses	Cells	SS AKC	Most likely in absence of reference profile, and given other samples in case.
[redacted]	0.0030	SUCCESS	swab	Driveway stain	Blood	SS	
[redacted]	0.0030	SUCCESS	swab	Bottle	Cells	SS	
[redacted]	0.0031	SUCCESS	tapelift	wipe EFRAC	Cells	SS	
[redacted]	0.0032	SUCCESS	swab	vehicle headlight	Cells	SS	
[redacted]	0.0032	SUCCESS	swab	Bottle	Cells	MIX NSIP/LR	
[redacted]	0.0032	SUCCESS	swab	Bottle	Cells	SS	
[redacted]	0.0032	SUCCESS	swab	fabric	Blood	SS AKC	
[redacted]	0.0033	SUCCESS	swab	HVS SFRAC	Cells	SS AKC	
[redacted]	0.0035	SUCCESS	swab	Anal/Rectal SFRAC	Cells	SS	
[redacted]	0.0036	SUCCESS	swab	Glove	Cells	MIX NSIP/LR	
[redacted]	0.0036	SUCCESS	swab	vaginal SFRAC	Cells	SS AKC	
[redacted]	0.0037	SUCCESS	swab	phone	Cells	MIX NSIP/LR	
[redacted]	0.0037	SUCCESS	tapelift	Glove	Cells	MIX NSIP/LR	
[redacted]	0.0038	SUCCESS	swab	Glasses	Cells	SS	
[redacted]	0.0039	SUCCESS	swab	LVS SFRAC	Unknown	MIX NSIP/LR	
[redacted]	0.0040	SUCCESS	swab	door	Blood	MIX NSIP/LR	
[redacted]	0.0041	SUCCESS	swab	Anal/Rectal SFRAC	Cells	SS AKC	
[redacted]	0.0041	SUCCESS	swab	tape	Cells	SS	
[redacted]	0.0043	SUCCESS	tapelift	hose	Cells	SS	
[redacted]	0.0043	SUCCESS	tapelift	Glove	Cells	MIX NSIP/LR	
[redacted]	0.0044	SUCCESS	cig butt	cig butt	Cells	SS	
[redacted]	0.0045	SUCCESS	swab	metal	Blood	MIX NSIP/LR	
[redacted]	0.0045	SUCCESS	swab	Window sill	Blood	MIX NSIP/LR	
[redacted]	0.0046	SUCCESS	swab	Nipple	Cells	MIX NSIP/LR	
[redacted]	0.0046	SUCCESS	swab	number plate	Cells	MIX NSIP/LR	
[redacted]	0.0046	SUCCESS	swab	Nipple	Cells	MIX NSIP/LR	
[redacted]	0.0047	SUCCESS	tapelift	Window ledge	Cells	MIX NSIP/LR	
[redacted]	0.0051	SUCCESS	swab	Glove	Cells	MIX NSIP/LR	
[redacted]	0.0051	SUCCESS	swab	straw	Cells	SS	
[redacted]	0.0053	SUCCESS	swab	penis SFRAC	Cells	SS AKC	
[redacted]	0.0054	SUCCESS	swab	carpet	Blood	MIX NSIP/LR	
[redacted]	0.0055	SUCCESS	fabric	Clothing SFRAC	Sperm	SS	
[redacted]	0.0055	SUCCESS	swab	HVS SFRAC	Cells	SS AKC	
[redacted]	0.0055	SUCCESS	swab	drink can	Cells	MIX NSIP/LR	
[redacted]	0.0056	SUCCESS	swab	vulval SFRAC	Cells	SS AKC	
[redacted]	0.0056	SUCCESS	swab	toothbrush	Cells	MIX NSIP/LR	
[redacted]	0.0056	SUCCESS	swab	straw	Cells	SS	
[redacted]	0.0057	SUCCESS	swab	Labia SFRAC	Unknown	MIX NSIP/LR	
[redacted]	0.0057	SUCCESS	scraping	Clothing SFRAC	Unknown	MIX NSIP/LR	
[redacted]	0.0057	SUCCESS	swab	plastic bag	Cells	SS	
[redacted]	0.0058	SUCCESS	swab	Labia	Cells	SS AKC	
[redacted]	0.0059	SUCCESS	fabric	Clothing	Blood	SS	

	Assumed contributor (SS or MIX)	SS	MIX NSIP/LR
Cells	33	30	43
Blood	4	10	10
Sperm	0	4	0
Hair	0	3	2
Unknown	0	1	14



	Assumed contributor (SS or MIX)	SS	MIX NSIP/LR
Swab	35	35	43
Tapelift	0	3	14
Cig Butt	0	2	0
Fabric	1	2	2
Hair	0	3	2
Scraping	1	2	8
Paper	0	1	0



Barcode	Quant	EXHinterp	Sample type	Sampled Substrate type	? Possible biological type	Profile type
[redacted]	.0060	SUCCESS	swab	skin	Cells	SS
[redacted]	.0060	SUCCESS	tapelift	knife	Blood	MIX NSIP/LR
[redacted]	.0060	SUCCESS	swab	penis	Cells	MIX NSIP/LR
[redacted]	.0061	SUCCESS	swab	Nipple	Cells	SS AKC
[redacted]	.0061	SUCCESS	swab	clothing	Blood	MIX NSIP/LR
[redacted]	.0061	SUCCESS	tapelift	plastic gear knob	Cells	MIX NSIP/LR
[redacted]	.0062	SUCCESS	swab	vulval SFRAC	Cells	SS AKC
[redacted]	.0063	SUCCESS	swab	glass window	Blood	SS
[redacted]	.0063	SUCCESS	swab	bottle	Cells	MIX NSIP/LR
[redacted]	.0063	SUCCESS	swab	Driveway stain	Blood	SS
[redacted]	.0063	SUCCESS	swab	lighter	Cells	MIX NSIP/LR
[redacted]	.0063	SUCCESS	swab	nail	Cells	SS
[redacted]	.0064	SUCCESS	scraping	blanket	Unknown	MIX NSIP/LR
[redacted]	.0064	SUCCESS	swab	Bottle	Cells	SS
[redacted]	.0065	SUCCESS	swab	tiles	Blood	SS
[redacted]	.0065	SUCCESS	swab	firearm	Cells	MIX NSIP/LR
[redacted]	.0065	SUCCESS	swab	handle	Cells	MIX NSIP/LR
[redacted]	.0065	SUCCESS	tapelift	glasses	Cells	MIX NSIP/LR
[redacted]	.0065	SUCCESS	fabric	clothing	Cells	MIX NSIP/LR
[redacted]	.0066	SUCCESS	scraping	SFRAC	Sperm	SS
[redacted]	.0066	SUCCESS	swab	bottle	Cells	SS
[redacted]	.0066	SUCCESS	swab	plastic	Cells	MIX NSIP/LR
[redacted]	.0067	SUCCESS	swab	handle	Blood	SS
[redacted]	.0067	SUCCESS	swab	bottle	Cells	SS
[redacted]	.0067	SUCCESS	swab	window	Cells	MIX NSIP/LR
[redacted]	.0067	SUCCESS	hair	tape	hair	SS
[redacted]	.0067	SUCCESS	tapelift	fabric	Cells	MIX NSIP/LR
[redacted]	.0067	SUCCESS	tapelift	plastic	Cells	MIX NSIP/LR
[redacted]	.0067	SUCCESS	swab	vaginal SFRAC	Unknown	MIX NSIP/LR
[redacted]	.0068	SUCCESS	paper	stain	Blood	SS
[redacted]	.0068	SUCCESS	swab	knife	Cells	SS
[redacted]	.0069	SUCCESS	swab	ring	Blood	MIX NSIP/LR
[redacted]	.0069	SUCCESS	swab	Unknown	Cells	SS
[redacted]	.0069	SUCCESS	swab	perianal SFRAC	Blood	SS AKC
[redacted]	.0070	SUCCESS	swab	penis	Cells	SS AKC
[redacted]	.0070	SUCCESS	swab	skin	Cells	MIX AKC
[redacted]	.0071	SUCCESS	swab	Nipple	Cells	MIX NSIP/LR
[redacted]	.0071	SUCCESS	swab	hand	Cells	SS AKC
[redacted]	.0071	SUCCESS	swab	LVS SFRAC	Cells	SS AKC
[redacted]	.0071	SUCCESS	swab	needle	Blood	SS
[redacted]	.0071	SUCCESS	swab	cup	Cells	MIX NSIP/LR
[redacted]	.0072	SUCCESS	swab	penis	Cells	MIX NSIP/LR
[redacted]	.0072	SUCCESS	swab	toothbrush	Cells	SS
[redacted]	.0072	SUCCESS	swab	plastic bag	Cells	MIX NSIP/LR
[redacted]	.0072	SUCCESS	tapelift	glove	Cells	MIX NSIP/LR
[redacted]	.0073	SUCCESS	swab	condom SFRAC	Unknown	SS
[redacted]	.0073	SUCCESS	tapelift	plastic	Cells	MIX NSIP/LR
[redacted]	.0073	SUCCESS	swab	plastic	Blood	MIX NSIP/LR
[redacted]	.0073	SUCCESS	tapelift	steering wheel	Cells	SS
[redacted]	.0073	SUCCESS	scraping	fabric SFRAC	Unknown	MIX NSIP/LR
[redacted]	.0074	SUCCESS	swab	clothing	Blood	MIX NSIP/LR
[redacted]	.0074	SUCCESS	swab	shoes	Blood	SS
[redacted]	.0074	SUCCESS	swab	gear knob	Cells	MIX NSIP/LR
[redacted]	.0074	SUCCESS	swab	can	Cells	SS
[redacted]	.0075	SUCCESS	swab	breast	Cells	MIX NSIP/LR
[redacted]	.0076	SUCCESS	scraping	clothing	Cells	MIX NSIP/LR
[redacted]	.0077	SUCCESS	cig butt	cig butt	Cells	SS
[redacted]	.0078	SUCCESS	swab	glove	Cells	MIX NSIP/LR
[redacted]	.0078	SUCCESS	swab	floor EFRAC	Cells	SS
[redacted]	.0079	SUCCESS	swab	condom packet	Cells	MIX NSIP/LR
[redacted]	.0080	SUCCESS	swab	HVS SFRAC	Cells	SS AKC
[redacted]	.0080	SUCCESS	tapelift	fabric SFRAC	Unknown	MIX NSIP/LR
[redacted]	.0081	SUCCESS	swab	bottle	Cells	SS
[redacted]	.0081	SUCCESS	scraping	fabric SFRAC	Unknown	MIX NSIP/LR
[redacted]	.0082	SUCCESS	hair	condom	hair	SS
[redacted]	.0082	SUCCESS	tapelift	cartridge	Cells	MIX NSIP/LR
[redacted]	.0082	SUCCESS	scraping	clothing SFRAC	Unknown	MIX NSIP/LR
[redacted]	.0082	SUCCESS	swab	tool	Cells	SS
[redacted]	.0082	SUCCESS	fabric	clothing	Cells	MIX AKC
[redacted]	.0082	SUCCESS	swab	breast	Cells	MIX NSIP/LR
[redacted]	.0083	SUCCESS	swab	endocervical SFRAC	Cells	SS AKC
[redacted]	.0083	SUCCESS	swab	perianal SFRAC	Sperm	SS
[redacted]	.0083	SUCCESS	scraping	clothing SFRAC	Cells	MIX AKC
[redacted]	.0084	SUCCESS	swab	can	Cells	SS
[redacted]	.0084	SUCCESS	fabric	clothing	Blood	MIX NSIP/LR

[redacted]	Quant	EXHinterp	Sample type	Sampled Substrate type	? Possible biological type	Profile type
[redacted]	0.0085	SUCCESS	scraping	fabric SFRAC	Unknown	MIX NSIP/LR
[redacted]	0.0085	SUCCESS	scraping	bedding SFRAC	Unknown	MIX NSIP/LR
[redacted]	0.0085	SUCCESS	swab	can	Cells	SS
[redacted]	0.0085	SUCCESS	swab	can	Cells	MIX NSIP/LR
[redacted]	0.0085	SUCCESS	swab	tiles EFRAC	Cells	MIX NSIP/LR
[redacted]	0.0086	SUCCESS	swab	bottle	Cells	MIX NSIP/LR
[redacted]	0.0086	SUCCESS	swab	penis	Cells	MIX AKC
[redacted]	0.0087	SUCCESS	swab	hand	Blood	MIX AKC
[redacted]	0.0087	SUCCESS	swab	gun	Cells	MIX NSIP/LR
[redacted]	0.0088	SUCCESS	swab	can	Cells	SS
[redacted]	0.0088	SUCCESS	scraping	fabric SFRAC	Sperm	SS
[redacted]	0.0088	SUCCESS	swab	straw	Cells	SS
[redacted]	0.0088	SUCCESS	swab	HVS SFRAC	Unknown	MIX NSIP/LR

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0089	FAIL	-1	Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.009	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.009	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.009	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0091	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0091	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0091	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0091	FAIL	-1	CMPU
[redacted]	0.0091	SUCCESS	1	consistent elsewhere
[redacted]	0.0091	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0091	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0092	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0092	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0092	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0092	SUCCESS	1	P SS
[redacted]	0.0093	FAIL	-1	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0093	SUCCESS	1	P SS
[redacted]	0.0093	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0093	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0094	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0094	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0094	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0094	FAIL	-1	CMPU
[redacted]	0.0094	FAIL	-1	CMPU
[redacted]	0.0094	SUCCESS	1	3p
[redacted]	0.0094	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion 3 person mix - support for contribution 100 to 1000
[redacted]	0.0094	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 3 person mix - supports non contribution
[redacted]	0.0094	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix remaining - supports non contribution
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	CMPU
[redacted]	0.0095	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD
[redacted]	0.0095	SUCCESS	1	3p
[redacted]	0.0095	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0095	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0095	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	0.0095	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib
[redacted]	0.0096	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0096	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0096	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0096	SUCCESS	1	cond
[redacted]	0.0096	SUCCESS	1	ss akc
[redacted]	0.0096	SUCCESS	1	SS DNA profile 9 loci and above LR > 100 billion Possible sub-threshold information
[redacted]	0.0096	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - supports non contribution
[redacted]	0.0096	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0097	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0098	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0098	SUCCESS	1	Hair located. Submitted-results pending Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	0.0099	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0099	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.01	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.01	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.01	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.01	FAIL	-1	cmpu
[redacted]	0.01	FAIL	-1	cmpu
[redacted]	0.01	FAIL	-1	cmpu
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	SUCCESS	1	ss
[redacted]	0.0101	SUCCESS	1	Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem - support for contrib 1 billion -100 billion
[redacted]	0.0101	SUCCESS	1	Submitted-results pending. Single source DNA profile
[redacted]	0.0101	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	0.0102	FAIL	-1	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0102	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0102	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0102	SUCCESS	1	ss
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Micro neg for sperm Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	0.0103	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0104	FAIL	-1	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	SUCCESS	1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	SUCCESS	1	Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	0.0105	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0105	SUCCESS	1	ss
[redacted]	0.0106	FAIL	-1	Submitted-results pending. ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	0.0106	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0107	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0107	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0107	FAIL	-1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	cmpu
[redacted]	0.0109	FAIL	-1	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0109	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0109	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0109	FAIL	-1	cmpu
[redacted]	0.0109	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib 3 person mix remaining - supports non contribution
[redacted]	0.011	FAIL	-1	Labelling discrepancy Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.011	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.011	SUCCESS	1	2p
[redacted]	0.011	SUCCESS	1	3p
[redacted]	0.011	SUCCESS	1	2p
[redacted]	0.011	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Single evidence sample excluded 3 person mix - supports non contribution

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.011	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion
[redacted]	0.0111	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0111	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0111	FAIL	-1	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	0.0111	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile
[redacted]	0.0111	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0112	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	SUCCESS	1	Submitted as cells Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0112	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile Suspect check - supports non contribution
[redacted]	0.0113	FAIL	-1	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0113	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0113	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0113	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0113	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0113	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed Single evidence sample excluded 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0114	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0114	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	0.0115	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0115	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0115	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0115	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0116	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0116	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0117	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	cmpu
[redacted]	0.0118	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0118	SUCCESS	1	ss
[redacted]	0.0118	SUCCESS	1	2p
[redacted]	0.0118	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix profile - support for contrib > 100 billion 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0118	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0119	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0119	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0119	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0119	SUCCESS	1	2p
[redacted]	0.0119	SUCCESS	1	ss
[redacted]	0.0119	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	0.0119	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.012	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.012	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.012	SUCCESS	1	mix
[redacted]	0.012	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	SUCCESS	1	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0122	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0122	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0122	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0122	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0123	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0123	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0123	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0123	FAIL	-1	cmpu
[redacted]	0.0123	SUCCESS	1	mix
[redacted]	0.0123	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0123	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution
[redacted]	0.0124	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0124	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0124	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0124	SUCCESS	1	mix
[redacted]	0.0124	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0124	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0125	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0125	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0125	SUCCESS	1	mix
[redacted]	0.0125	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0126	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0126	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0126	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0126	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
				Micro positive for sperm. Submitted-Results pending
				Complex mixed profile unsuitable for interp or comparison
				This sample has undergone further processing
				Two person mixed DNA profile
				2 person mixed profile - conditioned on
				2 person mix rem - support for contribution > 100 billion
[redacted]	0.0128	FAIL	-1	Possible sub-threshold information
				Semen not detected
				Submitted as cells
[redacted]	0.0128	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0128	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0128	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0128	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Interim result- mixed profile obtained. Rework Reqd
				Three person mixed DNA profile
				3 person mix profile - support for contrib > 100 billion
				Mixture-low support for contrib or supports non contrib
[redacted]	0.0128	SUCCESS	1	3 person mix - support for contrib 100 000 to 1 million
				Submitted-results pending.
[redacted]	0.0128	SUCCESS	1	Single source 20 loci DNA profile LR > 100 billion
				Submitted-results pending.
				Single source DNA profile
[redacted]	0.0128	SUCCESS	1	Possible sub-threshold information
				Sample on hold - awaiting advice
				Submitted-results pending.
[redacted]	0.0129	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Single source DNA profile
				NCIDD upload single source DNA profile
[redacted]	0.0129	SUCCESS	1	Possible sub-threshold information
				Submitted-results pending.
				Single source DNA profile
				Possible sub-threshold information
[redacted]	0.0129	SUCCESS	1	NCIDD upload single source DNA profile
				Submitted-results pending.
[redacted]	0.013	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.013	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.013	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.013	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.013	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Single Source DNA profile - assumed known contributor
[redacted]	0.013	SUCCESS	1	Possible sub-threshold information
[redacted]	0.0131	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0131	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0131	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Three person mixed DNA profile
				No statistical interpretation performed
				3 person mix profile - support for contrib > 100 billion
				Two person mixed DNA profile
[redacted]	0.0131	SUCCESS	1	2 person mix profile - support for contrib > 100 billion
				Submitted-results pending.
				Interim result- mixed profile obtained. Rework Reqd
[redacted]	0.0132	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0132	SUCCESS	1	mix
				Micro positive for sperm. Submitted-Results pending
				Three person mixed DNA profile
				3 person mixed profile - conditioned on
[redacted]	0.0132	SUCCESS	1	3 person mix remaining - supports non contribution
				Submitted-results pending.
[redacted]	0.0133	FAIL	-1	Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0133	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0133	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0133	FAIL	-1	cmpu
[redacted]	0.0133	FAIL	-1	cmpu
[redacted]	0.0133	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0133	SUCCESS	1	Submitted-results pending. Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0133	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution
[redacted]	0.0134	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0134	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0134	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0134	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0134	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0135	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0135	FAIL	-1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	0.0135	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0135	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0135	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Mixture-low support for contrib or supports non contrib 3 person mix - low support for contribution
[redacted]	0.0135	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded
[redacted]	0.0136	FAIL	-1	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0136	SUCCESS	1	Submitted as cells Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0136	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million Mixture-low support for contrib or supports non contrib Excluded from mixed DNA profile
[redacted]	0.0137	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0137	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0138	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0138	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0138	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0138	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0139	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0139	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile NCIDD upload - mixed DNA profile Excluded from mixed DNA profile
[redacted]	0.0139	SUCCESS	1	Submitted-results pending. Single source DNA profile SS DNA profile 9 loci and above LR > 100 billion
[redacted]	0.0139	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.014	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.014	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.014	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.014	SUCCESS	1	ss
[redacted]	0.014	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information Single Source DNA profile - assumed known contributor
[redacted]	0.014	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution
[redacted]	0.014	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.014	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	0.014	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile Mix Rem DNA contrib < NCIDD matching Stringency
[redacted]	0.0141	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0141	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0141	SUCCESS	1	Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person rem- support for contrib 1 billion-100 billion
[redacted]	0.0142	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0142	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0142	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
				Presump. PSA test positive, no sperm found
				Two person mixed DNA profile
				2 person mixed profile - conditioned on
[redacted]	0.0142	SUCCESS	1	2 person rem- support for contrib 1 million to 1 billion
				Submitted-results pending.
				Two person mixed DNA profile
				Suspect check inconclusive - mixed DNA profile
[redacted]	0.0142	SUCCESS	1	Suspect check - supports non contribution
[redacted]	0.0143	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0143	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0143	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Two person mixed DNA profile
				Single source DNA profile
				NCIDD upload single source DNA profile
[redacted]	0.0143	SUCCESS	1	Possible sub-threshold information
				Micro positive for sperm. Submitted-Results pending
				Three person mixed DNA profile
				3 person mixed profile - conditioned on
				3 person mix remaining - supports non contribution
				Two person mixed DNA profile
				2 person mixed profile - conditioned on
				Single evidence sample excluded
[redacted]	0.0143	SUCCESS	1	Possible sub-threshold information
				Submitted-results pending.
				Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0143	SUCCESS	1	Possible sub-threshold information
				Submitted-results pending.
				Three person mixed DNA profile
[redacted]	0.0143	SUCCESS	1	3 person mix profile - support for contrib > 100 billion
				Submitted-results pending.
[redacted]	0.0144	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0144	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0144	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted as cells
				Single source DNA profile
				NCIDD upload single source DNA profile
				Single Source DNA profile - assumed known contributor
[redacted]	0.0144	SUCCESS	1	DNA profile removed from NCIDD
				Submitted-results pending.
				Interim result- mixed profile obtained. Rework Reqd
				Three person mixed DNA profile
				3 person mix profile - support for contrib > 100 billion
				Excluded from mixed DNA profile
[redacted]	0.0144	SUCCESS	1	3 person mix profile - support for contrib > 100 billion
				Submitted-results pending.
[redacted]	0.0145	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0145	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Three person mixed DNA profile
[redacted]	0.0145	SUCCESS	1	3 person mix profile - support for contrib > 100 billion
				Submitted-results pending.
[redacted]	0.0146	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0146	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0146	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Single source DNA profile
[redacted]	0.0146	SUCCESS	1	NCIDD upload single source DNA profile
				Submitted for cells. Presumptive saliva test pending.
				Presump Saliva test negative
				Two person mixed DNA profile
				Single evidence sample excluded
				This sample has undergone further processing
[redacted]	0.0147	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0147	FAIL	-1	Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0147	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0148	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0148	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0148	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0148	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0148	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0149	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0149	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0149	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.015	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.015	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.015	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.015	SUCCESS	1	ss
[redacted]	0.015	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.015	SUCCESS	1	Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Single evidence sample excluded
[redacted]	0.0151	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0151	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0151	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0151	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0151	FAIL	-1	cmpu
[redacted]	0.0152	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0152	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0152	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0153	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0153	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0154	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0154	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0154	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0154	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0154	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0155	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0155	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0156	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0156	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0156	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Excluded from mixed DNA profile
[redacted]	0.0156	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile Single evidence sample excluded
[redacted]	0.0157	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0157	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0158	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0158	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0158	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix rem - support for contribution > 100 billion Single evidence sample excluded
[redacted]	0.0159	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.016	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.016	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.016	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.016	SUCCESS	1	Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	0.016	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution
[redacted]	0.016	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0161	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0161	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0161	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0162	FAIL	-1	Semen not detected Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0162	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0162	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0162	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0162	SUCCESS	1	2 person mix remaining - supports non contribution Submitted as cells Two person mixed DNA profile 2 person mix - supports non contribution Sample undergone further work - conditioned Two person mixed DNA profile 2 person mixed profile - conditioned on

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0162	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0162	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix- support for contrib 1 billion - 100 billion 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0163	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0163	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0163	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0163	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0164	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0164	FAIL	-1	cmpu
[redacted]	0.0164	SUCCESS	1	ss
[redacted]	0.0164	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0165	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0165	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0165	FAIL	-1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	0.0165	SUCCESS	1	Single evidence sample excluded Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0166	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0166	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	0.0167	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0167	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0167	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0167	SUCCESS	1	mix
[redacted]	0.0168	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0168	FAIL	-1	cmpu
[redacted]	0.0168	FAIL	-1	cmpu
[redacted]	0.0168	SUCCESS	1	Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.0168	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	0.0169	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0169	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0169	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.017	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information This sample has undergone further processing Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.017	SUCCESS	1	mix
[redacted]	0.0171	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 Mixture-low support for contrib or supports non contrib
[redacted]	0.0172	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0172	SUCCESS	1	ss
[redacted]	0.0172	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0173	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0173	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0173	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0173	SUCCESS	1	Single source DNA profile NCIDD upload single source DNA profile Single Source DNA profile - assumed known contributor DNA profile removed from NCIDD
[redacted]	0.0173	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution 3 person mix - support for contrib 10 000 - 100 000 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 2 person mix rem - support for contrib 10 000 to 100 000 2 person mix remaining - supports non contribution 2 person mix remaining - supports non contribution 3 person mix rem - support for contrib 10 000 to 100 000 3 person mix remaining - supports non contribution 3 person mix remaining - supports non contribution
[redacted]	0.0174	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0174	FAIL	-1	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0174	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0174	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 1 million - 1 billion Excluded from mixed DNA profile
[redacted]	0.0175	SUCCESS	1	mix
[redacted]	0.0175	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	0.0176	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0176	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0176	FAIL	-1	cmpu
[redacted]	0.0176	FAIL	-1	cmpu
[redacted]	0.0176	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0178	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0178	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0178	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0178	SUCCESS	1	mix

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0178	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0179	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0179	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - supports non contribution
[redacted]	0.018	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.018	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0181	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0183	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0183	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0183	SUCCESS	1	mix
[redacted]	0.0184	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0184	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0184	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD
[redacted]	0.0185	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0185	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0185	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0186	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0186	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0186	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0186	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0186	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.0187	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0187	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
				Suspect Check Actioned - No Match
				Suspect Check Actioned - No Match
				Suspect Check Actioned - No Match
				Suspect Check Actioned - No Match
				Suspect check - low support for contribution
				Micro positive for sperm. Submitted-Results pending
				Interim result- mixed profile obtained. Rework Reqd
				Two person mixed DNA profile
				2 person mixed profile - conditioned on
				Excluded from mixed DNA profile
				Mix remaining DNA contrib unsuitable for NCIDD searching
				Suspect Check Actioned - No Match
				Suspect Check Actioned - No Match
				Suspect Check Actioned - No Match
[redacted]	0.0187	FAIL	-1	Suspect Check Actioned - No Match
				Submitted-results pending.
[redacted]	0.0189	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Micro positive for sperm. Submitted-Results pending
				Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0189	SUCCESS	1	Possible sub-threshold information
				Submitted-results pending.
[redacted]	0.019	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.019	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0191	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0191	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0192	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0192	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0193	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0193	SUCCESS	1	ss
[redacted]	0.0194	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0195	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0195	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0195	SUCCESS	1	Three person mixed DNA profile
				Submitted-results pending.
				Three person mixed DNA profile
[redacted]	0.0195	SUCCESS	1	3 person mix profile - support for contrib > 100 billion
				Submitted-results pending.
				Three person mixed DNA profile
				No statistical interpretation performed
				3 person mix profile - support for contrib > 100 billion
[redacted]	0.0195	SUCCESS	1	Excluded from mixed DNA profile
				Submitted-results pending.
[redacted]	0.0195	SUCCESS	1	Two person mixed DNA profile
				Submitted-results pending.
[redacted]	0.0196	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
				Single source DNA profile
				Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0197	SUCCESS	1	Possible sub-threshold information
				Submitted-results pending.
				Three person mixed DNA profile
[redacted]	0.0197	SUCCESS	1	3 person mix profile - support for contrib > 100 billion
				Submitted-results pending.
				Three person mixed DNA profile
				Excluded from mixed DNA profile
				3 person mix profile - support for contrib > 100 billion
[redacted]	0.0197	SUCCESS	1	3 person mix - support for contribution 100 to 1000
				Submitted-results pending.
[redacted]	0.0198	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
				Submitted-results pending.
[redacted]	0.0198	FAIL	-1	Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0198	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000
[redacted]	0.0198	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0198	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on
[redacted]	0.0199	FAIL	-1	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0199	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - low support for contribution
[redacted]	0.0199	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0199	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	0.02	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.02	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Suspect Check Actioned - No Match
[redacted]	0.0201	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0202	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0202	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0202	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0202	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD Intel upload - single source partial profile NCIDD upload single source DNA profile
[redacted]	0.0202	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0203	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0203	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0203	FAIL	-1	Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0203	SUCCESS	1	ss
[redacted]	0.0203	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0203	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix- support for contrib 1 billion - 100 billion 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0204	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0204	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0204	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded 3 Person Mix Rem contrib unsuitable for NCIDD

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0205	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0205	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0205	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0205	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0205	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	0.0205	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0206	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0208	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0208	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0208	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0208	SUCCESS	1	Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0209	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.021	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.021	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Excluded from mixed DNA profile
[redacted]	0.0211	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mixture-low support for contrib or supports non contrib
[redacted]	0.0211	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion
[redacted]	0.0211	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	0.0211	SUCCESS	1	Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0212	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0212	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0212	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0212	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0213	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0213	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0215	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0215	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0215	SUCCESS	1	mix
[redacted]	0.0215	SUCCESS	1	mix
[redacted]	0.0216	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0216	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0218	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0218	FAIL	-1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	0.0218	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution
[redacted]	0.0219	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0219	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0219	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.022	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.022	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.022	FAIL	-1	cmpu
[redacted]	0.022	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution
[redacted]	0.022	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0221	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0221	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0222	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0222	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0222	SUCCESS	1	Submitted-results pending. Single source DNA profile
[redacted]	0.0222	SUCCESS	1	This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 10 000 - 100 000 Mixture-low support for contrib or supports non contrib
[redacted]	0.0223	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0223	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0223	SUCCESS	1	Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0224	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0225	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0226	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0226	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0226	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Remaining contribution - inconclusive
[redacted]	0.0227	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0227	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000 3 person mix - support for contribution 100 to 1000 3 person mix - low support for contribution
[redacted]	0.0228	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0228	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0228	SUCCESS	1	Three person mixed DNA profile No statistical interpretation performed Sample undergone further work - conditioned Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0229	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0229	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution
[redacted]	0.023	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.023	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution
[redacted]	0.0231	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0231	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0232	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0232	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0234	SUCCESS	1	mix
[redacted]	0.0234	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0235	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0235	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0235	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0235	SUCCESS	1	mix
[redacted]	0.0235	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0235	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0236	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0238	FAIL	-1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0239	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0239	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 100 to 1000 3 person mix - supports non contribution
[redacted]	0.0239	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	0.024	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Cond mix rem-low supp for contrib or supp non contrib 3 person mixed profile - conditioned on
[redacted]	0.0241	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0241	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0241	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0241	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion
[redacted]	0.0241	SUCCESS	1	Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution 3 person mix remaining - supports non contribution Single evidence sample excluded Suspect check - support for contrib 100 000 - 1 million Suspect check - supports non contribution Suspect check - supports non contribution Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect check - supports non contribution Suspect check - supports non contribution Suspect Check Actioned - No Match
[redacted]	0.0242	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0243	FAIL	-1	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0244	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0244	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0244	SUCCESS	1	Submitted-results pending. Single source DNA profile
[redacted]	0.0244	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0245	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0245	SUCCESS	1	ss
[redacted]	0.0246	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0246	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0246	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0247	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0247	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0247	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0248	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0248	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0248	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mixture-low support for contrib or supports non contrib Single evidence sample excluded This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0248	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0248	SUCCESS	1	mix
[redacted]	0.0248	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0249	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0249	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0249	FAIL	-1	cmpu
[redacted]	0.0249	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0252	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0253	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0253	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0255	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0255	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0256	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	0.0256	SUCCESS	1	mix
[redacted]	0.0256	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0257	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0257	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0257	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0258	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0258	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0259	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million
[redacted]	0.026	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.026	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0261	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0261	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0262	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0263	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0263	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0263	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0265	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0266	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0267	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0267	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.027	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0271	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0272	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0273	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0273	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0274	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0274	SUCCESS	1	Semen not detected Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0274	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0275	SUCCESS	1	Semen not detected Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	0.0275	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - low support or non contrib Suspect check - low support or non contrib
[redacted]	0.0276	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0276	FAIL	-1	cmpu
[redacted]	0.0276	SUCCESS	1	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	0.0277	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0277	SUCCESS	1	Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.0278	SUCCESS	1	presump Saliva test positive Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - support for contrib 100 to 1000
[redacted]	0.0278	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib
[redacted]	0.0278	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded 3 person mix profile - support for contrib > 100 billion

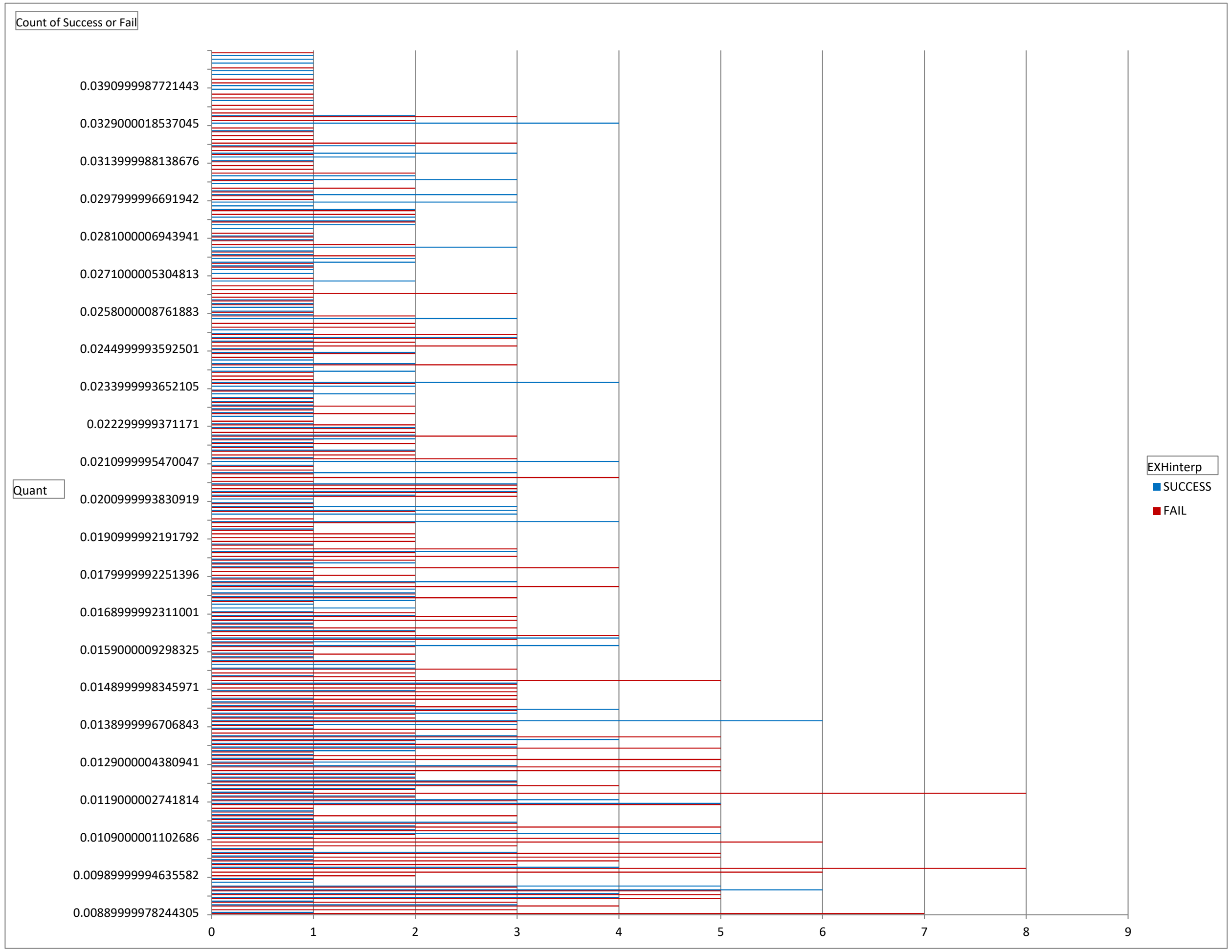
Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0279	FAIL	-1	Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0279	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.028	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.028	SUCCESS	1	mix
[redacted]	0.0281	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0281	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0284	FAIL	-1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0285	SUCCESS	1	mix
[redacted]	0.0287	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	0.0287	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0289	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0289	FAIL	-1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0289	SUCCESS	1	Presumptive blood test pos. Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.0289	SUCCESS	1	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion
[redacted]	0.029	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.029	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion Submitted as cells, Presump saliva test pending presump Saliva test positive
[redacted]	0.0292	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0292	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0293	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0293	FAIL	-1	cmpu
[redacted]	0.0293	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0293	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile
[redacted]	0.0294	SUCCESS	1	mix
[redacted]	0.0296	SUCCESS	1	Submitted as cells Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.0296	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	0.0296	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0298	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0299	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0299	SUCCESS	1	mix
[redacted]	0.0299	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Possible sub-threshold information

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0299	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.03	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.03	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution
[redacted]	0.0301	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0301	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0304	SUCCESS	1	Submitted as cells Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0305	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0305	SUCCESS	1	Submitted as cells Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion
[redacted]	0.0305	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000
[redacted]	0.0305	SUCCESS	1	Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Three person mixed DNA profile 3 person mixed profile - conditioned on Suspect check- support for contribution 10 000 to 100 000 Mixture-low support for contrib or supports non contrib Suspect check - supports non contribution Suspect check - supports non contribution
[redacted]	0.0306	SUCCESS	1	ss
[redacted]	0.0306	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0309	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0309	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0311	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0312	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0314	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0314	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0315	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0315	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 Single evidence sample excluded 3 person mix remaining - supports non contribution
[redacted]	0.0316	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0316	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion Excluded from mixed DNA profile
[redacted]	0.0316	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Single evidence sample excluded 3 person mix - support for contribution 100 to 1000
[redacted]	0.0316	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 3 person mix remaining - supports non contribution
[redacted]	0.0318	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0319	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0319	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0319	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix- support for contrib 1 billion - 100 billion Excluded from mixed DNA profile
[redacted]	0.0321	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0321	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0321	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0322	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0325	FAIL	-1	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0327	FAIL	-1	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0327	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 1 million - 1 billion 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0328	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 Person Mix Rem contrib unsuitable for NCIDD 3 person mix remaining - low support for contrib
[redacted]	0.0329	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile DNA profile removed from NCIDD
[redacted]	0.0329	SUCCESS	1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 3 person mix - support for contribution 100 to 1000
[redacted]	0.0329	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0329	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution
[redacted]	0.033	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.033	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0346	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0346	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0346	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0346	SUCCESS	1	Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0346	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0349	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0362	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0364	FAIL	-1	cmpu
[redacted]	0.0368	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0369	FAIL	-1	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0382	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0384	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix - supports non contribution
[redacted]	0.0391	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0396	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0397	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0446	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0474	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded 2 person mix profile - support for contrib > 100 billion This sample has undergone further processing Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0533	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0577	SUCCESS	1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000 3 person mix - supports non contribution
[redacted]	0.0611	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0743	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0907	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Count of Success or Fail	**Column Labels**		
Row Labels	**FAIL**	**SUCCESS**	**Grand Total**
0.0089	7	1	8
0.009	3		3
0.0091	4	3	7
0.0092	3	1	4
0.0093	5	4	9
0.0094	5	4	9
0.0095	5	6	11
0.0096	3	5	8
0.0097		1	1
0.0098	1	1	2
0.0099	2		2
0.01	6		6
0.0101	8	4	12
0.0102	3	1	4
0.0103	4	1	5
0.0104	5	1	6
0.0105	5	3	8
0.0106	1	1	2
0.0107	3		3
0.0108	6		6
0.0109	4	1	5
0.011	2	5	7
0.0111	3	2	5
0.0112	5	2	7
0.0113	3	3	6
0.0114	1	1	2
0.0115	3	1	4
0.0116	1	1	2
0.0117	1		1
0.0118	5	5	10
0.0119	3	4	7
0.012	2	2	4
0.0121	8	1	9
0.0122	2	2	4
0.0123	4	3	7
0.0124	3	3	6
0.0125	2	2	4
0.0126	2	2	4
0.0127	5		5
0.0128	5	3	8
0.0129	1	2	3
0.013	5	1	6
0.0131	3	1	4
0.0132	1	2	3
0.0133	5	3	8
0.0134	3	2	5
0.0135	2	4	6
0.0136	5	3	8
0.0137	2		2
0.0138	3	1	4
0.0139	1	3	4
0.014	3	6	9
0.0141	2	1	3
0.0142	2	3	5
0.0143	3	4	7
0.0144	3	2	5
0.0145	2	1	3
0.0146	3	1	4
0.0147	3		3
0.0148	3	2	5
0.0149	3		3
0.015	3	3	6
0.0151	5		5
0.0152	2	1	3
0.0153	2		2
0.0154	3	2	5
0.0155		2	2
0.0156	2	2	4
0.015699999	1	1	2



Count of Success or Fail	Column Labels		
Row Labels	**FAIL**	**SUCCESS**	**Grand Total**
0.015799999	2	1	3
0.015900001	1		1
0.016000001	2	4	6
0.016100001	1	2	3
0.0162	3	4	7
0.0163	4		4
0.0164	2	2	4
0.0165	3	1	4
0.0166	1	1	2
0.0167	3	1	4
0.016799999	3	2	5
0.016899999	2	1	3
0.017000001		2	2
0.017100001		1	1
0.017200001	1	2	3
0.0173	3	2	5
0.0174	2	2	4
0.0175		2	2
0.0176	4	1	5
0.0178	2	3	5
0.017899999	1	1	2
0.017999999	2		2
0.018100001	1		1
0.018200001	4	1	5
0.018300001	1	2	3
0.0184	2	1	3
0.0185	3		3
0.0186	2	3	5
0.0187	3		3
0.0189	1	1	2
0.018999999	2		2
0.019099999	2		2
0.019200001	2		2
0.019300001	1	1	2
0.019400001	1		1
0.0195	2	4	6
0.0196	1		1
0.0197		3	3
0.0198	2	3	5
0.0199	1	3	4
0.02	1	1	2
0.020099999		1	1
0.020199999	3	2	5
0.020300001	3	3	6
0.020400001	3		3
0.020500001	3	3	6
0.0206	1		1
0.0207	4		4
0.0208	1	3	4
0.0209	1		1
0.021	1	1	2
0.0211		4	4
0.021199999	3	1	4
0.021299999	2		2
0.021500001	2	2	4
0.021600001	1	1	2
0.0218	2	1	3
0.0219	1	2	3
0.022	3	2	5
0.0221	2		2
0.0222	2	2	4
0.022299999	2	1	3
0.022399999	1		1
0.022500001		1	1
0.022600001	2	1	3
0.022700001	1	1	2
0.0228	2	1	3
0.0229	1	1	2
0.023	1	1	2

Count of Success or Fail	Column Labels		
Row Labels	FAIL	SUCCESS	Grand Total
0.0231		2	2
0.0232	1	1	2
0.023399999		2	2
0.023499999	2	4	6
0.023600001	1		1
0.023800001	1		1
0.0239	1	2	3
0.024		1	1
0.0241	3	2	5
0.0242		1	1
0.0243	1		1
0.0244	2	2	4
0.024499999	1	1	2
0.024599999	3		3
0.024700001	2	1	3
0.024800001	3	3	6
0.024900001	3	1	4
0.0252		1	1
0.0253	2		2
0.0255	2		2
0.025599999		3	3
0.025699999	2	1	3
0.025800001	1	1	2
0.025900001		1	1
0.026000001	1	1	2
0.0261	1	1	2
0.0262	1		1
0.0263	3		3
0.0265	1		1
0.0266	1		1
0.026699999		2	2
0.027000001	1		1
0.027100001		1	1
0.0272		1	1
0.0273	1	1	2
0.0274	1	2	3
0.0275		2	2
0.0276	2	1	3
0.0277	1	1	2
0.027799999		3	3
0.027899999	2		2
0.028000001	1	1	2
0.028100001	1	1	2
0.0284	1		1
0.0285		1	1
0.0287		2	2
0.028899999	2	2	4
0.028999999		2	2
0.029200001	2		2
0.029300001	2	2	4
0.0294		1	1
0.0296		3	3
0.0298	1		1
0.029899999	1	3	4
0.029999999	1	1	2
0.030099999	2		2
0.030400001		1	1
0.0305	1	3	4
0.0306		2	2
0.0309	2		2
0.031099999	1		1
0.031199999	1		1
0.031399999	1	1	2
0.031500001		2	2
0.031599998	1	3	4
0.031800002	1		1
0.0319	1	2	3
0.032099999	3		3
0.032200001	1		1

Count of Success or Fail	**Column Labels**		
Row Labels	**FAIL**	**SUCCESS**	**Grand Total**
0.032499999	1		1
0.032699998	1	1	2
0.0328	1		1
0.032900002		4	4
0.033	2		2
0.034600001	3	2	5
0.034899998	1		1
0.036200002	1		1
0.036400001	1		1
0.036800001		1	1
0.036899999	1		1
0.038199998	1		1
0.038400002		1	1
0.039099999		1	1
0.0396	1		1
0.039700001	1		1
0.044599999		1	1
0.047400001		1	1
0.053300001	1		1
0.057700001		1	1
0.061099999		1	1
0.074299999		1	1
0.090700001	1		1
Grand Total	**432**	**320**	**752**

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.009	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0126	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0131	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0142	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0143	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0169	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0174	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0194	FAIL	-1	Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0255	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Hair located. Submitted-results pending
[redacted]	0.0089	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Labelling discrepancy Submitted-results pending.
[redacted]	0.011	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending
[redacted]	0.0093	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending
[redacted]	0.0112	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.0128	FAIL	-1	Possible sub-threshold information Sample on hold - awaiting advice Submitted-results pending.
[redacted]	0.0129	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells
[redacted]	0.0109	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells
[redacted]	0.0128	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells
[redacted]	0.0136	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells
[redacted]	0.0243	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells
[redacted]	0.0325	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells
[redacted]	0.0327	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells
[redacted]	0.0369	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted-results pending.
[redacted]	0.0162	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted as cells
[redacted]	0.0102	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted as cells
[redacted]	0.0174	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted as cells
[redacted]	0.0199	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted as cells
[redacted]	0.0279	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted as cells, Presump saliva test pending Presump Saliva test negative
[redacted]	0.0113	FAIL	-1	Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0104	FAIL	-1	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0147	FAIL	-1	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Two person mixed DNA profile Single evidence sample excluded This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0284	FAIL	-1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0089	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.009	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.009	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0091	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0091	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0092	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0092	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0092	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0093	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0094	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0094	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0094	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0095	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0096	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0096	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0096	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0098	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0099	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0099	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.01	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.01	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.01	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0101	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0102	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0102	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0104	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0105	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0107	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0107	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0108	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0109	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0109	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.011	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0111	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0111	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0112	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0113	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0113	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0114	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0115	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0115	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0115	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0116	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0117	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0118	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0119	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0119	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0119	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.012	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.012	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0121	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0122	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0122	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0123	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0123	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0123	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0124	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0124	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0124	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0125	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0125	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0126	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0127	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0128	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0128	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0128	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.013	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.013	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.013	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.013	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.013	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0131	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0131	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0133	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0133	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0133	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0134	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0134	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0134	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0135	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0136	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0137	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0137	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0138	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0138	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0138	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0139	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.014	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.014	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.014	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0141	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0141	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0142	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0143	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0143	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0144	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0144	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0144	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0145	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0145	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0146	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0146	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0146	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0147	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0147	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0148	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0148	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0148	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0149	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
				Submitted-results pending.
[redacted]	0.0149	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0149	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.015	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.015	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.015	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0151	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0151	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0151	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0151	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0152	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0152	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0153	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0153	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0154	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0154	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0154	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0156	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0156	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0157	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0158	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0158	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0159	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.016	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.016	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0161	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0162	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0162	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0163	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0163	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0163	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0163	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0164	FAIL	-1	Complex mixed profile unsuitable for interp or comparison Submitted-results pending.
[redacted]	0.0165	FAIL	-1	Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0165	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0166	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0167	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0167	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0167	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0168	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0169	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0172	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0173	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0173	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0173	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0176	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0176	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0178	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0178	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0179	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.018	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.018	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0181	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0182	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0183	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0184	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0184	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0185	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0185	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0185	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0186	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0186	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0187	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0187	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0189	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.019	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.019	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0191	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0191	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0192	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0192	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0193	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0195	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0195	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0196	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0198	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0198	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.02	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0202	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0202	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0202	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0203	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0203	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0204	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0205	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0205	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0205	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0206	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0207	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0208	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0209	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.021	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0212	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0212	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0212	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0213	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0213	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0215	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0215	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0216	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0218	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0219	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.022	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.022	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0221	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0221	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0222	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0222	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0223	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0223	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0224	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0226	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0226	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0227	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0228	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0228	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0229	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.023	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0232	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0235	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0235	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0236	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0239	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0241	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0241	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0241	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0244	FAIL	-1	Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0244	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0245	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0246	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0246	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0246	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0247	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0247	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0248	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0248	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0249	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0249	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0253	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0253	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0255	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0257	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0257	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0258	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.026	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0261	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0262	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0263	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0263	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0263	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0265	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0266	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.027	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0273	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0274	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0276	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0277	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0279	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.028	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0281	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0289	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0292	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0292	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0293	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0298	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0299	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.03	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0301	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0301	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0305	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0309	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0309	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0311	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0312	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0314	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0316	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0318	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0319	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0321	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0321	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0321	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0322	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.033	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.033	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0346	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0346	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0346	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0349	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0362	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0382	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0396	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0397	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0533	FAIL	-1	Complex mixed profile unsuitable for interp or comparison

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0907	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0091	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0106	FAIL	-1	Submitted-results pending. ENVM- Complex mixture unsuitable for interp or comparison
[redacted]	0.0107	FAIL	-1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0132	FAIL	-1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0289	FAIL	-1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0103	FAIL	-1	Submitted-results pending. Micro neg for sperm Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	0.0111	FAIL	-1	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
[redacted]	0.0204	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0328	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 Person Mix Rem contrib unsuitable for NCIDD 3 person mix remaining - low support for contrib
[redacted]	0.0248	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mixture-low support for contrib or supports non contrib Single evidence sample excluded This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0204	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded 3 Person Mix Rem contrib unsuitable for NCIDD
[redacted]	0.0203	FAIL	-1	Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0238	FAIL	-1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0.0135	FAIL	-1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0165	FAIL	-1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	0.0218	FAIL	-1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching
[redacted]	0.0187	FAIL	-1	Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect check - low support for contribution Micro positive for sperm. Submitted-Results pending Interim result- mixed profile obtained. Rework Reqd Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile Mix remaining DNA contrib unsuitable for NCIDD searching Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match
[redacted]	0.0091	FAIL	-1	CMPU
[redacted]	0.0094	FAIL	-1	CMPU
[redacted]	0.0094	FAIL	-1	CMPU
[redacted]	0.0095	FAIL	-1	CMPU
[redacted]	0.01	FAIL	-1	cmpu
[redacted]	0.01	FAIL	-1	cmpu
[redacted]	0.01	FAIL	-1	cmpu
[redacted]	0.0108	FAIL	-1	cmpu
[redacted]	0.0109	FAIL	-1	cmpu
[redacted]	0.0118	FAIL	-1	cmpu
[redacted]	0.0123	FAIL	-1	cmpu
[redacted]	0.0133	FAIL	-1	cmpu
[redacted]	0.0133	FAIL	-1	cmpu
[redacted]	0.0151	FAIL	-1	cmpu
[redacted]	0.0164	FAIL	-1	cmpu
[redacted]	0.0168	FAIL	-1	cmpu
[redacted]	0.0168	FAIL	-1	cmpu
[redacted]	0.0176	FAIL	-1	cmpu
[redacted]	0.0176	FAIL	-1	cmpu
[redacted]	0.022	FAIL	-1	cmpu
[redacted]	0.0249	FAIL	-1	cmpu
[redacted]	0.0276	FAIL	-1	cmpu
[redacted]	0.0293	FAIL	-1	cmpu
[redacted]	0.0364	FAIL	-1	cmpu
[redacted]	0.0091	SUCCESS	1	consistent elsewhere
[redacted]	0.0105	SUCCESS	1	Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	0.0139	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile NCIDD upload - mixed DNA profile Excluded from mixed DNA profile
[redacted]	0.0173	SUCCESS	1	Single source DNA profile NCIDD upload single source DNA profile Single Source DNA profile - assumed known contributor DNA profile removed from NCIDD
[redacted]	0.0112	SUCCESS	1	Submitted as cells Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0144	SUCCESS	1	Submitted as cells Single source DNA profile NCIDD upload single source DNA profile Single Source DNA profile - assumed known contributor DNA profile removed from NCIDD
[redacted]	0.029	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0111	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile
[redacted]	0.0118	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0091	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0248	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0133	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0314	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0202	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD Intel upload - single source partial profile NCIDD upload single source DNA profile
[redacted]	0.0105	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0106	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0111	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0146	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0154	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0162	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0174	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0178	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0183	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0208	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0315	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0446	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
[redacted]	0.0329	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile DNA profile removed from NCIDD
[redacted]	0.0113	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0129	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0142	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.016	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0273	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0095	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD
[redacted]	0.0093	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0184	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD
[redacted]	0.0134	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0241	SUCCESS	1	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion
[redacted]	0.0129	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0135	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile
[redacted]	0.0219	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.017	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information This sample has undergone further processing Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0121	SUCCESS	1	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	0.0276	SUCCESS	1	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile
[redacted]	0.0155	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.0235	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 3 person mix profile - support for contrib > 100 billion
[redacted]	0.03	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution
[redacted]	0.0261	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0256	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	0.0384	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix - supports non contribution
[redacted]	0.0091	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0211	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mixture-low support for contrib or supports non contrib
[redacted]	0.0219	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0136	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0225	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0166	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	0.0089	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0143	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information
[redacted]	0.0092	SUCCESS	1	P SS
[redacted]	0.0093	SUCCESS	1	P SS
[redacted]	0.0094	SUCCESS	1	3p

[redacted]	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0095	SUCCESS	1	3p
[redacted]	0.0096	SUCCESS	1	cond
[redacted]	0.0096	SUCCESS	1	ss akc
[redacted]	0.0101	SUCCESS	1	ss
[redacted]	0.0102	SUCCESS	1	ss
[redacted]	0.0105	SUCCESS	1	ss
[redacted]	0.011	SUCCESS	1	2p
[redacted]	0.011	SUCCESS	1	3p
[redacted]	0.011	SUCCESS	1	2p
[redacted]	0.0118	SUCCESS	1	ss
[redacted]	0.0118	SUCCESS	1	2p
[redacted]	0.0119	SUCCESS	1	2p
[redacted]	0.0119	SUCCESS	1	ss
[redacted]	0.012	SUCCESS	1	mix
[redacted]	0.0123	SUCCESS	1	mix
[redacted]	0.0124	SUCCESS	1	mix
[redacted]	0.0125	SUCCESS	1	mix
[redacted]	0.0132	SUCCESS	1	mix
[redacted]	0.014	SUCCESS	1	ss
[redacted]	0.015	SUCCESS	1	ss
[redacted]	0.0164	SUCCESS	1	ss
[redacted]	0.0167	SUCCESS	1	mix
[redacted]	0.017	SUCCESS	1	mix
[redacted]	0.0172	SUCCESS	1	ss
[redacted]	0.0175	SUCCESS	1	mix
[redacted]	0.0178	SUCCESS	1	mix
[redacted]	0.0183	SUCCESS	1	mix
[redacted]	0.0193	SUCCESS	1	ss
[redacted]	0.0203	SUCCESS	1	ss
[redacted]	0.0215	SUCCESS	1	mix
[redacted]	0.0215	SUCCESS	1	mix
[redacted]	0.0234	SUCCESS	1	mix
[redacted]	0.0235	SUCCESS	1	mix
[redacted]	0.0245	SUCCESS	1	ss
[redacted]	0.0248	SUCCESS	1	mix
[redacted]	0.0256	SUCCESS	1	mix
[redacted]	0.028	SUCCESS	1	mix
[redacted]	0.0285	SUCCESS	1	mix
[redacted]	0.0294	SUCCESS	1	mix
[redacted]	0.0299	SUCCESS	1	mix
[redacted]	0.0306	SUCCESS	1	ss
[redacted]				2 person mix remaining - supports non contribution
[redacted]				Submitted as cells
[redacted]				Two person mixed DNA profile
[redacted]				2 person mix - supports non contribution
[redacted]				Sample undergone further work - conditioned
[redacted]				Two person mixed DNA profile
[redacted]	0.0162	SUCCESS	1	2 person mixed profile - conditioned on
[redacted]				Hair located. Submitted-results pending
[redacted]				Single Source DNA profile - assumed known contributor
[redacted]	0.0098	SUCCESS	1	Possible sub-threshold information
[redacted]				Interim result- mixed profile obtained. Rework Reqd
[redacted]				Three person mixed DNA profile
[redacted]				3 person mixed profile - conditioned on
[redacted]				3 person mix remaining - supports non contribution
				3 person mix remaining - supports non contribution
				Single evidence sample excluded
				Suspect check - support for contrib 100 000 - 1 million
				Suspect check - supports non contribution
				Suspect check - supports non contribution
				Suspect Check Actioned - No Match
				Suspect Check Actioned - No Match
				Suspect Check Actioned - No Match
				Suspect check - supports non contribution
				Suspect check - supports non contribution
690166221	0.0241	SUCCESS	1	Suspect Check Actioned - No Match

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0095	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0189	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0095	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0116	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0132	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0143	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Possible sub-threshold information
[redacted]	0.0094	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion 3 person mix - support for contribution 100 to 1000
[redacted]	0.011	SUCCESS	1	Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Single evidence sample excluded 3 person mix - supports non contribution
[redacted]	0.0278	SUCCESS	1	presump Saliva test positive Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - support for contrib 100 to 1000
[redacted]	0.0101	SUCCESS	1	Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem - support for contrib 1 billion -100 billion
[redacted]	0.0142	SUCCESS	1	Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion
[redacted]	0.0289	SUCCESS	1	Presumptive blood test pos. Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.0274	SUCCESS	1	Semen not detected Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0275	SUCCESS	1	Semen not detected Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	0.0165	SUCCESS	1	Single evidence sample excluded Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0096	SUCCESS	1	SS DNA profile 9 loci and above LR > 100 billion Possible sub-threshold information

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	[redacted]	SUCCESS	1	Submitted as cells Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion
[redacted]	[redacted]	SUCCESS	1	Submitted as cells Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	[redacted]	SUCCESS	1	Submitted as cells Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person rem- support for contrib 1 billion-100 billion
[redacted]	[redacted]	SUCCESS	1	Submitted as cells Three person mixed DNA profile No statistical interpretation performed
[redacted]	[redacted]	SUCCESS	1	Submitted as cells Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	[redacted]	SUCCESS	1	Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	[redacted]	SUCCESS	1	Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	[redacted]	SUCCESS	1	Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	[redacted]	SUCCESS	1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	[redacted]	SUCCESS	1	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000 3 person mix - supports non contribution
[redacted]	[redacted]	SUCCESS	1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	[redacted]	SUCCESS	1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 100 000 to 1 million
[redacted]	[redacted]	SUCCESS	1	Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 3 person mix - support for contribution 100 to 1000
[redacted]	[redacted]	SUCCESS	1	Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
				Submitted-results pending. Micro positive for sperm. Submitted-Results pending
[redacted]	0.0133	SUCCESS	1	Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0128	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.026	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0743	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0143	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0186	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0234	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0272	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0281	SUCCESS	1	Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0101	SUCCESS	1	Submitted-results pending. Single source DNA profile
[redacted]	0.0222	SUCCESS	1	Submitted-results pending. Single source DNA profile
[redacted]	0.0244	SUCCESS	1	Submitted-results pending. Single source DNA profile
[redacted]	0.0119	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	0.013	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	0.0175	SUCCESS	1	Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information
[redacted]	0.0095	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	0.0101	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	0.0128	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	0.0296	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information
[redacted]	0.014	SUCCESS	1	Submitted-results pending. Single source DNA profile Possible sub-threshold information Single Source DNA profile - assumed known contributor
[redacted]	0.0223	SUCCESS	1	Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion
[redacted]	0.0197	SUCCESS	1	Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information
[redacted]	0.0139	SUCCESS	1	Submitted-results pending. Single source DNA profile SS DNA profile 9 loci and above LR > 100 billion

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	.0289	SUCCESS	1	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion
[redacted]	.0113	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0134	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0135	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	0.015	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0154	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0164	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0182	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0195	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0202	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0244	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0252	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0256	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0258	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0293	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0296	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0319	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0329	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0368	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0391	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile
[redacted]	.0199	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - low support for contribution
[redacted]	.0174	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 1 million - 1 billion Excluded from mixed DNA profile
[redacted]	.0198	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000
[redacted]	.0171	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 Mixture-low support for contrib or supports non contrib
[redacted]	.0305	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000
[redacted]	.0162	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	0.016	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.023	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution
[redacted]	0.0173	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution 3 person mix - support for contrib 10 000 - 100 000 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 2 person mix rem - support for contrib 10 000 to 100 000 2 person mix remaining - supports non contribution 2 person mix remaining - supports non contribution 3 person mix rem - support for contrib 10 000 to 100 000 3 person mix remaining - supports non contribution 3 person mix remaining - supports non contribution
[redacted]	0.0218	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution
[redacted]	0.0093	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0122	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0124	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0143	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0145	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0161	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0169	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0176	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0178	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0195	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0197	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0212	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0271	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0346	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0133	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0156	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Excluded from mixed DNA profile
[redacted]	0.0135	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Mixture-low support for contrib or supports non contrib 3 person mix - low support for contribution
[redacted]	0.011	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion
[redacted]	0.0158	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix rem - support for contribution > 100 billion Single evidence sample excluded
[redacted]	0.0316	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion Excluded from mixed DNA profile
[redacted]	0.0259	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million
[redacted]	0.0239	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 100 to 1000 3 person mix - supports non contribution
[redacted]	0.0157	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0267	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution
[redacted]	0.0148	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0119	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0124	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0198	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0199	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0096	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - supports non contribution
[redacted]	0.0179	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - supports non contribution
[redacted]	0.0316	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Single evidence sample excluded 3 person mix - support for contribution 100 to 1000
[redacted]	0.0162	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mix- support for contrib 1 billion - 100 billion 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0118	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix profile - support for contrib > 100 billion 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0306	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0278	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib
[redacted]	0.0109	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib 3 person mix remaining - supports non contribution
[redacted]	0.0139	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0148	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0186	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0316	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 3 person mix remaining - supports non contribution
[redacted]	0.0315	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 Single evidence sample excluded 3 person mix remaining - supports non contribution

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0287	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	0.021	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Excluded from mixed DNA profile
[redacted]	0.024	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Cond mix rem-low supp for contrib or supp non contrib 3 person mixed profile - conditioned on
[redacted]	0.0197	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 100 to 1000
[redacted]	0.0156	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile Single evidence sample excluded
[redacted]	0.0095	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib
[redacted]	0.0125	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0126	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0103	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0115	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0122	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0203	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0205	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0208	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0231	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0235	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0235	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0247	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0248	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0249	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0267	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0287	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed
[redacted]	0.0195	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0201	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0123	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0131	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0113	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed Single evidence sample excluded 3 person mix profile - support for contrib > 100 billion
[redacted]	0.0199	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	0.0205	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded
[redacted]	0.0278	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded 3 person mix profile - support for contrib > 100 billion
[redacted]	0.02	SUCCESS	1	Submitted-results pending. Three person mixed DNA profile Suspect Check Actioned - No Match
[redacted]	0.0093	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0152	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0155	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0195	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0242	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile
[redacted]	0.0211	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion
[redacted]	0.0123	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution
[redacted]	0.0229	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution

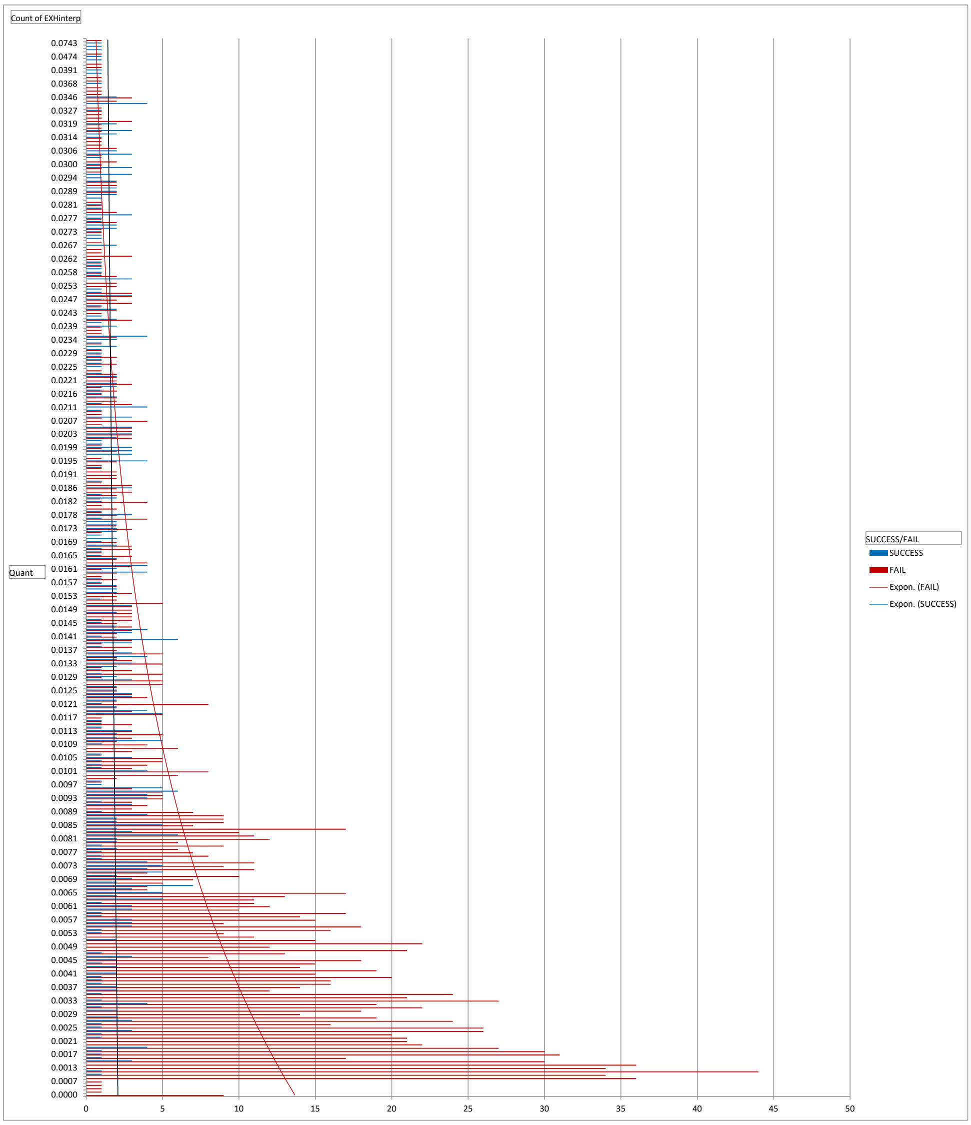
Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0118	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0161	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0172	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0257	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0611	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.014	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution
[redacted]	0.022	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution
[redacted]	0.0327	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 1 million - 1 billion 2 person mix profile - support for contrib > 100 billion
[redacted]	0.012	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution
[redacted]	0.0329	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution
[redacted]	0.0203	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix- support for contrib 1 billion - 100 billion 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0096	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0275	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - low support or non contrib Suspect check - low support or non contrib
[redacted]	0.0114	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	0.0126	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded
[redacted]	0.0211	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0299	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Possible sub-threshold information
[redacted]	0.0112	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile Suspect check - supports non contribution
[redacted]	0.016	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0205	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0216	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.022	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0231	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0299	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed
[redacted]	0.0135	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded
[redacted]	0.0474	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded 2 person mix profile - support for contrib > 100 billion This sample has undergone further processing Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0142	SUCCESS	1	Submitted-results pending. Two person mixed DNA profile Suspect check inconclusive - mixed DNA profile Suspect check - supports non contribution
[redacted]	0.0305	SUCCESS	1	Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Three person mixed DNA profile 3 person mixed profile - conditioned on Suspect check- support for contribution 10 000 to 100 000 Mixture-low support for contrib or supports non contrib Suspect check - supports non contribution Suspect check - supports non contribution
[redacted]	0.0222	SUCCESS	1	This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 10 000 - 100 000 Mixture-low support for contrib or supports non contrib
[redacted]	0.015	SUCCESS	1	Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Single evidence sample excluded

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0094	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 3 person mix - supports non contribution
[redacted]	0.0232	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion Mixture-low support for contrib or supports non contrib
[redacted]	0.0136	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million Mixture-low support for contrib or supports non contrib Excluded from mixed DNA profile
[redacted]	0.0227	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000 3 person mix - support for contribution 100 to 1000 3 person mix - low support for contribution
[redacted]	0.0319	SUCCESS	1	Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix- support for contrib 1 billion - 100 billion Excluded from mixed DNA profile
[redacted]	0.014	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
[redacted]	0.0094	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix remaining - supports non contribution
[redacted]	0.029	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion Submitted as cells, Presump saliva test pending presump Saliva test positive
[redacted]	0.0239	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib
[redacted]	0.0226	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Remaining contribution - inconclusive
[redacted]	0.0097	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0138	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0274	SUCCESS	1	Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded
[redacted]	0.0228	SUCCESS	1	Three person mixed DNA profile No statistical interpretation performed Sample undergone further work - conditioned Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution
[redacted]	0.0208	SUCCESS	1	Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion
[redacted]	0.0211	SUCCESS	1	Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile
[redacted]	0.0198	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on

Barcode	Quant	EXHinterp	Success (+1) or Fail (-1)	EXH
[redacted]	0.0186	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion
[redacted]	0.014	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	0.0168	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information
[redacted]	0.0293	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile
[redacted]	0.014	SUCCESS	1	Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile Mix Rem DNA contrib < NCIDD matching Stringency

Count of EXHinterp	**Column Labels**		
Row Labels	**FAIL**	**SU(**	**Grand Total**
0.0000	9		9
0.0003	1		1
0.0004	1		1
0.0005	1		1
0.0007	1		1
0.0010	36		36
0.0011	34	1	35
0.0012	44	1	45
0.0013	34		34
0.0014	36		36
0.0015	30	3	33
0.0016	17	1	18
0.0017	31	1	32
0.0018	30	1	31
0.0019	27	4	31
0.0020	22		22
0.0021	21		21
0.0022	21	1	22
0.0023	20	1	21
0.0024	26	3	29
0.0025	26	1	27
0.0026	16	1	17
0.0027	24	3	27
0.0028	19	2	21
0.0029	14		14
0.0030	18	2	20
0.0031	22	1	23
0.0032	19	4	23
0.0033	27	1	28
0.0034	21		21
0.0035	24	1	25
0.0036	12	2	14
0.0037	14	2	16
0.0038	16	1	17
0.0039	16	1	17
0.0040	20	1	21
0.0041	15	2	17
0.0042	19		19
0.0043	14	2	16
0.0044	15	1	16
0.0045	18	2	20
0.0046	8	3	11
0.0047	13	1	14
0.0048	21		21
0.0049	12		12
0.0050	22		22
0.0051	15	2	17
0.0052	11		11
0.0053	9	1	10
0.0054	16	1	17
0.0055	18	3	21
0.0056	9	3	12
0.0057	15	3	18
0.0058	14	1	15
0.0059	17	1	18
0.0060	10	3	13
0.0061	12	3	15
0.0062	11	1	12
0.0063	11	5	16
0.0064	13	2	15
0.0065	17	5	22
0.0066	4	3	7
0.0067	4	7	11
0.0068	5	2	7
0.0069	7	3	10
0.0070	10	2	12
0.0071	4	5	9
0.0072	11	4	15
0.0073	9	5	14
0.0074	11	4	15
0.0075	5	1	6
0.0076	8	1	9
0.0077	7	1	8
0.0078	6	2	8
0.0079	9	1	10
0.0080	6	2	8
0.0081	12	2	14
0.0082	11	6	17
0.0083	10	3	13
0.0084	17	2	19
0.0085	7	5	12
0.0086	9	2	11
0.0087	9	2	11
0.0088	9	4	13
0.0089	7	1	8
0.0090	3		3
0.0091	4	3	7
0.0092	3	1	4
0.0093	5	4	9
0.0094	5	4	9
0.0095	5	6	11
0.0096	3	5	8
0.0097		1	1
0.0098	1	1	2
0.0099	2		2
0.0100	6		6
0.0101	8	4	12
0.0102	3	1	4
0.0103	4	1	5
0.0104	5	1	6
0.0105	5	3	8
0.0106	1	1	2
0.0107	3		3
0.0108	6		6
0.0109	4	1	5
0.0110	2	5	7
0.0111	3	2	5
0.0112	5	2	7
0.0113	3	3	6
0.0114	1	1	2
0.0115	3	1	4
0.0116	1	1	2
0.0117	1		1
0.0118	5	5	10
0.0119	3	4	7
0.0120	2	2	4
0.0121	8	1	9
0.0122	2	2	4
0.0123	4	3	7
0.0124	3	3	6
0.0125	2	2	4
0.0126	2	2	4
0.0127	5		5
0.0128	5	3	8
0.0129	1	2	3
0.0130	5	1	6
0.0131	3	1	4
0.0132	1	2	3
0.0133	5	3	8
0.0134	3	2	5
0.0135	2	4	6
0.0136	5	3	8
0.0137	2		2
0.0138	3	1	4
0.0139	1	3	4
0.0140	3	6	9
0.0141	2	1	3
0.0142	2	3	5
0.0143	3	4	7
0.0144	3	2	5
0.0145	2	1	3
0.0146	3	1	4
0.0147	3		3
0.0148	3	2	5
0.0149	3		3
0.0150	3	3	6
0.0151	5		5
0.0152	2	1	3
0.0153	2		2
0.0154	3	2	5
0.0155		2	2
0.0156	2	2	4
0.0157	1	1	2
0.0158	2	1	3
0.0159	1		1
0.0160	2	4	6
0.0161	1	2	3
0.0162	3	4	7
0.0163	4		4
0.0164	2	2	4
0.0165	3	1	4



Count of EXHinterp	Column Labels		
Row Labels	**FAIL**	**SU(**	**Grand Total**
0.0166	1	1	2
0.0167	3	1	4
0.0168	3	2	5
0.0169	2	1	3
0.0170		2	2
0.0171		1	1
0.0172	1	2	3
0.0173	3	2	5
0.0174	2	2	4
0.0175		2	2
0.0176	4	1	5
0.0178	2	3	5
0.0179	1	1	2
0.0180	2		2
0.0181	1		1
0.0182	4	1	5
0.0183	1	2	3
0.0184	2	1	3
0.0185	3		3
0.0186	2	3	5
0.0187	3		3
0.0189	1	1	2
0.0190	2		2
0.0191	2		2
0.0192	2		2
0.0193	1	1	2
0.0194	1		1
0.0195	2	4	6
0.0196	1		1
0.0197		3	3
0.0198	2	3	5
0.0199	1	3	4
0.0200	1	1	2
0.0201		1	1
0.0202	3	2	5
0.0203	3	3	6
0.0204	3		3
0.0205	3	3	6
0.0206	1		1
0.0207	4		4
0.0208	1	3	4
0.0209	1		1
0.0210	1	1	2
0.0211		4	4
0.0212	3	1	4
0.0213	2		2
0.0215	2	2	4
0.0216	1	1	2
0.0218	2	1	3
0.0219	1	2	3
0.0220	3	2	5
0.0221	2		2
0.0222	2	2	4
0.0223	2	1	3
0.0224	1		1
0.0225		1	1
0.0226	2	1	3
0.0227	1	1	2
0.0228	2	1	3
0.0229	1	1	2
0.0230	1	1	2
0.0231		2	2
0.0232	1	1	2
0.0234		2	2
0.0235	2	4	6
0.0236	1		1
0.0238	1		1
0.0239	1	2	3
0.0240		1	1
0.0241	3	2	5
0.0242		1	1
0.0243	1		1
0.0244	2	2	4
0.0245	1	1	2
0.0246	3		3
0.0247	2	1	3
0.0248	3	3	6
0.0249	3	1	4
0.0252		1	1
0.0253	2		2
0.0255	2		2
0.0256		3	3
0.0257	2	1	3
0.0258	1	1	2
0.0259		1	1
0.0260	1	1	2
0.0261	1	1	2
0.0262	1		1
0.0263	3		3
0.0265	1		1
0.0266	1		1
0.0267		2	2
0.0270	1		1
0.0271		1	1
0.0272		1	1
0.0273	1	1	2
0.0274	1	2	3
0.0275		2	2
0.0276	2	1	3
0.0277	1	1	2
0.0278		3	3
0.0279	2		2
0.0280	1	1	2
0.0281	1	1	2
0.0284	1		1
0.0285		1	1
0.0287		2	2
0.0289	2	2	4
0.0290		2	2
0.0292	2		2
0.0293	2	2	4
0.0294		1	1
0.0296		3	3
0.0298	1		1
0.0299	1	3	4
0.0300	1	1	2
0.0301	2		2
0.0304		1	1
0.0305	1	3	4
0.0306		2	2
0.0309	2		2
0.0311	1		1
0.0312	1		1
0.0314	1	1	2
0.0315		2	2
0.0316	1	3	4
0.0318	1		1
0.0319	1	2	3
0.0321	3		3
0.0322	1		1
0.0325	1		1
0.0327	1	1	2
0.0328	1		1
0.0329		4	4
0.0330	2		2
0.0346	3	2	5
0.0349	1		1
0.0362	1		1
0.0364	1		1
0.0368		1	1
0.0369	1		1
0.0382	1		1
0.0384		1	1
0.0391		1	1
0.0396	1		1
0.0397	1		1
0.0446		1	1
0.0474		1	1
0.0533	1		1
0.0577		1	1
0.0611		1	1
0.0743		1	1
0.0907	1		1
Grand Total	**1727**	**##**	**2201**

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0000	FAIL	-1
[redacted]	0.0000	FAIL	-1
[redacted]	0.0000	FAIL	-1
[redacted]	0.0000	FAIL	-1
[redacted]	0.0000	FAIL	-1
[redacted]	0.0000	FAIL	-1
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0018	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0015	FAIL	-1
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[redacted]	0.0015	SUCCESS	1
[redacted]	0.0015	SUCCESS	1
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[redacted]	0.0016	SUCCESS	1
[redacted]	0.0017	FAIL	-1
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[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	FAIL	-1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	SUCCESS	1
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[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	SUCCESS	1
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[redacted]	0.0019	SUCCESS	1
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[redacted]	0.0020	FAIL	-1
[redacted]	0.0021	FAIL	-1
[redacted]	0.0021	FAIL	-1
[redacted]	0.0021	FAIL	-1
[redacted]	0.0021	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	SUCCESS	1
[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	FAIL	-1
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[redacted]	0.0019	FAIL	-1
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[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	SUCCESS	1
[redacted]	0.0019	SUCCESS	1
[redacted]	0.0019	SUCCESS	1
[redacted]	0.0019	SUCCESS	1
[redacted]	0.0020	FAIL	-1
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[redacted]	0.0020	FAIL	-1
[redacted]	0.0021	FAIL	-1
[redacted]	0.0021	FAIL	-1
[redacted]	0.0021	FAIL	-1
[redacted]	0.0021	FAIL	-1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0018	FAIL	-1
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[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	FAIL	-1
[redacted]	0.0018	SUCCESS	1
[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	FAIL	-1
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[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	FAIL	-1
[redacted]	0.0019	SUCCESS	1
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[redacted]	0.0021	FAIL	-1
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[redacted]	0.0021	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0019	SUCCESS	1
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[redacted]	0.0021	FAIL	-1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0024	FAIL	-1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0024	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0031	FAIL	-1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0031	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0031	FAIL	-1
[redacted]	0.0031	FAIL	-1
[redacted]	0.0031	SUCCESS	1
[redacted]	0.0032	FAIL	-1
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[redacted]	0.0034	FAIL	-1
[redacted]	0.0034	FAIL	-1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0037	SUCCESS	1
[redacted]	0.0037	SUCCESS	1
[redacted]	0.0038	FAIL	-1
[redacted]	0.0038	FAIL	-1
[redacted]	0.0038	FAIL	-1
[redacted]	0.0038	FAIL	-1
[redacted]	0.0038	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0038	FAIL	-1
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[redacted]	0.0038	FAIL	-1
[redacted]	0.0038	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0037	FAIL	-1
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0041	SUCCESS	1
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[redacted]	0.0042	FAIL	-1

[redacted]	uant <0.01	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0042	FAIL	-1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0046	SUCCESS	1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0046	SUCCESS	1
[redacted]	0.0046	SUCCESS	1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0046	SUCCESS	1

[redacted]	uant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0047	FAIL	-1
[redacted]	0.0047	SUCCESS	1
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[redacted]	0.0051	FAIL	-1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0058	FAIL	-1
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[redacted]	0.0059	FAIL	-1
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[redacted]	0.0059	FAIL	-1
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[redacted]	0.0060	FAIL	-1
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[redacted]	0.0060	SUCCESS	1
[redacted]	0.0060	SUCCESS	1
[redacted]	0.0060	SUCCESS	1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0056	FAIL	-1
[redacted]	0.0056	FAIL	-1
[redacted]	0.0056	SUCCESS	1
[redacted]	0.0056	SUCCESS	1
[redacted]	0.0056	SUCCESS	1
[redacted]	0.0057	FAIL	-1
[redacted]	0.0057	FAIL	-1
[redacted]	0.0057	FAIL	-1
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[redacted]	0.0057	FAIL	-1
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[redacted]	0.0057	SUCCESS	1
[redacted]	0.0057	SUCCESS	1
[redacted]	0.0057	SUCCESS	1
[redacted]	0.0058	FAIL	-1
[redacted]	0.0058	FAIL	-1
[redacted]	0.0058	FAIL	-1
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[redacted]	0.0058	SUCCESS	1
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[redacted]	0.0059	FAIL	-1
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[redacted]	0.0060	FAIL	-1
[redacted]	0.0060	FAIL	-1
[redacted]	0.0060	SUCCESS	1
[redacted]	0.0060	SUCCESS	1
[redacted]	0.0060	SUCCESS	1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0056	FAIL	-1
[redacted]	0.0056	SUCCESS	1
[redacted]	0.0056	SUCCESS	1
[redacted]	0.0056	SUCCESS	1
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[redacted]	0.0057	FAIL	-1
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[redacted]	0.0057	SUCCESS	1
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[redacted]	0.0058	FAIL	-1
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[redacted]	0.0058	SUCCESS	1
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[redacted]	0.0060	FAIL	-1
[redacted]	0.0060	FAIL	-1
[redacted]	0.0060	SUCCESS	1
[redacted]	0.0060	SUCCESS	1
[redacted]	0.0060	SUCCESS	1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0061	SUCCESS	1
[redacted]	0.0061	SUCCESS	1
[redacted]	0.0061	SUCCESS	1
[redacted]	0.0062	FAIL	-1
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[redacted]	0.0062	FAIL	-1
[redacted]	0.0062	FAIL	-1
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[redacted]	0.0064	FAIL	-1
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[redacted]	0.0064	SUCCESS	1
[redacted]	0.0064	SUCCESS	1
[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	FAIL	-1
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[redacted]	0.0065	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0061	FAIL	-1
[redacted]	0.0061	FAIL	-1
[redacted]	0.0061	FAIL	-1
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[redacted]	0.0061	FAIL	-1
[redacted]	0.0061	FAIL	-1
[redacted]	0.0061	FAIL	-1
[redacted]	0.0061	FAIL	-1
[redacted]	0.0061	SUCCESS	1
[redacted]	0.0061	SUCCESS	1
[redacted]	0.0061	SUCCESS	1
[redacted]	0.0062	FAIL	-1
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[redacted]	0.0062	FAIL	-1
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[redacted]	0.0062	FAIL	-1
[redacted]	0.0062	FAIL	-1
[redacted]	0.0062	FAIL	-1
[redacted]	0.0062	FAIL	-1
[redacted]	0.0062	SUCCESS	1
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[redacted]	0.0063	FAIL	-1
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[redacted]	0.0063	FAIL	-1
[redacted]	0.0063	FAIL	-1
[redacted]	0.0063	FAIL	-1
[redacted]	0.0063	FAIL	-1
[redacted]	0.0063	SUCCESS	1
[redacted]	0.0063	SUCCESS	1
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[redacted]	0.0063	SUCCESS	1
[redacted]	0.0063	SUCCESS	1
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[redacted]	0.0064	SUCCESS	1
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[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	FAIL	-1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0064	SUCCESS	1
[redacted]	0.0064	SUCCESS	1
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[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	FAIL	-1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
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[redacted]	0.0067	FAIL	-1
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[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	SUCCESS	1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	SUCCESS	1
[redacted]	0.0068	SUCCESS	1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	SUCCESS	1

[redacted]	Quant <0.0133	EXHinterp	SUCCESS/FAIL
[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	SUCCESS	1
[redacted]	0.0068	SUCCESS	1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	SUCCESS	1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0065	FAIL	-1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0065	SUCCESS	1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	FAIL	-1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0066	SUCCESS	1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	FAIL	-1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0067	SUCCESS	1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	FAIL	-1
[redacted]	0.0068	SUCCESS	1
[redacted]	0.0068	SUCCESS	1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	FAIL	-1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0069	SUCCESS	1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	FAIL	-1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0070	SUCCESS	1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	FAIL	-1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0071	SUCCESS	1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	FAIL	-1
[redacted]	0.0072	SUCCESS	1

	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	SUCCESS	1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	SUCCESS	1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	SUCCESS	1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	SUCCESS	1
[redacted]	0.0078	SUCCESS	1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	SUCCESS	1
[redacted]	0.0080	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	SUCCESS	1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	SUCCESS	1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	SUCCESS	1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	SUCCESS	1
[redacted]	0.0078	SUCCESS	1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	SUCCESS	1
[redacted]	0.0080	FAIL	-1

	nt <0.0133	EXHinterp	SUCCESS/FAIL
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	SUCCESS	1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	SUCCESS	1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	SUCCESS	1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	SUCCESS	1
[redacted]	0.0078	SUCCESS	1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	SUCCESS	1
[redacted]	0.0080	FAIL	-1

	Quant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0072	SUCCESS	1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	FAIL	-1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0073	SUCCESS	1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	FAIL	-1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0074	SUCCESS	1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	FAIL	-1
[redacted]	0.0075	SUCCESS	1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
[redacted]	0.0076	FAIL	-1
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[redacted]	0.0076	FAIL	-1
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[redacted]	0.0076	SUCCESS	1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	FAIL	-1
[redacted]	0.0077	SUCCESS	1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	FAIL	-1
[redacted]	0.0078	SUCCESS	1
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[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
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[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	FAIL	-1
[redacted]	0.0079	SUCCESS	1
[redacted]	0.0080	FAIL	-1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0080	FAIL	-1
[redacted]	0.0080	FAIL	-1
[redacted]	0.0080	FAIL	-1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
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[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
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[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
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[redacted]	0.0083	SUCCESS	1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	SUCCESS	1
[redacted]	0.0084	SUCCESS	1
[redacted]	0.0085	FAIL	-1
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[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0080	FAIL	-1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
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[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
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[redacted]	0.0082	FAIL	-1
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[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
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[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	SUCCESS	1
[redacted]	0.0083	SUCCESS	1
[redacted]	0.0083	SUCCESS	1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	SUCCESS	1
[redacted]	0.0084	SUCCESS	1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1

[redacted]	nt <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0080	FAIL	-1
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[redacted]	0.0080	FAIL	-1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
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[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0082	FAIL	-1
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[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
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[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
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[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
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[redacted]	0.0083	SUCCESS	1
[redacted]	0.0083	SUCCESS	1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	SUCCESS	1
[redacted]	0.0084	SUCCESS	1
[redacted]	0.0085	FAIL	-1
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[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0080	FAIL	-1
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[redacted]	0.0080	FAIL	-1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0080	SUCCESS	1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	FAIL	-1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0081	SUCCESS	1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	FAIL	-1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0082	SUCCESS	1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	FAIL	-1
[redacted]	0.0083	SUCCESS	1
[redacted]	0.0083	SUCCESS	1
[redacted]	0.0083	SUCCESS	1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	FAIL	-1
[redacted]	0.0084	FAIL	-1
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[redacted]	0.0084	SUCCESS	1
[redacted]	0.0084	SUCCESS	1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0085	FAIL	-1
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[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
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[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	SUCCESS	1
[redacted]	0.0087	SUCCESS	1
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[redacted]	0.0088	FAIL	-1
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[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
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[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
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[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	SUCCESS	1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	SUCCESS	1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
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[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
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[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	SUCCESS	1
[redacted]	0.0087	SUCCESS	1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
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[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0089	FAIL	-1
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[redacted]	0.0089	FAIL	-1
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[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	SUCCESS	1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	SUCCESS	1
[redacted]	0.0093	FAIL	-1
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[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
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[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
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[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0087	FAIL	-1
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[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	SUCCESS	1
[redacted]	0.0087	SUCCESS	1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	SUCCESS	1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	SUCCESS	1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1

[redacted]	ant <0.015	EXHinterp	SUCCESS/FAIL
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[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	FAIL	-1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0085	SUCCESS	1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	FAIL	-1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0086	SUCCESS	1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
[redacted]	0.0087	FAIL	-1
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[redacted]	0.0087	SUCCESS	1
[redacted]	0.0087	SUCCESS	1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	FAIL	-1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0088	SUCCESS	1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	FAIL	-1
[redacted]	0.0089	SUCCESS	1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0090	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	FAIL	-1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0091	SUCCESS	1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	FAIL	-1
[redacted]	0.0092	SUCCESS	1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	FAIL	-1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1
[redacted]	0.0093	SUCCESS	1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0097	SUCCESS	1
[redacted]	0.0098	FAIL	-1
[redacted]	0.0098	SUCCESS	1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	SUCCESS	1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	SUCCESS	1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	SUCCESS	1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	SUCCESS	1
[redacted]	0.0105	SUCCESS	1
[redacted]	0.0105	SUCCESS	1

[redacted]	nt <0.01	EXHinterp	SUCCESS/FAIL
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0097	SUCCESS	1
[redacted]	0.0098	FAIL	-1
[redacted]	0.0098	SUCCESS	1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0097	SUCCESS	1
[redacted]	0.0098	FAIL	-1
[redacted]	0.0098	SUCCESS	1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	SUCCESS	1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	SUCCESS	1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	SUCCESS	1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	SUCCESS	1
[redacted]	0.0105	SUCCESS	1
[redacted]	0.0105	SUCCESS	1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	FAIL	-1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0094	SUCCESS	1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	FAIL	-1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0095	SUCCESS	1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	FAIL	-1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0096	SUCCESS	1
[redacted]	0.0097	SUCCESS	1
[redacted]	0.0098	FAIL	-1
[redacted]	0.0098	SUCCESS	1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0099	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0100	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	FAIL	-1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0101	SUCCESS	1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	FAIL	-1
[redacted]	0.0102	SUCCESS	1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	FAIL	-1
[redacted]	0.0103	SUCCESS	1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	FAIL	-1
[redacted]	0.0104	SUCCESS	1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	FAIL	-1
[redacted]	0.0105	SUCCESS	1
[redacted]	0.0105	SUCCESS	1
[redacted]	0.0105	SUCCESS	1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0106	FAIL	-1
[redacted]	0.0106	SUCCESS	1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0107	FAIL	-1
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[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	SUCCESS	1
[redacted]	0.0110	FAIL	-1
[redacted]	0.0110	FAIL	-1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	SUCCESS	1
[redacted]	0.0111	SUCCESS	1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	SUCCESS	1
[redacted]	0.0112	SUCCESS	1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0114	FAIL	-1
[redacted]	0.0114	SUCCESS	1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	SUCCESS	1
[redacted]	0.0116	FAIL	-1
[redacted]	0.0116	SUCCESS	1
[redacted]	0.0117	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	SUCCESS	1
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[redacted]	0.0119	SUCCESS	1
[redacted]	0.0120	FAIL	-1
[redacted]	0.0120	FAIL	-1
[redacted]	0.0120	SUCCESS	1
[redacted]	0.0120	SUCCESS	1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
[redacted]	0.0106	FAIL	-1
[redacted]	0.0106	SUCCESS	1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	SUCCESS	1
[redacted]	0.0110	FAIL	-1
[redacted]	0.0110	FAIL	-1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	SUCCESS	1
[redacted]	0.0111	SUCCESS	1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	SUCCESS	1
[redacted]	0.0112	SUCCESS	1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0114	FAIL	-1
[redacted]	0.0114	SUCCESS	1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	SUCCESS	1
[redacted]	0.0116	FAIL	-1
[redacted]	0.0116	SUCCESS	1
[redacted]	0.0117	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0120	FAIL	-1
[redacted]	0.0120	FAIL	-1
[redacted]	0.0120	SUCCESS	1
[redacted]	0.0120	SUCCESS	1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0106	FAIL	-1
[redacted]	0.0106	SUCCESS	1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0107	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0108	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	FAIL	-1
[redacted]	0.0109	SUCCESS	1
[redacted]	0.0110	FAIL	-1
[redacted]	0.0110	FAIL	-1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0110	SUCCESS	1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	FAIL	-1
[redacted]	0.0111	SUCCESS	1
[redacted]	0.0111	SUCCESS	1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	FAIL	-1
[redacted]	0.0112	SUCCESS	1
[redacted]	0.0112	SUCCESS	1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	FAIL	-1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0113	SUCCESS	1
[redacted]	0.0114	FAIL	-1
[redacted]	0.0114	SUCCESS	1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	FAIL	-1
[redacted]	0.0115	SUCCESS	1
[redacted]	0.0116	FAIL	-1
[redacted]	0.0116	SUCCESS	1
[redacted]	0.0117	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	FAIL	-1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0118	SUCCESS	1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	FAIL	-1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0119	SUCCESS	1
[redacted]	0.0120	FAIL	-1
[redacted]	0.0120	FAIL	-1
[redacted]	0.0120	SUCCESS	1
[redacted]	0.0120	SUCCESS	1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	SUCCESS	1
[redacted]	0.0122	FAIL	-1
[redacted]	0.0122	FAIL	-1
[redacted]	0.0122	SUCCESS	1
[redacted]	0.0122	SUCCESS	1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0125	FAIL	-1
[redacted]	0.0125	FAIL	-1
[redacted]	0.0125	SUCCESS	1
[redacted]	0.0125	SUCCESS	1
[redacted]	0.0126	FAIL	-1
[redacted]	0.0126	FAIL	-1
[redacted]	0.0126	SUCCESS	1
[redacted]	0.0126	SUCCESS	1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0129	FAIL	-1
[redacted]	0.0129	SUCCESS	1
[redacted]	0.0129	SUCCESS	1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	SUCCESS	1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	SUCCESS	1
[redacted]	0.0132	FAIL	-1
[redacted]	0.0132	SUCCESS	1
[redacted]	0.0132	SUCCESS	1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0134	FAIL	-1
[redacted]	0.0134	FAIL	-1
[redacted]	0.0134	FAIL	-1
[redacted]	0.0134	SUCCESS	1
[redacted]	0.0134	SUCCESS	1
[redacted]	0.0135	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	SUCCESS	1
[redacted]	0.0122	FAIL	-1
[redacted]	0.0122	FAIL	-1
[redacted]	0.0122	SUCCESS	1
[redacted]	0.0122	SUCCESS	1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0125	FAIL	-1
[redacted]	0.0125	FAIL	-1
[redacted]	0.0125	SUCCESS	1
[redacted]	0.0125	SUCCESS	1
[redacted]	0.0126	FAIL	-1
[redacted]	0.0126	FAIL	-1
[redacted]	0.0126	SUCCESS	1
[redacted]	0.0126	SUCCESS	1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0129	FAIL	-1
[redacted]	0.0129	SUCCESS	1
[redacted]	0.0129	SUCCESS	1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	SUCCESS	1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	SUCCESS	1
[redacted]	0.0132	FAIL	-1
[redacted]	0.0132	SUCCESS	1
[redacted]	0.0132	SUCCESS	1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0133	SUCCESS	1

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	FAIL	-1
[redacted]	0.0121	SUCCESS	1
[redacted]	0.0122	FAIL	-1
[redacted]	0.0122	FAIL	-1
[redacted]	0.0122	SUCCESS	1
[redacted]	0.0122	SUCCESS	1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	FAIL	-1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0123	SUCCESS	1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	FAIL	-1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0124	SUCCESS	1
[redacted]	0.0125	FAIL	-1
[redacted]	0.0125	FAIL	-1
[redacted]	0.0125	SUCCESS	1
[redacted]	0.0125	SUCCESS	1
[redacted]	0.0126	FAIL	-1
[redacted]	0.0126	FAIL	-1
[redacted]	0.0126	SUCCESS	1
[redacted]	0.0126	SUCCESS	1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0127	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	FAIL	-1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0128	SUCCESS	1
[redacted]	0.0129	FAIL	-1
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[redacted]	0.0129	SUCCESS	1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
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[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	FAIL	-1
[redacted]	0.0130	SUCCESS	1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	FAIL	-1
[redacted]	0.0131	SUCCESS	1
[redacted]	0.0132	FAIL	-1
[redacted]	0.0132	SUCCESS	1
[redacted]	0.0132	SUCCESS	1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	FAIL	-1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0133	SUCCESS	1
[redacted]	0.0134	FAIL	-1
[redacted]	0.0134	FAIL	-1
[redacted]	0.0134	FAIL	-1
[redacted]	0.0134	SUCCESS	1
[redacted]	0.0134	SUCCESS	1
[redacted]	0.0135	FAIL	-1

[redacted]	uant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0135	FAIL	-1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	SUCCESS	1
[redacted]	0.0136	SUCCESS	1
[redacted]	0.0136	SUCCESS	1
[redacted]	0.0137	FAIL	-1
[redacted]	0.0137	FAIL	-1
[redacted]	0.0138	FAIL	-1
[redacted]	0.0138	FAIL	-1
[redacted]	0.0138	FAIL	-1
[redacted]	0.0138	SUCCESS	1
[redacted]	0.0139	FAIL	-1
[redacted]	0.0139	SUCCESS	1
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[redacted]	0.0139	SUCCESS	1
[redacted]	0.0140	FAIL	-1
[redacted]	0.0140	FAIL	-1
[redacted]	0.0140	FAIL	-1
[redacted]	0.0140	SUCCESS	1
[redacted]	0.0140	SUCCESS	1
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[redacted]	0.0140	SUCCESS	1
[redacted]	0.0140	SUCCESS	1
[redacted]	0.0140	SUCCESS	1
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[redacted]	0.0141	FAIL	-1
[redacted]	0.0141	SUCCESS	1
[redacted]	0.0142	FAIL	-1
[redacted]	0.0142	FAIL	-1
[redacted]	0.0142	SUCCESS	1
[redacted]	0.0142	SUCCESS	1
[redacted]	0.0142	SUCCESS	1
[redacted]	0.0143	FAIL	-1
[redacted]	0.0143	FAIL	-1
[redacted]	0.0143	FAIL	-1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0144	FAIL	-1
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[redacted]	0.0144	SUCCESS	1
[redacted]	0.0144	SUCCESS	1
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[redacted]	0.0146	FAIL	-1
[redacted]	0.0146	FAIL	-1
[redacted]	0.0146	FAIL	-1
[redacted]	0.0146	SUCCESS	1
[redacted]	0.0147	FAIL	-1
[redacted]	0.0147	FAIL	-1
[redacted]	0.0147	FAIL	-1
[redacted]	0.0148	FAIL	-1
[redacted]	0.0148	FAIL	-1
[redacted]	0.0148	FAIL	-1
[redacted]	0.0148	SUCCESS	1
[redacted]	0.0148	SUCCESS	1
[redacted]	0.0149	FAIL	-1
[redacted]	0.0149	FAIL	-1
[redacted]	0.0149	FAIL	-1
[redacted]	0.0150	FAIL	-1
[redacted]	0.0150	FAIL	-1
[redacted]	0.0150	FAIL	-1
[redacted]	0.0150	SUCCESS	1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL

[redacted]	uant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0135	FAIL	-1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0135	SUCCESS	1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	FAIL	-1
[redacted]	0.0136	SUCCESS	1
[redacted]	0.0136	SUCCESS	1
[redacted]	0.0136	SUCCESS	1
[redacted]	0.0137	FAIL	-1
[redacted]	0.0137	FAIL	-1
[redacted]	0.0138	FAIL	-1
[redacted]	0.0138	FAIL	-1
[redacted]	0.0138	FAIL	-1
[redacted]	0.0138	SUCCESS	1
[redacted]	0.0139	FAIL	-1
[redacted]	0.0139	SUCCESS	1
[redacted]	0.0139	SUCCESS	1
[redacted]	0.0139	SUCCESS	1
[redacted]	0.0140	FAIL	-1
[redacted]	0.0140	FAIL	-1
[redacted]	0.0140	FAIL	-1
[redacted]	0.0140	SUCCESS	1
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[redacted]	0.0140	SUCCESS	1
[redacted]	0.0140	SUCCESS	1
[redacted]	0.0140	SUCCESS	1
[redacted]	0.0140	SUCCESS	1
[redacted]	0.0141	FAIL	-1
[redacted]	0.0141	FAIL	-1
[redacted]	0.0141	SUCCESS	1
[redacted]	0.0142	FAIL	-1
[redacted]	0.0142	FAIL	-1
[redacted]	0.0142	SUCCESS	1
[redacted]	0.0142	SUCCESS	1
[redacted]	0.0142	SUCCESS	1
[redacted]	0.0143	FAIL	-1
[redacted]	0.0143	FAIL	-1
[redacted]	0.0143	FAIL	-1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0143	SUCCESS	1
[redacted]	0.0144	FAIL	-1
[redacted]	0.0144	FAIL	-1
[redacted]	0.0144	FAIL	-1
[redacted]	0.0144	SUCCESS	1
[redacted]	0.0144	SUCCESS	1
[redacted]	0.0145	FAIL	-1
[redacted]	0.0145	FAIL	-1
[redacted]	0.0145	SUCCESS	1
[redacted]	0.0146	FAIL	-1
[redacted]	0.0146	FAIL	-1
[redacted]	0.0146	FAIL	-1
[redacted]	0.0146	SUCCESS	1
[redacted]	0.0147	FAIL	-1
[redacted]	0.0147	FAIL	-1
[redacted]	0.0147	FAIL	-1
[redacted]	0.0148	FAIL	-1
[redacted]	0.0148	FAIL	-1
[redacted]	0.0148	FAIL	-1
[redacted]	0.0148	SUCCESS	1
[redacted]	0.0148	SUCCESS	1
[redacted]	0.0149	FAIL	-1
[redacted]	0.0149	FAIL	-1
[redacted]	0.0149	FAIL	-1
[redacted]	0.0150	FAIL	-1
[redacted]	0.0150	FAIL	-1
[redacted]	0.0150	FAIL	-1
[redacted]	0.0150	SUCCESS	1

[redacted]	uant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0150	SUCCESS	1
[redacted]	0.0150	SUCCESS	1
[redacted]	0.0151	FAIL	-1
[redacted]	0.0151	FAIL	-1
[redacted]	0.0151	FAIL	-1
[redacted]	0.0151	FAIL	-1
[redacted]	0.0151	FAIL	-1
[redacted]	0.0152	FAIL	-1
[redacted]	0.0152	FAIL	-1
[redacted]	0.0152	SUCCESS	1
[redacted]	0.0153	FAIL	-1
[redacted]	0.0153	FAIL	-1
[redacted]	0.0154	FAIL	-1
[redacted]	0.0154	FAIL	-1
[redacted]	0.0154	FAIL	-1
[redacted]	0.0154	SUCCESS	1
[redacted]	0.0154	SUCCESS	1
[redacted]	0.0155	SUCCESS	1
[redacted]	0.0155	SUCCESS	1
[redacted]	0.0156	FAIL	-1
[redacted]	0.0156	FAIL	-1
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[redacted]	0.0156	SUCCESS	1
[redacted]	0.0157	FAIL	-1
[redacted]	0.0157	SUCCESS	1
[redacted]	0.0158	FAIL	-1
[redacted]	0.0158	FAIL	-1
[redacted]	0.0158	SUCCESS	1
[redacted]	0.0159	FAIL	-1
[redacted]	0.0160	FAIL	-1
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[redacted]	0.0160	SUCCESS	1
[redacted]	0.0160	SUCCESS	1
[redacted]	0.0160	SUCCESS	1
[redacted]	0.0161	FAIL	-1
[redacted]	0.0161	SUCCESS	1
[redacted]	0.0161	SUCCESS	1
[redacted]	0.0162	FAIL	-1
[redacted]	0.0162	FAIL	-1
[redacted]	0.0162	FAIL	-1
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[redacted]	0.0162	SUCCESS	1
[redacted]	0.0162	SUCCESS	1
[redacted]	0.0162	SUCCESS	1
[redacted]	0.0163	FAIL	-1
[redacted]	0.0163	FAIL	-1
[redacted]	0.0163	FAIL	-1
[redacted]	0.0163	FAIL	-1
[redacted]	0.0164	FAIL	-1
[redacted]	0.0164	FAIL	-1
[redacted]	0.0164	SUCCESS	1
[redacted]	0.0164	SUCCESS	1
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[redacted]	0.0165	FAIL	-1
[redacted]	0.0165	FAIL	-1
[redacted]	0.0165	SUCCESS	1
[redacted]	0.0166	FAIL	-1
[redacted]	0.0166	SUCCESS	1
[redacted]	0.0167	FAIL	-1
[redacted]	0.0167	FAIL	-1
[redacted]	0.0167	FAIL	-1
[redacted]	0.0167	SUCCESS	1
[redacted]	0.0168	FAIL	-1
[redacted]	0.0168	FAIL	-1
[redacted]	0.0168	FAIL	-1
[redacted]	0.0168	SUCCESS	1
[redacted]	0.0168	SUCCESS	1
[redacted]	0.0169	FAIL	-1
[redacted]	0.0169	FAIL	-1
[redacted]	0.0169	SUCCESS	1
[redacted]	0.0170	SUCCESS	1
[redacted]	0.0170	SUCCESS	1
[redacted]	0.0171	SUCCESS	1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0150	SUCCESS	1
[redacted]	0.0150	SUCCESS	1

	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0172	FAIL	-1
[redacted]	0.0172	SUCCESS	1
[redacted]	0.0172	SUCCESS	1
[redacted]	0.0173	FAIL	-1
[redacted]	0.0173	FAIL	-1
[redacted]	0.0173	FAIL	-1
[redacted]	0.0173	SUCCESS	1
[redacted]	0.0173	SUCCESS	1
[redacted]	0.0174	FAIL	-1
[redacted]	0.0174	FAIL	-1
[redacted]	0.0174	SUCCESS	1
[redacted]	0.0174	SUCCESS	1
[redacted]	0.0175	SUCCESS	1
[redacted]	0.0175	SUCCESS	1
[redacted]	0.0176	FAIL	-1
[redacted]	0.0176	FAIL	-1
[redacted]	0.0176	FAIL	-1
[redacted]	0.0176	FAIL	-1
[redacted]	0.0176	SUCCESS	1
[redacted]	0.0178	FAIL	-1
[redacted]	0.0178	FAIL	-1
[redacted]	0.0178	SUCCESS	1
[redacted]	0.0178	SUCCESS	1
[redacted]	0.0178	SUCCESS	1
[redacted]	0.0179	FAIL	-1
[redacted]	0.0179	SUCCESS	1
[redacted]	0.0180	FAIL	-1
[redacted]	0.0180	FAIL	-1
[redacted]	0.0181	FAIL	-1
[redacted]	0.0182	FAIL	-1
[redacted]	0.0182	FAIL	-1
[redacted]	0.0182	FAIL	-1
[redacted]	0.0182	FAIL	-1
[redacted]	0.0182	SUCCESS	1
[redacted]	0.0183	FAIL	-1
[redacted]	0.0183	SUCCESS	1
[redacted]	0.0183	SUCCESS	1
[redacted]	0.0184	FAIL	-1
[redacted]	0.0184	FAIL	-1
[redacted]	0.0184	SUCCESS	1
[redacted]	0.0185	FAIL	-1
[redacted]	0.0185	FAIL	-1
[redacted]	0.0185	FAIL	-1
[redacted]	0.0186	FAIL	-1
[redacted]	0.0186	FAIL	-1
[redacted]	0.0186	SUCCESS	1
[redacted]	0.0186	SUCCESS	1
[redacted]	0.0186	SUCCESS	1
[redacted]	0.0187	FAIL	-1
[redacted]	0.0187	FAIL	-1
[redacted]	0.0187	FAIL	-1
[redacted]	0.0189	FAIL	-1
[redacted]	0.0189	SUCCESS	1
[redacted]	0.0190	FAIL	-1
[redacted]	0.0190	FAIL	-1
[redacted]	0.0191	FAIL	-1
[redacted]	0.0191	FAIL	-1
[redacted]	0.0192	FAIL	-1
[redacted]	0.0192	FAIL	-1
[redacted]	0.0193	FAIL	-1
[redacted]	0.0193	SUCCESS	1
[redacted]	0.0194	FAIL	-1
[redacted]	0.0195	FAIL	-1
[redacted]	0.0195	FAIL	-1
[redacted]	0.0195	SUCCESS	1
[redacted]	0.0195	SUCCESS	1
[redacted]	0.0195	SUCCESS	1
[redacted]	0.0195	SUCCESS	1
[redacted]	0.0196	FAIL	-1
[redacted]	0.0197	SUCCESS	1
[redacted]	0.0197	SUCCESS	1
[redacted]	0.0197	SUCCESS	1
[redacted]	0.0198	FAIL	-1
[redacted]	0.0198	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0198	SUCCESS	1
[redacted]	0.0198	SUCCESS	1
[redacted]	0.0198	SUCCESS	1
[redacted]	0.0199	FAIL	-1
[redacted]	0.0199	SUCCESS	1
[redacted]	0.0199	SUCCESS	1
[redacted]	0.0199	SUCCESS	1
[redacted]	0.0200	FAIL	-1
[redacted]	0.0200	SUCCESS	1
[redacted]	0.0201	SUCCESS	1
[redacted]	0.0202	FAIL	-1
[redacted]	0.0202	FAIL	-1
[redacted]	0.0202	FAIL	-1
[redacted]	0.0202	SUCCESS	1
[redacted]	0.0202	SUCCESS	1
[redacted]	0.0203	FAIL	-1
[redacted]	0.0203	FAIL	-1
[redacted]	0.0203	FAIL	-1
[redacted]	0.0203	SUCCESS	1
[redacted]	0.0203	SUCCESS	1
[redacted]	0.0203	SUCCESS	1
[redacted]	0.0204	FAIL	-1
[redacted]	0.0204	FAIL	-1
[redacted]	0.0204	FAIL	-1
[redacted]	0.0205	FAIL	-1
[redacted]	0.0205	FAIL	-1
[redacted]	0.0205	FAIL	-1
[redacted]	0.0205	SUCCESS	1
[redacted]	0.0205	SUCCESS	1
[redacted]	0.0205	SUCCESS	1
[redacted]	0.0206	FAIL	-1
[redacted]	0.0207	FAIL	-1
[redacted]	0.0207	FAIL	-1
[redacted]	0.0207	FAIL	-1
[redacted]	0.0207	FAIL	-1
[redacted]	0.0208	FAIL	-1
[redacted]	0.0208	SUCCESS	1
[redacted]	0.0208	SUCCESS	1
[redacted]	0.0208	SUCCESS	1
[redacted]	0.0209	FAIL	-1
[redacted]	0.0210	FAIL	-1
[redacted]	0.0210	SUCCESS	1
[redacted]	0.0211	SUCCESS	1
[redacted]	0.0211	SUCCESS	1
[redacted]	0.0211	SUCCESS	1
[redacted]	0.0211	SUCCESS	1
[redacted]	0.0212	FAIL	-1
[redacted]	0.0212	FAIL	-1
[redacted]	0.0212	FAIL	-1
[redacted]	0.0212	SUCCESS	1
[redacted]	0.0213	FAIL	-1
[redacted]	0.0213	FAIL	-1
[redacted]	0.0215	FAIL	-1
[redacted]	0.0215	FAIL	-1
[redacted]	0.0215	SUCCESS	1
[redacted]	0.0215	SUCCESS	1
[redacted]	0.0216	FAIL	-1
[redacted]	0.0216	SUCCESS	1
[redacted]	0.0218	FAIL	-1
[redacted]	0.0218	FAIL	-1
[redacted]	0.0218	SUCCESS	1
[redacted]	0.0219	FAIL	-1
[redacted]	0.0219	SUCCESS	1
[redacted]	0.0219	SUCCESS	1
[redacted]	0.0220	FAIL	-1
[redacted]	0.0220	FAIL	-1
[redacted]	0.0220	FAIL	-1
[redacted]	0.0220	SUCCESS	1
[redacted]	0.0220	SUCCESS	1
[redacted]	0.0221	FAIL	-1
[redacted]	0.0221	FAIL	-1
[redacted]	0.0222	FAIL	-1
[redacted]	0.0222	FAIL	-1
[redacted]	0.0222	SUCCESS	1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0222	SUCCESS	1
[redacted]	0.0223	FAIL	-1
[redacted]	0.0223	FAIL	-1
[redacted]	0.0223	SUCCESS	1
[redacted]	0.0224	FAIL	-1
[redacted]	0.0225	SUCCESS	1
[redacted]	0.0226	FAIL	-1
[redacted]	0.0226	FAIL	-1
[redacted]	0.0226	SUCCESS	1
[redacted]	0.0227	FAIL	-1
[redacted]	0.0227	SUCCESS	1
[redacted]	0.0228	FAIL	-1
[redacted]	0.0228	FAIL	-1
[redacted]	0.0228	SUCCESS	1
[redacted]	0.0229	FAIL	-1
[redacted]	0.0229	SUCCESS	1
[redacted]	0.0230	FAIL	-1
[redacted]	0.0230	SUCCESS	1
[redacted]	0.0231	SUCCESS	1
[redacted]	0.0231	SUCCESS	1
[redacted]	0.0232	FAIL	-1
[redacted]	0.0232	SUCCESS	1
[redacted]	0.0234	SUCCESS	1
[redacted]	0.0234	SUCCESS	1
[redacted]	0.0235	FAIL	-1
[redacted]	0.0235	FAIL	-1
[redacted]	0.0235	SUCCESS	1
[redacted]	0.0235	SUCCESS	1
[redacted]	0.0235	SUCCESS	1
[redacted]	0.0235	SUCCESS	1
[redacted]	0.0236	FAIL	-1
[redacted]	0.0238	FAIL	-1
[redacted]	0.0239	FAIL	-1
[redacted]	0.0239	SUCCESS	1
[redacted]	0.0239	SUCCESS	1
[redacted]	0.0240	SUCCESS	1
[redacted]	0.0241	FAIL	-1
[redacted]	0.0241	FAIL	-1
[redacted]	0.0241	FAIL	-1
[redacted]	0.0241	SUCCESS	1
[redacted]	0.0241	SUCCESS	1
[redacted]	0.0242	SUCCESS	1
[redacted]	0.0243	FAIL	-1
[redacted]	0.0244	FAIL	-1
[redacted]	0.0244	FAIL	-1
[redacted]	0.0244	SUCCESS	1
[redacted]	0.0244	SUCCESS	1
[redacted]	0.0245	FAIL	-1
[redacted]	0.0245	SUCCESS	1
[redacted]	0.0246	FAIL	-1
[redacted]	0.0246	FAIL	-1
[redacted]	0.0246	FAIL	-1
[redacted]	0.0247	FAIL	-1
[redacted]	0.0247	FAIL	-1
[redacted]	0.0247	SUCCESS	1
[redacted]	0.0248	FAIL	-1
[redacted]	0.0248	FAIL	-1
[redacted]	0.0248	FAIL	-1
[redacted]	0.0248	SUCCESS	1
[redacted]	0.0248	SUCCESS	1
[redacted]	0.0248	SUCCESS	1
[redacted]	0.0249	FAIL	-1
[redacted]	0.0249	FAIL	-1
[redacted]	0.0249	FAIL	-1
[redacted]	0.0249	SUCCESS	1
[redacted]	0.0252	SUCCESS	1
[redacted]	0.0253	FAIL	-1
[redacted]	0.0253	FAIL	-1
[redacted]	0.0255	FAIL	-1
[redacted]	0.0255	FAIL	-1
[redacted]	0.0256	SUCCESS	1
[redacted]	0.0256	SUCCESS	1
[redacted]	0.0256	SUCCESS	1
[redacted]	0.0257	FAIL	-1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL

Barcode	Quant all	EXHinterp	SUCCESS/FAIL
[redacted]	0.0257	FAIL	-1
[redacted]	0.0257	SUCCESS	1
[redacted]	0.0258	FAIL	-1
[redacted]	0.0258	SUCCESS	1
[redacted]	0.0259	SUCCESS	1
[redacted]	0.0260	FAIL	-1
[redacted]	0.0260	SUCCESS	1
[redacted]	0.0261	FAIL	-1
[redacted]	0.0261	SUCCESS	1
[redacted]	0.0262	FAIL	-1
[redacted]	0.0263	FAIL	-1
[redacted]	0.0263	FAIL	-1
[redacted]	0.0263	FAIL	-1
[redacted]	0.0265	FAIL	-1
[redacted]	0.0266	FAIL	-1
[redacted]	0.0267	SUCCESS	1
[redacted]	0.0267	SUCCESS	1
[redacted]	0.0270	FAIL	-1
[redacted]	0.0271	SUCCESS	1
[redacted]	0.0272	SUCCESS	1
[redacted]	0.0273	FAIL	-1
[redacted]	0.0273	SUCCESS	1
[redacted]	0.0274	FAIL	-1
[redacted]	0.0274	SUCCESS	1
[redacted]	0.0274	SUCCESS	1
[redacted]	0.0275	SUCCESS	1
[redacted]	0.0275	SUCCESS	1
[redacted]	0.0276	FAIL	-1
[redacted]	0.0276	FAIL	-1
[redacted]	0.0276	SUCCESS	1
[redacted]	0.0277	FAIL	-1
[redacted]	0.0277	SUCCESS	1
[redacted]	0.0278	SUCCESS	1
[redacted]	0.0278	SUCCESS	1
[redacted]	0.0278	SUCCESS	1
[redacted]	0.0279	FAIL	-1
[redacted]	0.0279	FAIL	-1
[redacted]	0.0280	FAIL	-1
[redacted]	0.0280	SUCCESS	1
[redacted]	0.0281	FAIL	-1
[redacted]	0.0281	SUCCESS	1
[redacted]	0.0284	FAIL	-1
[redacted]	0.0285	SUCCESS	1
[redacted]	0.0287	SUCCESS	1
[redacted]	0.0287	SUCCESS	1
[redacted]	0.0289	FAIL	-1
[redacted]	0.0289	FAIL	-1
[redacted]	0.0289	SUCCESS	1
[redacted]	0.0289	SUCCESS	1
[redacted]	0.0290	SUCCESS	1
[redacted]	0.0290	SUCCESS	1
[redacted]	0.0292	FAIL	-1
[redacted]	0.0292	FAIL	-1
[redacted]	0.0293	FAIL	-1
[redacted]	0.0293	FAIL	-1
[redacted]	0.0293	SUCCESS	1
[redacted]	0.0293	SUCCESS	1
[redacted]	0.0294	SUCCESS	1
[redacted]	0.0296	SUCCESS	1
[redacted]	0.0296	SUCCESS	1
[redacted]	0.0296	SUCCESS	1
[redacted]	0.0298	FAIL	-1
[redacted]	0.0299	FAIL	-1
[redacted]	0.0299	SUCCESS	1
[redacted]	0.0299	SUCCESS	1
[redacted]	0.0299	SUCCESS	1
[redacted]	0.0300	FAIL	-1
[redacted]	0.0300	SUCCESS	1
[redacted]	0.0301	FAIL	-1
[redacted]	0.0301	FAIL	-1
[redacted]	0.0304	SUCCESS	1
[redacted]	0.0305	FAIL	-1
[redacted]	0.0305	SUCCESS	1
[redacted]	0.0305	SUCCESS	1

Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL

Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL

Barcode	Quant all	EXHinterp	SUCCESS/FAIL	Barcode	Quant <0.01	EXHinterp	SUCCESS/FAIL	Barcode	Quant <0.0133	EXHinterp	SUCCESS/FAIL	Barcode	Quant <0.015	EXHinterp	SUCCESS/FAIL
[redacted]	0.0305	SUCCESS	1												
[redacted]	0.0306	SUCCESS	1												
[redacted]	0.0306	SUCCESS	1												
[redacted]	0.0309	FAIL	-1												
[redacted]	0.0309	FAIL	-1												
[redacted]	0.0311	FAIL	-1												
[redacted]	0.0312	FAIL	-1												
[redacted]	0.0314	FAIL	-1												
[redacted]	0.0314	SUCCESS	1												
[redacted]	0.0315	SUCCESS	1												
[redacted]	0.0315	SUCCESS	1												
[redacted]	0.0316	FAIL	-1												
[redacted]	0.0316	SUCCESS	1												
[redacted]	0.0316	SUCCESS	1												
[redacted]	0.0316	SUCCESS	1												
[redacted]	0.0318	FAIL	-1												
[redacted]	0.0319	FAIL	-1												
[redacted]	0.0319	SUCCESS	1												
[redacted]	0.0319	SUCCESS	1												
[redacted]	0.0321	FAIL	-1												
[redacted]	0.0321	FAIL	-1												
[redacted]	0.0321	FAIL	-1												
[redacted]	0.0322	FAIL	-1												
[redacted]	0.0325	FAIL	-1												
[redacted]	0.0327	FAIL	-1												
[redacted]	0.0327	SUCCESS	1												
[redacted]	0.0328	FAIL	-1												
[redacted]	0.0329	SUCCESS	1												
[redacted]	0.0329	SUCCESS	1												
[redacted]	0.0329	SUCCESS	1												
[redacted]	0.0329	SUCCESS	1												
[redacted]	0.0330	FAIL	-1												
[redacted]	0.0330	FAIL	-1												
[redacted]	0.0346	FAIL	-1												
[redacted]	0.0346	FAIL	-1												
[redacted]	0.0346	FAIL	-1												
[redacted]	0.0346	SUCCESS	1												
[redacted]	0.0346	SUCCESS	1												
[redacted]	0.0349	FAIL	-1												
[redacted]	0.0362	FAIL	-1												
[redacted]	0.0364	FAIL	-1												
[redacted]	0.0368	SUCCESS	1												
[redacted]	0.0369	FAIL	-1												
[redacted]	0.0382	FAIL	-1												
[redacted]	0.0384	SUCCESS	1												
[redacted]	0.0391	SUCCESS	1												
[redacted]	0.0396	FAIL	-1												
[redacted]	0.0397	FAIL	-1												
[redacted]	0.0446	SUCCESS	1												
[redacted]	0.0474	SUCCESS	1												
[redacted]	0.0533	FAIL	-1												
[redacted]	0.0577	SUCCESS	1												
[redacted]	0.0611	SUCCESS	1												
[redacted]	0.0743	SUCCESS	1												
[redacted]	0.0907	FAIL	-1												

[redacted]	TRUE	0.0046	Auto	Submitted as cells QPS advised no further work required - results available
[redacted]	TRUE	0.0022	Auto	Submitted as cells QPS advised no further work required - results available
[redacted]	TRUE	0.0088	Auto	Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.0074	Auto	Submitted-results pending. QPS advised no further work required - results available
[redacted]	TRUE	0.0088	Auto	
[redacted]	TRUE	0.0037	Auto	
[redacted]	TRUE	0.0071	Auto	
[redacted]	TRUE	0.0052	Auto	
[redacted]	TRUE	0.0031	Auto	Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.0031	Auto	Submitted-results pending. QPS advised no further work required - results available
[redacted]	TRUE	0.0036	Auto	
[redacted]	TRUE	0.0074	Auto	
[redacted]	TRUE	0.0037	Auto	
[redacted]	TRUE	0.0055	Auto	Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.0073	Auto	Submitted-results pending.
[redacted]	TRUE	0.0029	Auto	Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.0024	Auto	ENVM - Complex mixed DNA profile
[redacted]	TRUE	0.0073	Auto	Submitted-results pending.
[redacted]	TRUE	0.0029	Auto	Submitted-results pending.
[redacted]	TRUE	0.0041	Auto	
[redacted]	TRUE	0.0038	Auto	
[redacted]	TRUE	0.005	Auto	
[redacted]	TRUE	0.0067	Auto	
[redacted]	TRUE	0.0039	Auto	
[redacted]	TRUE	0.0068	Auto	
[redacted]	TRUE	0.0049	Auto	
[redacted]	TRUE	0.0032	Auto	
[redacted]	TRUE	0.0078	Auto	
[redacted]	TRUE	0.0029	Auto	
[redacted]	TRUE	0.0038	Auto	
[redacted]	TRUE	0.0022	Auto	
[redacted]	TRUE	0.0073	Auto	
[redacted]	TRUE	0.0023	Auto	
[redacted]	TRUE	0.0029	Auto	
[redacted]	TRUE	0.0071	Auto	
[redacted]	TRUE	0.0049	Auto	
[redacted]	TRUE	0.0033	Auto	
[redacted]	TRUE	0.0044	Auto	
[redacted]	TRUE	0.0051	Auto	
[redacted]	TRUE	0.003	Auto	
[redacted]	TRUE	0.0033	Auto	
[redacted]	TRUE	0.0022	Auto	
[redacted]	TRUE	0.0066	Auto	
[redacted]	TRUE	0.0052	Auto	Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	TRUE	0.0066	Auto	
[redacted]	TRUE	0.0066	Auto	
[redacted]	TRUE	0.0066	Auto	Submitted-results pending.
[redacted]	TRUE	0.0046	Auto	
[redacted]	TRUE	0.0074	Auto	
[redacted]	TRUE	0.0053	Auto	
[redacted]	TRUE	0.0086	Auto	
[redacted]	TRUE	0.0022	Auto	Submitted-results pending. Quality control failure - results not reportable
[redacted]	TRUE	0.0023	Auto	

[redacted]	TRUE	0.0045	Auto	Submitted-results pending.
[redacted]	TRUE	0.0078	Auto	
[redacted]	TRUE	0.0032	Auto	
[redacted]	TRUE	0.0066	Auto	
[redacted]	TRUE	0.0057	Auto	
[redacted]	TRUE	0.0085	Auto	
[redacted]	TRUE	0.0033	Auto	
[redacted]	TRUE	0.0038	Auto	Submitted-results pending.
[redacted]	TRUE	0.008	Auto	Submitted-results pending.
[redacted]	TRUE	0.006	Auto	Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS
[redacted]	TRUE	0.0044	Auto	
[redacted]	TRUE	0.0028	Auto	
[redacted]	TRUE	0.0064	Auto	
[redacted]	TRUE	0.0047	Auto	
[redacted]	TRUE	0.0026	Auto	
[redacted]	TRUE	0.0022	Auto	
[redacted]	TRUE	0.0028	Auto	
[redacted]	TRUE	0.0059	Auto	
[redacted]	TRUE	0.0053	Auto	
[redacted]	TRUE	0.0038	Auto	
[redacted]	TRUE	0.0054	Auto	
[redacted]	TRUE	0.0027	Auto	
[redacted]	TRUE	0.0086	Auto	
[redacted]	TRUE	0.0025	Auto	
[redacted]	TRUE	0.0036	Auto	
[redacted]	TRUE	0.0052	Auto	
[redacted]	TRUE	0.0036	Auto	
[redacted]	TRUE	0.0026	Auto	
[redacted]	TRUE	0.008	Auto	
[redacted]	TRUE	0.008	Auto	
[redacted]	TRUE	0.005	Auto	
[redacted]	TRUE	0.0068	Auto	
[redacted]	TRUE	0.0031	Auto	
[redacted]	TRUE	0.0031	Auto	
[redacted]	TRUE	0.0029	Auto	
[redacted]	TRUE	0.0062	Auto	
[redacted]	TRUE	0.0056	Auto	
[redacted]	TRUE	0.0054	Auto	
[redacted]	TRUE	0.005	Auto	
[redacted]	TRUE	0.0072	Auto	
[redacted]	TRUE	0.0023	Auto	
[redacted]	TRUE	0.0057	Auto	
[redacted]	TRUE	0.0066	Auto	
[redacted]	TRUE	0.0082	Auto	
[redacted]	TRUE	0.0025	Auto	
[redacted]	TRUE	0.0045	Auto	
[redacted]	TRUE	0.0075	Auto	
[redacted]	TRUE	0.0071	Auto	
[redacted]	TRUE	0.0023	Auto	
[redacted]	TRUE	0.0065	Auto	
[redacted]	TRUE	0.0055	Auto	
[redacted]	TRUE	0.0074	Auto	
[redacted]	TRUE	0.0049	Auto	
[redacted]	TRUE	0.0031	Auto	
[redacted]	TRUE	0.0045	Auto	
[redacted]	TRUE	0.0057	Auto	
[redacted]	TRUE	0.0085	Auto	
[redacted]	TRUE	0.0088	Auto	
[redacted]	TRUE	0.005	Auto	
[redacted]	TRUE	0.0039	Auto	
[redacted]	TRUE	0.0042	Auto	
[redacted]	TRUE	0.003	Auto	
[redacted]	TRUE	0.0038	Auto	
[redacted]	TRUE	0.0044	Auto	
[redacted]	TRUE	0.003	Auto	
[redacted]	TRUE	0.0028	Auto	
[redacted]	TRUE	0.0037	Auto	
[redacted]	TRUE	0.0066	Auto	
[redacted]	TRUE	0.0081	Auto	
[redacted]	TRUE	0.0033	Auto	
[redacted]	TRUE	0.0067	Auto	
[redacted]	TRUE	0.0035	Auto	
[redacted]	TRUE	0.0033	Auto	
[redacted]	TRUE	0.0044	Auto	
[redacted]	TRUE	0.005	Auto	
[redacted]	TRUE	0.0029	Auto	
[redacted]	TRUE	0.006	Auto	
[redacted]	TRUE	0.0078	Auto	
[redacted]	TRUE	0.0083	Auto	
[redacted]	TRUE	0.0045	Auto	
[redacted]	TRUE	0.0025	Auto	
[redacted]	TRUE	0.0051	Auto	

[redacted]	RUE	0.008	Auto		
[redacted]	RUE	0.0043	Auto		
[redacted]	RUE	0.0036	Auto		
[redacted]	RUE	0.0077	Auto		
[redacted]	RUE	0.0025	Auto		
[redacted]	RUE	0.0029	Auto		
[redacted]	RUE	0.0033	Auto		
[redacted]	RUE	0.0028	Auto		
[redacted]	RUE	0.0039	Auto		
[redacted]	RUE	0.0043	Auto		
[redacted]	RUE	0.0067	Auto		
[redacted]	RUE	0.0034	Auto		
[redacted]	RUE	0.0031	Auto		
[redacted]	RUE	0.0031	Auto		
[redacted]	RUE	0.004	Auto		
[redacted]	RUE	0.0041	Auto		
[redacted]	RUE	0.0026	Auto		
[redacted]	RUE	0.0038	Auto		
[redacted]	RUE	0.0031	Auto		
[redacted]	RUE	0.0044	Auto		
[redacted]	RUE	0.0041	Auto		
[redacted]	RUE	0.0088	Auto		
[redacted]	RUE	0.0037	Auto		
[redacted]	RUE	0.0063	Auto		
[redacted]	RUE	0.0086	Auto		
[redacted]	RUE	0.0037	Auto		
[redacted]	RUE	0.0063	Auto		
[redacted]	RUE	0.0067	Auto		
[redacted]	RUE	0.0028	Auto		Submitted-results pending.
[redacted]	RUE	0.0034	Auto		Submitted-results pending.
[redacted]	RUE	0.003	Auto		Submitted-results pending.
[redacted]	RUE	0.0059	Auto		Submitted-results pending.
[redacted]	RUE	0.0074	Auto		Submitted-results pending.
[redacted]	RUE	0.0045	Auto		Submitted-results pending.
[redacted]	RUE	0.0055	Auto		Submitted-results pending.
[redacted]	RUE	0.0034	Auto		Submitted-results pending.
[redacted]	RUE	0.0082	Auto		Submitted-results pending.
[redacted]	RUE	0.0054	Auto		Submitted-results pending.
[redacted]	RUE	0.0044	Auto		Submitted-results pending.
[redacted]	RUE	0.0023	Auto		Submitted-results pending.
[redacted]	RUE	0.0042	Auto		Submitted-results pending.
[redacted]	RUE	0.0025	Auto		Hair located. Submitted-results pending
[redacted]	RUE	0.0023	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	RUE	0.007	Auto		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
[redacted]	RUE	0.0031	Auto		Submitted-results pending. Sample processed and final results under
[redacted]	RUE	0.0039	Auto		Submitted-results pending. Sample processed and final results under
[redacted]	RUE	0.0038	Auto		Submitted-results pending. Sample processed and final results under
[redacted]	RUE	0.0044	Auto		Micro positive for sperm. Submitted-Results pending
[redacted]	RUE	0.007	Auto		presump Saliva test positive
[redacted]	RUE	0.0054	Auto		Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
[redacted]	RUE	0.0087	Auto		Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative
[redacted]	RUE	0.0046	Auto		Submitted-results pending. Micro neg for sperm
[redacted]	RUE	0.0022	Auto		Submitted-results pending. Micro neg for sperm
[redacted]	RUE	0.0062	Auto		Submitted-results pending. Micro neg for sperm
[redacted]	RUE	0.0023	Auto	SUCCESS	Submitted-results pending. Presump Saliva test negative Micro neg for sperm Single Source DNA profile - assumed known contributor

[redacted]	0.0079	SUCCESS	Micro positive for sperm. Submitted-Results pending Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion		not auto
[redacted]	0.0057	SUCCESS	SS DNA profile 9 loci and above LR > 100 billion		not auto
[redacted]	0	FAIL	-1	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison	

[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. DNA insufficient for further processing This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix- support for contrib 1 billion - 100 billion 3 person mix - supports non contribution 3 person mix - supports non contribution This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
[redacted]	0	FAIL	-1	Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison

7.1E+08	TRUE	0	Manual	FAIL	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0	Manual	FAIL	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
6.95E+08	TRUE	0	Manual		
5.99E+08	TRUE	0	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
5.99E+08	TRUE	0	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
5.82E+08	TRUE	0	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
7.1E+08	TRUE	0	Manual	FAIL	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0	Manual	FAIL	Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison
5.99E+08	TRUE	0	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
5.8E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		ENVM -Partial DNA profile
7.28E+08	TRUE	0	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
7.28E+08	TRUE	0	Manual		ENVM - No DNA profile
3.83E+08	TRUE	0	Manual		Submitted-results pending. No DNA detected
7.1E+08	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile

7.1E+08	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Possible sub-threshold information
7.1E+08	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Possible sub-threshold information
7.1E+08	TRUE	0	Manual		Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		ENVM - No DNA profile
7.28E+08	TRUE	0	Manual		
7.28E+08	TRUE	0	Manual		
5.24E+08	TRUE	0	Manual		Submitted-results pending. No DNA detected
5.99E+08	TRUE	0.0002	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
5.82E+08	TRUE	0.0002	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0002	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
7.28E+08	TRUE	0.0002	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
7.28E+08	TRUE	0.0002	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0002	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0002	Manual		
7.28E+08	TRUE	0.0002	Manual		
5.99E+08	TRUE	0.0002	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
6.9E+08	TRUE	0.0002	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
7.27E+08	TRUE	0.0002	Manual		ENVM - No DNA profile
6.9E+08	TRUE	0.0002	Manual		
6.95E+08	TRUE	0.0003	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
7.1E+08	TRUE	0.0003	Manual		Submitted-results pending. No DNA detected
5.99E+08	TRUE	0.0003	Manual		ENVM - No DNA profile
5.99E+08	TRUE	0.0003	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
5.99E+08	TRUE	0.0003	Manual		ENVM -Partial DNA profile
5.99E+08	TRUE	0.0003	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
6.9E+08	TRUE	0.0003	Manual		
6.95E+08	TRUE	0.0004	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
5.99E+08	TRUE	0.0004	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
6.9E+08	TRUE	0.0004	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.27E+08	TRUE	0.0004	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
5.99E+08	TRUE	0.0005	Manual		ENVM -Partial DNA profile
6.9E+08	TRUE	0.0005	Manual		
6.9E+08	TRUE	0.0005	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes

6.9E+08	TRUE	0.0005	Manual	FAIL	Submitted-results pending. Presump. PSA test positive, no sperm found Partial DNA profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0006	Manual		ENVM -Partial DNA profile
7.27E+08	TRUE	0.0006	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
5.99E+08	TRUE	0.0007	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
5.99E+08	TRUE	0.0007	Manual	FAIL	Micro positive for sperm. Submitted-Results pending No DNA detected This sample has undergone further processing Partial DNA profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0007	Manual		ENVM - No DNA profile
6.9E+08	TRUE	0.0007	Manual		ENVM -Partial DNA profile
6.95E+08	TRUE	0.0007	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
5.99E+08	TRUE	0.0008	Manual		
5.99E+08	TRUE	0.0008	Manual	FAIL	ENVM- Complex mixture unsuitable for interp or comparison
7.28E+08	TRUE	0.0009	Manual		ENVM -Partial DNA profile
7.27E+08	TRUE	0.0009	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.001	Manual		Submitted-results pending.
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.19E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.19E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.29E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

6.72E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
4.56E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.95E+08	TRUE	0.001	Manual		
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.89E+08	TRUE	0.001	Manual		
6.45E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.001	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.001	Manual		
6.86E+08	TRUE	0.001	Manual		Submitted-results pending.
5.8E+08	TRUE	0.001	Manual		
7.11E+08	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks

7.1E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.001	Manual		
7.28E+08	TRUE	0.001	Manual		
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.001	Manual		
7.13E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.28E+08	TRUE	0.001	Manual		
7.12E+08	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
5.99E+08	TRUE	0.001	Manual		
6.9E+08	TRUE	0.001	Manual		
6.9E+08	TRUE	0.001	Manual	FAIL	Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.001	Manual		
7.12E+08	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.27E+08	TRUE	0.001	Manual		

7.1E+08	TRUE	0.001	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.95E+08	TRUE	0.001	Manual		
7.12E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.001	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0011	Manual		Submitted-results pending. No DNA profile
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.89E+08	TRUE	0.0011	Manual	FAIL	ENVM - Partial profile unsuitable for comparison purposes
6.86E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.55E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.1E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0011	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0011	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0011	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.1E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.44E+08	TRUE	0.0011	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0011	Manual		Submitted-results pending. No DNA profile Possible sub-threshold information
6.91E+08	TRUE	0.0011	Manual		
6.9E+08	TRUE	0.0011	Manual		
7.28E+08	TRUE	0.0011	Manual		
6.95E+08	TRUE	0.0011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0011	Manual		Submitted-results pending. No DNA profile
7.12E+08	TRUE	0.0011	Manual	FAIL	Semen not detected Submitted as cells Partial DNA profile unsuitable for comparison purposes
6.55E+08	TRUE	0.0011	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0011	Manual		
7.28E+08	TRUE	0.0011	Manual		

7.13E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.1E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0011	Manual		Single Source DNA profile - assumed known contributor
6.9E+08	TRUE	0.0011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0011	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
5.99E+08	TRUE	0.0011	Manual		
6.9E+08	TRUE	0.0011	Manual		
7.27E+08	TRUE	0.0011	Manual		
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.27E+08	TRUE	0.0011	Manual		Submitted-results pending. Semen not detected No DNA profile - possible sub-threshold peaks
7.27E+08	TRUE	0.0011	Manual		
7.11E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.13E+08	TRUE	0.0011	Manual		Submitted-results pending. Sample processed and final results under
6.73E+08	TRUE	0.0011	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0011	Manual		
3.83E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.06E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.1E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.1E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0012	Manual	FAIL	Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
6.85E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0012	Manual	FAIL	Submitted as cells, Presump saliva test pending presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0012	Manual	FAIL	Submitted as cells Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.11E+08	TRUE	0.0012	Manual		Submitted-results pending. No DNA profile
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.86E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.63E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.0012	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
6.9E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0012	Manual		
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.55E+08	TRUE	0.0012	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
6.45E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.29E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0012	Manual	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0012	Manual		
6.63E+08	TRUE	0.0012	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0012	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0012	Manual		
5.8E+08	TRUE	0.0012	Manual		Single Source DNA profile - assumed known contributor
7.11E+08	TRUE	0.0012	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.13E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0012	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0012	Manual	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0012	Manual		
7.1E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0012	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks

6.9E+08	TRUE	0.0012	Manual	FAIL	Presumptive blood test pos. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.9E+08	TRUE	0.0012	Manual		
7.12E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.91E+08	TRUE	0.0012	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.45E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. No DNA profile
6.03E+08	TRUE	0.0013	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.1E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.89E+08	TRUE	0.0013	Manual		
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0013	Manual		
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.29E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes

7.11E+08	TRUE	0.0013	Manual	FAIL	Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0013	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
5.99E+08	TRUE	0.0013	Manual		ENVM -Partial DNA profile
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0013	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison
6.02E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0013	Manual		
7.28E+08	TRUE	0.0013	Manual		

7.12E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0013	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Partial DNA profile unsuitable for comparison purposes
7.72E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.0013	Manual		Submitted-results pending. No DNA profile Possible sub-threshold information
7.1E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.27E+08	TRUE	0.0013	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Micro positive for sperm. Submitted-Results pending Partial DNA profile unsuitable for comparison purposes
6.29E+08	TRUE	0.0013	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
6.9E+08	TRUE	0.0013	Manual		
7.13E+08	TRUE	0.0013	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.28E+08	TRUE	0.0013	Manual		
7.91E+08	TRUE	0.0013	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.27E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interp or comparison

6.86E+08	TRUE	0.0013	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.95E+08	TRUE	0.0014	Manual		
6.63E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.06E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.85E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.99E+08	TRUE	0.0014	Manual		
6.29E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.1E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0014	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
6.63E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

6.19E+08	TRUE	0.0014	Manual		Submitted-results pending. No DNA profile
7.11E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0014	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.55E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.64E+08	TRUE	0.0014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.29E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.0014	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.12E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0014	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.12E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.27E+08	TRUE	0.0014	Manual		
7.27E+08	TRUE	0.0014	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0014	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
6.95E+08	TRUE	0.0014	Manual		Micro positive for sperm. Submitted-Results pending
7.11E+08	TRUE	0.0014	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
6.29E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.0014	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0014	Manual		
6.85E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.55E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.03E+08	TRUE	0.0015	Manual		
6.86E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.11E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.85E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0015	Manual		Submitted-results pending. No DNA profile Possible sub-threshold information
7.11E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.89E+08	TRUE	0.0015	Manual		Submitted as cells Single Source DNA profile - assumed known contributor
7.11E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0015	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.1E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

6.63E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0015	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.45E+08	TRUE	0.0015	Manual	SUCCESS	Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile DNA profile removed from NCIDD
7.11E+08	TRUE	0.0015	Manual		Submitted-results pending.
7.28E+08	TRUE	0.0015	Manual		
7.11E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.13E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0015	Manual	FAIL	Hair located. Submitted-results pending Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.95E+08	TRUE	0.0015	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0015	Manual		No DNA profile - possible sub-threshold peaks
5.24E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0015	Manual		Submitted-results pending. Micro neg for sperm Semen not detected Single source DNA profile Single source DNA profile < 9 loci LR 1000 - 10 000
7.27E+08	TRUE	0.0015	Manual		

7.1E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0015	Manual		Submitted-results pending. No DNA profile
7.28E+08	TRUE	0.0015	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0015	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0015	Manual		
7.11E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.45E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.91E+08	TRUE	0.0016	Manual		
7.1E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
3.42E+08	TRUE	0.0016	Manual		
6.89E+08	TRUE	0.0016	Manual	FAIL	Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.12E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.91E+08	TRUE	0.0016	Manual		
6.9E+08	TRUE	0.0016	Manual		
7.1E+08	TRUE	0.0016	Manual		Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile No statistical interpretation performed
7.12E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
3.83E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0016	Manual		
7.12E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0016	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.27E+08	TRUE	0.0016	Manual		
7.13E+08	TRUE	0.0016	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0016	Manual		Submitted-results pending.
5.06E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.99E+08	TRUE	0.0017	Manual	SUCCESS	Presump. PSA test positive, no sperm found Single source DNA profile < NCIDD matching stringency Single Source DNA profile - assumed known contributor

7.11E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.45E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.91E+08	TRUE	0.0017	Manual		
7.11E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0017	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.1E+08	TRUE	0.0017	Manual		Submitted-results pending. No DNA profile
7.1E+08	TRUE	0.0017	Manual		Submitted-results pending. No DNA profile
7.12E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

6.85E+08	TRUE	0.0017	Manual		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
7.12E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0017	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0017	Manual		
7.12E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.85E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.13E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.1E+08	TRUE	0.0017	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.11E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0017	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0017	Manual		
6.73E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.89E+08	TRUE	0.0018	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.86E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0018	Manual		Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
7.11E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0018	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
6.89E+08	TRUE	0.0018	Manual		
7.1E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.89E+08	TRUE	0.0018	Manual		

6.73E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0018	Manual	FAIL	Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.11E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.29E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.9E+08	TRUE	0.0018	Manual	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison

6.9E+08	TRUE	0.0018	Manual		Hair located. Submitted-results pending Interim result - sample undergoing rework Two person mixed DNA profile 2 person mix - supports non contribution 2 person mix profile - support for contrib > 100 billion
7.13E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.73E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0018	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
5.06E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0018	Manual		
7.11E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0018	Manual		Submitted-results pending. No DNA profile
6.95E+08	TRUE	0.0018	Manual		
7.12E+08	TRUE	0.0018	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0018	Manual	FAIL	Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.11E+08	TRUE	0.0019	Manual	SUCCESS	Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile
6.63E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.73E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.89E+08	TRUE	0.0019	Manual		
7.1E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.82E+08	TRUE	0.0019	Manual		
5.99E+08	TRUE	0.0019	Manual		
7.1E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.89E+08	TRUE	0.0019	Manual		Submitted as cells, Presump saliva test pending Presump Saliva test negative Single Source DNA profile - assumed known contributor
7.11E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.11E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
6.63E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.12E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.54E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.02E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.99E+08	TRUE	0.0019	Manual	FAIL	Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0019	Manual	SUCCESS	Hair located. Submitted-results pending Single source DNA profile NCIDD upload single source DNA profile
7.12E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.12E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0019	Manual		
7.28E+08	TRUE	0.0019	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
7.28E+08	TRUE	0.0019	Manual		

7.11E+08	TRUE	0.0019	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0019	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion
6.95E+08	TRUE	0.0019	Manual	FAIL	Submitted as cells, Presump saliva test pending Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
7.27E+08	TRUE	0.0019	Manual		Micro positive for sperm. Submitted-Results pending
7.27E+08	TRUE	0.0019	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0019	Manual		Submitted-results pending. Micro neg for sperm
6.9E+08	TRUE	0.0019	Manual		Micro positive for sperm. Submitted-Results pending
7.27E+08	TRUE	0.0019	Manual		Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor
7.1E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

6.19E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.89E+08	TRUE	0.002	Manual		
7.1E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.45E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.29E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.73E+08	TRUE	0.002	Manual		Submitted-results pending. No DNA profile Possible sub-threshold information
7.12E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes

7.1E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.002	Manual	FAIL	Partial DNA profile unsuitable for comparison purposes
6.44E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
7.13E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.002	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.27E+08	TRUE	0.002	Manual		
7.1E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.86E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.91E+08	TRUE	0.0021	Manual		
7.1E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.63E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
5.82E+08	TRUE	0.0021	Manual	FAIL	Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison
7.28E+08	TRUE	0.0021	Manual		

7.1E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Partial DNA profile unsuitable for comparison purposes
5.06E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0021	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0021	Manual	FAIL	Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison
7.1E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.72E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.11E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
6.45E+08	TRUE	0.0021	Manual		Submitted-results pending. No DNA profile - possible sub-threshold peaks
7.13E+08	TRUE	0.0021	Manual		Submitted-results pending. No DNA detected
6.9E+08	TRUE	0.0021	Manual		
6.9E+08	TRUE	0.0021	Manual	FAIL	Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison
6.9E+08	TRUE	0.0021	Manual		
6.9E+08	TRUE	0.0021	Manual		
7.13E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison

7.12E+08	TRUE	0.0021	Manual	FAIL	Submitted-results pending. Complex mixed profile unsuitable for interp or comparison
7.13E+08	TRUE	0.0021	Manual		Submitted-results pending.
7.12E+08	0.0091		Submitted-results pending.		
7.28E+08	0.0121			nfa	
7.28E+08	0.023			nfa	
6.9E+08	0.0155		Micro positive for sperm. Submitted-Results pending QPS advised no further work required - results available		
7.12E+08	0.0115		Submitted-results pending.		
7.11E+08	0.0119		Submitted-results pending.		
7.12E+08	0.0128		Submitted-results pending.		
7.11E+08	0.0139		Submitted-results pending.		
6.72E+08	0.0141		Submitted-results pending.		
7.11E+08	0.0142		Submitted-results pending.		
5.85E+08	0.0143		Submitted-results pending.		
7.12E+08	0.0146		Submitted-results pending.		
6.86E+08	0.0165		Submitted-results pending.		
7.11E+08	0.0191		Submitted-results pending.		
7.12E+08	0.0195		Submitted-results pending.		
7.13E+08	0.0196		Submitted-results pending.		
7.1E+08	0.0238		Submitted-results pending.		
7.1E+08	0.0247		Submitted-results pending.		
7.13E+08	0.0268		Submitted-results pending.		
7.12E+08	0.0304		Submitted-results pending.		
7.11E+08	0.0305		Submitted-results pending.		
7.1E+08	0.0239		Submitted-results pending. Intel report required for further interpretation		

7.1E+08	0.016	Submitted-results pending. Interim result - sample undergoing rework Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
6.95E+08	0.0181	Submitted-results pending. Micro neg for sperm

JH-11

No DNA detected

DNA was not detected in this sample during initial the stages of DNA analysis and as such this sample was not submitted for DNA profiling.

DNA insufficient

This sample contained insufficient DNA to be suitable for analysis and therefore was not submitted for DNA profiling.