

FBS23 — FBU Report Wording Guidelines

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1. Scope

- 1.1. The guidelines listed below are provided for analysts to use when writing Forensic Biology Unit reports to relay the results and scientifically supported conclusions relative to the testing conducted in as concise a manner as possible.

2. Background

- 2.1. The content of Forensic Biology Unit laboratory reports must conform to the requirements of the Department of Forensic Sciences (DFS) Forensic Science Laboratory (FSL) *Quality Assurance Manual*, the accreditation standards under ISO/IEC 17025:2005, the supplemental standards set by the FSL's accrediting body, and the FBI's *Quality Assurance Standards for Forensic DNA Testing Laboratories*.
- 2.2. The function of this document is to set forth the report statements for the Results and Conclusions and Examination Methods Notes sections of Forensic Biology Unit Reports of Examination.

3. Safety

- 3.1. Not applicable

4. Materials Required

- 4.1. Not applicable

5. Standards and Controls

- 5.1. Refer to *LOM02 – Practices for Case Documentation and Report Writing* for letterhead requirements for all Reports of Examination, Amended Reports of Examination, Database Hit Notifications and Discontinuation of Analysis.
- 5.2. Refer to *LOM02 – Practices for Case Documentation and Report Writing* for general framework/report information requirements for laboratory reports.

6. Calibration

- 6.1. Not applicable

7. Procedures

- 7.1. In general, FBU reports will contain sections in the following order:
- 7.1.1. Report name (e.g., Report of Examination, Forensic Biology Unit)
 - 7.1.2. Case information block
 - 7.1.3. Items Submitted, including Item Number / Description listing
 - 7.1.4. Requested Analysis
 - 7.1.5. Results and Conclusions (with subsections for *Serology*, *Real-Time PCR Analysis (Quantitation)*, *DNA Analysis*, and *CODIS*, as needed)
 - 7.1.6. Examination Methods Notes
 - 7.1.7. Disposition of Evidence
 - 7.1.8. Signature block
- 7.2. Guidelines – Basic Information:
- 7.2.1. The guidelines are listed in the order in which they are used in the laboratory report.
 - 7.2.1.1. In general, all listed criteria associated with a selected report statement should be met or addressed.
 - 7.2.1.2. Within a criteria and statement table, it may be appropriate to select statements from multiple sections (e.g., in the Single

Source Inclusion portion of the table in section 7.4.2.5., a full report statement would be comprised of selections from Part 1A or Part 1B and Part 2A (and Part 2B, when applicable)).

- 7.2.2. An entry in ALL CAPITAL LETTERS indicates the need to insert the indicated information.
- 7.2.3. Entries in [brackets] should be included as needed.
- 7.2.4. Collective statements may be applied to samples that yield the same results, such as:
 - 7.2.4.1. For evidence items: “**The same** DNA profile was obtained from Items...”
 - 7.2.4.2. For reference samples: “DNA **profiles were** obtained from Items...”
- 7.2.5. When results and conclusions statements have been combined, redundant wording may be removed (as long as the meaning is clear).
- 7.2.6. A male contributor may only be reported when the Amelogenin Y allele is present above the analytical threshold.
 - 7.2.6.1 When interpreting epithelial and sperm fractions generated from a single sample, if one of the fractions contains a male profile with the Amelogenin Y allele above analytical threshold and the other fraction contains alleles consistent with that male donor, regardless of the Amelogenin Y allele, the findings may be reported as “alleles consistent with the male profile” for the fraction that contains the partial profile.
- 7.2.7. When a reported typing result is a composite of multiple injections for a single sample, the report statement will reflect this (e.g., the statement will read “A composite DNA profile was obtained from Item...”).
 - 7.2.7.1. When a composite profile is reported for a case, the following statement will be included in the “Examination Methods Notes” section: A composite DNA profile is generated by combining typing results from different loci obtained from multiple injections of the same amplified sample and/or multiple amplifications of the same DNA extract. When separate extracts from different locations on a given evidentiary item are combined prior to amplification, the resultant DNA profile is not considered a composite profile.
- 7.2.8. When reporting results in a supplemental report that have already been provided in a released/published report, the following wording will be used:
 - 7.2.8.1. “The DNA profile **previously** obtained from Item...”

7.3. Serology Analysis Results/Conclusions Wording:

7.3.1. When the Serology subheader is used in the “Results and Conclusions” section and testing for blood has been conducted, the following statement(s) will be included in the “Examination Methods Notes” section, as applicable:

7.3.1.1. Phenolphthalein (Kastle-Meyer) chemical testing is conducted to presumptively screen for the presence of blood. It is noted that a positive result is strongly indicative of the presence of blood, particularly when red-brown staining is observed. A negative result indicates that blood is not present; however, it does not preclude the possibility that blood may be present.

7.3.1.2. ABACard[®] Hematrace[®] immunological testing is conducted to confirm the presence of human blood. While blood from higher primates and ferrets may also yield a positive result, the laboratory considers a positive Hematrace[®] test result to be confirmatory for the presence of human blood. A negative result is a strong indication that the sample in question is not human blood; however, it does not preclude the possibility that human blood may be present.

7.3.2. When the Serology subheader is used in the “Results and Conclusions” section and testing for semen has been conducted, the following statement(s) will be included in the “Examination Methods Notes” section, as applicable:

7.3.2.1. An alternate light source (ALS) may be used to screen clothing, bedding and other similar types of evidence for the presence of biological stains, including semen. It is noted that many substances fluoresce under the conditions used to screen evidence for the presence of body fluid stains. Accordingly, the observation of fluorescence is used solely as a tool to visualize a location(s) to conduct further testing. Conversely, failure to observe fluorescence does not preclude a decision to conduct further testing for body fluids since; for example, fluorescence may not be detected due to sensitivity limits of the apparatus, age of the stain, and/or if interfering substances or substrates fluoresce.

7.3.2.2. Acid phosphatase (AP) chemical testing may be used as a presumptive screen for the presence of semen. It is noted that a positive AP result is indicative of the presence of semen; however, some false positive results are possible. A negative result indicates that semen is not present; however, it does not preclude the possibility that trace amounts of semen or intact sperm cells may be present, or that an older stain/deposit with little or no enzymatic activity may be present.

- 7.3.2.3. Seratec[®] p30 immunological testing is used to confirm the presence of semen. While semen from higher primates may also yield a positive result, the laboratory considers a positive Seratec[®] p30 test result to be confirmatory for the presence of human semen. A negative result is a strong indication that the sample in question is not human semen; however, it does not preclude the possibility that human semen may be present.
- 7.3.2.4. Microscopic visualization of spermatozoa (including a single spermatozoon) stained with nuclear fast red and picroindigocarmine dyes (Christmas tree stain) is used to confirm the presence of semen. Failure to visualize spermatozoa is a strong indication that human semen is not present, particularly when coupled with a negative p30 testing result. However, failure to visualize spermatozoa in and of itself it does not preclude the possibility that trace amounts of human semen may be present, particularly for samples with a large amount of cellular debris, or that semen from a vasectomized, aspermic, or azoospermic male may be present.

7.3.3. Refer to the following table for the statement(s) to be used when the *Serology* subheader is used in the “Results and Conclusions” section:

BIOLOGICAL SCREENING RESULTS – NEGATIVE VISUAL EXAMINATION ONLY	
To select this statement, the criteria listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> Item visually negative for the presence of blood or semen Further testing may or may not be performed 	No [blood] [and/or] [semen] was observed on DESCRIPTION (Item ITEM NUMBER) using [a] [an] [visual examination/] [microscopic examination] [and/or] [alternate light source screening] method[s]. [No further testing was performed.]
BIOLOGICAL SCREENING RESULTS – TESTING FOR BLOOD	
For the selected statement, the criteria listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> Positive Hematrace result Positive, negative or inconclusive phenolphthalein testing result or no phenolphthalein testing conducted Further testing may or may 	Human blood was detected on DESCRIPTION (Item ITEM NUMBER). [Due to limited quantity, no presumptive screening testing was conducted.] [No further testing was performed.]
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not be performed	
<ul style="list-style-type: none"> Negative phenolphthalein testing result Further testing may or may not be performed 	No blood was detected on DESCRIPTION (Item ITEM NUMBER). [No further testing was performed.]
<ul style="list-style-type: none"> Positive phenolphthalein testing result Further testing may or may not be performed 	The presence of blood was indicated on DESCRIPTION (Item ITEM NUMBER). [Due to limited quantity, no confirmatory testing was conducted.] [No further testing was performed.]
<ul style="list-style-type: none"> Positive phenolphthalein testing result Negative or inconclusive hematrace result Further testing may or may not be performed 	The presence of blood was indicated on DESCRIPTION (Item ITEM NUMBER); however, it could not be confirmed as human blood due to [an inconclusive] [a negative] Hematrace [®] test result. [No further testing was performed.]
<ul style="list-style-type: none"> Inconclusive phenolphthalein testing result Further testing may or may not be performed 	Testing for the presence of blood was inconclusive on DESCRIPTION (Item ITEM NUMBER). [Due to limited quantity, no confirmatory testing was conducted.] [No further testing was performed.]
<ul style="list-style-type: none"> Negative hematrace result Inconclusive phenolphthalein testing result Further testing may or may not be performed 	A confirmatory test for the presence of human blood was negative while the screening test for the presence of blood was inconclusive on DESCRIPTION (Item ITEM NUMBER). Accordingly, no determination can be made regarding the possible presence of blood. [No further testing was performed.]
<ul style="list-style-type: none"> Inconclusive phenolphthalein testing result Inconclusive hematrace result Further testing may or may not be performed 	Testing for the presence of blood was inconclusive on DESCRIPTION (Item ITEM NUMBER) using both screening and confirmatory tests. Accordingly, no determination can be made regarding the possible presence of blood. [No further testing was performed.]

BIOLOGICAL SCREENING RESULTS – TESTING FOR SEMEN
For the selected statement, the criteria listed in the left column must be met:

Criteria	Statement
<ul style="list-style-type: none"> Positive p30 testing result Spermatozoa visualized microscopically, no 	Human [seminal fluid] [semen] was detected on DESCRIPTION (Item ITEM NUMBER). [No further testing was performed.]

<p>spermatozoa detected microscopically or no microscopic examination conducted</p> <ul style="list-style-type: none"> • Positive, negative or inconclusive ALS screening result, or no ALS screening conducted • Positive, negative or inconclusive AP testing result, or no AP testing conducted • Further testing may or may not be performed 	<p>NOTE: when only a positive p30 testing result has been obtained, the results will be reported as human seminal fluid was detected. When spermatozoa are visualized along with the positive p30 result, the results will be reported as human semen was detected.</p>
<ul style="list-style-type: none"> • Option A: Visualization of spermatozoa microscopically • Option B: Visualization of a spermatozoon microscopically • Positive, negative or inconclusive p30 testing result, or no p30 testing conducted • Positive, negative or inconclusive ALS screening result, or no ALS screening conducted • Positive, negative or inconclusive AP testing result, or no AP testing conducted • Further testing may or may not be performed 	<p>Option A: Human semen was detected on DESCRIPTION (Item ITEM NUMBER). [No further testing was performed.]</p> <p>Option B: Human semen was detected on DESCRIPTION (Item ITEM NUMBER); however, only one spermatozoon was observed. [No further testing was performed.]</p>
<ul style="list-style-type: none"> • Inconclusive p30 testing result • No spermatozoa detected microscopically or no microscopic examination conducted • Positive, negative or inconclusive ALS screening result, or no ALS screening conducted • Positive, negative or inconclusive AP testing result • Further testing may or may 	<p>Testing for the presence of seminal fluid was inconclusive on DESCRIPTION (Item ITEM NUMBER) [; however, no spermatozoa were detected in a microscopic examination]. [No further testing [including a microscopic examination for spermatozoa] was performed.]</p>

<p>not be performed</p>	
<ul style="list-style-type: none"> • Inconclusive AP testing result • Negative or inconclusive p30 testing result and/or no spermatozoa detected microscopically • Positive, negative or inconclusive ALS screening result, or no ALS screening conducted • Further testing may or may not be performed 	<p>Testing for the presence of seminal fluid was inconclusive on DESCRIPTION (Item ITEM NUMBER) [; however, no spermatozoa were detected in a microscopic examination]. [No further testing was performed.]</p>
<ul style="list-style-type: none"> • Positive AP testing result • Negative p30 testing result • No spermatozoa detected microscopically • Positive, negative or inconclusive ALS screening result, or no ALS screening conducted • Further testing may or may not be performed 	<p>The presence of seminal fluid was indicated on DESCRIPTION (Item ITEM NUMBER) [but could not be confirmed]. [Due to limited quantity, no confirmatory testing was conducted.] [No further testing was performed.]</p>
<ul style="list-style-type: none"> • Negative AP testing result • Negative p30 testing result and/or no spermatozoa detected microscopically or no p30 testing conducted and/or no microscopic examination conducted • Positive, negative or inconclusive ALS screening result, or no ALS screening conducted • Further testing may or may not be performed 	<p>No [seminal fluid] [semen] was detected on DESCRIPTION (Item ITEM NUMBER). [No further testing was performed.]</p> <p>NOTE: when a microscopic examination is conducted and no spermatozoa are detected, the results will be reported as no semen was detected. When no microscopic examination is conducted, the results will be reported as no seminal fluid was detected.</p>

7.4. DNA Analysis Results/Conclusions Wording:

7.4.1. When the *Real-Time PCR Analysis (Quantitation)* subheader is used in the “Results and Conclusions” section:

7.4.1.1. The following statement will be included in the “Examination”

Methods Notes” section: The DNA extracts isolated from the appropriate items were quantified using the Quantifiler® Duo DNA Quantification Kit (Applied Biosystems). This laboratory employs a quantitation cut-off of 200 picograms (pg) using the Quantifiler® Duo DNA Quantification Kit. When a sample yields quantitation result below this cut-off value, no further testing is conducted

7.4.1.2. Refer to the following table for the statement(s) to be used in the “Results and Conclusions” section:

QUANTITATION RESULTS	
For the selected statement, the criterion listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> For samples with quantitation values $\leq 0.02\text{ng}/\mu\text{L}$ or $20\text{pg}/\mu\text{L}$ (a total amplification target of $\leq 200\text{pg}/10\mu\text{L}$) but greater than $0.0001\text{ng}/\mu\text{L}$ or $0.1\text{pg}/\mu\text{L}$ 	Real-time PCR testing determined that human DNA was detected on DESCRIPTION (Item ITEM NUMBER); however, it was insufficient for conducting the PCR DNA testing performed in this laboratory. This sample was not processed any further than quantitation.
<ul style="list-style-type: none"> For samples with quantitation values $\leq 0.0001\text{ng}/\mu\text{L}$ or $0.1\text{pg}/\mu\text{L}$ (undet.) 	Real-time PCR testing determined that no human DNA suitable for STR testing was found on DESCRIPTION (Item ITEM NUMBER). This sample was not processed any further than quantitation.

7.4.2. When the *DNA Analysis* subheader is used in the “Results and Conclusions” section:

7.4.2.1. The following statement will be included in the “Examination Methods Notes” section: The DNA extracts isolated from the appropriate items were quantified using the Quantifiler® Duo DNA Quantification Kit (Applied Biosystems) and subsequently amplified and typed using the AmpF/STR Identifiler Plus® Kit (Applied Biosystems). The Identifiler Plus® Kit analyzes the 13 core CODIS short tandem repeat (STR) loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, vWA, TPOX, D18S51, D5S818 and FGA), as well as the D2S1338, D19S433, and Amelogenin loci. Appropriate positive and negative controls were used concurrently throughout the analysis. The DNA profiles reported in this case were determined by procedures that have been validated according to standards established by the Scientific Working Group on DNA Analysis Methods (SWGDM) and adopted as Federal Standards.

- 7.4.2.2. The following statement will also be included in the “Examination Methods Notes” section: All DNA testing results are assessed to determine if the findings are consistent with the DNA profile having originated from a single individual or if the results are consistent with a mixture of DNA from two or more people. Typing results from mixture DNA profiles may enable the analyst to use available case information and/or mathematically separate out the profiles of the contributors based on the amount of DNA present from each individual. When this is possible, the mixture profile is said to be distinguishable. A major contributor to a mixture is the individual whose DNA is present in a greater amount. A minor contributor to a mixture is an individual who can account for a lesser portion of the DNA in a mixed sample.
- 7.4.2.3. The reference sample results statements will be listed first, before listing the “Results and Conclusions” for evidence profiles. Every reference sample will have an associated results statement.

REFERENCE SAMPLE RESULTS	
For the selected statement, the criterion listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> Results at ≥ ten (10) loci (excluding Amelogenin) 	A DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER).
<ul style="list-style-type: none"> Results at nine (9) loci to one (1) locus (excluding Amelogenin) 	A partial DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). [The results obtained from this reference sample are not suitable for meaningful comparison purposes.] [Should comparison of this individual to the evidence profile(s) obtained be desired, another known sample (buccal or blood) from NAME must be obtained and submitted to the laboratory.]
<ul style="list-style-type: none"> No profile obtained (no alleles detected above AT at all loci) 	No DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). [Should comparison of this individual to the evidence profile(s) obtained be desired, another known sample (buccal or blood) from NAME must be obtained and submitted to the laboratory.]

- 7.4.2.4. A results statement will be provided for all evidence profiles. The results statement is provided independent of comparison(s) to reference samples and describes the evidence profile as either:

- *no result*
- *single source*
- *mixture (non-complex)*
- *low level partial or complex mixture*

In addition, when comparisons are conducted, one of the following primary conclusions can be reached:

- cannot exclude / inclusion (match)
- can exclude
- inconclusive / uninterpretable

7.4.2.4.1. Results/conclusions statements for all evidence profiles are listed sequentially.

7.4.2.4.2. Designations such as Male 1 and Female 1 may be used when such clarification will be helpful to the reader.

7.4.2.5. The following guidelines will be used to report evidence profiles as *no result*.

NO DNA RESULTS – EVIDENCE	
To select this statement, the criterion listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> • No profile obtained (no alleles detected above AT at all loci) 	No DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER).

7.4.2.6. The following guidelines will be used to report “Results and Conclusions” for evidence *single source* profiles:

PART 1A – SINGLE SOURCE INCLUSION OR INCONCLUSIVE – DNA RESULTS/CONCLUSION	
For the selected statement, the criteria listed in the left column must be met (if low level partial results were obtained, refer to Part 1B):	
Criteria	Statement
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at ≥10 loci (excluding Amelogenin) • Inclusion of 1 individual 	The single source [male] [female] DNA profile obtained from DESCRIPTION (Item ITEM NUMBER) matches the DNA profile obtained from REFERENCE SAMPLE DESCRIPTION (Item ITEM NUMBER).
<ul style="list-style-type: none"> • 1-2 alleles at all loci*, except 1 	The single source [male] [female] DNA profile obtained

<p>additional minor allele at 1 locus; results at ≥ 10 loci (excluding Amelogenin)</p> <ul style="list-style-type: none"> • Inclusion of 1 individual 	<p>from DESCRIPTION (Item ITEM NUMBER) matches the DNA profile obtained from REFERENCE SAMPLE DESCRIPTION (Item ITEM NUMBER). One additional allele was obtained at the [locus name] locus.</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*, 3 alleles at one locus in possible triallelic pattern**; results at ≥ 10 loci (excluding Amelogenin) • Inclusion of 1 individual 	<p>The single source [male] [female] DNA profile obtained from DESCRIPTION (Item ITEM NUMBER) matches the DNA profile obtained from REFERENCE SAMPLE DESCRIPTION (Item ITEM NUMBER). A possible triallelic pattern was obtained at the [locus name] locus.</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at 6-9 loci (excluding Amelogenin) Option A: Inclusion of 1 individual • Option B: When the comparison is inconclusive 	<p>Option A: REFERENCE SAMPLE DESCRIPTION (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> contributor of the partial single source [male] [female] DNA profile obtained from DESCRIPTION (Item ITEM NUMBER)..</p> <p>Option B: A partial [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Due to the limited data obtained, no conclusion can be made in relation to NAME (Item ITEM NUMBER) as a possible contributor to this profile.</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at 6-9 loci (no Amelogenin results) Option A: Inclusion of 1 individual • Option B: When the comparison is inconclusive 	<p>Option A: REFERENCE SAMPLE DESCRIPTION (Item ITEM NUMBER) cannot be excluded as a possible contributor of the partial single source DNA profile obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: A partial DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Due to the limited data obtained, no conclusion can be made in relation to NAME (Item ITEM NUMBER) as a possible contributor to this profile.</p>
<p>*Since it may assist in the interpretation of results, when analyzing a sample using the >1000 rfus analysis method, signals below the >1000 rfus AT parameters that are \geq to the <1000 rfus AT parameters should be considered in the determination of whether a sample is most likely single source or a mixture.</p> <p>**Triallelic patterns are possible and may be significantly imbalanced. Case file documentation will support the reproducibility of the pattern, though it is noted that the peak height ratios may differ.</p> <p>NOTE: these symbols will have the same meaning in subsequent sections of this table.</p>	

PART 1B – LOW LEVEL PARTIAL SINGLE SOURCE INCLUSION OR INCONCLUSIVE – DNA RESULTS/CONCLUSION

For the selected statement, the criteria listed in the left column must be met (if low level partial results were not obtained, refer to Part 1A):

Criteria	Statement
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at 3-5 loci (excluding Amelogenin); potential for stochastic effects and/or indication of degradation • Option A: Inclusion of 1 individual • Option B: When it is possible to make inconclusive comparisons • Option C: When it is not possible to make any comparisons/the profile is deemed uninterpretable 	<p>Option A: REFERENCE SAMPLE DESCRIPTION (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> contributor of the partial [male] [female] DNA profile obtained from DESCRIPTION (Item ITEM NUMBER) at a limited number of loci.</p> <p>Option B: A partial [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Due to the limited data obtained, no conclusion can be made in relation to NAME (Item ITEM NUMBER) as a possible contributor to this profile.</p> <p>Option C: A partial [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Due to the limited data obtained, no conclusions can be made regarding this partial profile, nor can it be compared to any known/reference profiles.</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at 3-5 loci (no Amelogenin results); potential for stochastic effects and/or indication of degradation • Option A: Inclusion of 1 individual • Option B: When it is possible to make inconclusive comparisons • Option C: When it is not possible to make any comparisons/the profile is deemed uninterpretable 	<p>Option A: REFERENCE SAMPLE DESCRIPTION (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> contributor of the partial DNA profile obtained from DESCRIPTION (Item ITEM NUMBER) at a limited number of loci.</p> <p>Option B: A partial DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Due to the limited data obtained, no conclusion can be made in relation to NAME (Item ITEM NUMBER) as a possible contributor to this profile.</p> <p>Option C: A partial DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Due to the limited data obtained, no conclusions can be made regarding this partial profile.</p>
<ul style="list-style-type: none"> • Alleles above AT \leq2 loci (may or may not include Amelogenin); potential for stochastic effects and/or indication of degradation; no indication of more than one contributor • It is not possible to make any comparisons/the partial profile 	<p>Uninterpretable DNA profile data was obtained from DESCRIPTION (Item ITEM NUMBER). Accordingly, it cannot be compared to known/reference profiles.</p>

is deemed uninterpretable

PART 2A – SINGLE SOURCE INCLUSION – DNA RESULTS/CONCLUSION – STATISTICS

Use the following statement immediately below the Part 1 results/conclusion statement when use of a statistical statement is appropriate:

The probability of selecting an unrelated individual at random having a STR profile matching the [partial] single source [male] [female] DNA profile obtained from the DESCRIPTION (Item ITEM NUMBER) is approximately:

Approximate Frequency	Population Database
1 in ###	African-American
1 in ###	US Caucasian
1 in ###	US Hispanic

The following associated statement will be included in the “Examination Methods Notes” section whenever a random match statistic is included in a report:

Random match statistical calculations are performed according to the National Research Council’s recommendation 4.1 in “The Evaluation of Forensic DNA Evidence” (1996) and the allele frequencies used are provided in *Appendix A of FBS22 – STR Statistical Calculations Guidelines*. As stated in NRC II (1996) “It is probably safe to assume that within a race, the uncertainty of a value calculated from adequate databases (at least several hundred persons) by the product rule is within a factor of about 10 above and below the true value.”

PART 2B – SINGLE SOURCE INCLUSION – DNA RESULTS/CONCLUSION – STATISTICS

Use the following statement immediately below the Part 2A results/conclusion statistical statement when appropriate:

The following STR [locus was] [loci were] used for comparisons but not used in the statistical calculation: [locus name] (NOTE: add names of additional loci, as needed). [The following STR [locus was] [loci were] not used in the comparison[s] or the statistical calculation: [locus name] (NOTE: add names of additional loci, as needed)].

SINGLE SOURCE EXCLUSION (“NON-MATCH”) – DNA RESULTS/CONCLUSION

For the selected statement, the criteria listed in the left column must be met:

Criteria	Statement
<ul style="list-style-type: none"> 1-2 alleles at all loci*; results at ≥10 loci (excluding Amelogenin) Exclusion of 1 or more individual(s) 	<p>A single source [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). NAME OF EXCLUDED INDIVIDUAL (Item ITEM NUMBER) is excluded as a possible contributor of this profile. [NAME(S) of additional excluded individual(s) (Item ITEM NUMBER) should be added, as applicable.]</p>

<ul style="list-style-type: none"> • 1-2 alleles at all loci*, except 1 additional minor allele at 1 locus; results at ≥ 10 loci (excluding Amelogenin) • Exclusion of 1 or more individual(s) 	<p>A single source [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). One additional allele was obtained at the [locus name] locus. NAME OF EXCLUDED INDIVIDUAL (Item ITEM NUMBER) is excluded as a possible contributor of this profile. [NAME(S) of additional excluded individual(s) (Item ITEM NUMBER) should be added, as applicable.]</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*, 3 alleles at one locus in possible triallelic pattern**; results at ≥ 10 loci (excluding Amelogenin) • Exclusion of 1 or more individual(s) 	<p>A single source [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). A possible triallelic pattern was obtained at the [locus name] locus. NAME OF EXCLUDED INDIVIDUAL (Item ITEM NUMBER) is excluded as a possible contributor of this profile. [NAME(S) of additional excluded individual(s) (Item ITEM NUMBER) should be added, as applicable.]</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at 6-9 loci (excluding Amelogenin) • Exclusion of 1 or more individual(s) 	<p>A partial single source [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). NAME OF EXCLUDED INDIVIDUAL (Item ITEM NUMBER) is excluded as a possible contributor of this profile. [NAME(S) of additional excluded individual(s) (Item ITEM NUMBER) should be added, as applicable.]</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at 6-9 loci (no Amelogenin results) • Exclusion of 1 or more individual(s) 	<p>A partial single source DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). NAME OF EXCLUDED INDIVIDUAL (Item ITEM NUMBER) is excluded as a possible contributor of this profile. [NAME(S) of additional excluded individual(s) (Item ITEM NUMBER) should be added, as applicable.]</p>
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at 3-5 loci (excluding Amelogenin); potential for stochastic effects and/or indication of degradation; no indication of more than one contributor • Exclusion of 1 or more individual(s) 	<p>A partial DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). NAME OF EXCLUDED INDIVIDUAL (Item ITEM NUMBER) is excluded as a possible contributor of this profile. [NAME(S) of additional excluded individual(s) (Item ITEM NUMBER) should be added, as applicable.]</p>

SINGLE SOURCE DNA RESULTS – NO REFERENCE SAMPLE(S) SUBMITTED

For the selected statement, the criterion listed in the left column must be met:

Criteria	Statement
<ul style="list-style-type: none"> • 1-2 alleles at all loci*; results at ≥ 10 loci (excluding Amelogenin) 	<p>A single source unknown [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Comparisons can be conducted upon submission of a known sample(s) (buccal or blood) from [a person(s) of interest] [NAME] to the laboratory.</p>

	(NOTE: refer to section 1A, above, for additional wording in the event that 1 additional allele is noted at 1 locus or a possible triallelic pattern** is noted)
<ul style="list-style-type: none"> 1-2 alleles at all loci*; results at 6-9 loci (excluding Amelogenin) 	<p>A partial single source unknown [male] [female] DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Comparisons can be conducted upon submission of a known sample(s) (buccal or blood) from [a person(s) of interest] [NAME] to the laboratory.</p> <p>(NOTE: refer to section 1A, above, for additional wording in the event that 1 additional allele is noted at 1 locus or a possible triallelic pattern** is noted)</p>
<ul style="list-style-type: none"> 1-2 alleles at all loci*; results at 6-9 loci (no Amelogenin results) 	<p>A partial single source unknown DNA profile was obtained from DESCRIPTION (Item ITEM NUMBER). Comparisons can be conducted upon submission of a known sample(s) (buccal or blood) from [a person(s) of interest] [NAME] to the laboratory.</p> <p>(NOTE: refer to section 1A, above, for additional wording in the event that 1 additional allele is noted at 1 locus or a possible triallelic pattern** is noted)</p>

7.4.2.7. The following guidelines will be used to report non-complex evidence *mixture* profiles:

7.4.2.7.1. The majority of mixture profiles falling into this category will consist of mixtures of only two individuals or a mixture of two individuals plus a minor component that has rfu significantly below those comprising the major alleles. The minor component, particularly when considered non-probative, may have indications of multiple contributors without affecting the categorization of the profile as non-complex.

7.4.2.7.2. The principal component(s) of non-complex mixtures will most often have rfu values above, or primarily above, 1000. The presence or suspected presence of degradation, inhibition and/or apparent stochastic effects does not necessarily preclude a mixture profile from being considered non-complex; however, when any of these are noted, caution will be exercised during the interpretation process.

PART 1 – MIXTURE DNA RESULTS (NON-COMPLEX) – RESULTS/CONCLUSION

For the selected statement, the criteria listed in the left column must be met:

Criteria	Statement
<ul style="list-style-type: none"> • >1000 rfus analysis method used • >2 alleles at >1 locus; results at ≥10 loci (excluding Amelogenin) • Option A: 1-4 alleles per locus*; no signals observed below the >1000 rfus AT parameters that are ≥ to the <1000 rfus AT parameters; when use of a CPI calculation is applicable, 6 or greater loci suitable for inclusion in the statistical calculation • Option B: 1-4 alleles per locus*; no signals observed below the >1000 rfus AT parameters that are ≥ to the <1000 rfus AT parameters; when use of a CPI calculation is applicable, <6 loci suitable for inclusion in a statistical calculation • [Amelogenin Y present] 	<p>Option A: A DNA profile consistent with a mixture of two [individuals] [individuals, at least one of which is a male,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this DNA mixture profile is suitable for exclusionary purposes only.</p>
<ul style="list-style-type: none"> • >1000 rfus analysis parameters used • >2 alleles at >1 locus; results at ≥10 loci (excluding Amelogenin) • Option A: 1-4 alleles per locus (may have >4 alleles at 1 locus)*; when use of a CPI calculation is applicable, 6 or greater loci suitable for inclusion in the statistical calculation • Option B: 1-4 alleles per locus*; when use of a CPI calculation is applicable, <6 loci suitable for inclusion in a statistical calculation 	<p>Option A: A DNA profile consistent with a mixture of at least two [individuals] [individuals, at least one of which is a male,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this DNA mixture profile is suitable for exclusionary purposes only.</p>

<ul style="list-style-type: none"> • [Amelogenin Y present] 	
<ul style="list-style-type: none"> • >1000 rfus analysis parameters used • >2 alleles at >1 locus; results at ≥10 loci (excluding Amelogenin) • Option A: >4 alleles at >2 or more loci*; when use of a CPI calculation is applicable, 6 or greater loci suitable for inclusion in the statistical calculation • Option B: >4 alleles at >2 or more loci*; when use of a CPI calculation is applicable, <6 loci suitable for inclusion in a statistical calculation • Option C: >4 alleles at >2 or more loci*; when profile is deemed uninterpretable due to the complexity of the results/the number of indistinguishable contributors • [Amelogenin Y present] 	<p>Option A: A DNA profile consistent with a mixture of three or more [individuals] [individuals, at least one of which is a male,] [individuals, at least two of which are males,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this DNA mixture profile is suitable for exclusionary purposes only.</p> <p>Option C: Due to the complexity of the data and the laboratory's current interpretation guidelines, the DNA profile obtained has been deemed unsuitable for interpretation.</p>
<ul style="list-style-type: none"> • >1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 6-9 loci (excluding Amelogenin) • Option A: 1-4 alleles per locus*; no signals observed below the >1000 rfus AT parameters that are ≥ to the <1000 rfus AT parameters; when use of a CPI calculation is applicable, 6 or greater loci suitable for inclusion in the statistical calculation • Option B: 1-4 alleles per locus*; no signals observed below the >1000 rfus AT parameters that are ≥ to the <1000 rfus AT parameters; when use of a CPI calculation is applicable, <6 loci suitable for inclusion in a 	<p>Option A: A partial DNA profile consistent with a mixture of two [individuals] [individuals, at least one of which is a male,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>

<p>statistical calculation</p> <ul style="list-style-type: none"> • [Amelogenin Y present] 	
<ul style="list-style-type: none"> • >1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 6-9 loci (excluding Amelogenin) • Option A: 1-4 alleles per locus (may have >4 alleles at 1 locus)*; when use of a CPI calculation is applicable, 6 or greater loci suitable for inclusion in the statistical calculation • Option B: 1-4 alleles per locus (may have >4 alleles at 1 locus)*; when use of a CPI calculation is applicable, <6 loci suitable for inclusion in a statistical calculation • [Amelogenin Y present] 	<p>Option A: A partial DNA profile consistent with a mixture of at least two [individuals] [individuals, at least one of which is a male,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>
<ul style="list-style-type: none"> • >1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 6-9 loci (excluding Amelogenin) • Option A: >4 alleles at >2 or more loci*; when use of a CPI calculation is applicable, 6 or greater loci suitable for inclusion in the statistical calculation • Option B: >4 alleles at >2 or more loci*; when use of a CPI calculation is applicable, <6 loci suitable for inclusion in a statistical calculation • Option C: >4 alleles at >2 or more loci*; when profile is deemed uninterpretable due to the complexity of the results/the number of indistinguishable contributors • [Amelogenin Y present] 	<p>Option A: A partial DNA profile consistent with a mixture of three or more [individuals] [individuals, at least one of which is a male,] [individuals, at least two of which are males,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p> <p>Option C: Due to the complexity of the data and the laboratory's current interpretation guidelines, the partial DNA profile obtained has been deemed unsuitable for interpretation.</p>

*Since it may assist in the interpretation of results, when analyzing a sample using the >1000 rfus analysis method, signals below the >1000 rfus AT parameters that are \geq to the <1000 rfus AT parameters should be considered in the determination of how many contributors may be in a mixture.

PART 2A – MIXTURE DNA RESULTS (NON-COMPLEX) – NO REFERENCE SAMPLE(S) SUBMITTED – RESULTS/CONCLUSION

When selecting this statement is applicable, the criterion listed in the left column must be met:

Criteria	Statement
<ul style="list-style-type: none"> No reference sample(s) submitted 	This [mixture] profile is suitable for comparison purposes.

PART 2B – MIXTURE DNA RESULTS (NON-COMPLEX) – CONTRIBUTOR PROFILES INDISTINGUISHABLE – RESULTS/CONCLUSION

When selecting one of these statements is applicable, the criteria listed in the left column must be met :

Criteria	Statement
<ul style="list-style-type: none"> Contributor profiles indistinguishable Inclusion of 1 individual [inclusion of 2 individuals – typically mixtures that include >2 indistinguishable individuals are considered complex; in the event that another individual(s) is included as a contributor to the mixture, the additional name(s) and item number(s) should be listed] 	NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> contributor to this profile. [NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) cannot be excluded as <i>possible</i> contributors to this profile.]
<ul style="list-style-type: none"> Contributor profiles indistinguishable Exclusion of 1 individual [exclusion of 2 individuals – in the event that another individual(s) is excluded as a contributor to the mixture, the additional name(s) and item number(s) should be listed] 	NAME (Item ITEM NUMBER) is excluded as a contributor to this profile. [NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as [the] contributors to this profile.]
<ul style="list-style-type: none"> Contributor profiles indistinguishable Insufficient information to include or exclude 	[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) as a possible contributor to this profile.

<p>[inconclusive comparisons for 2 individuals – in the event that another individual(s) comparison is also inconclusive with respect to being a potential contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	<p>[[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as a possible contributor(s) to this profile.]</p>
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PART 2C – MIXTURE DNA RESULTS (NON-COMPLEX) – MAJOR CONTRIBUTOR PROFILE(S) DISCERNABLE – RESULTS/CONCLUSION

When selecting one of these statements is applicable, the criteria listed in the left column must be met:

Criteria	Statement
<ul style="list-style-type: none"> • 1 major contributor discernable • Inclusion of 1 individual as the major contributor 	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> major contributor to this profile.</p>
<ul style="list-style-type: none"> • 1 major contributor discernable • Exclusion of 1 individual as the major contributor <p>[exclusion of 2 individuals – in the event that another individual(s) is excluded as the major contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	<p>NAME (Item ITEM NUMBER) is excluded as the major contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as the major contributor to this profile.]</p>
<ul style="list-style-type: none"> • 1 major contributor discernable • Insufficient information to include or exclude <p>[inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed]</p>	<p>[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) as the major contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as the major contributor to this profile.]</p>
<ul style="list-style-type: none"> • 2 major contributors discernable • Inclusion of 1 individual as a major contributor <p>[inclusion of 2 individuals as the major contributors]</p>	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> major contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) cannot be excluded as <i>possible</i> major contributors to this profile.]</p>

<ul style="list-style-type: none"> • 2 major contributors discernable • Exclusion of 1 individual as a major contributor <p>[exclusion of 2 individuals – in the event that another individual(s) is excluded as a major contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	<p>NAME (Item ITEM NUMBER) is excluded as a major contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as the major contributors to this profile.]</p>
<ul style="list-style-type: none"> • 2 major contributors discernable • Insufficient information to include or exclude • [inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed] 	<p>[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) as a major contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as a major contributor to this profile.]</p>

PART 2D – MIXTURE DNA RESULTS (NON-COMPLEX) – MINOR CONTRIBUTOR(S) DISCERNABLE – RESULTS/CONCLUSION

When selecting one of these statements is applicable, the criteria listed in the left column must be met :

Criteria	Statement
<ul style="list-style-type: none"> • 1 minor contributor discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Inclusion of 1 individual as the minor contributor 	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> minor contributor to this profile.</p>
<ul style="list-style-type: none"> • 1 minor contributor discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Exclusion of 1 individual as the 	<p>NAME (Item ITEM NUMBER) is excluded as the minor contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as the minor contributor to this profile.]</p>

<p>minor contributor</p> <p>[exclusion of 2 individuals – in the event that another individual(s) is excluded as the minor contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	
<ul style="list-style-type: none"> • 1 minor contributor discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Insufficient information to include or exclude <p>[inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed]</p>	<p>[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) as the minor contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as the minor contributor to this profile.]</p>
<ul style="list-style-type: none"> • 2 [or more] minor contributors discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Inclusion of 1 individual as a minor contributor <p>[inclusion of 2 individuals as the major contributors]</p>	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> major contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) cannot be excluded as <i>possible</i> minor contributors to this profile.]</p>
<ul style="list-style-type: none"> • 2 [or more] minor contributors discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met 	<p>NAME (Item ITEM NUMBER) is excluded as a minor contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as [the] minor contributors to this profile.]</p>

<ul style="list-style-type: none"> • Exclusion of 1 individual as a minor contributor [exclusion of 2 individuals – in the event that another individual(s) is excluded as a minor contributor to the mixture, the additional name(s) and item number(s) should be listed] 	
<ul style="list-style-type: none"> • 2 [or more] minor contributors discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Insufficient information to include or exclude • [inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed] 	<p>[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) as a minor contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as a minor contributor to this profile.]</p>
<ul style="list-style-type: none"> • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • The reference sample(s) submitted match the major contributor(s) 	<p>The minor contributor profile is suitable for comparison purposes.</p>
<ul style="list-style-type: none"> • Minor contributor profile at 5 or fewer loci (excluding Amelogenin); signals may be observed below the >1000 rfus AT parameters that are \geq to the <1000 rfus AT parameters • RMP calculation requirements met • Option A: Inclusion of 1 individual as a minor contributor 	<p>Option A: NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> minor contributor to this profile.</p> <p>Option B: NAME (Item ITEM NUMBER) is excluded as a minor contributor to this profile.</p> <p>Option C: [Due to the limited data obtained,] no conclusion can be made in relation to NAME (Item ITEM NUMBER) as the minor contributor to this profile</p>

<ul style="list-style-type: none"> • Option B: Exclusion of 1 individual as a minor contributor • Option C: Insufficient information to include or exclude 	
<ul style="list-style-type: none"> • Minor contributor profile at 5 or fewer loci (excluding Amelogenin); signals may be observed below the >1000 rfus AT parameters that are \geq to the <1000 rfus AT parameters; CPI calculation cannot be conducted at 6 or more loci and RMP calculation requirements not met 	<p>Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>

PART 3A – MIXTURE DNA RESULTS (NON-COMPLEX) – RESULTS/CONCLUSION – RANDOM MATCH STATISTICS

When applicable, choose the following:

Assuming [two] [three] contributors, the probability of selecting an unrelated individual at random having a STR profile which matches [the] [a] [partial] [major] [minor] [contributor to the mixture] profile obtained from DESCRIPTION (Item ITEM NUMBER) is approximately:

Approximate Frequency	Population Database
1 in ###	African-American
1 in ###	US Caucasian
1 in ###	US Hispanic

The following associated statement will be included in the “Examination Methods Notes” section whenever a random match statistic is included in a report:

Random match statistical calculations are performed according to the National Research Council’s recommendation 4.1 in “The Evaluation of Forensic DNA Evidence” (1996) and the allele frequencies used are provided in Appendix A of *FBS22 – STR Statistical Calculations Guidelines*. As stated in NRC II (1996) “It is probably safe to assume that within a race, the uncertainty of a value calculated from adequate databases (at least several hundred persons) by the product rule is within a factor of about 10 above and below the true value.”

PART 3B – MIXTURE DNA RESULTS (NON-COMPLEX) – RESULTS/CONCLUSION – CPI STATISTICS

When applicable, choose the following:

The probability of selecting an unrelated individual at random having a STR profile which would be included as [the] [a] [partial] [major] [minor] contributor to the mixture profile obtained from DESCRIPTION (Item ITEM NUMBER) is approximately:

Approximate Frequency	Population Database
1 in ###	African-American
1 in ###	US Caucasian
1 in ###	US Hispanic

The following associated statement will be included in the “Examination Methods Notes” section whenever a random match statistic is included in a report:

Combined probability of inclusion (CPI) statistical calculations are the product of the probability of inclusion (PI) values for individual loci. A PI is calculated as (sum of allele frequencies with population substructure corrections) squared for each locus. Unrestricted CPI calculations do not take quantitative peak height information or inference of contributor mixture ratios into consideration. The allele frequencies used in calculations are provided in Appendix A of *FBS22 – STR Statistical Calculations Guidelines*. As stated in NRC II (1996) “It is probably safe to assume that within a race, the uncertainty of a value calculated from adequate databases (at least several hundred persons) by the product rule is within a factor of about 10 above and below the true value.”

PART 4 – MIXTURE DNA RESULTS (NON-COMPLEX) – RESULTS/CONCLUSION – STATISTICS

Use the following statement immediately below the Part 3A or 3B results/conclusion statistical statement when appropriate:

The following STR [locus was] [loci were] used for comparisons but not used in the statistical calculation: [locus name] (NOTE: add names of additional loci, as needed). [The following STR [locus was] [loci were] not used in the comparison[s] or the statistical calculation: [locus name] (NOTE: add names of additional loci, as needed)].

7.4.2.8. The following guidelines will be used to assess how *low level partial mixture* and/or *complex mixture* profiles are to be reported, including when they are to be reported as being for exclusion purposes only:

7.4.2.8.1. A low level partial mixture profile is typically defined as a profile appearing to have full/complete results at five or fewer loci. Complete results at a locus necessitate all relevant alleles being above the stochastic threshold (even after taking allele sharing

into consideration) and there being no apparent dropout (i.e., alleles below the stochastic threshold). The presence of degradation, stochastic effects to due low template and/or potential inhibition is commonplace in low level partial mixture profiles.

7.4.2.8.2. A complex mixture profile is typically defined as a mixture of three or more individuals, particularly when the profiles of three or more persons are indistinguishable/no major contributor(s) can be distinguished, where all, or the vast majority, of rfu values are below 1000. The presence of degradation, stochastic effects to due low template and/or potential inhibition may also lead to a profile being deemed a complex mixture, particularly when their presence affects deconvolution.

7.4.2.8.3. Low level partial mixture profiles and complex mixture profiles not meeting the statistical cut-off requirement will be deemed inconclusive/not suitable for comparisons. However, it is noted that in some instances these profiles may be suitable for exclusionary purposes.

7.4.2.8.3.1. For low level partial/ complex mixture profile CPI calculations, only those loci with no apparent allelic dropout may be included.

PART 1 – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – RESULTS/CONCLUSION	
For the selected statement, the criteria listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> • <1000 rfus analysis parameters used • >2 alleles at >1 locus; results at ≥10 loci (excluding Amelogenin) • 1-4 alleles per locus (may have >4 alleles at 1 locus) • Option A: 6 or greater loci suitable for inclusion in the statistical calculation • Option B: <6 loci suitable for inclusion in a statistical calculation 	<p>Option A: A DNA profile consistent with a mixture of at least two [individuals] [individuals, at least one of which is a male,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this DNA mixture profile is suitable for exclusionary purposes only.</p>
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UNCONTROLLED WHEN PRINTED	

<ul style="list-style-type: none"> • [Amelogenin Y present] 	
<ul style="list-style-type: none"> • <1000 rfus analysis parameters used • >2 alleles at >1 locus; results at ≥10 loci (excluding Amelogenin) • >4 alleles at >2 or more loci • Option A: 6 or greater loci suitable for inclusion in the statistical calculation • Option B: <6 loci suitable for inclusion in a statistical calculation • Option C: when profile is deemed uninterpretable due to the complexity of the results/the number of indistinguishable contributors • [Amelogenin Y present] 	<p>Option A: A DNA profile consistent with a mixture of [three] [four] or more [individuals] [individuals, at least one of which is a male,] [individuals, at least two of which are males,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this DNA mixture profile is suitable for exclusionary purposes only.</p> <p>Option C: Due to the complexity of the data and the laboratory's current interpretation guidelines, the DNA profile obtained has been deemed unsuitable for interpretation.</p>
<ul style="list-style-type: none"> • <1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 6-9 loci (excluding Amelogenin) • 1-4 alleles per locus • Option A: 6 or greater loci suitable for inclusion in the statistical calculation • Option B: <6 loci suitable for inclusion in a statistical calculation • [Amelogenin Y present] 	<p>Option A: A partial DNA profile consistent with a mixture of two [individuals] [individuals, at least one of which is a male,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>
<ul style="list-style-type: none"> • <1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 6-9 loci (excluding Amelogenin) • 1-4 alleles per locus (may have >4 alleles at 1 locus) • Option A: 6 or greater loci suitable for inclusion in the statistical calculation 	<p>Option A: A partial DNA profile consistent with a mixture of at least two [individuals] [individuals, at least one of which is a male,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>

<ul style="list-style-type: none"> • Option B: <6 loci suitable for inclusion in a statistical calculation • [Amelogenin Y present] 	
<ul style="list-style-type: none"> • <1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 6-9 loci (excluding Amelogenin) • >4 alleles at >2 or more loci • Option A: 6 or greater loci suitable for inclusion in the statistical calculation • Option B: <6 loci suitable for inclusion in a statistical calculation • Option C: when profile is deemed uninterpretable due to the complexity of the results/the number of indistinguishable contributors • [Amelogenin Y present] 	<p>Option A: A partial DNA profile consistent with a mixture of three or more [individuals] [individuals, at least one of which is a male,] [individuals, at least two of which are males,] [males] was obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p> <p>Option C: Due to the complexity of the data obtained and the laboratory's current interpretation guidelines, the partial DNA profile obtained has been deemed unsuitable for interpretation.</p>
<ul style="list-style-type: none"> • <1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 5 or fewer loci (excluding Amelogenin) • 1-4 alleles per locus (may have >4 alleles at 1 locus) 	<p>Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>
<ul style="list-style-type: none"> • <1000 rfus analysis parameters used • >2 alleles at >1 locus; results at 5 or fewer loci (excluding Amelogenin) • >4 alleles at >2 or more loci 	<p>Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>

PART 2A – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – NO REFERENCE SAMPLE(S) SUBMITTED – RESULTS/CONCLUSION	
When selecting this statement is applicable, the criterion listed in the left column must be met	
Criteria	Statement
<ul style="list-style-type: none"> No reference sample(s) submitted 	This [mixture] profile is suitable for comparison purposes.
PART 2B – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – CONTRIBUTOR PROFILES INDISTINGUISHABLE – RESULTS/CONCLUSION	
When selecting one of these statements is applicable, the criteria listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> Contributor profiles indistinguishable Inclusion of 1 individual [inclusion of 2 individuals – typically mixtures that include >2 indistinguishable individuals are considered complex; in the event that another individual(s) is included as a contributor to the mixture, the additional name(s) and item number(s) should be listed] 	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) cannot be excluded as <i>possible</i> contributors to this profile.]</p>
<ul style="list-style-type: none"> Contributor profiles indistinguishable Exclusion of 1 individual [exclusion of 2 individuals – in the event that another individual(s) is excluded as a contributor to the mixture, the additional name(s) and item number(s) should be listed] 	<p>NAME (Item ITEM NUMBER) is excluded as a contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as [the] contributors to this profile.]</p>
<ul style="list-style-type: none"> Contributor profiles indistinguishable Insufficient information to include or exclude [inconclusive comparisons for 2 individuals – in the event that another individual(s) 	<p>[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) as a possible contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as a possible contributor(s) to this</p>

comparison is also inconclusive with respect to being a potential contributor to the mixture, the additional name(s) and item number(s) should be listed]	profile.]
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PART 2C – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – MAJOR CONTRIBUTOR PROFILE(S) DISCERNABLE – RESULTS/CONCLUSION

When selecting one of these statements is applicable, the criteria listed in the left column must be met:

Criteria	Statement
<ul style="list-style-type: none"> 1 major contributor discernable Inclusion of 1 individual as the major contributor 	NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> major contributor to this profile.
<ul style="list-style-type: none"> 1 major contributor discernable Exclusion of 1 individual as the major contributor <p>[exclusion of 2 individuals – in the event that another individual(s) is excluded as the major contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	<p>NAME (Item ITEM NUMBER) is excluded as the major contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as the major contributor to this profile.]</p>
<ul style="list-style-type: none"> 1 major contributor discernable Insufficient information to include or exclude <p>[inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed]</p>	<p>[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) as the major contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as the major contributor to this profile.]</p>
<ul style="list-style-type: none"> 2 major contributors discernable Inclusion of 1 individual as a major contributor <p>[inclusion of 2 individuals as the major contributors]</p>	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> major contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) cannot be excluded as <i>possible</i> major contributors to this profile.]</p>
<ul style="list-style-type: none"> 2 major contributors discernable Exclusion of 1 individual as a 	NAME (Item ITEM NUMBER) is excluded as a major contributor to this profile.

<p>major contributor</p> <p>[exclusion of 2 individuals – in the event that another individual(s) is excluded as a major contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	<p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as the major contributors to this profile.]</p>
<ul style="list-style-type: none"> • 2 major contributors discernable • Insufficient information to include or exclude • [inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed] 	<p>[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) as a major contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as a major contributor to this profile.]</p>
<p>PART 2D – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – MINOR CONTRIBUTOR(S) DISCERNABLE – RESULTS/CONCLUSION</p> <p>When selecting one of these statements is applicable, the criteria listed in the left column must be met:</p>	
Criteria	Statement
<ul style="list-style-type: none"> • 1 minor contributor discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Inclusion of 1 individual as the minor contributor 	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> minor contributor to this profile.</p>
<ul style="list-style-type: none"> • 1 minor contributor discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Exclusion of 1 individual as the minor contributor <p>[exclusion of 2 individuals – in the event that another</p>	<p>NAME (Item ITEM NUMBER) is excluded as the minor contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as the minor contributor to this profile.]</p>

<p>individual(s) is excluded as the minor contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	
<ul style="list-style-type: none"> • 1 minor contributor discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Insufficient information to include or exclude <p>[inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed]</p>	<p>[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) as the minor contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as the minor contributor to this profile.]</p>
<ul style="list-style-type: none"> • 2 [or more] minor contributors discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Inclusion of 1 individual as a minor contributor <p>[inclusion of 2 individuals as the major contributors]</p>	<p>NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> major contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) cannot be excluded as <i>possible</i> minor contributors to this profile.]</p>
<ul style="list-style-type: none"> • 2 [or more] minor contributors discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Exclusion of 1 individual as a minor contributor <p>[exclusion of 2 individuals – in</p>	<p>NAME (Item ITEM NUMBER) is excluded as a minor contributor to this profile.</p> <p>[NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) are excluded as [the] minor contributors to this profile.]</p>

<p>the event that another individual(s) is excluded as a minor contributor to the mixture, the additional name(s) and item number(s) should be listed]</p>	
<ul style="list-style-type: none"> • 2 [or more] minor contributors discernable • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • Insufficient information to include or exclude • [inconclusive comparisons for 2 individuals – in the event that another comparison is also inconclusive, the additional name(s) and item number(s) should be listed] 	<p>[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) as a minor contributor to this profile.</p> <p>[[Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) and NAME (Item ITEM NUMBER) as a minor contributor to this profile.]</p>
<ul style="list-style-type: none"> • Minor contributor alleles at 6 or more loci (excluding Amelogenin); CPI calculation can be conducted at 6 or more loci or RMP calculation requirements met • The reference sample(s) submitted match the major contributor(s) 	<p>The minor contributor profile is suitable for comparison purposes.</p>
<ul style="list-style-type: none"> • Minor contributor profile at 5 or fewer loci (excluding Amelogenin) • RMP calculation requirements met • Option A: Inclusion of 1 individual as a minor contributor • Option B: Exclusion of 1 individual as a minor contributor • Option C: Insufficient information to include or exclude 	<p>Option A: NAME (Item ITEM NUMBER) cannot be excluded as a <i>possible</i> minor contributor to this profile.</p> <p>Option B: NAME (Item ITEM NUMBER) is excluded as a minor contributor to this profile.</p> <p>Option C: [Due to the limited data obtained,] no conclusion can be made relative to NAME (Item ITEM NUMBER) as the minor contributor to this profile</p>

<ul style="list-style-type: none"> Minor contributor profile at 5 or fewer loci (excluding Amelogenin); signals may be observed below the >1000 rfus AT parameters that are \geq to the <1000 rfus AT parameters; calculations cannot be conducted at 6 or more loci 	<p>Because no statistic can be applied, this partial DNA mixture profile is suitable for exclusionary purposes only.</p>
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PART 3A – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – RESULTS/CONCLUSION – RANDOM MATCH STATISTICS

When applicable, choose the following:

Assuming [two] [three] contributors, the probability of selecting an unrelated individual at random having a STR profile which matches [the] [a] [partial] [major] [minor] [contributor to the mixture] profile obtained from DESCRIPTION (Item ITEM NUMBER) is approximately:

Approximate Frequency	Population Database
1 in ###	African-American
1 in ###	US Caucasian
1 in ###	US Hispanic

The following associated statement will be included in the “Examination Methods Notes” section whenever a random match statistic is included in a report:

Random match statistical calculations are performed according to the National Research Council’s recommendation 4.1 in “The Evaluation of Forensic DNA Evidence” (1996) and the allele frequencies used are provided in Appendix A of *FBS22 – STR Statistical Calculations Guidelines*. As stated in NRC II (1996) “It is probably safe to assume that within a race, the uncertainty of a value calculated from adequate databases (at least several hundred persons) by the product rule is within a factor of about 10 above and below the true value.”

PART 3B – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – RESULTS/CONCLUSION – CPI STATISTICS

When applicable, choose the following:

The probability of selecting an unrelated individual at random having a STR profile which would be included as [the] [a] [partial] [major] [minor] contributor to the mixture profile obtained from DESCRIPTION (Item ITEM NUMBER) is approximately:

Approximate Frequency	Population Database
1 in ###	African-American
1 in ###	US Caucasian
1 in ###	US Hispanic

The following associated statement will be included in the “Examination Methods Notes” section whenever a random match statistic is included in a report:

Combined probability of inclusion (CPI) statistical calculations are the product of the probability of inclusion (PI) values for individual loci. A PI is calculated as (sum of allele frequencies with population substructure corrections)² for each locus. Unrestricted CPI calculations do not take quantitative peak height information or inference of contributor mixture ratios into consideration. The allele frequencies used in calculations are provided in Appendix A of *FBS22 – STR Statistical Calculations Guidelines*. As stated in NRC II (1996) “It is probably safe to assume that within a race, the uncertainty of a value calculated from adequate databases (at least several hundred persons) by the product rule is within a factor of about 10 above and below the true value.

PART 4 – LOW LEVEL PARTIAL MIXTURE AND COMPLEX MIXTURE PROFILES – RESULTS/CONCLUSION – STATISTICS

Use the following statement immediately below the Part 3A or 3B results/conclusion statistical statement when appropriate:

The following STR [locus was] [loci were] used for comparisons but not used in the statistical calculation: [locus name] (NOTE: add names of additional loci, as needed). [The following STR [locus was] [loci were] not used in the comparison[s] or the statistical calculation: [locus name] (NOTE: add names of additional loci, as needed)].

7.4.2.9. The following guidelines will be used to report comparisons between two evidence profiles (see above for appropriate results statement(s)):

SAMPLE TO SAMPLE COMPARISON CONCLUSIONS	
For the selected statement, the criteria listed in the left column must be met:	
Criteria	Statement
<ul style="list-style-type: none"> • Comparison of two unattributed evidence profiles • Differences in profiles noted 	The DNA from DESCRIPTION (Item ITEM NUMBER) did not originate from the same individual as the DNA obtained from DESCRIPTION (Item ITEM NUMBER).
<ul style="list-style-type: none"> • Comparison of two unattributed evidence profiles • No differences in profiles noted 	<p>Option A: The DNA obtained from DESCRIPTION (Item ITEM NUMBER) is consistent with having originated from the same individual as the DNA obtained from DESCRIPTION (Item ITEM NUMBER).</p> <p>Option B: The DNA obtained from DESCRIPTION (Item ITEM NUMBER) is consistent with having originated from the same individual as the DNA obtained from DESCRIPTION (Item ITEM NUMBER).</p>
<ul style="list-style-type: none"> • Comparison of two unattributed evidence profiles • When the comparison is 	Due to the limited data obtained, no determination can be made regarding whether or not the DNA from DESCRIPTION (Item ITEM NUMBER) may have originated from the same individual as the DNA obtained

inconclusive	from DESCRIPTION (Item ITEM NUMBER).
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8. Sampling

8.1. Not applicable

9. Calculations

9.1. Not applicable

10. Uncertainty of Measurement

10.1. When quantitative results are obtained, and the significance of the value may impact the report, the uncertainty of measurement must be determined. The method used to determine the estimation of uncertainty can be found in the *FSL Quality Assurance Manual – Estimation of Uncertainty of Measurement*.

11. Limitations

11.1. It is not possible to anticipate the nature of all potential DNA typing results, or the nature of the evidentiary samples from which they may be obtained. These guidelines do not exhaust the possible list of the results that may be encountered by the analyst nor the conclusions that the analyst may render based on his/her interpretation of those results. For results not specifically described, conclusion statements should be drafted using statements above that are similar in concept and/or origin. As needed, analysts will consult the FBU Technical Leader.

11.2. Not every situation can, or should, be covered by a pre-set reporting statement. It is important that the analyst follows interpretation criteria for a test when reporting examination results and conclusions.

11.3. Any report statements listed herein are intended as a guide only. Report statements may vary depending on the specifics of a case and are expected to evolve over time.

12. Documentation

12.1. FBU Report of Examination

13. References

- 13.1. *ISO/IEC 17025 – General Requirements for the Competence of Testing and Calibration Laboratories*, International Organization for Standardization, Geneva, Switzerland (current revision).
- 13.2. *Forensic Quality Services Supplemental Requirements for Forensic Testing*, FQS ANSI-ASQ Accreditation Board, Tampa, FL (current revision).
- 13.3. *ASCLD/LAB-International® Supplemental Requirements for the Accreditation of Forensic Science Testing and Calibration Laboratories*, American Society of Crime Laboratory Directors/Laboratory Accreditation Board, Garner, NC (current revision).
- 13.4. *Quality Assurance Standards for Forensic DNA Testing Laboratories*, Federal Bureau of Investigation (current revision).
- 13.5. National Research Council. *The Evaluation of Forensic DNA Evidence*, Washington, D.C.: National Academy Press, 1996.
- 13.6. *SWGDM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories* (2010 revision).
- 13.7. *Forensic Science Laboratory Quality Assurance Manual [DCN 1300]* (current revision)
- 13.8. *LOM02 – Practices for Case Documentation and Report Writing [DCN 1319]* (current revision)
- 13.9. *FBS22 – STR Statistical Calculations* (current revision)
- 13.10. *FBS21 – Identifiler Plus Interpretation Guidelines* (current revision)