Department of Forensic Science

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FORENSIC BIOLOGY PROCEDURES MANUAL

VIRGINIA DEPARTMENT OF FORENSIC SCIENCE

REPORT WRITING

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TABLE OF CONTENTS

1 General Formatting and Requirements

- **1.1 General Format**
- **1.2 METHODS Section**
- **1.3 Formatting a CONCLUSIONS Section if Used in the Report**
- **1.4 Termination/Discontinuation of Examinations**
- **1.5 Techniques and Methods of Sampling**
- **1.6 Results at Individual Loci**
- **1.7 Decision to Use ''profile' or 'type(s)'**
- **1.8 The Use of the Term 'different'**
- **1.9 The Use of 'as a contributor to' or 'as a contributor of'**
- **1.10 Assumptions Made During the Interpretation of Mixture Profiles**
- **1.11 Attribution Statements**
- **1.12 Sperm and Non-Sperm Fractions**
- **1.13 Mixture Samples for Which No Traditional Statistics Can/Will Be Calculated That Will Not Be Referred to TrueAllele®**
- **1.14 Cases for Which a Triaging Approach is Used to Discontinue DNA Analysis**
- **1.15 Certificates Addressing Samples Suitable for Y-STR Testing**
- **1.16 Multiple Samples Tested Within a Case**
- **1.17 Requests for Known Reference Samples**

2 Traditional Screening Results

- **2.1 General Reporting of Screening Results**
- **2.2 General Reporting for PERK Samples**
- **2.3 Preservation Only Items**
- **2.4 Blood Screening Results**
- **2.5 Semen/Seminal Fluid Screening Results**
- **2.6 Hair Screening Results**

3 DNA Results

- **3.1 Known Reference Samples and Alternate Knowns**
- **3.2 PowerPlex® 16 Samples That Were Discontinued Due to Low DNA Yields**
- **3.3 PowerPlex® Fusion Samples That Were Discontinued Due to Low DNA Yields**
- **3.4 Samples Taken Through Quantitation and Discontinued Based Upon Male Quant or Auto/Y Quant Ratio**
- **3.5 No DNA Typing Results (No Peaks Above LOD for the Sample)**
- **3.6 DNA Results of No Value**
- **3.7 DNA Results of No Value Due to Quality Control**
- **3.8 No DNA Typing Results Different from an Assumed Known**
- **3.9 DNA Typing Results – Single Source**
- **3.10 DNA Typing Results – Single Source Different from an Assumed Known**
- **3.11 DNA Typing Results – Mixtures**
- **3.12 DNA Typing Results – Mixture Different from Assumed Known**
- **3.13 Comparisons of Known Reference Profiles**

4 CODIS Searching/Entry and Related Report Writing

- **4.1 Samples With a Match to a Staff Member**
- **4.2 Profiles Removed from CODIS**
- **4.3 Samples Not Searched or Entered**
- **4.4 Potential Match Candidates to Profiles for Which a Statistic Cannot be Calculated (Typically Subsequent Hits), or When Compared, Do Not Meet the Minimum Requirements for a Conclusion of Not Eliminated to Be Reached**

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4.5 Matches Made
4.6 No Matches Made
4.7 Matches Made to Both Convicted Offender/Arrestee Samples AND Forensic Samples
4.8 Multiple Matches Made to Forensic Samples
4.9 Subsequent Hits

5 Statistical Statements

5.1 General Requirements
5.2 Random Match Probability (RMP)
5.3 Traditional Likelihood Ratio (LR)
5.4 Combined Probability of Inclusion (CPI) / Unrestricted Random Match (URM)
5.5 Likelihood Ratio Provided by TrueAllele®
5.6 Y Haplotype Frequency Estimates
5.7 Paternity/Maternity Index and Relationship Statistics

6 Table of Typing Results

7 Y-STR Testing Results

7.1 Known Reference Samples and Alternate Known Samples
7.2 No Y-STR Typing Results (No Peaks Above LOD for the Sample)
7.3 Y-STR DNA Results of No Value
7.4 Y-STR DNA Results of No Value Due to Quality Control
7.5 No Y-STR DNA Typing Results Different from an Assumed Known
7.6 Y-STR DNA Typing Results – Single Source
7.7 Y-STR DNA Typing Results – Single Source Different from an Assumed Known
7.8 Y-STR DNA Typing Results – Mixtures
7.9 Comparisons of Known Reference Profiles
7.10 Paternity, Missing Person, and Body Identification Cases
7.11 Y Haplotype Frequency Estimates

8 Paternity, Missing Person, and Body Identification Cases

8.1 Paternity Cases
8.2 Missing Person Cases
8.3 Body Identification Cases
8.4 Paternity Index and Probability of Paternity (Full Trio)
8.5 Sibling Statistics
8.6 Missing Person Statistics
8.7 Incorporation of a Mutation Calculation into a Kinship Statistical Analysis
8.8 Incorporation of a Y-STR Haplotype Statistic into an Autosomal Kinship Statistical Analysis

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1 GENERAL FORMATTING AND REQUIREMENTS

The Report wording offered in this manual is meant as a guide that can be applied to all cases. Because not all possible case scenarios can be anticipated or addressed individually, the author of a Report will use his/her judgement in applying the principles behind the wording offered here. The intent is that each author will attempt to conform as much as possible to the wording offered here. Grammatical changes and changes to fit a specific scenario more closely are acceptable and expected; however, unnecessary changes to the wording flow as a whole are not acceptable. Consultation with a Supervisor, Section Supervisor, the Program Manager (Technical Leader), and/or the Assistant Technical Leader is advised, if necessary.

For the purposes of this manual:

- Report = Certificate of Analysis
- Probative Evidence = Evidence through testing that demonstrates the proposition that a biological fluid may or may not have been deposited by a specific "individual of interest" who is believed to be associated with the evidence in question.

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In accordance with the FBI's "Quality Assurance Standards for Forensic DNA Testing Laboratories", all Forensic Biology Certificates of Analysis in which DNA analysis was conducted will contain at a minimum the following information:

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- Case identifier
- Description of evidence examined
- A description of the methodology
- Polymorphic loci examined or amplification system
- A quantitative or qualitative interpretative statement
- Statistical frequencies of inclusion
- Date issued
- Disposition of evidence
- A signature and title, or equivalent identification of the person accepting responsibility for the content of the report

Examples given in this General Formatting and Requirements section (as well as some of the sections below) may incorporate wording from each of the sections below. See a specific chapter/section for further guidance for particular wording needed/situations. The combination of wording from multiple sections/examples to fit a particular situation may be necessary.

Examples include the use of particular items of evidence. If the example uses 'stained swabs' but the item of evidence to be reported is a cigarette butt, substitute as necessary.

1.1 General Format

1.1.1 The Certificate of Analysis will contain a METHODS section (as appropriate) and RESULTS section, and may contain a CONCLUSIONS section.

1.1.1.1 All Certificates of Analysis that contain a METHODS section will include the following statement prior to the disposition statement:

Supporting examination documentation is maintained in the case file. The above listed methods are those approved for use at the time of analysis. Current methods can be found in the Forensic Biology Procedures Manuals, which can be found at www.dfs.virginia.gov/documentationpublications/manuals/.

1.1.2 The METHODS section will be placed prior to the RESULTS section in the Certificate of Analysis and will include the description of methodology, the PCR kit used (if applicable), and polymorphic loci tested (if applicable).

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1.1.3 METHODS will be included for each type of testing conducted, as applicable.

1.1.4 No METHODS section will be included in Supplemental Reports when no additional analyses have been performed (i.e., a subsequent hit report).

1.1.4.1 All Certificates of Analysis that do not contain a METHODS section will include the following statement prior to the disposition statement:

Supporting examination documentation is maintained in the case file.

1.1.5 The RESULTS section will contain the results of all analyses including screening results, DNA results, comparisons/conclusions (if applicable), Data Bank searches/entry (if applicable), and statistics (if applicable). The results section may list results in a bulleted format or a narrative format.

1.1.5.1 All items submitted for Forensic Biology examinations will be addressed in the Report. Items not examined will be addressed in the Report as not having been examined.

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1.1.5.1.1 If Forensic Biology examinations are terminated on an item examined by another Section, the FB termination may be addressed in the other Section's Report rather than in the FB Report.

1.1.5.2 For each item in a Report, the wording for the applicable testing and results below will be chosen and combined such that all associated results for a given item are reported as a whole.

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1.1.6 The CONCLUSIONS section, if included, will follow the RESULTS section. This section is reserved for reports containing multiple items tested and hence more results to be reported. It may be incorporated into the report to assist in streamlining results, thus creating a more reader friendly report. When incorporated, it will contain results of comparisons, Data Bank searches, conclusions and statistics, if applicable. Refer to the below examples for when a CONCLUSIONS section might be incorporated into the report.

EXAMPLE: A reconstruction case involving 2 victims and 2 suspects and 21 items were submitted for analysis. DNA profiles were developed from 17 of the 21 items; the results of comparison to the known samples may be summarized in a CONCLUSIONS section in the Certificate of Analysis. The RESULTS section would address whether DNA profiles were developed or not.

EXAMPLE: A homicide case involving 1 victim, 5 suspects, and multiple submissions with numerous items for examination were submitted for analysis. Grouping of evidence results for reporting purposes is minimal due to the varying results obtained (full profiles, no profiles different from an assumed known, mixtures suitable for searching, limited profiles different from an assumed known, etc.). A CONCLUSIONS section may be used to report the results of the comparisons and Data Bank searches. The RESULTS section of this report would address whether DNA profiles were developed or not.

1.2 METHODS Section

If both autosomal and Y-STR testing are Reported in one Report, "Y-CHROMOSOME" and "[AUTOSOMAL KIT USED]" may be added in the titles of the METHODS statements to clarify the Report for the reader.

1.2.1 METHODS for Body Fluid Testing (choose and use as appropriate based upon body fluid tested):

BODY FLUID DETECTION METHODS

- The indication of blood or seminal fluid is based on physical characteristics innate, but not unique, to the body fluid tested. Therefore, the testing for these body fluids is not confirmatory.
  - The indication of blood is conducted through visual and/or chemical examinations.

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  - The indication of seminal fluid is conducted through visual, chemical and/or immunological testing.
- The identification of spermatozoa is conducted through microscopic examinations and is confirmatory.

NOTE: The statement regarding identification of spermatozoa need only be included if a microscopic examination for spermatozoa is conducted.

1.2.2 METHODS for PowerPlex® Fusion Testing in Cases for Which No Differential Extraction Procedure Was Conducted

DNA ANALYSIS METHODS:

- The method of deoxyribonucleic acid (DNA) analysis used is the Polymerase Chain Reaction (PCR).
- The real-time PCR amplification kit used for DNA quantitation was the Plexor® HY System.
  - The Plexor® HY System quantitates both total human DNA and male DNA.
- The PCR amplification kit used for DNA typing was the PowerPlex® Fusion System.
  - The PowerPlex® Fusion System allows co-amplification and four-color detection of 24 loci (D3S1358, D1S1656, D2S441, D10S1248, D13S317, D16S539, D18S51, D2S1338, CSF1PO, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, D22S1045, and FGA plus Penta E, Penta D, DYS391 and Amelogenin).
  - Amelogenin and DYS391 aid in the determination of gender.

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1.2.3 METHODS for PowerPlex® Fusion Testing in Cases for Which a Differential Extraction Procedure Was Conducted

NOTE: As applicable to a particular case, the first bullet and sub-bullet seen below may be amended or omitted or the METHODS in 1.2.2 may be used.

DNA ANALYSIS METHODS:

- The terms sperm fraction and non-sperm fraction are used to denote two samples for analysis produced from one parent sample during the DNA extraction process.
  - DNA analysis of a sperm fraction does not necessarily imply the presence of spermatozoa.
- The method of deoxyribonucleic acid (DNA) analysis used is the Polymerase Chain Reaction (PCR).
- The real-time PCR amplification kit used for DNA quantitation was the Plexor® HY System.
  - The Plexor® HY System quantitates both total human DNA and male DNA.
- The PCR amplification kit used for DNA typing was the PowerPlex® Fusion System.
  - The PowerPlex® Fusion System allows co-amplification and four-color detection of 24 loci (D3S1358, D1S1656, D2S441, D10S1248, D13S317, D16S539, D18S51, D2S1338, CSF1PO, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, D22S1045, and FGA plus Penta E, Penta D, DYS391 and Amelogenin).
  - Amelogenin and DYS391 aid in the determination of gender.

1.2.4 METHODS for PowerPlex® 16 Testing

DNA ANALYSIS METHODS:

- The method of deoxyribonucleic acid (DNA) analysis used is the Polymerase Chain Reaction (PCR).
- The real-time PCR amplification kit used for DNA quantitation was the Plexor® HY System.
  - The Plexor® HY System quantitates both total human DNA and male DNA.
- The PCR amplification kit used for DNA typing was the PowerPlex® 16 system.
  - The PowerPlex® 16 system contains 16 genetic loci (D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA and Amelogenin, a gender determining locus which is not used for statistical purposes).

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NOTE: Amend as necessary to include the METHODS employed for cases for which a differential extraction procedure was conducted as shown for PowerPlex® Fusion testing.

1.2.5 METHODS for Yfiler™ Testing

(Y-CHROMOSOME) DNA ANALYSIS METHODS

- The method of deoxyribonucleic acid (DNA) analysis used is the Polymerase Chain Reaction (PCR).
- The PCR amplification kit used for Y-chromosome DNA typing was the AmpFℓSTR™ Yfiler™ system.
- The AmpFℓSTR™ Yfiler™ system contains 17 genetic loci (DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y_GATA_H4, DYS437, DYS438, and DYS448).
- Because the AmpFℓSTR™ Yfiler™ system targets only the Y-chromosome, all DNA profiles developed with this amplification kit originate from males.

1.2.6 METHODS for Statistical Calculations for PowerPlex® Fusion Data

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STATISTICAL ANALYSIS METHODS:

- The DNA statistics calculated herein used the 2017 revised population allele frequencies provided by the National Institute of Standards and Technology (NIST).
- The statistical calculation(s) have been performed in accordance with the Scientific Working Group on DNA Analysis Methods (SWGDAM) 2017 Interpretation Guidelines and Departmental procedures.
- The D12S391, DYS391 and Amelogenin loci are not used for statistical purposes.

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1.2.7 METHODS for Statistical Calculations for PowerPlex® 16 Data

STATISTICAL ANALYSIS METHODS:

- The DNA statistics calculated herein used the population allele frequencies generated by the Virginia Department of Forensic Science.
- The statistical calculation(s) have been performed in accordance with the Scientific Working Group on DNA Analysis Methods (SWGDAM) 2017 Interpretation Guidelines and Departmental procedures.

1.2.8 METHODS for Statistical Calculations for Yfiler™ Data

(Y-CHROMOSOME) STATISTICAL ANALYSIS METHODS

- The DNA statistics calculated herein used the Y-Chromosome STR Haplotype Reference Database (YHRD), which generated a statistic based upon the counting method and applied a 95% upper confidence interval.
- The statistical calculation(s) have been performed in accordance with the Scientific Working Group on DNA Analysis Methods (SWGDAM) 2014 Y-STR Interpretation Guidelines and Departmental procedures.

1.2.9 METHODS for Kinship Statistical Calculations

STATISTICAL ANALYSIS METHODS:

- The DNA statistics calculated herein used the 2017 revised population allele frequencies provided by the National Institute of Standards and Technology (NIST).
- The D12S391, DYS391 and Amelogenin loci are not used for statistical purposes.

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1.2.10 METHODS for Cases Which Were Terminated After Extraction Due to Low DNA Yields or because no male DNA was detected (N/A male quant value for certain types of samples):

DNA ANALYSIS METHODS:

- The method of deoxyribonucleic acid (DNA) analysis used is the Polymerase Chain Reaction (PCR).
- The real-time PCR amplification kit used for DNA quantitation was the Plexor® HY System.
  - The Plexor® HY System quantitates both total human DNA and male DNA.
- The PCR amplification kit, PowerPlex® Fusion, allows co-amplification and four-color detection of 24 loci (D3S1358, D1S1656, D2S441, D10S1248, D13S317, D16S539, D18S51, D2S1338, CSF1PO, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, D22S1045, and FGA plus Penta E, Penta D, DYS391 and Amelogenin).
  - Amelogenin and DYS391 aid in the determination of gender.

OR

DNA ANALYSIS METHODS:

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- The method of deoxyribonucleic acid (DNA) analysis used is the Polymerase Chain Reaction (PCR).
- The real-time PCR amplification kit used for DNA quantitation was the Plexor® HY System.
  - The Plexor® HY System quantitates both total human DNA and male DNA.
- The PCR amplification kit, PowerPlex® 16, contains 16 genetic loci (D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA and Amelogenin, a gender determining locus which is not used for statistical purposes).

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1.2.11 METHODS for Cases for Which Evidence Was Analyzed with PowerPlex® 16 and Newly Submitted Known References Were Analyzed with PowerPlex® Fusion:

DNA ANALYSIS METHODS:

- The method of deoxyribonucleic acid (DNA) analysis used is the Polymerase Chain Reaction (PCR).
- The real-time PCR amplification kit used for DNA quantitation was the Plexor® HY System.
  - The Plexor® HY System quantitates both total human DNA and male DNA.
- The PCR amplification kit used for DNA typing was the PowerPlex® Fusion System.
  - The PowerPlex® Fusion System allows co-amplification and four-color detection of 24 loci (D3S1358, D1S1656, D2S441, D10S1248, D13S317, D16S539, D18S51, D2S1338, CSF1PO, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, D22S1045, and FGA plus Penta E, Penta D, DYS391 and Amelogenin).
  - Amelogenin and DYS391 aid in the determination of gender.

STATISTICAL ANALYSIS METHODS:

- The DNA statistics calculated herein used the population allele frequencies generated by the Virginia Department of Forensic Science and were performed on data obtained using the PowerPlex® 16 System.
  - The PowerPlex® 16 system contains 16 genetic loci (D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA and Amelogenin, a gender determining locus which is not used for statistical purposes).
- The statistical calculation(s) have been performed in accordance with the Scientific Working Group on DNA Analysis Methods (SWGDAM) 2017 Interpretation Guidelines and Departmental procedures.

1.3 Formatting a CONCLUSIONS Section if Used in the Report

Depending on the number of samples tested and the complexity of the results, samples with similar conclusions can be listed in bullet/list format. Alternatively, the conclusions may be reported in a chart format which includes

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the item number, item description and names of individuals tested in the header row, and the results (i.e., eliminated, not eliminated) within the appropriate chart cells. Refer to the examples below.

1.3.1 Bullet/List Format

VICTIM cannot be eliminated, and SUSPECT is eliminated, as a contributor of the DNA profile developed from the following samples:

- Stained swabs (Items 1, 2 and 4)
- Stains A and C on T-shirt (Item 3)
- Stains A, B and C on pants (Item 5)
- Knife blade (Item 7)

SUSPECT cannot be eliminated, and VICTIM is eliminated, as a contributor of the DNA profile developed from the following samples:

- Stained swabs (Item 6)
- Stain B on T-shirt (Item 3)
- Knife handle (Item 7)

SUSPECT cannot be eliminated, and insufficient information exists to draw a conclusion regarding VICTIM as a contributor of the DNA profile developed from the following samples:

- Stained swabs (Item 6)
- Knife handle (Item 7)

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1.3.2 Chart Format

ITEM	ITEM DESCRIPTION	VICTIM	SUSPECT
1	Stained swabs	Not Eliminated	Eliminated
2	Stained swabs	Not Eliminated	Eliminated
3	T-shirt – Stains A and C	Not Eliminated	Eliminated
3	T-shirt – Stain B	Eliminated	Not Eliminated
4	Stained swabs	Not Eliminated	Eliminated
5	Pants – Stains A, B and C	Not Eliminated	Eliminated
6	Stained swabs	Inconclusive	Not Eliminated
7	Knife – Blade	Not Eliminated	Eliminated
7	Knife – Handle	Inconclusive	Not Eliminated

NOTE: If a CONCLUSIONS section is used for a Y-STR Report, a disclaimer statement will be added stating that for any Y-chromosome profile developed from an item of evidence from which a person cannot be eliminated, any/all of that person's patrilineally related male relatives are also not eliminated.

1.4 Termination/Discontinuation of Examinations

1.4.1 If a case is terminated, refer to the Department Quality Manual.

1.4.1.1 If a case is terminated and a Certificate of Analysis will be issued, use the wording below:

The Forensic Biology Examinations were terminated at the request of/per conversation with/per e-mail communication from/after consultation with INVESTIGATOR/CA of the AGENCY on DATE.

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1.4.2 If DNA analysis has begun in the case, and a request for termination is received, the reportable results obtained to this point will be reported along with the termination.

Blood was indicated on the swabs. The DNA analysis on the swabs was discontinued at the request of INVESTIGATOR/ COMMONWEALTH'S ATTORNEY of the AGENCY on DATE.

1.5 Techniques and Methods of Sampling

1.5.1 The technique used to collect a sample for DNA is considered part of the examination process and will not be reported in the Certificate of Analysis. For, example, if a bottle is submitted and a swab is used by the examiner to collect DNA from the mouth area of the bottle, the Report will refer to a DNA profile developed from the mouth area of the bottle, rather than a swab of the mouth area of the bottle.

1.5.2 The method of sampling will be reported:

1.5.2.1 If it is clearly inferred from the report wording that a sample was combined, there is no need to use the word combined in the Report.

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1.5.2.2 If samples are collected separately and combined or stains in different locations on items for which it would not be clearly inferred what method of sampling was used are combined, the Report will include the word combined.

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EXAMPLES: A DNA profile was developed from a selected stain.

A DNA profile was developed from the grip and trigger.

A DNA profile was developed from a combined sample of stains on the left sleeve and bottom back right of the shirt.

A DNA profile was developed from a representative sampling of stains.

DNA profiles were developed from a representative sampling of the stains.

1.6 Results at Individual Loci

1.6.1 Inconclusive results or a lack of results at individual loci will not be addressed in the Report but will be "INC" or "---"in the table when a table of typing results is included.

1.7 Decision to Use 'profile' or 'type(s)'

1.7.1 The term 'profile' will routinely be used to describe typing results for which conclusions can be drawn and/or entered into the Data Bank. However, it may also be used to describe typing results which have limited value, no value, and/or are not suitable for a Data Bank search.

1.7.2 The term 'type' or 'types' is described as components of a profile. These terms may be used instead of 'profile' when referring to typing results of limited value, no value and/or not suitable for a Data Bank search.

1.7.3 Examiner discretion will be used in deciding whether to use 'profile' or 'type/types' in the Report.

1.8 The Use of the Term 'different'

1.8.1 The term 'different' will routinely be used when evaluating a profile developed from an intimate/ownership sample or item of evidence for a DNA profile which is different than an assumed known's profile.

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1.9 The Use of 'as a contributor to' or 'as a contributor of'

1.9.1 When comparing a known reference to a single source profile or to only the deconvoluted single source portion of a mixture profile (major, minor or profile different from an assumed known), 'as a contributor of' will be used.

EXAMPLES: PERSON cannot be eliminated as a contributor of the DNA profile different from ASSUMED KNOWN.

PERSON cannot be eliminated as a contributor of this DNA profile.

PERSON cannot be eliminated as a contributor of this major DNA profile.

1.9.2 When comparing a known reference to a mixture profile, 'as a contributor to' will be used.

EXAMPLES: PERSON cannot be eliminated as a contributor to the DNA mixture profile developed from the swabs.

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PERSON 1 and PERSON 2 cannot be eliminated as contributors to this DNA mixture profile.

PERSON cannot be eliminated as a major contributor to this DNA mixture profile.

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1.10 Assumptions Made During the Interpretation of Mixture Profiles

1.10.1 The assumption of a contributor to a mixture developed from a non-intimate item of evidence will be stated as part of the conclusion statement or as part of the statistical statement.

EXAMPLE: Assuming this profile is a mixture of OWNER and (an) additional contributor(s)…

1.10.1.1 Assumptions need only be stated once for a mixture; they do not need to appear in both the conclusion statement and the statistical statement.

1.10.2 The assumption of the number of contributors to a mixture on which a URM will be calculated will be stated as part of the statistical statement.

EXAMPLES: Assuming the profile developed from the selected stain is a mixture of 3 contributors, the probability of randomly selecting an unrelated individual who would be included as a contributor [to this DNA mixture profile] at the PowerPlex® Fusion loci is…

Assuming this profile is a mixture of 2 contributors, the probability of randomly selecting an unrelated individual who would be included as a contributor [to this DNA mixture profile] at the PowerPlex® Fusion loci is…

1.10.3 The assumption of a contributor to a mixture developed from a non-intimate item of evidence which is then relied upon for searching/entry into CODIS will be stated as part of the CODIS searching/entry wording.

EXAMPLE: A DNA mixture profile was developed from the steering wheel swab. Assuming this profile is a mixture of OWNER and an additional contributor, the profile different from OWNER was searched against the Virginia DNA Data Bank…

1.10.4 Assumptions regarding the number of contributors made during the interpretation of a mixture profile which are not relied upon for searching/entry into CODIS do not need to be stated as part of the CODIS searching/entry wording, but will be addressed in a future Report, as applicable.

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EXAMPLE: An entire 2 person mixture on which a URM will be calculated, if necessary, is searched. The assumption of 2 contributors will not be stated until the Report including the URM calculation is written.

1.11 Attribution Statements

1.11.1 Attribution (qualitative) statements may be reported in lieu of calculating a statistic for inclusions of an assumed known in a profile.

1.11.1.1 An attribution statement MUST be included if the assumed known is considered to be donating types and an inclusion of that assumed known, along with a statistical statement supporting the inclusion, is not reported.

1.11.1.2 In some instances, it may be appropriate to attribute a profile to the donor of another evidence sample or to the other fraction of a sample differentially extracted. If so, this will be done in the same manner in which the attribution statements are reported for assumed knowns detailed in this section.

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1.11.1.3 In some instances, it may be appropriate to attribute a deduced portion (e.g., a major/minor portion) of a mixture to an assumed known.

1.11.2 The attribution statement must include the number of loci at which any of the assumed known's types are detected and are attributable to him/her.

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A DNA profile attributable to PERSON is present at 13 loci.

The major DNA profile developed is attributable to PERSON at 22 loci.

The minor DNA profile/types developed at 7 loci is/are attributable to PERSON.

1.11.2.1 Dosage across the profile as a whole should be considered when determining how many loci to attribute to the assumed known.

1.11.2.2 The minimum number of loci required to draw a conclusion regarding an assumed known and therefore report an attribution statement for specific sample types are detailed in the applicable Interpretation manual.

1.11.2.3 Amelogenin and DYS391 are not included in the locus count for attribution.

1.11.3 Attribution statements for multiple items of evidence may be combined as long as they are accurate in the number of loci listed for each item. If the number of loci differs, they must be reported independently.

A DNA profile attributable to victim is also present in each of the samples at 22 loci.

1.11.4 If 2 assumed knowns are used for the interpretation of an intimate sample, an attribution statement must be included for each assumed known.

EXAMPLES: A DNA profile attributable to VICTIM is present at 22 loci.

A DNA profile attributable to ELIMINATION is also present at 17 loci.

1.11.4.1 The statement may be combined if the number of loci is the same for each individual.

DNA profiles attributable to both VICTIM and ELIMINATION are present at 15 loci.

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1.12 Sperm and Non-Sperm Fractions

1.12.1 Results for a sample for which a sperm and non-sperm fraction were created may be reported in one of two ways.

1.12.1.1 If the results allow, the probative results for the sample as whole may be reported.

EXAMPLE: VC sample – single source male profile in sperm fraction; mixture of sperm fraction profile and victim in non-sperm fraction.

A DNA profile different from VICTIM was developed. A DNA profile attributable to VICTIM is also present at X loci.

1.12.1.2 If the results are made clearer to the reader of the Report by reporting the two fractions separately, they may be reported separately.

1.12.1.2.1 Types detected in one fraction due to carry over from the other fraction may, at the examiner's discretion, be addressed with an attribution statement.

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EXAMPLES: DNA types attributable to the sperm fraction are also present in the non-sperm fraction at 4 loci.

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A DNA mixture profile attributable to VICTIM and the additional contributor in the sperm fraction was developed from the non-sperm fraction.

- DNA types attributable to the additional contributor in the sperm fraction are present at 10 loci.
- DNA types attributable to VICTIM are present at 22 loci.

1.12.1.3 If one fraction is deemed to be of no value overall (e.g., >3C mixture, types of no value, etc.), the fractions should be reported separately and the fraction of no value left out of the table of typing results, as applicable (see Chapter 6 of this manual).

1.12.2 Regardless of the approach in reporting results, if a statistical calculation is reported, the Report must be clear as to which fraction on which the statistic is calculated.

EXAMPLE: The probability of randomly selecting an unrelated individual with a DNA profile matching that developed from the sperm fraction from the vaginal/cervical sample at the PowerPlex® Fusion loci is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

1.12.3 Attribution statements with regard to an assumed known must reflect the number of loci attributed for each fraction separately, if applicable. The statements may be made separately or combined as in the example below:

A DNA profile attributable to victim is present at 15 loci in the sperm fraction and in 22 loci in the non-sperm fraction.

1.13 Mixture Samples for Which No Traditional Statistics Can/Will Be Calculated That Will Not Be Referred to TrueAllele®

1.13.1 If the sample will not be referred to TrueAllele® because the inclusion is not probative or other probative samples exist:

No conclusions regarding PERSON as a contributor to this DNA mixture profile will be made at this time.

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1.13.2 If the sample will not be referred to TrueAllele® because the case is a non-person case:

The significance of this DNA mixture profile cannot be determined using traditional statistical methods. Accordingly, no conclusions regarding PERSON as a contributor will be offered.

1.14 Cases for Which a Triaging Approach is Used to Discontinue DNA Analysis

For cases that include a sample or samples that is/are discontinued for the purpose of limiting the number of samples on which DNA STR analysis is conducted but that may be suitable for either PowerPlex® or Y-chromosome DNA testing, the following wording will be used:

The samples not tested at this time may be suitable for DNA analysis and may be considered for analysis upon additional request.

NOTE: This wording may be amended grammatically as needed and used per individual sample to which it applies or as a statement at the end of the results section of the Certificate. It may also be amended to specify Y-chromosome DNA analysis, as applicable.

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1.15 Certificates Addressing Samples Suitable for Y-STR Testing

NOTE: This wording may be amended, combined with other wording, or placed according to the specifics of the case.

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The following statement may be included with regard to an individual sample:

This sample may be suitable for further (Y-chromosome) DNA testing.

The following statement(s) may be included at/near the end of the RESULTS section, as applicable:

The results of further (Y-chromosome) DNA testing on Items X and Y will be the subject of a separate report.

Further (Y-chromosome) DNA testing may be conducted upon re-submission of Item X along with the submission of two buccal (cheek) swabs from a male suspect to the Laboratory.

1.16 Multiples Samples Tested Within a Case

1.16.1 When multiple samples from a non-subject case are analyzed (e.g, 4 cigarette butts, 2 bottles and 1 can), the report may address, as follows, how many different profiles were obtained from these items and what the Data Bank searching results were.

DNA profiles were developed from the four cigarette butts, and the mouth openings of the two bottles and one can. Of these seven DNA profiles, four different profiles, indicative of four different contributors, were developed. Three of these profiles (Items 2, 3, and 5) were searched against the Virginia DNA Data Bank and no profile consistent with these profiles was found. These profiles are each indicative of a male contributor and will be submitted to the Virginia and National DNA Data Banks.

The fourth DNA profile (Item 7) was searched against the Virginia DNA Data Bank and found to be consistent with the following individual:…

1.16.2 When multiple samples from a non-subject case are analyzed and the profiles, although indicative of originating from the same contributor, are not identical, they may be reported in the following manner:

DNA profiles were developed from the five cigarette butts. These DNA profiles are consistent with originating from a common contributor. The DNA profile from the Item 3 cigarette butt was selected for searching against the Virginia DNA Data Bank and no profile consistent with this profile was found. This

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profile is indicative of a male contributor and will be submitted to the Virginia and National DNA Data Banks.

1.16.3 If multiple mixture profiles in a case are evaluated and appear to be similar, have a common contributor, or have contributor in common with a single source profile also developed in the case, and a single mixture profile was selected and taken through the complete workflow, they will be reported in the following manner:

DNA mixture profiles with a possible common contributor were developed from the knife handle, the stain on the shoe and the cigarette butt. The profile from the knife handle was selected for comparisons (OR for searching against the Virginia DNA Data Bank). [Remainder of reporting, as appropriate, for the selected mixture]

The mixture profiles from the stain on the shoe and the cigarette butt remain in the case file and can be compared upon request.

1.17 Requests for Known Reference Samples

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1.17.1 Requests will be made for known samples in the Report when unaccounted for profiles, unaccounted for mixtures or unaccounted for portions of mixture profiles are developed that, when compared, could provide investigative information of value.

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1.17.2 No requests for known samples need be made in cases for which the future submission of a known reference and subsequent comparison of a known reference profile will not provide any investigative information of value.

EXAMPLE: A request for known reference samples will not be made in the Report for a possession of a firearm by a felon case if a mixture is developed from which the person of interest is either not eliminated or eliminated.

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2 TRADITIONAL SCREENING RESULTS

2.1 General Reporting of Traditional Screening Results

2.1.1 Traditional screening results will be addressed in the RESULTS section of the Report for each item on which screening was conducted.

2.1.2 Presumptive (non-confirmatory) tests will be reported using the word 'indicated', as applicable.

2.1.3 Confirmatory tests (sperm identifications) will be reported using the word 'identified', as applicable.

2.1.4 The use of an alternate light source (ALS) is considered a visual examination.

2.1.4.1 When items were screened using an ALS and no stains were observed:

No seminal fluid was observed.

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2.1.4.2 When items were screened using an ALS and stains were observed, the results will be reported according to the further body fluid testing that was conducted.

2.1.5 The observation of the absence of blood on trauma-related evidence (evidence in homicides, assaults, rapes, etc.) will be reported, as this may provide investigative information.

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2.1.5.1 The submission of trace DNA samples or samples submitted for saliva in conjunction with homicides and assaults must be evaluated on a case-by-case basis with regard to blood testing and reporting since the presence or absence of blood may or may not be of importance in these situations, depending on the scenario.

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2.1.6 The observation of the absence of blood on non-trauma-related evidence such as samples presumed to be saliva, trace DNA samples, or known buccal samples may be included in the case notes, but is not required to be reported. If PTMB testing is conducted, however, the results of that testing must be reported.

2.1.7 The location of biological stains or sample recovery on an item will be included in the report if this information may be helpful to the reader. This determination will be made at the author's discretion.

EXAMPLES: Blood was indicated in a stain on the upper left thigh area of the jeans.

Spermatozoa were identified on the inside of the condom (as submitted).

2.1.8 When multiple stains are located in the same general vicinity, the results may be reported with respect to an area of staining, multiple stains, or selected stains, as applicable.

2.1.8.1 The report should be clear if individual stains were tested or if stains were grouped for testing.

2.1.9 If multiple stains on an item are chemically tested and only a subset are positive, both the positive and the negative stains will be addressed in the Report.

EXAMPLE: A bed sheet is examined and 8 stains are identified using an alternate light source for potential further chemical testing. Two of the stains are positive for AP and are taken forward for DNA analysis. Six of the stains are negative for AP and are therefore not examined further. One of the six appeared brownish and was PTMB negative. The report will include wording such as:

No seminal fluid was indicated in five (5) additional stains. No blood or seminal fluid was indicated in one (1) additional stain.

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OR

No seminal fluid was indicated in additional stains [on the sheet]. No blood or seminal fluid was indicated in an additional stain.

The decision to report the number of and location of the negative stains will be left to examiner discretion and will be based upon particular case specifics.

2.2 General Reporting for PERK Samples

2.2.1 The swabs and smears submitted from the same body area in the Physical Evidence Recovery Kit will be combined to be reported as a sample (i.e., vaginal/cervical smears and swabs will be reported as vaginal/cervical sample).

2.2.2 All contents (including known samples and buccal swabs) included in the Physical Evidence Recovery Kit which were not examined will be specified in the report.

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EXAMPLES: The thighs/external genitalia sample, the perianal/buttocks sample and the pubic combings were not examined.

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Thighs/external genitalia sample
Perianal/buttocks sample
Pubic combings

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- These samples were not examined.

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2.3 Preservation Only Items

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2.3.1 If an item is submitted only for the purposes of preservation, the preservation of that item will be documented in the case notes and the reporting will be as follows:

No examinations were conducted; however, the ITEM was preserved.

No examinations were conducted; however, a sample from the mouth area of the bottle was recovered and preserved.

2.3.2 If an item is submitted for examination, but due to a decision made regarding overall case approach the item is preserved but not tested, the preservation will be reported.

EXAMPLES: A knife is submitted for DNA and Latent Print examinations. Four distinct red/brown stains are observed on the knife and collected individually on swabs. One is tested, found to be positive for PTMB and taken forward for DNA analysis. The remaining three swabs are repackaged with the evidence.

Blood was indicated on and a DNA profile was developed from a selected stain on the blade of the knife……[DNA RESULTS CONTINUE].

Three other stains from the blade tip, hilt and handle were recovered and preserved.

OR

No examinations were conducted on three other stains from the blade tip, hilt and handle; however, they were recovered and preserved.

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Blood was indicated in three other stains on the blade tip, hilt and handle. No further testing was conducted on these stains; however, they were recovered and preserved.

2.4 Blood Screening Results

2.4.1 The following wording will be used in reporting Luminol or BLUESTAR® results, as applicable:

- Luminol/BLUESTAR® neg – No blood was observed…
- Luminol/BLUESTAR® pos, but no further testing with PTMB to conserve sample – The possible presence or absence of blood could not be determined due to insufficient information obtained from the chemical analysis. In order to conserve the sample for DNA analysis, no further blood detection testing was conducted.
- Luminol/BLUESTAR® pos, PTMB neg – report as PTMB neg below
- Luminol/BLUESTAR® pos, PTMB pos – report as PTMB pos below

2.4.2 The following wording will be used in reporting PTMB results, as applicable:

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- Visual exam only – No blood was observed….
- PTMB neg – No blood was indicated…
- PTMB pos – Blood was indicated…
- PTMB inconclusive – The possible presence or absence of blood could not be determined due to insufficient information obtained from the chemical analysis.
- In order to conserve the sample for DNA analysis, no blood detection testing was conducted.

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EXAMPLE: No blood was indicated on the swabs from the bedroom floor.

2.5 Semen/Seminal Fluid Screening Results

2.5.1 The following wording will be used in reporting screening results for semen/seminal fluid, as applicable:

- >1 sperm ID'd – Spermatozoa were identified…
- 1 sperm ID'd – A spermatozoon was identified…
- AP neg (or slow weak pink) and no sperm observed - No seminal fluid was indicated and no spermatozoa were identified…
- AP neg – No seminal fluid was indicated…
- AP pos, no sperm observed and p30 pos – Chemical and immunological testing indicated the presence of seminal fluid; however, no spermatozoa were identified…
- AP pos, no sperm observed and p30 neg – Immunological testing did not indicate the presence of seminal fluid and no spermatozoa were identified.
- AP pos but no further testing –
  - The possible presence or absence of seminal fluid could not be determined due to insufficient information obtained from the chemical analysis and the stain was of insufficient size to conduct further body fluid identification testing.
  - The possible presence or absence of seminal fluid could not be determined due to insufficient information obtained from the chemical analysis. In order to conserve sample for DNA analysis, no further body fluid identification testing was conducted.
- AP pos, no further testing on stain, sperm ID'd on sperm fraction of extract – Spermatozoa/a spermatozoon was identified.
- AP pos, no further testing on stain, no sperm ID'd on sperm fraction – The possible presence or absence of seminal fluid could not be determined due to insufficient information obtained from the chemical analysis. In order to conserve sample for DNA analysis, no further body fluid identification testing was conducted. No spermatozoa were identified on the sperm fraction from STAIN/SAMPLE.

2.5.2 If positive results are obtained for a confirmatory test (sperm identification), the results of the presumptive and/or immunological tests will not be reported.

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2.5.3 If positive results are obtained for sperm identification or p30, but the sample is not extracted because a different sample was chosen (see Chapter 12 of the FB PM Screening and Collection for DNA Analysis), the following statement will be reported after the screening results, as applicable:

No DNA analysis was conducted at this time.

2.5.4 If AP is performed on a sample and is positive, but no microscopic examination for spermatozoa or p30 testing is conducted prior to extraction and quantitation of that sample, the quantitation or DNA result is considered more conclusive than the presumptive AP result and will be reported in lieu of the AP result.

EXAMPLES: A vaginal/cervical sample is positive for AP. It is differentially extracted and both fractions are discontinued due to N/A male quantitation results. Refer to 3.4.1 for reporting. The Report will be silent regarding the AP testing.

A vaginal/cervical sample is positive for AP. A small portion of it is extracted using Casework Direct (CD) and quantitated. Although the male quantitation result is greater than N/A, it is not chosen for DNA STR analysis due to a different sample being chosen. Refer to 3.4 for reporting. The Report will be silent regarding the AP testing.

A vaginal/cervical sample is positive for AP. It is differentially extracted and DNA STR analysis is conducted. The DNA results will be reported. The Report will be silent regarding the AP testing.

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2.5.5 If AP is performed on a sample/stain and is negative and no further seminal fluid identification tests are performed, whether the sample/stain is taken forward for DNA analysis or not, the negative AP result will be reported. At the author's discretion, the following statement may also be reported:

No further body fluid identification testing was conducted [on the sample/stain].

2.5.6 If AP is performed on a sample/stain and is positive, but no further screening or DNA analysis is conducted, the following will be reported:

This sample was presumptively screened for seminal fluid; however, the presence or absence of seminal fluid was not determined. No further body fluid identification testing or DNA analysis was conducted at this time.

EXAMPLE: A sheet is screened for seminal fluid. Three stains observed with the ALS are AP positive. One gives a significantly faster and stronger AP result than the other two. The case scenario suggests that testing only one stain will be sufficient; therefore, only the one stain is extracted for DNA STR analysis. Report as follows:

Additional stains were presumptively screened for seminal fluid; however, the presence or absence of seminal fluid was not determined. No further body fluid identification testing or DNA analysis was conducted at this time.

2.6 Hair Screening Results

2.6.1 Hair examinations, or the lack thereof, will be addressed in the RESULTS sections of the Report for each item reported, as applicable. The term 'hair/fiber' may be used in lieu of the term 'hair', if appropriate.

2.6.1.1 No reference to hair examinations need be made for items for which probative DNA results were obtained and reported unless a specific hair request for that item was made.

2.6.1.2 No reference to hair examinations need be made for items on which it can be logically assumed no hairs would typically be present (i.e., blood swabs, soda can, buccal swabs, vaginal/cervical swabs and smear, etc.).

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2.6.1.2.1 If a hair/fiber is observed on an item such as this, choose the appropriate wording from the choices below.

2.6.2 No hairs were observed during the examination of an item that was searched for hairs/fibers:

No hairs were observed.

2.6.3 No hairs were observed during the examination of an item and the item was not thoroughly searched for hairs at the time of examination:

This item was not examined for the presence of hairs at this time.

2.6.4 Hairs/fibers were observed during the examination of an item, but no suitability examinations were conducted:

- Hairs/fibers were observed but not recovered for examination at this time.
- No hair examinations were conducted on the recovered hairs/fibers. (OPTIONAL: Others may remain.)

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2.6.5 Hair suitability examinations were conducted:

- No hairs suitable for nuclear DNA analysis were recovered. (OPTIONAL: Others may remain.)
- [DNA results on hairs taken forward.]
  - If other hairs/fibers were examined and found not to be suitable:

    The remaining hairs recovered are not suitable for nuclear DNA analysis. (OPTIONAL: Others may remain.)

    No other hairs suitable for nuclear DNA analysis were recovered. (OPTIONAL: Others may remain.)

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3 DNA RESULTS

In general, the results of DNA testing will fall within one of the following categories:

- No DNA typing results were obtained.
- DNA typing results of no value were developed.
  - This may be due to the limited nature of the information obtained.
  - This may be due to the complex nature of the results obtained.
  - This may be due to failure of any of the quality control standards.
- No DNA typing results different from an assumed known were developed.
- A DNA profile was developed/A DNA profile different from an assumed known was developed.
  - A compared known is eliminated.
  - A compared known is not eliminated.
  - Insufficient information exists to draw a conclusion regarding a compared known as a contributor.
  - The DNA profile is suitable for searching/entry into CODIS.
    - A Data Bank search results in a match.
      - The profile is entered/not entered into CODIS.
    - A Data Bank search results in no matches.
      - The profile is entered/not entered into CODIS.
  - The DNA profile is not suitable for searching/entry into CODIS (The DNA profile is suitable for comparison only).
- A DNA mixture profile was developed/A DNA mixture profile different from an assumed known was developed.
  - A compared known is eliminated.
  - A compared known is not eliminated.
  - Insufficient information exists to draw a conclusion regarding a compared known as a contributor.
  - The mixture profile (or a portion of it) is suitable for searching/entry into CODIS.
    - A Data Bank search results in a match.
      - The profile/portion of the profile is entered/not entered into CODIS.
    - A Data Bank search results in no matches.
      - The profile/portion of the profile is entered/not entered into CODIS.
  - The mixture profile is not suitable for searching/entry into CODIS (the mixture is suitable for comparison only).

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3.1 Known Reference Samples and Alternate Knowns

3.1.1 Typical Known Reference Sample Wording:

A DNA profile was developed from the buccal swabs/DNA card from PERSON.

3.1.2 Referencing a Previously Analyzed Known Reference Sample for Comparison to Current Evidence:

3.1.2.1 Same FS Lab#, Same Investigator

A DNA profile was developed from the stained swabs. PERSON (Item X, previously addressed in the Certificate of Analysis dated _____) cannot be eliminated as a contributor of this DNA profile.

Alternatively, a statement regarding the previous development of the profile can be included separately and then comparisons can be conducted throughout the report to various new items of evidence using the suspect's name:

A DNA profile was previously developed from the buccal swabs from PERSON (Item X, previously addressed in the Certificate of Analysis dated _____).

A different Investigator's name can be added, if necessary, similarly to how it appears in the example in 3.1.2.2.

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3.1.2.2 Known was reported for a different FS Lab #

A DNA profile was developed from the cigarette butt. SUSPECT (Item X, previously submitted under FS Lab # NXX-XXXX and reported in the Certificate of Analysis dated_____ and addressed to INVESTIGATOR of the AGENCY NAME, Agency Case # XXXXXXX), cannot be eliminated as a contributor of this DNA profile.

The other affected investigator will be cc'd.

3.1.2.3 Known was analyzed by an outside laboratory

If a known was analyzed by an outside laboratory, somewhat similar wording will be used as that in 3.1.2.2 making clear that the known profile used for comparison was supplied by that outside laboratory and should include their case number and the date of their report if at all possible.

3.1.3 Comparison of a New Known to Previously Analyzed Evidence

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3.1.3.1 This wording will be similar to the wording in 3.1.2 but with the information amended as applicable.

EXAMPLE: A DNA profile was developed from the buccal swabs from PERSON. Person cannot be eliminated as a contributor of the DNA profile previously developed from the stained swabs (Item 1) and addressed in the Certificate of Analysis dated_____.

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Add investigator or other case information, as necessary, and cc, as necessary.

3.1.4 Alternate Known Samples (cigarette butt in these examples)

A DNA profile was developed from the cigarette butt. If the cigarette butt is from PERSON, (then) PERSON is eliminated as a contributor of the DNA profile from the stained swabs from the broken window.

A DNA profile was developed from the cigarette butt. If the DNA profile developed from the cigarette butt is PERSON's DNA profile, then PERSON is eliminated as a contributor of the DNA profile developed from the stained swabs from the broken window.

3.2 PowerPlex® 16 Samples That Were Discontinued Due to Low DNA Yields

Due to the limited quantity of nuclear DNA obtained from the belt, it is not suitable for PCR analysis using the PowerPlex® 16 System; therefore, DNA analysis was discontinued on this sample.

Due to the limited quantity of nuclear DNA obtained from the swab from the firearm, this sample is not suitable for PCR analysis using the PowerPlex® 16 System; therefore, DNA analysis was discontinued.

3.3 PowerPlex® Fusion Samples That Were Discontinued Due to Low DNA Yields

Due to the limited quantity of nuclear DNA obtained from the belt, it is not suitable for PCR analysis using the PowerPlex® Fusion System; therefore, DNA analysis was discontinued on this sample.

Due to the limited quantity of nuclear DNA obtained from the swab from the firearm, this sample is not suitable for PCR analysis using the PowerPlex® Fusion System; therefore, DNA analysis was discontinued.

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3.4 Samples Taken Through Quantitation and Discontinued Based Upon Male Quant or Auto/Y Quant Ratio

3.4.1 Male Quant of N/A After CD Extraction

No male DNA was detected during screening; therefore, no DNA analysis using the PowerPlex® Fusion System was conducted. [Address Y-STR suitability, as applicable]

3.4.2 Male Quant >N/A After CD Extraction

Male DNA may be present in this sample; however, no further DNA analysis was conducted at this time. [Address future testing and/or Y-STR suitability, as applicable]

3.4.3 Male Quant of N/A After Full (Non-CD) Extraction

NOTE: This wording may apply to samples discontinued based upon the flowchart in the FB PM Plexor® HY Quantitation of DNA or based upon the PERK Triage Approach found in Chapter 12 of the FB PM Screening and Collection for DNA Analysis.

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No male DNA was detected [in the perianal/buttocks sample]; therefore, no further DNA analysis was conducted.

Because no male DNA was detected in the thighs/external genitalia sample, DNA analysis was discontinued.

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Because no male DNA was detected, DNA analysis on the breast swabs was discontinued.

3.4.4 Male Quant ≥ 0.010 ng/µL After Full (Non-CD) Extraction

NOTE: This wording will generally apply to samples discontinued based upon the PERK Triage Approach found in Chapter 12 of the FB PM Screening and Collection for DNA Analysis.

Male DNA was detected; however, no further DNA analysis was conducted at this time.

Male DNA was detected in the thighs/external genitalia sample; however, no further DNA analysis was conducted at this time.

3.4.5 Male Quant between N/A and 0.010 ng/µL After Full (Non-CD) Extraction

NOTE: This wording will generally apply to samples discontinued based upon the PERK Triage Approach found in Chapter 12 of the FB PM Screening and Collection for DNA Analysis.

Male DNA may be present in this sample; however, no further DNA analysis was conducted at this time.

3.4.6 Auto/Y quant ratio ≥ 20 After Full (Non-CD) Extraction

NOTE: This wording may apply to samples discontinued based upon the flowchart in the FB PM Plexor® HY Quantitation of DNA or based upon the PERK Triage Approach found in Chapter 12 of the FB PM Screening and Collection for DNA Analysis.

Due to the limited quantity of male DNA as compared to total human DNA, analysis using the PowerPlex® Fusion system was discontinued. [Address Y-STR suitability, as applicable]

3.5 No DNA Typing Results (No Peaks Above LOD for the Sample)

3.5.1 Typically:

No DNA typing results were obtained from the ITEM.

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3.5.2 In some instances:

Human DNA was isolated from the firearm; however, no DNA typing results were obtained.

3.6 DNA Results of No Value

A DNA profile of no value was developed from the swabs. Due to the limited information obtained, this DNA profile is not suitable for comparison, searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank.

A DNA mixture profile of no value was developed from the grip, trigger and sight of the firearm. Due to the unknown number of contributors and complex nature of this mixture profile, it is not suitable….
A DNA mixture profile of no value was developed from the cigarette butt. Due to the limited information obtained, this DNA mixture profile is not suitable….

DNA types different from ASSUMED KNOWN, but of no value, were developed from the vaginal/cervical sample. Due to the limited information obtained, these types are not suitable…. [Attribution statement, if applicable].

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3.7 DNA Results of No Value Due to Quality Control

No reportable DNA results were obtained because the quality control standard was not achieved.

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3.8 No DNA Typing Results Different from an Assumed Known

No DNA profile different from ASSUMED KNOWN was developed; however, DNA types attributable to her are present at 17 loci.

No DNA profile different from ASSUMED KNOWN was developed. [Attribution statement].

No DNA profile different from VICTIM and ELIM was developed. [Attribution statement(s)].

3.9 DNA Typing Results – Single Source

A DNA profile was developed from the swabs from the broken window.

A DNA profile suitable for comparison was developed from the mouth area of the bottle. Due to the limited information obtained, this profile is not suitable for searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank.

A DNA profile of limited value was developed from the swabs from the cartridges. Due to the limited information obtained, this profile is/may be suitable for comparison, but is not suitable for searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank.

NOTE: Gender statement may be added, as applicable

3.10 DNA Typing Results – Single Source Different from an Assumed Known

For use with non-intimate items with an assumed known:
A DNA mixture profile was developed from the cell phone. Assuming this profile is a mixture of ASSUMED KNOWN and one additional contributor,….[the profile different from ASSUMED KNOWN was searched…] OR [PERSON is eliminated/cannot be eliminated as the additional contributor]. [Will need attribution statement, if applicable]

For use with intimate items with an assumed known:
A DNA mixture profile attributable to ASSUMED KNOWN and one additional contributor was developed from the sperm fraction. [The profile different from ASSUMED KNOWN was searched…] OR [PERSON is

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eliminated/cannot be eliminated as the additional contributor]. DNA types attributable/A DNA profile attributable to ASSUMED KNOWN…

A DNA profile different from ASSUMED KNOWN was developed from a stain on the inside crotch area of the underpants. [Will need Attribution statement, if applicable]

A DNA profile different from ASSUMED KNOWN and ELIM was developed from the vaginal/cervical sample. [Will need attribution statements, if applicable]

The option to report these as mixtures with a comparison to ASSUMED KNOWN (and ELIM) individually is also available.

3.11 DNA Typing Results – Mixtures

A DNA mixture profile was developed from the mouth area of the bottle. (for use when the minor portion of the mixture will be deemed of no value)

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A DNA mixture profile suitable for comparison was developed from the mouth area of the bottle. (for use when an entire mixture (either as a whole or both parts – major AND minor) is suitable for comparison)

A DNA mixture profile suitable for comparison was developed from the mouth area of the bottle. Due to the limited information obtained, this mixture profile is not suitable for searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank.

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A DNA mixture profile of limited value was developed from the mouth area of the bottle. Due to the limited information obtained, this mixture profile is/may be suitable for comparison, but is not suitable for searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank.

A DNA mixture profile of limited value was developed from the mouth area of the bottle. Due to [the unknown number of contributors and] the complex nature of this mixture profile, it is/may be suitable for comparison, but is not suitable for searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank.

In RARE instances:

A DNA mixture profile of limited value was developed from the mouth area of the bottle. Due to [the unknown number of contributors and] the limited information obtained/complex nature of this mixture profile, it is suitable only for eliminations.

3.12 DNA Typing Results – Mixture Different from Assumed Known

3.12.1 Intimate Items of Evidence

A DNA mixture profile different from ASSUMED KNOWN and suitable for comparison was developed from the vaginal/cervical sample. [Will need attribution statement, if applicable]

A DNA mixture profile suitable for comparison was developed from the thighs/external genitalia sample. DNA types/A DNA profile attributable to ASSUMED KNOWN are/is present at X loci.

A DNA mixture profile attributable to ASSUMED KNOWN and two additional contributors was developed from the inside crotch area of the underpants. DNA types/A DNA profile attributable to ASSUMED KNOWN are/is present at X loci.

NOTE: The option to report this as a mixture with a separate comparison to ASSUMED KNOWN is available, and often preferable

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3.12.2 Non-Intimate Ownership Items of Evidence

NOTE: This wording is limited to samples for which a relatively certain assumption can be made that the owner/user's DNA profile will be detected AND for which the general approach comparison of the assumed known's profile resulted in a non-elimination (see the Conclusion Requirements Specific to Comparisons of Known References to Mixtures with DNA Typing Results detailed in the FB PM Interpretation of Fusion Data).

A DNA mixture profile suitable for comparison was developed from the cell phone. Assuming this is a mixture of ASSUMED KNOWN and additional contributors…[Will need attribution statement]

A DNA mixture profile suitable for comparison was developed from the steering wheel. Assuming this is a mixture of ASSUMED KNOWN 1, ASSUMED KNOWN 2, and an additional contributor…[Will need attribution statement(s)]

3.13 Comparisons of Known Reference Profiles

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3.13.1 If a comparison of a known reference results in a conclusion of not eliminated and traditional statistics will not be calculated and the sample will be referred to TrueAllele®, the following wording will be used:

Conclusions regarding NAME and statistics (if applicable) will be the subject of a separate report.

OR

Conclusions and statistics (if applicable) will be the subject of a separate report.

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3.13.2 Eliminations

PERSON is eliminated as a contributor of this DNA profile.

PERSON is eliminated as a major contributor to this DNA mixture profile.

PERSON is eliminated as a contributor of this major DNA profile.

PERSON is eliminated as a contributor to this DNA mixture profile.

NOTE: If a person is not eliminated as a major contributor to a mixture profile, no statement regarding that person as eliminated or not eliminated as a contributor of the minor profile need be made (and vice versa).

3.13.3 Non-Eliminations

PERSON cannot be eliminated as a contributor of this DNA profile.

PERSON cannot be eliminated as a major contributor to this DNA mixture profile.

PERSON cannot be eliminated as a contributor of this major DNA profile.

PERSON cannot be eliminated as a contributor to this DNA mixture profile.

3.13.4 Inconclusive Conclusion with Regard to a Known Reference

Insufficient information exists to draw a conclusion regarding PERSON as a contributor of this DNA profile.

Insufficient information exists to draw a conclusion regarding PERSON as a contributor to this DNA mixture profile.

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4 CODIS SEARCHING/ENTRY AND RELATED REPORT WRITING

For any unaccounted for profile or portion of a profile deemed of value for comparison, the suitability for searching/entry into CODIS and the results of a search, if applicable, will be reported.

EXCEPTION: For profiles from non-CODIS cases, such as possession cases, or ineligible profiles or suspect profiles, no CODIS/Data Bank suitability will be addressed.

The individual loci searched and/or entered into CODIS will not be addressed in the Report.

The results of all searches in CODIS, with the exception of staff index searches with no hits, will be reported.

If a match to an **individual occurs after previous matches** have been made to other unsolved cases, a separate Supplemental report will be issued for each linked case and contain the information of the individual.

Anytime a sample is entered into/uploaded to CODIS, a statement detailing the affected Data Bank (Virginia or National) will be included.

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EXAMPLES: This DNA profile will be entered into the Virginia DNA Data Bank, but is not suitable for searching against the National DNA Data Bank.

This DNA profile will be submitted to the Virginia and National DNA Data Banks.

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Anytime a sample is removed/deleted from a CODIS Index, a statement detailing the affected Data Bank (Virginia and/or National) will be included (see 4.2).

Wording from categories below may be combined with wording from other categorie(s) and/or amended, if necessary, to meet the particular scenario at hand. The wording should conform as much as possible to the wording examples offered here.

Appropriate parties will be cc'd, if applicable.

4.1 Samples With a Match to a Staff Member

4.1.1 If the match was deemed adventitious, it will not be reported.

4.1.2 If the match candidate cannot be eliminated as a possible contributor, the results for the affected item/sample will be reported as:

No reportable DNA results were obtained because the quality control standard was not achieved.

4.2 Profiles Removed from CODIS

The DNA profile from the gun swab has been removed from the Virginia (and National) DNA Data Bank(s).

4.3 Samples Not Searched or Entered

4.3.1 Samples not searched because they do not meet the requirements of CODIS eligibility:

This sample is not suitable for searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank.

4.3.2 Samples not searched due to current case information available, but may be searched in the future if further information is obtained:

This DNA profile will not be searched against the Virginia DNA Data Bank or submitted to the National DNA Data Bank at this time.

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EXAMPLE: A single source male DNA profile is developed from a vaginal/cervical sample and no known reference from the previous consensual partner has been submitted, the profile may be reported as above.

The known reference from the consensual partner will be requested and, if later eliminated, the evidence profile may be searched.

4.4 Potential Match Candidates to Profiles for Which a Statistic Cannot be Calculated (Typically Subsequent Hits), or When Compared, Do Not Meet the Minimum Requirements for a Conclusion of Not Eliminated to Be Reached

4.4.1 No Statistic Can Be Calculated (Typically a Historical Profile with a Subsequent Hit)

A subsequent search of the DNA mixture profile previously developed from the ITEM and addressed in the Certificate of Analysis dated _____was conducted. As a result of this search, a potential candidate was identified. However, because the significance of the evidence profile cannot be determined using traditional statistical methods, the identifying information for this individual will not be reported. No further searches will be conducted and the evidence profile will be removed from the Virginia DNA Data Bank.

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4.4.2 Insufficient Information Exists to Draw a Conclusion regarding the Candidate Based on Interpretation Rules

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This DNA profile was searched against the Virginia DNA Data Bank and a potential candidate was identified. However, insufficient information exists to draw a conclusion regarding the candidate and as a result, the identifying information for this individual will not be reported. No further searches will be conducted and the evidence profile will be removed from the Virginia and National DNA Data Banks.

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The wording in 4.4.1 and 4.4.2 should be modified to address mixture, types different, major, minor, single source, original search vs. subsequent search, and indices affected, etc., as applicable.

4.5 Matches Made

If multiple matches are made, ALL matches will be reported.

If matches are made to specimens in the convicted offender/arrestee AND the forensic indices, see 4.7.

If multiple matches are made to specimens in the forensic index, but none are made to the convicted offender/arrestee index, see 4.8.

NOTE: All wording for matches obtained to an individual will include the information below, as applicable, as shown in the wording for a single source match. The wording detailed for each scenario below is meant to highlight differences in wording required without repeating all the wording that will remain the same.

Name:
SSN:
DOC #
DCN #
SID #
Date of Birth:
Race:
Gender:

This information is provided only as an investigative lead, and any possible connection or involvement of this individual to the case must be determined through further investigation.

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In order to complete the direct DNA comparison, two buccal (cheek) swabs from INDIVIDUAL must be submitted to the Laboratory.

This profile will submitted to the Virginia (and National) DNA Data Bank(s).

NOTES: If the match is made to the **listed victim**, the statements following the hit information may be omitted. The request for the victim known may or may not be included, depending upon the case scenario.

If the match is made to the **listed suspect**, the statement referencing an investigative lead may be omitted. The request for a known and the submission to the Data Bank(s) statement will still be included.

No gender information will be provided for unresolved mixtures.

If the gender results are inconclusive, report as:

No conclusions can be made regarding the gender of the contributor of this profile.

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4.5.1 Single Source to an Individual

A DNA profile was developed from the swab from the floor. This profile was searched against the Virginia DNA Data Bank and found to be consistent with the following individual:

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Name:
SSN:
DOC #
DCN #
SID #
Date of Birth:
Race:
Gender:

This information is provided only as an investigative lead, and any possible connection or involvement of this individual to the case must be determined through further investigation.

In order to complete the direct DNA comparison, two buccal (cheek) swabs from INDIVIDUAL must be submitted to the Laboratory.

This profile will be submitted to the Virginia and National DNA Data Banks. (OR will be submitted to the Virginia DNA Data Bank but is not suitable for submission to the National DNA Data Bank).

4.5.2 Single Source to a Forensic Sample or Mixture

<u>Forensic Sample</u>

A DNA profile was developed from the swabs. This profile was searched against the Virginia DNA Data Bank and found to be consistent with the DNA profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ and addressed to INVESTIGATOR of the AGENCY, AGENCY CASE NUMBER. These results indicate that the DNA profile developed from both of these samples could have been deposited by the same individual.
This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.
Future searches will be conducted on a periodic basis. The DNA profile developed from the swabs is indicative of a male/female contributor and will be submitted to the Virginia (and National) DNA Data Bank(s).

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DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

Forensic Mixture

A DNA profile was developed from the swabs. This profile was searched against the Virginia DNA Data Bank. As a result of this search, the contributor of this profile cannot be eliminated as a contributor to the DNA mixture profile developed from the EVIDENCE, submitted under FS LAB # and the subject of the Certificate of Analysis dated _____, addressed to INVESTIGATOR of the AGENCY, AGENCY CASE NUMBER.

This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.

Future searches will be conducted on a periodic basis. The DNA profile developed from the swabs is indicative of a male contributor and will be submitted to the Virginia and National DNA Data Banks.

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DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

4.5.2.1 If there are multiple items addressed in the Certificate of Analysis:

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Permission to disseminate all information pertaining to the case to the other investigator/agency in one Certificate will be obtained and documented. One Certificate will then be written and cc'd to the additional appropriate investigator.

OR

The original Certificate of Analysis will include all information except the results of the search. The results of the search will be reported in a Supplemental Certificate and cc'd to the additional appropriate investigator.

See 4.7 and 4.8 for examples.

4.5.3 Resolved Mixture to an Individual

A DNA mixture profile was developed from the cigarette butt. The major profile was searched against the Virginia DNA Data Bank and found to be consistent with the following individual:

This major DNA profile is indicative of a male/female contributor and will be submitted to the Virginia (and National) DNA Data Bank(s).

A DNA profile different from ASSUMED KNOWN was developed from the EVIDENCE. This profile was searched against the Virginia DNA Data Bank and found to be consistent with the following individual:

This DNA profile different from ASSUMED KNOWN is indicative of a male/female contributor and will be submitted….
[Attribution statement, if applicable]

4.5.4 Unresolved Mixture to an Individual

Predominant Profile

A DNA mixture profile suitable for comparison was developed from the stained swabs. The predominant profile developed was searched against the Virginia DNA Data Bank and found to be consistent with the following individual:

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This predominant profile is indicative of a male/female contributor and will be submitted to the Virginia (and National) DNA Data Bank(s).

Entire Mixture

A DNA mixture profile suitable for comparison was developed from the inside neck area of the shirt. This mixture profile was searched against the Virginia DNA Data Bank. As a result of this search, the following individual has a DNA profile consistent with a possible contributor to this mixture:
[This mixture profile will be submitted to the Virginia (and National) DNA Data Bank(s)].

4.5.5 Resolved Mixture to a Forensic Sample or Mixture

Forensic Sample

A DNA mixture profile was developed from the swabs. The minor DNA profile developed was searched against the Virginia DNA Data Bank and found to be consistent with the DNA profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ and addressed to INVESTIGATOR of the AGENCY, AGENCY CASE NUMBER. These results indicate that the DNA profile developed from both of these samples could have been deposited by the same individual.

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This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.

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Future searches will be conducted on a periodic basis. The minor DNA profile developed from the swabs will be submitted to the Virginia (and National) DNA Data Bank(s).

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

Forensic Sample

A DNA mixture profile was developed from the swabs from the steering wheel. Assuming this profile is a mixture of ASSUMED KNOWN and one additional contributor, the profile different from ASSUMED KNOWN was searched against the Virginia DNA Data Bank and found to be consistent with the DNA profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ and addressed to INVESTIGATOR of the AGENCY, AGENCY CASE NUMBER. These results indicate that the DNA profile developed from both of these samples could have been deposited by the same individual.

This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.

Future searches will be conducted on a periodic basis. This DNA profile different from ASSUMED KNOWN will be submitted to the Virginia (and National) DNA Data Bank(s).

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory

Forensic Sample

A DNA profile different from ASSUMED KNOWN was developed from the vaginal/cervical sample. This profile was searched against the Virginia DNA Data Bank and found to be consistent with the DNA profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ and addressed to INVESTIGATOR of the AGENCY, AGENCY CASE NUMBER. These results indicate that the DNA profile developed from both of these samples could have been deposited by the same individual….

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Forensic Mixture

A DNA mixture profile was developed from the swabs. The major profile developed was searched against the Virginia DNA Data Bank. As a result of this search, a contributor to the DNA mixture profile developed from the EVIDENCE, submitted under FS LAB # and the subject of the Certificate of Analysis dated _____, addressed to INVESTIGATOR of the AGENCY, AGENCY CASE NUMBER, cannot be eliminated as the contributor of this profile.

This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.

Future searches will be conducted on a periodic basis. The major DNA profile developed from the swabs is indicative of a male contributor and will be submitted to the Virginia and National DNA Data Banks.

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory

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4.5.5.1 If there are multiple items addressed in the Certificate of Analysis:

Permission to disseminate all information pertaining to the case to the other investigator/agency in one Certificate will be obtained and documented. One Certificate will then be written and cc'd to the additional appropriate investigator.

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The original Certificate of Analysis will include all information except the results of the search. The results of the search will be reported in a Supplemental Certificate and cc'd to the additional appropriate investigator.

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See 4.7 and 4.8 for examples.

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4.5.6 Unresolved Mixture to a Forensic Sample or Mixture

Forensic Sample

A DNA mixture profile suitable for comparison was developed from the swabs. This mixture profile was searched against the Virginia DNA Data Bank. As a result of this search, the contributor of the profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____, addressed to INVESTIGATOR of the AGENCY, AGENCY CASE NUMBER has a DNA profile consistent with a possible contributor to this mixture.

This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.

Future searches will be conducted on a periodic basis. The DNA mixture profile developed from the swabs will be submitted to the Virginia (and National) DNA Data Bank(s).

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

Forensic Mixture

A DNA mixture profile suitable for comparison was developed from the swabs. This mixture profile was searched against the Virginia DNA Data Bank. As a result of this search, a contributor (or the major contributor/the minor contributor) to the DNA mixture profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ addressed to

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INVESTIGATOR, of the AGENCY, AGENCY CASE NUMBER has a profile consistent with a possible contributor to this mixture.

This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.

Future searches will be conducted on a periodic basis. The DNA mixture profile developed from the swabs will be submitted to the Virginia (and National) DNA Data Bank(s).

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

4.5.6.1 If there are multiple items addressed in the Certificate of Analysis:

Permission to disseminate all information pertaining to the case to the other investigator/agency in one Certificate will be obtained and documented. One Certificate will then be written and cc'd to the additional appropriate investigator.

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OR

The original Certificate of Analysis will include all information except the results of the search. The results of the search will be reported in a Supplemental Certificate and cc'd to the additional appropriate investigator.

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See 4.7 and 4.8 for examples.

4.6 No Matches Made

NOTE: All wording for no matches obtained will include the information below, as applicable, as shown in the wording for a single source no match. The wording detailed for each scenario is meant to highlight differences in wording required without repeating wording that will remain the same.

Future searches will be conducted on a periodic basis. This profile is indicative of a male (or female) contributor and will be submitted to the Virginia and National DNA Data Banks (OR will be submitted to the Virginia DNA Data Bank but is not suitable for submission to the National DNA Data Bank).

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

NOTES: No gender information will be provided for unresolved mixture profiles.

If the gender results are inconclusive, report as:

No conclusions can be made regarding the gender of the contributor of this profile.

4.6.1 Single Source

A DNA profile was developed from the cigar tip. This profile was searched against the Virginia DNA Data Bank and no DNA profile consistent with this profile was found.

Future searches will be conducted on a periodic basis. This profile is indicative of a male/female contributor and will be submitted to the Virginia (and National) DNA Data Bank(s) (OR will be submitted to the Virginia DNA Data Bank but is not suitable for submission to the National DNA Data Bank).

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

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4.6.2 Resolved Mixture

A DNA mixture profile was developed from the cell phone. The major profile developed was searched against the Virginia DNA Data Bank and no DNA profile consistent with this profile was found.

A DNA mixture profile was developed from the handle of the knife. The predominant profile developed was searched against the Virginia DNA Data Bank and no DNA profile consistent with this profile was found.

A DNA profile different from ASSUMED KNOWN was developed from the thighs/external genitalia sample. This profile was searched against the Virginia DNA Data Bank and no DNA profile consistent with this profile was found.

4.6.3 Unresolved Mixture

A DNA mixture profile was developed from a combined sample from the nose and mouth areas of the mask. This mixture profile was searched against the Virginia DNA Data Bank and no DNA profiles consistent with this profile were found. Future searches will be conducted on a periodic basis.

This mixture profile will be submitted to the Virginia and National DNA Data Banks. (OR This mixture profile will be submitted to the Virginia DNA Data Bank but is not suitable for submission to the National DNA Data Bank).

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

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4.7 Matches Made to both Convicted Offender/Arrestee Samples AND Forensic Samples

4.7.1 If a match is made to specimens in the **convicted offender/arrestee AND the forensic indices**, etc., the information associated with ALL matches will be reported.

4.7.2 Wording used will be that as detailed in 4.5 and should be modified to address mixture, types different, major, minor, single source, and indices affected, etc., as applicable.

4.7.3 If the item of evidence that was searched is the only item addressed in the Certificate, the information associated with ALL matches will be reported in the one Certificate of Analysis. The convicted offender/arrestee hit will be reported first. Then, the forensic index hit(s) will be reported with wording to make clear that these are hits to the same sample. The Certificate will be cc'd to all affected parties.

EXAMPLES: This profile was also found to be consistent with the DNA profile developed from the cigarette butt (Item X) submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ and addressed to INVESTIGATOR of the NAME OF AGENCY, AGENCY CASE NUMBER. These results indicate that the DNA profile developed from both of these samples could have been deposited by the same individual….

In addition, a contributor (or the major contributor/the minor contributor) to the DNA mixture profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ addressed to NAME OF INVESTIGATOR, NAME OF AGENCY, AGENCY CASE NUMBER cannot be eliminated as a contributor to this mixture profile….

4.7.4 If there are multiple items addressed in the Certificate of Analysis:

Permission to disseminate all information pertaining to the case to all affected investigators/agencies in one Certificate will be obtained and documented. One Certificate will then be written as described in 4.7.3.

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OR

The original Certificate of Analysis will include all information except the results of the search. The results of the search (ALL matches) will be reported in a Supplemental Certificate and cc'd to all affected parties.

EXAMPLE: Original Certificate:

Item 3 - A DNA profile was developed from the cigarette butt. John Doe cannot be eliminated as a contributor of this DNA profile… [remainder of reporting for Item 3]

Item 4 – Blood was indicated on and a DNA profile was developed from the swabs from the window sill. John Doe is eliminated as a contributor of this DNA profile. This profile was searched against the Virginia DNA Data Bank. The results of this search will be reported separately.

Supplemental Certificate:

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Item 4 – The results of the search against the Virginia DNA Data Bank previously addressed in the Certificate of Analysis dated XXXX (probably same date as original Cert) are as follows:
The profile developed from the swabs from the window sill was found to be consistent with the following individual:
[hit info as usual]

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This profile was also found to be consistent with the DNA profile developed from the cigarette butt….[see example in 4.7.3]

The wording should be modified to address mixture, types different, major, minor, single source, and indices affected, etc., as applicable.

4.8 Multiple Matches Made to Forensic Samples

4.8.1 If multiple matches are made to specimens in the forensic index, the information associated with ALL matches will be reported.

4.8.2 Wording used will be that as detailed in 4.5 and should be modified to address mixture, types different, major, minor, single source, and indices affected, etc., as applicable.

4.8.3 If the item of evidence that was searched is the only item addressed in the Certificate, the information associated with ALL matches will be reported in the one Certificate of Analysis with wording to make clear that these are hits to the same sample. The Certificate will be cc'd to all affected parties.

EXAMPLES: This profile was also found to be consistent with the DNA profile developed from the cigarette butt (Item X) submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ and addressed to INVESTIGATOR of the NAME OF AGENCY, AGENCY CASE NUMBER. These results indicate that the DNA profile developed from both of these samples could have been deposited by the same individual….

In addition, a contributor (or the major contributor/the minor contributor) to the DNA mixture profile developed from the EVIDENCE submitted under FS LAB # and the subject of the Certificate of Analysis dated _____ addressed to NAME OF INVESTIGATOR, NAME OF AGENCY, AGENCY CASE NUMBER cannot be eliminated as a contributor to this mixture profile….

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4.8.4 If there are multiple items addressed in the Certificate of Analysis:

Permission to disseminate all information pertaining to the case to all affected investigators/agencies in one Certificate will be obtained and documented. One Certificate will then be written as described in 4.8.3.

OR

The original Certificate of Analysis will include all information except the results of the search. The results of the search (ALL matches) will be reported in a Supplemental Certificate and cc'd to all affected parties.

EXAMPLE: Original Certificate:

Item 3 - A DNA profile was developed from the cigarette butt. John Doe cannot be eliminated as a contributor of this DNA profile… [remainder of reporting for Item 3]

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Item 4 – Blood was indicated on and a DNA profile was developed from the swabs from the window sill. John Doe is eliminated as a contributor of this DNA profile. This profile was searched against the Virginia DNA Data Bank. The results of this search will be reported separately.

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Supplemental Certificate:

Item 4 – The results of the search against the Virginia DNA Data Bank previously addressed in the Certificate of Analysis dated XXXX (probably same date as original Cert) are as follows:

The profile developed from the swabs from the window sill profile was found to be consistent with the DNA profile developed from the cigarette butt….[see example in 4.8.3]

The wording should be modified to address mixture, types different, major, minor, single source, and indices affected, etc., as applicable.

4.9 Subsequent Hits

All NDIS case to case hits will be reported.

If multiple matches are made, ALL matches will be reported. If matches are made to both an offender/arrestee AND forensic samples (either Virginia or NDIS), the offender/arrestee match will be reported first. Then, the forensic index hit(s) will be reported with wording to make clear that these are hits to the same sample.

NOTES: If the match made is from a sample in a **solved case** and the match is not probative, the two statements following the hit information may be omitted and the statement for removal from CODIS outlined above will be included in the Report.

If the match made is to a sample in a **solved case** for which the subject of the hit has been identified and named in a report (either previously or in the current report), it is not necessary to report the offender/arrestee information again.

Appropriate parties will be cc'd, as applicable.

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4.9.1 Virginia DNA Data Bank

NOTE: Wording may be adjusted to fit the particular scenario. Wording used for subsequent hits should be similar to that used for original hits in regard to unresolved mixtures vs. single source samples vs. resolved mixtures and hits to individuals vs. forensic samples.

A subsequent search of the DNA profile previously developed from the blood swabs and addressed in the Certificate of Analysis dated _____ against the Virginia DNA Data Bank found it to be consistent with the following individual:

Name:
SSN:
DOC #
DCN #
SID #
Date of Birth:
Race:
Gender:

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This information is provided only as an investigative lead, and any possible connection or involvement of this individual to the case must be determined through further investigation.
In order to complete the direct DNA comparison, two buccal (cheek) swabs from INDIVIDUAL must be submitted to the Laboratory.

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4.9.2 NDIS Hit to Another State or FBI Data Bank

A subsequent search of the DNA profile previously developed from EVIDENCE and addressed in the Certificate of Analysis dated _____ against the National DNA Data Bank found it to be consistent with the following individual in the STATE/Federal DNA Data Bank:

Name:
SSN:
DOC #
DCN #
SID #
Date of Birth:
Race:
Gender:

This information is provided only as an investigative lead, and any possible connection or involvement of this individual to the case must be determined through further investigation.

In order to complete the direct DNA comparison, two buccal (cheek) swabs from INDIVIDUAL must be submitted to the Laboratory.

NOTE: When a NDIS hit occurs and the information provided by another state is more comprehensive than the categories listed above, the additional identifying information (e.g., FBI number) will be provided in the Certificate of Analysis. No information regarding height, weight, hair color, eye color, etc., will be included in the Certificate of Analysis if this information is provided by the other state.

4.9.3 NDIS Case to Case Hits

A subsequent search of the DNA profile previously developed from the swabs and addressed in the Certificate of Analysis dated _____ against the National DNA Data Bank found it to be consistent with a DNA profile in the STATE DNA Data Bank developed from THE EVIDENCE/A SAMPLE/AN ITEM

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associated with AGENCY CASE #/INVESTIGATING AGENCY. These results indicate that the DNA profile developed from both of these samples could have been deposited by the same individual.

This information is provided only as an investigative lead, and any possible connection between these cases must be determined through further investigation.

Contact INVESTIGATOR with the INVESTIGATING AGENCY at INVESTIGATOR CONTACT INFO for more information.

Future searches will be conducted on a periodic basis.

DNA comparisons can be conducted following the submission of two buccal (cheek) swabs from a suspect to the Laboratory.

NOTE: Wording may be adjusted to fit the particular scenario. Wording used for subsequent hits should be similar to that used for original hits in regard to unresolved mixtures vs. single source samples vs. resolved mixtures and hits to individuals vs. forensic samples.

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5 STATISTICAL STATEMENTS

5.1 General Requirements

5.1.1 Routinely, statistical calculations will be reported for the Caucasian, African American, and Hispanic populations in accordance with The Evaluation of Forensic DNA Evidence, National Academy Press, Washington D.C., 1996 (i.e., National Research Council II).

5.1.1.1 Other population databases may be reported upon specific request with the approval of the Biology Program Manager.

5.1.2 Refer to 1.10 of this manual in determining when to include a statement addressing assumptions made with regard to number of contributors with these statistical statements.

5.1.3 Statistical statements will specify which loci were used in the calculation.

5.1.3.1 The statistical statement may state that the loci from the kit specified in the METHODS were used.

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The probability of randomly selecting an unrelated individual with a DNA profile matching that developed from the stained swabs at the PowerPlex® Fusion loci is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

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5.1.3.2 The statistical statement may state that the loci from the kit specified in the METHODS were used (with the exception of/excluding…).

The probability of randomly selecting an unrelated individual with a DNA profile matching that developed from the sperm fraction from the vaginal/cervical sample at the PowerPlex® 16 loci (excluding TPOX, D5S8181 and vWA) is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

5.1.3.3 The statistical statement may list the loci individually.

The probability of randomly selecting an unrelated individual with a DNA profile matching that developed from the stained swabs at the FGA, D8S1179, Penta E, D18S51, D21S11 and D13S317 loci is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

5.1.4 If a statistical statement applies to multiple items/samples in a case, they may be combined in the Report.

Two different RM calculations were conducted on two different samples. Each resulted in all population groups exceeding 7.2 billion.

The probability of randomly selecting an unrelated individual with a DNA profile matching that developed from the stained swabs and from the cigarette butt at the PowerPlex® Fusion loci is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

If one calculation incorporated 2p while one did not, use the more conservative wording for 2p as shown in 5.2.2.

If different loci were used for each calculation, the loci used for each will be specified.

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5.2 Random Match Probability (RMP)

For each RMP statement, adjustments will be made to accurately report the loci used in the calculation (see 5.1.3) and to address whether 2p or uncertainty was applied during the calculation (see 5.2.2).

5.2.1 When all population groups exceed 7.2 billion (approximate world population) and no 2p or uncertainty was applied:

The probability of randomly selecting an unrelated individual with a DNA profile matching that developed from the stained swabs at the PowerPlex® Fusion loci is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

5.2.2 When all population groups exceed 7.2 billion (approximate world population) and 2p or uncertainty was applied:

The probability of randomly selecting an unrelated individual who would be included as a contributor of the profile developed from the stained swabs at the PowerPlex® Fusion loci is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

NOTE: For samples for which statistics are reported together because they meet the same thresholds, if 2p or uncertainty was applied for any of the calculations, this wording will be used.

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5.2.3 When only one or two population groups exceed 7.2 billion (approximate world population):

The probability of randomly selecting an unrelated individual with a DNA profile matching that developed from the sperm fraction at the PowerPlex® Fusion loci is approximately 1 in _____ in the African American population, 1 in _____ in the Hispanic population, and 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian population.

5.2.4 When none of the population groups exceed 7.2 billion (approximate world population):

The probability of randomly selecting an unrelated individual who would be included as a contributor of the profile different from ASSUMED KNOWN developed from the thighs/external genitalia sample at the PowerPlex® Fusion loci is approximately 1 in _____ in the Caucasian population, 1 in _____ in the African American population, and 1 in _____ in the Hispanic population.

5.2.5 If it is suspected that a relative of the suspect may have left the DNA profile at the crime scene, the following wording will be used:

The probability of the RELATIVE having a DNA profile consistent with that of SUSPECT is approximately 1 in ____ in the Caucasian population, 1 in _____ in the African American population, and 1 in _____ in the Hispanic population.

NOTE: Based upon the question that is being asked above, the frequency provided will not be limited to 1 in greater than 7.2 billion (which is approximately the world population), but instead will be reported as the actual truncated probability that is obtained using the formulas described in the applicable Interpretation Manual. The reported value for the random match probability will be truncated to 2 significant figures.

5.3 Traditional Likelihood Ratio (LR)

An accurate description of the loci used in the calculation will be used (see 5.1.3).

The DNA profile developed from the sperm fraction from the inside crotch area of the underpants at the PowerPlex® Fusion loci is:

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_____ times more likely to be observed if it originated from the VICTIM and SUSPECT than if it originated from the VICTIM and an unknown individual in the Caucasian population.

_____ times more likely to be observed if it originated from the VICTIM and SUSPECT than if it originated from the VICTIM and an unknown individual in the African American population.

_____ times more likely to be observed if it originated from the VICTIM and SUSPECT than if it originated from the VICTIM and an unknown individual in the Hispanic population.

NOTES: Depending on the assumptions made during the likelihood ratio calculation, there may be other individuals (i.e., ELIMINATION SAMPLE, UNKNOWN INDIVIDUAL) that need to be included in the likelihood ratio statement.

The reported value for the likelihood ratio probability will be truncated to 2 significant figures.

5.4 Combined Probability of Inclusion (CPI) / Unrestricted Random Match (URM)

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An accurate description of the loci used in the calculation will be used (see 5.1.3).

5.4.1 When all population groups exceed 7.2 billion (approximate world population):

The probability of randomly selecting an unrelated individual who would be included as a contributor to the DNA mixture profile developed from the firearm at the PowerPlex® Fusion loci is 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian, African American, and Hispanic populations.

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5.4.2 When only one or two population groups exceed 7.2 billion (approximate world population):

The probability of randomly selecting an unrelated individual who would be included as a contributor to the DNA mixture profile developed from the combined sample from the trigger and grip of the firearm at the PowerPlex® Fusion loci is approximately 1 in _____ in the African American population, 1 in _____ in the Hispanic population, and 1 in greater than 7.2 billion (which is approximately the world population) in the Caucasian population.

5.4.3 When none of the population groups exceed 7.2 billion (approximate world population):

The probability of randomly selecting an unrelated individual who would be included as a contributor to the DNA mixture profile developed from the stained area on the sofa cushion at the PowerPlex® Fusion loci is approximately 1 in _____ in the Caucasian population, 1 in_____ in the African American population, and 1 in _____ in the Hispanic population.

NOTE: The reported value for the combined probability of inclusion will be truncated to 2 significant figures.

5.5 Likelihood Ratio Provided by TrueAllele®

Refer to the TrueAllele® Manual.

5.6 Y Haplotype Frequency Estimates

Refer to Chapter 7 of this manual.

5.7 Paternity/Maternity Index and Relationship Statistics

Refer to Chapter 8 of this manual.

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6 TABLE OF TYPING RESULTS

6.1 Tables of Typing Results will only be included in cases where there is a probative positive association (i.e., inclusion) to an item of evidence.

6.1.1 The table, if included, will be an appendix to the Certificate and an abbreviations appendix will also be included.

EXCEPTION: Body Identification cases may include only a table with no abbreviations appendix.

6.1.2 The following wording will be included in the Certificate just prior to the disposition statement(s).

Refer to Appendix 1 for the DNA typing results and Appendix 2 for the Abbreviations.

BODY ID CASE EXCEPTION: Refer to Appendix 1 for the DNA typing results.

6.2 The typing results (phenotype) obtained at amelogenin will be included in the table, regardless of the conclusions regarding gender.

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6.2.1 X (above or below STH) will be charted as X. X,Y will be charted as X,Y. Y (above or below STH) will be charted as Y.

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6.3 In cases where a table is included, all DNA evidence profiles suitable for comparison will be included in the table, regardless of what conclusion is reached for the profile (inclusion, elimination, insufficient information, elimination only).

EXCEPTION: Profiles not completely interpreted, analyzed, deconvoluted, etc., as referred to in 1.16.3, will not be included in the table.

6.4 In cases where a table is included, DNA reference profiles for individuals for which a conclusion of cannot be eliminated or insufficient information was reached will be included in the table. DNA reference profiles will NOT be included in the table if the individual is eliminated from all charted evidence.

6.5 Any DNA profile determined to be of no value for comparison (for any reason) will not be included in the chart. This includes DNA mixture and single source profiles of no value, intimate DNA samples with no profile different from the assumed known, and intimate DNA samples with DNA types different from the assumed known, but of no value.

EXCEPTION: For differentially extracted samples, if one fraction is included in the table, the other fraction may also be included in the table unless the profile developed is of no value overall (i.e., types of no value or a complex mixture of no value).

6.6 For cases (paternity/maternity, body ID, TrueAllele®) where conclusions and statistics are to be the subject of a supplemental report and/or the profiles are not suitable for traditional statistics, tables will be included with the original Certificate of Analysis.

6.7 In cases where the original analysis did not result in a table being included in the Certificate of Analysis and where the subsequent submission of new evidence or known standards results in probative positive associations to item(s) of evidence, a table will be included in a new Certificate of Analysis including all profiles developed in the case *following the guidelines above*.

6.8 In cases where the original analysis did result in a table being included in the Certificate of Analysis and where the subsequent submission of new evidence or known standards results in additional inclusions to probative item(s) of evidence, only the newly developed profiles need to be included in the table. Previously charted profiles are not required to be included in any subsequent tables.

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7 Y-STR TESTING RESULTS

The overall approach to report writing will conform to that detailed above for autosomal DNA. When applicable, the wording detailed above will be combined with the Y-chromosome specific wording addressed below and amended, as needed, to fit the case scenario.

The results of autosomal and Y-chromosome DNA testing may be combined into one Report. If this is done, all applicable METHODS must be included.

Unless the results of the autosomal and Y-chromosome DNA testing are combined into one Report, the Y-STR Report will generally be a Supplemental Report. Refer to the Department Quality Manual.

If the evidence item itself is transferred to the Y-STR examiner or the Y-STR examiner is the original autosomal examiner for the case, the item descriptions will match those in the original Report.

If only DNA extracts are transferred to the Y-STR examiner, the item description will indicate this.

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EXAMPLE: DNA extract from the sperm fraction from the vaginal/cervical sample from Jane Doe.

In general, the results of Y-chromosome DNA testing will fall into one of the following categories:

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- No Y-chromosome DNA typing results were obtained.
- Y-chromosome DNA typing results of no value were developed.
  - This may be due to the limited nature of the information obtained.
  - This may be due to the complex nature of the results obtained.
  - This may be due to failure of any of the quality control standards.
- No Y-chromosome DNA typing results different from an assumed known were developed.
- A Y-chromosome DNA profile was developed/A Y-chromosome DNA profile different from an assumed known was developed.
  - A compared known is eliminated.
  - A compared known is not eliminated, nor are any patrilineally related male relatives.
  - Insufficient information exists to draw a conclusion regarding a compared known as a contributor.
- A Y-chromosome DNA mixture profile was developed.
  - A compared known is eliminated.
  - A compared known is not eliminated as a major or minor contributor.
  - Insufficient information exists to draw a conclusion regarding a compared known as a contributor.

Y-chromosome DNA profiles are not suitable for searching in CODIS. If an unaccounted for Y-chromosome DNA profile/mixture profile is developed and it does not result in a match to the Staff Index, the following statement will be included:

> Y-chromosome DNA profiles are not suitable for searching against the Virginia DNA Data Bank or submission to the National DNA Data Bank; however, this profile/mixture profile is suitable for comparison.

When Y-STR results are obtained from an evidentiary sample or an alternate known sample, the phrase ‘originating from a male’ OR ‘originating from more than one male’ will be included in the report wording, as applicable.

EXCEPTIONS: If a single Y-chromosome DNA type is obtained, this phrase will be omitted.

> If the Y-STR results are limited such that it is unclear if the types obtained are from one or more than one male, this phrase may be omitted.

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7.1 Known Reference Samples and Alternate Known Samples

7.1.1 Known Reference Samples

A Y-chromosome DNA profile was developed from the buccal swabs from John Smith.

A Y-chromosome DNA profile was developed from the DNA extract from the DNA card from John Smith.

7.1.2 Referencing a Previously Analyzed Known Reference Sample for Comparison to Current Evidence and Comparison of a New Known to Previously Analyzed Evidence

7.1.2.1 The wording in 3.1.2 and 3.1.3 will be adapted such that the Y-chromosome specific wording will follow the same approach as that for autosomal wording.

7.1.3 Alternate Known Samples (cigarette butt in this example)

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A Y-chromosome DNA profile originating from a male was developed from the cigarette butt. If the cigarette butt is from John Doe, (then) John Doe is eliminated as a contributor of the DNA profile from the stained swabs from the broken window.

7.2 No Y-STR Typing Results (No Peaks Above LOD for the Sample)

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No Y-chromosome DNA typing results were obtained from the ITEM.

7.3 Y-STR Results of No Value

A Y-chromosome DNA profile originating from a male, but of no value, was developed from the swabs. Due to the limited information obtained, this Y-chromosome DNA profile is not suitable for comparison.

A Y-chromosome DNA mixture profile originating from more than one male, but of no value, was developed from the DNA extract from the grip, trigger and sight of the firearm. Due to the unknown number of contributors and the limited information obtained, this Y-chromosome DNA mixture profile it is not suitable for comparison.

Y-chromosome DNA types different from ASSUMED KNOWN, but of no value, were developed from the DNA extract from the penile swabs. Due to the limited information obtained, these Y-chromosome DNA types are not suitable for comparison. [Attribution statement, if applicable].

7.4 Y-STR DNA Results of No Value Due to Quality Control

No reportable Y-chromosome DNA results were obtained because the quality control standard was not achieved.

7.5 No Y-STR DNA Typing Results Different from an Assumed Known

No Y-chromosome DNA profile different from ASSUMED KNOWN was developed; however, DNA types attributable to him are present at 17 loci.

No Y-chromosome DNA profile different from ASSUMED KNOWN was developed. [Attribution statement].

7.6 Y-STR DNA Typing Results – Single Source

A Y-chromosome DNA profile originating from a male was developed from the inside rear area of the underpants.

7.7 Y-STR DNA Typing Results – Single Source Different from an Assumed Known

A Y-chromosome DNA profile originating from a male and different from ASSUMED KNOWN was developed from a stain on the inside crotch area of the underpants. [Will need Attribution statement, if applicable]

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The option to report these as mixtures with a comparison to ASSUMED KNOWN (and ELIM) individually is also available.

7.8 Y-STR DNA Typing Results – Mixtures

A Y-chromosome DNA mixture profile originating from more than one male was developed from the mouth area of the bottle. (for use when the minor portion of the mixture will be deemed of no value)

A Y-chromosome DNA mixture profile originating from more than one male and suitable for comparison was developed from the mouth area of the bottle. (for use when an entire mixture (either as a whole or both parts – major AND minor) is suitable for comparison)

A Y-chromosome DNA mixture profile originating from two males and suitable for comparison was developed from the mouth area of the bottle. (may be used for 2 person mixtures with both a major and minor component suitable for comparison)

In RARE instances:

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A Y-chromosome DNA mixture profile originating from more than one male, but of limited value, was developed from the DNA extract from the massager. Due to the unknown number of contributors and the limited information obtained/complex nature of this Y-chromosome DNA mixture profile, it is suitable only for eliminations.

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7.9 Comparisons of Known Reference Profiles

7.9.1 If a comparison of a known reference to an unresolved mixture results in a conclusion of not eliminated, the following will be reported:

Because statistical calculations will not be conducted, no conclusions regarding PERSON as a contributor will be offered.

7.9.2 Eliminations

PERSON is eliminated as a contributor of this Y-chromosome DNA profile.

PERSON is eliminated as a major contributor to this Y-chromosome DNA mixture profile.

PERSON is eliminated as a contributor of this major Y-chromosome DNA profile.

PERSON is eliminated as a contributor to this Y-chromosome DNA mixture profile.

NOTE: If a person is not eliminated as a major contributor to a mixture profile, no statement regarding that person as eliminated or not eliminated as a contributor of the minor profile need be made (and vice versa).

7.9.3 Non-Eliminations

NOTE: If a Report includes a non-elimination, the phrase ‘nor can any of his patrilineally related male relatives’ will be included. In addition, the following statement will be included just prior to either the Appendices statement or the disposition statement, whichever comes first: Patrilineally related male relatives can include, but are not limited to father, sons, brothers, uncles, cousins and grandfathers.

PERSON cannot be eliminated as a contributor of this Y-chromosome DNA profile, nor can any of his patrilineally related male relatives.

PERSON cannot be eliminated as a minor contributor, nor can any of his patrilineally related male relatives.

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PERSON cannot be eliminated as a major contributor to this Y-chromosome DNA mixture profile, nor can any of his patrilineally related male relatives.

PERSON cannot be eliminated as a contributor of this major Y-chromosome DNA profile, nor can any of his patrilineally related male relatives.

7.9.4 Inconclusive Conclusion with Regard to a Known Reference

Insufficient information exists to draw a conclusion regarding PERSON as a contributor of this Y-chromosome DNA profile.

Insufficient information exists to draw a conclusion regarding PERSON as a minor contributor to this Y-chromosome DNA mixture profile.

7.10 Paternity, Missing Person, and Body Identification Cases

When a comparison is made to a biological relative of an individual, rather than directly to the individual, the results will be reported in the following manner:

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7.10.1 Paternity Cases

7.10.1.1 Elimination

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A Y-chromosome DNA profile was developed from the CHILD'S KNOWN SAMPLE/EVIDENCE SAMPLE and from the blood (or buccal) sample from the ALLEGED FATHER. The ALLEGED FATHER is eliminated as the biological father of the CHILD/EVIDENCE SAMPLE.

7.10.1.2 Non-elimination

A Y-chromosome DNA profile was developed from the CHILD'S KNOWN SAMPLE/EVIDENCE SAMPLE and from the blood (or buccal) sample from the ALLEGED FATHER. Conclusions and statistics will be the subject of a separate report.

NOTE: If the examiner conducting the Y-STR analysis will also calculate the statistics, one report will be issued and the following statement will be used in lieu of the one above:

A Y-chromosome DNA profile was developed from the CHILD'S KNOWN SAMPLE/EVIDENCE SAMPLE and from the blood (or buccal) sample from the ALLEGED FATHER. The ALLEGED FATHER cannot be eliminated as the biological father of the CHILD/EVIDENCE SAMPLE, nor can any of his patrilineally related male relatvies.

7.10.2 Missing Person Cases

7.10.2.1 Elimination

Y-chromosome DNA profiles were developed from the EVIDENCE and from the blood (or buccal) sample from RELATIVE. RELATIVE is eliminated as a biological father/offspring/relative of the donor of the Y-chromosome DNA profile developed from EVIDENCE.

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7.10.2.2 Non-Elimination

Y-chromosome DNA profiles were developed from the EVIDENCE and from the blood (or buccal) sample from RELATIVE. Conclusions and statistics will be the subject of a separate report.

NOTE: If the examiner conducting the Y-STR analysis will also calculate the statistics, one report will be issued and the following statement will be used in lieu of the one above:

Y-chromosome DNA profiles were developed from the EVIDENCE and from the blood (or buccal) sample from RELATIVE. RELATIVE cannot be eliminated as a biological father/offspring/relative of the donor of the Y-chromosome DNA profile developed from EVIDENCE, nor can any of his patrilineally related male relatives.

7.10.2.3 Uploading Y-STR Results for a Relative of a Missing Person for Which No Comparison is Conducted

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A Y-chromosome DNA profile was developed from the KNOWN REFERENCE. This profile will be added to the nuclear short tandem repeat (STR) profile previously developed from this sample and addressed in the Certificate of Analysis dated DATE. This profile will be submitted to the Virginia and National DNA Data Banks. Future searches will be conducted on a periodic basis until the missing relative has been identified or located.

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NOTE: This wording should be adjusted, as necessary.

7.10.3 Body Identification Cases

7.10.3.1 Comparison to Personal Effects

7.10.3.1.1 Elimination

Y-chromosome DNA profiles were developed from the SAMPLE FROM DECEDENT and from the PERSONAL EFFECTS SAMPLE (ie., toothbrush, razor, etc.). If the Y-chromosome DNA profile developed from the PERSONAL EFFECTS SAMPLE is from DECEDENT, then DECEDENT is eliminated as a contributor of the Y-chromosome DNA profile developed from the SAMPLE FROM DECEDENT.

7.10.3.1.2 Non-Elimination

Y-chromosome DNA profiles were developed from the SAMPLE FROM DECEDENT and from the PERSONAL EFFECTS SAMPLE (ie., toothbrush, razor, etc.). Conclusions and statistics will be the subject of a separate report.

NOTE: If the examiner conducting the Y-STR analysis will also calculate the statistics, one report will be issued and the following statement will be used in lieu of the one above:
Y-chromosome DNA profiles were developed from the SAMPLE FROM DECEDENT and from the PERSONAL EFFECTS SAMPLE (ie., toothbrush, razor, etc.). If the Y-chromosome DNA profile developed from the PERSONAL EFFECTS SAMPLE is from DECEDENT, then DECEDENT cannot be eliminated as a contributor of the Y-chromosome DNA profile developed from the SAMPLE FROM DECEDENT, nor can any of his patrilineally related male relatives.

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7.10.3.2 Comparison to Biological Relatives

7.10.3.2.1 Elimination

A Y-chromosome DNA profile was developed from the SAMPLE FROM DECEDENT and from the blood (or buccal) samples from RELATIVE. RELATIVE is eliminated as a biological father/offspring/relative of the donor of the Y-chromosome DNA profile developed from EVIDENCE.

7.10.3.2.2 Non-Elimination

Y-chromosome DNA profiles were developed from the SAMPLE FROM DECEDENT and from the blood (or buccal) samples from RELATIVE. Conclusions and statistics will be the subject of a separate report.

NOTE: If the examiner conducting the Y-STR analysis will also calculate the statistics, one report will be issued and the following statement will be used in lieu of the one above:

Y-chromosome DNA profiles were developed from the SAMPLE FROM DECEDENT and from the blood (or buccal) samples from RELATIVE. RELATIVE cannot be eliminated as a biological father/offspring/relative of the contributor of the Y-chromosome DNA profile developed from EVIDENCE, nor can any of his patrilineally related male relatives.

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7.11 Y Haplotype Frequency Estimates

7.11.1 Statistical statements will specify which loci were used in the calculation. Refer to 5.1.3 of this manual for guidance, if necessary.

7.11.1.1 If the Y-STR haplotype frequency has been incorporated into an autosomal calculation, the loci used overall will be specified.

7.11.2 Statistical calculations will be reported to reflect the number of observations seen for the entire portion of the database searched and using a 95% upper confidence interval calculation for each of the Caucasian, African American, and Hispanic populations. The frequencies calculated for each of the sub-populations using the 95% upper confidence interval will be truncated to 2 significant figures.

The Y-chromosome DNA profile developed from EVIDENCE at the AmpFℓSTR™ Yfiler™ loci was observed 5 times in 6739 individuals. Applying a 95% upper confidence interval results in a frequency of approximately 1 in 370 individuals in the Caucasian population, 1 in 710 individuals in the African American population and 1 in 160 individuals in the Hispanic population.

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8 PATERNITY, MISSING PERSON, AND BODY IDENTIFICATON CASES

If the case will be referred for paternity/maternity/kinship statistics, the appendices (table of typing results and abbreviations) will be included with the original Report with the testing results.

If the statistics are reported in the same Report as the testing, the appendices will be included with this Report and the statistical statements may be amended as necessary.

An accurate description of the loci used in the calculation will be used (see 5.1.3).

8.1 Paternity Cases

DNA profiles were developed from the CHILD'S KNOWN SAMPLE/EVIDENCE SAMPLE and the blood (or buccal) sample from the MOTHER and ALLEGED FATHER.

8.1.1 If conclusions and statistics will be issued in a separate report by another examiner:

Conclusions and statistics will be the subject of a separate report.

8.1.2 If conclusions and/or statistics are to be included in the same report as the testing:

The ALLEGED FATHER cannot be eliminated (or is eliminated) as the biological parent (father) of the CHILD/EVIDENCE SAMPLE.

NOTES: If the mother is the alleged parent, the wording will be changed to reflect the appropriate conclusion.

If the mother and father are both alleged, the wording will be changed to reflect the appropriate conclusions.

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8.2 Missing Person Cases

A DNA profile was developed from the buccal swabs from RELATIVE. This profile will be submitted to the Virginia DNA Data Bank and the National DNA Data Bank. Future searches of this profile will be conducted on a periodic basis until the missing relative has been identified or located.

OR

DNA profiles were developed from the EVIDENCE and from the blood (or buccal) samples from RELATIVE.

8.2.1 If conclusions and statistics will be issued in a separate report by another examiner:

Conclusions and statistics will be the subject of a separate report.

8.2.2 If conclusions and/or statistics are to be included in the same report as the testing:

RELATIVE cannot be eliminated (or is eliminated) as a biological parent/offspring of the contributor of the DNA profile developed from EVIDENCE.

8.3 Body Identification Cases

8.3.1 Comparison to Personal Effects

DNA profiles were developed from the SAMPLE FROM DECEDENT and from the PERSONAL EFFECTS SAMPLE (e.g., toothbrush, razor). If the DNA profile developed from the PERSONAL EFFECTS SAMPLE is from DECEDENT, then DECEDENT cannot be eliminated (or is eliminated) as a contributor of the DNA profile developed from the SAMPLE FROM DECEDENT.

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Investigators are advised to evaluate all associated case information in addition to the provided genetic results before declaring the identity of the remains.

NOTE: If a mixture profile is developed from a personal effects sample, this can be used for comparison purposes as long as the major contributor to this mixture profile can be discerned. No reference will be made in the C of A regarding the remaining portion of the mixture in the personal effects sample.

8.3.2 Comparison to Biological Relatives

A DNA profile was developed from the SAMPLE FROM DECEDENT and from the blood (or buccal) sample(s) from RELATIVE(S).

8.3.2.1 If conclusions and statistics will be issued in a separate report by another examiner:

Conclusions and statistics will be the subject of a separate report.

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8.3.2.2 If conclusions and/or statistics are to be included in the same report as the testing:

RELATIVE cannot be eliminated (or is eliminated) as a biological parent/offspring of the contributor of the DNA profile developed from EVIDENCE.

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8.4 Paternity Index and Probability of Paternity (Full Trio)

Based on a review of the typing results for the ALLEGED FATHER (Item#) MOTHER (Item #) and CHILD (Item #), previously analyzed at the PowerPlex® Fusion loci and addressed in the Certificate of Analysis dated DATE, ALLEGED FATHER cannot be eliminated as the biological parent (father) of CHILD. The following Combined Paternity Index (CPI) and Probability of Paternity, using a prior probability of 0.5, were calculated for the following populations at the PowerPlex® Fusion loci:

Caucasian	CPI = XXXX	Probability of Paternity = XX.XXXX%
African American	CPI = XXXX	Probability of Paternity = XX.XXXX%
Hispanic	CPI = XXXX	Probability of Paternity = XX.XXXX%

The Combined Paternity Index is a likelihood ratio that expresses the odds that ALLEGED FATHER is the biological parent (father) of CHILD rather than another unrelated random man. Therefore, the odds are XXXX times more likely in the Caucasian population, XXXX million times more likely in the African American population and XXXX times more likely in the Hispanic population that these alleles would be observed if ALLEGED FATHER is the biological parent (father) of CHILD rather than another unrelated random man.

Supporting examination documentation is maintained in the case file.

Refer to Appendix 1 in the Certificate of Analysis dated DATE, for the DNA typing results.

The disposition of the evidence and the results of other requested examinations are the subject of another report.

8.4.1 The reported value for the combined paternity index will be truncated to 2 significant figures.

8.4.2 The Probability of Paternity percentage (%) will be truncated at 4 places after the decimal point.

8.4.3 Refer to Appendix A of the appropriate Interpretation Manual for acceptable values for the Probability of Paternity.

8.5 Sibling Statistics

The reported value for the likelihood ratio probability will be truncated to 2 significant figures.

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8.5.1 The values for all three population groups meet or exceed 33:

Based on a review of the typing results for the EVIDENCE (Item #) and the REFERENCE (Item #), previously analyzed at the PowerPlex® Fusion loci and addressed in the Certificate of Analysis dated DATE, the following Combined Full Sibling Indices (CSI) were calculated for the following populations at the PowerPlex® Fusion loci:

Caucasian	CSI = XXXX
African American	CSI = XXXX
Hispanic	CSI = XXXX

The Combined Full Sibling Index is a likelihood ratio that expresses the odds that the donor of the EVIDENCE and REFERENCE share common biological parents, rather than unrelated. Therefore, the odds are XXXX times more likely in the Caucasian population, XXXX times more likely in the African American population and XXXX times more likely in the Hispanic population that these alleles would be observed if the donor of the EVIDENCE and REFERENCE share common biological parents, rather than unrelated.

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These findings support the conclusion that the donor of the EVIDENCE and REFERENCE are siblings.

Investigators are advised to evaluate all associated case information in addition to the provided genetic results before declaring the identity of the remains.

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Supporting examination documentation is maintained in the case file.

Refer to Appendix 1 in the Certificate of Analysis dated DATE, for the DNA typing results.

The disposition of the evidence and the results of other requested examinations are the subject of another report.

8.5.2 The values for one or more of the population groups fall below 33:

Based on a review of the typing results for the EVIDENCE (Item #) and the REFERENCE (Item #), previously analyzed at the PowerPlex® Fusion loci and addressed in the Certificate of Analysis dated DATE, the following Combined Full Sibling Indices (CSI) were calculated for the following populations at the PowerPlex® Fusion loci:

Caucasian	CSI = XXXX
African American	CSI = XXXX
Hispanic	CSI = XXXX

The Combined Full Sibling Index is a likelihood ratio that expresses the odds that the donor of the EVIDENCE and REFERENCE share common biological parents, rather than unrelated. Therefore, the odds are XXXX times more likely in the Caucasian population, XXXX times more likely in the African American population and XXXX times more likely in the Hispanic population that these alleles would be observed if the donor of the EVIDENCE and REFERENCE share common biological parents, rather than unrelated.

The values reported do not meet the minimum value required in all population groups for an inclusion as siblings. Therefore, these results support a finding of inconclusive regarding the question of a sibling relationship between the donor of the EVIDENCE and REFERENCE.

Investigators are advised to evaluate all associated case information in addition to the provided genetic results before declaring the identity of the remains.

Supporting examination documentation is maintained in the case file.

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Refer to Appendix 1 in the Certificate of Analysis dated DATE, for the DNA typing results.

The disposition of the evidence and the results of other requested examinations are the subject of another report.

8.6 Missing Person Statistics

The reported value for the likelihood ratio probability will be truncated to 2 significant figures.

8.6.1 BOTH Parents Available for Testing

NOTE: This wording will also be used for other cases in which a reverse paternity calculation is the appropriate calculation to use (i.e. the questioned sample is from an alleged child of two known parents).

Based on a review of the typing results for the femur from the EVIDENCE (Item X) and the samples from REFERENCE and REFERENCE (Items X and X, respectively), previously analyzed at the PowerPlex® Fusion loci and addressed in the Certificate of Analysis dated DATE, the donor of the EVIDENCE cannot be eliminated as a biological child of REFERENCE and REFERENCE. Statistical analyses regarding these results were calculated for the following populations at the PowerPlex® Fusion loci:

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It is XXXX times more likely to observe the DNA profile developed from the EVIDENCE at the PowerPlex® Fusion loci if it were from a biological child of REFERENCE and REFERENCE than if it were from a random couple of the Caucasian population.

It is XXXX times more likely to observe the DNA profile developed from the EVIDENCE at the PowerPlex® Fusion loci if it were from a biological child of REFERENCE and REFERENCE than if it were from a random couple of the African American population.

It is XXXX times more likely to observe the DNA profile developed from the EVIDENCE at the PowerPlex® Fusion loci if it were from a biological child of REFERENCE and REFERENCE than if it were from a random couple of the Hispanic population.

Supporting examination documentation is maintained in the case file.

Refer to Appendix 1 in the Certificate of Analysis dated DATE, for the DNA typing results.

The disposition of the evidence and the results of other requested examinations are the subject of another report.

8.6.2 Only ONE Parent Available for Testing

NOTE: This wording will also be used for single parent criminal paternity cases. For these cases, the statement, “Investigators are advised to evaluate all associated case information in addition to the provided genetic results before declaring the identity of the remains,” will be replaced with, “A maternal sample was not submitted for paternity relationship evaluation in this matter. Without a maternal sample, a complete relationship evaluation cannot be performed. Without a full trio (mother, child, father), the relationship statistic is limited.” This wording may be adjusted, as appropriate, for single parent criminal maternity cases.

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Based on a review of the typing results for the sample from ALLEGED PARENT (Item #) and the sample from CHILD (Item #), previously analyzed at the PowerPlex® Fusion loci and addressed in the Certificate of Analysis dated DATE, ALLEGED PARENT cannot be eliminated as the biological parent (father/mother) of CHILD. The following Combined Paternity/Maternity Index (CPI/CMI) and Probability of Paternity/Maternity, using a prior probability of 0.5, were calculated for the following populations at the PowerPlex® Fusion loci:

Caucasian	CP/MI = XXXX	Probability of P/Maternity = XX.XXXX%
African American	CP/MI = XXXX	Probability of P/Maternity = XX.XXXX%
Hispanic	CP/MI = XXXX	Probability of P/Maternity = XX.XXXX%

The Combined P/Maternity Index is a likelihood ratio that expresses the odds that the donor of the sample from ALLEGED PARENT is the biological parent (father/mother) of CHILD rather than another unrelated random man/woman. Therefore, the odds are XXXX times more likely in the Caucasian population, XXXX times more likely in the African American population and XXXX times more likely in the Hispanic population that these alleles would be observed if the donor of sample from ALLEGED PARENT is the biological parent (father/mother) of CHILD rather than another unrelated random man/woman.

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Investigators are advised to evaluate all associated case information in addition to the provided genetic results before declaring the identity of the remains.

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Supporting examination documentation is maintained in the case file.

Refer to Appendix 1 in the Certificate of Analysis dated DATE, for the DNA typing results.

The disposition of the evidence and the results of other requested examinations are the subject of another report.

8.6.2.1 The reported value for the combined paternity index will be truncated to 2 significant figures.

8.6.2.2 The Probability of Paternity percentage (%) will be truncated at 4 places after the decimal point.

8.7 Incorporation of a Mutation Calculation into a Kinship Statistical Analysis

The reported values for the final calculations will be truncated to 2 significant figures.

8.7.1 When the possibility of a mutation is included in the statistical calculation, two sets of statistical calculations will be reported – one with a mutation incorporated and one with the locus excluded – each with the applicable assumption stated clearly.

EXAMPLE: Assuming a mutation occurred at the D13S317 locus [(allele 11 mutated to allele 10)], the following Combined Paternity Index (CPI) and Probability of Paternity, using a prior probability of 0.5, were calculated for the following populations at the PowerPlex® Fusion loci:...

AND

Assuming an undetected allele exists at the D13S317 locus for the SAMPLE, the following Combined Paternity Index (CPI)…

NOTE: These assumptions will be placed into the applicable wording based upon the type of statistical calculation conducted, (e.g., sibling statistics, reverse parentage statistics, etc.) and may be edited grammatically, as necessary.

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8.8 Incorporation of a Y-STR Haplotype Statistic into an Autosomal Kinship Statistical Analysis

The SAMPLE from ALLEGED FATHER (Item #), the SAMPLE from MOTHER (Item #), and the SAMPLE from CHILD (Item #) were previously analyzed at the PowerPlex® Fusion loci and addressed in the Certificate of Analysis dated DATE. The SAMPLE from ALLEGED FATHER and the SAMPLE from CHILD were also previously analyzed at the AmpFℓSTR™ Yfiler™ loci and addressed in the Certificate of Analysis dated DATE. Based upon a review of these typing results, ALLEGED FATHER cannot be eliminated as the biological parent (father) of CHILD.

The following Combined Paternity Index (CPI) and Probability of Paternity, using a prior probability of 0.5, were calculated for the following populations at the PowerPlex® Fusion and AmpFℓSTR™ Yfiler™ loci:…

NOTE: This wording will be incorporated into the applicable wording based upon the type of statistical calculation conducted, (e.g., sibling statistics, reverse parentage statistics, etc.) and may be edited grammatically or as necessary to apply to each individual case.

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