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.

NOTE: 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.

Appropriate parties will be cc'd, as applicable.

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:

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.

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 STATE/Federal DNA Data Bank found it to be consistent with the following individual:

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 STATE/Federal DNA Data Bank found it to be consistent with the DNA profile developed from the EVIDENCE in AGENCY CASE #. 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. 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).

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.

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.

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.

5.1.3.2 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.

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 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 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 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.

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:

_____ 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)

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.

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.

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.

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

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).

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 (note exception below), and intimate DNA samples with DNA types different from the assumed known, but of no value.

6.5.1 If a sperm or non-sperm fraction is suitable for comparison and is included in the table, the other fraction MUST be included in the table as well, regardless of the value of that fraction. This may affect which reference samples are charted. In the example of a non-sperm fraction with no types different from the victim now being charted, the victim reference sample should also be charted.

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.

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.

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:

- 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.

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)

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)

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]

A Y-chromosome DNA mixture profile was developed from the stain on the inside crotch area of the underpants. Assuming this profile is a mixture of ASSUMED KNOWN and one additional contributor…. [PERSON is eliminated/cannot be eliminated, nor can any of his patrilineally related male relatives, as the additional contributor].

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:

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.

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.

Assuming this profile is a mixture of a major contributor and minor contributor(s), PERSON is eliminated as a major contributor.

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.

Assuming this profile is a mixture of a (one) major contributor and a (one) minor contributor, PERSON cannot be eliminated as a minor contributor, nor can any of his patrilineally related male relatives.

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:

7.10.1 Paternity Cases

7.10.1.1 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. 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.

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.

7.10.3 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.

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.

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 figures.

The Y-chromosome DNA profile developed from EVIDENCE 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.

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.

8.2 Missing Person Cases

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.

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.

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.

8.4 Paternity Index and Probability of Paternity

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 PowerPlex® 16 Fusion 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 If a paternity calculation is being conducted in relation to a Body Identification case, the following statement will be added to the Certificate of Analysis:

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

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

8.4.4 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.

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 (CSI) and Combined Half-Sibling (CHSI) indices were calculated for the following populations at the PowerPlex® Fusion loci:

Caucasian	CSI = XXXX	CHSI = XXXX
African American	CSI = XXXX	CHSI = XXXX
Hispanic	CSI = XXXX	CHSI = 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 Combined Half-Sibling Index is a likelihood ratio that expresses the odds that the donor of the EVIDENCE and REFERENCE share one common biological parent, 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 one common biological parent, rather than unrelated.

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

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.

Refer to Appendix 1 in the Certificate of Analysis dated DATE, for the PowerPlex® Fusion 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 (CSI) and Combined Half-Sibling (CHSI) indices were calculated for the following populations at the PowerPlex® Fusion loci:

Caucasian	CSI = 0.00076	CHSI = 0.42
African American	CSI = 0.00021	CHSI = 0.14
Hispanic	CSI = 0.00048	CHSI = 0.29

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

Refer to Appendix 1in the Certificate of Analysis dated DATE, for the PowerPlex® Fusion 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

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:

It is XXXX times more likely to observe the DNA profile developed from the EVIDENCE at the PowerPlex® 16 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® 16 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® 16 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 PowerPlex® 16 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/ Grandparent Available for Testing

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® 16 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® 16 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.

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.

Refer to Appendix 1 in the Certificate of Analysis dated DATE, for the PowerPlex® 16 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.

8.6.2.3 Adjust the wording, as necessary for Grandparent cases.