Procedure for Autosomal DNA STR Interpretation

1.0 Purpose - The purpose of this document is to provide guidelines for the interpretation of autosomal DNA results.

2.0 Scope - This document applies to qualified DNA Forensic Scientists and trainees within the Forensic Biology Section.

3.0 Definitions

- **3:1 Peak Height to Noise Ratio:** As a general rule, the Peak Height to Noise (background) ratio should be 3:1. In other words, the Peak Height should be at least 3 times greater than the average background for a peak to be called.
- **Activity:** For casework, a peak that has a maximum height < 75 RFU. For Database, a peak less than the analytical threshold (between 100 and 175 RFU, see applicable DNA Database Procedures).
- **Allele:** An alternative form of a gene; allele designation is used to designate a specific size fragment of DNA for a specific locus in STR analysis.
- **Allelic Dropout:** An occurrence where one or more alleles from an individual's DNA profile fail(s) to amplify during PCR and as a result is(are) not detected in the profile. Allelic dropout may be detected by severe imbalance of loci where the smaller fragments are observed and the larger fragments are not observed and/or observance of activity as defined above.
- **Analytical Threshold:** The minimum height (RFU) requirement at and above which detected peaks may be reliably distinguished from background noise; peaks above this threshold are generally not considered noise and are either artifacts or true alleles.
- **Artifact:** Non-allelic byproducts of PCR technology (i.e., stutter, etc), anomalies which occur during capillary electrophoresis (e.g., pull-up, spike, etc), or byproducts of primer synthesis (i.e., dye blob, etc).
- **Cannot Be Excluded:** In a mixed DNA sample, a person cannot be excluded if the individuals' entire profile is present in the mixture or the individual's profile cannot be scientifically excluded from the mixture.
- **Combined Probability of Exclusion (CPE):** The probability that a random person (unrelated individual) would be excluded as a contributor to the observed DNA mixture.
- **Combined Probability of Inclusion (CPI):** The probability that a random person (unrelated individual) would be included as a contributor to the observed DNA mixture.
- **Composite Profile:** A DNA profile generated by combining typing results from different loci obtained from multiple injections of the same amplified sample and/or multiple amplifications of the same DNA extract. When separate extracts from different locations on a given evidentiary item are combined prior to amplification, the resultant DNA profile is not considered a composite profile.
- **Deconvolution:** Separation of contributors to a mixed DNA profile based on quantitative peak height information and underlying assumptions.
- **Distinguishable Mixture:** A DNA mixture in which relative peak height ratios allow deconvolution of the profiles of major/minor contributors.
- **DNA Profile:** The combination of genotypes obtained from DNA analysis testing of multiple loci.
- **Exclusion:** A conclusion reached after comparing the DNA profile of a known sample to the DNA profile of an evidentiary item and the individual in question is not a potential contributor.
- **Full Profile:** A DNA profile that exhibits genotypic information at each locus tested and there is no evidence of allelic dropout, degradation, or preferential amplification.
- **Inclusion:** A conclusion reached after comparing the DNA profile of a known sample to the DNA profile of an evidentiary item and the DNA profile of the individual in question is a potential contributor.
- **Injection:** When a DNA sample is electrokinetically introduced into a capillary for electrophoretic separation.

- **Inhibition:** The total or partial suppression of the PCR process that would result in partial or no DNA profile being obtained.
- **Intimate Sample:** A sample collected from a person's body or an object collected from a person that has made close physical contact with that person. There is an expectation that the person's DNA profile from whom the sample or object was collected may be observed when analyzing that sample or object.
- **Locus (plural=Loci):** The chromosomal location or location of a gene or DNA marker.
- **Match:** DNA profiles are considered to match if their patterns are the same after taking into consideration the properties of the substrate tested and limitations of the specific techniques used.
- **Microvariant:** An allele that varies by less than the consensus repeat unit and is not defined by a ladder allele. Microvariants are observed in-between the ladder alleles for a specific locus.
- **Mixture:** A DNA typing result originating from more than one individual. **NOTE**: If a DNA profile is observed to have more than two peaks at more than one locus, then there is a high possibility that there is a mixture of two or more individual's DNA profiles. If three peaks are observed at only one locus, then there may not be a mixture; the individual contributor may have a triallelic pattern at that locus. Both unknown sample and known sample shall express the triallelic pattern in order for a MATCH to be determined.
- **Noise:** Background signal detected by a data collection instrument.
- **Non-Match:** Assuming a single source from a forensic sample, two DNA profiles are considered to be a non-match if there is a difference of one allele after taking into consideration the circumstances of collection and preparation of samples and knowledge of the properties of the substrate tested and limitations of the specific techniques used.
- **Off-Ladder Allele:** An allele observed outside the region covered by the allelic ladder at a given locus.
- **Overblown/Off-Scale Data:** the result of excess DNA present in an electrophoresed sample, typically visualized by excessive artifacts as a result of peak heights consistently greater than 6000 RFUs.
- **Partial DNA Profile:** A DNA profile that does not produce DNA typing results for all loci tested.
- **Partially Predominant DNA Profile:** A Predominant DNA Profile (see definition below) where one or more loci do not exhibit predominance.
- **Peak:** A well defined point on an electropherogram that is on-ladder. See "Microvariant" and "Off-Ladder Alleles" for exceptions to the "on-ladder" requirement.
- **Peak Height/(Signal) to Noise Ratio:** An assessment used to establish an analytical threshold to distinguish allelic peaks (signal) from background/instrument noise.
- **Predominant Alleles/Predominance:** Given a mixture of two or more contributors at a specific locus, one or two alleles have an RFU value greater than approximately 50 % of the remaining alleles at that locus and a single source may be readily inferred by the observed data.
- **Predominant DNA Profile:** Given a mixture or two or more contributors, one or two alleles at every locus typed has an RFU value greater than 50 % of all other alleles and a single source may be readily inferred by the observed data.
- **Pull-up:** A signal from an allele labeled with one dye-set may show up as a peak or Off-Ladder Allele in another dye-set.
- **Run:** Each set of 16 samples that are injected and separated electrophoretically on the Capillary Electrophoresis Unit (ABI 3130XL or equivalent).
- **Random Match Probability (RMP):** The chance that a randomly selected unrelated individual from a population will have an identical STR profile to that obtained from a forensic sample. Due to genetic variations between ethnic groups, each group has different population databases and different RMP results.
- **Shoulder and Tail:** A "Shoulder" and "Tail" is an elongated or raised area to the immediate left and right of a main peak but is not separated from the main peak.
- **Spike/Electrical Spike:** An artifact believed to be caused by a spike in the current within a capillary that causes a sharp increase in signal. This artifact lacks the defined morphology of a peak.
- **Split peaks:** A split peak is where one allele is represented by two peaks. Lack of full "nucleotide A" addition may be observed when the amount of input DNA is greater than the recommended protocol. In

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this case, more time is needed for Taq Polymerase to add the "A" nucleotide to all molecules. Amplification of too much input DNA also results in off-scale/overblown data (saturation of signal) and may be manifested as split peaks.

- **Single Source Profile:** A combination of genotypes obtained from STR DNA testing that could only originate from a single individual. A sample may be considered to consist of a single contributor when no more than two alleles are observed at each locus. All loci are to be evaluated in making this decision.
  If three alleles are observed at one locus, then there may not be a mixture; the individual contributor may have a triallelic pattern at that locus.
- **Stochastic Effects:** The observation of intra-locus peak imbalance and/or allele drop-out resulting from random, disproportionate amplification of alleles in low-quantity template samples.
- **Stutter:** An artifact of PCR amplification that is typically one repeat unit less than the corresponding main allele peak resulting from strand slippage during amplification.
- **Triallelic Pattern:** Three peaks observed at a single locus and not the result of a mixture. These peaks may or may not be of equal intensity.
- **Unincorporated Dye:** Unincorporated dye (i.e., dye-blobs) may be observed in an electropherogram and are distinct morphologically from a labeled DNA fragment. A dye-blob does not exhibit the typical sharp, distinct peak that is produced by actual alleles and is observed as a wider, thicker peak and may be lacking the sharply defined slope to the apex of a peak.
- **Uninterpretable Profile:** A DNA typing result which results from an insufficient quantity of DNA, testing of degraded DNA, or preferential amplification. These type profiles provide insufficient data and shall not be used for comparison purposes.

4.0 Equipment, Materials and Reagents - N/A

5.0 Procedure

5.1 Introduction - The guidelines outlined herein are based upon this Laboratory's validation studies, review of literature, and over 15 years of forensic DNA casework experience. These guidelines are to be used in conjunction with the Forensic Scientist's training and experience to provide a solid scientific interpretation of the STR results.

5.2 Interpretation of Samples, Controls, and Allelic Ladders

5.2.1 Examining of the Electropherogram of Samples

Visually inspect the questioned samples and the known samples. Assess the quality of the peaks including RFU values and determine if artifacts are present. (Refer to the Forensic Biology Section Procedure for GeneMapper ID.)

If the question sample(s) contains more than two peaks at the same locus, then the results *may* indicate a mixture. NOTE: If three peaks are observed at only one locus, then there may not be a mixture; the individual contributor may have a triallelic pattern at that locus (see Procedure for GeneMapper ID and Procedure for DNA Database).

Failure of any locus (loci) to amplify for a multiplex STR system shall not preclude Forensic Scientists from reporting those loci that are present. For Database samples, the profile shall contain the 13 core loci for upload into CODIS.

Casework samples that are overblown shall be re-amplified using a lower DNA template or re-injected at a lower injection time, depending on the overall quality of the electropherogram.

Activity shall be used for qualitative data interpretation (including, but not limited to, evidence for a

mixture within a given sample or exclusions). Activity below threshold shall be used for exclusion purposes only. The Forensic Scientist/Database Analyst shall take into consideration possible artifacts, high noise, and general quality of data when making the decision to use data below threshold for this purpose.

It is permissible to combine results from different injections, dilutions and amplifications of the same sample when determining a final DNA profile. In order to call predominance at a locus, all results shall show the same predominance.

5.2.2 Examination of the Electropherogram of the Negative Controls

If any peaks are detected in the amplification negative control or the reagent control samples, then contamination *may* have occurred and the samples may not be interpreted at the locus or loci in question. If possible, the sample(s) associated with the negative controls shall be re-analyzed (i.e., re-injected, re-amplified, or re-extracted). If it is not possible to reanalyze the data because of sample depletion, the Forensic Scientist/Database Analyst may proceed to interpret the results of the samples.

If activity is detected in the negative control at a single locus or multiple loci, the Forensic Scientist/Database Analyst shall determine the effects of this activity when interpreting the corresponding samples. The controls and/or sample(s) associated with the negative controls may be re-analyzed (i.e., re-injected, re-amplified, or re-extracted).

Artifact(s) observed in the negative samples does not require the samples to be re-injected. Those artifacts shall be documented in the notes.

5.2.3 Examination of the Electropherogram of the Positive Amplification Control

The positive amplification control must have peaks that are in the proper location relative to the allelic markers. If these characteristic peaks are not in their correct position or are not present (too weak to interpret), that particular locus shall be considered inconclusive for all samples and shall be successfully re-injected, re-run, or re-amplified and analyzed before that locus may be used for analysis.

5.2.4 Examination of the Electropherogram of the Allelic Ladder(s)

Allelic ladder shall be analyzed as specified in the Forensic Biology Section Procedure for GeneMapper ID.

5.3 Artifacts - The PCR process produces artifacts that are known and well characterized. All by-products of PCR and/or capillary electrophoresis shall be labeled on electropherograms as "artifact" in the case notes.

5.3.1 Stutter

5.3.1.1 The STR results shall not be considered inconclusive if stutter peaks are present in single source samples.

5.3.1.2 The GeneMapper® ID software from ABI contains designated cutoff for peaks in stutter positions and shall be used for designating stutter. Based upon the scientist's training and experience, a minor peak in the stutter position that is called by the GeneMapper® ID software may be disregarded as stutter if the peak in question is 1) not in a mixed sample and 2) when compared to the predominant sister allele, it is close to the percent stutter

cutoff for that particular locus.

5.3.2 Pull up - Generally, pull-up can be noted when all the alleles are overlapped using the software and the pull-up is observed as a relatively small peak located directly under the larger peak. Scientists shall be aware of this phenomenon and use the computer software to aid in discerning actual alleles from pull-up.

5.3.3 Unincorporated Dye - Scientists shall not call dye-blobs as an actual allele. Dye-blobs shall not be considered for interpretation.

5.3.4 Shoulder and Tail - Shoulders and tails do not prevent the scientist from assigning the specific peak an allelic value.

5.3.5 n+4 peaks - An artifact peak may appear in the n+4 position. When an n+4 peak is suspected in casework, this shall be documented on the allele call sheets.

5.4 Amelogenin Results - Under rare circumstances a male individual may not display the Y chromosome of this test; therefore, scientists shall not interpret an X as originating from a female.

5.5 Balance - Samples shall be examined for balance at each locus. For single source casework and database samples exhibiting heterozygote imbalance ($< 50\%$), the sample shall be rerun if the imbalance does not allow for proper interpretation by the scientist.

5.6 Comparison of Profiles

5.6.1 The comparison and interpretation of DNA profiles by a qualified scientist is a qualitative judgment based on review of all information pertinent to the tests performed.

5.6.2 Matches and non-matches shall be determined by careful, objective, qualitative, and quantitative evaluation of the entire profile produced by the various loci tested. It is scientifically acceptable for a match or non-match to be determined for a case when one or more of the loci yield inconclusive results. A match shall be based only on those loci which yield conclusive results.

5.6.3 Match/consistent with statements shall only be used when the standard's, employee's, vendor's, or visitor's full locus profile is observed in a minimum of two loci. Samples which fail to meet these criteria shall be written per **5.7.10** of these guidelines.

5.7 Conclusions: Included below is a list of statements that shall be used when reporting the results of DNA analysis. The results statements shall reflect only the work that is performed. Portions of the statements listed under the reporting guidelines may be omitted to address testing actually performed. Any deviations from these statements require the approval of the DNA Technical Leader prior to the case being released for technical review.   Approval shall be documented in writing. Scientists shall provide the DNA Technical Leader with the requested wording. The DNA Technical Leader shall then reply with an approval or denial of the request in writing. This correspondence shall be placed in the FA Case Record Object Repository. In addition, a verification review shall be completed by the DNA Technical Leader when a result of un-interpretable profile is reported. If results are only obtained for Amelogenin, an un-interpretable profile shall be reported, but no verification review is required.

5.7.1 Single Source Profiles - Comparisons with a Full Unknown Profile:

Comparison between a known sample and a questioned sample (full profile) originating from one person:

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- **Match Statement:** The following statement shall be used when the DNA profile from a known matches the DNA profile of a questioned sample: *"The DNA profile obtained from _____ (Item _) **MATCHES** the DNA profile obtained from ____ (Item_)."*

- **Non-Match Statement:** The following statement shall be used when the DNA profile from a known sample does not match the DNA profile of a questioned sample, (or additional samples): *"An unknown male DNA profile obtained from _____ (Item_) **DOES NOT MATCH** the DNA profile obtained from _____ (Item_) (or the DNA profile obtained from _____ (Item_)."*

- **Match and Non-Match Statement:** The following statement shall be used when the DNA profile from more than one known sample is compared to a questioned sample where matches and non-matches occur: *"The DNA profile obtained from _____ (Item_) **MATCHES** the DNA profile obtained from _____ (Item_) and **DOES NOT MATCH** the DNA profile(s) obtained from _____ (Item(s)_)."*

- **Statistics**: Any statistical data generated from these scenarios shall be calculated using Random Match Probability (RMP) as provided in the Forensic Biology Section Procedure for Statistical Interpretation. The following statistical statement shall be used: *"The probability of randomly selecting an unrelated individual with a DNA profile that matches the DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."*

5.7.2 Single Source Profiles: Comparisons with a Partial Unknown Profile: Comparison between a known sample and a questioned sample (partial profile) originating from one person:

Note: Population data shall be generated prior to determining the MATCH or CONSISTENT WITH statement (if necessary).This data shall be compared to the current world census according to the U.S. Census Bureau World Population Clock (http://www.census.gov/main/www/popclock.html). If all four population groups exceed the world's population at the time the statistics are generated, the word MATCH shall be used. If one or more population groups are less than the world population at the time the statistics are generated, the phrase CONSISTENT WITH shall be used.

- **Match:** The following statements shall be used when the DNA profile from a known sample matches the partial DNA profile of a questioned sample (additional "non-match statements" may be added as necessary): *"The partial DNA profile obtained from _____ (Item_) **MATCHES** the DNA profile obtained from _____ (Item_)."* OR *"The partial DNA profile obtained from _____ (Item_) **IS CONSISTENT WITH** the DNA profile obtained from _____ (Item_)." (Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used).*

- **Non-Match:** The following statement shall be used when the DNA profile from a known sample does not match the partial DNA profile of a questioned sample (additional "non-match statements" may be added as necessary): *"A partial unknown male DNA profile was obtained from _____ (Item) that **DOES NOT MATCH** the DNA profile obtained from _____ (Item_)."*

- **Match and Non-Match Statement:** The following statement shall be used when more than one known sample is compared to the partial DNA profile from a questioned sample where

matches and non-matches occur (additional "non-match statements" may be added as necessary): *"The partial DNA profile obtained from _____ (Item)* **MATCHES/IS CONSISTENT WITH** *the DNA profile obtained from _____ (Item_) and* **DOES NOT MATCH** *the DNA profile obtained from _____ (Item_)."*

- Note: If the phrase CONSISTENT WITH is used, add the following statement: *(Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used).*

- **Statistics:** Any statistical data generated from these scenarios shall be calculated using Random Match Probability (RMP) as provided in the Forensic Biology Section Procedure for Statistical Interpretation. If all databases are above 1 trillion, Statement "A" shall be used. If one or more database is below 1 trillion, Statement "B" shall be used.

    Statement A: *"The probability of randomly selecting an unrelated individual with a DNA profile that matches the partial DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."*

    Or

    Statement B: *" The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with the partial DNA profile obtained from the _____ is approximately 1 in _____ in the NC Black population, 1 in _____ in the NC Hispanic population, 1 in _____ in the NC Lumbee Indian and 1 in _____ in the NC Caucasian population."*

5.7.3 Single Source Profiles: Comparisons with an Intimate Object: On occasion, body fluid scientists may obtain positive results for semen/sperm or saliva on intimate objects such as vaginal swabs, rectal swabs or panties. In the event that this DNA profile matches the respective "owner," the following statements shall be used:

5.7.3.1 Full profile:

"The DNA profile obtained from the _____ (Item_) is no different from that of the victim/subject (Item_) and **DOES NOT MATCH** *the DNA profile obtained from _____ (Item_)."*

- **Statistics**: Statistical data generated from this scenario shall be calculated using Random Match Probability (RMP) as provided in the Forensic Biology Section Procedure for Statistical Interpretation. The following statistical statement shall be used: *"The probability of randomly selecting an unrelated individual with a DNA profile that matches the DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."*

5.7.3.2 Partial profile:

"The partial DNA profile obtained from the _____ (Item_) is no different from that of the victim/subject (Item_) and **DOES NOT MATCH** *the DNA profile obtained from _____ (Item_)."*

- **Statistics:** Statistical data generated from this scenario shall be calculated using Random Match Probability (RMP) as provided in the Forensic Biology Section Procedure for Statistical Interpretation. If all databases are above 1 trillion, Statement "A" shall be used. If one or more database is below 1 trillion, Statement "B" shall be used.

  Statement A: "The probability of randomly selecting an unrelated individual with a DNA profile that matches the partial DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."

  Or

  Statement B: " The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with the partial DNA profile obtained from the _____ is approximately 1 in _____ in the NC Black population, 1 in _____ in the NC Hispanic population, 1 in _____ in the NC Lumbee Indian and 1 in _____ in the NC Caucasian population."

5.7.4 Mixture Profiles: Comparisons with a Full Profile Mixture (no evidence of allelic dropout):
Comparison between a known sample and a questioned sample (full profiles) originating from more than one person:

5.7.4.1 Predominant Profile

- **Match to Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a predominant and minor component(s) and the known sample matches the predominant profile: *"The DNA profile obtained from _____ (Item_) is __INDICATIVE OF A MIXTURE__ (a DNA typing result originating from more than one individual). The predominant profile __MATCHES__ the DNA profile obtained from _____ (Item_)."*

- **Non- Match to Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a predominant and minor component(s) and the known sample does not match the predominant profile: *"The DNA profile obtained from _____ (Item_) is __INDICATIVE OF A MIXTURE__. (a DNA typing result originating from more than one individual). The predominant profile DOES NOT MATCH the DNA profile obtained from ____ (Item _) and is from an unknown male individual."*

- **Cannot Exclude from Mixture Profile:**   The following statement shall be added to the MATCH and NON-MATCH statements above, if appropriate, when comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample cannot be excluded.   This statement may be extended to include other inclusions.   *"The DNA profile obtained from _____ (Item_) cannot be excluded as a contributor to the mixture."*

- **Excluded from Mixture Profile:** The following statement shall be added to the MATCH and NON-MATCH statements above, if appropriate, when comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample can be excluded. This statement may be extended to include other

exclusions. *"The DNA profile obtained from _____ (Item_) is excluded as a contributor to the mixture."*

- **Statistics**: Any statistical data generated from these scenarios shall be calculated in the following manner: If predominance exists, then Random Match Probability (RMP) as provided in the Forensic Biology Section Procedure for Statistical Interpretation shall be used and Statement "A" shall be used. If the known profile "cannot be excluded", then Combined Probability of Exclusion (CPE) as provided in the Procedure for Statistical Interpretation shall be used and Statement "B" shall be used.

  Statement A: "The probability of randomly selecting an unrelated individual with a DNA profile that matches the predominant DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."

  Or

  Statement B: "The chance of randomly selecting an unrelated individual who would be expected to be included for the observed DNA mixture profile is approximately:

  N.C. Caucasian: 1 in ___
  N.C. Black: 1 in ___
  N.C. Hispanic: 1 in ___
  N.C. Lumbee Indian: 1 in ___."

5.7.4.2 Partially Predominant Profile

NOTE: Population data shall be generated prior to determining the MATCH or CONSISTENT WITH statement (if necessary).This data shall be compared to the current world census according to the U.S. Census Bureau World Population Clock (http://www.census.gov/main/www/popclock.html). If all four population groups exceed the world's population at the time the statistics are generated, the word MATCH shall be used. If one or more population groups are less than the world population at the time the statistics are generated, the phrase CONSISTENT WITH shall be used.

- **Matches to/Consistent with Partially Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a partially predominant and minor component and the known sample matches the partially predominant profile: *"The DNA profile obtained from _____ (Item_) is **INDICATIVE OF A MIXTURE** (a DNA typing result originating from more than one individual). The partially predominant profile **MATCHES/IS CONSISTENT WITH** the DNA profile obtained from _____ (Item_)."*

- Note: If the phrase CONSISTENT WITH is used, add the following statement: *(Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used).*

- **Non-Match to Partially Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a partially predominant and minor component and the known sample does not match the partially predominant profile: *"The DNA profile obtained from _____ (Item_) is **INDICATIVE OF A MIXTURE** (a*

DNA typing result originating from more than one individual). The partially predominant profile DOES NOT MATCH the DNA profile obtained from _____ (Item_) and is from an unknown male individual."

- **Cannot Exclude from Mixture Profile:** The following statement shall be added to the MATCH and NON-MATCH statements above, if appropriate, when additional comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample cannot be excluded. This statement may be extended to include other inclusions. *"The DNA profile obtained from _____ (Item_) cannot be excluded as a contributor to the mixture."*

- **Excluded from Mixture Profile:** The following statement shall be added to the MATCH and NON-MATCH statements above, if appropriate, when additional comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample can be excluded. This statement may be extended to include other exclusions. *"The DNA profile obtained from _____ (Item_) is excluded as a contributor to the mixture."*

- **Statistics**: Any statistical data generated from these scenarios shall be calculated in the following manner: If partial predominance exists, at 10 or more core loci, RMP as provided in the Forensic Biology Section Procedure for Statistical Interpretation shall be used and if all four databases are above 1 trillion, then Statement "A" shall be used. If one or more databases are below 1 trillion, then Statement "B" shall be used. If the statement "Cannot Be Excluded" is used, or partial predominance is observed at less than 10 core loci, then CPE as provided in the Forensic Biology Section Procedure for Statistical Interpretation shall be used and Statement "C" shall be used.

  Statement A: "The probability of randomly selecting an unrelated individual with a DNA profile that matches the partially predominant DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."

  Or

  Statement B: " The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with the partially predominant DNA profile obtained from the ____ is approximately 1 in _____ in the NC Black population, 1 in _____ in the NC Hispanic population, 1 in _____ in the NC Lumbee Indian and 1 in ____ in the NC Caucasian population."

  Or

  Statement C: "The chance of randomly selecting an unrelated individual who would be expected to be included for the observed DNA mixture profile is approximately:

  N.C. Caucasian: 1 in ___
  N.C. Black: 1 in ___
  N.C. Hispanic: 1 in ___
  N.C. Lumbee Indian: 1 in ___."

5.7.4.3 No Predominant Profile

- **Primary Statement**: *"The DNA profile obtained from _____ (Item_) is* **_INDICATIVE OF A MIXTURE_** *(a DNA typing result originating from more than one individual) which does not contain a predominant or partially predominant profile."*

- **Cannot Exclude from Mixture Profile:** This statement is added to the primary statement above when comparisons are made to the mixture and the known sample cannot be excluded. This statement may be extended to include other inclusions. *"The DNA profile obtained from _____ (Item_) cannot be excluded as a contributor to the mixture."*

- **Excluded from Mixture Profile:** This statement shall be added to the primary statement above when additional comparisons are made to the mixture and the known sample can be excluded. This statement may be extended to include other exclusions: *"The DNA profile obtained from _____ (Item_) is excluded as a contributor to the mixture."*

- **Statistics**: Any statistical data generated from these scenarios shall be calculated using CPE as provided in the Forensic Biology Section Procedure for Statistical Interpretation using the statement below:

  "The chance of randomly selecting an unrelated individual who would be expected to be included for the observed DNA mixture profile is approximately:

  N.C. Caucasian: 1 in ___
  N.C. Black: 1 in ___
  N.C. Hispanic: 1 in ___
  N.C. Lumbee Indian: 1 in ___."

5.7.5 Mixture Profiles: Comparisons with a Partial Profile Mixture (evidence of allelic dropout): Comparison between a known sample and a questioned sample (partial profile) originating from more than one person.

Once a mixture is determined to be a partial profile, the scientist shall review the resulting profile to determine predominance, partial predominance or no-dominance. If the resulting profile is predominant, statements in **5.7.5.1** shall be used. If the resulting profile displays partial predominance, statements in **5.7.5.2** shall be used. If the resulting profile displays no-dominance, statements in **5.7.5.3** shall be used.

NOTE: Population data shall be generated prior to determining the MATCH or CONSISTENT WITH statement (if necessary).This data shall be compared to the current world census according to the U.S. Census Bureau World Population Clock (http://www.census.gov/main/www/popclock.html). If all four population groups exceed the world's population at the time the statistics are generated, the word MATCH shall be used. If one or more population groups are less than the world population at the time the statistics are generated, the phrase CONSISTENT WITH shall be used.

5.7.5.1 Predominant Profile

- **Match to Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a predominant and minor component and the known sample matches the predominant profile: *"The partial DNA profile obtained from _____ (Item_) is* **_INDICATIVE OF A MIXTURE_** *(a DNA typing result*

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*originating from more than one individual). The predominant profile **MATCHES/IS CONSISTENT WITH** the DNA profile obtained from _____ (Item_)."*

- Note: If the phrase **CONSISTENT WITH** is used, add the following statement: *(Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used).*

- **Non-Match to Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a predominant and minor component and the known sample does not match the predominant profile: *"The partial DNA profile obtained from _____ (Item_) is **INDICATIVE OF A MIXTURE** (a DNA typing result originating from more than one individual). The predominant profile is from an unknown male individual."*

- **Cannot Exclude from Mixture Profile:** The following statement shall be added to the MATCH and NON-MATCH statements above, if appropriate, when additional comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample cannot be excluded. This statement may be extended to include other inclusions. *"The DNA profile obtained from _____ (Item_) cannot be excluded as a contributor to the mixture."*

- **Excluded from Minor Profile:** The following statement shall be added to the above MATCH and NON-MATCH statements above, if appropriate, when additional comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample may be excluded. This statement can be extended to include other exclusions. *"The DNA profile obtained from _____ (Item _) is excluded as a contributor to the mixture."*

- **Statistics**: Any statistical data generated from these scenarios shall be calculated in the following manner: If predominance exists, RMP as provided in the Forensic Biology Section Procedure for Statistical Interpretation shall be used and if all four databases are above 1 trillion, then Statement "A" shall be used. If one or more databases are below 1 trillion, then Statement "B" shall be used. If the statement "Cannot Be Excluded" is used, then CPE as provided in the Forensic Biology Section Procedure for Statistical Interpretation shall be used and Statement "C" shall be used.

  Statement A: "The probability of randomly selecting an unrelated individual with a DNA profile that matches the predominant DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."

  Or

  Statement B: " The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with the predominant DNA profile obtained from the ____ is approximately 1 in _____ in the NC Black population, 1 in _____ in the NC Hispanic population, 1 in _____ in the NC Lumbee Indian and 1 in ____ in the NC Caucasian population."

  Or

Statement C: *"The chance of randomly selecting an unrelated individual who would be expected to be included for the observed DNA mixture profile is approximately:*

N.C. Caucasian: 1 in ___
N.C. Black: 1 in ___
N.C. Hispanic: 1 in ___
N.C. Lumbee Indian: 1 in ___."

5.7.5.2 Partially Predominant Profile

NOTE: Population data shall be generated prior to determining the MATCH or CONSISTENT WITH statement (if necessary). This data shall be compared to the current world census according to the U.S. Census Bureau World Population Clock (http://www.census.gov/main/www/popclockworld.html). If all four population groups exceed the world's population at the time the statistics are generated, the word MATCH shall be used. If one or more population groups are less than the world population at the time the statistics are generated, the phrase CONSISTENT WITH shall be used.

- **Match to Partially Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a partially predominant and minor component and the known sample matches the partial predominant profile: *"The partial DNA profile obtained from _____ (Item_) is* **INDICATIVE OF A MIXTURE** *(a DNA typing result originating from more than one individual). The partially predominant profile* **MATCHES/IS CONSISTENT WITH** *the DNA profile obtained from _____ (Item)."*

- Note: If the phrase **CONSISTENT WITH** is used, add the following statement: *(Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used).*

- **Non-Match to Partially Predominant Profile:** The following statement shall be used when the questioned sample produces a mixture of a partial predominant and minor component and the known sample does not match the partial predominant profile: *"The partial DNA profile obtained from _____ (Item) is* **INDICATIVE OF A MIXTURE** *(a DNA typing result originating from more than one individual). The partially predominant profile did not match the DNA profile obtained from _____ (Item_) and is from an unknown male individual."*

- **Cannot Exclude from Mixture Profile:** The following statement shall be added to the MATCH and NON-MATCH statements above, if appropriate, when additional comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample cannot be excluded. This statement may be extended to include other inclusions. *"The DNA profile obtained from _____ (Item_) cannot be excluded as a contributor to the mixture."*

- **Excluded from Mixture Profile:** The following statement shall be added to the above MATCH and NON-MATCH statements above, if appropriate, when additional comparisons are made to the mixture as a whole or to the minor component of the mixture and the known sample can be excluded. This statement may be extended to include other exclusions: *"The DNA profile obtained from _____ (Item_) is excluded as a contributor to the mixture."*

- **Statistics**: Any statistical data generated from these scenarios shall be calculated in the following manner: If partial predominance exists, at 10 or more core loci, RMP as provided in the Forensic Biology Section Procedure for Statistical Interpretation shall be used. If all four databases are above 1 trillion, then Statement "A" shall be used. If one or more databases are below 1 trillion, then Statement "B" shall be used. If the statement "Cannot Be Excluded" is used or partial predominance exists at less than 10 core loci, then CPE as provided in the Forensic Biology Section Procedure for Statistical Interpretation shall be used and Statement "C" shall be used.

    Statement A: *"The probability of randomly selecting an unrelated individual with a DNA profile that matches the partially predominant DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."*

    Or

    Statement B: *"The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with the partially predominant DNA profile obtained from the _____ is approximately 1 in _____ in the NC Black population, 1 in _____ in the NC Hispanic population, 1 in _____ in the NC Lumbee Indian and 1 in _____ in the NC Caucasian population."*

    Or

    Statement C: *"The chance of randomly selecting an unrelated individual who would be expected to be included for the observed DNA mixture profile is approximately:*

    N.C. Caucasian: 1 in ___
    N.C. Black: 1 in ___
    N.C. Hispanic: 1 in ___
    N.C. Lumbee Indian: 1 in ___."

5.7.5.3 No Predominant Profile

Primary Statement: *"The partial DNA profile obtained from _____ (Item_) is* **_INDICATIVE OF A MIXTURE_** *(a DNA typing result originating from more than one individual) which does not contain a predominant or partially predominant profile."*

- **Cannot Be Excluded from Mixture Profile:** The following statement shall be added to the primary statement above when comparisons are made to the mixture and the known sample cannot be excluded. This statement may be extended to include other inclusions. *"The DNA profile obtained from _____ (Item_) cannot be excluded as a contributor to the mixture."*

- **Excluded from Mixture Profile:** The following statement shall be added to the primary statement above when additional comparisons are made to the mixture and the known sample can be excluded. This statement may be extended to include other exclusions. *"The DNA profile obtained from _____ (Item_) is excluded as a contributor to the mixture."*

- **Statistics**: Any statistical data generated from these scenarios shall be calculated using

CPE as provided in the Forensic Biology Section Procedure for Statistical Interpretation using the statement below:

As provided in the Forensic Biology Section Procedure for Statistical Interpretation *"The chance of randomly selecting an unrelated individual who would be expected to be included for the observed DNA mixture profile is approximately:*

N.C. Caucasian: 1 in ___
N.C. Black: 1 in ___
N.C. Hispanic: 1 in ___
N.C. Lumbee Indian: 1 in ___."

5.7.6 Interpretation Based on Number of Contributors:

It is acceptable for scientists to qualify their conclusions based on the data observed in the notes. For example, the scientist may preface a mixture statement with "Assuming two contributors" or "Assuming multiple contributors."

5.7.7 Interpretation of Minor Profiles in Mixtures

In the event that a mixture profile with a major and minor profile (two identifiable contributors) is obtained, the Forensic Scientist shall declare the standard as a possible source of the minor contributor if the standard's full heterozygous profile is observed (independent of the major profile) in at least two loci of the minor component of the mixture.

If the above criterion fails to be met, the following interpretation shall be used:

"No conclusion can be rendered as to the contribution of _____ (Item ___) to the minor profile (Item __)."

5.7.8 Inconclusive Comparisons

The following statement shall be used when a comparison between a questioned sample and a known sample fails to give a conclusion as to the contribution of the known sample.

"The DNA profile obtained from _____ (Item_) is consistent with a mixture/single source profile. No conclusion can be rendered as to the contribution of the DNA profile from _____ (Item _) to the profile due to insufficient data to include or exclude."

Or

"The DNA profile obtained from _____ (Item_) is consistent with a mixture/single source profile. Due to the complexity of the sample, the analyst and reviewer were unable to come to a complete agreement as to the interpretation of the profile. As a result, no conclusion can be rendered as to the contribution of the DNA profile from _____ (Item _) to the profile."

5.7.9 Un-interpretable Profiles

The following statement shall be used when the DNA profile is insufficient for comparison purposes.

"No interpretable DNA profile was obtained from _____ (Item_)."(The DNA profile is not of

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sufficient quantity and/or quality for comparison purposes.).

5.7.10 Limited Information Profiles

The following statement shall be used to describe partial DNA profiles which only contain enough information to make statements of exclusion or no conclusion. Amelogenin results shall not be considered when determining the total number of alleles present.

"Examination of _____ (Item_) revealed the presence of __ alleles. Due to the limited amount of information obtained from this profile, it is unsuitable for upload into CODIS and cannot be used for inclusionary purposes. The DNA profile obtained from ___ (Item __) was excluded as being a contributor to this profile. No conclusion can be rendered as to the contribution of the DNA profile obtained from ___ (Item __) to this profile."

5.7.11 No DNA Results

The following statement shall be used when no DNA profile is obtained.

"No DNA profile was obtained from _____ (Item_)."

5.7.12 Employee, Vendor, Visitor and Batched Case Samples Profiles Obtained in Evidence:

5.7.12.1 Single Source Full Profiles

5.7.12.1.1 Match to the DNA Forensic Scientist who worked the case:

*"The DNA profile obtained from _____ (Item_) **MATCHES** to State Crime Laboratory Forensic Scientist _____ who performed the DNA analysis on this item of evidence."*

5.7.12.1.2 Match to a Prior Forensic Scientist or Field Agent involved in the case:

*"The DNA profile from _____ (Item_) **MATCHES** to State Crime Laboratory Forensic Scientist/Agent _____. This scientist/agent performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis."*

5.7.12.1.3 Match to an State Crime Laboratory employee, vendor, or visitor not involved in the case:

*"The DNA profile obtained from _____ (Item_) **MATCHES** to State Crime Laboratory (employee, vendor, visitor) _____. This individual has been present in a Laboratory area within the Forensic Biology Section on at least one occasion."*

5.7.12.1.4 Match to a sample in a batched case:

*"The DNA profile obtained from _____ (Item_) **MATCHES** to State Laboratory item number _____ which was analyzed along with items of evidence in this case."*

- **Statistics for 5.7.12.1.1, 5.7.12.1.2, 5.7.12.1.3 and 5.7.12.1.4:** Statistical

data generated from these scenarios shall be calculated using Random Match Probability (RMP) as provided in the Forensic Biology Section Procedure for Statistical Interpretation. The following statistical statement shall be used: *"The probability of randomly selecting an unrelated individual with a DNA profile that matches the DNA profile obtained from the ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."*

5.7.12.2 Single Source Partial Profiles with Seven or Greater Core Loci Obtained

5.7.12.2.1 Match to/consistent with the DNA Forensic Scientist who worked the case:

"The partial DNA profile obtained from _____ (Item_) **MATCHES /IS CONSISTENT WITH** *State Crime Laboratory Forensic Scientist _____ who performed the DNA analysis on this item of evidence."*

5.7.12.2.2 Match to/consistent with a prior Forensic Scientist/Field Agent involved in the case:

"The partial DNA profile obtained from_____ (Item_) **MATCHES/IS CONSISTENT WITH** *State Crime Laboratory Forensic Scientist/Agent _____. This scientist/agent performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis."*

5.7.12.2.3 Match to/consistent with an State Crime Laboratory employee, vendor, or visitor not involved in the case:

"The partial DNA profile obtained from_____ (Item_) **MATCHES /IS CONSISTENT WITH** *State Crime Laboratory (employee, vendor, visitor) _____. This individual has been present in a Laboratory area within the Forensic Biology Section on at least one occasion."*

5.7.12.2.4 Match to/consistent with a sample in a batched case:

"The DNA profile obtained from _____ (Item_) **MATCHES/IS CONSISTENT WITH** *State Crime Laboratory item number _____ which was analyzed along with items of evidence in this case."*

- If the phrase CONSISTENT WITH is used in these scenarios, add the following statement: *(Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used).*

- **Statistics for 5.7.12.2.1, 5.7.12.2.2, 5.7.12.2.3 and 5.7.12.2.4:** Population data shall be generated prior to determining the MATCH or CONSISTENT WITH statement (if necessary).This data shall be compared to the current world census according to the U.S. Census Bureau World Population Clock (http://www.census.gov/ipc/www/popclockworld.html). If all four population groups exceed the world's population at the time the statistics are generated, the word MATCH shall be used. If one or more population

groups are less than the world population at the time the statistics are generated, the phrase CONSISTENT WITH shall be used.

- Any statistical data generated from these scenarios shall be calculated using Random Match Probability (RMP) as provided in the Forensic Biology Section Procedure for Statistical Interpretation. If all databases are above 1 trillion, Statement "A" shall be used. If one or more database is below 1 trillion, Statement "B" shall be used.

Statement A: "The probability of randomly selecting an unrelated individual with a DNA profile that matches the partial DNA profile obtained from (the) ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."

Or

Statement B: " The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with the partial DNA profile obtained from (the) ____ is approximately 1 in _____ in the NC Black population, 1 in _____ in the NC Hispanic population, 1 in _____ in the NC Lumbee Indian and 1 in ____ in the NC Caucasian population."

5.7.12.3 Single Source Partial Profiles with Less than Seven Core Loci Obtained

When results are obtained at less than seven of the CODIS core loci, the Forensic Scientist shall evaluate data below the callable threshold to determine if a conclusion can be made. After review of all data and consultation with the DNA Technical Leader, one of the following statements shall be used:

5.7.12.3.1 Consistent with the Forensic Scientist who worked the case:

*"The partial DNA profile obtained from _____ (Item_) **IS CONSISTENT WITH** State Crime Laboratory Forensic Scientist _____ who performed the DNA analysis on this item of evidence. (Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used)."*

5.7.12.3.2 Consistent with a prior Forensic Scientist/Field Agent involved in the case:

*"The partial DNA profile obtained from_____ (Item_) **IS CONSISTENT WITH** State Crime Laboratory Forensic Scientist/Agent _____(Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used). This scientist/agent performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis."*

5.7.12.3.3 Consistent with an State Crime Laboratory employee, vendor, or visitor

not involved in the case:

"The partial DNA profile obtained from_____ (Item_) __IS CONSISTENT__ __WITH__ State Crime Laboratory(employee, vendor, visitor) _____(Per Laboratory policy, the term "is consistent with" means that the result of the population data statistics did not exceed the world's population; therefore, the term "match" cannot be used). This individual has been present in a laboratory area within the Forensic Biology Section on at least one occasion."

5.7.12.3.4 Consistent with sample in a batched case:

"The DNA profile obtained from _____ (Item_) __IS CONSISTENT__ __WITH__ State Crime Laboratory item number _____ which was analyzed along with items of evidence in this case. Although the Laboratory has made an association between an item of evidence in this case to another item in a batched case, it is based on limited information and does not necessarily mean that an unwanted transfer of DNA has occurred. In addition, this association should not deter the authorities from submitting additional standards for comparison, if necessary."

5.7.12.4 Mixture Profiles with Full Predominant Profile

5.7.12.4.1 Predominant Match to the DNA Forensic Scientist who worked the case:

"The DNA profile obtained from_____ (Item_) is __INDICATIVE OF A__ __MIXTURE__ (a DNA typing result originating from more than one individual). The predominant DNA profile __MATCHES__ to State Crime Laboratory Forensic Scientist_____ who performed the DNA analysis on this item of evidence."

5.7.12.4.2 Predominant Match to a Prior Forensic Scientist/Field Agent involved in the case:

"The DNA profile obtained from_____ (Item_) is __INDICATIVE OF A__ __MIXTURE__ (a DNA typing result originating from more than one individual). The predominant DNA profile __MATCHES__ to State Crime Laboratory Forensic Scientist/Agent _____. This scientist/agent performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis."

5.7.12.4.3 Predominant Match to a State Crime Laboratory employee, vendor, or visitor not involved in the case:

"The DNA profile obtained from_____ (Item) is __INDICATIVE OF A__ __MIXTURE__ (a DNA typing result originating from more than one individual). The predominant DNA profile __MATCHES__ to State Crime Laboratory (employee, vendor, visitor) _____. This individual has been present in a Laboratory area within the Forensic Biology Section on at least one occasion."

5.7.12.4.4 Predominant Match to a sample in a batched case:

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*"The DNA profile obtained from _____ (Item_) is **<u>INDICATIVE OF A MIXTURE</u>** (a DNA typing result originating from more than one individual). The predominant DNA profile **<u>MATCHES</u>** to State Crime Laboratory item number _____ which was analyzed along with items of evidence in this case."*

- **Statistics for 5.7.12.4.1, 5.7.12.4.2, 5.7.12.4.3 and 5.7.12.4.4:** Statistical data generated from these scenarios shall be calculated using Random Match Probability (RMP) as provided in the Procedure for Statistical Interpretation. The following statistical statement shall be used: *"The probability of randomly selecting an unrelated individual with a DNA profile that matches the predominant DNA profile obtained from (the) ___ is 1 in greater than 1 trillion (which is more than the world's population) in the NC Caucasian, Black, Hispanic, and Lumbee Indian populations."*

5.7.12.5 Mixture Profiles Not Exhibiting Full Predominance

5.7.12.5.1 Cannot exclude the DNA Forensic Scientist who worked the case

*"The DNA profile obtained from_____ (Item_) is **<u>INDICATIVE OF A MIXTURE</u>** (a DNA typing result originating from more than one individual). The DNA profile obtained from State Crime Laboratory Forensic Scientist _____ cannot be excluded as a contributor to the mixture. _____ performed the DNA analysis on this item of evidence."*

5.7.12.5.2 Cannot exclude the prior Forensic Scientist/Field Agent involved in the case

*"The DNA profile obtained from_____ (Item_) is **<u>INDICATIVE OF A MIXTURE</u>** (a DNA typing result originating from more than one individual). The DNA profile obtained from State Crime Laboratory Forensic Scientist/Agent _____ cannot be excluded as a contributor to the mixture. This scientist/agent performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis."*

5.7.12.5.3 Cannot exclude the State Crime Laboratory employee, vendor, or visitor not involved in the case

*"The DNA profile obtained from_____ (Item_) is **<u>INDICATIVE OF A MIXTURE</u>** (a DNA typing result originating from more than one individual). The DNA profile obtained from State Crime Laboratory (employee, vendor, visitor) _____ cannot be excluded as a contributor to the mixture. This individual has been present in a Laboratory area within the Forensic Biology Section on at least one occasion."*

5.7.12.5.4 Cannot exclude a sample in a batched case

*"The DNA profile obtained from _____ (Item_) is **<u>INDICATIVE OF A MIXTURE</u>** (a DNA typing result originating from more than one individual). The DNA profile obtained from State Crime Laboratory item number _____ which was analyzed with items of evidence in this case*

cannot be excluded as a contributor to the mixture."

- **Statistics for 5.7.12.5.1, 5.7.12.5.2, 5.7.12.5.3 and 5.7.12.5.4:** Statistical data generated from these scenarios shall be calculated using Combined Probability of Exclusion (CPE) as provided in the Forensic Biology Section Procedure for Statistical Interpretation. The following statistical statement shall be used: *"The chance of randomly selecting an unrelated individual who would be expected to be included for the observed DNA mixture profile is approximately:*

  N.C. Caucasian: 1 in ___
  N.C. Black: 1 in ___
  N.C. Hispanic: 1 in ___
  N.C. Lumbee Indian: 1 in ___."

5.7.12.6 Other Scenarios

Other scenarios may be encountered which are not addressed in these examples and shall have documented approval by the DNA Technical Leader before being stated in a Laboratory Report.

5.7.13 CODIS Hit Notifications: Refer to the Forensic Biology Section Procedures for CODIS and DNA Database for wording and requirements.

5.8 Known Samples that Produce Partial Profiles: In the event that a partial profile is obtained from a known sample, the word "partial" shall be incorporated into the result statement.

5.9 Reporting of Non-Sperm Fractions: Scientists are to report the results of all non-sperms fractions.

5.10 Additional Alleles

When additional alleles are present that cannot be attributed to any of the known reference standards provided, the following statement shall be used:

"Additional alleles were observed which cannot be accounted for by the standard(s) submitted."

5.11 Identity Statement

Forensic Scientists in the Forensic Biology Section may provide opinion testimony as to the uniqueness of a DNA profile in cases when population frequency calculations for all population groups exceed the current estimated population of the world.

Forensic Scientists are to use great care with the wording of their opinion on the uniqueness of the DNA profile and shall use a scientific equivalent of the following statement:

"It is my opinion that it is not scientifically reasonable to expect that the DNA profile derived from the (semen, blood, saliva) stain detected on State's Exhibit # _____ (description of the State's Exhibit item) could have originated from anyone other than _____, unless this individual has an identical sibling."

6.0 Limitations - N/A

7.0 Safety - N/A

8.0 References

Butler, J.M. *Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers*. 2nd ed. Burlington, MA: Elsevier Academic Press, 2005.

Federal Bureau of Investigation. "QUALITY ASSURANCE KNOWN SAMPLES FOR DNA DATABASING LABORATORIES." *Forensic Science Communications, October 2008, Volume 10, Number 4.*

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Forensic Biology Section Procedure for DNA Database

Forensic Biology Section Procedure for CODIS

9.0 Records – N/A

10.0 Attachments – N/A

Revision History		
Effective Date	Version Number	Reason
09/17/2012	1	Original Document
10/26/2012	2	5.7 – added sentence to allow portions of the statements to be omitted to reflect work actually performed; 5.7.4.1 - changed wording to be consistent with 5.7.4.2; unknown profile reporting statements throughout procedure - added "male" to reporting guidelines.
12/07/12	3	5.7.10 – Added wording to allow reporting of exclusion/ no conclusion to a limited profile result. Added statement for reporting of additional alleles as new 5.10, previous 5.10 renumbered as 5.11