**OSAC Technical Guidance Document**

# Human Forensic DNA Reporting Appendix Exemplar

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*Human Forensic Biology Subcommittee*

OSAC
Organization of Scientific Area Committees for Forensic Science

## OSAC Technical Guidance Document 0009

# Human Forensic DNA Reporting Appendix Exemplar

Prepared for
*The Organization of Scientific Area Committees (OSAC) for Forensic Science*

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**Abstract**

This publication aims to assist Forensic Science Service Providers with developing and refining statements to meet the reporting needs of their laboratory as well as any end users of the technical reports. Providing this information to the end user should assist them in comprehending the results and opinions in the report, especially as it pertains to the meaning and limitations of the DNA results.

This publication does not endorse or discourage particular procedures and practices but rather provides a template for the laboratory to adopt or modify the statements contained herein. While this document is directly applicable to autosomal short tandem repeat (STR) and Y-STR DNA testing, many of these concepts and suggested language can be applied to other types of DNA testing.

**Keywords**

Appendix, DNA, Template, Forensic Biology, Report, Limitations, Caveats, Notes

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## Executive Summary

This publication is an OSAC Technical Series Publication rather than a standard or best practice recommendation. It offers guidance for reporting statements, limitations, and caveats to accompany reports containing DNA results and conclusions. This publication does not recommend or discourage particular procedures and practices. This publication aims to assist Forensic Science Service Providers in developing and refining statements to meet the needs of their laboratory, as well as any end users and readers of the technical reports. This information helps end users better comprehend the results and opinions in the report, especially as it pertains to the limitations of DNA results and what they do not mean.

While this document directly applies to reporting data derived from autosomal short tandem repeat (STR) and Y-STR DNA methods and technologies, many of these concepts and suggested language can be applied to other DNA testing methodologies.

The example statements are intended to be used as a starting point for a laboratory to develop, modify, and refine a report appendix (however named) whether attached directly to the report or made publicly available for the following categories:

- Case record and discovery
- Y(male)-screening method: Extraction & Quantitation only
- Extraction
- Quantitation
- Amplification and Detection
- Interpretation and Comparison
- Statistical Analysis
- Quality Assurance and Quality Control
- CODIS
- Y-STR Testing

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## Foreword

This document was prepared, revised, and finalized as a technical guidance document by the Human Forensic Biology Subcommittee of the Organization of Scientific Area Committees (OSAC) for Forensic Science.

This publication was produced using a consensus process, as part of the Organization of Scientific Area Committees (OSAC) for Forensic Science, and is made available by the U.S. Government. Consensus for the purposes of the OSAC Technical Series publications means that all OSAC members had an opportunity to comment on the document and provide suggestions for revisions. Consensus does not mean that all OSAC members are in complete agreement with the contents of this publication. The views expressed in this publication and in the OSAC Technical Series publications do not necessarily reflect the views or policies of the U.S. Government. The publications are provided "as-is" as a public service, and the U.S. Government is not liable for their contents.

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# Introduction

This publication is an OSAC Technical Series Publication rather than a standard or best practice recommendation. It offers examples of reporting statements, limitations, and caveats to accompany reports containing DNA results and opinions. The purpose of these statements is to help the end user of the report comprehend what the DNA results mean and, more importantly, what they do not mean. Forensic Science Service Providers (FSSPs) may be able to adopt some statements as provided; however, FSSPs should modify or refine the statements to meet the needs of their laboratory and end users of these reports. The provided examples are meant to be a starting point and are not intended to be prescriptive or all-encompassing and will vary depending on the FSSP's policies and procedures.

Although this document is directly applicable to autosomal short tandem repeat (STR) and Y-STR DNA methods and technologies, many of these concepts and suggested language can be applied to other types of DNA testing.

# I. General Information

## Introductory statement for a reporting appendix

The following appendix includes supplemental information on the testing, analysis, and interpretation of the data performed along with caveats for some commonly used terms. Please contact the reporting analyst with any specific questions regarding the DNA testing performed and the data obtained in this case.

## Case Record and Discovery

The report does not contain all of the documentation associated with and necessary to understand and evaluate the testing performed and data obtained. The following materials may be necessary to perform an independent evaluation and are available upon request:

- A complete record of the chain of custody maintained by the laboratory.
- All testing records including all bench notes generated during the laboratory testing processes, photographic documentation, data obtained during the testing including all laboratory controls, records of statistical evaluations, and reports.
- Electronic raw data files and software output files, as relevant. Note that specialized software is required to access raw data files.
- Quality control documents including root cause analyses, contamination event/incident reports, unexpected results, non-conformances, corrective action documentation and other quality incident reviews.
- All administrative records to include all information provided to and communications with the laboratory regarding the evidence and/or testing.
- Records of CODIS or other profile-searchable database (e.g., elimination database, commercial database) associations.
- Relevant standard operating procedures used during testing.

- Relevant internal validation records.

## II. Y(male)-screening method: Extraction & Quantitation only

*Example 1*

Eligible items are moved through a screening workflow designed to detect DNA from male contributor(s) (referred to as "male DNA"). Eligibility for screening depends on the case circumstances and the value associated with the detection of male DNA. The quantitation results indicate whether or not male DNA was detected and are used to help select items for additional testing. (*Include the following additional language as appropriate*) Y-screen extracts are discarded as they are not suitable for additional DNA analysis. –OR– Y-screen extracts are retained for possible additional DNA analysis.

*Example 2*

The Y (or male)-screening method extracts DNA from a portion of the item without a purification step. The purpose of this screening method is to provide information about whether or not DNA from one or more males is detected. Y (or male)-screening may be used as an alternative to traditional serological testing; however, serological testing may be able to be performed by request. (*Include the following additional language as appropriate*) Y-screen extracts are discarded as they are not suitable for additional DNA analysis. –OR– Y-screen extracts are retained for possible additional DNA analysis.

## III. Extraction

Extraction is the process of recovering DNA from a biological sample for testing.

Items potentially containing semen were extracted with a differential extraction method. The method is designed to separate potential mixtures of sperm and non-sperm cells into two distinct fractions (*insert fraction names, respectively*). These two fractions are created regardless of the presence or absence of sperm. Incomplete separation/carryover can occur, resulting in the fractions containing DNA from both sperm and non-sperm cells. The use of a differential extraction method and the detection, or lack of detection, of male DNA alone cannot establish the presence, or absence, respectively, of sperm. A microscopic examination for sperm was not performed.

## IV. Quantitation

### General Quantitation Information

The quantitation data are used to decide whether DNA testing should be discontinued or continued to autosomal STR or Y-STR analysis. The decision to proceed with autosomal and/or Y-STR amplification is based on the total amount of DNA detected and/or the relative amounts of male

and female DNA in the extract. Meeting a minimum threshold or target ratio does not guarantee that an interpretable and comparable autosomal or Y-STR DNA profile would be obtained.

### Insufficient/Minimal or No DNA Detected

*Example 1*
Based on the laboratory's validation, DNA testing may be stopped due to the detection of either an insufficient amount of DNA or no DNA, as interpretable results are not expected. While testing could be performed upon request, halting testing at the quantitation step enables the laboratory to conserve evidence and DNA extract(s) for potential future testing.

*Example 2*
Based on the laboratory's validation studies, DNA testing may be stopped if the {concentration of DNA is less than _ng/µL or total amount of DNA is less than _ng}, as interpretable results are not expected. While additional testing could be performed upon request, halting testing at the quantitation step enables the laboratory to conserve evidence and DNA extract(s) for potential future testing.

### Ratio of DNA (Human:Male or Female:Male)

Based on the laboratory's validation studies, DNA testing may be stopped due to the detection of an abundance of female DNA compared to the amount of male DNA detected, as interpretable results are not expected from male contributor(s) with autosomal STR testing. While additional testing could be performed upon request (e.g., Y-STR), halting testing at the quantitation step enables the laboratory to conserve evidence and DNA extract(s) for potential future testing.

## V. Amplification and Detection

The PCR (polymerase chain reaction) technique produces many copies (products) of DNA from small starting amounts by repeated cycles of copying (DNA amplification) specific regions (loci) of the DNA recovered from an item.

Short tandem repeat (STR) autosomal loci were amplified using the polymerase chain reaction (PCR) with the amplification kit (*insert amplification kit*) and analyzed using capillary electrophoresis.

Short tandem repeat (STR) loci on the Y chromosome (which is male-specific) were amplified using the polymerase chain reaction (PCR) with the (*insert amplification kit*) and analyzed using capillary electrophoresis.

Capillary electrophoresis is the process where amplified DNA products are separated and detected. The DNA profile derived from the tested item is then analyzed using software, and an electropherogram (the visual representation of the profile as a series of peaks) representing the results is generated.

# VI. Interpretation and Comparison

## General Process Statements

DNA interpretation involves evaluating data to determine whether the data are suitable for comparison.

Comparison is the process of examining two or more DNA data sets to assess the degree of similarity or difference.

A number of factors may have been considered when interpreting the DNA profile data obtained from an evidence item and comparing it to reference profile(s) from known individuals. These factors may include the assigned number and relative proportions of contributors to a DNA mixture, assumed contributors, allele sharing, and undetected alleles. The ground truth for these factors can never be known.

All interpretations, comparisons, and evaluations of DNA data rely on established laboratory protocols. These protocols are grounded in validation studies using samples with known composition, which aid the evaluation and interpretation of profiles from unknown sources where ground truth can never be known.

Statistical statements are provided to give value to the DNA comparison(s).

## Specific Limitations and Caveats to DNA Interpretation and Comparisons

### Highlighting the importance of case information

Since the evaluation presented in this report is dependent on the information provided and the propositions formed using this information, any change in the case information may require a new evaluation. Contact the laboratory to re-evaluate the results as soon as possible if case information changes or new case information is added.

### Limitations of DNA test results and conclusions

The meaning of all DNA test results, subsequent conclusions, and statistical values should be considered by the end-user in the context of the case.

### Limitations regarding the value of DNA comparisons

*Example 1 - Likelihood Ratio*

This report and evaluation do not directly answer the question, “Who is the source of the DNA?”; instead, the interpretations may ***help*** answer that question by providing an evaluation of the results in light of the propositions (e.g., “The person of interest is the source of the DNA” versus “An unknown individual is the source of the DNA”). It is the role of the end-users (and not the DNA analyst) to integrate the DNA results with the other case information and evidence. The (magnitude of the) LR value alone cannot identify an individual as the source of the DNA.

*Example 2 - Random Match Probability*

This report and evaluation do not directly answer the question, "Who is the source of the DNA?"; instead, the interpretations may ***help*** answer that question. It is the role of the end-users (and not the DNA analyst) to integrate the DNA results with the other case information and evidence. The random match probability (RMP) alone is insufficient to identify an individual as the source of the DNA.

## Distinguishing between sub-source and activity level questions

This report and evaluation only provides information that helps address who may or may not be a contributor of the DNA, not how or when the DNA was deposited. This report cannot contribute any information regarding the mechanisms, timings, or actions that led to the deposition of the biological material or the meaning of its absence.

## Qualitative terms used to describe DNA profiles

Terms used to describe portions of a DNA profile (e.g., major/minor contributor) and label the DNA fractions generated by a differential extraction method (e.g., sperm/epithelial fraction) provide no direct information regarding the specific cell type or biological material from which the DNA was recovered.

## Assigning biological sex to portions of profiles

Biological (DNA-based) sex information reported here is based solely on the detection of X and Y chromosome markers. This information should not be misinterpreted to mean that an individual must identify as or appear as male or female based upon this indication alone.

## Assigning number of contributors

The true number of contributors to a DNA profile recovered from an item of evidence cannot be known. The assigned number of contributors is based on the laboratory's procedures that take into account the observed quantity and quality of the DNA profile data and any available case information.

## Assumptions or conditioning

An individual may be assumed to be a contributor to a DNA profile when their contribution is expected. This expectation may be based on the item type (e.g., intimate body swab) or case information (e.g., consensual partner), and where the profile data support the presence of their DNA. Assumptions or conditioning information may aid in evaluating the DNA profile of the remaining contributor(s) and has been shown to improve sensitivity and specificity.

## Suitability for Comparison

Decisions about the number of contributors, sex typing results, and suitability for interpretation and comparison of the DNA profile (or a portion of the DNA profile) were made prior to the comparison to any reference profiles.

Data that are determined to be unsuitable for comparison cannot be used. Reasons include, but are not limited to, poor or limited data quality, mixture complexity, or a failure to meet quality assurance requirements.

## Binary Comparison Terminology Caveats

### Inclusion/included/cannot be excluded/match

The terms “included,” “cannot be excluded,” and “match” indicate that a degree of similarity was observed between two DNA profiles. These terms should not be interpreted as indicating that an individual is the source of the DNA. The statistical statement provides a measure of the value of the DNA results.

### Exclusion/excluded

An individual (or unknown DNA donor to an item) may be excluded because either the DNA profile being compared was not present or the DNA was below the limit of detection for the testing method used. It is not possible to distinguish between these two alternatives.

*Example 1 - exclusion*
The term "exclusion" indicates that a degree of dissimilarity was observed between two DNA profiles to conclude, based on laboratory defined criteria, that the DNA profiles tested are from different sources.

*Example 2 - exclusion*
The term “exclusion” indicates that, based on DNA profile dissimilarity and laboratory criteria, the profiles are from different sources.

### Inconclusive

The term “inconclusive” indicates that neither an inclusion nor an exclusion can be determined from the comparison between two DNA profiles based on laboratory defined criteria.

## Probabilistic Genotyping Software

A probabilistic genotyping approach helps interpret DNA profiles by considering possible genotypes, and then assigning likelihood ratios, which provide the value of the DNA comparisons.

Probabilistic genotyping software uses biological modeling (i.e., statistical modeling informed by biological data), probability theory, computer algorithms, and probability distributions to infer genotypes and calculate likelihood ratios.

# VII. Statistical Analysis

## General Caveat for Statistical Calculations

Statistical calculations are performed using the population database in use by the laboratory at the time of reporting. Population databases are maintained by external organizations and may undergo periodic updates, which may or may not impact the values of any previously reported statistics.

Recalculation of statistics using the newest database version may be available upon request, where appropriate.

## Random Match Probability (RMP)

The RMP is a numerical value that conveys how common or rare a DNA profile is in a general population of unrelated individuals. It does not indicate how common or rare a DNA profile is among persons who are biologically related, and it is not the probability that a given individual is the source of the DNA in a specific sample.

The RMP is assigned to the DNA profile from the item of evidence, not to the reference profile.

## Combined probability of inclusion (CPI)

A CPI is a numerical value that represents the proportion of the general population of unrelated individuals that cannot be excluded/would be included as potential contributors to a mixed DNA profile. A CPI is not the probability that a given individual is a contributor to a mixture.

The CPI calculation takes into account all possible combinations of genetic profiles that could produce the DNA typing results obtained. The application of the CPI assumes that all of the alleles from each contributor to the mixture have been observed.

These probabilities are assigned to the DNA profile from the item of evidence, not to the reference profile.

## Combined probability of exclusion (CPE)

A CPE is a numerical value that represents the proportion of the general population of unrelated individuals that can be excluded as a potential contributor to a mixed DNA profile (i.e., 1 - CPI). A CPE is not the probability that a given individual is excluded as a contributor to a mixture.

The CPE calculation takes into account all possible combinations of genetic profiles that could produce the DNA typing results obtained. The application of the CPE assumes that all of the alleles from each contributor to the mixture have been observed.

These probabilities are assigned to the DNA profile from the item of evidence, not to the reference profile.

## Likelihood Ratio (LR) - Value of the DNA comparison

The likelihood ratio (LR) is a numerical value that compares the probabilities of observing the DNA results obtained considering two opposing propositions.

The propositions and LR value depend on known or assumed case information. An LR: (i) does not require that either of the propositions be true, only that both cannot be true at the same time; (ii) cannot determine whether a proposition is true or not; and (iii) will be obtained even if both propositions are false.

Additional pairs of propositions can be considered upon request (e.g., if there are changes to the case information, a biological relative needs to be considered as a possible source of DNA).

LR values indicate if and to what extent the DNA results provide relative support for one proposition versus an alternative proposition.

LRs greater than 1 may be obtained for comparisons to individuals who are not the source of the DNA just as LRs less than 1 may be obtained for comparisons to individuals who are a source of the DNA. Reasons for this include, but are not limited to, the quality of the DNA profile, and allele sharing between the true source of the DNA profile and the profile of the compared individual.

### Exclusion/excluded when using LRs

*Example 1 - manual exclusion*
The term "exclusion" indicates that a degree of dissimilarity is observed between two DNA profiles to conclude, based on laboratory-defined criteria, that the DNA profiles tested are from different sources. This dissimilarity is based on a manual assessment of the profiles or the probabilistic genotyping output.

*Example 2 - manual exclusion*
The term “exclusion” is based on a manual assessment of the dissimilarity of the profiles or the probabilistic genotyping output using laboratory-defined criteria.

*Example 3 - exclusion based on LR value*
An “exclusion” is based on an LR value of 0 or an LR value less than a laboratory-established value using probabilistic genotyping software.

### Uninformative

*Example 1*
The term “uninformative” is based on an LR value of 1 resulting from the comparison of two DNA profiles. This indicates that the DNA results are unable to provide support for one proposition versus the other proposition.

*Example 2*
An LR value of 1 indicates that the DNA results are uninformative, their value null or neutral. The term "uninformative" does not mean that the DNA results are meaningless, only that the findings are equally probable given the propositions selected.

### Verbal qualifiers

Words can be assigned to ranges of numerical LR values to further describe the extent of support that the DNA results provide for one proposition versus another. Several verbal equivalence tables have been published, and they are a matter of convention. The table below describes the verbal qualifiers used by this laboratory [insert table].

## VIII. Quality Assurance / Quality Control

### General Statements

Unless noted otherwise in the case record, the laboratory assumes the accuracy of the investigative information, collection, sampling or description of evidentiary samples prior to submission to the laboratory, and the association of these items to individuals as provided by the submitting agency. All item and reference sample descriptions are as received from the submitter unless otherwise noted.

The DNA unit employs a team-based approach to casework analysis; therefore, portions of the testing in this case may have been performed by someone other than the analyst who signed this report. Please contact the reporting analyst with any specific questions regarding the DNA analysis performed and the data obtained in this case.

The interpretation of the data and authorization of the results was performed by the undersigned forensic analyst. Other staff members may have performed laboratory activities concerning evidence associated with this report. For a complete listing of all staff members who performed laboratory activities in this case, please contact the laboratory via the telephone number provided.

The correct performance of controls and the use of other measures are intended to prevent and detect error; however, the potential for error is inherent in any testing process by any testing laboratory. If a portion of the original item and/or DNA extract remains, additional and/or independent testing could be conducted in order to assess concordance of the testing results.

All appropriate controls were processed and yielded expected results.

The data from the evidentiary item(s) were evaluated as suitable for interpretation, comparison and statistical calculations prior to comparison to the data from the reference standard(s).

The laboratory has a publicly available website (*provide website link*). This website contains standard operating procedures, other laboratory manuals and policies, documentation of quality

events, nonconformities and corrective actions, accreditation assessment activity reports, preventative action documentation, internal audit reports, and management review documentation.

## Additional Testing Methods and Technologies

Additional testing utilizing other methods and technologies could be performed on item(s) in this case (e.g., serology, Y-STR, mitochondrial DNA, forensic investigative genetic genealogy, Rapid DNA). This testing may be performed by the laboratory or may need to be performed by another laboratory. Please contact the laboratory to discuss additional testing options.

The laboratory limits the number and type of items for testing based on a combination of its available validated technologies, the known limitations of those technologies, laboratory capacity and/or CODIS database eligibility. However, testing may be able to be performed on additional items in this case. Please contact the laboratory to discuss additional testing options.

## Accreditation

Accredited laboratories must demonstrate compliance with a published standard and any additional requirements set forth by the accrediting body [*insert accrediting body(ies)*].

The laboratory is accredited to ISO/IEC 17025:2017 *General requirements for the competence of testing and calibration laboratories*. The logo(s) from the laboratory's accrediting body is featured on this report and signifies the testing and analysis performed in this case is within the laboratory's scope of accreditation.

Accredited laboratories undergo annual assessment activities by their respective accrediting body. Records of these assessment activities are available upon request.

Laboratories entering, uploading, and searching DNA profiles in the CODIS software must demonstrate compliance with the FBI Quality Assurance Standards for Forensic DNA Testing Laboratories, effective (*insert date*). Records of the assessment activities are available upon request.

## ANSI/ASB Published and OSAC Registry Standards

The laboratory has voluntarily implemented the following OSAC Registry Standard:

- ANSI/ASB Standard ###, Title, Edition #, year

The laboratory has voluntarily implemented the following ANSI/ASB published standard:

- ANSI/ASB Standard ####, Title, Edition #, year

The laboratory has voluntarily implemented the following proposed OSAC Registry Standard:

- 20XX-S-#### Title of proposed OSAC Registry Standard

## Technical Review

Technical reviews are performed by laboratory staff who are qualified in the procedures and software used in this case prior to releasing the report.

Any discrepancies between the case analyst and the technical reviewer are resolved and documented within the case record according to laboratory procedures.

## Validation

Validation studies conducted by this laboratory are available upon request.

*Example*
The laboratory's probabilistic genotyping validation was performed in accordance with the Scientific Working Group on DNA Analysis Methods's (SWGDAM) Guidelines for the Validation of Probabilistic Genotyping Systems, FBI Quality Assurance Standards for Forensic DNA Testing Laboratories, and ANSI/ASB Standard 018, *Standard for Validation of Probabilistic Genotyping Systems*, First Edition, 2020.

## Proficiency Testing

Laboratory analysts are required to undergo proficiency testing twice per year. Tests must be purchased from an external vendor and must be graded as satisfactory or containing non-consensus results. If non-consensus results are obtained, laboratories are required to investigate the root cause of the non-consensus results and take corrective action where appropriate.

## Additional Procedures and Guidelines

Accredited laboratories are required to have and follow documented standard operating procedures. In addition to technical or analytical procedures, additional procedures, such as Quality Assurance Manuals and CODIS manuals, are available for review upon request.

## Quality Event/Nonconformity/Corrective Action

There may be a quality event, nonconformity, and/or corrective action associated with this case. Additional documentation concerning the details is contained in the case record and is available upon request.

The case record may contain documentation regarding other events that may have occurred during testing, analysis and interpretation that are not tracked as part of a quality event, nonconformity, or corrective action.

Data in this case may be associated with a failed control. Documentation regarding the likely or known cause of the failed control, the impact of the failed control on the integrity of the DNA test results, and the determination of suitability for interpretation is contained in the case record.

# IX. CODIS

## General Statements

CODIS is the acronym for the COmbined DNA Index System, which is a DNA database software program administered by the FBI.

CODIS consists of three levels: the Local DNA Index System (LDIS), the State DNA Index System (SDIS), and the National DNA Index System (NDIS). Profiles are entered into the LDIS database, which is managed by the individual local laboratory, and searched locally. Profiles that meet state-specific eligibility criteria are also uploaded and searched at SDIS. Profiles that meet national eligibility criteria are also uploaded to NDIS where they are searched against other profiles that meet national eligibility criteria.

To be eligible for entry into CODIS, the profile must be of appropriate quality and reasonably assumed to have originated from the individual(s) who committed the alleged crime. If the same, or similar, profile is detected in multiple samples within a case, only one profile may be uploaded into CODIS.

Software (*insert name, version*) was used to aid in the determination of the CODIS entry.

## Elimination Samples

Reference samples from individual(s) possibly having contact with the evidence at the scene, during collection, or transport to the laboratory should be submitted to the laboratory for elimination purposes (e.g., consensual partner(s), officers, investigators). This aids in preventing the upload of profiles into CODIS from individuals who are not associated with the alleged crime.

## CODIS Database Searching Outcomes

CODIS searches can result in a potential association between profiles. The association can be between evidentiary DNA profiles or between an evidentiary DNA profile(s) and a DNA profile from a reference sample. A notification will be issued if a CODIS search results in an association between two or more DNA profiles.

CODIS notifications only provide investigative lead information, and therefore, it is important to evaluate this information in conjunction with the other available evidence.

While a CODIS notification provides the name of a potential person of interest, a reference sample for that individual should be collected and submitted to the laboratory for analysis and comparison. The notification can only be used to support probable cause in obtaining the reference sample and does not substitute for further testing.

If a CODIS notification provides case information from a potentially related case identified through a CODIS search, the applicable agency information will be provided to allow for further investigation.

A notification will be issued if a profile is subsequently removed from CODIS.

# X. Y-STR Testing

## Y-STR Analysis and Patrilineal Disclaimer

Y-STR analysis is a specialized type of DNA analysis that targets STR loci on the Y chromosome of biological males. Since the Y chromosome is paternally inherited *(i.e.*, from father to son), all biological male relatives in the paternal line are expected to share the same Y-STR profile, barring mutations. Therefore, two specimens that exhibit the same Y-STR profile may have originated from a common individual source; from individuals within a paternal lineage; or unrelated individuals who share the same Y-STR profile. Reference samples from relevant untested biological males should be submitted to the laboratory for comparison to evidentiary profiles.

## Y-STR Statistical Analysis

Unlike autosomal STR markers, the probability of a Y-STR profile, or "haplotype," is assigned by directly comparing it to profiles in a Y-STR reference database. This comparison reveals how often the profile is observed in the database used. As the database grows, the value assigned to the Y-STR profile is expected to change.

The YHRD (Y-Chromosome Haplotype Reference Database) database was used for assigning Y-STR statistical values. This publicly accessible database contains Y-STR data from male volunteers, but does not include data from convicted offenders, missing persons, or evidence.

### Direct Counting Method (Y haplotype sample frequency)

The Y-STR profile frequency in the reference database is assigned using a direct counting method that provides the number of times a matching profile is observed in the database. If the count is zero, it means this profile has not yet been submitted by any male donor; it does not necessarily mean the profile is rare in the overall population.

### Upper Confidence Interval (Profile Probability)

A Y-STR upper bound profile probability was calculated by applying a confidence value (95%) to the observed database count. This accounts for the effect of database size and sampling, but not population substructure.

The upper confidence interval does not indicate the confidence or probability that the DNA originated from a given individual, or other related or unrelated male.

### Likelihood Ratio (value of the Y-STR comparison)

A likelihood ratio (LR) expresses how many times more likely the Y-STR profile comparison is to be observed if the reference individual is the source of the male DNA than if an unknown unrelated male from the same population is. This method can account for the effect of the size of the population surveyed, sampling, and population substructure.

An LR value is not the probability that the male DNA detected on an item of evidence originated from a specific male of interest or any other related/unrelated male.

An LR value is not the probability that anyone other than the person of interest is a source of the DNA detected.

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