FORENSIC BIOLOGY SECTION

CODIS
TEST METHODS

INDIANA STATE POLICE
BIOLOGY SECTION
CODIS TEST METHODS

FOREWORD

The Laboratory Division of the Indiana State Police (ISP) maintains the Combined DNA Index System (CODIS) or DNA Database. The Laboratory organizes and funds the collection of legislatively mandated samples from convicted offenders and arrestees. The analysts of the Biology Section shall have a minimum of a baccalaureate or an advanced degree in a natural science or a closely related field. DNA analysts shall have successfully completed college course work covering the subject areas of genetics, biochemistry, molecular biology, and statistics. All analysts undergo an intensive formalized training program dealing with forensic techniques and instrumentation. Completion of the Training Program is required before analysis of databasing samples is performed. Additionally, all analysts shall participate in proficiency testing utilizing open trials, blind trials and/or re-examination techniques. The accuracy and specificity of test results are ensured by running known controls with each set of tests.

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1 LDIS (Local DNA Index System) Methods:

1.1 Scope:

This test method is designed for the guidance of laboratory personnel (at all four laboratories) who interact with the Combined DNA Index System (CODIS). The scope of this interaction may include but is not limited to submitting profiles from casework samples for entry into the database, performing CODIS Administrator functions, or being involved in hit confirmations and reporting. This test method may be expanded or altered as techniques, software and/or new legal authorities are found applicable.

1.1.1 Indiana Criminal Code 10-13-6 (Appendix 1) authorizes the Superintendent of the Indiana State Police (ISP) to establish and maintain the Indiana DNA Database. The purpose of this database is to assist federal, state and local criminal justice and law enforcement agencies in the putative identification, detection, or exclusion of individuals who are subjects of an investigation or prosecution of a crime in which biological evidence is recovered from a crime scene.

1.1.2 The Indiana DNA Database Administrative Rules (Appendix 2) assign the Commander of the Indiana State Police Laboratory (ISPL) the responsibility for the administration of the Indiana DNA Database subject to the authority and approval of the Superintendent.

1.1.3 In addition to these procedures, all current National DNA Index System (NDIS) Procedures, available on the CODIS Portal, shall be followed.

1.2 Precautions/Limitations:

1.2.1 Casework profiles submitted for entry into CODIS should be evaluated carefully for eligibility in accordance with National DNA Index System (NDIS) Operational Procedure "DNA Records Accepted at NDIS" and the flowchart "A Guide to Determining What is Allowable in the Forensic Index at NDIS," both available on the CODIS Portal.

1.3 Related Information:

1.3.1 Indiana Criminal Code 10-13-6

1.3.2 NDIS Operational Procedures

1.3.3 Worksheet Manual

1.4 Instruments: Designated computer terminals and software

1.5   Reagents/Materials: None

1.6   Hazards/Safety: None

1.7   Reference Materials/Controls/Calibration Checks:

   1.7.1   DNA profiles shall be developed in compliance with the DNA Identification Act of 1994 and the FBI Approved Quality Assurance Standards for Forensic DNA Testing Laboratories.

   1.7.2   Development of DNA profiles may be performed using validated and approved procedures as defined in any currently approved ISP Test Method.

1.8   Procedures/Instructions:

   1.8.1   CODIS Entry for Identity Searches

      1.8.1.1   Profiles for entry shall be recorded using an approved worksheet or program (i.e. CODIS Submission Worksheet, Pedigree CMF Tool or other approved worksheet) and technically reviewed. This technical review shall include verifying CODIS eligibility, correct DNA types and appropriate specimen category. Hand entry or import of a CMF may be used to enter the reviewed information into CODIS.

      1.8.1.2   Categories of casework DNA data eligible at LDIS/SDIS are Forensic Unknown, Forensic Mixture, Forensic Partial, Forensic Targeted, SDIS only SAK, Missing Person, Deduced Missing Person, and Unidentified Person.

         1.8.1.2.1   Profiles shall be entered as Forensic Unknown if the profile being entered is believed to be complete and from a single source.

         1.8.1.2.2   Profiles shall be entered as Forensic Mixture if the data being entered is believed to be a mixture of more than one individual.

         1.8.1.2.3   Profiles shall be entered as a Forensic Partial if either locus or allelic drop out are suspected.

         1.8.1.2.4   Profiles entered as Missing Person, Deduced Missing Person and Unidentified Person shall not enter partial loci or rapidly mutating Y loci.

1.8.1.2.5   All profiles shall have a minimum of 8 loci for entry. To be uploaded to NDIS, there shall be a minimum of 8 original core loci.

1.8.1.2.6   Forensic Mixtures or Forensic Partials shall meet the moderate match estimate (MME) threshold of 1 in 10 million to be uploaded to NDIS. They may be uploaded to the State DNA Index System (SDIS) if the MME is at least 1 in 100,000.

    1.8.1.2.6.1   If the moderate match estimate is less than the above thresholds, the profile may be changed to specimen category Forensic Targeted with the appropriate loci flagged as partial.

    1.8.1.2.6.2   Forensic Targeted profiles shall have match rarity estimate (MRE) of 1 in 10 million for NDIS or 1 in 100,000 for SDIS.

    1.8.1.2.6.3   Discretion should be used when evaluating profiles with a large amount of dropout. Profiles for which more than 2/3 of loci entered would be a single allele with suspected dropout are not appropriate for CODIS. It may be possible to "match" relatives of the perpetrator. These profiles should not be entered for identity searching, even if they meet the thresholds above.

1.8.1.2.7   Profiles from sexual assault kits for which it is unclear whether the profile is eligible for NDIS based on the information available may be entered in specimen category SDIS only SAK. These profiles shall meet the MME threshold of 1 in 100,000.

1.8.1.2.8   Other specimen categories shall be used as appropriate according to their definitions in NDIS Operational Procedure "NDIS DNA Records" and indicated on the CODIS Submission Worksheet.

1.8.1.3   The CODIS State or Local Administrator or other designated personnel shall have final determination of which profile(s) or alleles shall be entered into CODIS.

1.8.1.4   Double entry of allele calls is required if manually entered but may be conducted by the same individual.

1.8.1.5   A Specimen Detail Report shall be printed or saved as a PDF for each profile entered from the CODIS Submission Worksheet and placed with the case notes.

1.8.1.6   The Specimen Detail Report shall be reviewed to ensure entry of the correct profiles, accuracy of alleles and correct specimen category. This shall be done by the Technical Reviewer.

1.8.1.7   CODIS input shall include all loci with conclusive types and shall not be limited to the core STR loci. This may include Y-STR loci; however, they shall not be counted toward the minimums detailed above.

    1.8.1.7.1   Y-STR loci with duplications should be omitted.

1.8.1.8   All suitable data shall be marked for transfer to SDIS or NDIS at the time of entry.

1.8.1.9   A CODIS administrator shall upload new or changed data on a routine basis.

1.8.1.10   Deletion of a DNA profile shall be initiated when it has been determined a sample is not lawfully permitted or appropriate for retention in the system.

1.8.2   CODIS Entry for Pedigree Searches

1.8.2.1   Relatives of Missing Persons shall have profiles and relationships to the missing individual recorded within the case notes and technically reviewed. This technical review shall include verifying CODIS eligibility, correct DNA types and appropriate specimen category. Hand entry or import of a CMF may be used to enter the reviewed information into CODIS.

    1.8.2.1.1   Partial loci (drop out suspected) shall not be entered.

    1.8.2.1.2   All profiles shall have a minimum of 8 loci for entry. To be uploaded to NDIS, there shall be a minimum of 8 original core loci.

    1.8.2.1.3   A second technology (Y-STR) shall be entered whenever possible. Rapidly mutating Y-STRs shall not be entered.

    1.8.2.1.4   Pedigree Manager shall be used to create a tree depicting the relationships indicated in the case record.

        1.8.2.1.4.1   Category Missing Persons shall be used when two or more individuals have DNA typing information.

        1.8.2.1.4.2   Category Single Typed Node shall be used when only one individual has DNA typing information.

1.8.2.1.4.3   The missing person's node shall be designated as unknown.

1.8.2.1.4.4   Each typed node shall be associated with the specimen ID containing that individual's DNA profile.

1.8.2.1.5   Metadata from the case file may be entered as desired using a right-click on the unknown node of the tree.

1.8.2.2   The CODIS State or Local Administrator or other designated personnel shall have final determination of which profile(s) or alleles shall be entered into CODIS.

1.8.2.3   Double entry of allele calls is required if manually entered but may be conducted by the same individual.

1.8.2.4   All Specimen Detail Reports for each profile entered and the Pedigree Details Report shall be printed or saved as a PDF and placed with the case notes.

1.8.2.5   The reports shall be reviewed to ensure entry of the correct profiles, accuracy of alleles, correct specimen category, correct metadata and proper pedigree construction. This shall be done by the Technical Reviewer.

1.8.2.6   CODIS input shall include all appropriate autosomal STR and Y-STR loci with conclusive types and shall not be limited to the core STR loci.

1.8.2.7   All suitable data shall be marked for transfer to SDIS or NDIS at the time of entry.

1.8.2.8   A CODIS administrator shall upload new or changed data on a routine basis.

1.8.2.9   Deletion of a DNA profile shall be initiated when it has been determined a sample is not lawfully permitted or appropriate for retention in the system.

1.8.3   Profiles developed by Vendor Laboratories

1.8.3.1   If the desire is that profile(s) developed in the case be entered into CODIS, the following must be documented and approved by the ISPL Technical Leader prior to the start of analysis by the vendor laboratory:

1.8.3.1.1   Compliance with FBI Quality Assurance Standards and accreditation requirements

1.8.3.1.2 All technical specifications, including a technology, data platform and test kit which ISPL personnel are qualified to review in order to accept ownership of the data

1.8.3.1.3 An on-site visit that has occurred within 18 months of the conducted analysis

1.8.3.2 Ownership Review

1.8.3.2.1 The complete case record must be provided to the ISPL for technical review.

1.8.3.2.2 The ownership review shall include:

1.8.3.2.2.1 A review of all DNA types that the ISPL will take ownership of to verify that they are supported by the raw and/or analyzed data (electropherograms or images).

1.8.3.2.2.2 A review of all associated analytical controls, internal size standards, and allelic ladders to verify that the expected results were obtained.

1.8.3.2.2.3 A review of the final report to verify that the results/conclusions are supported by the data.

1.8.3.2.3 After technical review, qualifying profiles shall be entered into CODIS in the same manner as cases analyzed by ISP. A second individual shall verify accurate transcription of the profile(s) onto the CODIS Submission Worksheet.

1.8.3.2.4 The agency requesting analysis and entry shall be informed of the CODIS entry via memo on ISP letterhead. The memo shall state where the analysis took place and what profile(s) were entered using current report wording guidelines.

1.8.3.2.5 The outsourced case file, technical review worksheet, memo, and any other relevant documentation shall be maintained on a network drive (LIMS if an ISPL case exists or the Biology QA drive if no ISPL case exists).

1.8.3.3 If any of the requirements of 1.8.3 are not met, profiles developed by the vendor laboratory at the request of the contributing agency shall not be entered into CODIS.

1.8.4 Hit Confirmation and Reporting of Identity Searches

1.8.4.1 Evaluation of Matches

1.8.4.1.1 An effort shall be made to resolve all matches within 30 business days, except in circumstances beyond the control of ISPL personnel.

1.8.4.1.2 High Stringency matches that provide previously unknown information to an unsolved case (as determined by the case record and/or contact with the investigator) shall be confirmed.

1.8.4.1.3 Moderate Stringency matches shall be reviewed by an individual with mixture interpretation training/experience. The case analyst may also be consulted to determine if the match should be confirmed or given a disposition of No Match.

1.8.4.1.4 The laboratory with ownership of an unsolved casework profile involved in a match has primary responsibility to request any needed confirmation of that match.

1.8.4.2 Offender to Case Hits

1.8.4.2.1 State DNA Index System (SDIS) Hits

1.8.4.2.1.1 Confirmation shall be requested from the SDIS laboratory.

1.8.4.2.1.2 The case profile shall be verified by reviewing the original DNA analysis records. This shall be recorded on the Hit Confirmation Checklist.

1.8.4.2.1.3 The match shall be verified by a qualified or previously qualified analyst. This shall be recorded on the Hit Confirmation Checklist.

1.8.4.2.1.4 The Hit Confirmation Checklist shall be returned to the SDIS laboratory.

1.8.4.2.1.5 The disposition and Source ID fields shall be updated.

1.8.4.2.2 National DNA Index System (NDIS) Hits

1.8.4.2.2.1 Confirmation shall be requested from the NDIS laboratory.

1.8.4.2.2.2 The SDIS laboratory shall be notified for hit counting purposes.

1.8.4.2.2.3   The case profile shall be verified by reviewing the original DNA analysis records. This shall be recorded on the Hit Confirmation Checklist.

1.8.4.2.2.4   The match shall be verified by a qualified or previously qualified analyst. This shall be recorded on the Hit Confirmation Checklist.

1.8.4.2.2.5   When all verifications are complete, the Hit Confirmed line on the Hit Confirmation Checklist shall be signed by the CODIS Administrator.

1.8.4.2.2.6   A hit notification shall be generated stating the match results. No statistics shall be included. Notifications shall follow the format seen in 2.11.

1.8.4.2.2.7   Hit notifications shall be administratively reviewed for accuracy of identifying information. This review shall be documented on the CODIS Notification Administrative Review worksheet.

1.8.4.2.2.8   The disposition and Source ID fields shall be updated.

1.8.4.3   Case to Case Hits

1.8.4.3.1   When at least one case is unsolved, confirmation shall be requested from the laboratory with the unsolved case, if the cases are from different laboratories.

1.8.4.3.2   The SDIS laboratory shall be notified for hit counting purposes.

1.8.4.3.3   Each case profile shall be verified by reviewing the original DNA analysis records. This shall be recorded on the Hit Confirmation Checklist.

1.8.4.3.4   The match shall be verified by a qualified analyst. This shall be recorded on the Hit Confirmation Checklist.

1.8.4.3.5   When all verifications are complete, the Hit Confirmed line on the Hit Confirmation Checklist shall be signed by a CODIS Administrator at one of the laboratories involved in the match.

1.8.4.3.6   The cases should be related in LIMS and a hit notification shall be generated for each matching ISP case profile as in 2.11.

1.8.4.3.7   Hit notifications shall be administratively reviewed for accuracy of case information. This review shall be documented on the CODIS Notification Administrative Review worksheet.

1.8.4.3.8   If the match involves a laboratory from another state, a CODIS notification shall be forwarded to that laboratory.

1.8.4.3.9   The disposition and Source ID fields, if appropriate, shall be updated.

1.8.4.4   In instances where it is determined that the offender is not incarcerated and there are unusual public safety concerns, the investigating agency may be given verbal notification of the match with the reminder that the hit confirmation is in process. The hit notification shall not be issued until the match is confirmed.

1.8.4.5   The CODIS notification documenting the hit may be written by the CODIS Unit at the Indianapolis Regional Laboratory for any ISPL case.

1.8.5   Confirmation and Reporting of Pedigree Searches

1.8.5.1   Evaluation of Ranks

1.8.5.1.1   An effort shall be made to resolve all ranks within 30 business days, except in circumstances beyond the control of ISPL personnel.

1.8.5.1.2   Each typed technology should be considered when evaluating ranks. This shall be done by a qualified or previously qualified analyst in that technology.

1.8.5.1.3   In some cases, it may be necessary to have additional testing, such as mitochondrial DNA, performed to determine if the rank is a true association.

1.8.5.2   Missing Persons/Single Typed Node Associations

1.8.5.2.1   Confirmation shall be requested from the laboratory with the unidentified remains if the cases are from different laboratories.

1.8.5.2.2   The SDIS laboratory shall be notified for counting purposes.

1.8.5.2.3   Each case profile shall be verified by reviewing the original DNA analysis records. This shall be recorded on the Rank Confirmation Checklist.

1.8.5.2.4   Metadata for the rank shall be reviewed for consistency. This shall be recorded on the Rank Confirmation Checklist.

1.8.5.2.5   Kinship statistics for the potential relationships shall be calculated and printed for the file. Support or non-support of at least one relationship shall be recorded on the Rank Confirmation Checklist.

1.8.5.2.6   When all verifications are complete, the Association Confirmed line on the Rank Confirmation Checklist shall be signed by a CODIS Administrator at one of the laboratories involved in the association.

1.8.5.2.7   The cases should be related in LIMS and a CODIS notification shall be generated for each matching ISP case profile as in 2.11.

1.8.5.2.8   A Certificate of Analysis, including statistical information, shall be issued for the unidentified remains case.

1.8.5.2.9   Notifications shall be administratively reviewed for accuracy of case information. This review shall be documented on the CODIS Notification Administrative Review worksheet.

1.8.5.2.10   If the match involves a laboratory from another state, a notification shall be forwarded to that laboratory.

1.8.5.2.11   The disposition and Source ID fields, if appropriate, shall be updated.

1.8.5.2.12   The notification documenting the association may be written by the CODIS Unit at the Indianapolis Regional Laboratory for any ISPL case.

1.8.6   Systems Operations

1.8.6.1   Access to CODIS shall be limited to laboratory personnel designated by the CODIS Unit Supervisor.

1.8.6.2   Access by NDIS or NDIS contract personnel may be allowed for the purpose of diagnosing, repairing and servicing CODIS software.

1.8.6.3   All users shall log off or lock the CODIS computers after each session. Terminals shall lock after 10 minutes of non-use.

1.8.6.4   Backups of all files on the CODIS computers shall be performed at minimum once per week.

1.8.6.4.1 Backups may be documented by either automatic scheduling within backup software or a written log if done manually.

1.8.6.4.2 The backup media shall be stored in a secure location.

1.8.6.4.3 Backups shall be stored in a separate building in a secure area once per month.

1.8.6.4.4 The movement of backup media shall be recorded on the CODIS Backup Log.

1.9 Records:

1.9.1 The appropriate worksheets as contained in the Biology Section Worksheet Manual shall be used to record all procedures.

1.9.2 Notifications shall have an assigned memo number and be uploaded to the LIMS as an attachment when possible.

1.9.3 Documents relating to confirmations shall be maintained in the Hit/Family Reference Association File and/or in LIMS.

1.9.4 User documentation and backup logs shall be maintained by the CODIS Administrators at each laboratory.

1.10 Interpretation of Results: All Candidate Matches/Ranks shall be reviewed and evaluated by a DNA analyst currently or previously qualified in the technology being reviewed. Matches/Ranks shall be given a disposition in accordance with the disposition definitions provided in current NDIS Operational Procedures.

1.11 Reporting of Hits/Associations: See section 2.11

1.12 References: None

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2 SDIS (State DNA Index System) Methods

2.1 Scope:

This test method is designed for the guidance of CODIS Unit personnel who interact with the Combined DNA Index System (CODIS). The scope of this interaction may include but is not limited to entering profiles from casework or offenders, accessioning and preparing offender samples, performing CODIS Administrator functions, or being involved in hit confirmations and reporting. This test method may be expanded or altered as techniques, software and/or new legal authorities are found applicable.

2.1.1 Indiana Criminal Code 10-13-6 (Appendix 1) authorizes the Superintendent of the Indiana State Police (ISP) to establish and maintain the Indiana DNA Database. The purpose of this database is to assist federal, state and local criminal justice and law enforcement agencies in the putative identification, detection, or exclusion of individuals who are subjects of an investigation or prosecution of a crime in which biological evidence is recovered from a crime scene.

2.1.2 The Indiana DNA Database Administrative Rules (Appendix 2) assign the Commander of the Indiana State Police Laboratory (ISPL) the responsibility for the administration of the Indiana DNA Database subject to the authority and approval of the Superintendent.

2.1.3 In addition to these procedures, all current National DNA Index System (NDIS) Procedures, available on the CODIS Portal, shall be followed.

2.2 Precautions/Limitations:

2.2.1 Profiles submitted for entry into CODIS should be evaluated carefully for eligibility in accordance with National DNA Index System (NDIS) Operational Procedure "DNA Records Accepted at NDIS" and the flowchart "A Guide to Determining What is Allowable in the Forensic Index at NDIS," both available on the CODIS Portal.

2.2.2 Offender samples (convicted offenders and arrestees) collected for Combined DNA Index System (CODIS) shall be treated as reference materials and not considered evidence.

2.3 Related Information:

2.3.1 Indiana Criminal Code 10-13-6

2.3.2   Indiana DNA Database Administrative Rules

2.3.3   NDIS Operational Procedures

2.3.4   Worksheet Manual

2.4   Instruments: Designated computer terminals and software

2.5   Reagents/Materials: None

2.6   Hazards/Safety:

2.6.1   Universal Precautions shall be used whenever biological materials are being handled.

2.6.2   Biological waste shall be disposed of in the appropriate waste receptacle.

2.7   Reference Materials/Controls/Calibration Checks:

2.7.1   DNA profiles shall be developed in compliance with the DNA Identification Act of 1994, the FBI Approved Quality Assurance Standards for Forensic DNA Testing Laboratories and the FBI Approved Quality Assurance Standards for DNA Databasing Laboratories.

2.7.2   Offenders who are collected and analyzed more than once shall be compared to ensure their DNA profiles and identities match. An effort shall be made to resolve any discrepancies.

2.8   Procedures/Instructions:

2.8.1   Collection and Delivery of Offender Samples

2.8.1.1   DNA samples shall be collected in a medically approved manner by a physician, registered nurse, licensed vocational nurse, licensed clinical technologist, or other person trained to properly collect DNA samples.

2.8.1.2   The Department of Correction (DOC) Reception and Diagnostic Center and the DOC Indiana Women's Prison shall collect a DNA sample from all convicted felons entering the DOC. The county sheriff or their designee shall collect a sample from all arrestees and convicted felons not entering DOC. A private vendor may be used. When information is available that the offender has already been collected and entered into CODIS, a second collection is not necessary.

2.8.1.3   At the time of sample collection, the collecting agency shall complete an Indiana Offender DNA Database Sample Information Sheet, Live Scan Print Card, or another approved form. All relevant identifying information as well as at least one fingerprint of the offender shall be provided.

2.8.1.4   The person who collected the sample shall seal offender samples in appropriate containers. Samples should be stored in a secure location prior to delivery to the ISPL.

2.8.1.5   Samples may be delivered by hand transport to the ISPL or via a carrier that uses a package tracking system.

2.8.2   Handling and Storage of Offender Samples

2.8.2.1   Samples not immediately processed shall be stored in a secure location.

2.8.2.2   The offender name and/or identifying number of the sample may be compared to the ISP Offender sample tracking database of previously sampled offenders.

   2.8.2.2.1   Samples from offenders not previously in the tracking database shall be assigned a new Indiana Offender Database (INODB) number and added to the tracking database. The INODB number is a unique, non-identifying number assigned by the ISPL. INODB numbers start at 000001 and are assigned consecutively.

   2.8.2.2.2   Samples from offenders previously in the tracking database may be saved for potential use as quality assurance, training or validation samples.

      2.8.2.2.2.1   Samples not being retained for future use shall be destroyed, including associated paperwork.

2.8.2.3   The DNA sample(s), envelope(s) and Sample Information Sheet or Print Card shall all be labeled with the corresponding INODB number.

2.8.2.4   Samples shall be stored in a secure location until analysis. A sample may be consumed for analysis if necessary to develop a complete DNA profile.

2.8.2.5   Offender samples not used for analysis shall remain in storage, indefinitely, for future reference.

2.8.3   Sample and Information Access

2.8.3.1 Per the Indiana DNA Data Base Law, access to DNA samples and DNA analysis results is limited to criminal justice agencies for law enforcement identification purposes, defense counsel for criminal defense purposes, upon authorization by a court or statute, for a population statistics database, identification research and protocol development, or quality control purposes, but only if personal identifying information is removed. Federal, state and local law enforcement agencies may also have access through their servicing forensic DNA laboratories.

2.8.3.2 All requests for access to DNA samples or DNA analysis results except for requests from ISP Laboratories and the Indianapolis-Marion County Forensic Services Agency must be submitted in the form of a written request. The request must identify the requesting agency, the purpose for the request and the specific data requested. The CODIS Administrator or CODIS Unit Supervisor shall approve or deny such requests.

2.8.3.3 If DNA records that have been uploaded to NDIS are released to an individual, entity, agency, or laboratory other than another NDIS participating laboratory, the CODIS Administrator shall notify the FBI and remove those DNA records from NDIS.

2.8.4 Use of Contract Laboratories for analysis of Offender samples

2.8.4.1 A portion of the offender sample shall be removed from storage for analysis. The rest of the sample shall remain in storage for future reference.

2.8.4.2 Samples shall be shipped by a carrier that uses a package tracking system.

2.8.4.3 The contract laboratory shall follow sample storage procedures, analytical methods and administrative policies approved by the ISPL.

2.8.4.4 The sample analysis results shall be returned to the ISPL in an electronic format suitable for technical review.

2.8.4.5 Review of Data

2.8.4.5.1 All data from offender samples received from the contract laboratory shall be reviewed by ISPL personnel that have been trained and competency tested to interpret the data.

2.8.4.5.2 This technical review shall include verification that allele designations are correct, all extraction negative, amplification negative and amplification positive controls performed as expected

and technical specifications (as agreed upon by ISPL and the contract laboratory) are met.

2.8.4.5.3   Completion of the technical review shall be documented by handwritten initials of the reviewing analyst on each page of the profile print-out and completion of an Offender Data Technical Review Worksheet.

2.8.4.5.4   When ISPL review personnel question a sample allele assignment, a decision shall be made to classify the discrepancy as a possible clerical error or a possible analytical discrepancy.

2.8.4.5.4.1   If the questioned result is clearly due to a clerical error, the allele assignment shall be changed. A notation shall be made on the paperwork received from the contract laboratory.

2.8.4.5.4.2   If the questioned result is due to a possible analytical discrepancy, the ISPL shall reanalyze the corresponding sample retained by the ISPL, or the contract laboratory shall be requested to reanalyze the sample. Whenever possible, these samples shall be reviewed with the contract laboratory during on-site visits. The ISPL shall make the final decision regarding interpretation of the sample results. When a clear interpretation is not rendered, any affected loci shall not be entered into the DNA database.

2.8.4.6   After sample analysis results are approved, the ISPL shall give the contract laboratory an e-mail or written permission to dispose of approved samples or the samples may be returned to the ISPL for storage or destruction.

2.8.4.7   Quality Assurance

2.8.4.7.1   Random Re-analysis

2.8.4.7.1.1   Duplicate quality assurance samples shall be prepared from approximately 5% of offender samples received. These samples shall be assigned a database number different from the original sample, such that the duplicate cannot be associated with the original sample.

2.8.4.7.1.2   ISPL personnel shall ensure that original and duplicate quality assurance sample results are in agreement. CODIS search software can be used to conduct or assist with this task. Discrepancies shall be resolved as appropriate.

2.8.4.7.1.3   ISPL personnel may also re-analyze selected samples.

2.8.4.7.1.4   All data received from the contract laboratory shall be reviewed and approved by ISPL personnel as described in 2.8.4.5.

2.8.4.7.2   Quality Control (QC) samples which may be an external proficiency test purchased by the ISPL shall be sent to the contract laboratory at least once per year. All DNA analysis data shall be checked for correct results and approved by ISPL personnel.

2.8.4.7.3   ISPL personnel shall perform on-site visits of the vendor laboratory at least once, prior to the initiation of analysis, to ensure the vendor laboratory is in compliance with the Quality Assurance Standards for Forensic DNA Casework Laboratories. Subsequent yearly on-site visits may be performed by another NDIS participating laboratory with appropriate review and documentation by the ISPL Technical Leader.

2.8.5   CODIS Entry

2.8.5.1   Entry of casework profiles – follow procedures in 1.8.1-1.8.3.

2.8.5.2   Entry of offender profiles shall be by import of a CMF (Common Message Format) file whenever practical. Categories of offender DNA data eligible at SDIS are Arrestee, Convicted Offender and Multi-allelic Offender.

2.8.5.3   Manual entry of offender profiles shall be verified by a second analyst. This may be noted on the technical review worksheet or by entering a Verified By User in the CODIS software.

2.8.5.4   Older offender profiles may be updated with new loci in CODIS when reanalyzed in the current kit (such as during hit confirmations). Import validations shall be used to verify concordance with the original entry.

2.8.5.5   Upload to NDIS shall be in accordance with NDIS Operational Procedures.

2.8.6   Expungement/Administrative Deletion of Records (IC 10-13-6-18 and 34 U.S.C. § 12592(d)(2)(A))

2.8.6.1   A DNA profile may be removed (and sample destroyed) from CODIS for the following reasons:

2.8.6.1.1   All of the person's felony convictions have been reversed and the cases dismissed; the person was acquitted of all felony charges or all felonies were converted to misdemeanors; or all felony charges against the person were dismissed.

2.8.6.1.1.1   The person shall provide a written request for expungement and a certified copy of the court order evidencing the basis for removal.

2.8.6.1.1.2   The appropriate court jurisdiction may be contacted for verification of court action.

2.8.6.1.2   365 days have elapsed since the person's arrest and no felony charges have been filed.

2.8.6.1.2.1   The person shall notify the prosecuting attorney in writing.

2.8.6.1.2.2   The prosecuting attorney shall obtain a court order and provide a certified copy of that order to ISP.

2.8.6.1.3   An administrative deletion shall be initiated when it has been determined a sample is not lawfully permitted or appropriate for retention in the system.

2.8.6.1.3.1   This type of deletion request may be initiated by ISPL personnel, DOC personnel, county collection personnel, vendor collection personnel or the offender. The offender's conviction or arrest offense may be verified before removal.

2.8.6.2   Upon receipt and verification of the legitimacy of the request for removal, the CODIS State Administrator shall ensure deletion of all DNA profiles, records and identifiable information pertaining to the person.

2.8.6.3   All offender samples obtained from the individual shall be destroyed.

2.8.6.4   An Indiana State Police DNA Database Removal of Offender Sample Record shall be completed.

2.8.6.5   The NDIS Expungement Procedure shall also be followed to ensure proper expungement from NDIS when applicable.

2.8.6.6   The expungement court order, sample expungement record and any other pertinent documents shall be stored in the expungement file in a secure location when not in use.

2.8.7 CODIS Searches

2.8.7.1 Autosearches

2.8.7.1.1 On a routine basis, as determined by a CODIS Administrator or the CODIS Unit Supervisor, Autosearcher shall be initiated to search the following indexes against each other:

	Forensic	Offender	Missing Person	Relatives of Missing Person and Pedigrees	Unidentified Human (Remains)
Forensic	X	X	X		X
Offender	X		X		X
Missing Person	X	X			X
Relatives of Missing Person and Pedigrees					X
Unidentified Human (Remains)	X	X	X	X	X

2.8.7.1.2 Routine autosearches shall be done as described below with 8 loci required to report a match. If needed, the CODIS Administrator or CODIS Unit Supervisor may change the search parameters at their discretion.

2.8.7.1.2.1 Forensic Unknown and Forensic Targeted Indexes at High Stringency with up to 2 floating moderates

2.8.7.1.2.2 Forensic Partial and Forensic Mixture Indexes at Moderate Stringency

2.8.7.1.2.3 Missing Persons and Single Typed Node Trees with a combined likelihood ratio (CLR) of ≥ 10

2.8.7.2 DNA profiles from unsolved cases that qualify for both SDIS and NDIS may utilize the Emergency Upload and Search Request (EUSR) function of the CODIS software. This shall take place after technical review and with the approval of the CODIS State or Local Administrator or other designated personnel. An EUSR search should only be used in the event of a rush case or other unusual circumstance and shall be documented in the case record.

2.8.7.3   DNA Search Requests from other State Administrators may be searched against SDIS at the discretion of the CODIS Administrator.

2.8.7.4   When a DNA profile from an unsolved case is not acceptable for NDIS upload, but it may be beneficial to have it searched by other states, the DNA Search Request and Batch Target Files procedure may be utilized.

2.8.7.5   Staff Batch Searches

    2.8.7.5.1   Profiles obtained from ISPL personnel and other personnel who could potentially have contact with DNA evidence should be entered into the Staff Batch file on the SDIS CODIS Server.

    2.8.7.5.2   After addition of data into CODIS, but before it is uploaded to NDIS, the Staff Batch file should be searched against all profiles present in CODIS to ensure no profile is due to a contamination event.

    2.8.7.5.3   Any matches shall be immediately reported to the CODIS Administrator and/or DNA Technical Leader and the profile shall be removed from CODIS.

2.8.8   Hit Confirmation and Reporting

2.8.8.1   Evaluation of Matches – follow procedures in 1.8.4.1.

2.8.8.2   SDIS Offender to Case Hits

    2.8.8.2.1   The CODIS Administrator or CODIS Unit Supervisor shall ensure that the proper hit confirmation steps are performed. The Hit Confirmation Checklist shall be used to document completion of the steps.

    2.8.8.2.2   The qualifying offense of the offender should be verified through state or county resources. If no qualifying offense can be verified, the match shall be reported under IC 10-13-6-8(f).

    2.8.8.2.3   The case profile shall be verified by reviewing the original DNA analysis records.

    2.8.8.2.4   The match shall be verified by a qualified analyst by comparing the offender and case profiles.

    2.8.8.2.5   The remaining offender sample shall be re-analyzed by a qualified analyst.

2.8.8.2.5.1   This step need not be performed if:

    2.8.8.2.5.1.1   The individual has already been analyzed more than once and has been tested in the 2017 expanded core loci.

    2.8.8.2.5.1.2   No suitable sample remains.

2.8.8.2.6   The most complete offender sample profile shall be compared to the case profile to verify the match.

2.8.8.2.7   The thumbprint on the offender Sample Information Sheet shall be compared to the individual's 10 print fingerprint card to verify the identity of the offender sample, when possible.

    2.8.8.2.7.1   This step need not be performed for offenders submitted with Live Scan print cards as this would be a redundant comparison to itself.

2.8.8.2.8   After verifications are complete, the match shall be confirmed by the CODIS Unit Supervisor or CODIS Administrator.

2.8.8.2.9   A hit notification shall be generated stating the match results. No statistics shall be included. Hit notifications shall follow the format seen in 2.11.

2.8.8.2.10   Hit notifications shall be administratively reviewed for accuracy of identifying information. This review shall be documented on the CODIS Notification Administrative Review worksheet.

2.8.8.2.11   The disposition and Source ID fields, if appropriate, shall be updated.

2.8.8.2.12   If the offender is excluded as a possible contributor to the forensic sample, confirmation shall stop, and the Candidate Match shall be changed to a disposition of No Match. Identifying information of the offender shall not be released.

2.8.8.3   NDIS Offender to Case Hits

2.8.8.3.1   Matches involving an Indiana Offender – follow procedures in 2.8.8.2 as appropriate.

2.8.8.3.2   Matches involving an out of state offender – follow procedures in 1.8.4.2.2.

2.8.8.4 Case to Case Hits – follow procedures in 1.8.4.3.

2.8.8.5 Pedigree Tree Associations – follow procedures in 1.8.5.

2.8.8.6 In instances where it is determined that an offender is not incarcerated and there are unusual public safety concerns, the investigating agency may be given verbal notification of the match with the reminder that the hit confirmation is in process. The hit notification shall not be issued until the match is confirmed.

2.8.9 Systems Operations – follow procedures in 1.8.6.

2.9 Records:

2.9.1 The appropriate worksheets as contained in the Biology Section Worksheet Manual shall be used to record all procedures.

2.9.2 Notifications shall have an assigned memo number and be uploaded to the LIMS as an attachment for all ISPL cases.

2.9.3 Documents relating to confirmations shall be maintained in the Hit/Family Reference Association File and/or on a network drive. These documents shall be retained for a minimum of 2 years.

2.9.4 User documentation and backup logs shall be maintained by the CODIS Administrators.

2.9.5 Sample Information Sheets, Delivery Receipts, vendor data and all other documentation relating to the collection and analysis of offender samples shall be retained in a secure location for a minimum of 50 years.

2.10 Interpretations of Results: All Candidate Matches shall be reviewed and evaluated by a DNA analyst currently or previously qualified in the technology being reviewed. Matches shall be given a disposition in accordance with the disposition definitions provided in current NDIS Operational Procedures.

2.11 Reporting of Hits/Associations:

2.11.1 Formatting of notifications shall follow those shown on ISP letterhead (see Appendix 4). Exact information given may differ according to what is available.

2.11.2 Known aliases should be reported in parentheses after the true identifier.

2.11.3   Hit notifications should be distributed within 14 days of the completion of the confirmation procedure, whenever possible.

2.11.4   When appropriate, a Certificate of Analysis providing statistics may be issued after a pedigree association. Generally, this should be done if ISP owns the unidentified remains profile.

2.12 References: None

3   ISPL Analysis of Offender Samples

3.1   Scope:

This test method is designed for the guidance of Laboratory personnel who develop profiles from samples of offenders collected for inclusion in the CODIS database. Samples may include blood stain cards on FTA® or buccal/oral swabs. This manual may be expanded or altered as new techniques and/or genetic systems are available with the approval of the Division Commander.

3.1.1   The DNA is incubated, directly amplified to produce many fluorescently tagged copies of specific regions of the DNA and processed to separate and detect a DNA profile. These profiles are then entered into CODIS.

3.1.2   While most offenders will be analyzed using the procedure below, analysis of these samples may also be performed using any currently approved ISP Test Method.

3.2   Precautions/Limitations:

3.2.1   Offender samples collected for the Combined DNA Index System (CODIS) shall be treated as reference materials and not considered evidence.

3.3   Related Information:

3.3.1   Worksheet Manual

3.4   Instruments:

3.4.1   Capillary Electrophoresis Instrument - Simultaneously separates and detects multiple amplified DNA samples by size by capillary electrophoresis using fluorescently tagged primers.

3.4.2   Laminar Flow Hood - An air purifying biohazard cabinet that maintains a nominal inflow velocity of 80 fpm which prevents contaminants from entering or escaping the work area.

3.4.3   Miscellaneous Laboratory Equipment - Supportive laboratory equipment consisting of ovens, incubators, minifuges, pipettes, water baths, stirring/heating plates, vortex mixers, thermometers, temperature verification system, vacuum pump, refrigerators/freezers for storing of reagents, buffers and work product.

3.4.4   Thermal Cycler - An instrument that can be programmed to rapidly cycle between high and low temperatures. This process is used to make many fluorescently tagged copies of specific regions on a DNA strand(s).

3.4.5   Water Purification System - An apparatus that routes water through a series of filtering devices to produce high quality, uncontaminated water used in buffer preparation and DNA typing methods.

3.5   **Reagents/Materials:** Reagents critical to the DNA analysis process are listed in the Critical Reagents Manual.

3.5.1   Nuclease Free Water (NFH$_2$O)

3.5.2   SwabSolution™

3.5.3   AmpSolution™

3.6   **Hazards/Safety:**

3.6.1   All chemicals shall be handled in a safe method as referenced in the specific Safety Data Sheets (SDS).

3.6.2   The manual preparation of samples for electrophoresis by the addition of Hi-Di™ formamide shall be confined to a chemical fume hood. **Caution**: Formamide is an irritant and teratogen; therefore, universal precautions and a fume hood shall be utilized when manually working with formamide to avoid inhalation and contact with the skin.

3.6.3   Universal precautions shall be in use whenever biological materials are being handled.

3.6.4   Biological waste shall be disposed of in the appropriate waste receptacle.

3.7   **Reference Materials/Controls/Calibration Checks:**

3.7.1   DNA profiles shall be developed in compliance with the DNA Identification Act of 1994, the FBI Approved Quality Assurance Standards for Forensic DNA Testing Laboratories and the FBI Approved Quality Assurance Standards for DNA Databasing Laboratories.

3.7.2   The accuracy and specificity of test results are ensured by running known DNA controls and reagent controls at the same time as samples. See the specific test for the appropriate controls to be run and the interpretation of the results.

INDIANA STATE POLICE
BIOLOGY SECTION
CODIS TEST METHODS

3.8   Procedures/Instructions:

3.8.1   PowerPlex® Fusion 6C Introduction (Promega® Spectrum CE instrument)

3.8.1.1   The Promega PowerPlex® Fusion 6C System is a 27-locus multiplex that amplifies 23 autosomal short tandem repeat (STR) loci (CSF1PO, FGA, Penta D, Penta E, SE33, TH01, TPOX, vWA, D1S1656, D2S1338, D2S441, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, and D22S1045), two gender determining loci (Amelogenin and DYS391), and two additional rapidly mutating Y-STR loci (DYS570 and DYS576) in a single reaction. Separation and detection occur using capillary electrophoresis with overlapping loci visualized simultaneously by using PCR primers labeled with six different fluorescent tags (FL-6C, JOE-6C, TMR-6C, CXR-6C, TOM-6C, and WEN-6C).

3.8.1.2   The Promega® Spectrum CE instrument utilizes electrokinetic injection of DNA molecules into polymer-filled capillaries to separate the amplified DNA fragments by size. The fluorescently-labeled primers incorporated into the PowerPlex® Fusion 6C amplification products are responsive to the frequency of the 505nm solid state laser. Upon excitation, the fluorophores are raised to a higher energy level. When the fluorophores return to the lower energy level, fluorescent light is emitted. This signal is detected by a charge-coupled device (CCD) sensor, which records the light signal as data which can be visualized as a peak in an image called an electropherogram.

3.8.1.3   The data produced by the Spectrum CE instrument is analyzed with GeneMapper™ *ID*-X Software which results in peaks labeled with allele designations. The allele designations for each sample are accomplished by using an internal lane standard (ILS) which is injected with each sample. The ILS contains 21 fragments of known length, and determines the base pair size of the fragments in the sample. The software compares the sizes to an allelic ladder to determine the allele designation.

3.8.1.4   The PowerPlex® Fusion 6C System locus-specific and allelic ladder information is available at *www.promega.com/protocols/* in the PowerPlex® Fusion 6C System Technical Manual TMD051.

3.8.1.5   All PowerPlex® Fusion 6C components should be stored at -10 °C to -30 °C upon receipt in the appropriate laboratory locations. The PowerPlex® Fusion 6C Allelic Ladder Mix is packaged separately for shipping and should be stored in the post-amplification kit. Once thawed all components are stable at 2-10 °C for 6 months. Do not refreeze.

3.8.1.6   The PowerPlex® Fusion 6C 5X Primer Pair Mix, PowerPlex® Fusion 6C Allelic Ladder Mix, and WEN ILS 500 shall be protected from excessive exposure to light.

3.8.1.7   The preparation of the amplification reactions shall be performed in the PCR amplification set-up area.

3.8.2   PowerPlex® Fusion 6C Amplification

3.8.2.1   When programming the Applied Biosystems™ VeritiPro™ thermal cycler, use "9700 simulation mode" to optimize ramp speed.

3.8.2.2   Select 13 μL for the volume.

3.8.2.3   Applied Biosystems™ VeritiPro™ Thermal Cycler Program

3.8.2.3.1   96 °C for 60 seconds, then:

3.8.2.3.2   96 °C for 5 seconds

3.8.2.3.3   60 °C for 60 seconds

3.8.2.3.4   for 25 cycles, then:

3.8.2.3.5   60 °C for 10 minutes, then:

3.8.2.3.6   Soak at 4 °C until the plate is removed.

3.8.3   Promega® Spectrum CE – Spectrum Control Software v3.1.0 (8) - Instrument Set-up

3.8.3.1   Creating, Editing, and Sorting Instrument User Protocols

3.8.3.1.1   From the HOME screen, navigate to the PROTOCOLS screen as follows: HOME → SETTINGS → PROTOCOLS.

3.8.3.1.2   To create a new user protocol, either select an existing protocol and select SAVE AS (recommended) OR select NEW to begin a new protocol without using a template.

3.8.3.1.3   In the pop-up window, enter a unique descriptive name for the new protocol and select OK. The new protocol will appear in the list on the left panel of the screen.

3.8.3.1.4   To edit parameters of a user protocol, unlock the desired protocol by selecting the lock icon near the bottom of the screen. It should toggle to an unlocked icon, and the protocol can be edited.

3.8.3.1.5   Edit user protocol parameters in the right panel as desired and select SAVE when editing is complete. NOTE: Preset (factory installed) instrument protocols cannot be edited without using the SAVE AS option.

3.8.3.1.6   A user protocol may be deleted from the list if it is no longer desired. To do so, unlock the protocol as described above, and select DELETE from the menu.

3.8.3.1.7   The list of available protocols may be sorted if desired. The star icon may be selected to set a protocol as a favorite, which will then sort to the top of the list. Protocols may also be sorted by selecting any of the column headings.

3.8.3.1.8   The standard database protocol shall be created for each instrument as "ISP CODIS 6C", which is the 2kV15s injection protocol used for all CODIS analysis.

3.8.3.1.8.1   Select the "Promega 6-Dye (6C)" protocol. This is a pre-installed protocol on the instrument software.

3.8.3.1.8.2   Select SAVE AS in the bottom right.

3.8.3.1.8.3   In the pop-up window, type "ISP CODIS 6C" for the name and select OK when complete.

3.8.3.1.8.4   Click the lock icon to ensure no further changes are made.

3.8.3.1.8.5   No parameters from Promega 6-Dye (6C) are to be changed.

Instrument Protocol
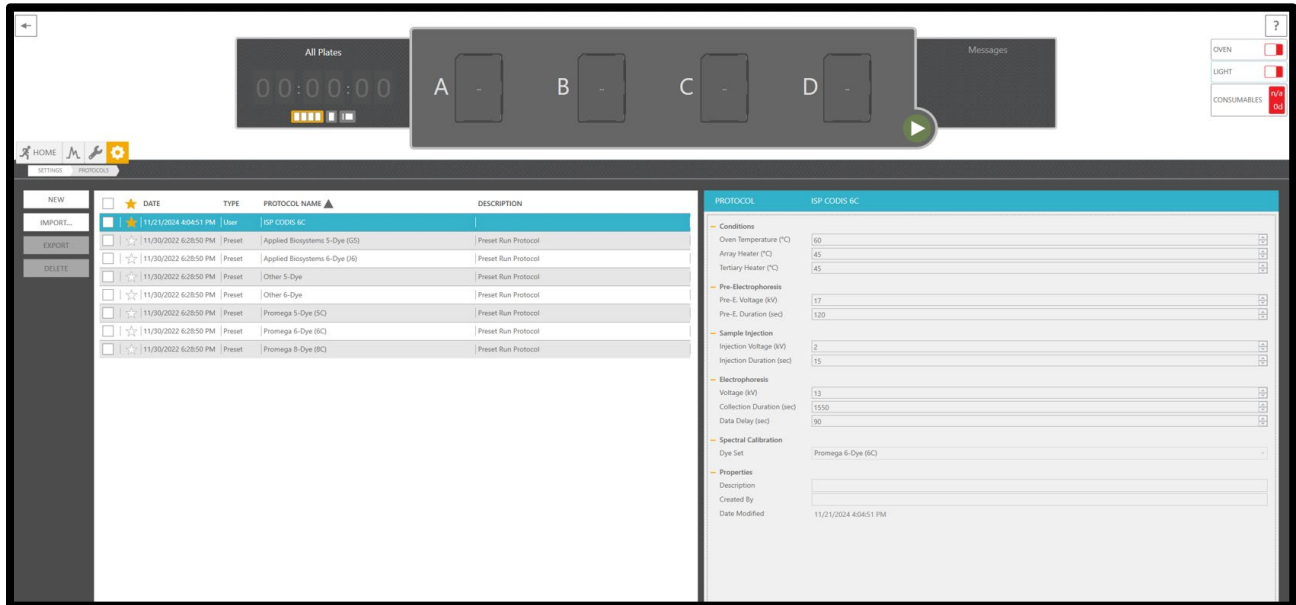
    3.8.3.2   Edit Exported Filename for data export (if desired).

        3.8.3.2.1   From the HOME screen, navigate to the DATA EXPORT screen as follows: SETTINGS → PREFERENCES → DATA EXPORT.

        3.8.3.2.2   To edit Exported Filename, use "+" to select or "-" to remove naming options in the lists marked "Includes" and "Available". Use "∧ / ∨" controls to edit the order of selected name components.

        3.8.3.2.3   The Preview area indicates the appearance of the filename with the selected components and chosen order.

        3.8.3.2.4   The file naming convention is saved immediately when edited and is automatically applied to future data exported from an instrument.

        3.8.3.2.5   For offender analysis, the Exported Filename shall be set to "Sample ID_Well Position".

Editing Exported Filename
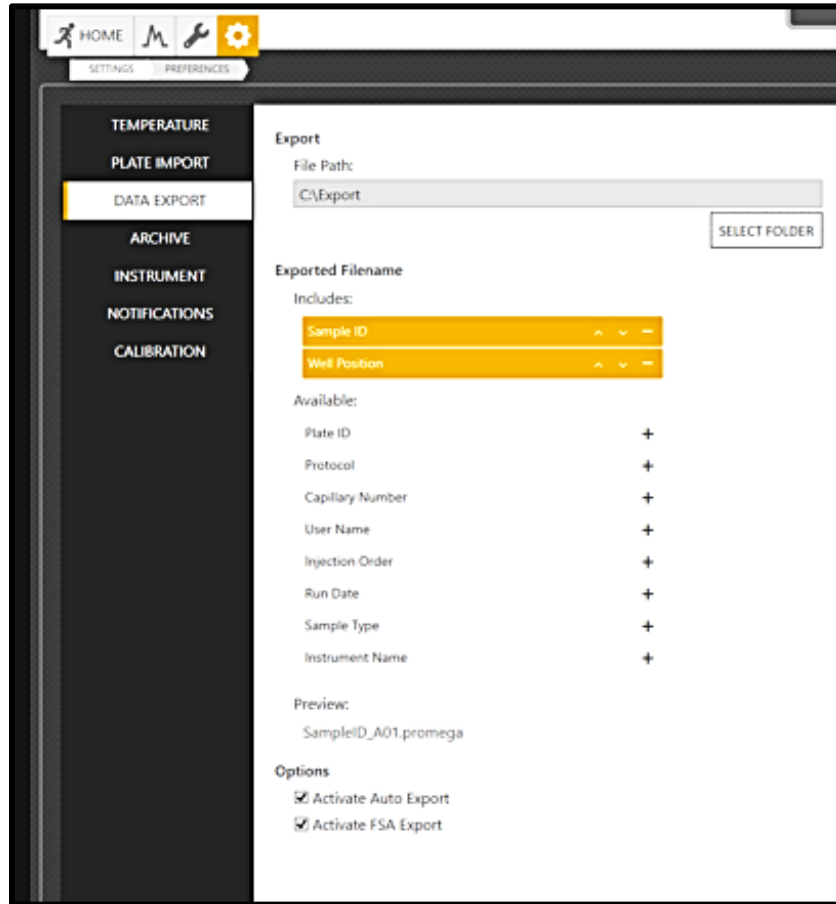
3.8.4 GeneMapper™ *ID*-X Software version 1.6 - PowerPlex® Fusion 6C Software Settings

3.8.4.1 Import Panel and Bin Files

3.8.4.1.1 Select "Tools", then "Panel Manager".

3.8.4.1.2 Highlight the Panel Manager icon in the upper left navigation pane.

3.8.4.1.3 Select "File", then "Import Panels".

3.8.4.1.4 Navigate to the saved panels and bins file. Select "PowerPlex_Fusion_6C_CODIS_ES_ISP_IDX_v1.1_Panels", then "Import". Choose the "ISP Databasing Security Group". Click "OK".

3.8.4.1.5   In the navigation pane, highlight the
              "PowerPlex_Fusion_6C_CODIS_ES_ISP_IDX_v1.1" folder.

3.8.4.1.6   Select "File", then "Import Bin Set".

3.8.4.1.7   Navigate to the bins file. Select
              "PowerPlex_Fusion_6C_CODIS_ES_ISP_IDX_v1.1_PowerPlex_Fus
              ion_6C_Bins_ISP_IDX_v1.1_bins", then "Import".

3.8.4.1.8   In the navigation pane, highlight the
              "PowerPlex_Fusion_6C_CODIS_ES_ISP_IDX_v1.1" folder.

3.8.4.1.9   Select "File", then "Import Marker Stutter". A warning box will
              appear asking if you want to overwrite current values. Select "Yes".

3.8.4.1.10   Navigate to the stutter file. Select
              "PowerPlex_Fusion_6C_CODIS_ES_ISP_IDX_v1.1_stutter", then
              "OK".

3.8.4.1.11   At the bottom of the Panel Manager window, select "Apply" and then
              "OK".

3.8.4.2   Create an Analysis Method

3.8.4.2.1   Select "Tools", then "GeneMapper™ *ID-X* Manager".

3.8.4.2.2   Select the "Analysis Methods" tab.

3.8.4.2.3   Select "New" and a new analysis method dialog box will open.

3.8.4.2.4   Enter the name "Fusion6C_CODIS_Spectrum" for the analysis
              method.

3.8.4.2.5   In the Analysis Method Editor window, select "ISP Databasing
              Security Group" as the Security Group.

3.8.4.2.6   Select the "Allele" tab.

3.8.4.2.7   Select "PowerPlex_Fusion_6C_Bins_ISP_IDX_v1.1"as the Bin Set.

3.8.4.2.8   Ensure that the global cut-off value is set at 0.2 for all.

Allele Tab

3.8.4.2.9 Select "Peak Detector" tab. Change the settings to those shown below. Alternatively, the Analysis Range may be set to "Partial Range" and the start point adjusted if the Instrument migration warrants it (to eliminate the primer peak).

Peak Detector Tab
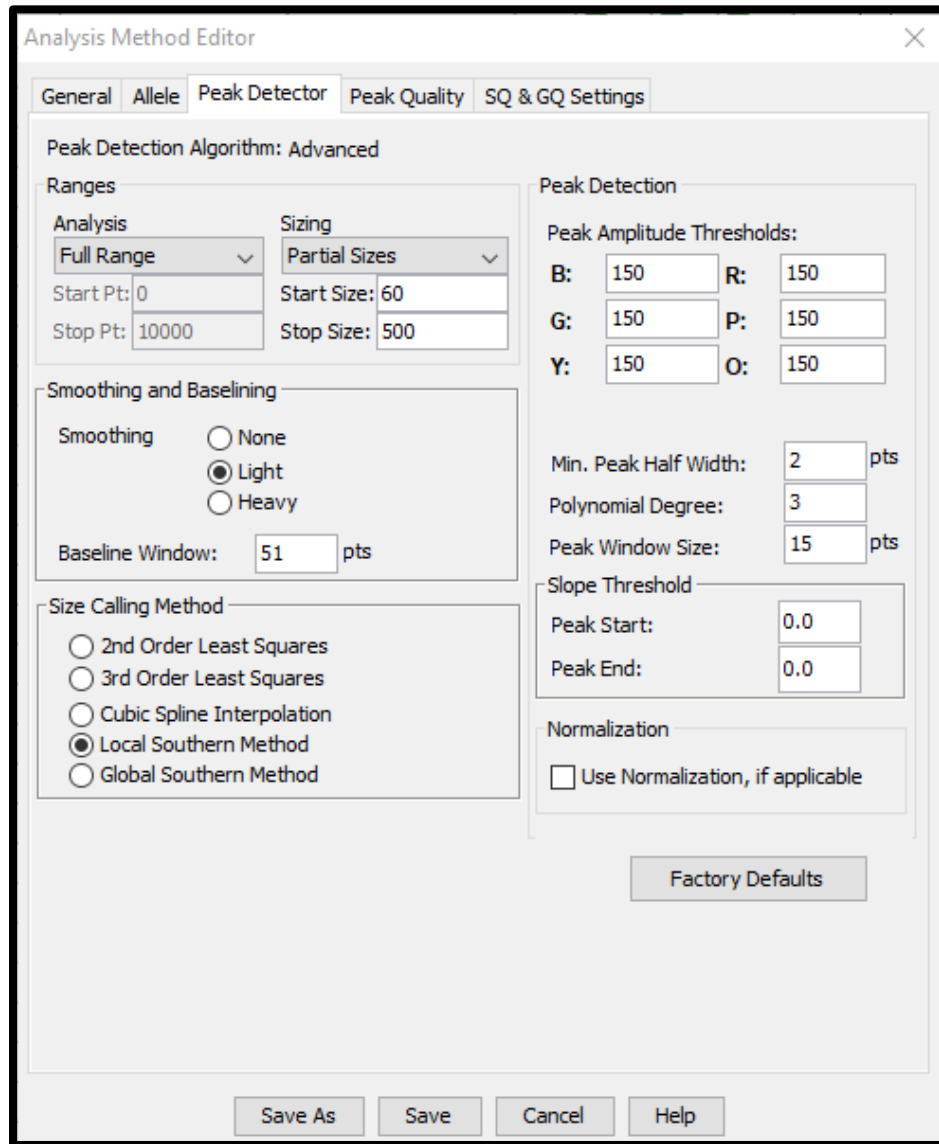
3.8.4.2.10   Select the "Peak Quality" tab. Change settings to those shown below.

Peak Quality Tab

3.8.4.2.11   Select the "SQ & GQ Settings" tab. Change settings to those shown below.

SQ & GQ Settings Tab

3.8.4.2.12   Click "Save".

3.8.4.3   Create a Size Standard

3.8.4.3.1   Select "Tools", then "GeneMapper™ *ID-X* Manager".

3.8.4.3.2   Select the "Size Standards" tab.

3.8.4.3.3   Select "New".

3.8.4.3.4   In the Size Standard Editor window, select "ISP Databasing Security Group" as the Security Group.

3.8.4.3.5   Enter the name as "WEN ILS 500".

3.8.4.3.6   Choose "Orange" for the Size Standard Dye.

3.8.4.3.7   Enter the sizes of the internal lane standard fragments (60, 65, 80, 100, 120, 140, 160, 180, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475 and 500 bases).

3.8.4.3.8   Click "OK".

3.8.4.4   Create a Table Setting

3.8.4.4.1   Select "Tools", then "GeneMapper™ *ID-X* Manager".

3.8.4.4.2   Select the "Table Setting" tab and click "New".

3.8.4.4.3   Under the "General" tab name the Table Setting "CODIS".

3.8.4.4.4   Select "ISP Databasing Security Group".

3.8.4.4.5   Select the "Samples" tab. Under column headings, ensure the following are checked: Status, Sample Name, Sample Type, Specimen Category, Analysis Method, Panel, Size Standard, Well Location, Sample Edit, Sample File Not Found, Sample Off-Scale, Sizing Quality, Sample Spike, Mixed Source, Outside Marker Range, Composite GQ and User Defined Column 2. Change other settings to those shown below.
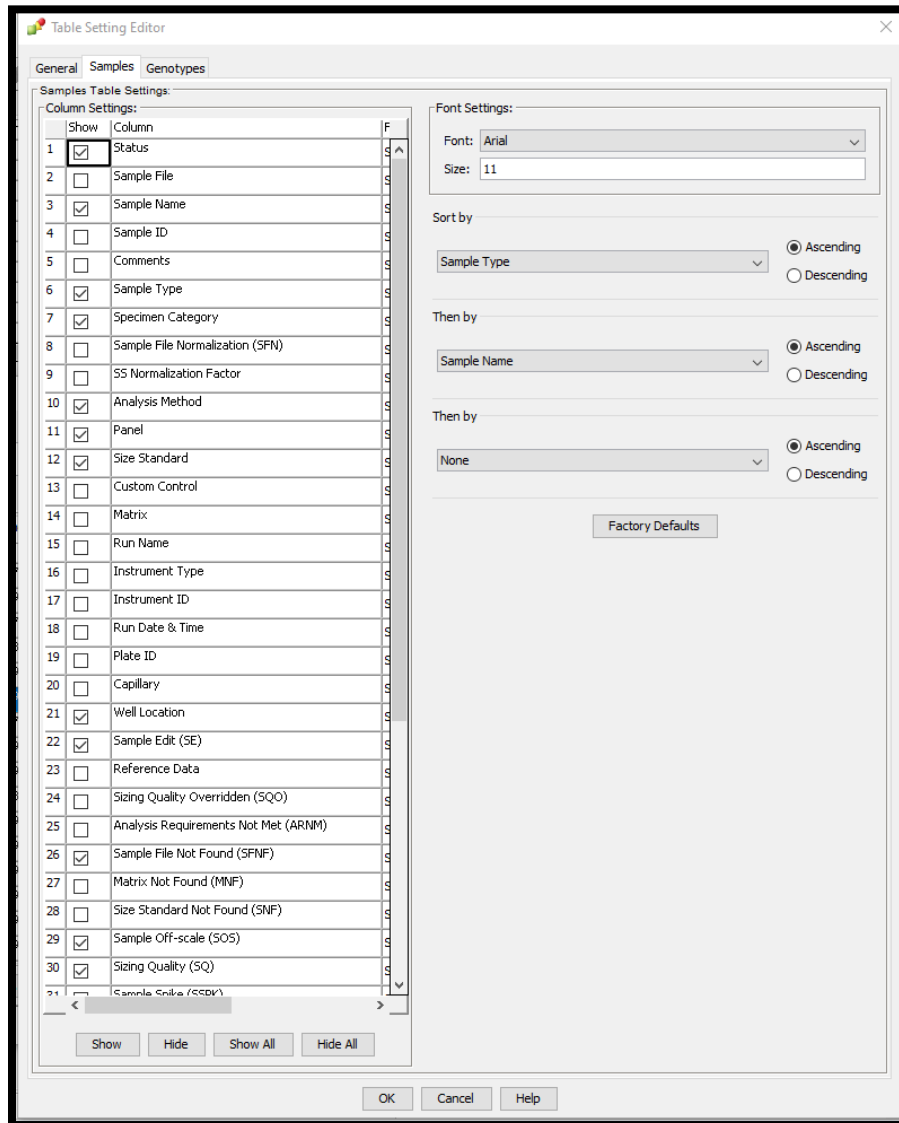
Samples Tab

3.8.4.4.6 Select the "Genotypes" tab. Under Column Settings, ensure the following are checked: Sample Name, Marker, Dye, Allele, Size, Height, Marker Edit, Off-Scale, Out of Bin Allele, Peak Height Ratio, Low Peak Height, Max Peak Height, Marker Spike, Allele Number, AMEL Cross Check, Broad Peak, Control Concordance, Overlap, Genotype Quality, User Defined Column 2, and User Defined Column 5. Change other settings to those shown below.

Genotypes Tab
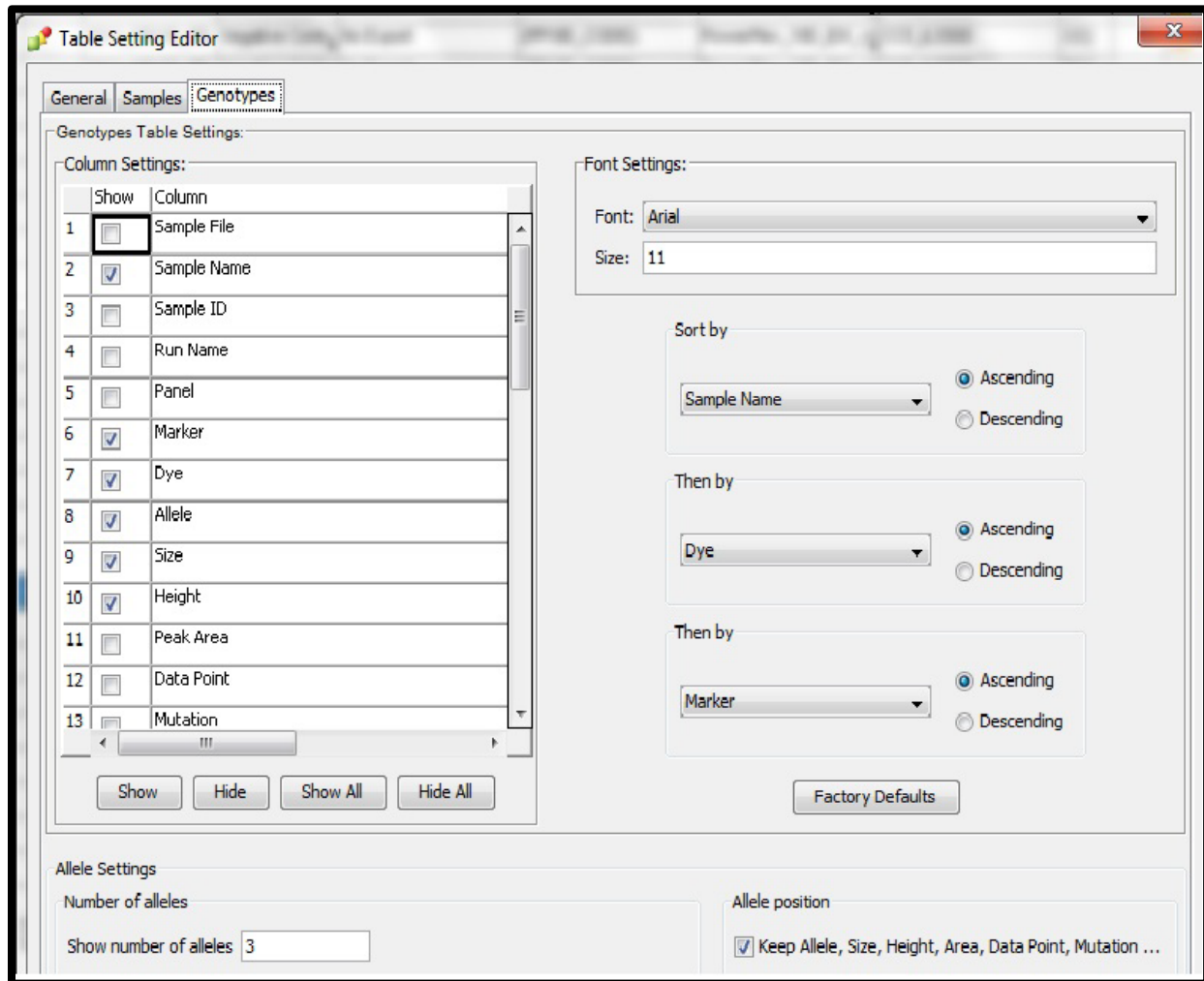
3.8.4.5   Create a Plot Setting – Samples and Controls

    3.8.4.5.1   Select "Tools", then "GeneMapper™ *ID-X* Manager".

    3.8.4.5.2   Select the "Plot Settings" tab and click "New".

    3.8.4.5.3   Under the "General" tab, name the Plot Setting "CODIS".

    3.8.4.5.4   Select "ISP Databasing Security Group".

    3.8.4.5.5   Select the "Sample Header" tab. Ensure the following are checked: Sample File, Sample Name, Panel, Sizing Quality Overridden, Sample Off-Scale, Sizing Quality, Sample Spike, Mixed Source, Outside Marker Range and Composite GQ.

3.8.4.5.6　Select the "Genotype Header" tab. Ensure the following are checked: Sample File, Sample Name, Panel, Marker, Off-Scale, Out of Bin Allele, Peak Height Ratio, Low Peak Height, Max Peak Height, Marker Spike, Allele Number, AMEL Cross Check, Broad Peak, Control Concordance, Overlap and Genotype Quality.

3.8.4.5.7　Select the "Sizing Table" tab. Ensure the following are checked: Dye/Sample Peak, Sample File Name, Marker, Allele, Size, Height, Area and Data Point. Set the font as Arial 11.

3.8.4.5.8　Select the "Labels" tab. Change the setting to those shown below.

Labels Tab

3.8.4.5.9　Select the "Display Settings" tab. Change the settings to those shown below.

Display Settings Tab
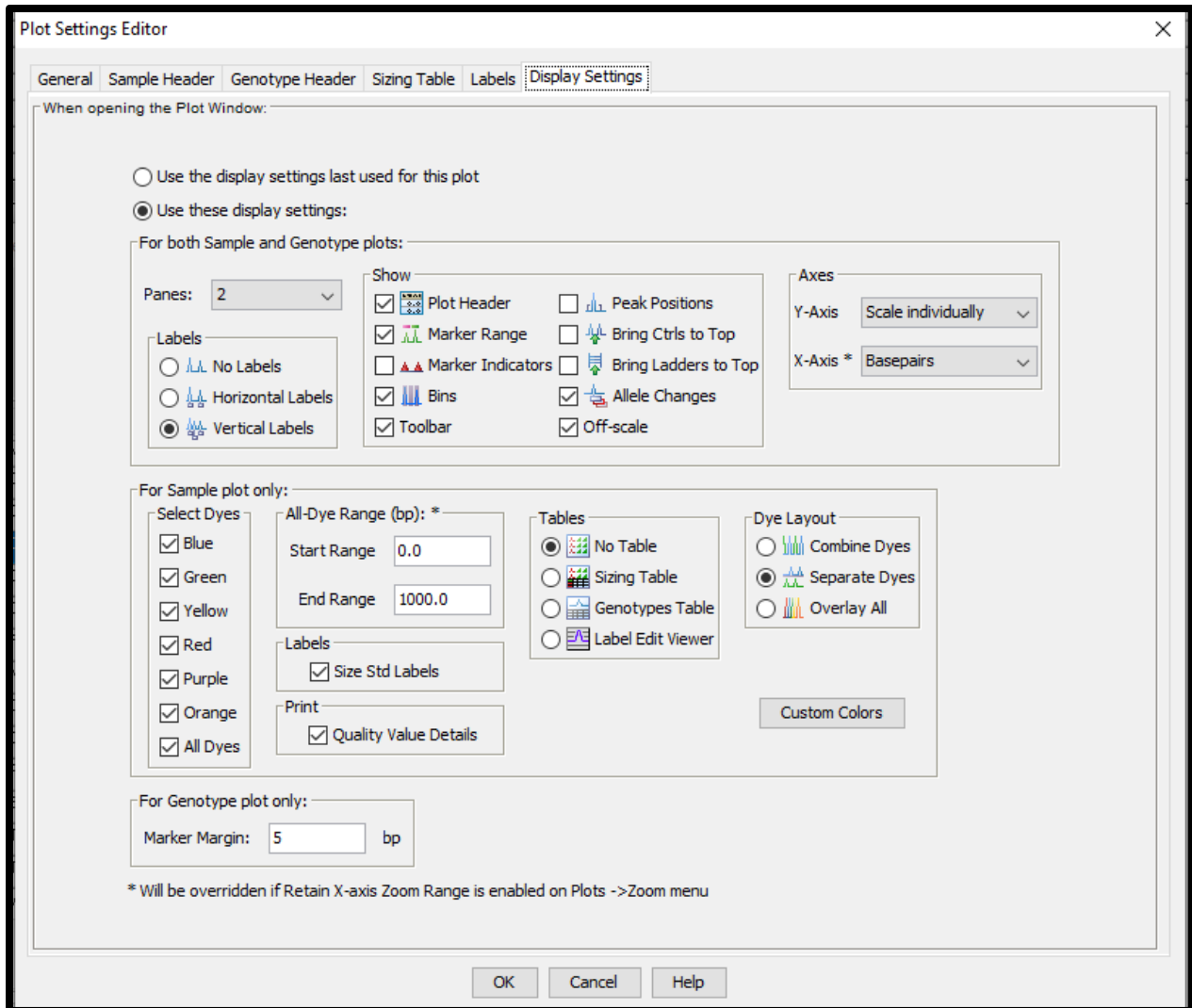
3.8.4.5.10   Select "OK" and click "DONE".
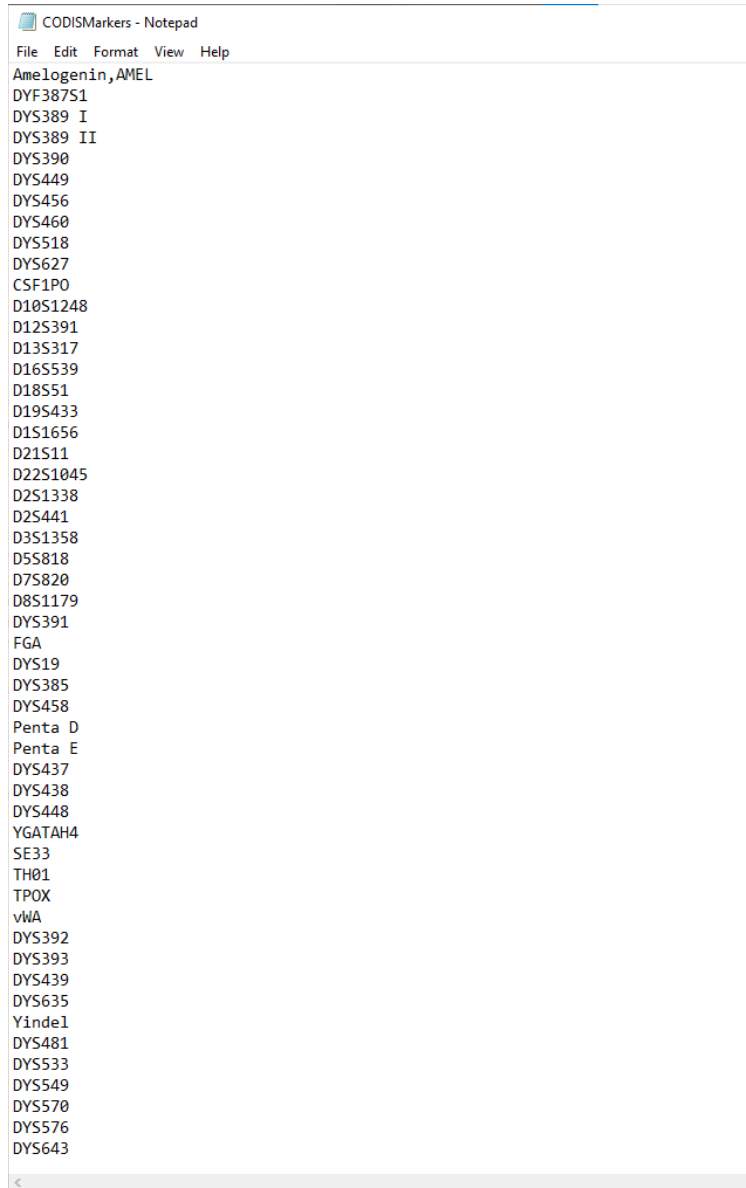
3.8.4.6   Locus names in CODISMarkers

3.8.4.6.1   Navigate to C:/AppliedBiosystems/GeneMapperID-X/Client on your state issued computer.

3.8.4.6.2   Open CODISMarkers in Notepad.

3.8.4.6.3   Alter the file as necessary so all loci are named exactly as shown below. Save without changing the name of the file.

```
CODISMarkers - Notepad
File  Edit  Format  View  Help
Amelogenin,AMEL
DYF387S1
DYS389 I
DYS389 II
DYS390
DYS449
DYS456
DYS460
DYS518
DYS627
CSF1PO
D10S1248
D12S391
D13S317
D16S539
D18S51
D19S433
D1S1656
D21S11
D22S1045
D2S1338
D2S441
D3S1358
D5S818
D7S820
D8S1179
DYS391
FGA
DYS19
DYS385
DYS458
Penta D
Penta E
DYS437
DYS438
DYS448
YGATAH4
SE33
TH01
TPOX
vWA
DYS392
DYS393
DYS439
DYS635
Yindel
DYS481
DYS533
DYS549
DYS570
DYS576
DYS643
```

3.8.5   Sampling

3.8.5.1   For oral swabs

3.8.5.1.1   Place the head of one swab in a deep well plate.

3.8.5.1.2   Using a fresh pipette tip every time, place 1 mL SwabSolution™ into each well containing a swab head.

3.8.5.1.3   For the reagent blank, place the solution only into well E12 for a full plate. A different well may be chosen for partial plates.

3.8.5.1.4   Incubate at 70 °C for approximately 1 hour.

3.8.5.2   For FTA® stain cards (non-FTA stain cards shall not be directly amplified)

3.8.5.2.1   Using the 1.2 mm Harris punch, take one punch of the stained area and place directly in the 96-well plate to be used in amplification set-up.

3.8.5.2.2   An unused stain card shall be punched between each stain card sample as a cleaning punch.

3.8.5.2.3   Repeat for all samples.

3.8.5.2.4   For the reagent blank, place one punch from an unused stain card in the appropriate well.

3.8.5.3   Wells F12, G12, and H12 shall be left empty for the placement of positive and negative amplification controls. Different wells may be chosen for partial plates.

3.8.5.4   Wells H01, H04, H07, and H10 shall be left empty for the placement of allelic ladders during CE plate setup. Different wells may be chosen for partial plates.

3.8.6   PowerPlex® Fusion 6C Amplification Set-Up

3.8.6.1   Full plates of oral swabs

3.8.6.1.1   The following steps shall be performed in the PCR amplification set-up area.

3.8.6.1.2   Thaw the Amplification Grade Water, PowerPlex® Fusion 6C 5X Master Mix and PowerPlex® Fusion 6C 5X Primer Pair Mix. When thawed, it is important to vortex the PowerPlex® Fusion 6C 5X Master Mix and PowerPlex® Fusion 6C 5X Primer Pair Mix tubes for 5 to 10 seconds. After first use, components shall be stored refrigerated.

3.8.6.1.3   Place 0.2 mL 96-well plate(s) in the PCR setup area and label appropriately.

3.8.6.1.4   To prepare master mix for a full plate of samples, add the following to a tube and mix gently:

     3.8.6.1.4.1   550 µL Amplification Grade Water

     3.8.6.1.4.2   250 µL PowerPlex® Fusion 6C 5X Master Mix

     3.8.6.1.4.3   250 µL PowerPlex® Fusion 6C 5X Primer Pair Mix

3.8.6.1.5   Add 10.5 µL of PCR master mix to each well for all samples and controls.

3.8.6.1.6   Pipette 2 µL of liquid from each sample into the respective well containing master mix, using a new tip for each sample. Samples may be stored refrigerated until no longer needed.

3.8.6.1.7   For the positive control, dilute the 2800M DNA standard or other approved positive DNA standard supplied with the PowerPlex® Fusion 6C kit to 5.0 ng/µL. Pipette 2 µL into the designated well(s) containing 10.5 µL of PCR master mix. A positive control shall be included on each plate.

3.8.6.1.8   For the negative amplification control, pipette 2 µL of nuclease free or amplification grade water into the designated well containing 10.5 µL of the PCR master mix. A negative amplification control shall be included on each plate.

3.8.6.1.9   Cover the amplification plate with a foil seal and centrifuge briefly to remove air bubbles from the wells.

3.8.6.1.10   Place the 96-well plate in a thermal cycler.

3.8.6.1.11   Select and run the "fusion6C-25cycle" thermal cycling protocol.

3.8.6.1.12   Remove the plate after the amplification process is completed.

3.8.6.1.13   Store the amplified samples in the freezer (or refrigerator if they are to be used within 24 hours).

3.8.6.2   Partial plates or those containing a combination of oral and blood samples

3.8.6.2.1   The following steps shall be performed in the PCR amplification set-up area.

3.8.6.2.2   Thaw the Amplification Grade Water, PowerPlex® Fusion 6C 5X Master Mix and PowerPlex® Fusion 6C 5X Primer Pair Mix. When thawed, it is important to vortex the PowerPlex® Fusion 6C 5X Master Mix and PowerPlex® Fusion 6C 5X Primer Pair Mix tubes for 5 to 10 seconds. After first use, components shall be stored refrigerated.

3.8.6.2.3   Place a 0.2 mL 96-well plate in the PCR setup area and label appropriately.

3.8.6.2.4   Determine the number of samples of each type to be amplified, including controls (reagent blank, positive control and amplification blank). Add 2 to 4 reactions to this number to compensate for the loss that occurs during reagent transfer.

3.8.6.2.5   Stain card punches require a separate master mix preparation from the master mix for oral swabs and controls.

3.8.6.2.6   For oral swabs and controls, calculate the required amount of each component of the PCR master mix. Multiply the volume per sample (noted below) by the total number of reactions to obtain the final volume needed for each component.

    3.8.6.2.6.1   5.5 µL Amplification Grade Water

    3.8.6.2.6.2   2.5 µL PowerPlex® Fusion 6C 5X Master Mix

    3.8.6.2.6.3   2.5 µL PowerPlex® Fusion 6C 5X Primer Pair Mix

3.8.6.2.7   Add the calculated volume of each component to a tube. Mix gently.

3.8.6.2.8   Add 10.5 µL of PCR master mix to each well for all samples and controls.

3.8.6.2.9   Pipette 2 µL of liquid from each sample into the respective well containing master mix, using a new tip for each sample. Samples may be stored refrigerated until no longer needed.

3.8.6.2.10   For the positive control, dilute the 2800M DNA standard or other approved positive DNA standard supplied with the PowerPlex® Fusion 6C kit to 5.0 ng/µL. Pipette 2 µL into the designated well(s)

containing 10.5 µL of PCR master mix. A positive control shall be included on each plate.

3.8.6.2.11   For the negative amplification control, pipette 2 µL of nuclease free or amplification grade water into the designated well containing 10.5 µL of the PCR master mix. A negative amplification control shall be included on each plate and shall be the last sample in the batch.

3.8.6.2.12   For stain card punches, calculate the required amount of each component of the PCR master mix. Multiply the volume per sample (noted below) by the total number of reactions to obtain the final volume needed for each component.

3.8.6.2.12.1   5.0 µL Amplification Grade Water

3.8.6.2.12.2   2.5 µL PowerPlex® Fusion 6C 5X Master Mix

3.8.6.2.12.3   2.5 µL PowerPlex® Fusion 6C 5X Primer Pair Mix

3.8.6.2.12.4   2.5 µL 5X AmpSolution™ Reagent

3.8.6.2.13   Add the calculated volume of each component to a tube. Mix gently.

3.8.6.2.14   Add 12.5 µL of PCR master mix to each well containing a stain card punch. Use a new disposable tip for each well.

3.8.6.2.15   Cover the amplification plate with a foil seal and centrifuge briefly to remove air bubbles from the wells.

3.8.6.2.16   Place the 96-well plate in a thermal cycler.

3.8.6.2.17   Select and run the "fusion6C-25cycle" thermal cycling protocol.

3.8.6.2.18   Remove the plate after the amplification process is completed.

3.8.6.2.19   Store the amplified samples in the freezer (or refrigerator if they are to be used within 24 hours).

3.8.7   Promega® Spectrum CE Instrument – Spectrum Control Software v3.1.0 (8)-PowerPlex® Fusion 6C Electrophoresis

3.8.7.1   Sample Preparation

3.8.7.1.1   **Note:** The quality of formamide is critical for the successful detection of a DNA profile. Deionized formamide shall be used that has a conductivity of less than 100 µS/cm, such as Hi-Di™ Formamide. The formamide shall be frozen in aliquots at -20 °C and the remainder of each aliquot shall be discarded after it is thawed. Multiple freeze-thaw cycles or long-term refrigerated storage may cause breakdown of the formamide which can create ions that compete with DNA during injection. This will cause lower peak heights and decreased sensitivity.

3.8.7.1.2   **Caution:** Formamide is an irritant and teratogen; therefore, universal precautions and a fume hood shall be utilized when manually working with formamide to avoid inhalation and contact with the skin.

3.8.7.1.3   For initial use, thaw the WEN ILS 500, PowerPlex® Fusion 6C allelic ladder, and an aliquot of Hi-Di™ Formamide. When thawed, vortex to mix, then centrifuge briefly. The ILS and allelic ladder shall be stored at 2-10 °C after first use.

3.8.7.1.4   For a full plate, prepare a loading cocktail by combining 50 µL internal lane standard with 950 µL Hi-Di™ Formamide.

3.8.7.1.5   For a partial plate, calculate the required amount of each component of the loading cocktail. Multiply the volume per sample (noted below) by the total number of sample wells to obtain the final volume.

    3.8.7.1.5.1   9.5 µL Hi-Di™ Formamide

    3.8.7.1.5.2   0.5 µL WEN ILS 500

3.8.7.1.6   Vortex to mix.

3.8.7.1.7   Pipette 10 µL of the loading cocktail into each well.

3.8.7.1.8   Add 1 µL of amplified sample or 1 µL of the allelic ladder mix to each well, using a new tip for each sample. At least one allelic ladder is required within each run folder.

    3.8.7.1.8.1   If the plate is not full, add formamide or loading cocktail into empty wells to complete an injection set of 8. Every well in which an injection is occurring must contain liquid.

3.8.7.1.9   Cover the samples with a plate septum and centrifuge briefly to remove air bubbles from the wells.

3.8.7.1.10 OPTIONAL: Just prior to loading, denature the plate at 95 °C for ~3 minutes and immediately chill for ~3 minutes. Avoid denaturing for longer than 3 minutes as this may lead to the appearance of increased artifacts.

3.8.7.2 Prepare the Instrument

3.8.7.2.1 Open the Spectrum Control Software (SCS). The HOME screen will launch.

Home Screen

3.8.7.2.2 Check oven status. Ensure oven is ON using toggle button at the upper right of the HOME screen.

3.8.7.2.3 Check consumables status to ensure a sufficient supply for the samples to be loaded. Details are found on the consumables screen by selecting the status indicator at the upper right of the HOME screen.

3.8.7.2.4 Check that buffers and polymer have not exceeded 14 days on the instrument or the manufacturer expiration date.

3.8.7.2.5   Once all scheduled runs are complete, consumables may be replaced as needed, using the wizard button(s) for the appropriate supplies.

Consumables screen
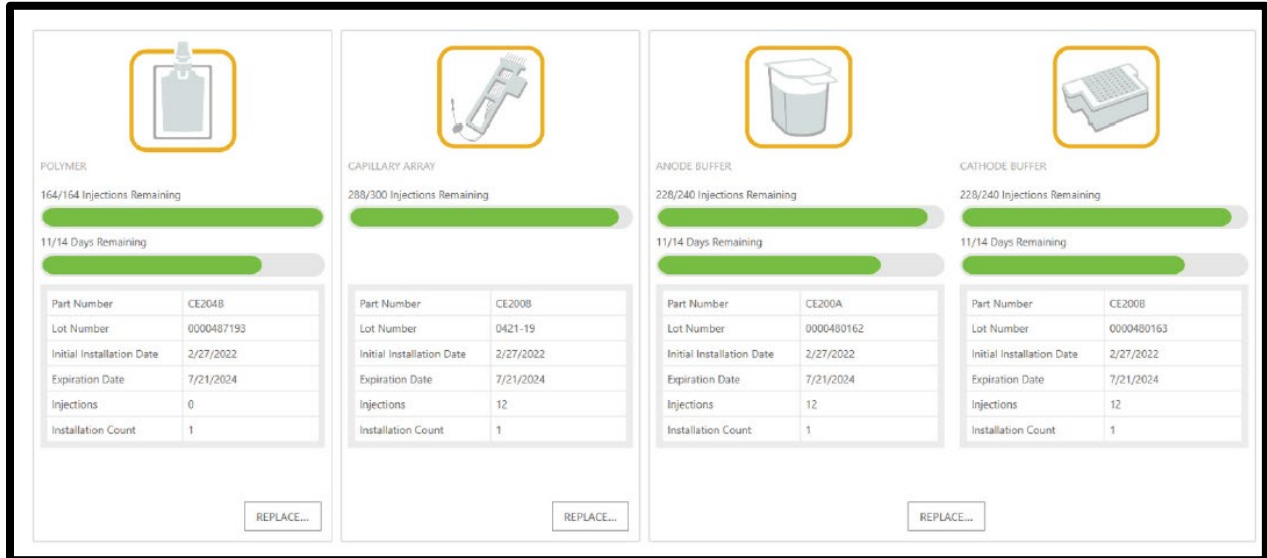
3.8.7.3   Creating a plate record by importing a plate record file (recommended)

3.8.7.3.1   Select IMPORT PLATE from the HOME screen to open a browsing window.

3.8.7.3.2   Navigate to the location of the plate record file. The file location will be preserved for future imports.

3.8.7.3.3   Select the plate record import file and select Open.

3.8.7.3.4   The plate screen will display the imported plate information including the plate ID, sample IDs, sample types, and instrument protocol.

3.8.7.4   Creating a new plate record manually

3.8.7.4.1   Select NEW PLATE from the HOME screen to open the NEW PLATE screen.

New Plate Screen

3.8.7.4.2 Enter a unique plate ID including year, database plate number, sample type, and injection number (ex: 2025_DB001A_01).

3.8.7.4.3 Enter a User (initials and/or PE# of plate creator).

3.8.7.4.4 Enter a sample ID for each sample by selecting the appropriate well(s) and typing the information, or in the 'Sample' tab of the Sample Information section.

3.8.7.4.5 Select the correct sample type for all samples, positive and negative controls, and allelic ladders.

3.8.7.4.6 Select "PowerPlex_Fusion_6C" GeneMarker template in the "GMHID-Spectrum" field for all wells to be injected.

3.8.7.4.7 Select the "ISP CODIS 6C" run protocol for all wells to be injected.

3.8.7.4.7.1 Protocols are added to samples or injections using the "+" button after selecting desired samples. Protocols may be added to a

plate in draft, queued, or running status (not completed or aborted). An injection number will be assigned and displayed in the injection set box.

3.8.7.4.7.2   To reorder injections, right-click the desired injection and select the appropriate command. The Protocol Queue (toggle "≡" icon to view) displays all scheduled injections with remaining injection time, status, column(s), and assigned run protocol.

3.8.7.4.7.3   To remove a protocol, use the "–" button.

3.8.7.4.8   Sample type, run protocol, and GeneMarkerHID template can be added to multiple samples at once by highlighting all desired wells in the plate map before selecting these options. To select multiple samples, left-click and drag to select a range of wells or use CTRL+click to select specific wells as a group.

Plate view left pane - protocol assignment

3.8.7.5   Accessing draft plates

3.8.7.5.1   A created plate record remains in "draft" status until linked to a plate position. Status changes to "queued" once linked but will revert to "draft" if unlinked before processing begins.

3.8.7.5.2   To access a list of plates in draft status, select the DRAFT PLATES button from the HOME screen.

3.8.7.5.3   NOTE: Plate, sample, and injection information can only be modified while a plate record is in draft status.

3.8.7.6   Loading a plate

3.8.7.6.1   Assemble the plate by placing the 96-well plate in a yellow base and attaching a white plate retainer over the 96-well plate. Check alignment of notched corners on all three components.

3.8.7.6.2   Verify the drawer is not locked or wait for unlocked status.

     3.8.7.6.2.1   The drawer handle light should be illuminated, indicating the drawer is unlocked and ready for plate loading.

     3.8.7.6.2.2   "Drawer Locked" is displayed in the Message Center if a previously loaded plate is actively injecting.

3.8.7.6.3   Open the plate drawer. The Message Center will now display the "Drawer Open" message.

3.8.7.6.4   Check the Plate Position indicator to determine an open plate position (A, B, C or D) that does not already contain a plate.

     3.8.7.6.4.1   NOTE: If a new plate is placed in a position reserved for an active plate currently on the autosampler, the system will display an error indicating the plate position cannot be used.

3.8.7.6.5   Place the plate assembly in an open position with the notched corner in the upper left. The Plate Positions indicator will update that position to Occupied, but not Linked.

3.8.7.6.6   Close the plate drawer. The Plate Drawer Status indicator will change from Open to Closed.

Plate Status Indicator
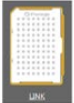
3.8.7.7   Linking a Plate for a Run

     3.8.7.7.1   After placing a plate into the plate drawer, a plate must be linked to add it to the run queue.

3.8.7.7.2   Select the appropriate plate in the Plate Positions indicator and select LINK under the plate position. The option under the position will change to UNLINK and the plate name will appear above the position.

   3.8.7.7.2.1   If a new plate is linked while no runs are in progress, the green START button must be selected to begin.

   3.8.7.7.2.2   If a plate is linked while a previous run is in progress, the newly linked plate will enter the run queue and automatically run when all previously scheduled plates are complete.

   3.8.7.7.2.3   The status of linked plates will update in the Plate Positions indicator as the run queue progresses.

3.8.7.7.3   To access the plate screen for linked plates, select the plate image in the Plate Positions indicator. The Plate Status is indicated as follows:

Plate Positions Indicator status icons

Icon	Status		Icon	Status
	No plate is detected in plate drawer.		(green plate icon)	The plate is linked and all injections on the plate have completed.
LINK	The plate is detected in the plate drawer. No plate record is linked. Clicking a plate icon in this state opens the Review Plates screen with the Draft filter applied. See Section 5.1.		(red plate icon)	The plate is linked and the run was aborted.
Run 2016.12.29 15:05:14 A 1	The plate record is linked to the plate in the designated position and is scheduled to run. The run name is displayed. The number inside the square indicates the order of the plate in the run queue (i.e., 1, 2, 3 or 4).		(orange plate icon) REMOVE	The new plate in is a position linked to the plate currently running on the instrument. You must remove the plate from the position.
Promega 6-Dye IST) [2017.10.23 16:27:54] A 1	The plate is linked and currently running on the instrument.			

3.8.7.7.4   Caution! Any plates linked to a plate position will be unlinked if the software is closed or if the instrument is turned off. If this occurs while a plate is running, the run will be aborted upon restart. Plates will also be unlinked when removed from the plate drawer.

3.8.7.7.5   To reorder injections, right-click the desired plate in the Plate Positions Indicator and select the appropriate command: Order Up, Order Down, Order First, Order Last.

3.8.7.7.6   To unlink a plate, select UNLINK in the Plate Position indicator under the appropriate plate.

3.8.7.7.7   To abort a run, select the Stop button in the header. This will abort the current run and clear the plate queue.

3.8.7.8   Monitoring a Run

3.8.7.8.1   To view status or data from an injection in progress or a completed injection, select the plate in the Plate Positions indicator.

3.8.7.8.1.1   The 'Electropherogram' tab displays the raw data electropherogram for the selected well(s). Each is labeled by the well position of the selected sample followed by the injection number [e.g., A1 (1)].

3.8.7.8.1.1.1   The display may be modified by zooming in or out, selecting a view range, or selecting dye channels as needed. To restore the default view, select the "Reset View" button

Electropherogram Tab

3.8.7.8.1.2   The Quality Table will populate with GMHID-Spectrum quality flags only if a GeneMarker®HID template was selected when the plate record was created. (See 3.8.7.4.6)

         3.8.7.8.1.2.1   The quality table lists samples in order by well position with allelic ladders and controls sorted to the bottom.

         3.8.7.8.1.2.2   This table displays the size score for each sample as well as a flag for each quality reason detected in the sample.

Quality Table

Well	Sample ID	Injection	Size Score	SQ	OL	OB	SD	SP	HI	LO	BC
C1	6C 1 ng Amp 1	1	96	■	■	■					
D1	6C 1 ng Amp 2	1	--	■							
E1	6C 1 ng Amp 3	1	78	■	■	■					
F1	6C 1 ng Amp 4	1	95	■	■	■			■		
G1	6C AL 1	1	96	■		■					
H1	6C AL 2	1	96	■		■					
A1	6C NTC 1	1	96	■	■	■					
B1	6C NTC 2	1	96	■	■	■					

Re-analyze

3.8.7.8.2   If samples require reinjection, a new injection may be added to a plate while it remains in the running status. Injections may not be added if the plate is already in the completed status.

3.8.7.8.3   To monitor the run conditions and log for a current run, expand the Status Bar by selecting the "∧" button at the bottom left of the screen.

         3.8.7.8.3.1   The monitor graph may be modified by zooming in and out or by checking and unchecking the boxes for desired parameters. To reset the view, select the "Zoom All" button.

         3.8.7.8.3.2   To review the system operations and error messages recorded throughout the run, use scroll bar on the right of the log list.

         3.8.7.8.3.3   To minimize the Status Bar, select the "∨" button at the bottom left of the screen.

Monitor graph
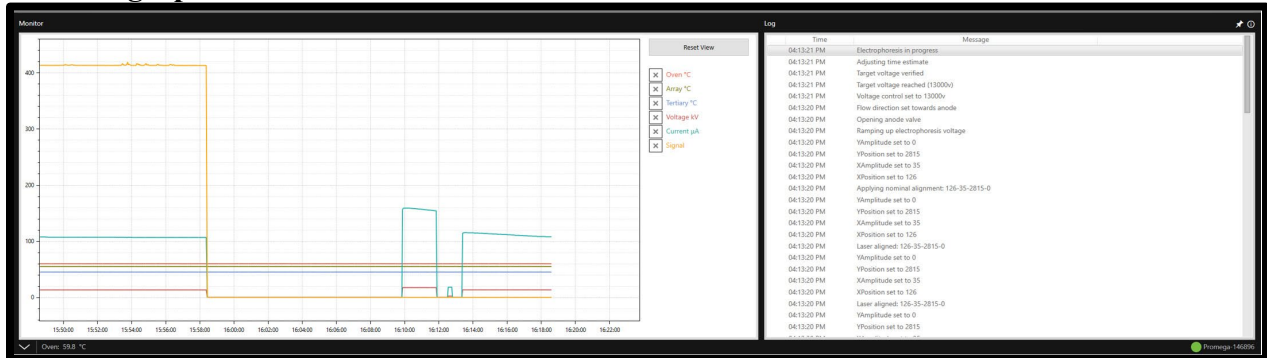
3.8.8   GeneMapper™ *ID-X* Version 1.6 Software - PowerPlex® Fusion 6C Data Analysis

3.8.8.1   Processing Sample Data

3.8.8.1.1   Import the sample files from a single run folder by clicking on "Edit", then selecting "Add Samples to Project".

3.8.8.1.2   In the "Add Samples to Project" screen, navigate to the run folder that contains the sample files.

3.8.8.1.2.1   If the entire run folder is to be imported, click on the folder to highlight it, then click the "Add to List" button at the bottom of the window.

3.8.8.1.2.2   If only a portion of samples need to be selected, expand the folder to view the samples. Highlight the appropriate samples, ensuring that the allelic ladder(s), controls and all the desired samples are selected. Once all the samples are selected, click the "Add to List" button at the bottom of the window.

3.8.8.1.3   Ensure that the necessary files are now located in the "Samples to Add" window by double-clicking on the folder in the right pane, then click "Add".

3.8.8.1.4   After the samples have been added to the project, the raw data can be viewed to ensure that a bad injection did not occur. To check the raw data, first expand the project folder in the left navigation pane, then click on a sample file, then click on the "Raw Data" tab in the right GeneMapper™ *ID-X* window. To return to the "Samples" window, click on the project folder at the top of the left navigation pane.

3.8.8.1.5   The GeneMapper™ *ID-X* project shall contain at least one allelic ladder from each run folder included in the project for proper

genotyping. Multiple allelic ladders within a run folder will be averaged by the software to calculate the allelic bins.

3.8.8.1.6   Ensure the table setting at the top of the screen is set to "CODIS".

3.8.8.1.7   In the "Analysis Method" column, for each sample select "Fusion6C_CODIS_Spectrum" from the drop-down menu. Click the column header cell to highlight the entire column, then select "Edit", then "Fill Down" (or the shortcut Ctrl + D).

3.8.8.1.8   In the "Panel" column, for each sample select "PowerPlex_Fusion_6C_CODIS_ES_Panels_ISP_IDX_v1.1" from the drop-down menu. Click the column header cell to highlight the entire column, then select "Edit", then "Fill Down" (or the shortcut Ctrl + D).

3.8.8.1.9   In the "Size Standard" column, select "WEN ILS 500" from the drop-down menu. Click the column header cell to highlight the entire column, then select "Edit", then "Fill Down" (or the shortcut Ctrl + D).

3.8.8.1.10   The Analysis Method, Size Standard and Panel can be set as defaults when a GeneMapper™ *ID-X* project is opened. Under the "File" menu, select "Project Options". Under the "Add Samples" tab, select the above settings as the default in the drop-down menus for Analysis Method, Size Standard and Panel. Click "OK".

3.8.8.1.11   Select the green "Analyze" arrow button to start the data analysis. At the project name prompt, save the project. At a minimum, the project name shall contain the plate name for the project. Select the "ISP Databasing Security Group".

3.8.8.2   Evaluating Sample Data

3.8.8.2.1   The Sizing Quality PQV will be yellow or red if the sizing quality is less than 0.75. These samples should be interpreted with caution and may be re-run at the analyst's discretion. All appropriate ILS peaks shall be present and labeled correctly.

3.8.8.2.2   Verify that the correct allele calls are made for each ladder peak and positive control sample.

3.8.8.2.3   For negative controls, ensure that no allelic peaks above analytical threshold are present.

3.8.8.2.4   Highlight all sample rows. Then click "View", then "Display Plots". Magnify the area from approximately 50 bp to 500 bp. Evaluate all allele calls.

3.8.8.2.5   Set "Specimen Category" for all passing offender samples as either "Convicted Offender" or "Arrestee." "Specimen Category" for samples to be re-run, controls, and ladders shall be "No Export" to exclude them from the CMF.

3.8.8.2.6   Create a CMF for import into CODIS.

   3.8.8.2.6.1   Ensure all samples are displayed.

   3.8.8.2.6.2   Click on "File" then "Export Table for CODIS".

   3.8.8.2.6.3   Under "Export File As", select either CMF 3.2 or CMF 3.3 as the file format.

   3.8.8.2.6.4   Under "CODIS Laboratory IDs", select "INISP5200" for both the "Source" and "Destination".

   3.8.8.2.6.5   Click "OK".

   3.8.8.2.6.6   Name the CMF with, at minimum, the plate name included. (e.g., 2025_DB001A_01).

3.8.8.2.7   After all analysis is complete, save the Run Folder containing the sample files, associated projects and CMFs under the batch folder in the zCODIS folder located on the server. Periodically delete projects from GeneMapper™ *ID-X* Manager to maintain computer disk space. Data files will be deleted from the database on a routine basis.

3.8.9   Interpretation Guidelines for PowerPlex® Fusion 6C

3.8.9.1   Once a determination has been made whether a peak is to be considered a true allele, the following interpretation guidelines shall be used. The analytical threshold is established at 150 relative fluorescent units (RFU) for GeneMapper™ *ID-X* software. The stochastic threshold for data interpretation is 400 RFU.

3.8.9.2   Peaks below 150 RFU shall not be interpreted for CODIS entry. If allelic drop-out is suspected in any of the CODIS core loci, the sample shall be re-run, when possible, to attempt to obtain a full profile. If allelic drop-out is

suspected in a non-core locus, that locus may be omitted from CODIS entry and allele calls deleted. Hit confirmations may be used with drop-out present.

3.8.9.3　Samples with a single peak in an autosomal locus between 150-399 RFU shall be re-run if being used for CODIS entry. If the single peak in this range is in a non-core locus, that locus may be omitted from CODIS entry and the allele call deleted.

3.8.9.4　Heterozygous alleles with peak height balance less than 60% should be interpreted with caution. The interpretation of profiles containing imbalance shall be at the discretion of the analyst based on their training and experience.

3.8.9.5　Controls

　　3.8.9.5.1　Failed controls require notification to the Technical Leader with appropriate documentation in the batch folder located on the server.

　　3.8.9.5.2　The appearance of pull-up or known artifact peaks does not render the following controls inconclusive.

　　3.8.9.5.3　Reagent Blank

　　　　3.8.9.5.3.1　The purpose of the reagent blank is to determine if the reagents used to extract the associated samples were contaminated by human DNA. Therefore, no signal should be detected in this sample well other than the internal lane standard. If a signal is detected in the reagent blank, all results of samples associated with that reagent blank shall be considered inconclusive.

　　　　3.8.9.5.3.2　A reagent blank with possible peaks below 150 RFU shall not prevent associated samples from being interpreted.

　　　　3.8.9.5.3.3　A reagent blank with allelic peaks of 150 RFU and above shall be considered a failed negative control.

　　3.8.9.5.4　Positive Control

　　　　3.8.9.5.4.1　The 2800M positive DNA control supplied with the PowerPlex® Fusion 6C kits is used as a positive control to demonstrate that the kit is performing properly. A positive control is considered a failed positive control if expected alleles are not detected, a single peak is < 400 RFU, or if extra alleles are detected.

2800M Profile

X, Y	17, 18	12, 13	10, 14	13, 15	9, 11	7, 14
Amelogenin	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E

9, 13	16, 18	22, 25	12	12, 13
D16S539	D18S51	D2S1338	CSF1PO	Penta D

6, 9.3	16, 19	29, 31.2	8, 11	12	11
TH01	vWA	D21S11	D7S820	D5S818	TPOX

14, 15	18, 23	13, 14	15, 16	16
D8S1179	D12S391	D19S433	SE33	D22S1045

10	20, 23	18	17
DYS391	FGA	DYS576	DYS570

3.8.9.5.5   Amplification Blank

3.8.9.5.5.1   The purpose of the amplification blank is to determine if human DNA contaminated the samples at the amplification step. Because no template DNA was placed in the reaction, the sample well should be blank except for the internal lane standard peaks. If amplified product is detected in the amplification blank well, the test is considered inconclusive.

3.8.9.5.5.2   An amplification blank with possible peaks below 150 RFU shall not prevent associated samples from being interpreted.

3.8.9.5.5.3   An amplification blank with allelic peaks of 150 RFU and above shall be considered a failed negative control.

3.8.9.5.6   Interpreting, Comparing and Reporting DNA results associated with Failed Controls and Contamination Events

3.8.9.5.6.1   The Technical Leader shall be notified if a positive or negative control fails and/or if sample contamination occurs. Sample contamination is defined as additional peaks present in a sample that can be conclusively identified to not have originated in the sample (e.g., a mixture in an offender sample).

3.8.9.5.6.2   Assessment of the integrity of the associated DNA results shall be done in consultation with the Technical Leader. This shall include the possible cause and effect of the failed control or contamination. Additionally, an assessment of the risk

associated with moving forward with interpretation shall be documented.

3.8.9.5.6.3   Documentation in the batch file shall include at a minimum: the sample, reference, or control test result that failed or was contaminated, the likely or known cause of the failed control or contamination, the likely or known source of the contamination, the impact on the integrity of the DNA results, and the determination if the test result is suitable or unsuitable for interpretation.

3.8.9.6   The analytical and stochastic threshold shall be determined during validation. It shall be at the analyst's discretion, based on experience and training, as to which peaks are suitable for interpretation. If an analyst has determined that a peak that has been labeled by the GeneMapper™ *ID-X* software is not a true allele peak, the analyst can delete the allele call label in the software. The GeneMapper™ *ID-X* software is set to record all allele changes. Therefore, any change or deletion in an allele call shall be maintained in the saved project.

3.8.9.7   An analyst is required to confirm all allelic ladders used for allele designation performed correctly and the allele calls for all positive controls are correct.

3.8.9.8   A Global filter shall be set in the GeneMapper™ *ID-X* software to 20%. Therefore, any peaks that are less than 20% of the major peak at a locus will be automatically filtered out by the software and not labeled. This should significantly reduce the frequency of many of the following types of peaks that will be labeled as alleles by the software.

3.8.9.9   Stutter peaks are artifacts of the amplification process and display less intensity than the true parent peak. Stutter peaks will typically be observed one repeat unit shorter than the parent peak (e.g., n-4 at a tetranucleotide STR) but may also occur two repeats shorter (e.g., n-8 at a tetranucleotide STR), or one repeat longer (e.g., n+4 at a tetranucleotide STR). Additionally, n-2 artifact peaks have been reported at several loci amplified with PowerPlex® Fusion 6C.

3.8.9.9.1   The interpretation of these peaks, similar to the other artifact peaks, shall be at the discretion of the analyst based on their training and experience.

3.8.9.10   Artifacts have been observed and documented utilizing the PowerPlex® Fusion 6C amplification kit. A complete list of artifacts, including

nonhuman cross-reactivity, can be found in the PowerPlex® Fusion 6C Technical Manual. It is the analyst's discretion to determine which allele calls may be deleted in GeneMapper™ *ID-X* analysis.

3.8.9.11 Pull-up or bleedthrough peaks can occur if signal intensity of sample or ILS peaks are too high or if a new spectral calibration needs to be run. Any pull-up peaks called as alleles by the GeneMapper™ *ID-X* software should be deleted. The sample should be re-run if a pull-up peak interferes with the analyst's ability to evaluate the profile based on their experience and training.

3.8.9.12 Spikes are peaks that generally appear in all colors and are sharper than regular peaks; however, they can occur predominantly in one color. Spikes are a natural consequence of capillary electrophoresis and can be caused by dust or urea crystals in the system. It is essential that the instrumentation be maintained and cleaned regularly to minimize the appearance of spikes. All spikes called as alleles by the GeneMapper™ *ID-X* software should be deleted. The sample should be re-injected when a spike interferes with the analyst's ability to evaluate the profile based on their experience and training.

3.8.9.13 Crosstalk peaks can occur within a single injection when intense signal from one capillary is detected by the CCD sensor on pixels mapped to a different capillary with lower signal intensity. Crosstalk signal seldom shows effects beyond adjacent capillaries. The sample should be re-run if crosstalk interferes with the analyst's ability to evaluate the profile based on their experience and training.

3.8.9.14 Rare variants (microvariants) have been described in the literature. These peaks will have a similar intensity to the other major peak for that locus but will not line up with the allelic ladder or have a bin in the GeneMapper™ *ID-X* PowerPlex® Fusion 6C panels and bins settings.

   3.8.9.14.1 Any allele peak that is not present in the allelic ladder and does not have an associated "bin" in the GeneMapper™ *ID-X* analysis software, will be called "OL" by the software. The analyst can rename the allele.

   3.8.9.14.2 Alleles located between two full-repeat alleles on the ladder shall be described as the short repeat followed by the number of base pairs it is larger (i.e., X.1, X.2, etc.). A full-repeat microvariant larger than an allele on the ladder may be designated with the full repeat number.

3.8.9.14.3 Alleles which are located outside the range of the ladder or bin set for a given locus (above or below) shall be designated as "<[smallest allele]" or ">[largest allele]" for that locus.

3.8.9.14.4 If an allele falls outside the marked range of any discrete locus, it will be designated as "OMR" by the GeneMapper™ *ID-X* software. In this case, it is necessary to both name the allele and assign the locus to which it belongs.

3.8.9.15 Mixed DNA samples shall be investigated for possible contamination and re-run as appropriate. All loci shall be taken into consideration when determining if a mixture is present. A three-peak pattern at one or more loci may be an indication of a mixture. However, three-peak patterns have been reported for single source profiles. If a three-peak pattern is observed for a single locus and is believed to be tri-allelic, the sample should be re-amplified to confirm the possible tri-allelic locus.

3.8.9.16 If it is determined a sample needs to be re-run, it shall be labeled "No Export" in the GeneMapper™ *ID-X* analysis software and either re-injected or entered on the current re-amplification plate record(s).

3.8.9.17 All re-amplifications shall be checked against the original run for concordance.

3.8.9.17.1 Creating a concordance project

3.8.9.17.1.1 Ensure all original GeneMapper™ *ID-X* projects containing samples to be used for concordance checks have already been imported into GeneMapper™ *ID-X*.

3.8.9.17.1.2 Open the project containing the re-amplification samples by selecting "File" then "Open Project". Navigate to the appropriate project and select "OK".

3.8.9.17.1.3 Select "Edit" then "Add Samples to Project".

3.8.9.17.1.4 Choose the tab labeled "GMID-X Database" then press the "Search" button.

3.8.9.17.1.5 Navigate to the folder(s) containing the desired concordance sample(s) and expand.

3.8.9.17.1.6 Select the sample(s) and then "Add To List". Once all samples for concordance have been selected, press the "Add" button.

3.8.9.17.1.6.1 Allelic ladders and controls shall not be added to the concordance project from the original project.

3.8.9.17.1.6.2 Concordance samples shall not be re-analyzed.

3.8.9.17.1.7 Save the updated project according to previously established guidelines with "_concordance" at the end of the name. (e.g., 2025_DB001RA_concordance)

3.8.9.18 Rare circumstances, such as an allele between markers or a low-level tri-allele that is present but not always above threshold, require interpretation by the analyst using their experience and best judgement. If two genotypes appear equally feasible, that offender may be entered in CODIS twice with the database identifier and either A or B (e.g., INODB123456A and INODB123456B). This covers both possibilities for matching purposes.

3.9 **Records:**

3.9.1 The appropriate worksheets as contained in the Worksheet Manual or the equivalent workbooks shall be used to record all procedures.

3.9.2 The technical review of data shall be recorded on the worksheet provided for that purpose.

3.9.3 All data (Spectrum run folders, GeneMapper™ *ID-X* project files and CMFs) and documentation (plate records, emails, technical review worksheets) shall be saved in each batch folder located in the zCODIS folder on the server. All files stored on the server shall be routinely backed up to ensure security of data and maintained for a minimum of 50 years.

3.10 **Interpretations of Results:**

3.10.1 Profiles with conclusive results at all CODIS core loci shall be entered into SDIS.

3.10.2 If test results from a sample cannot be clearly interpreted, that sample should be repeated. An additional collection from the individual may be requested.

3.10.3 See Interpretation guidelines in 3.8.9 and 3.8.10 for specific guidelines.

3.11 **Reporting of Hits:** Not applicable

3.12 **References:**

3.12.1 Federal Bureau of Investigation. Procedures for the Detection of Restriction Fragment Length Polymorphisms in Human DNA. FBI Laboratory. 1990.

3.12.2 Federal Bureau of Investigation. PCR-Based Typing Protocols. FBI Laboratory. 1994.

3.12.3 Thermo Fisher Scientific®. Applied Biosystems™ VeritiPro™ Thermal Cycler Installation, Use, and Maintenance. Publication Number: MAN0019157 Revision B.0 https://assets.thermofisher.com/TFS-Assets/LSG/manuals/MAN0019157_veritipro_UG.pdf

3.12.4 Promega Corporation. *PowerPlex® Fusion 6C System for use on the Spectrum CE SystemTechnical Manual*. Part No. TMD051. Madison, WI 7/22 (or current version). Sections referencing software and instruments not used may be skipped. Print and web. https://www.promega.com/-/media/files/resources/protocols/technical-manuals/tmd/powerplex-fusion-6c-system-for-spectrum-ce-system-protocol-tmd051.pdf?rev=8cb5fd159cf746d8bd9a1bd25db375b0&sc_lang=en?la=en

3.12.5 Promega Corporation. SwabSolution™ Kit Technical Manual. Part No. TMD037. Most current issue.

3.12.6 Promega Corporation. PowerPlex® 6C Matrix Standard. Part No. TMD046. Most current issue.

3.12.7 Promega® Corporation. Spectrum CE System Operating Manual. Part No. TMD052, Madison, WI Revised 04/24 (or current version). https://www.promega.com/-/media/files/resources/protocols/technical-manuals/tmd/spectrum-ce-system-protocol-tmd052.pdf?rev=e61a0f81e975490a8ba3d18b567c9579&sc_lang=en

3.12.8 Bär W. et al. "DNA recommendations: Further report of the DNA Commission of the ISFH regarding the use of short tandem repeat systems". *Int. J. Legal Med.* (1997) 110, 175-176.

3.12.9 Gill P. et al. "Considerations from the European DNA profiling group (EDNAP) concerning STR nomenclature." *Forensic Science International* (1997) 87, 185-192.

3.12.10 Ensenberger, M. et al. "Developmental Validation of the PowerPlex® Fusion 6C System." *Forensic Science International: Genetics* 21 (2016): 134-144. Print and web. http://www.fsigenetics.com/article/S1872-4973(15)30107-1/abstract

3.12.11 Applied Biosystems®. *GeneMapper^{TM} ID-X Software Version 1.5 Reference Guide*. Part Number 100031707, Rev. A (or current version). Foster City, CA, 2015. Print and web. https://assets.thermofisher.com/TFS-Assets/LSG/manuals/100031707_GeneMapIDX_ver1_5_ReferenceGuide.pdf

3.12.12 Applied Biosystems. GeneMapper™ *ID-X* Software Version 1.6 User Bulletin. Publication No. 100073905 Rev B. Foster City, CA. 02/2019.

4   ISPL Familial Searching

4.1   Scope:

This test method is designed for the guidance of Laboratory personnel who assist in the deliberate search of CODIS offenders for relatives of a contributor to a crime scene sample. This manual may be expanded or altered as new techniques and/or genetic systems are available with the approval of the Division Commander.

4.2   Precautions/Limitations:

4.2.1   A familial search (FS) is an investigative lead and should not be interpreted as the identification of an individual contributing to a DNA profile but rather as a possible close relative (parent-child or full sibling).

4.2.2   Any leads generated should be confirmed by traditional direct comparison to an evidentiary standard.

4.3   Related Information:

4.3.1   Worksheet manual (current version)

4.3.2   Biology Casework Test Methods (current version)

4.4   Instruments:

4.4.1   Designated computer terminals and software

4.4.2   Biomek NXP Automated Laboratory Workstation - robotic DNA processing system

4.4.3   Biomek 3000¬ - robotic DNA processing system

4.4.4   Applied Biosystems® 3500xL Genetic Analyzer Capillary Electrophoresis Instrument - Simultaneously separates and detects multiple amplified DNA samples by size by capillary electrophoresis using fluorescently tagged primers.

4.4.5   Laminar Flow Hood - An air purifying biohazard cabinet that maintains a nominal inflow velocity of 80 fpm which prevents contaminants from entering or escaping the work area.

4.4.6   Miscellaneous Laboratory Equipment - Supportive laboratory equipment consisting of ovens, incubators, minifuges, pipettes, water baths, stirring/heating

plates, vortex mixers, thermometers, temperature verification system, vacuum pump, refrigerators/freezers for storing of reagents, buffers, and work product.

4.4.7   Thermal Cycler - An instrument that can be programmed to rapidly cycle between high and low temperatures. This process is used to make many fluorescently tagged copies of specific regions on a DNA strand(s).

4.4.8   Water Purification System - An apparatus that routes water through a series of filtering devices to produce high quality, uncontaminated water used in buffer preparation and DNA typing methods.

4.5   Reagents/Materials:

4.5.1   Reagents critical to the DNA analysis process are listed in the Critical Reagents Manual.

4.6   Hazards/Safety:

4.6.1   All chemicals shall be handled in a safe method as referenced in the specific Safety Data Sheets (SDS).

4.6.2   The manual preparation of samples for electrophoresis by the addition of Hi-Di™ Formamide shall be confined to a chemical fume hood. **Caution:** Formamide is an irritant and teratogen; therefore, universal precautions and a fume hood shall be utilized when manually working with formamide to avoid inhalation and contact with the skin.

4.6.3   Universal precautions shall be in use whenever biological materials are being handled.

4.6.4   Biological waste shall be disposed of in the appropriate waste receptacle.

4.7   Reference Materials/Controls/Calibration Checks:

4.7.1   DNA profiles shall be developed in compliance with the DNA Identification Act of 1994, the FBI Approved Quality Assurance Standards for Forensic DNA Testing Laboratories, and the FBI Approved Quality Assurance Standards for DNA Databasing Laboratories.

4.7.2   The accuracy and specificity of test results are ensured by running known DNA controls and reagent controls at the same time as samples. See the specific test for the appropriate controls to be run and the interpretation of the results.

4.8   Procedures/Instructions:

4.8.1   Selection of Cases/Profiles

4.8.1.1   The case and associated profile being considered shall meet the following criteria for a FS to be conducted. Exceptions shall be approved by the CODIS Unit Supervisor and documented in the case file.

4.8.1.1.1   Case Criteria

4.8.1.1.1.1   The case is an unsolved violent crime against a person or an investigation of an unidentified person.

4.8.1.1.1.2   The investigation is still active.

4.8.1.1.1.3   Other investigative leads have been exhausted.

4.8.1.1.1.4   In criminal investigations, if a FS would lead to the development of a named suspect, prosecution would be pursued.

4.8.1.1.2   Profile Criteria

4.8.1.1.2.1   The profile has been searched in CODIS at state and national levels with no hits.

4.8.1.1.2.2   The sample is a single source or a fully deduced single source male profile.

4.8.1.1.2.3   The sample has a Y-STR profile or enough sample remaining to perform testing.

4.8.1.1.2.4   The sample has 20 CODIS Core Loci or enough sample remaining to perform testing.

4.8.1.1.2.5   If insufficient genetic data is obtained upon additional testing, the sample is not suitable for a FS.

4.8.1.2   The CODIS Unit Supervisor shall have final determination of which case(s) and associated profile(s) are eligible for a FS.

4.8.1.2.1   A genotypes table for the searched profile may be created by the case analyst and stored in the batch folder.

4.8.1.3   A FS shall be conducted once per case and associated profile. If the search does not yield a lead, the agency may request the profile(s) be searched

again after a period of one year. Such requests may be approved or denied by the CODIS Unit Supervisor.

4.8.2   Performing a Familial Search

4.8.2.1   Additional testing as noted above shall be completed and the profile updated in CODIS before the search is performed. All entry procedures shall be followed and documented as described in section 1.8.

4.8.2.1.1   Rapidly mutating loci shall not be included in the search profile.

4.8.2.2   Use Pedigree Manager to create a new pedigree, including parents and one sibling for the forensic sample.

4.8.2.2.1   Set pedigree type to Familial Search.

4.8.2.2.2   The father and brother nodes shall be designated unknown.

4.8.2.2.3   Associate the forensic sample to the known sibling node.

4.8.2.2.4   Save the pedigree, but do not mark for upload to NDIS.

4.8.2.2.5   Print the Pedigree Details Report to PDF for the FS file.

4.8.2.3   Searcher shall be used to perform the STR search using the Familial Search configuration as follows:

4.8.2.3.1   All candidates returned

4.8.2.3.2   Minimum CLR of 10

4.8.2.3.3   Search against Offender and Unidentified Persons Indexes

4.8.2.4   Perform separate searches to target either parent-child or sibling relationships and save all ranks to rank manager.

4.8.2.5   Export rank list from rank manager.

4.8.2.5.1   Display ranks from current search with both nodes combined.

4.8.2.5.2   Sort by CLR. Highlight desired number of ranks. Disposition as Pending.

4.8.2.5.3   Sort Pending ranks by Candidate Specimen ID.

4.8.2.5.4   Look for duplicated candidates. For each pair, disposition the lower CLR as Investigative Information.

4.8.2.5.5   Export the Rank Inventory Report as a txt file.

4.8.3   Candidate List Evaluation

4.8.3.1   The 172 highest ranking candidates (according to CLR) will be considered for further evaluation. Analysis with PowerPlex® Fusion 6C and/or PowerPlex® Y23 Y-STR will be performed as appropriate.

4.8.3.2   Offender samples may include blood stain cards or buccal/oral swabs.

4.8.3.3   The DNA is incubated, amplified to produce many fluorescently tagged copies of specific regions of the DNA, and processed to separate and detect a DNA profile. These profiles are then entered into CODIS.

4.8.3.4   Sampling

All samples may be processed by protocols outlined in the current versions of the Biology Casework Test Methods and the Biology CODIS Test Methods or as detailed below.

4.8.3.4.1   For Automated Processing

4.8.3.4.1.1   Buccal/Oral swabs

4.8.3.4.1.1.1   Remove the collar from Promega Slicprep™ Device. Place the head of one swab in a well of the Promega Slicprep™ Device.

4.8.3.4.1.1.2   Repeat for all samples.

4.8.3.4.1.2   FTA® or non-FTA stain cards

4.8.3.4.1.2.1   Remove the collar from Promega Slicprep™ Device. Take a ~3 x 3 mm cutting of the stained area and place directly in a well of the Slicprep™ Device.

4.8.3.4.1.2.2   Repeat for all samples.

4.8.3.4.1.3   For each sample, combine 350 µL Stain Extraction Buffer for Automation (SEBA) with 10 µL Pro K (18 mg/mL) and 40 µL DTT (1M).

4.8.3.4.1.4   Reagent blanks: Place only SEBA master mix in an appropriate well.

4.8.3.4.1.5   Cover Slicprep™ Device with a foil seal and incubate overnight at 56 °C. Optional: Prior to incubation, quick spin the plate at 1450 RCF to move samples to the bottom of the 96 Spin Basket.

4.8.3.4.1.6   Following incubation, insert Slicprep™ collar and centrifuge the plate for 5 minutes at 1450 RCF.

4.8.3.4.1.7   Remove the 96 Spin Basket, Slicprep™ collar, and then cover with a foil seal.

4.8.3.4.1.8   Submit to automation team using pre-extraction processing form within 24 hours, leaving the Case field blank and using the INODB number as the sample name. Samples will be processed using PowerPlex® Fusion 6C and PowerPlex® Y23 using Automation methods.

   4.8.3.4.1.8.1   Assign the plate names with the year, familial search batch number, and plate identifier since two plates will be submitted for extraction for each FS (e.g., 2023_FS01A and 2023_FS01B).

   4.8.3.4.1.8.2   Note that an injection time of 20 seconds will be used on a 3500xL as per Appendix 3.

4.8.3.4.2   For Manual Processing

   Follow Maxwell® Preparation of Samples and Maxwell® FSC or RSC 48 Instrument Automated DNA Purification in current version of Biology Test Methods, except as below:

4.8.3.4.2.1   PowerPlex® Y23 System Amplification

   4.8.3.4.2.1.1   Follow Biology Casework Test Methods (current version); however, targeting 2.0 ng of template DNA is recommended. Amplification of greater than 2.0 ng of template DNA could lead to off-scale peak heights and may result in increased artifacts and interfere with interpretation.

For the positive amplification control (2800M or another approved positive DNA standard), target 0.1 – 0.5 ng.

4.8.3.5 GeneMapper™ *ID-X* Version 1.6 Software - PowerPlex® Fusion 6C and PowerPlex® Y23 Data Analysis (use Biology Casework Test Methods and Biology CODIS Test Methods (current versions)) except as listed below:

4.8.3.5.1 For PowerPlex® Y23

4.8.3.5.1.1 Analysis Methods

4.8.3.5.1.1.1 Select "Tools", then "GeneMapper™ *ID-X* Manager".

4.8.3.5.1.1.2 Select the "Analysis Methods" tab.

4.8.3.5.1.1.3 Select "New" and a new analysis method dialog box will open.

4.8.3.5.1.1.4 Enter the name "PowerPlex Y23_CODIS" for the analysis method.

4.8.3.5.1.1.5 In the Analysis Method Editor window, select "ISP Databasing Security Group" as the Security Group.

4.8.3.5.1.1.6 Select the "Allele" tab.

4.8.3.5.1.1.7 Select "PowerPlexY23_Bins_IDX_v2.0"as the Bin Set.

4.8.3.5.1.1.8 Ensure that the global cut-off value is set at 0.3 for all.

4.8.3.5.1.2 Interpretation Guidelines

4.8.3.5.1.2.1 Global Filter – A Global filter shall be set in the GeneMapper™ *ID-X* software to 30%. Therefore, any peaks that are less than 30% of the major peak at a locus will be automatically filtered out by the software and not labeled. This should significantly reduce the detection of most of the artifacts described in the Biology Casework Test Methods. It should be noted that this is not an expert system but merely a visual aid in interpretation.

4.8.3.5.1.2.2 Peak Heights – Peak heights will occasionally exceed 28,000 RFU when amplified at 2.0 ng. Data can be used; however, caution should be taken to confirm that peak

heights above 28,000 RFU do not interfere with the allele calls in those samples. Samples shall be re-amplified if allele calls are impacted by excessive artifacts.

4.8.3.5.1.2.3 Omit any locus with a duplication.

4.8.3.5.2 Creating a CMF

4.8.3.5.2.1 Ensure Table Setting is set to "CODIS" and "Specimen category" is set appropriately for all samples.

4.8.3.5.2.2 Create a CMF as outlined in 3.8.8.2.6.

4.8.3.5.2.2.1 If necessary, open the CMF in WordPad and ensure all user names match your CODIS ID. Resave.

4.8.4 Re-evaluation of ranks

4.8.4.1 After technical review, new genetic data shall be imported into CODIS as an update to the existing offender specimen.

4.8.4.2 Use rank manager to view the candidate ranks under consideration for the FS.

4.8.4.3 Re-evaluate the ranks affected and observe the new CLR, JPLR, and Y-STR LR for each candidate rank. Depending on the number of ranks chosen, this may take several hours.

4.8.4.3.1 Export the Final Rank Inventory Report including all affected ranks for the FS file.

4.8.4.3.2 Any candidate ranks with a CLR = 0 should be considered eliminated as an association. Disposition as No Match.

4.8.4.3.2.1 If the values of the JPLR and Y-STR LR appear to conflict, non-genetic information and/or manual comparisons of the profiles may be used to eliminate or support an association.

4.8.4.3.3 Candidate ranks without at least 12 Y-STR loci for comparison and with a JPLR < 1,000,000 should be considered eliminated as an association. Disposition as No Match.

4.8.4.3.3.1   If the values of the JPLR and Y-STR LR appear to conflict, non-genetic information and/or manual comparisons of the profiles may be used to eliminate or support an association.

4.8.4.3.4   Any remaining candidates shall be considered for reporting as an association. Additional human interpretation of the rank as well as non-genetic data may be used to further eliminate or support potential candidates.

4.8.5   Association Confirmation and Reporting of Results

4.8.5.1   If no candidate ranks remain, report negative FS as shown in [Appendix 4](#).

4.8.5.2   Offender to Case Associations

4.8.5.2.1   The CODIS Unit Supervisor shall ensure that the proper association steps are performed. The Familial Search Confirmation Checklist shall be used to document completion of the steps.

4.8.5.2.2   The qualifying offense of the offender should be verified through state or county resources. If no qualifying offense can be verified, the candidate rank shall be reported under IC 10-13-6-8(f).

4.8.5.2.3   The most complete offender sample profile shall be compared to the case profile to verify the candidate rank.

4.8.5.2.4   The thumbprint on the offender Sample Information Sheet shall be compared to the individual's 10 print fingerprint card to verify the identity of the offender sample, when possible.

4.8.5.2.4.1   This step need not be performed for offenders submitted with Live Scan print cards as this would be a redundant comparison to itself.

4.8.5.2.5   The case profile shall be verified by reviewing the original DNA analysis records.

4.8.5.2.6   Kinship statistics for the potential relationships shall be calculated by a qualified analyst and printed for the file. Support or non-support of at least one relationship shall be recorded on the Familial Search Confirmation Checklist.

4.8.5.2.7   After verifications are complete, the association shall be confirmed by the CODIS Unit Supervisor.

4.8.5.2.8   A written notification shall be generated stating the FS results. No statistics shall be included. Written notifications shall follow the format seen in [Appendix 4](#).

4.8.5.3   Written notifications shall be administratively reviewed for accuracy. This review shall be documented on the CODIS Notification Administrative Review worksheet.

4.8.5.4   Written notifications of associations shall only be released after a representative of the agency and the CODIS Unit Supervisor or other designated laboratory personnel meet to discuss the results of the FS either in-person or through a digital meeting platform (Microsoft Teams, Zoom, etc.).

4.8.5.5   The disposition and Source ID fields, if appropriate, shall be updated.

4.9   Records:

4.9.1   The appropriate worksheets as contained in the Worksheet Manual, or the equivalent workbooks shall be used to record all procedures.

4.9.2   The technical review of data shall be recorded on the worksheet provided for that purpose.

4.9.3   Familial Search Case Selection forms shall be uploaded to the LIMS imaging module for all ISPL cases.

4.9.4   Notifications shall have an assigned memo number and be uploaded to the LIMS imaging module along with their administrative review worksheet for all ISPL cases.

4.9.5   All data (3500/3500xL run folders, GeneMapper™ *ID-X* project files and CMFs) and related documentation (plate records, emails, technical review worksheets, etc.) shall be saved in each batch folder located in the zCODIS folder on the server. All files stored on the server shall be routinely backed up to ensure security of data and maintained for a minimum of 50 years.

4.9.6   Additional documentation of the search and results (Pedigree Details Report, exported rank lists, Familial Search Confirmation Worksheet, Kinship comparison statistics, etc.) shall be maintained in the appropriate Familial Search File. These documents shall be retained for a minimum of 2 years.

4.10   Interpretation of Results:

4.10.1 If any candidates remain and are still supported, a memo will be generated, and a meeting scheduled with the investigating agency to report the association as a lead.

4.10.2 If no candidates remain, a memo will be generated to report the negative FS.

4.10.2.1 The law enforcement agency may request the case be searched again after one year due to new offenders continually being added to CODIS.

4.11 Reporting of Investigative Leads:

4.11.1 Formatting of notifications shall follow those shown on ISP letterhead. Exact information given may differ according to what is available. Identification of potential familial relationship shall be included.

4.11.2 Known aliases should be reported in parentheses after the true identifier.

4.11.3 Investigative leads should be distributed at an investigative meeting either in-person or through a digital meeting platform. Investigative meetings should include the primary investigator, the prosecutor, the analyst(s) and the CODIS Unit Supervisor.

4.12 References:

4.12.1 Federal Bureau of Investigation. Familial Searching Manual for CODIS 8.0. Quantico, VA. Version 1.1. August 2018.

4.12.2 Myers SP et al. "Searching for first-degree familial relationships in California's offender DNA database: validation of a likelihood ratio-based approach." Forensic Science International: Genetics, vol. 5 2011, pp. 493-500.

4.12.3 Organization of Scientific Area Committees (OSAC) for Forensic Science. 2021-S-0029 Standard for Familial DNA Searching. Version 2.0. Nov 2022.

4.12.4 SWGDAM. Recommendations from the SWGDAM Ad Hoc Working Group on Familial Searching Executive Summary. 2012, pp. 1-34. http://media.wix.com/ugd/4344b0_46b5263cab994f16aeedb01419f964f6.pdf

4.12.5 Forensic Biology Section Casework Test Methods. Indiana State Police Laboratory. Current Edition. Indianapolis, IN.

Appendix 1
Indiana Criminal Code 10-13-6

IC 10-13-6Chapter 6. Indiana DNA Data Base

IC 10-13-6-1"Combined DNA Index System"
   Sec. 1. As used in this chapter, "Combined DNA Index System" refers to the Federal Bureau of Investigation's national DNA identification index system that allows the storage and exchange of DNA records submitted by state and local forensic DNA laboratories.

   [Pre-2003 Recodification Citation: 10-1-9-1.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-2"DNA"
   Sec. 2. As used in this chapter, "DNA" means deoxyribonucleic acid that:

   (1) is located in the nucleated cells;

(2) provides an individual's personal genetic blueprint; and

(3) encodes genetic information that is the basis of human heredity and forensic identification.

[Pre-2003 Recodification Citation: 10-1-9-2.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-3"DNA analysis"

Sec. 3. As used in this chapter, "DNA analysis" means an identification process in which the unique genetic code of an individual that is carried by the individual's DNA is compared with the genetic codes of another individual.

[Pre-2003 Recodification Citation: 10-1-9-3.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-4"DNA profile"

Sec. 4. As used in this chapter, "DNA profile" means the results of all DNA identification tests on an individual's DNA sample.

[Pre-2003 Recodification Citation: 10-1-9-4.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-5"DNA record"

Sec. 5. As used in this chapter, "DNA record" refers to DNA identification information stored in the state DNA data base or the Combined DNA Index System for the purpose of generating investigative leads or supporting statistical interpretation of DNA test results that:

(1) is the result obtained from DNA typing tests; and

(2) is comprised of the characteristics of a DNA sample that are of value in establishing the identity of individuals.

[Pre-2003 Recodification Citation: 10-1-9-5.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-6"DNA sample"

Sec. 6. As used in this chapter, "DNA sample" means a blood, tissue, or other body fluid sample:

(1) provided by a person with respect to offenses covered by this chapter; or

(2) submitted to the state police laboratory under this chapter for analysis or storage, or both.

[Pre-2003 Recodification Citation: 10-1-9-6.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-7"Superintendent"

Sec. 7. As used in this chapter, "superintendent" includes the superintendent or the superintendent's designee.

[Pre-2003 Recodification Citation: 10-1-9-7.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-8Establishment of DNA data base; mandatory and discretionary testing and analysis

Sec. 8. (a) The superintendent may establish a data base of DNA identification records of:

(1) convicted criminals;

(2) persons arrested for a felony;

(3) crime scene specimens;

(4) unidentified missing persons; and

(5) close biological relatives of missing persons.

(b) The superintendent shall maintain the Indiana DNA data base.

(c) The superintendent may contract for services to perform DNA analysis of:

(1) convicted offenders; and

(2) persons arrested for a felony;

under section 10 of this chapter to assist federal, state, and local criminal justice and law enforcement agencies in the putative identification, detection, or exclusion of individuals who are subjects of an investigation or prosecution of a sex offense, a violent crime, or another crime in which biological evidence is recovered from the crime scene.

(d) The superintendent:

(1) may perform or contract for performance of testing, typing, or analysis of a DNA sample collected from a person described in section 10 of this chapter at any time; and

(2) shall perform or contract for the performance of testing, typing, or analysis of a DNA sample collected from a person described in section 10 of this chapter if federal funds become available for the performance of DNA testing, typing, or analysis.

(e) The superintendent shall adopt rules under IC 4-22-2 necessary to administer and enforce the provisions and intent of this chapter.

(f) The detention, arrest, or conviction of a person based on a data base match or data base information is not invalidated if a court determines that the DNA sample was obtained or placed in the Indiana DNA data base by mistake.

[Pre-2003 Recodification Citation: 10-1-9-8.]

As added by P.L.2-2003, SEC.4. Amended by P.L.69-2005, SEC.1 and P.L.142-2005, SEC.1; P.L.111-2017, SEC.1.

IC 10-13-6-9Duties of superintendent

Sec. 9. The superintendent shall ensure that the Indiana DNA data base:

(1) supports development of a population statistics data base when personal identifying information is removed;

(2) supports identification research and protocol development of forensic DNA analysis;

(3) assists in achieving quality control; and

(4) assists in the recovery or identification of human remains from mass disasters or for other humanitarian purposes, including identification of missing persons who may be alive.

[Pre-2003 Recodification Citation: 10-1-9-9.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-9.5DNA sample processing fund
Sec. 9.5. (a) The DNA sample processing fund is established for the purpose of funding the collection, shipment, analysis, and preservation of DNA samples and the conduct of a DNA data base program under this chapter. The fund shall be administered by the superintendent.

(b) The expenses of administering the fund shall be paid from money in the fund.

(c) The treasurer of state shall invest the money in the fund not currently needed to meet the obligations of the fund in the same manner as other public money may be invested.

(d) Money in the fund at the end of a state fiscal year does not revert to the state general fund.

As added by P.L.176-2005, SEC.1.

IC 10-13-6-10Persons required to provide DNA sample; buccal swab; right to removal; probable cause required
Sec. 10. (a) This section applies to the following:

(1) A person arrested for a felony after December 31, 2017.

(2) A person convicted of a felony under IC 35-42 (offenses against the person) or IC 35-43-2-1 (burglary):

(A) after June 30, 1996, whether or not the person is sentenced to a term of imprisonment; or

(B) before July 1, 1996, if the person is held in jail or prison on or after July 1, 1996.

(3) A person convicted of a criminal law in effect before October 1, 1977, that penalized an act substantially similar to a felony described in IC 35-42 or IC 35-43-2-1 or that would have been an included offense of a felony described in IC 35-42 or IC 35-43-2-1 if the felony had been in effect:

(A) after June 30, 1998, whether or not the person is sentenced to a term of imprisonment; or

(B) before July 1, 1998, if the person is held in jail or prison on or after July 1, 1998.

(4) A person convicted of a felony, conspiracy to commit a felony, or attempt to commit a felony:

(A) after June 30, 2005, whether or not the person is sentenced to a term of imprisonment; or

(B) before July 1, 2005, if the person is held in jail or prison on or after July 1, 2005.

(b) A person described in subsection (a) shall provide a DNA sample to the:

(1) department of correction or the designee of the department of correction if the offender is committed to the department of correction;

(2) county sheriff or the designee of the county sheriff if the offender is held in a county jail or other county penal facility, placed in a community corrections program (as defined in IC 35-38-2.6-2), placed on probation, or released on bond;

(3) agency that supervises the person, or the agency's designee, if the person is on conditional release in accordance with IC 35-38-1-27; or

(4) sheriff, in the case of a person arrested for a felony.

A DNA sample provided under subdivision (4) may be obtained only by buccal swab. A person is not required to submit a blood sample if doing so would present a substantial and an unreasonable risk to the person's health.

(c) The detention, arrest, or conviction of a person based on a data base match or data base information is not invalidated if a court determines that the DNA sample was obtained or placed in the Indiana DNA data base by mistake.

(d) The officer, employee, or designee who obtains a DNA sample from a person under this section shall:

(1) inform the person of the person's right to DNA removal under section 18 of this chapter; and

(2) provide the person with instructions and a form that may be used for DNA removal.

(e) This subsection applies only to a DNA sample provided by a person arrested for a felony. A person described in subsection (b)(1), (b)(2), (b)(3), or (b)(4) may not ship a DNA sample collected from a felony arrestee for DNA identification testing unless:

(1) the arrestee was arrested pursuant to a felony arrest warrant; or

(2) a court has found probable cause for the felony arrest.

[Pre-2003 Recodification Citation: 10-1-9-10.]

As added by P.L.2-2003, SEC.4. Amended by P.L.69-2005, SEC.2 and P.L.142-2005, SEC.2; P.L.140-2006, SEC.8 and P.L.173-2006, SEC.8; P.L.111-2017, SEC.2.

IC 10-13-6-11 Guidelines for DNA sample collection and shipment
Sec. 11. (a) The superintendent may issue specific guidelines relating to procedures for DNA sample collection and shipment within Indiana for DNA identification testing.

(b) The superintendent shall issue specific guidelines related to procedures for DNA sample collection and shipment by the:

(1) county sheriff or designee of the county sheriff under section 10(b)(2) of this chapter; or

(2) supervising agency or designee of the supervising agency under section 10(b)(3) of this chapter.

The superintendent shall provide each county sheriff and supervising agency with the guidelines issued under this subsection. A county sheriff and supervising agency shall collect and ship DNA samples in compliance with the guidelines issued under this subsection.

(c) The superintendent may delay the implementation of the collection of DNA samples under section 10(b)(2) or 10(b)(3) of this chapter in one (1) or more counties until the earlier of the following:

(1) A date set by the superintendent.

(2) The date funding becomes available by grant through the criminal justice institute.

If the superintendent delays implementation of section 10(b)(2) or 10(b)(3) of this chapter or terminates a delay under section 10(b)(2) or 10(b)(3) of this chapter in any county, the superintendent shall notify the county sheriff in writing of the superintendent's action.

[Pre-2003 Recodification Citation: 10-1-9-11.]

As added by P.L.2-2003, SEC.4. Amended by P.L.140-2006, SEC.9 and P.L.173-2006, SEC.9.

IC 10-13-6-12Collection of samples

Sec. 12. DNA samples for the Indiana DNA data base must be collected in a medically approved manner by one (1) of the following:

(1) A physician.

(2) A registered nurse.

(3) A licensed vocational nurse.

(4) A licensed clinical laboratory technologist.

(5) Any other person trained to collect DNA samples properly.

[Pre-2003 Recodification Citation: 10-1-9-12.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-13Purposes of testing

Sec. 13. (a) Tests performed on the DNA samples are for the following purposes:

(1) To analyze and type the genetic markers contained in or derived from DNA.

(2) For law enforcement identification purposes.

(3) For research or administrative purposes, including:

(A) development of a population statistics data base after personal identifying information is removed;

(B) support of identification research and protocol development of forensic DNA analysis methods;

(C) quality control; and

(D) assisting in the recovery or identification of human remains from mass disasters or for other humanitarian purposes, including identification of missing persons who may be alive.

(b) Tests performed under this chapter must be conducted in a manner that produces compatible results with procedures specified by the Federal Bureau of Investigation Laboratory to ensure that DNA records are fully exchangeable between DNA laboratories.

[Pre-2003 Recodification Citation: 10-1-9-13.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-14Adherence to nationally recognized standards
   Sec. 14. (a) A laboratory conducting forensic DNA analysis in Indiana must implement and follow nationally recognized standards for DNA quality assurance and proficiency testing, such as those approved by the American Society of Crime Laboratory Directors Laboratory Accreditation Board.

   (b) Quality assurance guidelines issued by the Technical Working Group on DNA Analysis Methods serve as the standard for DNA testing under this chapter until national standards are set.

   (c) A laboratory conducting forensic DNA analysis in Indiana shall forward relevant DNA data base records to the state police laboratory.

   [Pre-2003 Recodification Citation: 10-1-9-14.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-15Disclosure of DNA samples and analysis
   Sec. 15. A laboratory conducting forensic DNA analysis in Indiana may disclose or allow access to collected DNA samples and DNA analysis results only under the following circumstances:

   (1) To criminal justice agencies for law enforcement identification purposes.

   (2) To defense counsel for criminal defense purposes.

   (3) Upon authorization by a court or statute.

   (4) For a population statistics data base, identification research and protocol development, or quality control purposes, but only if personal identifying information is removed.

   (5) For purposes of postconviction DNA testing and analysis under IC 35-38-7.

   [Pre-2003 Recodification Citation: 10-1-9-17.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-16Collection of information for certain purposes prohibited
   Sec. 16. The information contained in the Indiana DNA data base may not be collected or stored to obtain information about human physical traits or predisposition for disease.

   [Pre-2003 Recodification Citation: 10-1-9-18.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-17Personal information limited
   Sec. 17. Personal information stored in the Indiana DNA data base is limited to:

   (1) data necessary to:

      (A) generate investigative leads; and

(B) support statistical interpretation of test results; and

(2) any other information necessary to allow for the successful implementation of the Indiana DNA data base system.

[Pre-2003 Recodification Citation: 10-1-9-19.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-18Removal of DNA profile
　　Sec. 18. (a) A person whose DNA profile has been included in the Indiana DNA data base may request removal of the profile from the DNA data base on the grounds that:

　　(1) the conviction on which the authority for inclusion in the Indiana DNA data base was founded has been reversed and the case has been dismissed; or

　　(2) the person's DNA profile has been included in the Indiana DNA data base on the basis of the person's arrest for one (1) or more felonies, and:

　　　　(A) the person was acquitted of all the felony charges, or all of the felonies were converted to misdemeanors under IC 35-38-1-1.5 or IC 35-50-2-7;

　　　　(B) all felony charges against the person were dismissed; or

　　　　(C) three hundred sixty-five (365) days have elapsed since the person's arrest and no felony charges have been filed against the person.

　　(b) All identifiable information in the Indiana DNA data base pertaining to a person requesting removal under subsection (a) shall be removed, and all samples from the person shall be destroyed, upon receipt of:

　　(1) a letter or form requesting removal under subsection (a); and

　　(2) a certified copy of a court order establishing a basis for removal described in this section; as described in subsections (c) and (d).

　　(c) This subsection applies to a person if:

　　(1) the person's conviction has been reversed and the case dismissed (as described in subsection (a)(1));

　　(2) the person was acquitted of all felony charges or all felonies against the person were converted to misdemeanors (as described in subsection (a)(2)(A)); or

　　(3) all felony charges were dismissed (as described in subsection (a)(2)(B)).

A person to whom this subsection applies may request DNA removal by obtaining a certified copy of a court order evidencing a basis for removal described in subdivisions (1) through (3) and transmitting the certified copy of the order with a letter or form requesting DNA removal to the superintendent.

　　(d) This subsection applies to a person if three hundred sixty-five (365) days have elapsed since the person's arrest and no felony charges have been filed against the person (as described in subsection (a)(2)(C)). A person to whom this subsection applies may request DNA removal by notifying the prosecuting attorney, in writing, that:

　　(1) three hundred sixty-five (365) days have elapsed since the person's arrest;

　　(2) no felony charges have been filed against the person; and

(3) the person wishes to have the person's DNA removed from the data base.

Not later than thirty (30) days after receipt of a request for removal under this subsection, the prosecuting attorney shall consult the records maintained by the prosecuting attorney. If the person's claim appears to be meritorious, the prosecuting attorney shall file a request for removal with a court with jurisdiction. Upon receipt of a court order granting removal, the prosecuting attorney shall transmit a certified copy of the court order and a copy of the person's letter requesting DNA removal to the superintendent.

(e) Upon removal of a person's DNA profile from the Indiana DNA data base, the superintendent shall request removal of the person's DNA profile from the national DNA data base.

[Pre-2003 Recodification Citation: 10-1-9-20.]

As added by P.L.2-2003, SEC.4. Amended by P.L.111-2017, SEC.3.

IC 10-13-6-19Access to DNA data base; confidentiality
Sec. 19. (a) The DNA data base is confidential. Access to the Indiana DNA data base is limited to federal, state, and local law enforcement agencies through their servicing forensic DNA laboratories.

(b) The superintendent shall take appropriate measures to ensure that the Indiana DNA data base is protected against unauthorized access.

[Pre-2003 Recodification Citation: 10-1-9-21.]

As added by P.L.2-2003, SEC.4. Amended by P.L.111-2017, SEC.4.

IC 10-13-6-20Denial of privileges due to failure to follow quality control and privacy standards
Sec. 20. The superintendent may deny the privilege of a laboratory performing forensic DNA analysis within Indiana to exchange DNA identification records with federal, state, or local criminal justice agencies if required quality control and privacy standards described in this chapter for the Indiana DNA data base are not met by the laboratory.

[Pre-2003 Recodification Citation: 10-1-9-22.]

As added by P.L.2-2003, SEC.4.

IC 10-13-6-21Unlawful tampering
Sec. 21. A person who knowingly or intentionally without lawful authority tampers with or attempts to tamper with any DNA sample or a container collected under section 10 of this chapter commits a Level 6 felony.

[Pre-2003 Recodification Citation: 10-1-9-15.]

As added by P.L.2-2003, SEC.4. Amended by P.L.158-2013, SEC.167.

IC 10-13-6-22Unlawful use of data base information or DNA samples
Sec. 22. A person who knowingly or intentionally disseminates, receives, or otherwise uses or attempts to use information in the Indiana DNA data base or DNA samples used in DNA analyses, knowing that such dissemination, receipt, or use is for a purpose other than authorized by law, commits a Level 6 felony.

[Pre-2003 Recodification Citation: 10-1-9-16.]

As added by P.L.2-2003, SEC.4. Amended by P.L.111-2017, SEC.5.

Appendix 2
Indiana DNA Database Administrative Rules

ARTICLE 8. INDIANA DNA DATA BASE

Rule 1. Application and Administration

240 IAC 8-1-1 Application of article
Authority: IC 10-11-2-10; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 1. This article governs the administration of the Indiana DNA data base established by IC 10-1-9 *[IC 10-1 was repealed by P.L.2-2003, SECTION 102, effective July 1, 2003. See IC 10-13-6.]*.

(State Police Department; 240 IAC 8-1-1; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3333; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-1-2 Administration
Authority: IC 10-11-2-10; IC 10-13-6-7; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 2. The commander of the state police laboratory has responsibility for the administration of the Indiana DNA data base established by IC 10-1-9 *[IC 10-1 was repealed by P.L.2-2003, SECTION 102, effective July 1, 2003. See IC 10-13-6.]* subject to the authority and approval of the superintendent.

(State Police Department; 240 IAC 8-1-2; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3333; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR240220286RFA)

Rule 2. Definitions

240 IAC 8-2-1 Applicability
Authority: IC 10-11-2-10; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 1. The definitions in this rule apply throughout this article.

(State Police Department; 240 IAC 8-2-1; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3333; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

INDIANA STATE POLICE
BIOLOGY SECTION
CODIS TEST METHODS

240 IAC 8-2-2 "DNA" defined
Authority: IC 10-11-2-10; IC 10-13-6-2; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 2. "DNA" means deoxyribonucleic acid. DNA is located in the nucleated cells and provides an individual's personal genetic blueprint. DNA encodes genetic information that is the basis of human heredity and forensic identification.

(State Police Department; 240 IAC 8-2-2; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-2-3 "DNA analysis" defined
Authority: IC 10-11-2-10; IC 10-13-6-3; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 3. "DNA analysis" means an identification process in which the unique genetic code of an individual that is carried by the individual's DNA is compared with the genetic codes of another individual.

(State Police Department; 240 IAC 8-2-3; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-2-4 "DNA profile" defined
Authority: IC 10-11-2-10; IC 10-13-6-4; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 4. "DNA profile" means the results of all DNA identification tests on an individual's DNA sample.

(State Police Department; 240 IAC 8-2-4; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-2-5 "DNA sample" defined
Authority: IC 10-11-2-10; IC 10-13-6-6; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 5. "DNA sample" means a blood, tissue, or other body fluid sample:

(1) provided by a person with respect to offenses covered by IC 10-1-9 *[IC 10-1 was repealed by P.L.2-2003, SECTION 102, effective July 1, 2003. See IC 10-13-6.]*; or

(2) submitted to the state police laboratory under IC 10-1-9 *[IC 10-1 was repealed by P.L.2-2003, SECTION 102, effective July 1, 2003. See IC 10-13-6.]* for analysis or storage, or both.

(State Police Department; 240 IAC 8-2-5; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-2-6 "Qualifying offender" defined
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-10
Affected: IC 10-13-6; IC 35-42-4-6; IC 35-43-2-1

Sec. 6. "Qualifying offender" means a person convicted of a felony under IC 35-42 (offense against the person), IC 35-43-2-1 (burglary), or IC 35-42-4-6 (child solicitation):

  (1) after June 30, 1996, whether or not sentenced to a term of imprisonment; and

  (2) before July 1, 1996, if the person is held in jail or prison on or after July 1, 1996.

(State Police Department; 240 IAC 8-2-6; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-2-7 "Superintendent" defined
Authority: IC 10-11-2-10; IC 10-13-6-7; IC 10-13-6-8
Affected: IC 10-13-6

Sec. 7. "Superintendent" means the superintendent of the state police department or the superintendent's designee.

(State Police Department; 240 IAC 8-2-7; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

Rule 3. Collection and Submission of Samples

240 IAC 8-3-1 Responsibilities
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-10
Affected: IC 10-13-6

Sec. 1. The department of correction shall collect a DNA sample from a qualifying offender, if the qualifying offender has not previously had a sample collected, and:

  (1) is serving a term of incarceration in a facility under the control of the department of correction; or

  (2) is transferred to a facility under the control of the department of correction.

(State Police Department; 240 IAC 8-3-1; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct

6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-3-2 Approved procedure
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-12; IC 10-13-6-17
Affected: IC 10-13-6

Sec. 2. (a) DNA samples shall be collected in a medically approved manner by a physician, registered nurse, licensed vocational nurse, licensed clinical technologist, or other person at the direction of a physician or under a protocol approved by a physician.

(b) Procedures used by the department of correction to extract and obtain liquid blood samples shall be with the approval and at the direction of the medical director of the department of correction.

(State Police Department; 240 IAC 8-3-2; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 2010081820161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-3-3 Collection guidelines
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-10; IC 10-13-6-11
Affected: IC 10-13-6

Sec. 3. (a) The following guidelines apply to the collection of blood samples for submission to the state police laboratory for the Indiana DNA data base:

(1) Blood samples shall only be drawn from qualifying offenders for use as DNA samples.

(2) A qualifying offender is not required to submit a blood sample if doing so would present a substantial and an unreasonable risk to the offender.

(3) Blood samples shall be collected using vacutainer tubes containing EDTA preservative or by a finger stick procedure using stain cards.

(4) After collection of the blood sample, a label approved by the state police laboratory shall be affixed to the blood sample container; this label shall be completed with required information, including the name and inmate number of the qualifying offender.

(5) Information shall be recorded on a form approved by the state police laboratory to accompany each blood sample to include the following:

(A) The qualifying offender's:

(i) name;

(ii) inmate number; and

   (iii) inked right thumb print.

 (B) If the qualifying offender has no right thumb, then the inked print of another finger and a written notation identifying the finger used shall be recorded.

(6) The blood sample of the qualifying offender shall be placed in a container approved by the state police laboratory.

(7) An initialed integrity seal shall be placed across the lid of the approved container.

(8) Blood samples may be refrigerated for up to seven (7) days before submission to the state police laboratory.

(9) Blood samples shall be refrigerated until delivery to the state police laboratory.

(b) When it is not possible to obtain a blood sample, the department of correction shall obtain an oral swab.

(c) The following guidelines apply to the collection of oral swabs for submission to the state police laboratory for the Indiana DNA data base:
(1) Oral swabs shall only be collected from qualifying offenders for use as DNA samples.

(2) Oral swabs shall be collected using sterile cotton tipped applicators.

(3) The following procedure shall be used to collect a sample with an oral swab:

 (A) Remove a sterile tipped applicator from its package.

 (B) Swab the inner surface of the cheek using a circular motion and complete fifteen (15) to twenty (20) circles.

 (C) Repeat the steps in clauses (A) and (B) with a second sterile tipped applicator.

 (D) Place the used swabs into two (2) separate envelopes approved by the state police laboratory for the collection of DNA samples by oral swabs and place the two (2) smaller envelopes into a larger envelope approved by the state police laboratory.

(4) A label approved by the state police laboratory shall be affixed across the flap of the larger envelope; this label shall be completed with required information, including the name and inmate number of the qualifying offender.

(5) Information shall be recorded on a form approved by the state police laboratory to accompany each oral swab sample to include the following:

 (A) The qualifying offender's:

  (i) name;

  (ii) inmate number; and

(iii) inked right thumb print.

(B) If the qualifying offender has no right thumb, then the inked print of another finger and a written notation identifying the finger used shall be recorded.

(6) Oral swab samples may be refrigerated for up to seven (7) days before submission to the state police laboratory.

(7) Oral swab samples shall be refrigerated until delivery to the state police laboratory.

(State Police Department; 240 IAC 8-3-3; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3334; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

Rule 4. Quality Control

240 IAC 8-4-1 Quality control testing
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-13
Affected: IC 10-13-6

Sec. 1. The state police laboratory shall perform tests on DNA samples for quality control and assurance.

(State Police Department; 240 IAC 8-4-1; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3335; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-4-2 Quality assurance standards
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-14
Affected: IC 10-13-6

Sec. 2. (a) A laboratory conducting forensic DNA analysis in Indiana shall comply with nationally recognized standards for quality assurance and proficiency testing.

(b) In the event of competing quality assurance standards, the state police laboratory commander shall identify the nationally recognized standard that a laboratory conducting forensic DNA analysis in Indiana must implement and follow.

(State Police Department; 240 IAC 8-4-2; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3335; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

240 IAC 8-4-3 Participation
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-20
Affected: IC 10-13-6

Sec. 3. If a laboratory performing forensic DNA analysis in Indiana fails to meet required quality control standards, the superintendent shall deny the laboratory the right to exchange DNA identification records with federal, state, or local criminal justice agencies.

(State Police Department; 240 IAC 8-4-3; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3335; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

Rule 5. Authorized Access

240 IAC 8-5-1 Request for access; denial
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-19
Affected: IC 10-13-6

Sec. 1. (a) A forensic DNA laboratory seeking access to the DNA data base must submit a written request to the commander of the state police laboratory.

  (b) The written request required by subsection (a) must state the following:

  (1) The identity of the federal, state, or local law enforcement agency requesting access.

  (2) The purpose of the testing to be performed.

  (c) A request submitted under subsection (a) that does not identify a requesting law enforcement agency or fails to state a proper purpose for testing under IC 10-1-9 *[IC 10-1 was repealed by P.L.2-2003, SECTION 102, effective July 1, 2003. See IC 10-13-6.]* shall be denied.

(State Police Department; 240 IAC 8-5-1; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3335; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 9:27 a.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 20161228-IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)

Rule 6. Expungement

240 IAC 8-6-1 Request for expungement
Authority: IC 10-11-2-10; IC 10-13-6-8; IC 10-13-6-18
Affected: IC 10-13-6

Sec. 1. (a) A person whose DNA profile has been included in the Indiana DNA data base and who is eligible for expungement under IC 10-1-9-20 *[IC 10-1 was repealed by P.L.2-2003, SECTION 102, effective July 1, 2003. See IC 10-13-6-18.]* may submit a written request for expungement to the superintendent.

(b) All identifiable information pertaining to the person in the DNA data base and all DNA samples related to the request shall be destroyed upon receipt of the following:

(1) the written request for expungement under subsection (a);

(2) a certified copy of the court order reversing and dismissing the conviction that made the person a qualifying offender; and

(3) identifying information to include the following:

(A) The full name of the person requesting expungement.

(B) The inmate number and name of the person that contributed the DNA sample correlating to the DNA profile to be expunged.

(C) The inked right thumb print of the person requesting expungement, or if the person has no right thumb, then the inked print of another finger and information identifying the finger actually used.

(State Police Department; 240 IAC 8-6-1; filed Apr 23, 1998, 9:25 a.m.: 21 IR 3336; readopted filed Oct 6, 2004, 5:10 p.m.: 28 IR 677; readopted filed Jul 23, 2010, 3:02 p.m.: 20100818-IR-240100362RFA; readopted filed Nov 30, 2016, 9:27 a.m.: 20161228IR-240160432RFA; readopted filed Nov 23, 2022, 9:36 a.m.: 20221221-IR-240220286RFA)*

Appendix 3
Definitions

1. Allele – the alternative form of a gene.
2. Allelic Ladder – a set of DNA fragments of the commonly known alleles for each locus. By comparing the samples to the allelic ladder, the correct allele designation may be assigned.
3. Amelogenin – the marker for determining the gender of the individual contributor to a DNA profile.
4. Amplification – using the PCR process to create many copies of a specific DNA sequence(s). An increase in the number of copies of a specific DNA fragment.
5. Analyst Discretion - The use of individual judgment, based on an analyst's training and experience to determine the optimum modes of analysis for sample.
6. Artifact – non-allelic product of the amplification process, an anomaly of the detection process, or a by-product of primer synthesis. A data peak that does not represent a true allele.
7. Association – A search result that pairs an unidentified sample with one or more known samples using Pedigree searching; it does not reflect a direct identity match between profiles.
8. Autosearch – A CODIS program, which automatically searches all DNA profiles in a user specified index against all profiles in one or more other user specified indexes.
9. Candidate Match – A possible match between two or more DNA profiles discovered by CODIS software.
10. Candidate Rank – A possible association between two or more DNA profiles discovered by the CODIS software.
11. Capillary Electrophoresis – a method to separate DNA fragments based on size using electrical current. The DNA sample is placed in thin tube (capillary) containing gel (polymer) and subjected to high voltage current allowing the DNA fragments to migrate through the tube.
12. CODIS Administrator – An employee of the laboratory responsible for administration and security of the laboratory's CODIS.
13. Combined DNA Index System (CODIS) – refers to the DNA database and its software. It is composed of National (NDIS), State (SDIS), and Local (LDIS) components. It contains DNA profiles form offenders, crime scenes, and includes a missing persons database.
14. Contamination – the process of making a sample impure or unusable.
15. Convicted Offender (specimen category) – The known sample from a person who has been convicted of a qualifying offense.
16. Convicted Offender Index – consists of DNA records from offenders convicted of qualifying state crimes and juveniles required by relevant jurisdiction to provide DNA samples.
17. Deduced Missing Person – The DNA profile of a reported missing person that has been generated by examining items purported to belong to the missing person such as a toothbrush.
18. Deoxyribonucleic Acid (DNA) - the genetic material present in the nucleus of most cells. Also located in cell mitochondria.

19. DNA Profile – The genetic constitution of an individual at defined locations (also known as loci) in the DNA.
20. DNA Record – A database record that includes the DNA profile as well as data required to manage and operate NDIS.
21. DNA Sequence – a specific order of base pairs.
22. Electropherogram – the visual representation of the DNA fragments contained in each sample; generated by the analysis software of the Capillary Electrophoresis Instrument.
23. Electrophoresis – the method to separate molecules based on their size by placing them in a medium and applying an electrical current. The molecules will travel through the medium at different rates, the smaller molecules traveling through the medium more quickly than the larger ones.
24. Enzyme – a protein which acts as a catalyst, speeding up a specific chemical reaction without being changed or consumed in the process.
25. Familial Search (FS) – deliberate search of a DNA database conducted for the intended purpose of potentially identifying close biological relatives to the unknown forensic profile obtained from crime scene evidence or unidentified human remains.
26. First-order relative – relatives, such as siblings or parent-child relationships, that share more genetic data in common than unrelated individuals or more distantly related individuals.
27. Forensic Index – consists of DNA records originating from and associated with an evidence sample from a single source from a crime scene.
28. Forensic Mixture – DNA results originating from a biological sample found at the scene of a crime that contains DNA contributed from more than one source.
29. Forensic Partial – A DNA profile that originates from a single source biological sample found at the scene of a crime and has suspected locus or allelic dropout.
30. Forensic Targeted – A DNA profile that would otherwise be categorized as a Forensic Partial or Forensic Mixture but has increased its match rarity through searching at specified stringency by locus (high or moderate).
31. Forensic Unknown – A DNA profile that originates from a single source biological sample found at the scene of a crime, with no dropout suspected.
32. High Stringency – requires all alleles to match.
33. Hit – A confirmed match that aids an investigation and one or more of the case(s) involved in the match are unsolved.
34. Internal Lane Standard (ILS) – a set of DNA fragments of known length(s). The ILS is simultaneously injected with all DNA samples during electrophoresis. This allows accurate measurement of the length of each allele in a DNA sample.Match – A match occurs when CODIS links two or more DNA profiles.
35. Missing Person (specimen category) – The known reference sample from an individual that is missing.
36. Missing Persons Index – consists of DNA records from missing persons and deduced missing persons.
37. Mixture – A DNA profile containing 3 or more alleles at more than 2 loci.
38. Moderate Stringency – requires all alleles to match, but the target and candidate profiles can contain a different number of alleles.
39. Multi-allelic Offender – An offender profile having three or more alleles at two or more loci.

40. Negative Amplification Control – used to detect DNA contamination of the amplification reagents, consisting of only amplification reagents without the addition of template DNA.

41. Pedigree Tree – A family tree constructed in CODIS using Family Reference Standards. A Missing Persons tree contains genetic information from two or more biological relatives of the missing person (or person of interest). A Single Typed Node Pedigree contains genetic information from only one biological relative of a missing person or person of interest.

42. Platform – The type of analytical system utilized to generate DNA profiles, such as capillary electrophoresis and real-time gel.

43. Polymerase – an enzyme that initiates the duplication of a DNA molecule.

44. Polymerase Chain Reaction (PCR) – a process for amplifying (copying) the DNA molecule.

45. Positive Amplification Control – an analytical control sample used to determine if the PCR performed properly consisting of amplification reagents and a known DNA sample.

46. Primer – a short nucleotide fragment of known sequence used to locate its complementary sequence on the DNA molecule for the initiation of PCR. Primers target the specific loci to be amplified.

47. Proficiency Testing – a test to evaluate the competency of an analyst in a specific procedure.

48. Qualified DNA Analyst – A DNA analyst who has satisfied and continues to satisfy the experience, education, training, proficiency testing and continuing education requirements of the FBI Director's Quality Assurance Standards issued in accordance with the DNA Identification Act of 1994, as well as successful completion of a qualifying test prior to beginning casework or databasing responsibilities.

49. Reagent Blank Control – an analytical control sample that contains no template DNA and is used to monitor contamination from extraction to final fragment analysis.

50. Reference Material – material obtained from a known source and collected for purposes of comparison to forensic samples.

51. Relatives of Missing Persons Index – consists of DNA records from the biological relatives of individuals reported missing.

52. Short Tandem Repeat (STR) – small sections of DNA that contain short segments (2, 3, 4 or more base pairs) which repeat several times. The number of repeat units may vary between individuals. STRs are located between specific genes and are considered non-functional.

53. Source ID – A field in the CODIS software used to indicate whether or not the source of a forensic profile is known.

54. Stochastic effect – peak imbalance observed in a locus and/or allele drop-out due to random, disproportionate amplification of alleles in low quality/quantity template samples.

55. Stutter – an artifact that occurs as a by-product of the PCR process. It is observed as a minor peak typically observed one repeat unit smaller than a primary STR allele caused by strand slippage during amplification.

56. Technical Review – an evaluation of reports, notes, data, and other documents to ensure there is an appropriate and sufficient basis for the scientific conclusions.

57. Test Kit – A preassembled set of reagents that allow the user to conduct a specific DNA extraction, quantification, or amplification.

58. Unidentified Human (Remains) Index – The DNA profile developed from the recovered deceased (including body parts and tissue) or an individual who is unidentified (e.g., children who can't and others who won't or refuse to identify themselves).

59. Unidentified Person – The DNA profile developed from the recovered deceased (including body parts and tissue) or an individual who is unidentified (such as persons who can't or refuse to identify themselves).

60. Work Product – the material that is generated as a function of analysis, which may include extracts and amplified product, in tubes or plates, and any aliquots thereof.

Appendix 4
Notification Templates

Example: Offender Hits for ISPL cases

Name
Agency

Date
Laboratory Case
Agency Case

This notice is to inform you of a potential investigative lead. A search of the Combined DNA Index System (CODIS) resulted in a high/moderate stringency computer match between the convicted offender/arrestee sample named below and the DNA profile entered from the swab (item 001A). {Fingerprint verification of the offender's identity was not possible in this case.}

A database sample is not an evidentiary standard. Your agency needs to obtain an evidentiary standard (such as blood standard or oral swab) and submit it to the laboratory for examination if criminal prosecution is desired.

Please note that if your case is past its original statute of limitations, Indiana Code 35-41-4-2b may still allow for prosecution of that case in the event of a DNA match. It states that prosecution may begin within one year of a DNA match (essentially renewing the statute of limitations) for Class B, Class C, Level 3, Level 4, or Level 5 felonies. Class D or Level 6 felonies and misdemeanors may only be prosecuted within their normal statute of limitations.

Name:	DOB:
Race:	Gender:
FBI No:	SID No:
Qualifying Offense:	

This information is as it appears on laboratory records; other names and dates of birth may exist.

Author's Name
CODIS Unit
Indiana State Police Laboratory

YY/CODIS/001

INDIANA STATE POLICE
BIOLOGY SECTION
CODIS TEST METHODS

Example: Offender Hits for Non-ISPL cases

Name
Agency

Date
Match ID
IN Specimen ID

This notice is to inform you of a potential investigative lead. A search of the Combined DNA Index System (CODIS) resulted in a high/moderate stringency computer match between the convicted offender/arrestee sample named below and the DNA profile entered from Agency Specimen ID XXX. {Fingerprint verification of the offender's identity was not possible in this case.}

A database sample is not an evidentiary standard. Your agency needs to obtain an evidentiary standard (such as blood standard or oral swab) and submit it to your laboratory for examination if criminal prosecution is desired.

Name:	DOB:
Race:	Gender:
FBI No:	IN SID No:
Qualifying Offense:	

This information is as it appears on laboratory records; other names and dates of birth may exist.

Author's Name
CODIS Unit
Indiana State Police Laboratory

YY/CODIS/001

INDIANA STATE POLICE
BIOLOGY SECTION
CODIS TEST METHODS

Example: Forensic Hits

Name
Agency

Date
Laboratory Case/Match ID
Agency Case/IN Specimen ID

This notice is to inform you of a potential investigative lead. A search of the Combined DNA Index System (CODIS) resulted in a high/moderate stringency computer match between the case sample detailed below and the DNA profile entered from the swab (item 001)/Agency Specimen ID XXX.

If your case is unsolved, please contact the agency involved for more information.

Case Information:

Agency:	
Investigator Name:	
Phone:	
Offense:	
Agency case #:	
Evidence:	

<div style="text-align:right">

Author's Name
CODIS Unit
Indiana State Police Laboratory

</div>

YY/CODIS/001

Example: Family Reference Associations

Name
Agency

Date
Laboratory Case/Rank ID
Agency Case(s)/IN Specimen ID

This notice is to inform you of a potential investigative lead. A search of the Combined DNA Index System (CODIS) resulted in an association between ISP Lab case/Pedigree Tree ID and the DNA profile entered from the unidentified human remains (item 001)/Agency Specimen ID XXX.

Below is the case information regarding the missing/unidentified person.

Case Information:

Agency:	
Investigator Name:	
Phone:	
Offense:	
Agency case #:	
Missing Person Name:	
NamUs Identifier:	
Date of Last Contact/Remains Found:	

Author's Name
CODIS Unit
Indiana State Police Laboratory

YY/CODIS/001

Example: Familial Search Positive Association
Name
Agency

Date

FAMILIAL SEARCH RESULTS
Laboratory Case
Agency Case(s)

This notice is to inform you of a potential investigative lead. A familial search was performed on the DNA profile entered from the *description* (item XXX). The database sample detailed below cannot be excluded as a **close relative** of the DNA profile. **[The individual named is not the person who left the DNA evidence.]** The search result is best explained by a (parent-child [or full sibling]); however, other familial relationships are possible and should be considered. {The statistical results for the familial relationships are in a range where adventitious support with unrelated individuals can occur. These results should be considered in the context of other information known in the case when making determinations of the identity of the individual.}

Please submit an appropriate standard (such as an oral/buccal swab standard) from any suspect(s) for direct forensic comparison. The genetic results described here are based only on the data developed at the time of reporting and do not supersede any additional genetic testing that may be performed.

Please note that if your case is past its original statute of limitations, Indiana Code 35-41-4-2b may still allow for prosecution of that case in the event of a DNA match. It states that prosecution may begin within one year of a DNA match (essentially renewing the statute of limitations) for Class B, Class C, Level 3, Level 4, or Level 5 felonies. Class D or Level 6 felonies and misdemeanors may only be prosecuted within their normal statute of limitations.

Name:	DOB:
Race:	Gender:
FBI No:	IN SID No:
Qualifying Offense:	

This information is as it appears on laboratory records; other names and dates of birth may exist.
{Fingerprint verification of the offender's identity was not possible in this case.}

Author's Name
CODIS Unit
Indiana State Police Laboratory

YY/CODIS/001

INDIANA STATE POLICE
BIOLOGY SECTION
CODIS TEST METHODS

Example: Familial Search Negative

Name
Agency

Date

FAMILIAL SEARCH RESULTS
Laboratory Case
Agency Case(s)

A familial search was performed on the DNA profile entered from the *description* (item XXX). No database samples were identified as a **close relative** of the DNA profile.

This type of search is not performed on a routine basis. You may request another familial search of this profile after a period of one year by contacting the CODIS Administrator.

                                        Author's Name
                                        CODIS Unit
                                        Indiana State Police Laboratory

YYCODIS/001