Reference Batch Analysis, Interpretation and Review

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Although typically used for processing batches of offender samples, batches of casework reference samples may also be processed in this manner.

Section 1 Data Analysis with GeneMapper™ ID-X

References: GeneMapper™ ID-X Software User Guide
GeneMapper™ ID-X Software Tutorial
GeneMapper™ ID-X Software User Bulletin

1.1 Logging in to GeneMapper™ ID-X

- Open GeneMapper™ ID-X
- Select the User Name and Database Host from the drop-down list and enter the appropriate password.
- Click OK.
- The main project window will open.

1.2 Creating a Project

- To add samples from the collection software at a workstation, go to the edit menu and select **Add Samples to Project**. Navigate to **My Computer > Uncontrolled Documents > Section Shares > DNA Share > CE Data** on the laboratory "I Drive" as per current designation(s).

Note: Location is dependent on network mapping and may vary slightly.

- Select the raw data folder to be imported or select individual samples and click **Add to list**.
- When all samples have been selected, click **Add**.
- Select the appropriate Sample Type, Analysis Method (refer to section 1.2.1), Panel (Promega_Bins_IDX_alpha) and Size Standard (ILS_80-550_Adv) for each sample and click the green arrow on the tool bar to analyze the samples.
- The user will be prompted to name and save the project to the appropriate Security Group (GeneMapper ID-X Security Group). Name the project with the Batch name. Click OK.
    - Example: DB13-0319A_KAH

- Analysis is complete when the green arrows in the Status column on the left are gone.

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1.2.1 Analysis Methods

A range of Analysis Methods are available to analyze database samples. Options for Analysis Methods vary by RFU and analysis range. These methods shall not be modified. New methods shall only be created or modified with permission from the DNA Technical Manager.

- 250RFU Database-2400
- 250RFU Database-2800
- 250RFU Database-3200

- 700RFU Database-2400
- 700RFU Database-2800
- 700RFU Database-3200

- Blank Database Global

The settings for the Analysis Methods are viewed by selecting GeneMapper ID-X Manager under the Tools drop-down menu, clicking on the Analysis Methods tab, then double clicking to select a particular Analysis Method.

Based on the laboratory's internal validation, allelic ladders will typically need to be analyzed at 250RFU to achieve complete allele calling. The most efficient analysis and review will generally be achieved by first analyzing all samples at 250RFU. Samples with baseline artifacts can be identified and re-analyzed at 750RFU.

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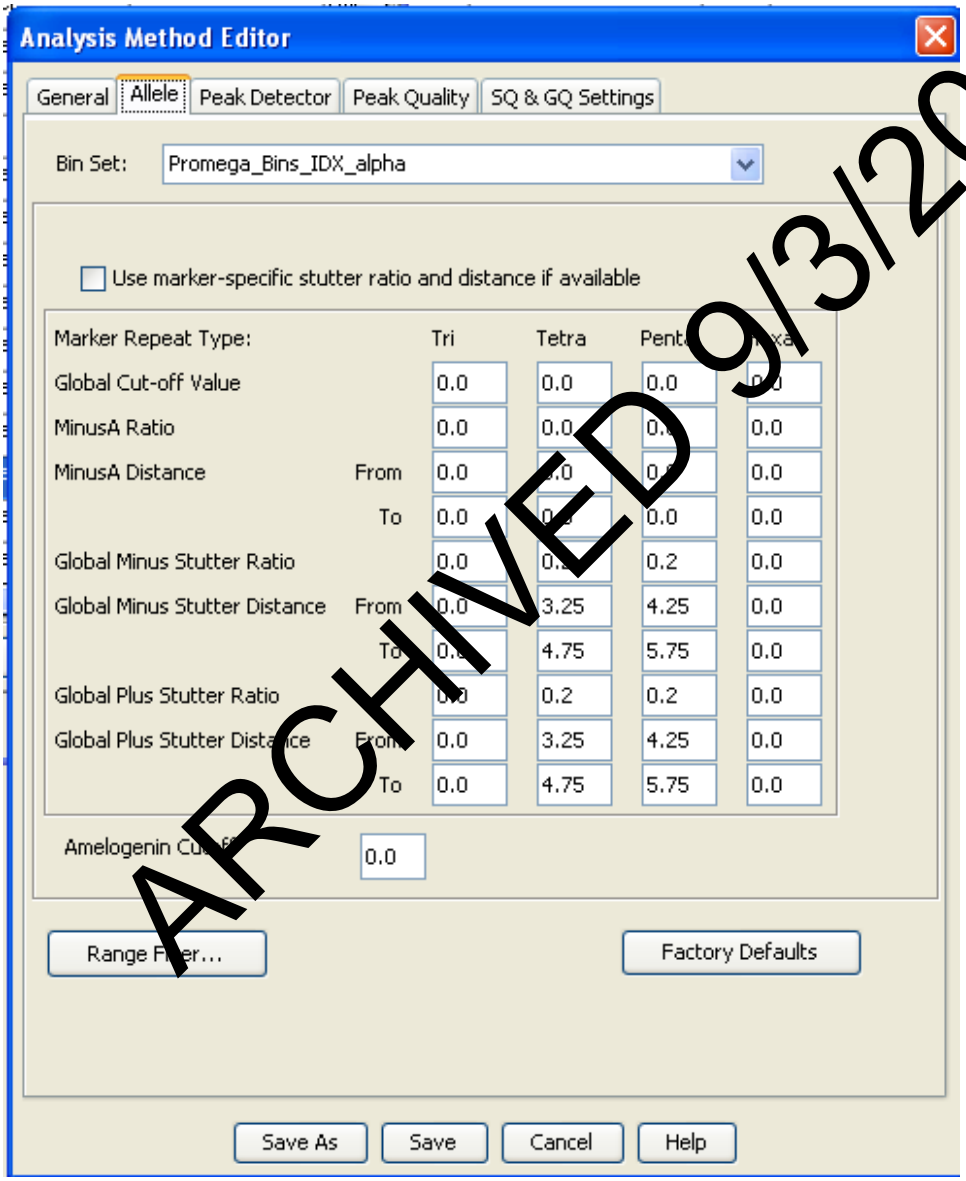
1.2.1.1 Allele Tab Settings

The Allele Tab Settings are viewed by opening a selected analysis method. These settings are consistent within all database methods.

<u>All Analysis Methods</u>



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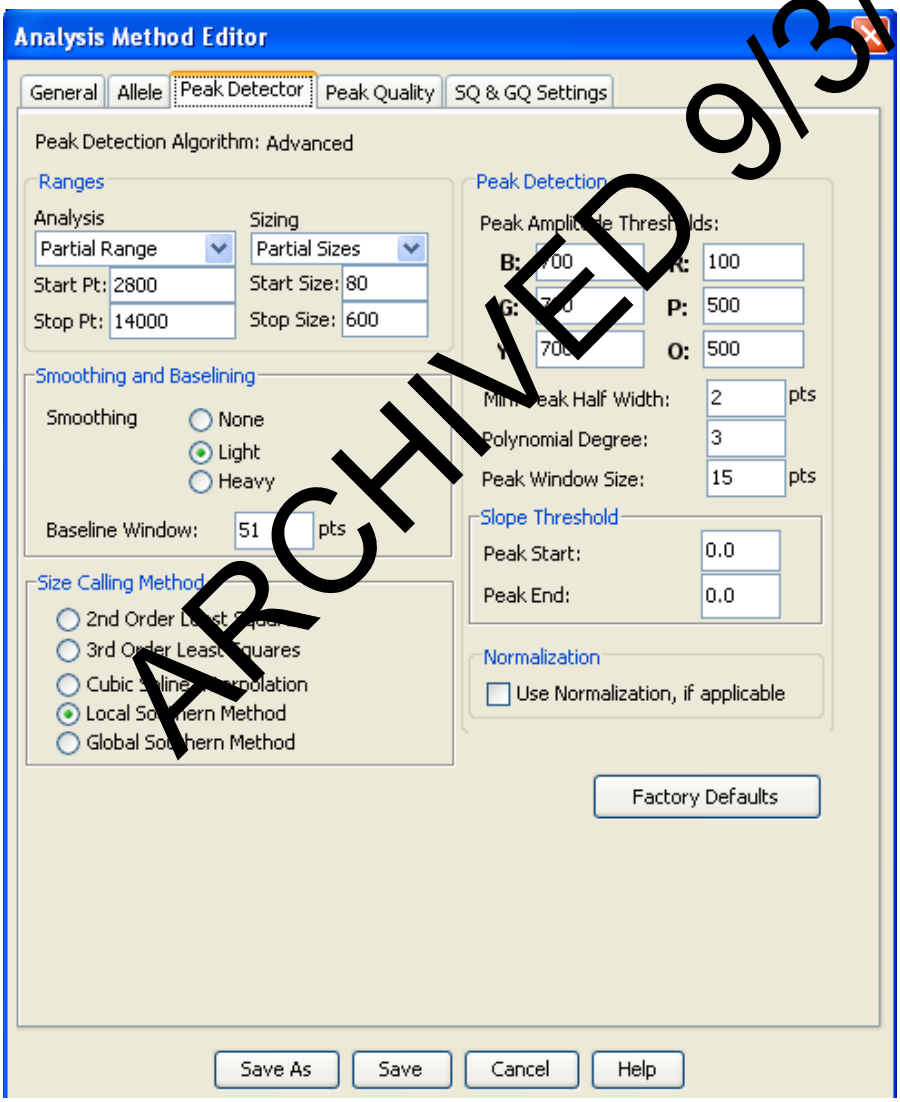
1.2.1.2 Peak Detector Tab Settings

The Analysis Range and/or the Peak Amplitude Thresholds are the only settings that vary between the alternative Analysis Methods. The Analysis Range is selected to ensure capture of the 80bp ILS peak for all allelic ladders, positive controls, and questioned and known samples in the project. The Analysis Range is selected to capture the primer peaks for reagent blanks, negative amplification controls, and samples that do not yield at least a partial profile. Peak Amplitude Thresholds (for blue, green and yellow) of 250RFU and 700RFU are approved for database analyses. For each RFU threshold, there are methods with analysis start points of 2400, 2800 and 3200. All other settings are the same among the methods.

<u>Example: 700RFU Database-2800 Analysis Method</u>



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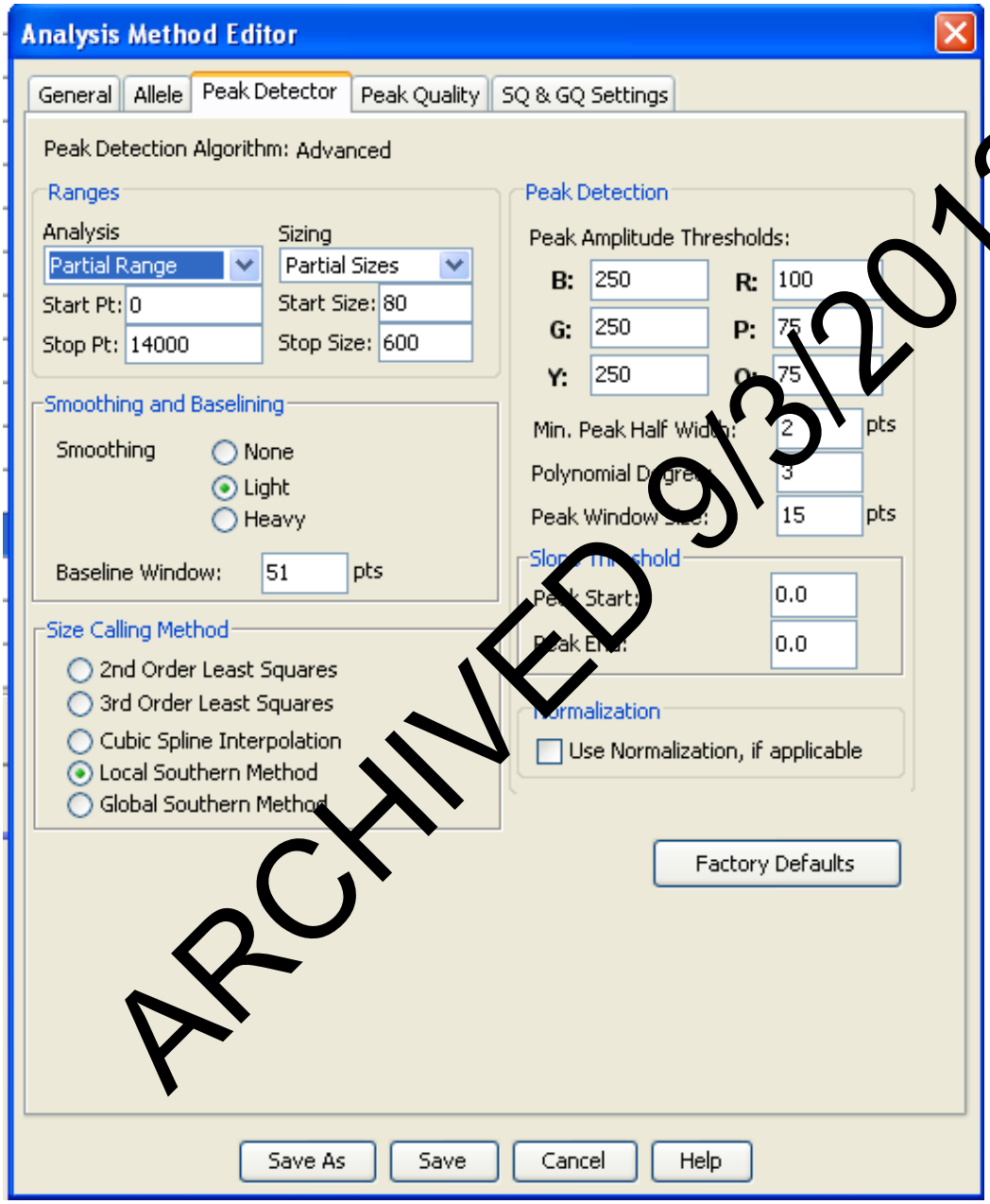
Blank Database Global Analysis Method



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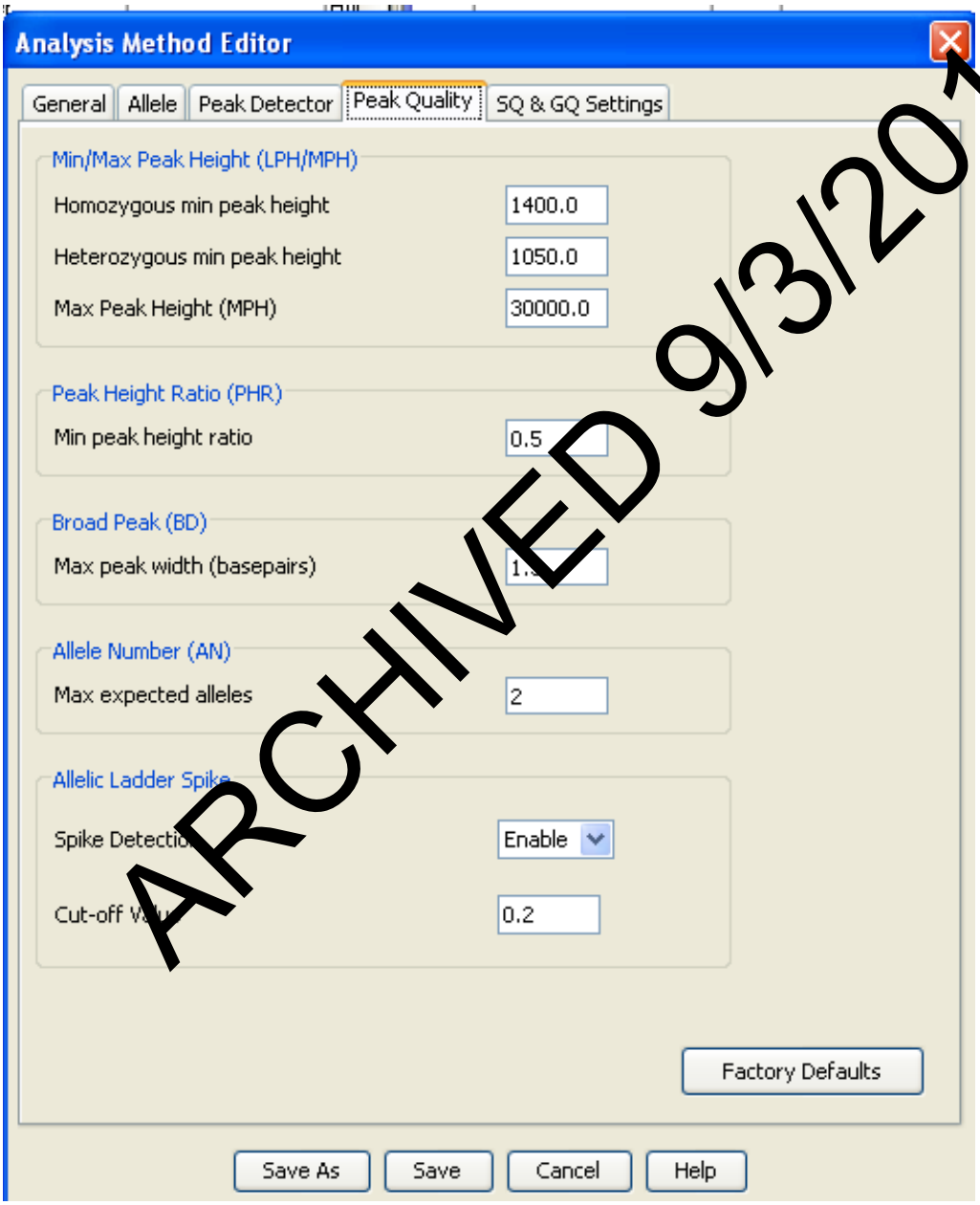
1.2.1.3 Peak Quality Tab Settings

These settings do not vary among the methods, and they are not relevant in analysis of any samples where the sample type is set to Negative Control.

<u>700RFU Analysis Methods</u>



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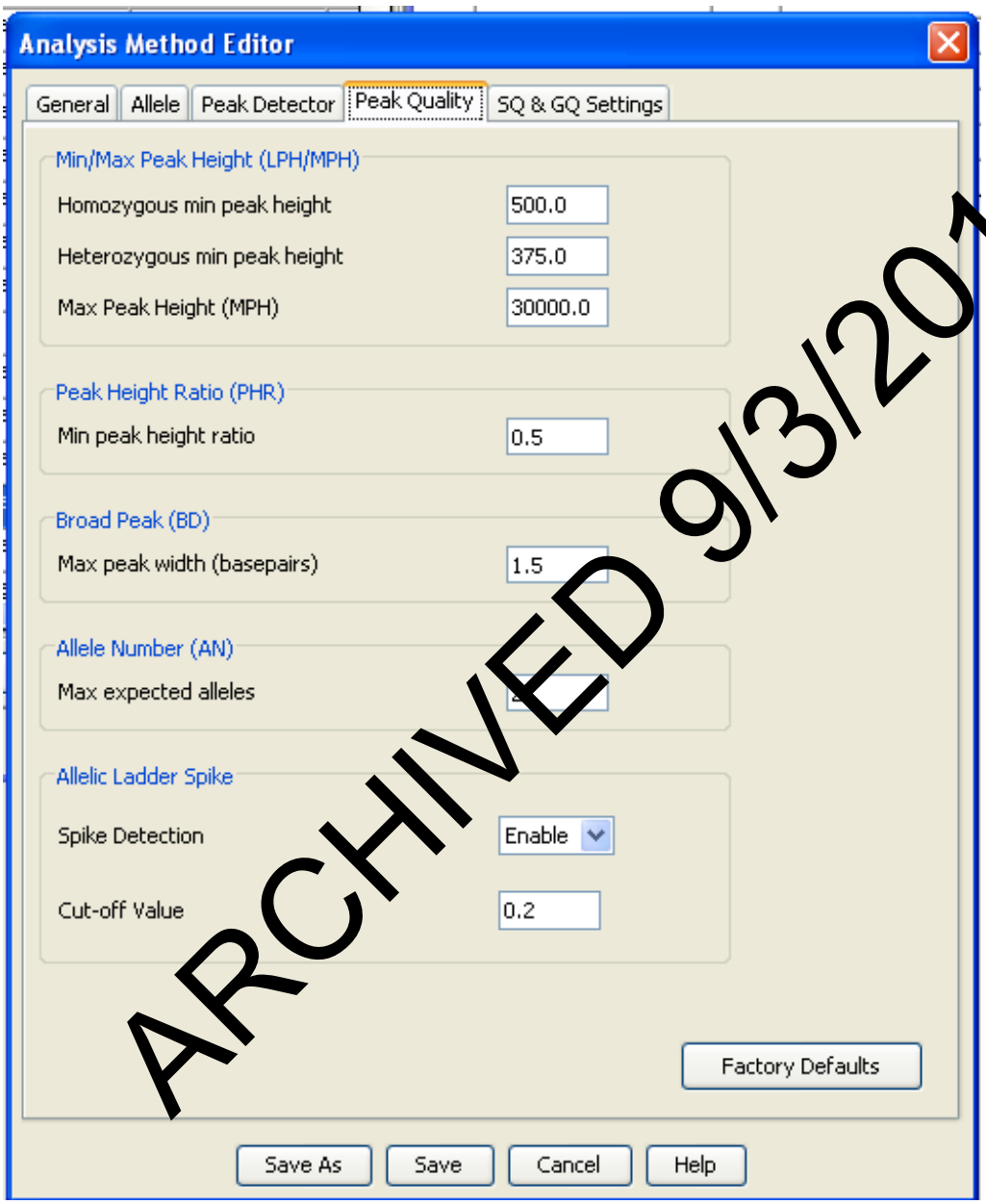
250RFU Analysis Methods



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1.2.1.4 SQ and GQ Tab Settings

These settings do not vary among any of the analysis methods, and they are not relevant, as all samples are currently manually reviewed and interpreted, regardless of flagging.

<u>All Analysis Methods</u>

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1.3 Viewing the Data

- The ILS is viewed by highlighting all samples and clicking on the Size Match Editor, the icon with the red peaks on the toolbar.
- To view each sample, highlight the sample and click on the icon with the colored peaks to display plots. (This can also be done by View > display plots or Ctrl + L).
- Electropherograms can be printed from the sample's plot window. Various plots have been created for different sample types. Commonly used plot displays include: Traditional Genotype Plot, Casework Blank, Casework artifacts and Casework zoom view.
- To view information on a sample's injection time and other run information, highlight the sample of interest and click **View** on the toolbar > Sample Info (Ctrl + F1).
- To view raw data for a sample, click **View > Raw Data**.
- To view allele calls by sample and locus click the Genotypes tab from the main project window.

1.4 Data Retention

Raw data files will be retained electronically on the laboratory network share drive.

GeneMapper ID-X project files are not retained long term and may be deleted after the technical and administrative reviews of a batch are completed.

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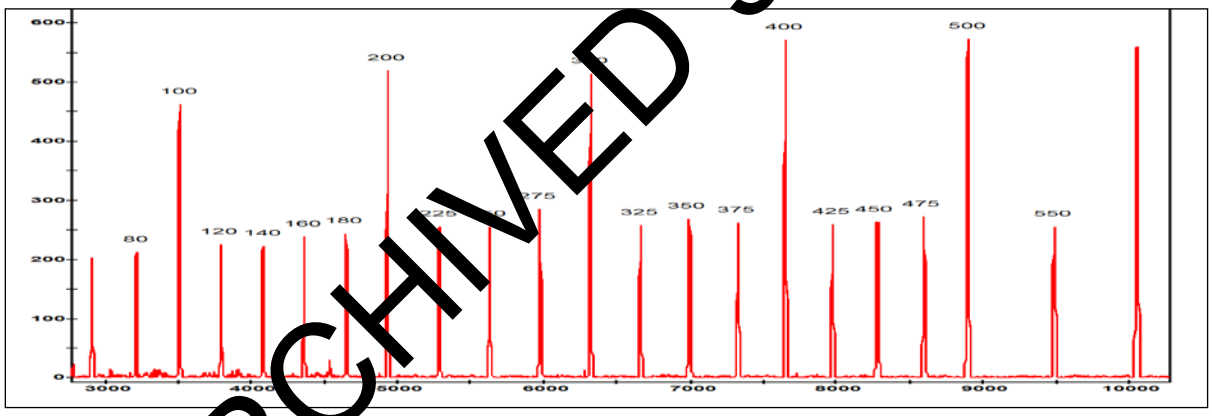
Section 2 STR Data Interpretation

Interpretation of database samples is based on the guidelines contained in this section, as well as the qualified DNA analyst's training and experience. The DNA Technical Manager may authorize the interpretation/reporting of data outside of the criteria defined herein and will document this approval by initialing and dating comments on the relevant paperwork.

The minimum peak height acceptable for database sample STR loci alleles is 250RFU. The threshold may be raised to a maximum of 700RFU for samples with an elevated baseline. Lower threshold limits for hit confirmations or ILS (Internal Lane Standard) may be authorized by the DNA Technical Manager.

2.1 Internal Lane Standard (ILS)

The first step in interpreting data from a run is to assess the ILS for each sample (including all controls and allelic ladders). The Promega PowerPlex16® System uses ILS 600. The analyst should verify that all peaks from 80-550 base pairs are present and labeled as shown.



The peak heights for the ILS peaks must be at least 100RFU (relative fluorescence units) to be identified and labeled by the GeneMapper™ ID-X software with a database method.

When the peaks are not labeled as shown above, the analyst must determine the cause for the incorrect labeling. If the peaks at either the low or high ends are not visible, the data may be re-analyzed after changing the analysis range in the Analysis Method. It is also possible to manually label peaks above the 100RFU ILS threshold. Refer to the GeneMapper™ID-X Software User Guide for details on manually labeling the size standard.

If a peak is not labeled because it falls below the reporting threshold, the analyst may, with the documented approval of the DNA Technical Manager, lower the acceptable

threshold for the ILS peak(s). The Technical Manager may also approve use of samples when one of the ILS peaks (between 80 and 550bp) is not labeled. Approval is documented on the either the electropherogram or the batch worksheet by the Technical Manager's initials and date of approval.

Use caution when allowing for lower ILS peak heights since sample peaks may also fall below the reporting threshold when ILS peaks do. The analyst may re-inject the sample and/or set up an additional plate with the same amplified product in order to obtain proper ILS sizing. On occasion, adding more ILS to the sample well and re-injecting may be sufficient to achieve this.

2.2 Allelic Ladder

When the analyst has verified the correct labeling of the ILS for the samples in a run, the next step is to verify that the peaks in the allelic ladder(s) are labeled correctly. The GeneMapper™ ID-X software uses the allele calls of the ladder to assign allele calls to all the other samples in the project. The allele calls for the Promega PowerPlex16® System allelic ladder are shown below:

The allelic ladder contains the most common alleles determined for each of the loci. In addition, alleles not labeled in the allelic ladder (virtual alleles), may be detected and labeled in some of the samples analyzed.

At least one allelic ladder must be included in a GeneMapper™ ID-X project with the sample type designated as "allelic ladder". All the peaks in the allelic ladder must be labeled correctly for the software to assign the correct allele calls to samples in the run. When more than one ladder in a project has the sample type designated as "allelic ladder", the software will average the allelic ladders to make the allele calls for the samples in the project.

Artifacts such as spikes or "pull-up" peaks may be present that are labeled as off- ladder (OL) peaks in the allelic ladder. If all the true allele peaks are labeled correctly, such OL peaks will not affect the sample allele calls. If a spurious peak (not a true allelic peak) is labeled as a true allele (i.e. it falls within an allele size range and is designated and labeled as an allele) at any particular locus, the remaining allele designations / labels at the locus shift and will impact the correct allele call / labeling of the samples in the project. Allelic ladders with such artifacts shall not be used to analyze data in the project.

Additional information about the allelic ladder can be found in the Promega PowerPlex16® System Technical Manual.

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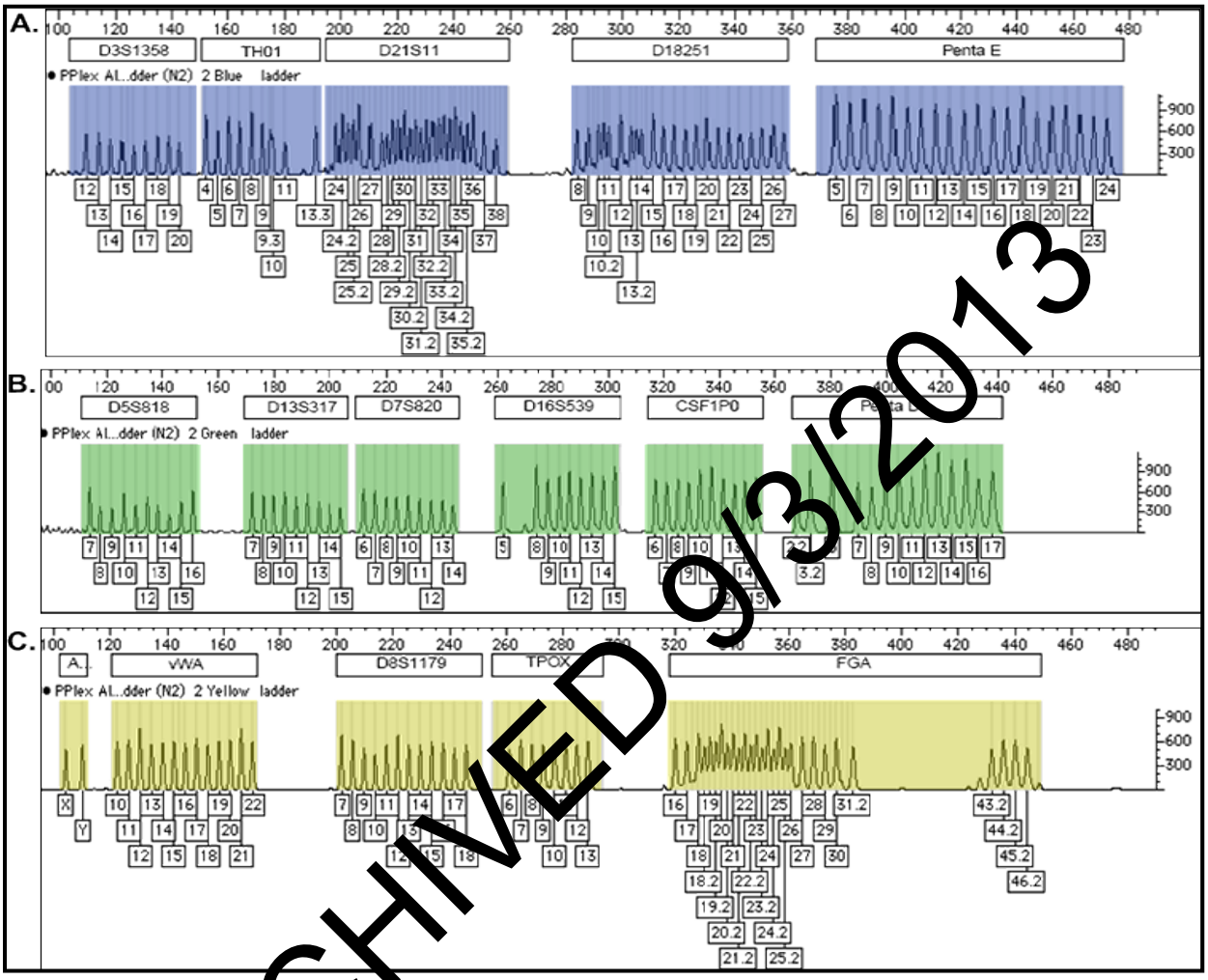
PowerPlex16® Allelic Ladder



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2.3 Positive Amplification Control

The standard DNA template 2800M is currently used as the positive amplification control for the Promega PowerPlex16® System. The positive control is used to evaluate the performance of the amplification and typing procedures.

If the incorrect STR profile is obtained for the positive control, the analyst should verify that the ILS and allelic ladder peaks are labeled properly. If the ILS and allelic ladder are labeled correctly, but one or more of the alleles in the positive amplification control are labeled incorrectly or labeled as “OL”, then the analyst when appropriate may remove a ladder(s) from the project or create different projects for different injections in an order to obtain acceptable allele calls for the positive amplification control. If the allele peak heights of the positive control fall below the reporting threshold, but the other samples in the batch have acceptable allele peak heights, then the positive control

sample data may be analyzed at 50RFU to verify allele calls with the technical manager's approval.

Generally, approximately 5% of the samples in a database batch will be quality control samples such as a duplicate offender sample or a staff duplicate sample. One of these samples may also serve as the positive amplification control when the kit control fails. Failure to obtain the expected profile for at least one positive control sample requires re-amplification of the entire plate.

When an incorrect STR profile is obtained for one or more of the positive control samples in a batch, other profiles in the batch will not be entered into CODIS until the issue is resolved. The CODIS Administrator, or a designated individual, may approve the entry of select profiles on a case by case basis.

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STR profile of 2800M

2.4 Negative Controls

A reagent blank is carried through the entire analytical process as part of each extraction or type of extraction. It contains all the reagents - except DNA template - used during extraction, amplification and typing.

The negative amplification control contains only the PCR master mix (reagents used to prepare the PCR amplification mixture) for each batch of samples and the water used to dilute the DNA samples.

The purpose of the negative controls is to detect DNA contamination that might occur from the reagents, the laboratory environment, between the samples being processed, and/or due to improper handling of the samples by the analyst. The negative controls must be run at the most stringent set of conditions for the batch (e.g. lowest reporting threshold, largest capillary electrophoresis preparation volume).

Verification of the presence of amplified product in the negative controls is performed by viewing the presence of unincorporated primer peaks.

The negative controls should not yield any true STR allelic peaks above the reporting threshold. When peaks greater than or equal to the reporting threshold are present in the range between 80-550 base pairs, the analyst will determine if the peaks are artifacts (e.g. spike, pull-up) or true allele peaks. Artifacts will be documented on the electropherogram or the database batch worksheet.

Although appropriate quality assurance practices are stringently applied and enforced, it is not unexpected that low-levels of adventitious DNA (i.e., levels that result in peak heights for allelic data that are below the Laboratory's reporting threshold) attributable to staff scientists and/or consumable products directly involved in the analytical steps of such a highly sensitive technique may be detected at a few loci. Low-level DNA in a blank will be documented on the electropherogram, along with comments regarding the presence or absence of the peaks in actual samples. As long as the low-level DNA is not also observed as a contaminant in offender samples, re-analysis may not be required. Contaminated offender samples should be re-processed (to the extent required) to determine the source of the contamination or obtain a clean result.

When probable true allele peaks are detected above the reporting threshold (in a negative control sample), at several or all STR loci, the Technical Manager will be consulted to determine the appropriate course of action.

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2.5 Interpretation of Samples

Typically, each locus is characterized by one or two labeled peaks or alleles of approximately equal intensity.

Allele peak heights should typically lie between 1000 and 6000RFU. Peak heights outside this range may be acceptable; however, it is possible that these samples will require careful interpretation. Alleles with peak heights less than 1000RFU may occasionally exhibit peak height imbalance due to stochastic effects caused by low template copy number.

Batches of database samples are uploaded into SDIS by creating an Export Table for CODIS. Prior to creating this table, the analyst must confirm that only eligible profiles are marked for export (as Convicted Offender, CO Duplicate, Arrestee, Staff Duplicate). This is done by selecting the appropriate Specimen Category while in GeneMapper ID-X. Samples not exported to CODIS are marked “no export”.

Peak height ratios (PHR) are calculated by dividing the peak height (in RFUs) of the lower RFU allele by the peak height of the higher RFU allele, and then multiplying this dividend by 100 to express the PHR as a percentage. The GeneMapper™ ID-X software is set to flag samples with an intralocus PHR below the expected minimum of 50%. PHR imbalance (in a single source sample) may occur with low quantities of template DNA, degraded template DNA or in the presence of PCR inhibitors. Severe imbalance may result in allelic dropout, where one or more alleles occur below the detection threshold or are not visible at all.

The presence of more than two peaks or severe PHR imbalance at a locus may be explained by a tri-allele, primer binding site mutation, variant allele, or other biological or procedural artifact. The presence of these at several loci is indicative of a mixed sample.

2.5.1 Tri-alleles

Tri-allelic patterns (three alleles at a single locus) are known to occur in single source samples and there are documented instances where different tissues from the same individual may or may not exhibit the tri-allelic pattern.

Samples exhibiting tri-allelic patterns with all alleles of approximately equal intensity, or with the 3rd allele having a peak height greater than or equal to 20% of the neighboring peak, are entered as such in CODIS.

Samples exhibiting possible tri-allelic patterns where the 3rd allele is less than 20% the height of the neighboring peak will be re-amplified to verify the pattern. If the pattern reproduces, the 3rd allele is designated as A/TA (artifact/possible true allele) on the

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batch worksheet and the comments section in CODIS. Only the larger two alleles are entered into CODIS.

2.5.2 Off-Ladder (OL) Alleles

The allelic ladder contains the most commonly observed alleles for the STR loci. True alleles are peaks that are detected and labeled by the GeneMapper™ ID-X software with a number and should lie within the range of the alleles in the ladder. Alleles which are not assigned a numeric designation in the standard ladder will be designated as off-ladder (OL) alleles.

Peaks that are labeled as OL (off ladder) at a particular locus have a base size that is different from any of the alleles in the ladder and any of the virtual alleles. These peaks may be true alleles but additional analysis is required to verify this. Before determining whether an OL is a true allele or an artifact, the analyst must consider all other possible causes of OL occurrence.

True OL alleles will exhibit peak morphology similar to the other alleles in the sample and the PHR should be appropriate relative to the other allelic peaks in the sample. When the overall sample quality is poor, the analyst should consider re-amplification prior to designating an OL peak as a true allele.

When a true OL allele lies within the range of alleles for a particular locus, the allele will be reported as a variant of the integer (i.e. X.1, X.2, etc.). The appropriate allele call is determined by simultaneously examining the base sizes for the sample allele peak and the associated allelic ladder peaks in the relevant locus.

When the OL allele lies either above or below the largest or smallest allele in the ladder, the OL allele will be designated as either greater than (>) or less than (<) the allele from the ladder that is closest in proximity to the OL allele.

2.5.3 Low-Level DNA Samples

Peaks may be observed that are below the reporting threshold of 250RFU. When these peaks exhibit peak morphology similar to allelic peaks and fall within an allele bin, the analyst should consider the possibility of allelic dropout. If allelic dropout is suspected in one or more core STR loci, the analyst will make a “best attempt” to re-process the sample in order to generate a complete genetic profile. The repeat analysis may include any or all of the following: re-extraction using more sample, maximum template input in PCR, and maximum “prep” or amplified sample loading volume for capillary electrophoresis.

Note: The reagent blank and negative PCR control shall be processed under the most stringent conditions utilized for any associated sample.

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If the above "best attempt" also fails to generate a complete genetic profile, a maximum of three core STR loci with elevated stutter and/or stochastic issues (e.g., partial dropout, heterozygous peak height ratio less than 50%) may be permissible in a sample. Samples that do not contain at least partial data at each of the 13 core STR loci are not eligible for upload to NDIS. The known allele 10 variant at the D5 locus is an accepted phenomenon and is not counted towards the maximum three core STR loci with stochastic issues. The presence of this variant, when observed, should be documented on the database batch worksheet.

When incomplete typing results are suspected at one or more STR loci, it is indicated by selecting "Yes" in the "Partial Profile" field in CODIS. The comments field in CODIS may be used to indicate in which loci the dropout is suspected.

Data will not be composited from multiple amplifications/injections of a database sample to obtain a more complete profile.

2.5.4 Artifacts

Artifacts are data peaks resulting from the analytical process and are not attributable to an individual contributor to the sample.

When artifacts are not pervasive throughout the sample and do not interfere with data interpretation, the sample does not require re-analysis. When an artifact is present within the size range of the alleles in a core locus and the presence of the artifact interferes with interpretation of the data in that locus, or when a sample exhibits artifacts in several loci, interpretation of the sample becomes more challenging and it may be necessary to reprocess the sample. Artifacts may be resolved by merely re-injecting a sample, or may require re-amplification or re-extraction to resolve. If the interfering artifact is located in one of the Penta loci, the analyst may choose to enter the profile, omitting all data from the affected Penta locus.

Samples uploaded into CODIS must not contain any labeled artifacts or OL alleles. The analyst may remove the artifact label. Artifact or OL peaks are either deleted or re-labeled by right clicking on the peak and selecting one of the given options. The analyst should note any changes made to the allele calls in the appropriate column on the database batch worksheet.

2.5.4.1 Incomplete 'A' nucleotide addition (-A or split peaks)

AmpliTaq Gold™, like many other DNA polymerases, catalyzes the addition of a single nucleotide (predominantly adenosine) to the 3' ends of double-stranded PCR products. This non-template addition results in a PCR product that is one base longer than the actual template, and the PCR product with the extra nucleotide is referred to as the "+A" (base peak) form. The final step of the STR amplification process is a terminal

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extension step to promote complete non-template 'A' nucleotide addition. The "-A" form is the peak that represents the actual template length. The "+A" peak will be the predominant form, with the "-A" peak typically not being detected.

Failure to attain complete terminal nucleotide addition (typically due to an excess of template DNA) results in "split peaks", two peaks above threshold that are one base apart. If the labeled "-A" peaks are not pervasive throughout the sample and the sample appears to otherwise be a single source sample, the peaks may be documented and such on the paperwork and the OL labels removed. When split peaks occur at several loci, re-amplification with less template DNA may be appropriate.

2.5.4.2 Pull-up

Multi-component analysis is the process that separates the four different fluorescent dye colors into distinct spectral components. The four dyes (Fluorescein, JOE, TMR and CXR) emit their maximum fluorescence at different wavelengths, but there is some overlap of the emission spectra. A spectral calibration is performed for a specific dye set to create a matrix that corrects for the spectral overlap.

Pull-up is the result of incomplete separation of the emission spectra and is typically observed as a non-allelic peak at the same base size as a peak in another dye. This typically occurs at high RFU values, when an excess of template DNA has been amplified.

Pull-up may also occur when the matrix file is not current. A new spectral calibration is performed whenever a new capillary array is placed on the instrument or whenever any part of the optics have been realigned and/ or replaced. A new spectral calibration may also need to be performed when an overall decrease in spectral separation is observed.

If the pull-up is prevalent enough to interfere with data interpretation, the sample may need to be re-injected or re-amplified with less DNA template. Otherwise, it can be noted on the batch worksheet and the label(s) manually removed.

2.5.4.3 Stutter

The PCR amplification of tetranucleotide STR loci typically produces a minor product peak four bases shorter than the corresponding base peak. This artifact is the result of slippage of the Taq polymerase and is referred to as the stutter peak or stutter product. Stutter products four bases longer, or two bases shorter, than the corresponding base peak are less frequently observed. Two base pair stutter products are so rare that peaks in these positions are not filtered out in the analysis parameters. In the penta-nucleotide loci, the stutter peak is five bases shorter than the corresponding base peak.

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The proportion of stutter product relative to the main allele peak is calculated by dividing the height of the stutter peak by the height of the main allele peak. The stutter percentage is fairly reproducible for a particular locus.

The GeneMapper™ ID-X database analysis methods have a global stutter filter of 20%. Peaks in the stutter position greater than 20% may indicate the presence of DNA from more than one individual. When there is no indication of a mixture, and the data is determined to be elevated stutter, the analyst will document the elevated stutter on the database batch worksheet and manually remove the stutter label.

It is unlikely that the presence of stutter peaks would interfere with the interpretation of database samples and therefore, re-amplification and/or re-injection of the sample may not be required.

2.5.4.4 Spikes

Spikes are non-allele peaks that may arise due to air bubbles, urea crystals or voltage spikes. Spikes are typically quite sharp and easy to distinguish from a true allele, usually appearing in more than one color at the same base size, and not reproducible by re-injection.

Peaks labeled as such by the GeneMapper™ ID software cannot be manually removed. However, they do not interfere with upload to CODIS and no re-analysis is required if the spike does not interfere with interpretation of the sample.

2.5.4.5 Dye Blobs

Dye blobs, like spikes, are non-allele peaks that are easily distinguished from true alleles. Dye blobs may be the result from residual dye molecules left over from the synthesis of the primers or they may be dye molecules that fell off the primer during the amplification.

If the artifact is labeled but does not interfere with data interpretation, the dye blob(s) shall be documented on the batch worksheet and the label manually removed.

2.5.4.6 Persistent Kit Artifacts

Occasionally, PCR kits may exhibit persistent artifacts that may or may not appear as true alleles. Typically, these artifacts are observed and documented during kit verification process.

As with other artifacts, if the artifact does not interfere with data interpretation, it may be documented on the batch worksheet and the label manually removed, if necessary.

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Section 3 Review of Data

3.1 Review of Offender Database Samples Analyzed In-House

Genetic profiles and all supporting documentation generated in the course of analysis will be subjected to a technical review. The DNA analyst will submit a packet containing the database batch worksheet and any electropherograms requiring documented review to another qualified database analyst for technical review. This review will be conducted in accordance with the FBI QAS Guidelines and includes the following, at a minimum, to ensure compliance with the interpretation guidelines contained within this document:

- Review of the ILS for all passing samples
- Review of all allelic ladders designated as such
- Review of all amplification positive controls and quality control samples
- Review of all reagent blanks and negative amplification controls
- Review of all DNA typing data for all passing samples
- Verification of eligibility for all profiles marked for export, to include selection of an appropriate specimen category

The analyst and the reviewer may consult a third qualified DNA analyst, if necessary, when there is a disagreement on how to report a result. If the analysts are unable to come to an agreement, the DNA Technical Manager will be consulted to make the final decision.

A review checklist is used to document completion of the individual components of the technical and administrative review. Upon completion of the technical review, the analyst may import the passing samples to SDIS. The analyst or a CODIS Administrator will then complete an administrative review, to include performing a duplicate offender search in SDIS. Upon completion of the technical and administrative review, NDIS eligible samples are uploaded by a CODIS Administrator. Additional information on CODIS procedures is contained in the CODIS Administrative Manual.

Upon completion of the upload, the following paperwork is archived as a .pdf in the LIMS:

- Database batch worksheet
- Electropherograms requiring documented review
- STR Offender Batch Review Checklist
- SDIS Import Reconciliation Report

3.2 Review of Outsourced Offender Database Samples

The laboratory does not currently use a vendor laboratory for DNA analysis. Should the laboratory enter into a contract for DNA analysis of database samples with a vendor laboratory, a procedure for the in-house review of samples analyzed under the contract will be created prior to the analysis of any samples.

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STR Offender Batch Review Checklist

Date:_____
Technical Review Started: _____
Administrative Review Started: _____
Database Batch Number: _____

	Analyst:	Tech. Review:	Admin. Review:
Database batch # and analyst's initials on each page			
Reagent worksheet complete: analysis dates, instruments, # samples, reagent lot # and expiration dates, raw data folder(s) and project name(s)			
Batch worksheet complete: well #s, sample IDs, upload eligibility, specimen category and analysis range.			
Technical Reviewer checked batch worksheet (inc. reagents): initialed and dated each page			
ILS labeled correctly (80-550) for all passing samples			
Allelic Ladder(s): correct allele calls obtained [1]			
Positive control(s): correct DNA profile obtained [1]			
Negative control(s): results are acceptable [1]			
Reagent blank(s): results are acceptable [1]			
Check for consistency between NO EXPORT samples on paperwork and in project			
Confirm appropriateness of NO EXPORT status			
Technical review of passing samples: ≤3 problem core loci, RFU 250/700, appropriate allele edits, OL allele documentation			
Correct specimen categories are assigned			
Confirm specimen category is either convicted offender or arrestee for passing samples (check for agreement between paperwork and project)			
Samples for SDIS only are flagged on paperwork			

[1] includes verification of ILS and controls for reworked samples

Eligible profiles uploaded into SDIS (in the Offender Index)			
Reconciliation report: #samples uploaded consistent with batch worksheet			
Problem samples corrected and documentation attached			
Duplicate offender search performed and all high stringency matches reconciled			
AK new moderate stringency search performed (only after previous step completed) * may be completed by analyst or administrative reviewer			

Performed by SDIS Administrator

Upload to NDIS performed			
Reconciliation report received; consistent with # samples uploaded			

NOTES:

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Appendix A Revision History

Sections of this manual were taken from the current versions of the Forensic Biology Procedures, Forensic Biology Work Instructions, and the DNA Quality Assurance Manual. The instructions and guidelines in this manual supercede the relevant sections in those manuals.

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