
Procedure for GeneMapper® ID-X for Casework

1.0 Purpose-This procedure specifies the steps for performing analysis on DNA samples amplified with AmpF ℓ STR® Identifiler® Plus using the GeneMapper® ID-X (GMID-X) software.

2.0 Scope- This procedure applies to casework analysts and trainees in the Forensic Biology Section who perform DNA analysis using GMID-X.

3.0 Definitions

- **Amelogenin** – Gender-determining locus.
- **Artifact** – Non-allelic byproducts of PCR technology (e.g., stutter, etc.), anomalies which occur during capillary electrophoresis (e.g., pull-up, spike, etc.), or byproducts of primer synthesis (e.g., dye blob, etc.).
- **Bin** – An expected location for a particular allele within a locus; a binset is a collection of expected locations for alleles at loci amplified as a set.
- **Consensus Allele** – An allele that conforms to an incremental repeat pattern at an STR locus.
- **Electropherogram (egram)** - The computer generated electronic/visual result from an analysis performed by electrophoresis.
- **.fsa File** - A raw data file generated during sample electrophoresis as part of a run; only viewable through GMID software (or equivalent).
- **Identifiler® Plus** - A commercially produced amplification kit which contains the following loci: CSF1PO, FGA, THO1, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, D2S1338, D19S433, and Amelogenin.
- **Injection** - See the Forensic Biology Section Procedure for Use of the 3130XL Genetic Analyzer for Casework.
- **LIZ Sizing Standard** - A commercially produced set of DNA fragments of known size, used to determine the size of DNA fragments in an electrophoresed sample.
- **Locus (plural = Loci)** - The chromosomal location or location of a gene or DNA marker.
- **Microvariant** - An allele that varies by less than the consensus repeat unit and is not defined by a ladder allele. Microvariants are observed in-between the ladder alleles for a specific locus.
- **Noise** - Signal detected by a data collection instrument.
- **Off Ladder Allele** - Alleles that size outside the allele categories (bins) represented in the ladder.
- **Off-Scale Data** - The result of excess DNA present in an electrophoresed sample, typically visualized by excessive artifacts as a result of peak heights consistently greater than 7000 RFUs.
- **Panel** – A collection of markers specific to an amplification kit (i.e., Identifiler® Plus).
- **Project** – A set of data saved as a single entity in GMID-X.
- **Relative Fluorescence Units (RFUs)** – A unit of measurement in electrophoresis when fluorescence detection is used; determines peak height.
- **Run** - See the Forensic Biology Section Procedure for Use of the 3130XL Genetic Analyzer for Casework.
- **Split Peaks** - A split peak is where one allele is represented by two peaks. Lack of full nucleotide A addition may be observed when the amount of input DNA is greater than the recommended protocol. In this case, more time is needed for Taq Polymerase to add the A nucleotide to all molecules.

Amplification of too much input DNA also results in off-scale/overblown data (saturation of signal) and may be manifested as split peaks.

4.0 Equipment and Materials

- Computer with GeneMapper® ID-X (version 1.4 or most current) software
- Microsoft Excel, Word
- Print2PDF software

5.0 Procedure


5.1 Creating a Project

5.1.1 Open GMID-X and log in under the Forensic Scientist's name/log-in. Analysis under the generic gmidx log-in name is not permitted. Forensic Scientists shall log into and use the Casework Database Host.

5.1.2 Select "Edit" and "Add samples" to add samples to be analyzed to the project.


5.1.3 Locate the run folder containing the samples to be added to the project under the "Files" tab. Highlight the run folder (or select the specific samples to be analyzed) and select add to List. The file(s) then appears on the right-hand side. Select "Add."

5.1.4 In the Samples pane, the category Sample Type shall have the samples labeled as follows when amplified with Identifiler® Plus:


- Ladder: Allelic Ladder
- 9947A (Positive Amplification Control): Positive Control
- All Negative Controls (extraction and amplification): Negative Control
- All other samples shall be Samples
- Sample File names appear by well number (e.g., A12) followed by the sample name as entered by the Forensic Scientist prior to electrophoresis. Also, until the samples are analyzed, the Status icon to the left of the Sample File name has the unanalyzed icon () present next to it. Verify that the table setting (in top center of the main GMID-X window) is set to 31XX Data Analysis.

5.1.5 The remaining categories shall be filled out as follows:

- Specimen Category: no export
- Analysis Method: Identifiler_Plus_AnalysisMethod
- Panel: Identifiler_Plus_v1.3X
- Size Standard: Identifiler_Plus_G5_GS500
- Instrument Type: ABI3130, or similar (note: automatically filled in by the software and instrument)

5.1.6 Once all samples and categories are properly labeled and identified, select the Analyze icon () to analyze the data. When prompted, create a project name for the set of samples and select the “Casework Security Group” and select “OK.”

5.1.6.1 The Analysis Summary and Genotypes tabs become available in the main GMID-X window once analysis is complete.

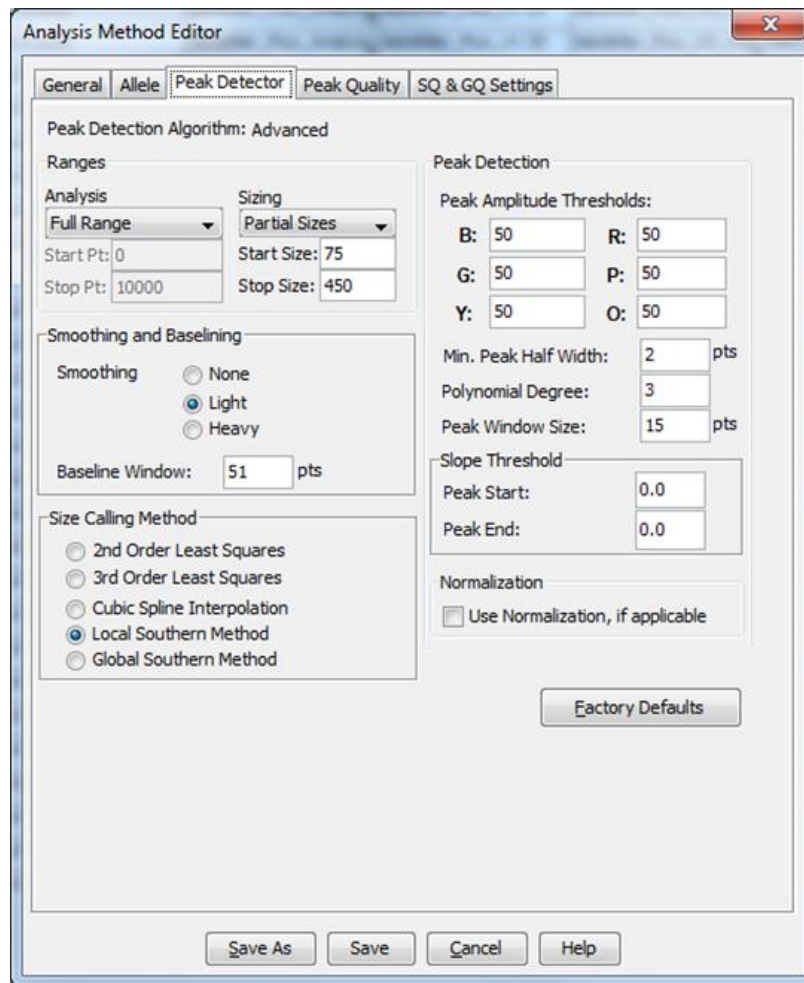
5.1.6.2 If any sample displays a solid red stop sign icon () on the right-hand side of the GMID-X window, assess the data as described in **5.2**.

5.1.6.3 Forensic Scientists shall delete their projects from the software after a copy of the project has been added to the case record associated with it and the case record has been published.

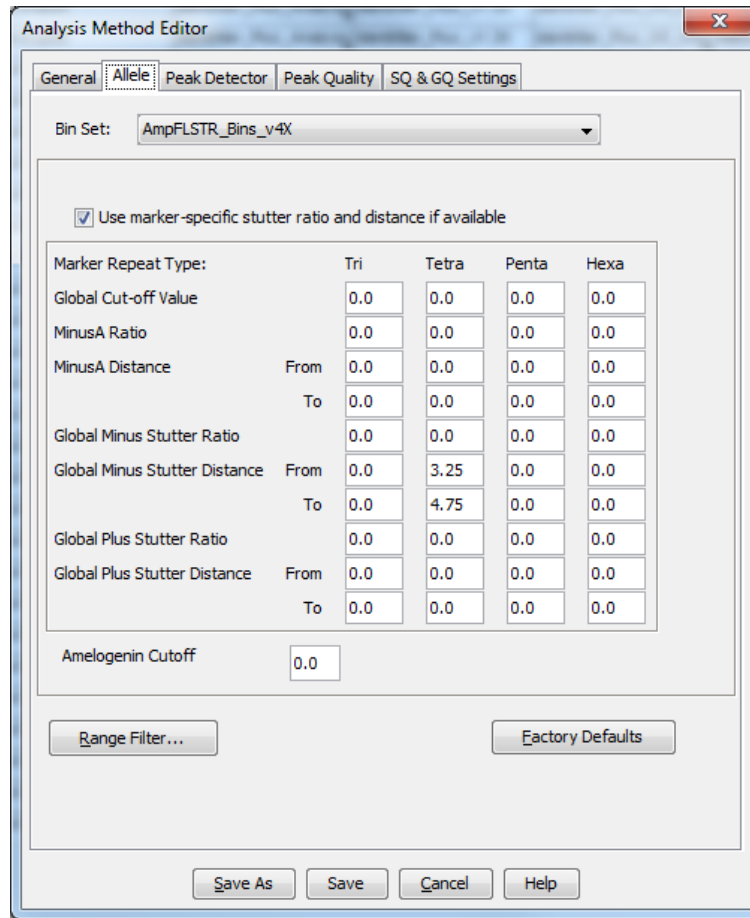
5.1.7 Analysis and Plot Settings

5.1.7.1 Access the Analysis Method Editor by selecting “Tools” from the menu in the main GMID-X window, and then select “Analysis Method Editor.” Note that the user must have a single sample in the main GMID-X window selected in order to access the Editor.

5.1.7.2 Select the “Peak Detector” tab and ensure that the settings for Peak Detection, Smoothing and Baselineing, and Size Calling Method appear as below when the samples have been amplified with Identifiler® Plus. Note that the Peak Threshold is set to 50 for all dye channels.



5.1.7.3 Next select the “Allele” tab; the contents should appear as below:

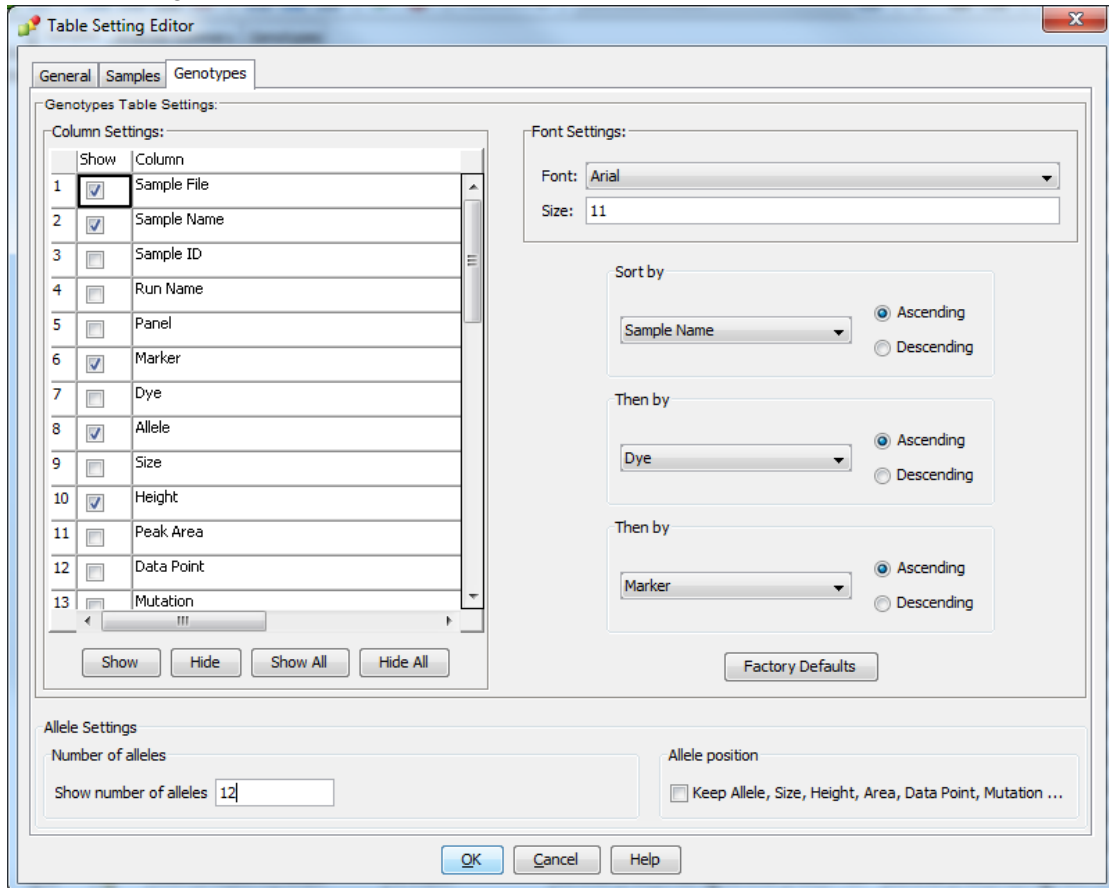


5.1.7.4 Marker-specific stutter filter percentages for Identifiler® Plus are listed below.

Locus	% Stutter
D8S1179	10.3155
D21S11	10.6714
D7S820	9.6926
CSF1PO	9.2041
D3S1358	12.2719
TH01	4.0813
D13S317	9.9348
D16S539	10.3945
D2S1338	12.4409
D19S433	11.2096
vWA	12.446
TPOX	6.3832
D18S51	13.6799
D5S818	10.0599

FGA	13.028
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5.1.7.5 In the main GMID-X window, ensure that the Traditional Allele Table is chosen; select “Tools” from the top menu; then select “Table Setting Editor.” Under the “Genotypes” tab, at the bottom of the window, ensure that the “Number of Alleles” under Allele Settings is set to at least 12.



5.1.7.6 Only the DNA Technical Leader or the GMID-X Administrators shall change settings for the Analysis Method Editor or the Table Setting Editor.

5.1.8 Adding/Deleting samples

5.1.8.1 If a Forensic Scientist must add additional sample(s) to a current project, follow **5.1.2** through **5.1.8**. The newly added sample shall be analyzed (select the Analyze icon) before the data can be viewed.


5.1.8.1.1 If the sample is from a different injection (e.g., run folder), the associated Allelic ladder shall also be imported in order for the sample data to be sized properly.


5.1.8.2 If a Forensic Scientist must remove a sample(s) that has been added to the project (e.g., a sample from an unrelated case), highlight the sample to be removed and in the menu bar, select Edit and Delete from Project. Select “OK” when prompted.

5.1.8.2.1 Samples from the same case that are present in a project, but are not used (e.g., redundancy, sizing data issues or similar), shall not be deleted (refer to **5.2.3.2**).

5.2 Analyzing/Preliminary Evaluation of Data of Each GMID-X Project

5.2.1 Evaluate Sizing Data (e.g., LIZ)

5.2.1.1 Select Edit from the GMID-X menu bar at the top of the window and Select All. Click on the Size Match Editor Icon (). The new window that opens displays the LIZ sizing data for all selected samples; scroll through each one and confirm that all sizing peaks are correct (75, 100, 139, 150, 160, 200, 300, 350, 400 and 450-base pairs). Close this window.

5.2.1.2 Again select all the samples in the main GMID-X window and select the Display Plots icon (). This opens the Sample Plot window for all selected samples. Change the Plot Setting to Overlay LIZ Dye by selecting it from the dropdown menu in the top left portion of the Sample Plot window. Zoom in to the area near the 250-base pair peak (bp) by holding the mouse just above the horizontal scale, indicating bp size, and then clicking and dragging to zoom.

5.2.1.2.1 The 250-bp peak was not defined by the manufacturer in the size standard. The purpose of checking this sizing peak is to determine if the 250-bp peak within the samples and controls are within +/- 0.5 bp of the 250-bp sizing peak of the allelic ladder with which they were injected. Therefore, no sample or control run in-house shall be used for analysis if its 250-bp peak falls outside this window in relation to the allelic ladder. Any sample or control that exceeds the window shall be re-injected (refer to the Forensic Biology Section Procedure for Use of the 3130XL Genetic Analyzer for Casework for reinjection requirements).

5.2.1.3 Highlight the 250-bp peak and hold down the “Ctrl” and “G” keys on the keyboard to select all samples at the 250-bp peak. The sizing table then displays the 250-bp peak size for all selected samples. If any sample has a 250-bp peak which is greater than +/- 0.5 bp from the 250-bp peak in the associated allelic ladder, refer to **5.2.1.2.1**.

5.2.1.4 If any sample or reagent blank in the project indicates no sizing data (e.g., LIZ failure), then that sample or reagent blank shall not be used for comparison. This information shall be noted on the Casework Table Worksheet. If there is no sizing data for an allelic ladder, then no data associated with that ladder can be sized.

5.2.1.4.1 If the allelic ladder has no sizing data, a ladder may be imported from another run to size the run. Note: The source of this imported ladder shall be documented in the case file.

5.2.1.4.2 If an amplification control has no sizing data, a duplicate control from the same amplification may be used.

5.2.1.4.3 Any sample/reagent blank that has no sizing data shall be re-injected.

5.2.2 Assess Overall Quality of Data

5.2.2.1 Allelic Ladders and Controls

5.2.2.1.1 Once all samples have been analyzed, the Analysis Summary tab will appear. This tab shows an overview of all samples, ladders and controls for the run.

5.2.2.1.2 For any ladder not showing a green square, select the allelic ladder(s) and open the sample plot window by selecting the Display Plots icon. In the Samples Plot window, ensure that the Plot Setting is set to Data Interpretation.

5.2.2.1.3 Scroll through each of the color channels (blue, green, yellow, red) and verify that all the alleles are sized and labeled correctly according to the expected calls for the Identifiler® Plus Allelic ladder. All expected peaks must be present and above the appropriate analytical threshold. Close this Sample Plot window.

5.2.2.1.4 For any positive or negative control not showing a green square, select the appropriate control and open the sample plot window as described previously.

5.2.2.1.5 Examine the positive control(s) for the expected allelic results and to ensure that the negative controls meet the required interpretive guidelines (see the Forensic Biology Section Procedure for Casework DNA Interpretation with Identifiler® Plus). Remove any artifacts as described in **5.2.2.2.1.1**.

5.2.2.2 Samples

5.2.2.2.1 Examine all samples in the manner as described for the allelic ladders and controls.

5.2.2.2.1.1 Artifacts: If any peaks are to be removed from consideration as true alleles due to their presence as a known artifact (e.g., pull-up, dye-blob, stutter, spike), highlight the sizing box associated with the peak and right-click the mouse. Select Delete Label(s) (multiple peaks can be deleted simultaneously by selecting them at the same time-when the warning dialog box appears, select OK). When prompted, type in artifact as the Reason(s) for Change.

5.2.2.2.1.1.1 OMR: GMID-X software flags peaks that fall outside the range of known alleles for a locus with the label “OMR” (Outside Marker Range). Forensic Scientists shall assess all instances of OMR to ensure that a true allele was not mislabeled by the software. If the OMR call is an artifact, the Forensic Scientist shall leave the peak labeled as OMR.

5.2.2.2.1.1.2 Spike: GMID-X software provides automatic labelling of artifacts known as “spikes” based upon peak morphology and typical presence in multiple dye channels. Peaks automatically labeled by the software as “spikes” can also include spectral pull-up. Forensic Scientists shall assess all instances of “spike” to ensure that a true allele was not mislabeled by the software. If the “spike” call is an artifact, the Forensic Scientist shall leave the peak labeled as “spike.”

5.2.2.2.1.2 Off-ladder Alleles, Tri-alleles and Microvariants: If a sample(s) contains an off-ladder allele that is not an artifact or a microvariant is present in a sample and GMID-X has not automatically assigned it an allelic value, Forensic Scientists shall document the proper sizing/locus assignment of the off-ladder alleles, tri-alleles, and/or microvariants as follows:

5.2.2.2.1.2.1 If the allele in question lies outside the marker range of a locus (e.g., between two loci, above or below the end of the color channel), the Forensic Scientist shall attempt to determine which locus the allele should be assigned to based upon the presence or absence of heterozygosity at the loci in question.

5.2.2.2.1.2.2 If one locus exhibits homozygosity and the second heterozygosity, the off-ladder allele shall be assigned to the homozygous locus.


5.2.2.2.1.2.3 If both loci exhibit homozygosity or heterozygosity, the Forensic Scientist shall document either on the allele call table or the electropherograms that the allele was observed, but not assign the allele to a particular locus, and mark the allele as inconclusive

(INC). The called (non off-ladder) alleles at these loci shall be reported and uploaded into CODIS.

5.2.2.2.1.2.4 In some instances, an off-ladder allele from one locus may appear within an adjacent locus (i.e., appears to be a potential tri-allele next to a homozygous locus). If based on training and experience the Forensic Scientist believes such a situation has occurred, the entire locus containing that allele may be marked as inconclusive.

5.2.2.2.1.2.5 A microvariant or an off-ladder shall be named/assigned per NDIS standards. For CODIS eligibility, refer to the Forensic Biology Section Procedure for CODIS.

5.2.2.2.1.2.6 In the main GMID-X window, select the sample(s) containing the microvariant/off-ladder allele and the allelic ladder. Display Plots. Zoom in to the locus containing the microvariant/off-ladder allele; the Sample Plot displays the allelic ladder in the top half of the Plot window and the sample is in the bottom half.

5.2.2.2.1.2.7 Highlight the microvariant/off-ladder allele in the sample, along with the alleles in the allelic ladder that lie the closest in size to the microvariant/off-ladder allele (to select peaks simultaneously, hold down the Ctrl key on the keyboard while selecting). Select the sizing table icon (). Select Ctrl + G to make the sizing table display the selected alleles.

5.2.2.2.1.2.8 Based upon the sizing information provided in the table, determine the appropriate allele call for the microvariant/off-ladder allele.

5.2.2.2.1.2.8.1 The correct allele call for the microvariant/off-ladder allele is dependent upon the base pair size when compared to the allelic ladder.

5.2.2.2.1.2.8.2 Microvariants that vary by less than the consensus repeat unit for that locus must be designated as an

integer of that variation (e.g., the 9.3 allele at TH01).

5.2.2.2.1.2.9 Rename the allele by right-clicking on it and selecting Rename Allele Label. Select Custom Allele Label and enter the call in the box. When prompted by the Reason(s) for Change box, type microvariant or off-ladder allele.

5.2.2.2.1.2.10 With the alleles highlighted in **5.2.2.2.1.2.7** still present in the sizing table, add a copy to the appropriate Case Record Object Repository in FA.

5.2.2.2.1.3 Verification of Off-Ladder Alleles, Tri-alleles, Microvariants:

5.2.2.2.1.3.1 Verification

5.2.2.2.1.3.1.1 For single occurrence off-ladder alleles and microvariants, verification shall be performed by re-injection of the sample or re-amplification.

5.2.2.2.1.3.1.2 Tri-alleles shall be re-amplified in order to verify their presence and size (if applicable).

5.2.2.2.1.3.1.3 When multiple occurrences of the same off-ladder, tri-allele, or microvariant are seen within the questioned samples of the same case, no verification is required.

5.2.2.2.1.3.2 Shifted alleles/loci shall not be used for comparison in any control, ladder or sample.

5.2.2.2.1.3.3 A known sample cannot be used to verify the presence of an off-ladder allele, a tri-allele, or a microvariant in a questioned sample.

5.2.2.2.1.4 Off-scale Samples: Off-scale samples shall not be used for comparison. Such samples shall be re-amplified with a lower concentration.

5.2.3 Printing Egrams Electronically

5.2.3.1 The egrams for any well in which data is collected (e.g., blank, ladder, item, etc.) shall be printed and the egrams for each GMID-X project shall exist as an individual PDF file. Ensure the plot setting is set to “Traditional Genotype Plot” when printing to PDF. The egrams for the questioned items in a case shall be printed prior to the known items.

5.2.3.1.1 GMID-X projects are added to the FA case record object repository by exporting the projects: in GMID-X, select “Tools,” “GeneMapper® ID-X Manager,” select the applicable project and select “export.” The file is exported/saved as a .ser file.

5.2.3.2 Any individual sample/control/ladder with the case that is not used for comparison purposes (e.g., LIZ failure, redundancy, further analysis) shall be added to the appropriate FA Case Record Object Repository. Such samples/controls/ladders shall appear in the Casework Table explaining why it was not used for comparison (e.g., LIZ failure, redundancy, re-analysis).

5.2.3.2.1 Even if not used for comparison purposes, all .fsa files associated with such samples/controls/ladders shall be present in the run folder containing the electronic data in the FA case record object repository.

5.2.3.2.2 For any sample/control/ladder that is not used for comparison purposes, corrections (labeling of artifacts) are not required.

5.2.3.3 If an entire run or project for a case is not used for comparison purposes, it shall be added to the case record object repository. Corrections (e.g., labeling of artifacts) are not required in this instance. A Casework Table shall be generated for this instance and the reason for not using the entire run/project shall be noted on this page (also Print2PDF; see **5.3.1**). An Allele Call Table is not required for such runs/projects.

5.2.3.4 The LIZ sizing standard shall be printed as a separate set of egrams and added to the overall egram PDF file for each project. The LIZ must be present for all samples/controls/ladders and all peaks (75 through 450) must be visible.

5.2.4 View Raw Data

5.2.4.1 In order to verify the addition of amplification kit primers to all samples and controls which do not show amplification of at least one allele (which includes instances of LIZ or injection failure), the raw data for these samples/controls shall be added to the case record object repository. Any sample/control that shows at least one allele is not required to be printed, as it may be inferred that the presence of an allele indicates primers were added to the sample/control. Note: If the entire run is not used for analysis, then the negative raw data is not required to be printed.

5.2.4.1.1 In the main GMID-X window, highlight the sample/control and select Raw Data from the View option in the main GMID-X menu.

- 5.2.4.1.2** The subsequent window displays the raw data on the right-hand side and the sample and run information on the left-hand side. Expand the left-hand window so that the full run file name (including run number) is clearly visible. The right-hand window shall show the maximum vertical and horizontal axis.
- 5.2.4.1.3** Using the “Alt” and “Print Screen” buttons on the computer, take a snapshot of the raw data. Open up a Word document and paste this snapshot into the document. Repeat this process for all samples/controls in each project that do not show amplification of at least one allele.
- 5.2.4.1.3.1** This raw data Word document shall contain at least the following information in the header: full case number, date and Forensic Scientist’s initials.
- 5.2.4.1.4** The Word document(s) containing the snapshots of the raw data shall be saved/printed as a .pdf file and included in case record object repository.

5.3 Exporting and Creating Tables

5.3.1 Casework Table

- 5.3.1.1** In the main GMID-X window, select the “Traditional Allele Table” from the Table Setting menu.
- 5.3.1.2** Select all samples and under “File” in the main GMID-X menu, select “Export Table.” Save the table to a location easily located by the Forensic Scientist (e.g., desktop or thumb drive). Ensure the file is exported/saved in the Tab-delimited Text (.txt) format.
- 5.3.1.3** Open Excel; open the .txt file saved in the previous step (note: the Forensic Scientist may have to change the file of type to All Files in order for the software to access the .txt file).
- 5.3.1.4** When the Text Import Wizard opens, select “Finish.”
- 5.3.1.5** Adjust the columns to accommodate the full text for each line.
- 5.3.1.6** Select “Page Setup.” Under the Page tab, select landscape and fit to 1 page wide by 1 page tall; under the Header/Footer tab, select Custom Header – at a minimum, the Forensic Scientist shall enter the full case number, initials and the date; under the Sheet tab, select only the Gridlines box. Finish by selecting “OK.”
- 5.3.1.7** Forensic Scientists shall note on this page any samples that are not to be used for comparison and why, or those that are to have additional analysis performed on them (see **5.2.3.2**).

5.3.1.8 The Casework Table Worksheet shall exist independently of the egrams and the Allele Call Table Worksheet(s). It may be merged with the 3130 setup sheet and saved/printed as a .pdf file.

5.3.1.9 Only samples and controls specific to the case shall be present in the Casework Table.

5.3.2 Allele Call Table

5.3.2.1 In the main GMID-X window, select the “Traditional Allele Table” from the Table Setting menu. With all samples selected, select the “Genotypes” tab in the main GMID-X menu.

5.3.2.2 Under the “File” menu in the main GMID-X window, select “Export Table.” Save the table to a location easily located by the Forensic Scientist on his/her computer (e.g., desktop or thumb drive). Ensure the file is exported/saved in the Tab-delimited Text (.txt) format.

5.3.2.3 Open Excel; open the .txt file saved in the previous step (note: the Forensic Scientist may have to change the files of type to All Files in order for the software to access the .txt file).

5.3.2.4 When the Text Import Wizard opens, select “Finish.”

5.3.2.5 Open the Allele Call Table Excel file in the Forensic Biology Shared Folder. Copy and paste the allele calls generated from the .txt file in **5.3.2.4** (Select All) into the Results tab in the appropriate Allele Call Table Worksheet.

5.3.2.6 Return to the Allele Call Table tab (or the Mixture tabs if any samples have more than 2 alleles at any given locus) and verify that the copy and paste function worked properly.

5.3.2.7 If minor alleles or profiles are to be marked, the Forensic Scientist shall indicate these with parentheses. Alleles that fall within the stochastic range (i.e., between the AT and the ST) shall have their cells highlighted. Minor alleles shall be marked if an analyst is calling that/those locus/loci predominant in a mixture. Analysts shall not mark minor alleles if predominance is not being reported.

5.3.2.8 If multiple injections are present in a case file due to re-extraction, re-amplification, or re-injection (non-serial in nature), the Forensic Scientist shall indicate from which run number the sample came. Item descriptions shall also be typed into the designated areas in the worksheet. The Forensic Scientist shall ensure their initials are typed on each page of the worksheets, as well as the full case number and the date.

5.3.2.9 It is permissible for the Forensic Scientist to combine all Allele Call Table Worksheets into one Excel spreadsheet.

5.3.2.10 Any and all notes, remarks, and observations used by the Forensic Scientist to make an interpretation and/or conclusion regarding a question sample shall be noted on the Allele Call Table Worksheet(s). Full, single source samples above stochastic threshold and samples that produce no DNA profiles do not have to be noted. (See Forensic Biology Section Procedures for Casework DNA Interpretation and Statistical Calculations.)

5.3.2.11 Allele call tables for the question and known samples shall be generated and included as separate .pdf files in the appropriate Case Record Object Repository.

5.3.2.12 Only samples specific to the case shall be present in the Allele Call Table (i.e., controls, unlabeled/unassigned allele call tables, and ladders shall not be printed).

5.3.3 CODIS Table

5.3.3.1 Refer to the Procedure for CODIS for CODIS Table Export.

5.3.3.2 Refer to the Procedure for CODIS for Specimen Upload.

6.0 Limitations - GMID-X cannot be used on computers operating on Windows XP or older.

7.0 Safety - N/A

8.0 References

Applied Biosystems™. GeneMapper® ID Software Version 3.1 User's Guide. P/N 4338775 Rev. C.

Applied Biosystems™. AmpFℓSTR® Identifiler® Plus PCR Amplification Kit User's Manual. P/N 4440211 Rev. D.

Forensic Biology Section Procedure for Casework DNA Interpretation

Forensic Biology Section Procedure for Use of the 3130XL Genetic Analyzer for Casework

Forensic Biology Section Procedure for CODIS

NDIS STR Data Entry Software (accessible by registered CODIS users only)

9.0 Records

- Identifiler® Plus Allelic Ladder Expected Results
- Identifiler® Plus 9947A Expected Results

10.0 Attachments - N/A

Revision History		
Effective Date	Version Number	Reason
07/01/2014	1	Original Document
08/29/2014	2	5.2.2.1.5 – corrected symbol header, clarified location in project window; 5.2.2.2.1.5 – added requirement to mark headers green after review; 5.2.4.1 – added note for raw data printing
02/27/2015	3	5.2.1.4.1 – clarified importing ladder for use in case; 5.2.2.2.1.1 – clarified renaming of software deleted artifacts; 5.2.2.2.1.3 – added microvariants to section; 5.2.2.2.1.5 – removed requirement to change marker headers; 5.2.3.1 – added requirement to print Q samples before K
12/28/2015	4	5.2.1.4.2 – clarified wording; 5.2.2.1.5 – amended wording to make controls and samples wording agree; 5.2.2.2.1.2 – added tri-allele throughout section; 5.2.2.2.1.3 – clarified wording; 5.2.3.4 – removed alternative for printing LIZ; 5.2.4.1, 5.2.4.1.1, 5.2.4.1.3 – updated wording to clarify when raw data is to be printed; 5.3.2.7 – clarified wording on marking