
Procedure for GeneMapper® ID

1.0 Purpose – This procedure specifies the steps for performing analysis on DNA samples using GeneMapper® ID (GMID) software.

2.0 Scope – This procedure applies to Forensic Scientists and Database Analysts in the Forensic Biology Section who perform DNA analysis using GMID.

3.0 Definitions

- **Amelogenin** - Gender-determining short tandem repeat (STR) locus.
- **Artifact** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure.
- **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).
- **Heterozygote Peak Imbalance** - A difference of greater than approximately 50% between two peaks of a single source sample at a given locus.
- **Identifiler™** - A commercially produced amplification kit which contains the following STRs: CSF1PO, FGA, THO1, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, D2S1338, D19S433, and Amelogenin.
- **Injection** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure.
- **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)** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure; also referred to as a marker.
- **Microvariant** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure.
- **Off Ladder Allele** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure.
- **Overblown/Off-Scale Data** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure.
- **Panel** - A collection of markers specific to an amplification kit (i.e., Identifiler™).
- **Project** - A set of data saved as a single entity in GMID.
- **Relative Fluorescence Units (RFUs)** - A unit of measurement used in electrophoresis when fluorescence detection is utilized; determines peak height.
- **Run** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure.
- **Split Peaks** - See Forensic Biology Section Autosomal DNA STR Interpretation Procedure.

4.0 Equipment and Materials

- Computer with GeneMapper® ID (version 3.2.1 or most current) software
- Microsoft Excel, Word
- Print2PDF software

5.0 Procedure

5.1 Setting Analysis Parameters for GMID: Each user shall import from the Section Shared Drive the following files as required for the type of analysis being performed into his/her copy of GMID prior to analysis (if not already present):

5.1.1 Analysis Methods:

- G5_Advanced.xml
- NCSBI Robot.xml (Database Robot runs only)
- North Carolina v2.xml (Database Contractor Data Review only, provided by contract laboratory)

5.1.2 Panels/Bins:

- AmpFLSTR_Panels_v2.txt
- AmpFLSTR_Panels_v2_AmpFLSTR_Bins_v2_bins.txt
- AmpFLSTR_Panels_NC_v2_Panels.txt (Database Contractor Data Review only, provided by contract laboratory)
- AmpFLSTR_Panels_NC_v2_AmpFLSTR_Bins_NC_v2_bins.txt (Database Contractor Data Review only, provided by contract laboratory)

5.1.3 Size Standards:

- GS500LIZ_Advanced.xml

5.1.4 Tables and Plot Settings:

- SBI Casework Table.xml
- AmpFLSTR Sizing plot.xml
- Case Allele Table.xml
- Overlay LIZ plot.xml
- AmpFLSTR Genotyping plot.xml
- AmpFLSTR Table.xml
- CODIS Export Table.xml

5.2 Creating a Project

5.2.1 Open GMID and log in under Forensic Scientist's/Database Analyst's name/log-in. Analysis under the generic "gmid" log-in name is not permitted.

5.2.2 For Database review of contractor data, the contractor-provided .ser file(s) shall be imported using GeneMapper Manager. The following files must be added to GMID prior to review:

- Analysis Method: North Carolina v2.xml
- Panels/Bins: AmpFLSTR_Panels_NC_v2_Panels.txt and AmpFLSTR_Panels_NC_v2_AmpFLSTR_Bins_NC_v2_bins.txt

Refer to DNA Database Review of Contractor Data for review procedure.

5.2.3 Select "File" and "Add samples to project."

-
- 5.2.4** 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.”
- 5.2.5** In the Samples pane, the category “Sample Type” shall have the samples labeled as follows when amplified with Identifiler™:
- Ladder: Allelic Ladder
 - 9947A (Positive Amplification Control): Positive Control
 - Negative Amplification Control: Negative Control
 - All other samples shall be “Samples”
 - Note: Sample File names appear by well number (ie, A12) followed by the sample name as entered by the Forensic Scientist/Database Analyst 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. If no “Status” category or icons are present, verify that the table setting (in top center of the main GMID window) is set to “AmpFLSTR Table.”
- 5.2.6** The remaining categories shall be filled out as follows:
- Specimen Category: no export
 - Analysis Method: G5_Advanced or NCSBI Robot (for Robot runs)
 - Panel: Identifiler_v2
 - Size Standard: GS500LIZ_Advanced
 - Instrument Type: ABI3130, or similar (note: automatically filled in by the software and instrument)
- 5.2.7** 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 “Save.”
- 5.2.7.1** Note: GMID auto-saves data after every 10 samples have been processed.
- 5.2.7.2** Note: The Genotypes tab becomes available in the main GMID window once analysis is complete.
- 5.2.7.3** Note: If any sample displays a solid red “stop” sign icon () on the right-hand side of the GMID window, assess the data as described in 5.3.
- 5.2.8** Analysis and Plot Settings
- 5.2.8.1** Access the Analysis Method Editor by selecting “Analysis” from the menu in the main GMID window, and then select “Analysis Method Editor.” Note that the user must have a single sample in the main GMID window selected in order to access the Editor.
- 5.2.8.2** Select the “Peak Detector” tab, and for casework ensure that the settings are as seen below when the samples have been amplified with Identifiler™. Note that the Peak Threshold is set to 75 for the blue, green, yellow and red channels for
-

casework. Note that the threshold for orange (LIZ) is set to 80 RFU for all casework and database samples.

Analysis Method Editor - HID

General | **Allele** | **Peak Detector** | Peak Quality | Quality Flags

Peak Detection Algorithm: Advanced

Ranges

Analysis: Partial Range
Start Pt: 1500
Stop Pt: 12000

Sizing: All Sizes
Start Size: 0
Stop Size: 000

Smoothing and Baseline

Smoothing: ☐ None ☒ Light ☐ Heavy

Baseline Window: 51 pts

Size Calling Method

☐ 2nd Order Least Squares
☐ 3rd Order Least Squares
☐ Cubic Spline Interpolation
☒ Local Southern Method
☐ Global Southern Method

Peak Detection

Peak Amplitude Thresholds:

B: 75 R: 75
G: 75 O: 80
Y: 75

Min. Peak Half Width: 2 pts
Polynomial Degree: 3
Peak Window Size: 15 pts

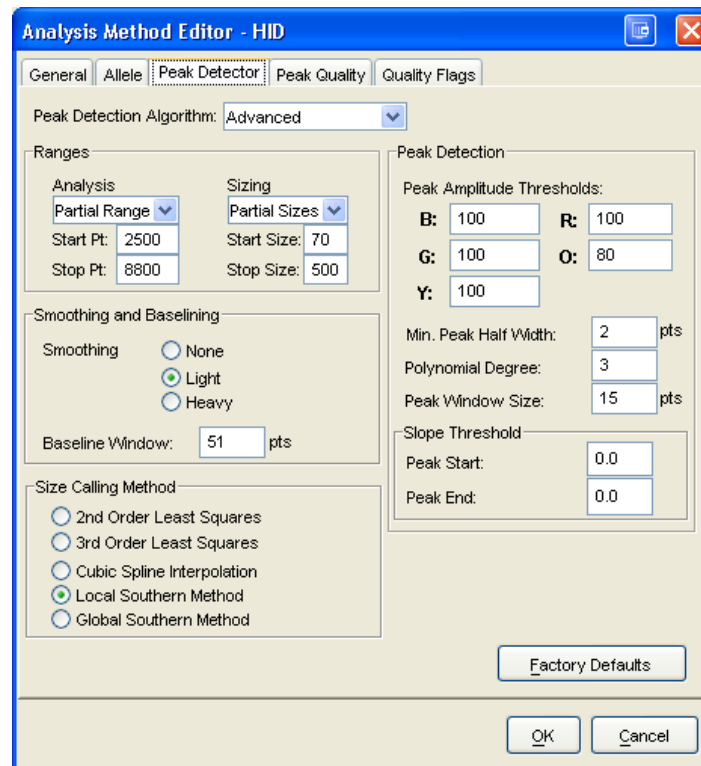
Slope Threshold

Peak Start: 0.0
Peak End: 0.0

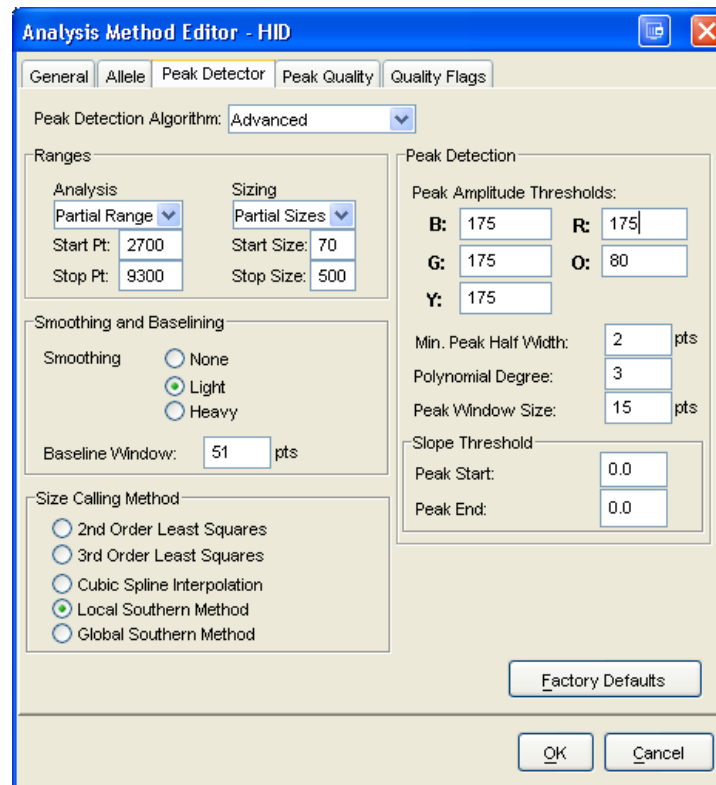
Factory Defaults

OK Cancel

For Database samples generated in-house, the Peak Threshold for the blue, green, yellow and red channels shall be set according to the screenshot below.



For Database robot samples, the Peak Threshold for the blue, green, yellow and red channels shall be set according to the screenshot below.



For Database samples generated by contractors, the Peak Threshold for the blue, green, yellow and red channels shall be set according to the screenshot below.

Analysis Method Editor - HID

General | **Allele** | Peak Detector | Peak Quality | Quality Flags

Peak Detection Algorithm: Advanced

Ranges

Analysis	Sizing
Partial Range	Partial Sizes
Start Pt: 2500	Start Size: 75
Stop Pt: 9000	Stop Size: 450

Smoothing and Baseline

Smoothing: ☐ None ☒ Light ☐ Heavy

Baseline Window: 51 pts

Size Calling Method

☐ 2nd Order Least Squares
☐ 3rd Order Least Squares
☐ Cubic Spline Interpolation
☒ Local Southern Method
☐ Global Southern Method

Peak Detection

Peak Amplitude Thresholds:

B: 50	R: 50
G: 50	O: 50
Y: 50	

Min. Peak Half Width: 2 pts
 Polynomial Degree: 3
 Peak Window Size: 15 pts

Slope Threshold

Peak Start: 0.0
Peak End: 0.0

Factory Defaults

OK Cancel

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

Analysis Method Editor - HID

General | **Allele** | Peak Detector | Peak Quality | Quality Flags

Bin Set: AmpFLSTR_Bins_v2

☒ Use marker-specific stutter ratio if available

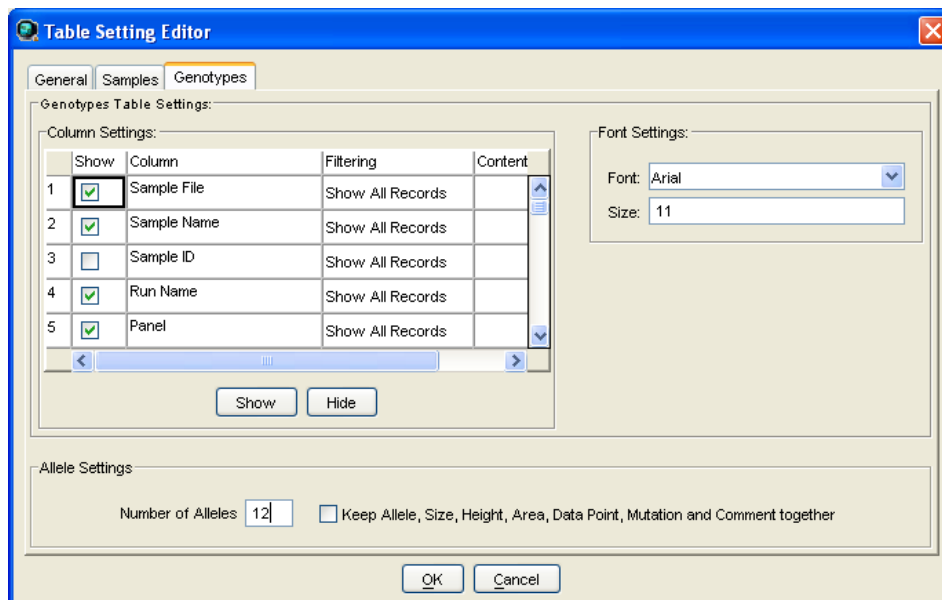
Marker Repeat Type :		Tri	Tetra	Penta	Hexa
Cut-off Value		0.2	0.0	0.25	0.25
MinusA Ratio		0.0	0.0	0.95	0.95
MinusA Distance	From	0.0	0.0	0.0	0.0
	To	0.0	0.0	1.6	1.6
Minus Stutter Ratio		0.95	0.0	0.15	0.15
Minus Stutter Distance	From	0.0	3.25	0.0	0.0
	To	3.5	4.75	5.5	6.5
Plus Stutter Ratio		0.0	0.0	0.0	0.0
Plus Stutter Distance	From	0.0	0.0	0.0	0.0
	To	0.0	0.0	0.0	0.0

Amelogenin Cutoff: 0.0

Range Filter... Factory Defaults

OK Cancel

- 5.2.8.4** In the main GMID window, select “Tools” from the top menu, and 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 for casework. Forensic Scientists/Database Analysts may adjust this number if necessary (i.e., to maximum number of called allele at any locus).



5.2.9 Adding/Deleting samples

- 5.2.9.1** If a Forensic Scientist/Database Analyst must add an additional sample(s) to a current project, follow 5.2.3 through 5.2.8. The newly added sample shall be analyzed (select the “Analyze” icon) before the data can be viewed.

5.2.9.1.1 Note: if the sample is from a different injection (i.e., run folder), the associated Allelic ladder shall also be imported in order for the sample data to be sized properly.

- 5.2.9.2** If a Forensic Scientist/Database Analyst must remove a sample(s) that has been added to the project (i.e., a sample from an unrelated case or CODIS confirmation), highlight the sample to be removed and in the menu bar, select “Edit” and “Delete from Project.” Select “OK” when prompted.

5.2.9.2.1 Note: samples from the same case or confirmation that are present in a project but are not used (i.e., redundancy, sizing data issues, or similar) shall not be deleted (refer to 5.3.2.3.2).

5.3 Analyzing/Preliminary Evaluation of Data of Each GMID Project

5.3.1 Evaluate Sizing Data (i.e., LIZ)

- 5.3.1.1** Select “Edit” from the GMID 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, 340, 350, 400, and 450- base pairs). Close this window.

5.3.1.1.1 Note: If all peaks are not called, the analysis range may need to be extended: view the Analysis Settings in **5.2.8. 2** and change the analysis range to “Full Range” in the “Peak Detector” tab.

5.3.1.2 Again select all the samples in the main GMID window and select the “Display Plots” icon (). This opens the Sample Plot window for all selected samples. Change the Plot Setting to “Overlay LIZ” 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.

5.3.1.2.1 Note: 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 they were injected with. Therefore, no sample or control run in-house shall be used for analysis if its 250-bp peak falls outside of 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 reinjection requirements).

5.3.1.3 Highlight the 250-bp peak and hold down the Ctrl and “S” key 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 **5.3.1.2.1**.

5.3.1.4 If any sample or control in the project indicates “no sizing data” (i.e., LIZ failure), then that sample or control shall not be used for comparison and shall be re-injected to achieve proper sizing information. 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 and the entire set shall be re-injected.

5.3.2 Assess Overall Quality of Data

5.3.2.1 Allelic Ladders and Controls

5.3.2.1.1 In the main GMID window, 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 “AmpFLSTR Genotyping.”

- 5.3.2.1.2 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™ Allelic ladder. All expected peaks must be present and above the appropriate analytical threshold (i.e., database or casework thresholds). Close this Sample Plot window.
- 5.3.2.1.3 In the main GMID window, select the positive and negative amplification and extraction controls if used. Open the sample plot window as described previously.
- 5.3.2.1.4 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 Autosomal DNA STR Interpretation). Remove any artifacts as described in 5.3.2.2.1.1. Close the Sample Plot window.

5.3.2.2 Samples

- 5.3.2.2.1 Examine all samples in the manner as described for the allelic ladders and controls.
 - 5.3.2.2.1.1 **Artifacts:** If any peaks are to be removed from consideration as true alleles due their presence as a known artifact (i.e., pull-up, dye-blob, stutter, spike), highlight the sizing box associated with the peak and right-click the mouse. Select “Delete Allele(s)” (multiple peaks can be deleted simultaneously by selecting them at the same time—when the warning dialog box appears, select “OK”). When prompted by the “Delete Allele Comment,” type in “artifact” and the Forensic Scientist’s/Database Analyst’s initials.
 - 5.3.2.2.1.2 **Microvariants:** If a microvariant is present in a sample and GMID has not automatically assigned it an allelic value, Forensic Scientists/Database Analysts shall document the proper sizing of the microvariant as follows:
 - 5.3.2.2.1.2.1 In the main GMID window, select the sample(s) containing the microvariant and the allelic ladder. Display Plots. Zoom in to the locus containing the microvariant; the Sample Plot displays the allelic ladder in the top half of the Plot window and the sample is in the bottom half.
 - 5.3.2.2.1.2.2 Highlight the microvariant in the sample, along with the alleles in the allelic ladder that lie the closest in size to the microvariant (to

select peaks simultaneously, hold down the Ctrl key on the keyboard while selecting). Select the sizing table icon (). Select Ctrl + S to make the sizing table display the selected alleles.

5.3.2.2.1.2.3 Based upon the sizing information provided in the table, determine the appropriate allele call for the microvariant. For CODIS eligibility, refer to the Procedure for CODIS.

5.3.2.2.1.2.3.1 Note: the correct allele call for the microvariant is dependent upon the microvariant's base pair size when compared to the allelic ladder.

5.3.2.2.1.2.3.2 Note: microvariants that vary by less than the consensus repeat unit for that locus must be designated as an integer of that variation (i.e., the 9.3 allele at TH01).

5.3.2.2.1.2.4 Rename the allele by right-clicking on it and selecting "Rename Allele." If the correct allele call is not already present in the subsequent drop-down list, select "Custom" and enter the call in the "Create Custom Allele Name" box. When prompted by the "Edit Allele Comment" box, type in "microvariant" and the Forensic Scientist's/Database Analyst's initials.

5.3.2.2.1.2.5 With the alleles highlighted in **5.3.2.2.1.2.2** still present in the sizing table (remove any extraneous), select "File" and "Print" and select "Print2PDF."

5.3.2.2.1.2.6 In casework samples, if a microvariant is observed in a single instance in a case, it shall be reamplified to verify its presence in the sample. If the microvariant is observed throughout the case, across more than one sample (question or known), then the sample(s) containing the microvariant do not need to be re-amplified. For database samples,

re-amplification or re-extraction of the sample shall be at the Forensic Scientist's/Database Analyst's discretion (see the Forensic Biology Section DNA Database procedures).

5.3.2.2.1.3 Off Ladder Alleles: If a sample(s) contains an off ladder allele that is not an artifact, the Forensic Scientist/Database Analyst shall assign the allele to the correct locus if possible (see below). For CODIS eligibility, refer to the Forensic Biology Section Procedure for CODIS.

5.3.2.2.1.3.1.1 If the allele in question lies between two loci, the Forensic Scientist/Database Analyst 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.

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

5.3.2.2.1.3.1.3 If both loci exhibit homozygosity or heterozygosity, the Forensic Scientist/Database Analyst 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.

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

5.3.2.2.1.3.2 If the off ladder allele can be assigned to a locus, the allele must be designated as either greater than (>) or less than (<) the last respective allele for that locus called by the allelic ladder. For CODIS

eligibility, refer to the Forensic Biology Section Procedure for CODIS.

5.3.2.2.1.3.3 Follow the steps outlined for microvariants for assigning a value to the off ladder allele, as well as the printing format, with the exception that the “comment” shall be “off ladder allele” instead of “microvariant.”

5.3.2.2.1.3.4 In casework samples, if an off ladder allele occurs as a single instance, it shall be re-amplified. In database samples, re-amplification or re-extraction shall be at the Forensic Scientist’s/Database Analyst’s discretion (see **5.3.2.2.1.2.6**).

5.3.2.2.1.3.5 If the GMID software does not allow the Forensic Scientist/Database Analyst to assign a value to the off ladder allele, the Forensic Scientist/Database Analyst shall follow the same procedure for documentation and assignment of microvariants. The Forensic Scientist/Database Analyst shall be required to print out the sizing table/egram combination and manually write the proper sizing designation to the off ladder allele along with the Forensic Scientist’s/Database Analyst’s initials. These pages shall then be scanned into PDF format.

5.3.2.2.1.3.5.1 Note: the Allele Call Table Worksheet also needs to be changed to reflect the proper allele call for the off ladder allele that cannot be exported through the GMID software.

5.3.2.2.1.4 Sizing Shifts: If any allele at any locus has been sized outside of the appropriate bin which results in an “off ladder” call by GMID, the sample shall be re-injected (or re-amplified, if necessary) in order to size the allele(s) properly if the Forensic Scientist/Database Analyst wants to use the results at that locus. Shifted alleles/loci shall not be used for comparison in any control, ladder or sample.

5.3.2.2.1.5 Overblown/Off-scale Samples: overblown samples in casework shall not be used for comparison. Such samples shall be either re-injected for a lower injection time (i.e., 22 to 10 seconds) or re-amplified with a lower concentration. The use of overblown samples in Database samples shall be at the

discretion of the Forensic Scientist/Database Analyst based upon the training and experience of the Forensic Scientist/Database Analyst.

5.3.2.2.1.6 Tri-alleles: For casework, the sample shall be re-extracted unless the tri-allelic pattern appears at least twice within a case. For database, the sample shall be re-extracted except in CODIS confirmations.

5.3.2.3 Printing Egrams Electronically

5.3.2.3.1 All egrams shall be printed using the Print2PDF printer, with the exception of **5.3.2.2.1.3.5**. The egrams for each GMID project shall exist as its own PDF file.

5.3.2.3.1.1 Note: GMID projects are added to the FA case record object repository by exporting the projects: in GMID, select “Tools,” “GeneMapper Manager,” select the applicable project and select “export.” The file is exported/saved as an .ser file.

5.3.2.3.2 Any individual sample/control/ladder with the case or CODIS confirmation that is not used for comparison purposes (i.e., LIZ failure, redundancy, further analysis) shall be printed in PDF format. Such samples/controls/ladders shall appear in the Casework Table explaining it was not used for comparison (e.g., LIZ failure, redundancy, re-analysis).

5.3.2.3.2.1 Note: 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.

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

5.3.2.3.3 If an entire run or project for a case or CODIS confirmation is not used for comparison purposes, it shall be printed as Print2PDF and added to the case record object repository. Corrections (i.e., 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 **5.4.1**). An Allele Call Table is not required for such runs/projects.

5.3.2.3.4 The LIZ sizing standard shall be printed (Print2PDF) as a separate set of egrams which may be added to the overall egram PDF file for each project, or kept separately as an independent document. The LIZ must

be present for all samples/controls/ladders and all peaks (75 through 450) must be visible.

5.3.3 View Raw Data

5.3.3.1 In order to verify the addition of amplification kit primers to all negative controls and negative samples (which includes instances of LIZ or injection failure), the raw data for such samples from each project must be present in each case record object repository.

5.3.3.1.1 In the main GMID window, highlight the negative control or negative sample and select “Raw Data” from the “View” option in the main GMID menu.

5.3.3.1.2 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.

5.3.3.1.3 Using the Alt + Print Screen buttons on the computer, take a “snapshot” of the raw data window. Open up a Word document and paste this “snapshot” into the document. Repeat this process for all negative samples and negative controls in each project.

5.3.3.1.3.1 This raw data Word document shall contain at least the following information in the header: full case number (or batch number for Database; refer to the DNA Database Procedures), date, Forensic Scientist’s/Database Analyst’s initials.

5.3.3.1.4 The Word document(s) containing the “snapshots” of the raw data shall be included in the scanned or Print2PDF case notes.

5.4 Exporting and Creating Tables

5.4.1 Casework Table

5.4.1.1 In the main GMID window, select the “SBI Casework Table” from the Table Setting menu.

5.4.1.2 Select all samples and under “File” in the main GMID menu, select “Export Table.” Save the table to a location easily located by the Forensic Scientist/Database Analyst (i.e., desktop or thumb drive). Ensure the file is exported/saved in the “Tab- and Comma-delimited Text” (.txt) format.

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

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

5.4.1.5 Adjust the columns to accommodate the full text for each line.

5.4.1.6 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/Database Analyst shall enter the full case number (or batch number for Database), initials, and the date; under the “Sheet” tab, select only the “Gridlines” box. Finish by selecting “OK.” Alternately, Forensic Scientist /Database Analysts may use the Casework Table Worksheet to create this table.

5.4.1.7 Forensic Scientists/Database Analysts 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 5.3.2.3.2).

5.4.1.8 Print the Casework Table Worksheet by using the Print2PDF printer. The Casework Table Worksheet shall exist independently of the egrams and the Allele Call Table Worksheet(s). It may be merged with the set-up sheet.

5.4.1.9 Note: only samples and controls specific to the case or CODIS confirmation shall be present in the Casework Table.

5.4.2 Allele Call Table

5.4.2.1 In the main GMID window, select the “Case Allele Table” from the Table Setting menu. With all samples selected, select the “Genotypes” tab in the main GMID menu.

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

5.4.2.2.1 Note: the Forensic Scientist/Database Analyst may need to add additional information to the .txt file name in order to avoid copying over the Casework Table file.

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

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

5.4.2.5 Open the Allele Call Table Excel file in the Forensic Biology Shared Folder. For Robot runs, use the Robot Allele Call Table. For manual runs performed in the database, either the Robot Allele Call table or manual allele call table may be used. Copy and paste the allele calls generated from the .txt file in 5.4.2.4 (Select “All”) into the “Results” tab in the appropriate Allele Call Table Worksheet.

- 5.4.2.6** 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.
- 5.4.2.7** If minor alleles or profiles are to be marked, the Forensic Scientist/Database Analyst shall highlight the cells containing the minor allele/profile. The Forensic Scientist/Database Analyst shall make a key at the bottom (or in the footer) of the Allele Call Table indicating what the highlighted cell represents.
- 5.4.2.8** If multiple injections are present in a case file, the Forensic Scientist/Database Analyst 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/Database Analyst shall ensure their initials are typed on each page of the worksheets, as well as the full case number (or batch number for Database) and the date.
- 5.4.2.9** In casework, it is permissible for the Forensic Scientist to combine all Allele Call Table Worksheets into one Excel spreadsheet.
- 5.4.2.10** In casework, Forensic Scientists shall note any activity or allelic dropout (or similar notations) on the Allele Call Table Worksheet(s).
- 5.4.2.11** Print the Allele Call Table Worksheet(s) using the Print2PDF printer. This file must be separate from the file containing the egrams or the Casework Table.
- 5.4.2.12** Note: only samples specific to the case or CODIS confirmation are required to be present in the Allele Call Table (i.e., controls and ladders).

5.4.3 CODIS Table

- 5.4.3.1** For casework, refer to the Procedure for CODIS for CODIS Table Export.
- 5.4.3.2** For casework, refer to the Procedure for CODIS for Specimen Upload.
- 5.4.3.3** For Database, refer to the Procedure for CODIS, Procedure for DNA Database Review Contractor Data, and the Procedure for DNA Analysis and Technical Review of Database Samples for CODIS sample export and specimen upload.

6.0 Limitations – GMID cannot be used on computers operating on Windows 7 or higher.

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™ PCR Amplification Kit User’s Manual. P/N 4323291 Rev. B.

Forensic Biology Section Procedure for Autosomal DNA STR Interpretation

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

Forensic Biology Section Procedure for CODIS

Forensic Biology Section DNA Database Procedures

Forensic Biology Section Procedure for DNA Database Review of Contractor Data

Forensic Biology Section Procedure for DNA Database Analysis and Technical Review of Database Samples

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

9.0 Records

- Identifiler™ Allelic Ladder Expected Results
- Identifiler™ 9947A and MJB Expected Results

10.0 Attachments – N/A

Revision History		
Effective Date	Version Number	Reason
09/17/2012	1	Original Document
10/26/2012	2	Changed wording in 5.4.2.12 from “shall” to “are required” to allow analyst to add control results if warranted. Added option to 5.4.2.5 to allow either the Robot or manual allele call tables to be used for manual runs in the Database. Added 5.3.2.3.2.2, note to not require corrections to egrams that are not used for comparisons.