	Intermountain Forensics	SOP #	IAC-205
		Revision #	01
Forensic DNA Technical Leader Approval		**Issue Date**	
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Genemapper® ID-X

1.   Purpose

To provide instruction and explanation on icons for using the Genemapper® ID-X software for Capillary Electrophoresis data interpretation.

2.   Summary

GeneMapper® ID-X Software is used to convert the data generated by a genetic analyzer (3130, 3500, etc.) into a visual format that can be interpreted by a DNA Analyst. The software provides may tools to assist in interpretation and print documentation for inclusion in reports.

3.   Procedure

Casework Analysis using GeneMapper® ID-X

1. Log into the software by selecting your username from the drop-down menu and typing in your password.

2. Select "Add samples to project" under the file menu or click the "Add Samples to Project" icon   . Browse the system to find the .hid GeneMapper® ID-X project file folder.

3. Select the folder containing the .hid files, then "Add to List". When you add samples from .hid files to a project you specify the location of the files on the network. The sample files remain in their original location on the drive and are not stored in the GeneMapper® ID-X Software project or database.

4. In the Project window, select the appropriate table setting from the Table Settings drop-down list.

5. Select the appropriate size standard, analysis method, and panel from the dropdown menus in the sample table in the GeneMapper® ID-X project window.

6. Change the sample type for the allelic ladder to Allelic Ladder in the Sample Type field.

7. Click the "Analyze" icon   to begin analysis of the selected GeneMapper® ID-X files.

8. Save project files using the load plate number for plate projects and the case number for individual case projects.

9. If there are multiple ladders in the project protocol and one fails, the Allelic Ladder Analysis Summary Table will appear. Select "Continue analysis of folders with at least one passing allelic ladder" before clicking OK.

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Analyzes run folders with at least one passing ladder and uses the passing ladder(s) to calculate bin offsets. Run folders with no passing ladders are not analyzed.

Allelic Ladder Analysis Summary

Quality indicators shown here are based on SQ and CGQ only.

Run Folder	Total # of Analyzed Ladders	🟩	⚠️	🔴
Identifier Samples	2	1	0	1

What would you like to do next?

◉ Continue analysis of folders with at least one passing allelic ladder

○ Continue analysis of all folders

○ View allelic ladder samples with yellow and/or red quality indicators

[OK] [Cancel] [Help]

Icons:

GeneMapper® ID-X Project Window Toolbar

New Project, Save Project, Export Table, Report Manager, Size Match Editor, Panel Manager, Analyze, Table Setting Menu, Print, Products and Services

Open Project, Add Samples to Project, Display Plots, Label Edit Viewer, Analysis Method Editor, GeneMapper® ID-X Manager, Low Quality to Top, Find, Print Preview, GeneMapper® ID-X Help

Table Setting: HID Table

10. The "New Project" icon is used to open a new project that does not contain any .hid files.

11. The "Open Project" icon is used to open a project that has previously been created and will contain .hid files.

12. The "Save Project" icon can be used to save any changes to the project that have not already been saved. A * in the project name indicates that changes have been made and have not been saved.

13. The "Add Samples to Project" icon is used to add samples to a new project or can also be used to add samples to a project that has already been completed.

14. The "Export Table" exports the contents of the currently selected table in a .txt file. It can export tables from the Samples tab or the Genotypes tab.

15. The "Display Plots" icon is used to show the electropherogram for the sample(s) highlighted.

16. The "Label Edit Viewer" icon contains a detailed list of edits made to allele and artifact labels in a Sample plot, with the reasons for the changes.

17. The "Size Match Editor" icon is used to display the ILS of the sample(s) highlighted.

18. The "Analysis Method Editor" icon is used to change any parameters in the analysis methods, such as the analysis range.

19. The "Panel Manager" icon is used to import, export, review the panels, bins, or stutter percentages for the STR multiplexes.

20. The "GeneMapper® ID-X Manager" icon allows you to view analysis methods, plot settings, table settings, matrices, size standards, panels, and previously analyzed projects".

21. The "Analyze" icon will start the analysis of the project.

22. The "Low Quality to top" icon will move any samples that have a red octagon for quality to the top of the sample list.

23. The "Table Settings Menu" lists available table settings in a drop-down menu.

24. The "Table Setting Editor" icon allows you to edit the parameters of new and existing table settings.

25. The "Find" icon allows you to search the Sample tab or Genotypes tab columns.

26. The "Print" icon allows you to print reports, tables, plots, sample information, raw data, or EPT data; as long as the item is currently open.

27. The "Print Preview" icon allows you to review the printout before printing.

28. The "Products and Services" icon will open the Life Technologies Corporation online Store.
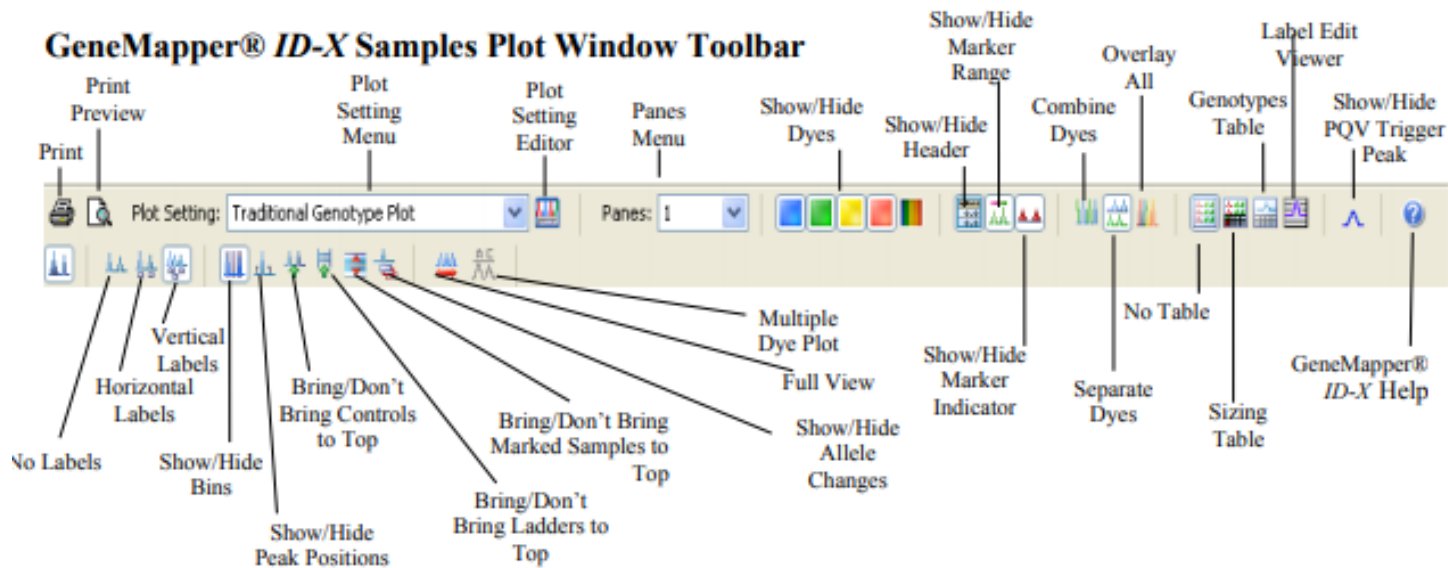
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29. The "GeneMapper® ID-X Help" icon can be opened to display help for the Project window.

GeneMapper® ID-X Samples Plot Window Toolbar

30. The "Print" icon allows you to print reports, tables, plots, sample information, raw data, or EPT data; as long as the item is currently open.

31. The "Print Preview" icon allows you to review the printout before printing.

32. The "Plot Setting Menu" icon lists available plot settings in the drop-down menu.

33. The "Plot Setting Editor" icon allows you to edit the parameters of new and existing plot settings.

34. The "Panes Menu" icon allows you to change the number of panes (from 1 to 8) that can be displayed.

35. The "Show/Hide Header" icon allows you to display or hide the sample headers in the plot window.

36. The "Show/Hide Marker Range" icon allows you to display or hide the color-coded marker headers in the plot window.

37. The "Show/Hide Marker Indicator" icon allows you to display or hide the red marker size range indicators in the plot window.

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38. The "Show/Hide PQV Trigger Peak" icon allows you to display or hide a peak label suffix for peaks with Low Peak Height (LPH), Max Peak Height (MPH), Broad Peak (BD), or Off-scale (OS) PQVs.

39. The "GeneMapper® ID-X Help" icon can be opened to display help for the Plot window.

40. The "No Labels" icon allows you to hide all peak labels.

41. The "Horizontal Labels" icon allows you to display peak labels in a horizontal format. This may cause overlapping of labels if not zoomed in sufficiently.

42. The "Vertical Labels" icon allows you to display labels in a vertical format. This will prevent overlapping labels.

43. The "Show/Hide Bins" icon allows you to display or hide allele bins. Note: Bins are not displayed when the x-axis scale is set to data points.

44. The "Show/Hide Peak Positions" icon allows you to display or hide peak position indicators (for start of peak, peak apex, and end of peak).

45. The "Bring/Don't Bring Controls to Top" icon moves control samples to the top of the plot in one scrollable pane, or to the bottom of the plot.

46. The "Show/Hide Allele Changes" icon allows you to display or hide any allele label edits manually applied after software analysis.

47. The "Full View" icon restores the plot to the maximum magnification.

48. The "Multiple Dye Plot" icon displays a plot showing all dyes in the range of the selected marker.

49. The "Show/Hide Dyes" icon allows you to select the dyes to display or hide in the plot.

50. The "Combine Dyes" icon allows you to display all dyes for a sample in one pane.

51. The "Separate Dyes" icon allows you to display each dye of s ample in a separate pane.

52. The "Overlay All" icon allows you to overlay all samples and display all dyes for all samples in one pane.

53. The "No Table" icon removes any tables from the plot window.

54. The "Sizing Table" icon displays the Sizing table which contains allele, size, peak height, peak area, and data point associated with an allele).

55. The "Genotypes Table" displays the Genotypes table which contains panel, marker, allele and PQV associated with a sample.

56. The "Label Edit Viewer" icon displays the Label Edit Viewer which contains allele and artifact label edits, and reasons for change associated with a sample.

57. The "Bring/Don't Bring Marked Samples to Top" icon moves samples marked for deletion to the top of the Samples plot in one scrollable pane or moves them to the bottom of the Samples plot.

Analyzing Data

58. Select appropriate sample(s) or control(s).

59. Press the "Display Plots" button .

60. In the plot settings drop down menu, choose the appropriate plot setting.

61. Samples containing < or > alleles, microvariants that are not extrapolated, or loci that are deemed inconclusive must have the locus (all alleles present at the locus deleted) omitted from the STRmix™ project file and have the locus omitted (i.e. ignored) from the STRmix™ analysis.

62. A genotypes table will be exported from GMIDX for the evidence and reference samples.

Exporting GeneMapper® ID-X Table for the Allele Summary Table or STRmix™

63. Following Data Analysis, open the project folder and select the Genotypes tab.

64. Select the appropriate table setting:

   a. Allele Summary Table
   b. STRmix_Export_Evidence
   c. STRMix_Export_Reference

65. Highlight samples to be exported.

66. Select File, then Export Table from the toolbar menu or the Export Table icon on the GeneMapper® ID-X toolbar.

67. Name the .txt file with the project's name and select the export table button. Export the .txt file.

Archiving Run Folders

68. Export (.ser) file:

   a. Select GeneMapper® Manager under the tools menu or the GeneMapper® ID-X Manager icon .
   b. Under the Project tab, select project name.
   c. Select Export.

69. Delete (.ser) file:

   a. Select GeneMapper® Manager under the tools menu or the GeneMapper® ID-X Manager icon .

      b.   Under the Project tab, select project name.

      c.   Select Delete.

70. Re-import (.ser) file:

      a.   Select GeneMapper® ID-X Manager under the tools menu or the GeneMapper® ID-X Manager icon .

      b.   Under the Project tab, select import.

      c.   Select appropriate file, select import.

      d.   Select Done.

      e.   Under file menu, choose open project.

      f.   Select appropriate project.

GeneMapper® ID-X Settings

Table Settings

71. HID Table:

      a.   For Samples Tab:

            i.   #1 Status

            ii.   #2 Sample File

            iii.   #3 Sample Name

            iv.   #6 Sample Type

            v.   #9 Analysis Method

            vi.   #10 Panel

            vii.   #11 Size Standard

            viii.   #14 Run Name

            ix.   #23 Sizing Quality Overridden

            x.   #28 Off-Scale

            xi.   #29 Sizing Quality

      b.   For Genotypes Tab:

            i.   #1 Sample File

            ii.   #2 Sample Name

            iii.   #4 Run Name

            iv.   #5 Panel

            v.   #6 Marker

            vi.   #7 Dye

            vii.   #8 Allele

            viii.   #10 Height

            ix.   #28 Genotype Quality

            x.   In Allele Settings box type 50 for number of alleles

            xi.   Check box for keep allele, size height, area, data, point mutation, and comment together.

72. Allele Summary Table:
    a. For the Genotypes Tab:
        i. #2 Sample Name
        ii. #6 Marker
        iii. #8 Allele
        iv. #9 Size
        v. #10 Height
        vi. #16 Allele Display Overflow (ADO)
        vii. #30 User Defined Column 1
        viii. In the Allele Settings box type 35 for show number of alleles
        ix. Check box for keep allele, size height, area, data, point mutation, and comment together.

73. STRMix_Export_Evidence:
    a. For the Genotypes Tab:
        i. #1 Sample File
        ii. #6 Marker
        iii. #8 Allele
        iv. #9 Size
        v. #10 Height
        vi. In the Allele Settings box type 25 for show number of alleles
        vii. Uncheck the box for keep allele, size height, area, data, point mutation, and comment together

74. STMix_Export_Reference:
    a. For the Genotypes Tab:
        i. #1 Sample File
        ii. #6 Marker
        iii. #8 Allele
        iv. #9 Size
        v. In the Allele Settings box type 25 for show number of alleles
        vi. Uncheck the box for keep allele, size height, area, data, point mutation, and comment together

Plot Settings
75. HID Genotyping:
    a. Sample Header Tab
        i. #1 Sample File
        ii. #2 Sample Name
        iii. #3 Panel
    b. Genotype Header Tab
        i. #2 Sample Name
        ii. #3 Panel

           iii.   #4 Marker
        c.   Sizing Table Tab
            i.   All settings selected
        d.   Labels Tab
            i.   Label #1: Allele Call
           ii.   Label #2: Height
          iii.   Label #3: Size
          iv.   Label #4: "AE Reason for Change"
           v.   Label Color: Dye-Color Border

Display Settings

76. From the GeneMapper® ID-X manager select plot settings. A window will appear, click the "Labels" tab.

77. Label 1 must be "allele call", Label 2 must be "height", Label 3 must be "size", Label 4 must be "AE Comment", Font size should be 8.

78. For the Display Settings click the "Display Settings" tab. Under the display settings, the number of panels can be adjusted, show/hide off scale data, overlay/separate channels, and select the number of dyes, etc. The blue, green, yellow, red and orange dyes should be selected. Select the allele changes box from the show field. This will display deleted artifact and allele calls on the electropherogram.

79. Click Okay.

4.　　**References**

1. Applied Biosystems. Quick Reference Guide: GeneMapper® ID-X Software v1.2. 2009.

2. Applied Biosystems. GeneMapper® ID-X Software Version 1.0 Getting Started Guide. 2007.

5.　　**Definitions**

Clarify any terms used within the document