GeneMapper™ *ID-X* Software v1.7

New features and software verification and validation

Publication Number MAN0029209 Revision A.0

This user bulletin describes new features and software verification and validation. For more information on using the software, see “Related documentation” on page 31.

New features in GeneMapper™ *ID-X* Software v1.7

Feature	See
The Oracle™ Database has been replaced by the PostgreSQL Database. **Note:** The Oracle™ Database Dashboard does not exist in GeneMapper™ *ID-X* Software v1.7. However, the Dashboard functionality has been migrated to GeneMapper™ *ID-X* Software v1.7.	*GeneMapper™ ID-X Software v1.7 Administration Guide*
The GeneMapper™ *ID-X* Software administrator can perform ad hoc and scheduled database backups.	“Perform a database backup or restore” on page 3
Support for FSA files generated by the SeqStudio™ Flex Series Genetic Analyzer.	NA
Support for FSA and SER files generated by future RapidHIT™ ID Systems.	NA
Support for Microsoft™ Windows™ 10 and 11 operating systems.	NA
(SeqStudio™ Flex Series Genetic Analyzer, SeqStudio™ Genetic Analyzer, and 3500/3500xL Genetic Analyzer only) The GeneMapper™ *ID-X* Software can automatically populate the analysis method, size standard, and panel columns in the Samples table, if these columns are configured when the plate file is created in the instrument software.	“Add custom columns to an instrument plate file” on page 5
Optional ability to enable allele-specific stutter and additive stutter filtering.	“Enable allele-specific and/or additive stutter filtering” on page 6
Optional ability to enable marker-specific thresholds.	“Enable marker-specific thresholds” on page 9
Optional ability to enable pull-up filtering.	“Enable pull-up filtering” on page 11

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(continued)

Feature	See
Ability to autosave projects. **Note:** The autosave interval can be set from 0–120 minutes. To disable the autosave feature, select **0** minutes (**0** is the default setting).	"Configure autosave" on page 13
Ability to show the peak height ratio of any two selected peaks.	"View the peak height ratio of any two peaks" on page 14
Ability to add notes to a plot. The notes are displayed on the plot screen and in printouts of the plot.	"Add notes to a Samples Plot or Genotypes Plot" on page 15
In the Plot Settings Editor, ability to add analysis method, panel, size standard, and analytical threshold to electropherograms. Plot settings appear in reports.	"Display analysis settings in a Samples Plot or Genotypes Plot" on page 16
In the Plot Settings Editor, ability to gray out stutter peaks to distinguish them from allelic peaks.	"Gray out stutter peaks" on page 18
Ability to open multiple projects at one time.	"Open and close multiple projects" on page 19
Ability to open multiple plots at one time.	"Open multiple plots" on page 20
Updates to the Profile Comparison tool: • The tool can be used across multiple projects. • A new threshold for the number of allele matches has been added to the tool to allow filtering of trivial matches. • The tool has been tested for use with up to 2,000 laboratory reference samples and 100 customer control/QA samples.	"Use new features in the Profile Comparison tool" on page 22
For printed reports: Increased print job batch size from 10 pages to 500 pages and improved sample name legibility.	NA
New consolidated bins and panels for Thermo Fisher Scientific STR kits.	NA
Enhanced command line interface functionality: new options to keep the application open after command execution and to close projects.	*GeneMapper™ ID-X Software v1.7 Administration Guide*

Perform a database backup or restore

There are three new options for backing up and restoring the database:

- **Backup Now**—Perform an ad hoc backup (export) of the database; a copy of the database is saved as a DUMP file
- **Automate Backup Configuration**—Perform a scheduled backup (export) of the database; a copy of the database is automatically saved as a DUMP file at scheduled frequencies
- **Database Restore**—Restore (import) previously created DUMP files

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Note: For detailed procedures, see the *GeneMapper™ ID-X Software v1.7 Administration Guide*.

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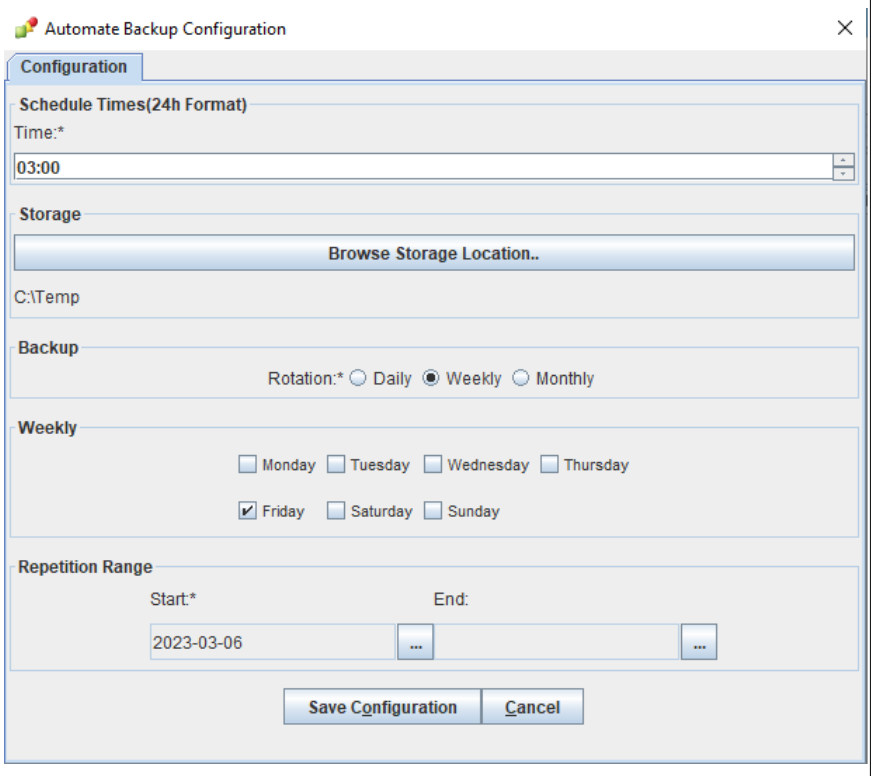
1. In the main window, select **Admin ▸ Database Backup**.

2. Select a database backup option.

Option	Action
Backup Now	1. Select **Admin** ▸ **Database Backup** ▸ **Backup Now**. 2. Select a save location and enter a name for the backup file.
Automate Backup Configuration **Note:** For automated backups to occur, a separate utility (the pgAgent tool) must be installed and running on the full installation computer during a backup. The GeneMapper™ *ID-X* Software (full or client installation) does not need to be running during a backup. After backups are scheduled, the backup job is passed to the pgAgent tool, which will run even if the GeneMapper™ *ID-X* Software is closed. For detailed information, see the *GeneMapper™ ID-X Software v1.7 Installation Guide*.	1. Select **Admin** ▸ **Database Backup** ▸ **Automate Backup Configuration**. 2. Specify the following parameters to configure the automated backups: • The time of day for the backups to occur (in 24-hour format) • The storage (save) location for the DUMP file • The frequency of the backups: – **Daily** – **Weekly**—The day of week that the backups should be performed; you can select more than one day per week – **Monthly**—The day of the month that the backups should be performed • *(Optional)* **Repetition Range**—When the backup schedule starts and ends 
Database Restore **IMPORTANT!** When you restore the database, you erase the current data and recreate the database. You lose all existing data when you import the data from the exported DUMP file.	1. Select **Admin** ▸ **Database Backup** ▸ **Database Restore**. 2. In the **Quit Application** dialog box, click **Yes** to close the GeneMapper™ *ID-X* Software. 3. Navigate to the backup (DUMP) file to restore.

Add custom columns to an instrument plate file

If you add the appropriate custom columns to an instrument plate file, the GeneMapper™ *ID-X* Software can automatically populate the Samples table with the following information:

- Analysis method
- Size standard
- Panel

The custom column headings to include in the instrument plate files are listed in Table 1.

Note: For information on creating custom columns in a plate file, see your instrument user guide.

Table 1 Custom column headings to include in the instrument plate files

Information in the custom column	Custom column headings in the instrument plate file			Corresponding column headings in the GeneMapper™ *ID-X* Software Samples table
	SeqStudio™ Flex[1]	SeqStudio™[1]	3500/3500xL	
Analysis method	CustomFields1	CustomFields1	User Defined Field 1	UD1 (User-defined column 1)
Size standard	CustomFields2	CustomFields2	User Defined Field 2	UD2 (User-defined column 2)
Panel	CustomFields3	CustomFields3	User Defined Field 3	UD3 (User-defined column 3)
Other values	CustomFields4, CustomFields5, and so on	CustomFields4, CustomFields5, and so on	User Defined Field 3, User Defined Field 4, and so on	UD4, UD5, and so on

[1] For the SeqStudio™ Flex Series Genetic Analyzer and SeqStudio™ Genetic Analyzer, you can also use the SeqStudio™ Plate Manager Software to create a plate file and add the custom columns.

If a plate file includes standard columns for the analysis method, size standard, or panel, you do not need to enter that information in the corresponding custom columns. For example, SeqStudio™ Plate Manager Software plate files already include **Size Standard** and **Panel** columns; therefore, you can leave the **CustomFields2** (size standard) and **CustomFields3** (panel) custom columns empty in the plate file.

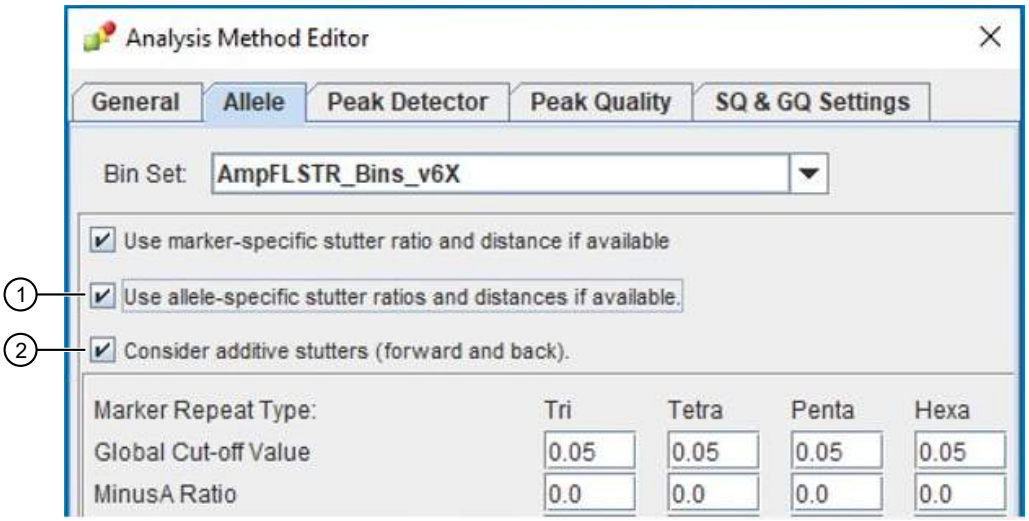
IMPORTANT! Information in the custom columns takes precedence. The standard columns are used to auto-populate the Samples table in the GeneMapper™ *ID-X* Software only when the custom columns are empty.

This may have consequences if you use custom columns 1–3 for other values. If you want to automatically import the analysis settings, move the other values to custom column 4 or greater and use custom columns 1-3 only as described in Table 1.

Enable allele-specific and/or additive stutter filtering

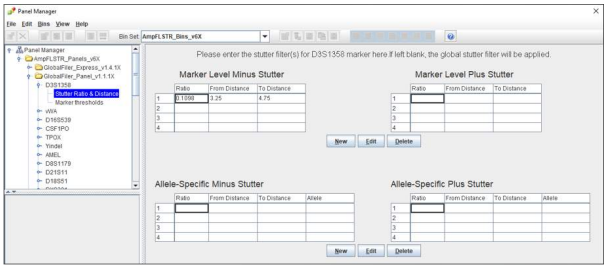
You can apply different stutter filters at individual loci, based on the specific alleles that are observed.

1. Open the Analysis Method Editor, then select the **Allele** tab.

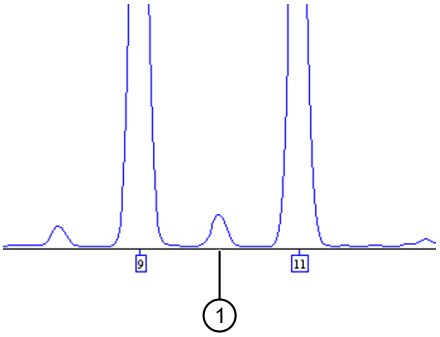


① Allele-specific stutter filtering
② Additive stutter filtering

2. Select the stutter filter options.

Option	Action	Additional information
Use allele-specific stutter ratios and distances if available	Select (☑) to use allele-specific Stutter Ratio from the panel in addition to the Global Plus and Minus Stutter ratios specified in this tab. **Note:** To use allele-specific filtering, the marker-specific stutter filter must also be enabled. Otherwise, the allele-specific stutter option is disabled.	Values for allele-specific stutter are in the Panel Manager in the same location as marker-specific stutter values.  Allele-specific values have precedence over marker-specific values. If allele-specific stutter filtering is enabled, the software checks for a relevant allele-specific value for a given peak. The software uses that value if it exists. If no allele-specific value exists, the software uses the marker-specific value. As such, a higher marker-specific value will not override a lower allele-specific value.

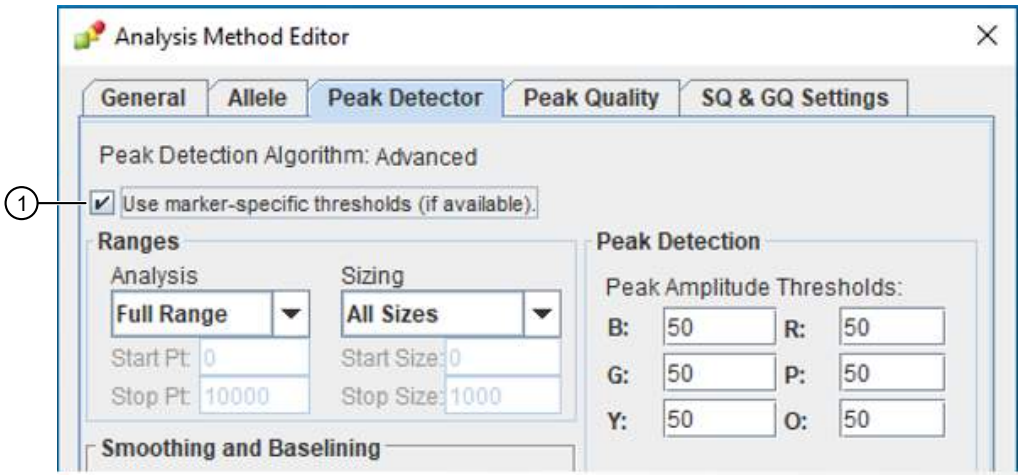
(continued)

Option	Action	Additional information
Consider additive stutters (forward and back)	Select (☑) to have overlapping stutter filters calculated additively. That is, if two stutter filters refer to the same peak, the filter used will be calculated as the sum of the two individual filters.	When this option is selected, the stutter filters are applied together (that is, "additively"). This is also known as "combined stutter". Additive stutter filtering can be used with or without allele-specific stutter filtering. **Example**  ① Potential minus stutter from 11 and plus stutter from 9 Consider the 9 and 11 alleles in the image: • 9 allele = 800 RFU • 11 allele = 1,000 RFU • Minus-4 stutter filter is 10% • Plus-4 stutter filter is 1% • The peak in the 10 bin qualifies as both minus stutter of the 11 allele and plus stutter of the 9 allele • If additive stutter filtering is enabled, the peak in the 10 bin will be filtered at 108 RFU The filter is: [1% of 800 + 10% of 1,000] = [8 + 100] = 108 RFU

Enable marker-specific thresholds

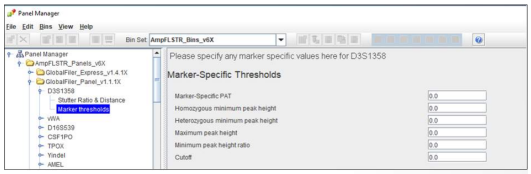
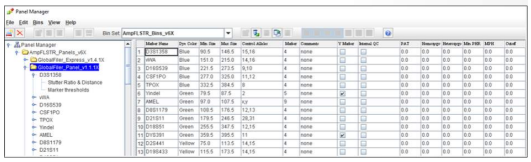
You can apply different analysis thresholds at individual loci, instead of having only one value for the entire profile.

1. Open the Analysis Method Editor, then select the **Peak Detector** tab.



① Marker-specific thresholds

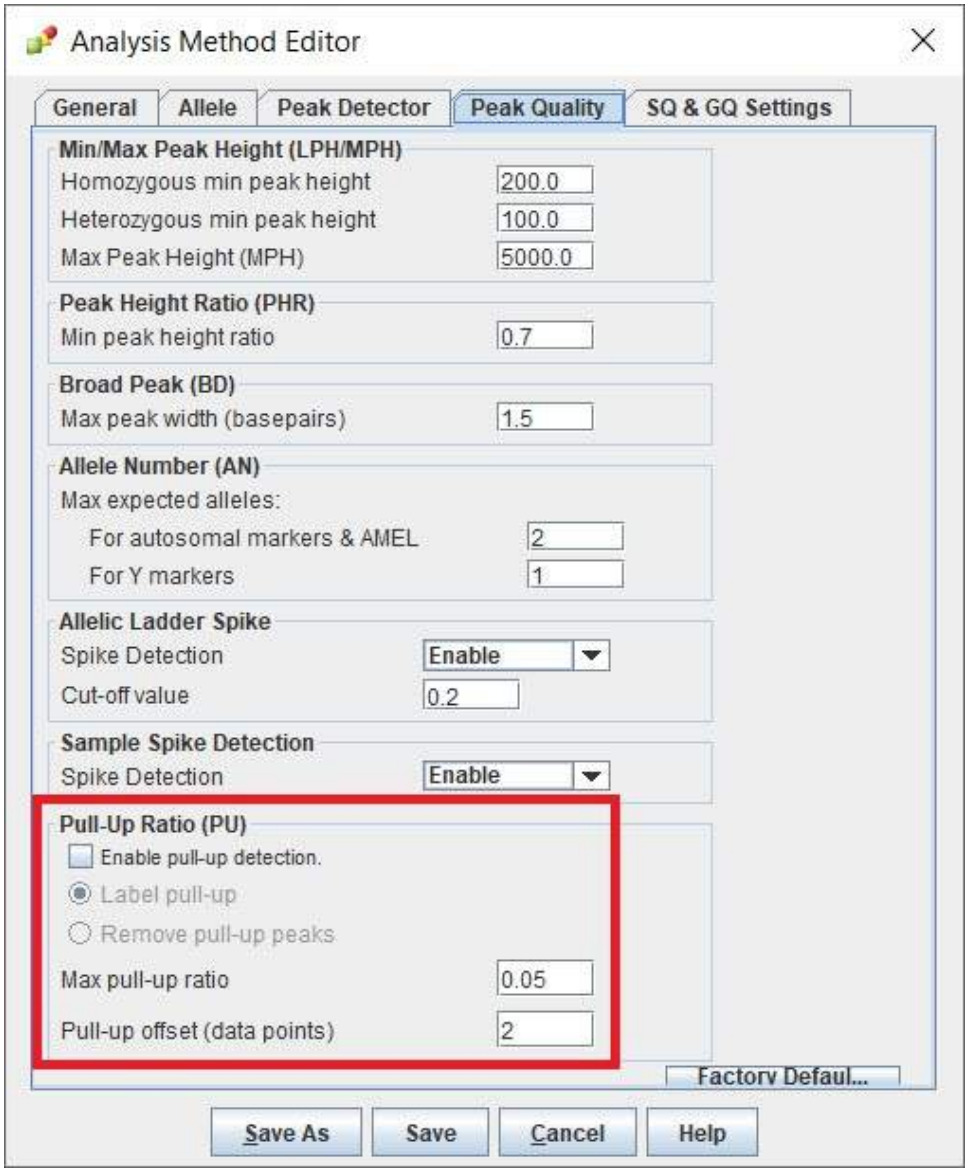
2. Select marker-specific threshold options.

Option	Action	Additional information
Use marker-specific thresholds (if available)	1. Select (☑) to use marker-specific analysis parameters from the panel. 2. Open the Panel Manager to enter the desired settings. You can enter the settings at the marker level or at the panel level. These two areas are linked—a change in one is automatically applied in the other.   3. In the **Marker-Specific Thresholds** view, click **Apply** to save changes before moving between loci.	The following thresholds can now be set at the marker level: • Peak Amplitude Threshold (PAT) • Homozygous minimum peak height • Heterozygous minimum peak height • Maximum peak height • Minimum Peak Height Ratio (PHR) • Cut-off Marker-specific values have precedence over global values. For example, if the PAT is set to 100 RFU in the analysis method and 50 RFU at a locus in the Panel Manager, then 50 RFU will be used as the PAT for that locus. **Note:** A value of **0** (zero) for any marker-specific threshold is equivalent to "off". That is, if a marker-specific setting is set to **0**, then the value used for that locus will be the global setting defined in the analysis method.

Enable pull-up filtering

You can configure the software to automatically label or filter possible pull-up peaks by looking at peaks that align across dyes. Peaks that are below the specified percentage height of large peaks in another dye are flagged as pull-up peaks.

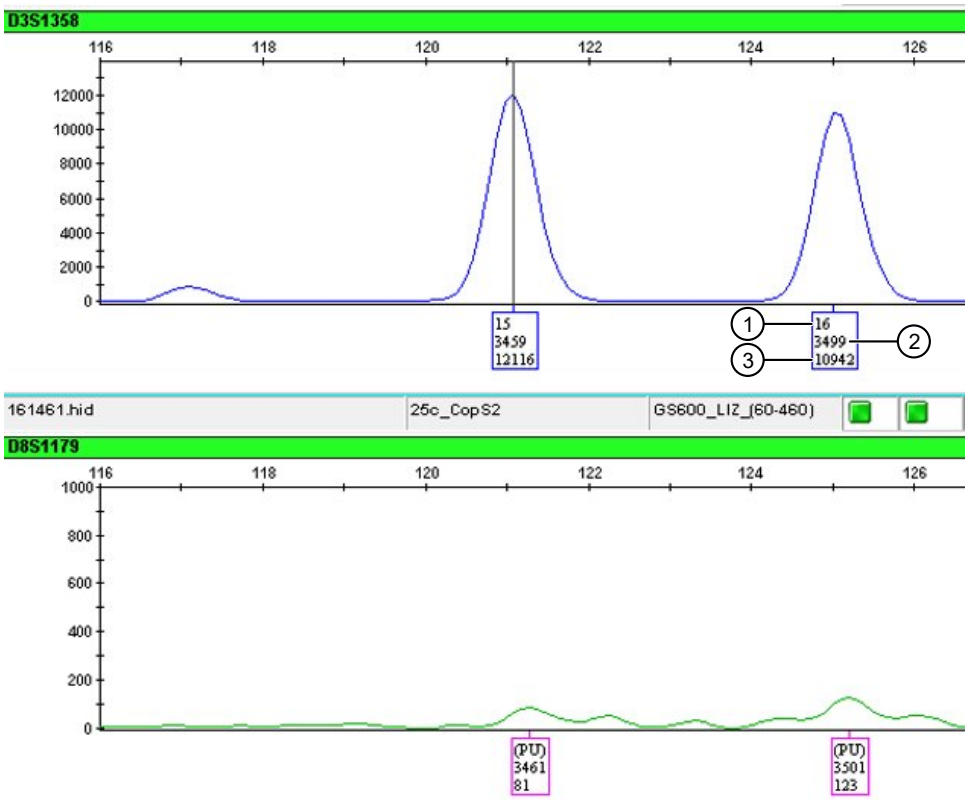
1. Open the Analysis Method Editor, then select the **Peak Quality** tab.



2. Select the pull-up filtering options.

Option	Action
Enable pull-up detection	Select (☑) to automatically detect possible pull-up peaks. When deselected, no pull-up detection is performed, as in earlier versions of the GeneMapper™ *ID-X* Software.
Label pull-up	Select (☑) to apply the **PU** artifact label to possible pull-up peaks.
Remove pull-up peaks	Select (☑) to filter (without labeling) possible pull-up peaks.
Max pull-up ratio	Enter the cut-off percentage of the pull-up peak height to the parent peak height. A peak below this percentage in another dye that aligns with the parent peak will be called as pull-up. The default value is 5%.
Pull-up offset (data points)	Enter a value to determine how close the peaks in different dyes must be to be considered aligned. The value is plus/minus in data points (or scan number). The default value is 2.

Example



Label values:

① Name/allele
② Data point
③ Height

Consider the alleles in the image:

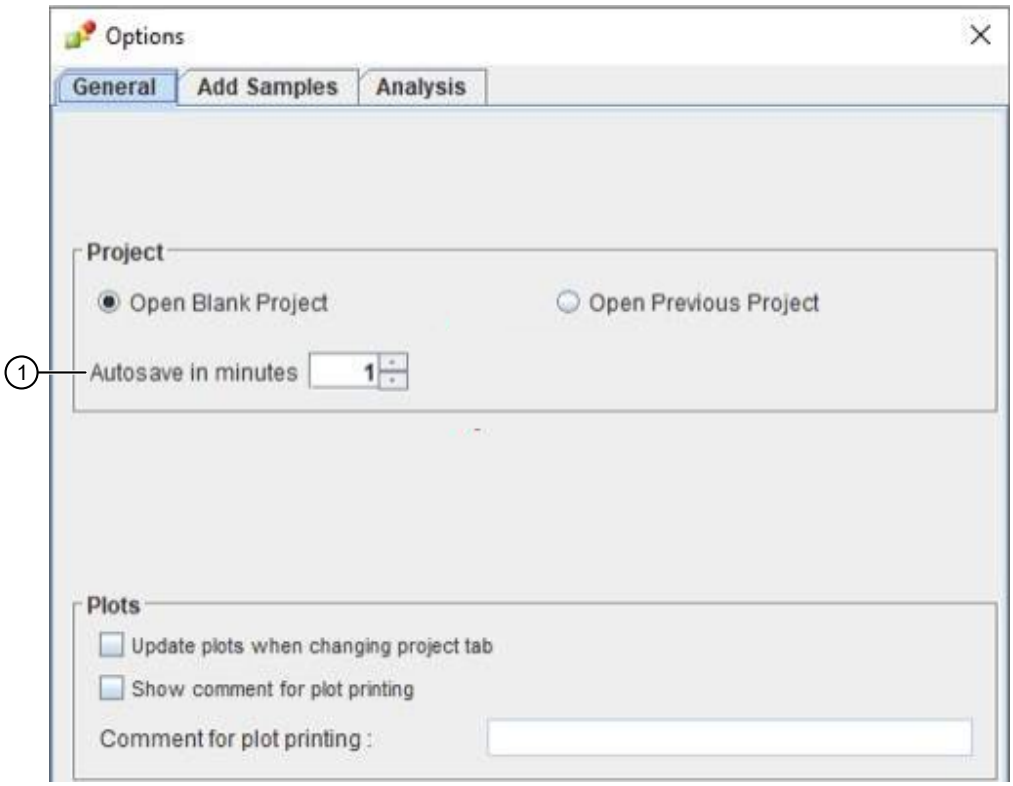
- The max pull-up ratio is set to 5% and the pull-up offset is set to 2 (default values).
- 15 and 16 alleles in D3S1358 are the parent peaks.
- Peaks detected in green dye are flagged as pull-up because:
  - The peaks align with the parent peaks
    - 3461 is ±2 data points of 3459
    - 3501 is ±2 data points of 3499

    And
  - The peaks are below the 5% height cutoff value
    - 81 ÷ 12,116 = 0.7%
    - 123 ÷ 10,942 = 1.1%

Configure autosave

You can configure the software to autosave projects. With autosave enabled, changes to projects are automatically saved after a user-defined time period.

1. In the **Project** window, select **File ▸ Project Options**.
2. Select the **General** tab.
3. Use the up/down arrows to select the autosave interval (in minutes).



① Autosave setting

Note: The autosave interval can be set from 0–120 minutes. To disable the autosave feature, select **0** minutes (**0** is the default setting).

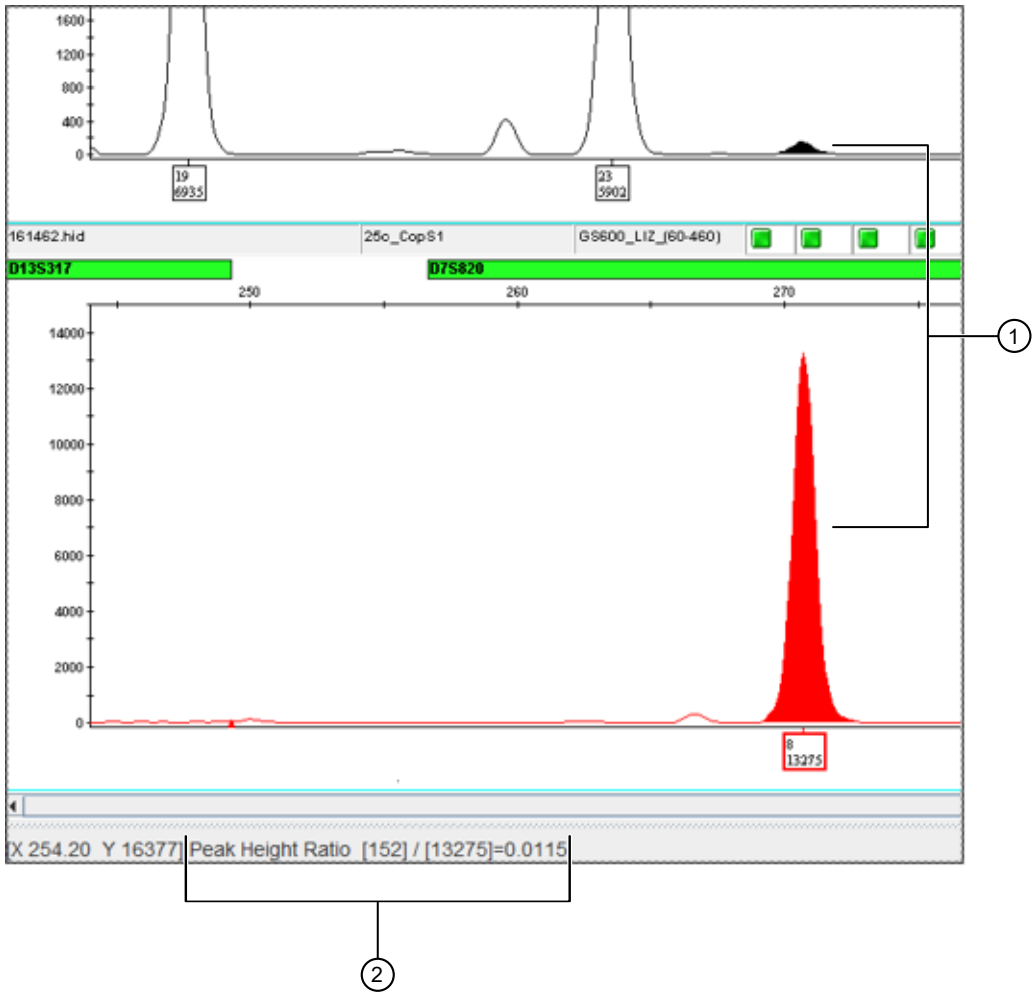
4. Click **OK**.

View the peak height ratio of any two peaks

You can view the peak height ratio of any two peaks in the Samples Plot or Genotypes Plot. In earlier versions of the GeneMapper™ *ID-X* Software, this view was limited to two peaks in the same dye channel.

1. Display the Samples Plot or Genotypes Plot of interest.

2. Select the two peaks of interest.
   The peak height ratio is displayed at the bottom of the plot.

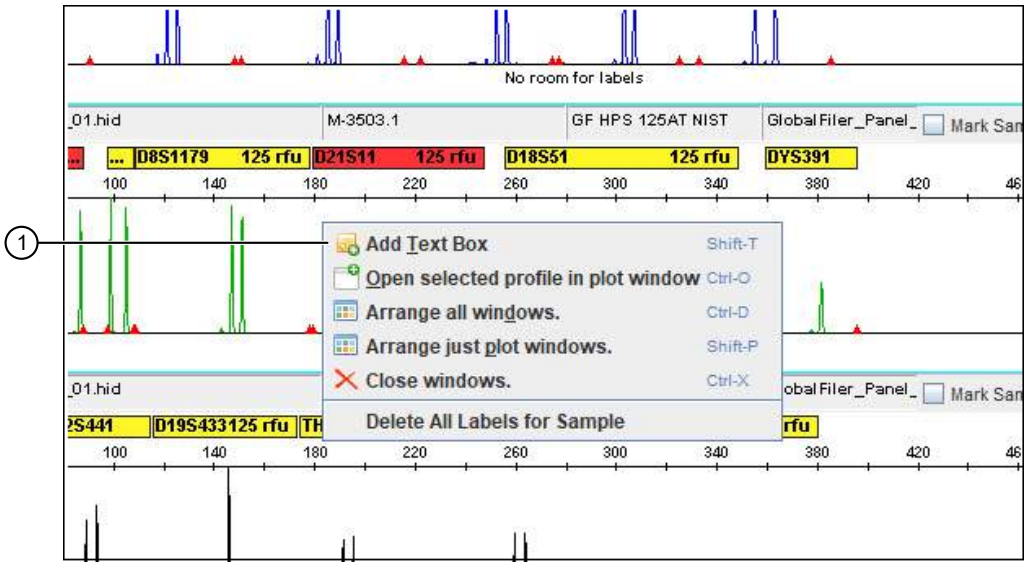


① Select two peaks
② Peak height ratio for the selected peaks

Add notes to a Samples Plot or Genotypes Plot

You can add notes to profiles in the Samples Plot or Genotypes Plot. The notes are displayed on the screen and in printouts of the plot.

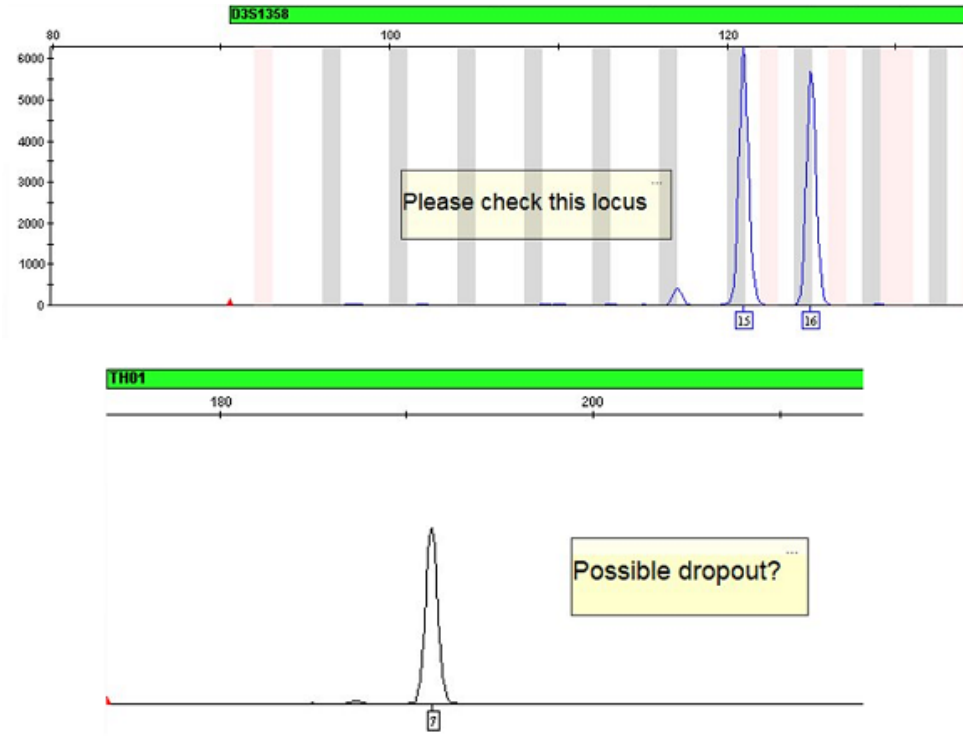
1. Display the Samples Plot or Genotypes Plot of interest.
2. Right-click inside the plot, then select **Add Text Box**.



① Select to add a text box to a plot

Note: The **Add Text Box** option is not available for any plot setting that has **Overlay All** selected in the **Dye Layout** pane.

3. Enter text, then click **Save**.
4. *(Optional)* Click the ellipses (**...**) at the top for options to change the text, font, and color of the note.
5. *(Optional)* Click and drag the top of the note to reposition it.



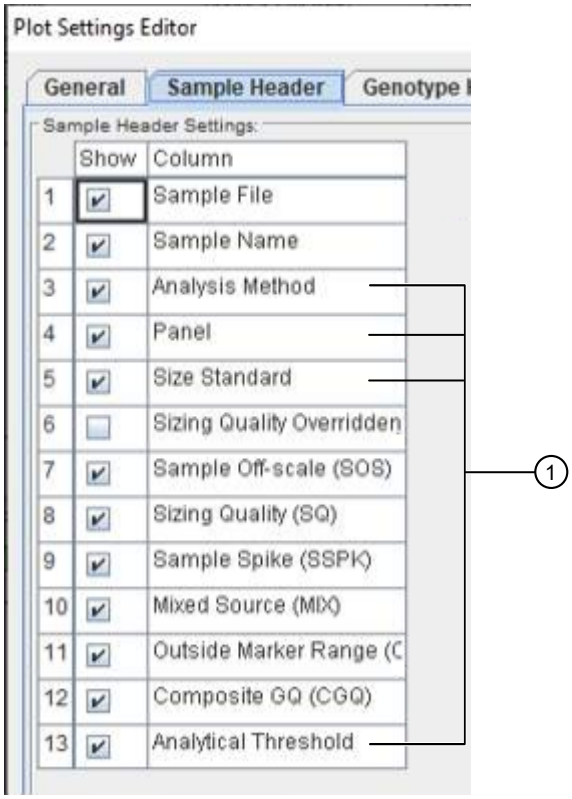
Display analysis settings in a Samples Plot or Genotypes Plot

You can display the settings that were used to analyze profiles in a Samples Plot or Genotypes Plot. This setting is configured in the Plot Settings Editor.

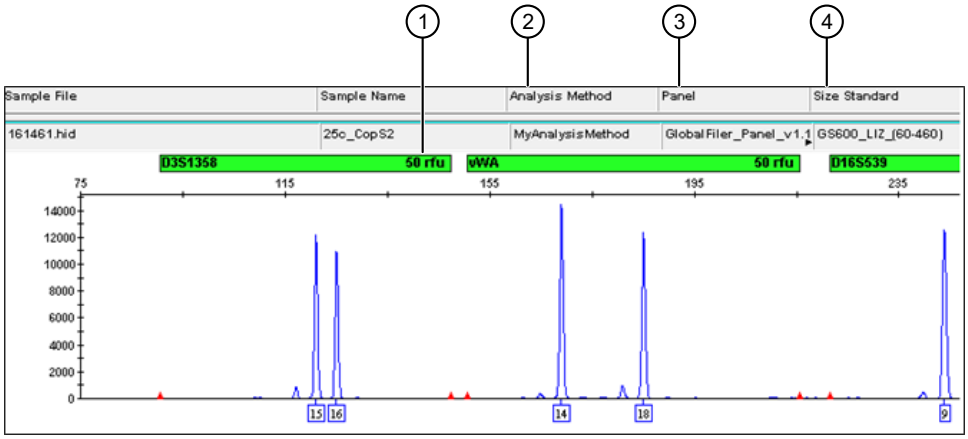
1. Display the Samples Plot or Genotypes Plot of interest, then click **(Plot Setting Editor)**.
2. Select the **Sample Header** tab.
3. Select the checkbox for each item to display in the plot.

   The following are the new analysis setting options:

   - **Analysis Method**, displayed in the plot sample header
   - **Panel**, displayed in the plot sample header
   - **Size Standard**, displayed in the plot sample header
   - **Analytical Threshold** (also known as peak amplitude threshold), displayed in the plot locus headers



① New analysis settings available in the **Samples Header** tab

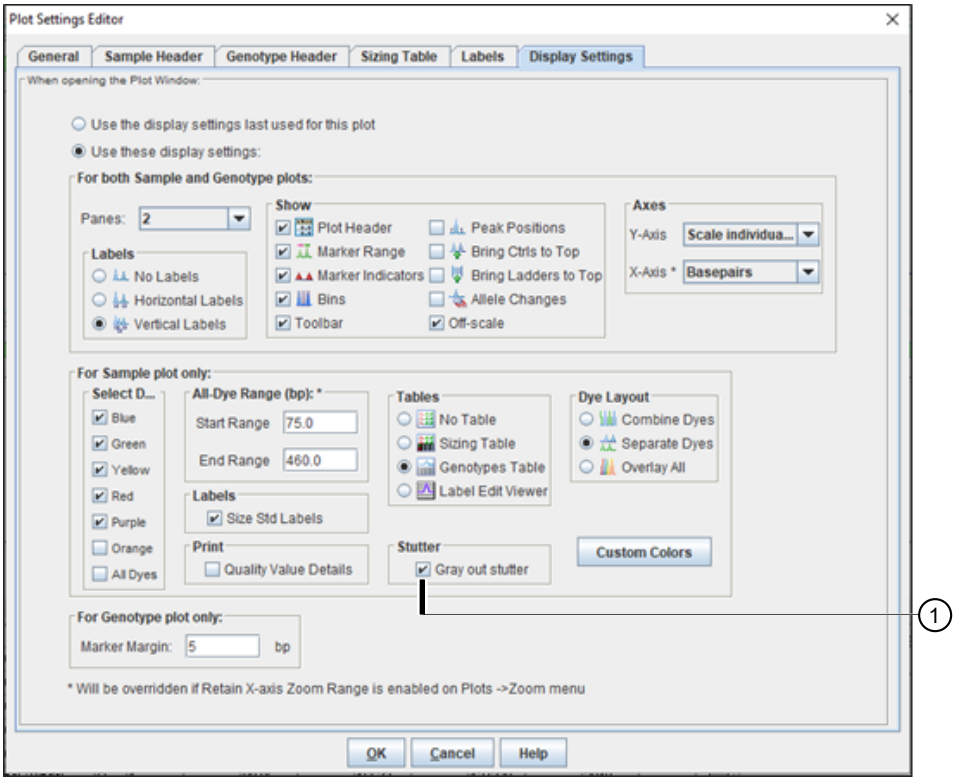


① Analytical threshold; example = **50 rfu**
② Analysis method; example = **MyAnalysisMethod**
③ Panel; example = **GlobalFiler_Panel_v1.1**
④ Size standard; example = **GS600_LIZ_(60-460)**

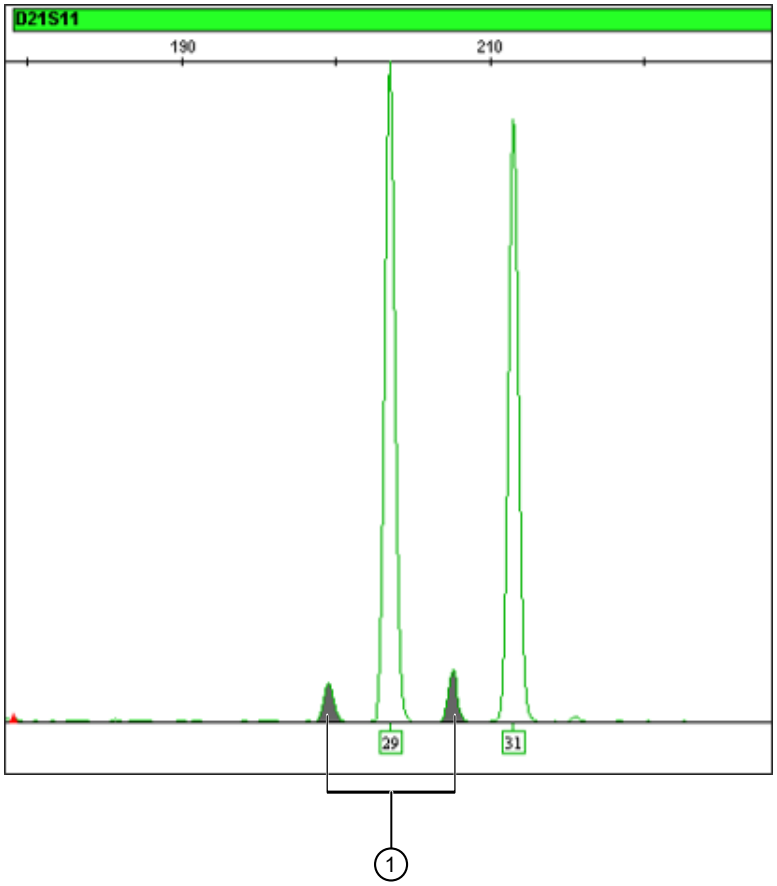
Gray out stutter peaks

You can display stutter peaks in gray. This setting is configured in the Plot Settings Editor.

1. Display the Samples Plot or Genotypes Plot of interest, then click **(Plot Setting Editor)**.
2. Select the **Display Settings** tab.
3. Select the **Gray out stutter** checkbox.



① **Gray out stutter** checkbox



① Grayed-out stutter peaks

Open and close multiple projects

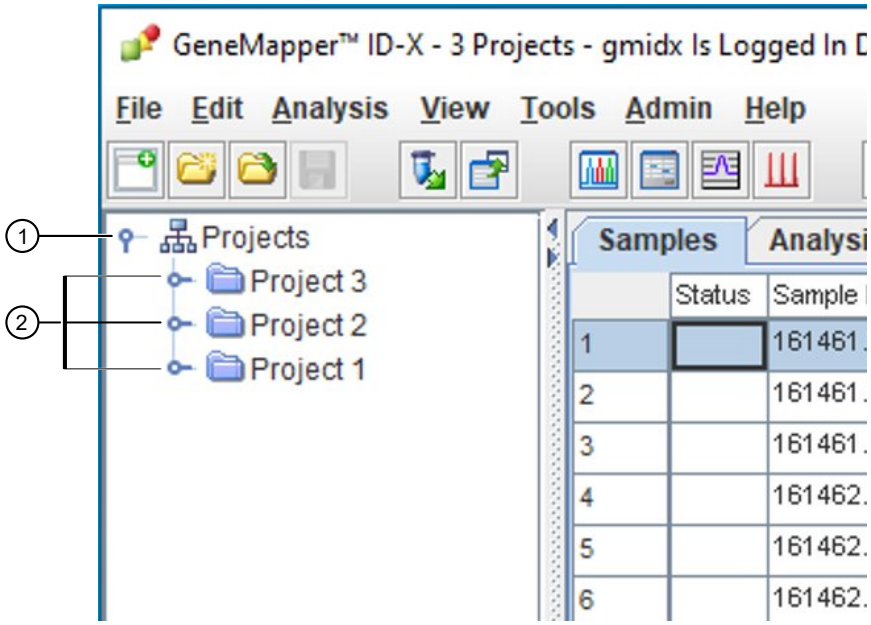
You can open and close multiple projects simultaneously.

1. In the **Project** window, select **File** ▸ **Open Project** or click **(Open Project)**.
2. In the **Open Project** dialog box, list the projects of interest.
   You can:
   - List all projects in the database
   - List projects with specific names
   - List projects with specific dates
   - Search for projects in the project list

   Note: Only projects that are associated with the security group of the signed-in user are available to list.
3. Select one or more projects from the project list, then click **Open**.
   - **Ctrl+Click** to select multiple, non-contiguous projects
   - **Shift+Click** to select multiple, contiguous projects

The selected projects are displayed in the navigation pane.

4. Display project samples in the **Samples** tab.
   - To display samples for all open projects: In the navigation pane, select **Projects**.
   - To display samples for an individual project: In the navigation pane, select an individual project.



① Select to display all samples in all open projects
② Select an individual project to display only samples in that project

Note: The **Analysis Summary** tab is separate for each project. The **Analysis Summary** tab that is displayed depends on the project selected in the navigation pane. If **Projects** at the top of the navigation pane is selected, the software displays the analysis summary for the most recently selected project.

5. Close projects.
   - To close all projects: Select **File** ▸ **Close all projects** (or press **Shift+X**).
   - To close an individual project: In the navigation pane, right-click the project, then select **Close**.

Open multiple plots

You can open and close multiple plots simultaneously.

1. In the **Project** window, select **File** ▸ **Open Project** or click **(Open Project)**.
2. In the Samples table, select the samples of interest.
   - **Ctrl+Click** to select multiple, non-contiguous samples
   - **Shift+Click** to select multiple, contiguous samples

3. In the **View** menu, select one of the new display options.
   - **View ▸ Display plots** opens all samples simultaneously, replacing any other open plots.
   - **View ▸ Display all plots together in a new window** opens all samples simultaneously in a new plot, leaving any existing plot open
   - **View ▸ Display each plot in a new window** opens a new, separate plot for each sample selected

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Note: Alternatively, you can right-click the row number in the Samples table to access the view options listed above for the selected samples.

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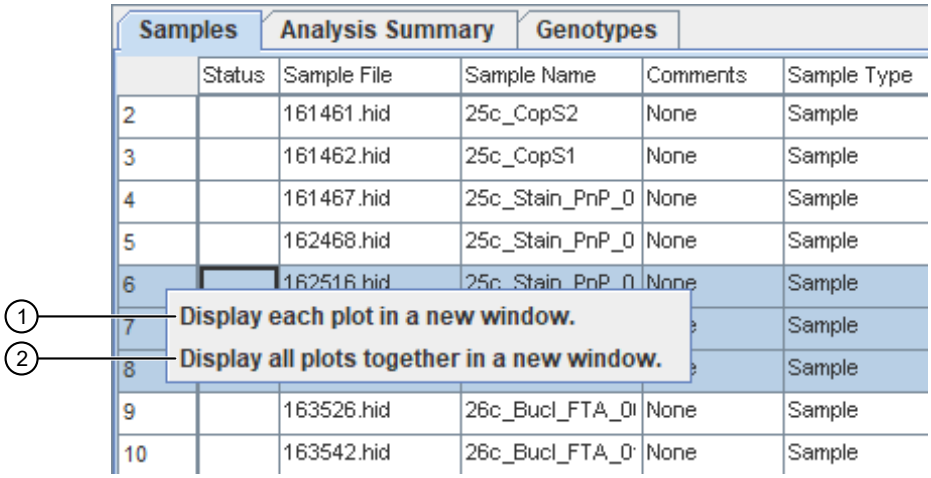
4. *(Optional)* Right-click any open plot for additional viewing options.



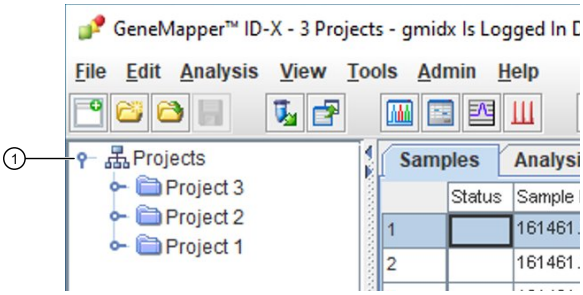
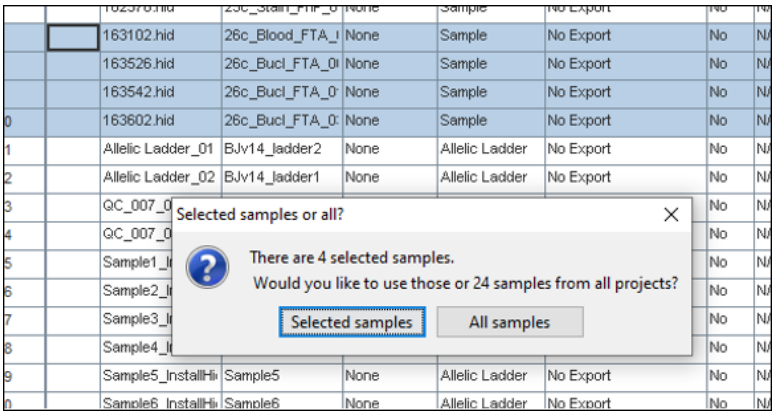
① Open a profile for the selected sample in its own plot
② Arrange the plot windows

Use new features in the Profile Comparison tool

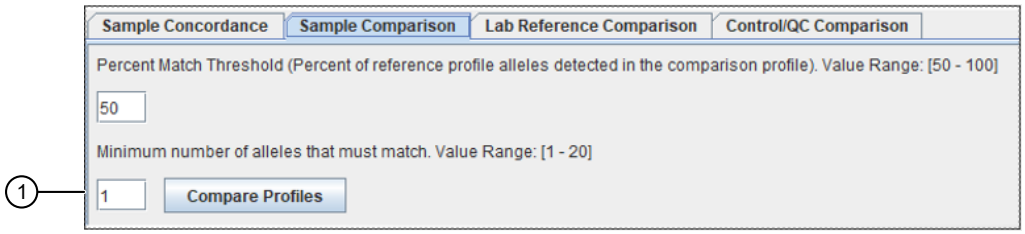
There are two new features available in the Profile Comparison tool:

- **Compare profiles in different projects**—The new ability to open multiple projects simultaneously (see "Open and close multiple projects" on page 19) also allows you to use the Profile Comparison tool to compare profiles across all open projects.
- **Remove trivial matches from results**—You can set the minimum number of alleles that must be in a match. This prevents chance matches with only a small number of matching alleles being shown.

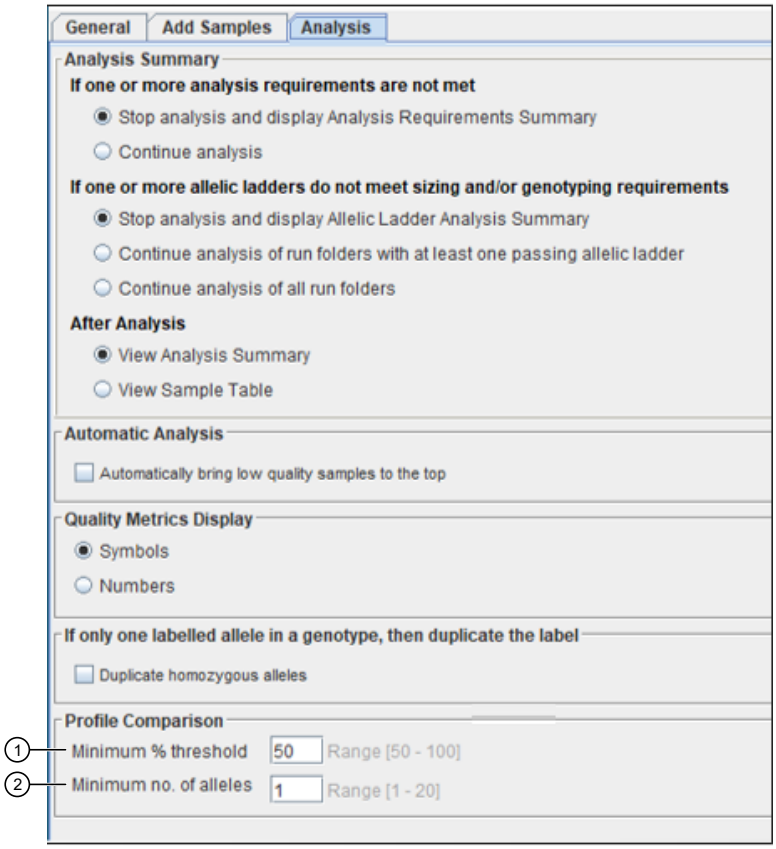
As needed, use the new features in the Profile Comparison tool.

Option	Action
Compare profiles in different projects	**1.** In the **Project** window navigation pane, select **Projects** to display all samples in all open projects.  ① Displays all samples in all open projects **2.** In the **Samples** tab, select the samples to compare. **3.** Select **Tools** ▸ **Profile Comparison**. **4.** At the prompt, confirm your sample selection (from step 2).  **5.** Select the **Sample Concordance** or **Sample Comparison** tab, then click **Compare Profiles**.

(continued)

Option	Action
Remove trivial matches from results	Option 1: Set the minimum number of alleles for a specific profile comparison. **1.** In the **Project** window, select samples and open the Profile Comparison tool as described in the row above ("Compare profiles in different projects", steps 1–3). **2.** Select the **Sample Comparison** tab. **3.** Enter a value in the **Minimum number of alleles that must match** field. The accepted range is 1–20; the value indicates the minimum number of alleles that must match for the match to be reported.  ① The minimum number of alleles that must match **Note:** If the value is **1**, all matches are shown. This is the same behavior as earlier GeneMapper™ *ID-X* Software versions. **4.** Click **Compare Profiles**.

(continued)

Option	Action
Remove trivial matches from results	Option 2: Set a default value for the minimum number of alleles. Use this option to avoid setting values each time that you use the Profile Comparison tool. **1.** In the **Project** window, select **File ▸ Project Options**. **2.** Select the **Analysis** tab. **3.** Enter a value in the **Minimum no. of alleles** field. The accepted range is 1–20; the value indicates the minimum number of alleles that must match for the match to be reported. **Note:** If the value is **1**, all matches are shown. This is the same behavior as earlier GeneMapper™ *ID-X* Software versions. **4.** *(Optional)* Enter a value in the **Minimum % threshold** field. The accepted range is 50–100; the value indicates how closely a comparison profile must match a reference profile. **Note:** Any samples that are greater than or equal to the specified percentage will be displayed in the **Profile Comparison** tab. Any samples that are less than the specified percentage will not be displayed in the **Profile Comparison** tab. **5.** Click **OK**.  ① How closely a comparison profile must match a reference profile ② The minimum number of alleles that must match

GeneMapper™ *ID-X* Software v1.7 verification and validation

The verification and validation were performed according to SWGDAM Validation Guidelines for DNA Analysis Methods (SWGDAM, December 2016) and the FBI Quality Assurance Standards (QAS, July 2020).

Computers used for verification testing

Make/model	Memory	Operating system (OS)
Dell Latitude 5420	32 GB	Windows™ 11 Enterprise
Dell Latitude 3571	16 GB	Windows™ 10 IOT Enterprise LTSC
Dell Latitude 5570	16 GB	Windows™ 10 IOT Enterprise LTSC
Dell Latitude 7550	32 GB	Windows™ 10 Enterprise

Tests cases performed

Test	Test description	Result	Comments
Instrument compatibility	User can read, open, and analyze data from the following instruments: • SeqStudio™ Flex Series Genetic Analyzer • SeqStudio™ Genetic Analyzer • 3730 Genetic Analyzer • 3500/3500xL Genetic Analyzer • 3130/3130*xl* Genetic Analyzer • 3100-*Avant*™/3100 Genetic Analyzer • 310 Genetic Analyzer	Pass	GeneMapper™ *ID-X* Software v1.7 can open, read, and analyze data from all listed instruments. For a list of chemistries and instrument platforms tested as part of the concordance testing, see Table 2. Table 2 includes data from all instruments listed here, except for the SeqStudio™ Flex Series Genetic Analyzer. The SeqStudio™ Flex instrument was not part of the concordance testing because data from this instrument is not compatible with earlier versions of the GeneMapper™ *ID-X* Software. To verify compatibility of GeneMapper™ *ID-X* Software v1.7 with the SeqStudio™ Flex instrument, 23 samples from each of 8 chemistries were run on the SeqStudio™ Flex instrument and analyzed in GeneMapper™ *ID-X* Software v1.7. Full compatibility was confirmed. For detailed information, see the *SeqStudio™ Flex Series Genetic Analyzer for HID Validation User Bulletin*.

(continued)

Test	Test description	Result	Comments
Backwards compatibility	User can open, read, and reanalyze project and settings files from GeneMapper™ *ID-X* Software v1.1 through v1.6.	Pass	GeneMapper™ *ID-X* Software v1.7 can open, read, and reanalyze project and settings files from GeneMapper™ *ID-X* Software v1.1 through v1.6.
Sizing and genotyping	There is 100% concordance of peak sizes, heights, data points, and allele calls between data analyzed in GeneMapper™ *ID-X* Software v1.6 and v1.7.	Pass	3,146 samples from multiple chemistries were analyzed in GeneMapper™ *ID-X* Software v1.6 and v1.7. The v1.6 data was analyzed with **v6X** panels and bins; the v1.7 data was analyzed with **v7X** panels and bins. There was 100% concordance of peak sizes, heights, data points, and allele calls between data. For a list of samples, chemistries, and instrument platforms tested, see "Samples used for concordance testing" on page 28.
	There is 100% concordance of peak sizes, heights, data points, and allele calls between data analyzed with GeneMapper™ *ID-X* Software v1.7 installed on a computer running the Windows™ 10 OS and GeneMapper™ *ID-X* Software v1.7 installed on a computer running the Windows™ 11 OS.	Pass	94 samples from GlobalFiler™ IQC chemistry, run on the 3500xL instrument, were analyzed with GeneMapper™ *ID-X* Software v1.7 on the Windows™ 10 OS and GeneMapper™ *ID-X* Software v1.7 on the Windows™ 11 OS. There was 100% concordance of peak sizes, heights, data points, and allele calls between data analyzed with GeneMapper™ *ID-X* Software v1.7 on the Windows™ 10 OS and GeneMapper™ *ID-X* Software v1.7 on the Windows™ 11 OS.
Database	User can perform ad hoc database backups.	Pass	All functions operate as expected.
	User can restore from a database backup file.	Pass	
	User can perform scheduled backups.	Pass	
Auto-populate settings	Analysis method, size standard, and panel can be automatically imported from data run on the SeqStudio™ Flex Series Genetic Analyzer and 3500/3500xL Genetic Analyzer.	Pass	Analysis settings were successfully imported into GeneMapper™ *ID-X* Software v1.7 as defined during setup of the instrument plate file.

(continued)

Test	Test description	Result	Comments
Data analysis and review	User can display the peak ratio for any two peaks.	Pass	All functions operate as expected.
	User can perform automatic pull-up detection and choose to filter pull-up peaks or label the peaks as **PU**.	Pass	
	User can specify allele-specific stutter filters.	Pass	
	User can apply additive stutter filters.	Pass	
	User can apply marker-specific analysis thresholds.	Pass	
	User can color stutter peaks gray.	Pass	
Interface	User can open multiple projects simultaneously.	Pass	The function operates as expected. Up to 5 projects, each with 384 samples (the maximum tested), can be simultaneously opened.
	User can open multiple plot windows simultaneously.	Pass	The function operates as expected. Up to 8 plot windows (the maximum tested), can be simultaneously opened.
	User can add a panel name, analysis method, and size standard to a profile.	Pass	The function operates as expected.
	User can add configurable text notes to profiles.	Pass	The function operates as expected.
Printing	Printing is not restricted to a 10-page limit.	Pass	Print jobs up to 500 pages successfully performed.
Profile Comparison tool	User can compare samples within and across all open projects.	Pass	All functions operate as expected.
	User can compare all open projects to Lab Reference and Control/QC data profiles.	Pass	
	User can configure the match percentage and the minimum number of alleles to match.	Pass	

(continued)

Test	Test description	Result	Comments
Profile Comparison tool	User can configure default values for the match percentage and the minimum number of alleles to match.	Pass	All functions operate as expected.
	20 GlobalFiler™ chemistry mixture samples return correct results for Sample Concordance, Sample Comparison, Lab Reference Comparison, and Control/QC Comparison.	Pass	All test cases return expected match results.

Samples used for concordance testing

A total of 3,146 sample files (FSA and HID files) and >160,000 genotypes were used in the sizing and genotyping concordance test. These samples were analyzed using GeneMapper™ *ID-X* Software v1.6 and GeneMapper™ *ID-X* Software v1.7. 100% concordance between v1.6 and v1.7 was seen in all cases.

Table 2 Chemistry and instrument platforms tested for concordance between GeneMapper™ *ID-X* Software v1.6 and v1.7

Chemistry	Platform	No. of samples	No. of genotypes	Concordance				
				Allele call	Size	Height	Area	Data point
Profiler Plus™	310	28	1,458	100%	100%	100%	100%	100%
	3100	39	1.202	100%	100%	100%	100%	100%
SEfiler™	310	23	1,337	100%	100%	100%	100%	100%
	3100	21	954	100%	100%	100%	100%	100%
COfiler™	310	26	609	100%	100%	100%	100%	100%
	3100	37	603	100%	100%	100%	100%	100%
Yfiler™	310	97	2,693	100%	100%	100%	100%	100%
	3130	87	4,317	100%	100%	100%	100%	100%
	3500	192	4,740	100%	100%	100%	100%	100%
	SeqStudio™	192	4,675	100%	100%	100%	100%	100%
Identifiler™	310	26	2,140	100%	100%	100%	100%	100%
	3100	38	1,748	100%	100%	100%	100%	100%
	3130	99	3,683	100%	100%	100%	100%	100%
Identifiler™ Plus	3730	30	2,101	100%	100%	100%	100%	100%
	3500	190	7,690	100%	100%	100%	100%	100%
	SeqStudio™	192	7,688	100%	100%	100%	100%	100%
MiniFiler™	3130	90	6,574	100%	100%	100%	100%	100%
	3500	96	768	100%	100%	100%	100%	100%
	SeqStudio™	192	4,806	100%	100%	100%	100%	100%
Yfiler™ Plus	3500	236	10,804	100%	100%	100%	100%	100%

Table 2 Chemistry and instrument platforms tested for concordance between GeneMapper ID-X Software v1.6 and v1.7 *(continued)*

Chemistry	Platform	No. of samples	No. of genotypes	Concordance				
				Allele call	Size	Height	Area	Data point
Yfiler™ Plus	SeqStudio™	192	8,839	100%	100%	100%	100%	100%
NGM Detect™	3500	96	5,443	100%	100%	100%	100%	100%
	SeqStudio™	240	15,663	100%	100%	100%	100%	100%
NGM SElect™	3500	144	5,094	100%	100%	100%	100%	100%
GlobalFiler™ Express	3730	96	29,667	100%	100%	100%	100%	100%
	3500	55	3,141	100%	100%	100%	100%	100%
VeriFiler™ Express	3500	138	9,591	100%	100%	100%	100%	100%
	3730	144	4,574	100%	100%	100%	100%	100%
Yfiler™ Pt-CW	3130	15	865	100%	100%	100%	100%	100%
	3500	48	4,291	100%	100%	100%	100%	100%
GlobalFiler™	3500	47	2,510	100%	100%	100%	100%	100%

Conclusions

- GeneMapper™ *ID-X* Software v1.7 can be used to process sample files generated on all HID CE instruments and with existing PCR amplification kits.
- The same results for sizing, genotyping, profile comparison, and mixture analysis were obtained using GeneMapper™ *ID-X* Software v1.6 and v1.7.
- All new features and updates to GeneMapper™ *ID-X* Software v1.7 were successfully and correctly implemented without deleterious effects on other software functionality.

Based on the nature of the modifications addressed in this update, and the testing that we performed, we recommend that users evaluate this software as it pertains to their laboratory workflow to demonstrate concordance to previously validated GeneMapper™ *ID-X* Software versions. Laboratories should determine the appropriate level of testing required based on their internal software validation guidelines and those of the appropriate governing agencies.

Documentation and support

Related documentation

Document	Publication number
GeneMapper™ ID-X Software v1.7 Administration Guide	MAN0029245
GeneMapper™ ID-X Software v1.7 Installation Guide	MAN0029246
GeneMapper™ ID-X Software v1.7 New Features and Software Verification and Validation User Bulletin	MAN0029209
GeneMapper™ ID-X Software v1.5 Getting Started Guide— Basic Features	100031701
GeneMapper™ ID-X Software v1.5 Quick Reference— Basic Features	100031702
GeneMapper™ ID-X Software v1.5 Getting Started Guide— Mixture Analysis Tool	100031704
GeneMapper™ ID-X Software v1.5 Quick Reference— Mixture Analysis Tool	100031705
GeneMapper™ ID-X Software v1.5 Reference Guide	100031707
SeqStudio™ Flex Series Genetic Analyzer for HID Validation User Bulletin	MAN0028463
Technical Note: Compendium of GeneMapper™ ID-X Software version changes from version 1.0.1 through version 1.7	NA

Customer and technical support

For support:

- **In North America**—Send an email to **HIDTechSupport@thermofisher.com**, or call **888-821-4443 option 1**.
- **Outside North America**—Contact your local support office.

For the latest services and support information for all locations, go to **thermofisher.com/support** to obtain the following information.

- Worldwide contact telephone numbers
- Product support
- Order and web support
- Safety Data Sheets (SDSs; also known as MSDSs)

Additional product documentation, including user guides and Certificates of Analysis, are available by contacting Customer Support.

Limited product warranty

Life Technologies Corporation and/or its affiliate(s) warrant their products as set forth in the Life Technologies' General Terms and Conditions of Sale at **www.thermofisher.com/us/en/home/global/terms-and-conditions.html**. If you have any questions, please contact Life Technologies at **www.thermofisher.com/support**.

Life Technologies Corporation | 6055 Sunol Blvd | Pleasanton, California 94566 USA

Revision history: Pub. No. MAN0029209

Revision	Date	Description
A.0	17 May 2023	New document for GeneMapper™ *ID-X* Software v1.7.

The information in this guide is subject to change without notice.

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