GeneMapper™ *ID-X* Software v1.7

Software features, Verification, and Validation

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This user bulletin describes software features and software verification and validation. For more information on using the software, see "Related documentation" on page 53.

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The Oracle™ Database has been replaced by the PostgreSQL Database.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 (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 (page 5)
Optional ability to enable allele-specific stutter and additive stutter filtering.	Enable allele-specific and/or additive stutter filtering (page 6)
Optional ability to enable marker-specific thresholds.	Enable marker-specific thresholds (page 9)

For Research, Forensic or Paternity and Cell Line Authentication. Not for use in Diagnostic and Therapeutic applications.

ThermoFisher SCIENTIFIC

(continued)

Feature	See
Optional ability to enable pull-up filtering.	Enable pull-up filtering (page 10)
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 (page 12)
Ability to show the peak height ratio of any two selected peaks.	View the peak height ratio of any two peaks (page 13)
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 (page 14)
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 (page 15)
In the Plot Settings Editor, ability to gray out stutter peaks to distinguish them from allelic peaks.	Gray out stutter peaks (page 17)
Ability to open multiple projects at one time.	Open and close multiple projects (page 18)
Ability to open multiple plots at one time.	Open multiple plots (page 19)
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 (page 20)
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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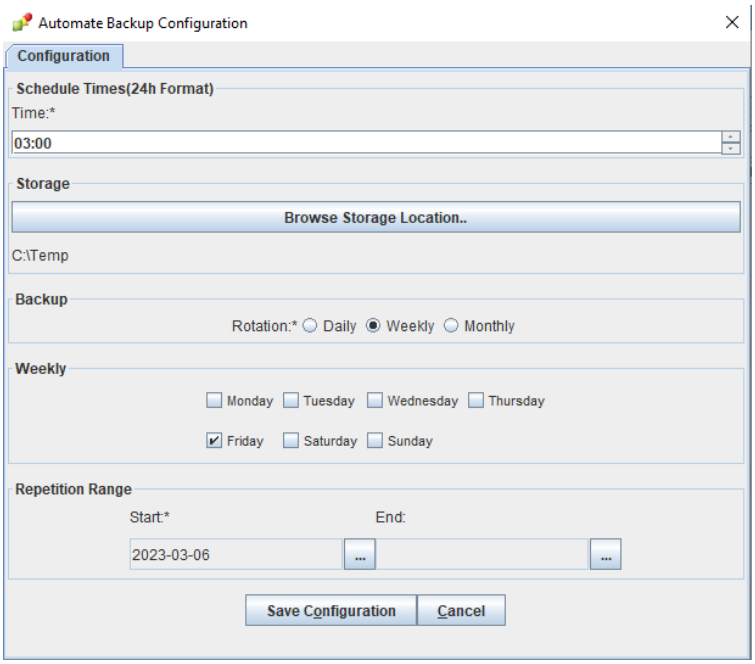
Note: For detailed procedures, see the *GeneMapper™ ID-X Software v1.7 Administration Guide*.

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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 

(continued)

Option	Action
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 about creating custom columns in a plate file, see the 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™/SeqStudio™ Flex[1]	3500/3500xL	
Analysis method	CustomFields1	User Defined Field 1	UD1 (User-defined column 1)
Size standard	CustomFields2	User Defined Field 2	UD2 (User-defined column 2)
Panel	CustomFields3	User Defined Field 3	UD3 (User-defined column 3)
Other values	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.

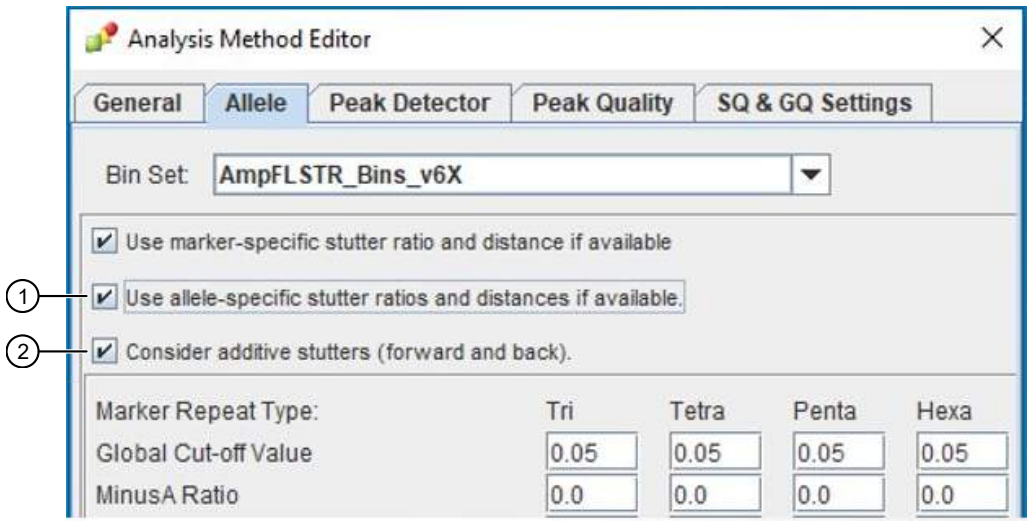
IMPORTANT! Values in custom columns have priority over values in standard columns. The **Samples** table in GeneMapper™ *ID-X* Software is populated from standard columns only when the corresponding custom columns are empty.

This can cause issues if custom columns 1–3 are used for other values. 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

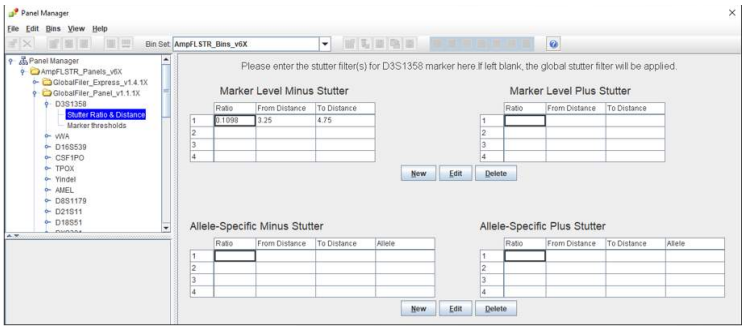
You can apply different stutter filters at individual loci, based on the specific alleles that are observed.

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

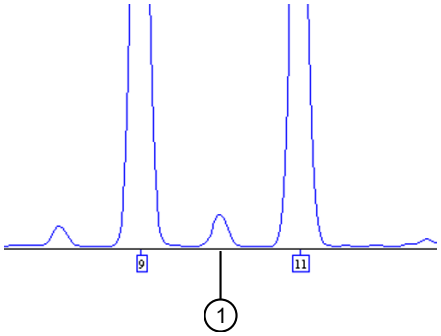


① Allele-specific stutter filtering
② Additive stutter filtering

2. Select the stutter filter options.

Option	Action	Additional information
Use allele-specific stutter ratios and distances if available	Select ☑ **(checkbox)** 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 priority 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.

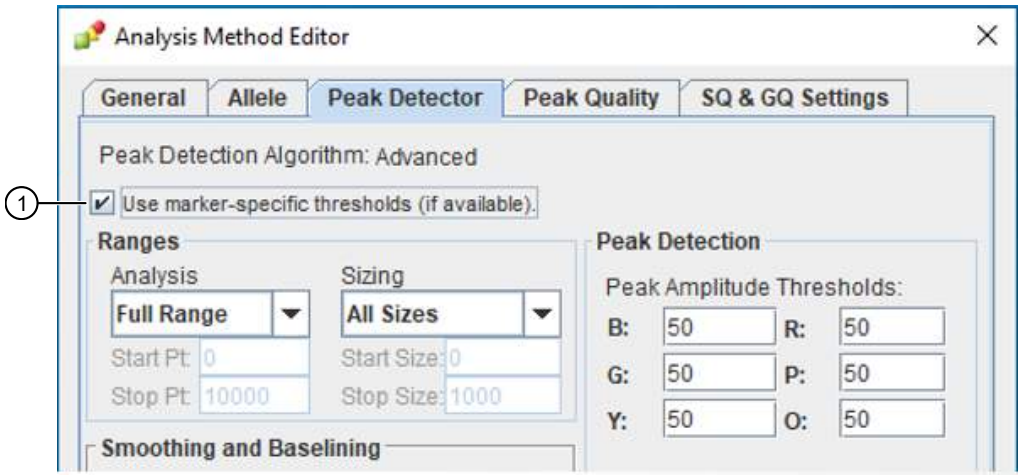
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Option	Action	Additional information
Consider additive stutters (forward and back)	Select ☑ **(checkbox)** to have overlapping stutter filters calculated additively. That is, if two stutter filters refer to the same peak, the filter used will be calculated 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

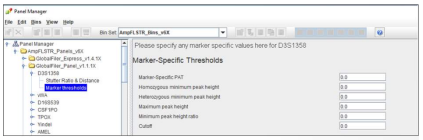
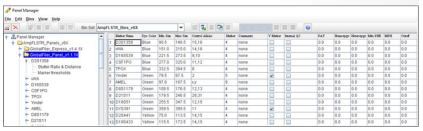
You can apply different analysis thresholds at individual loci, instead of having only one value for the entire profile.

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



① Marker-specific thresholds

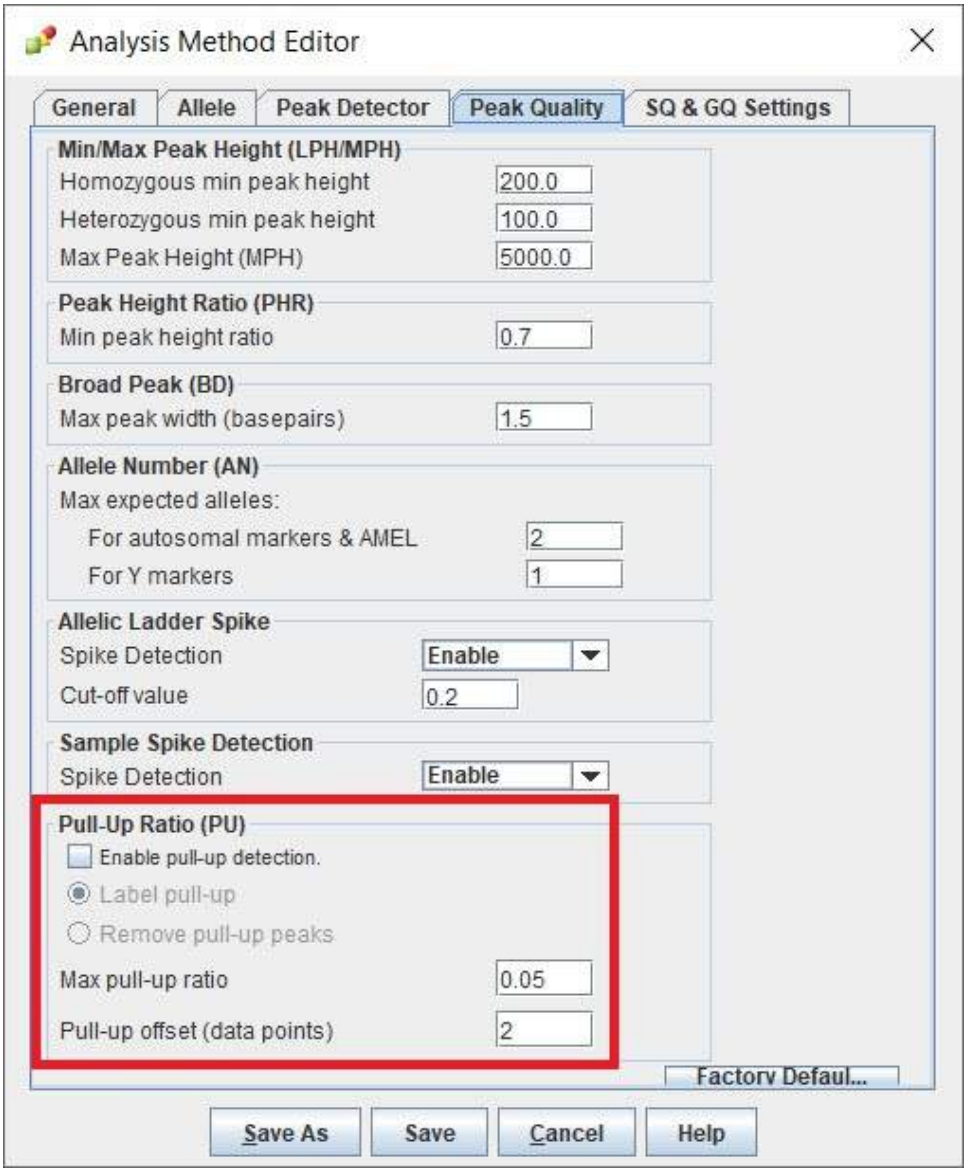
2. Select marker-specific threshold options.

Option	Action	Additional information
Use marker-specific thresholds (if available)	1. Select ☑ **(checkbox)** 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.

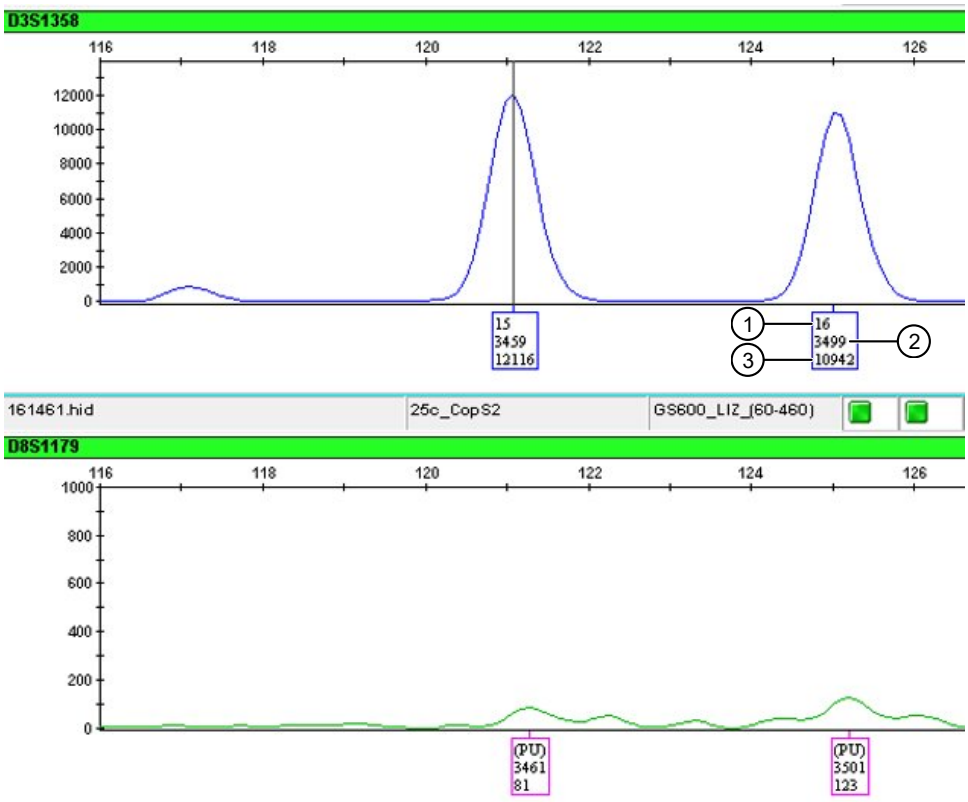
1. Open the **Analysis Method Editor**, then select the **Peak Quality** tab.



2. Select the pull-up filtering options.

Option	Action
Enable pull-up detection	Select ☑ **(checkbox)** 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 ☑ **(checkbox)** to apply the **PU** artifact label to possible pull-up peaks.
Remove pull-up peaks	Select ☑ **(checkbox)** 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:

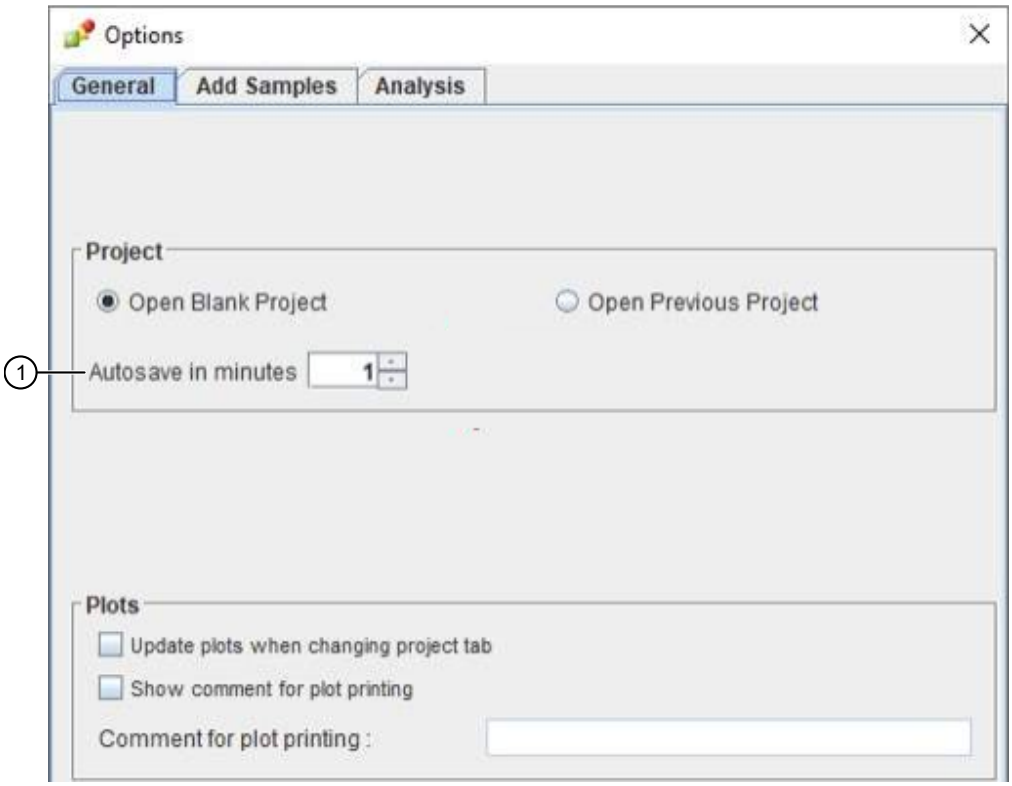
- The max pull-up ratio is set to 5% and the pull-up offset is set to 2 (default values).
- 15 and 16 alleles in D3S1358 are the parent peaks.
- Peaks detected in green dye are flagged as pull-up because:
  - The peaks align with the parent peaks
    - 3461 is ±2 data points of 3459
    - 3501 is ±2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

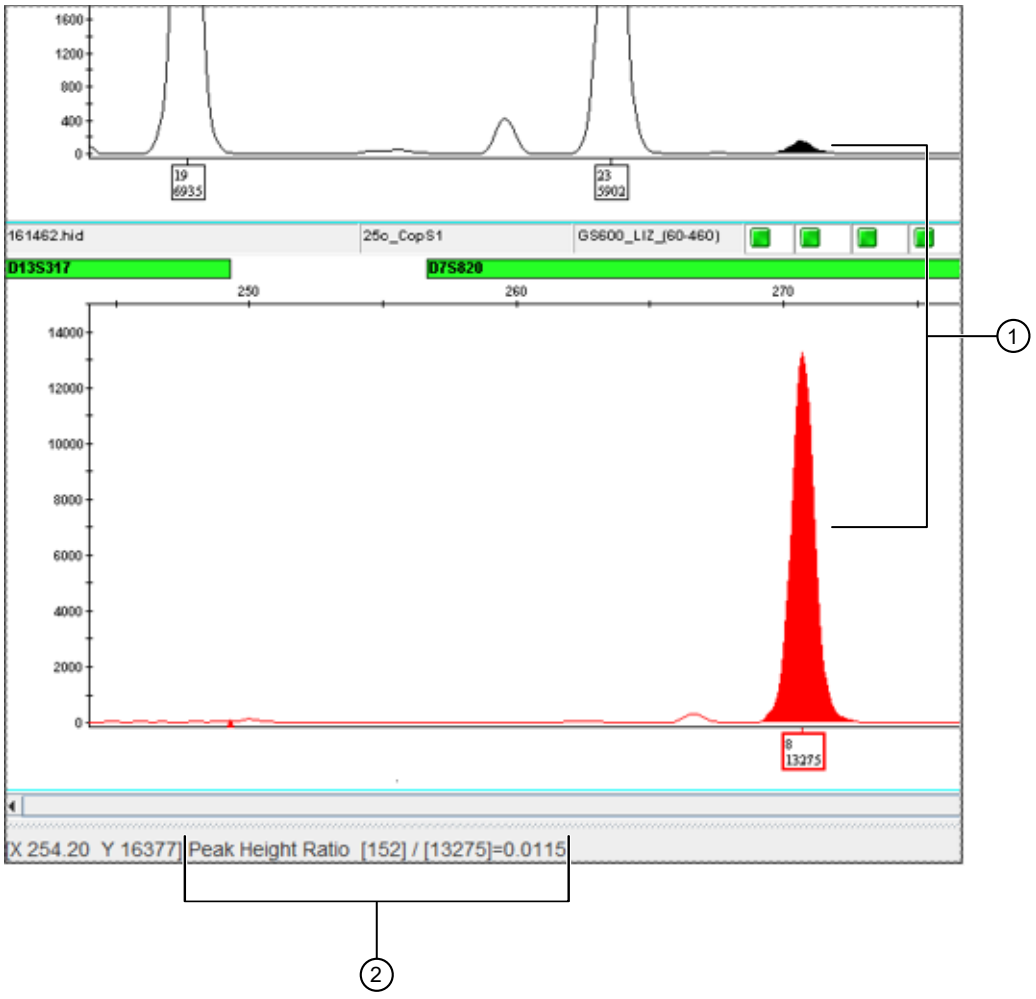
Note: The autosave interval can be set from 0–120 minutes. To disable the autosave feature, select **0** minutes (**0** is the default setting).

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.

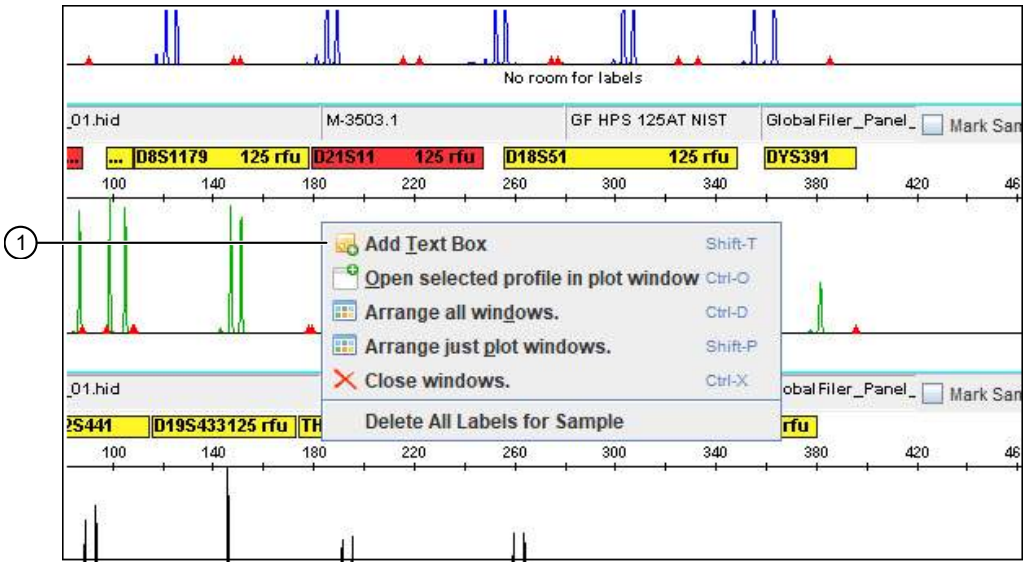


① Select two peaks
② Peak height ratio for the selected peaks

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.

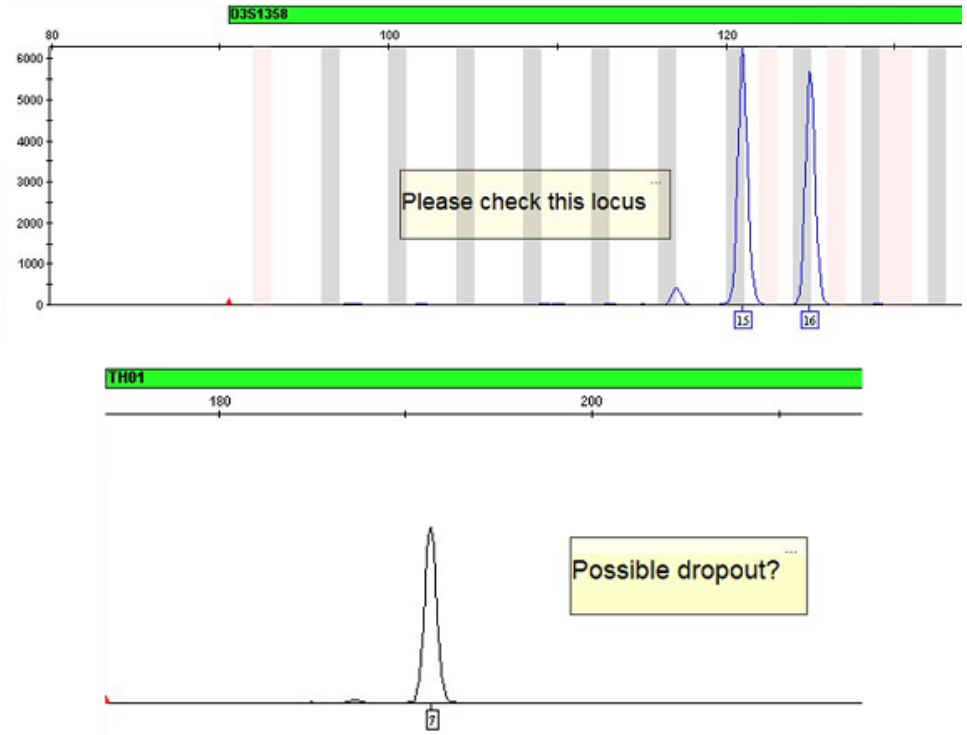
1. Display the Samples Plot or Genotypes Plot of interest.
2. Right-click inside the plot, then select **Add Text Box**.



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.



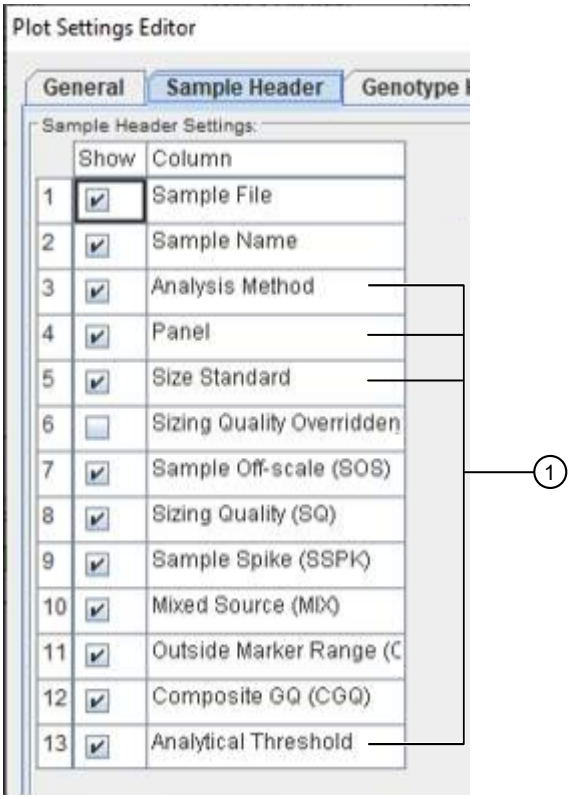
Display analysis settings in a Samples Plot or Genotypes Plot

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.

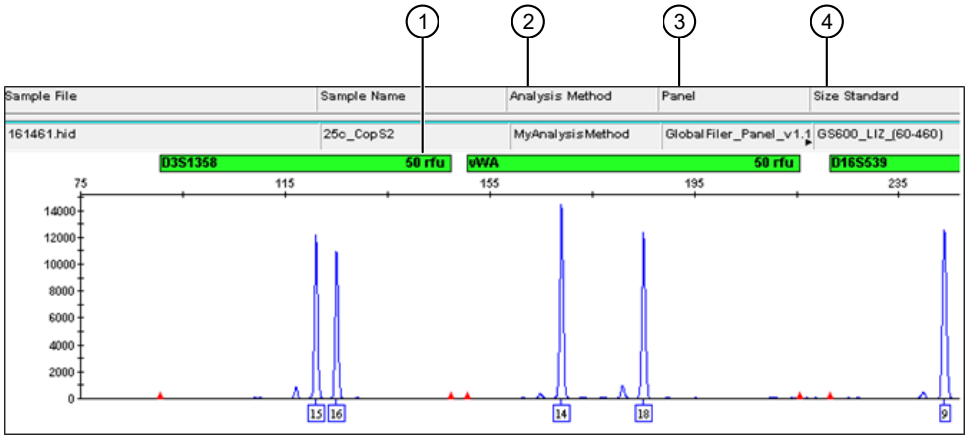
1. Display the Samples Plot or Genotypes Plot of interest, then click **(Plot Setting Editor)**.
2. Select the **Sample Header** tab.
3. Select the checkbox for each item to display in the plot.

   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

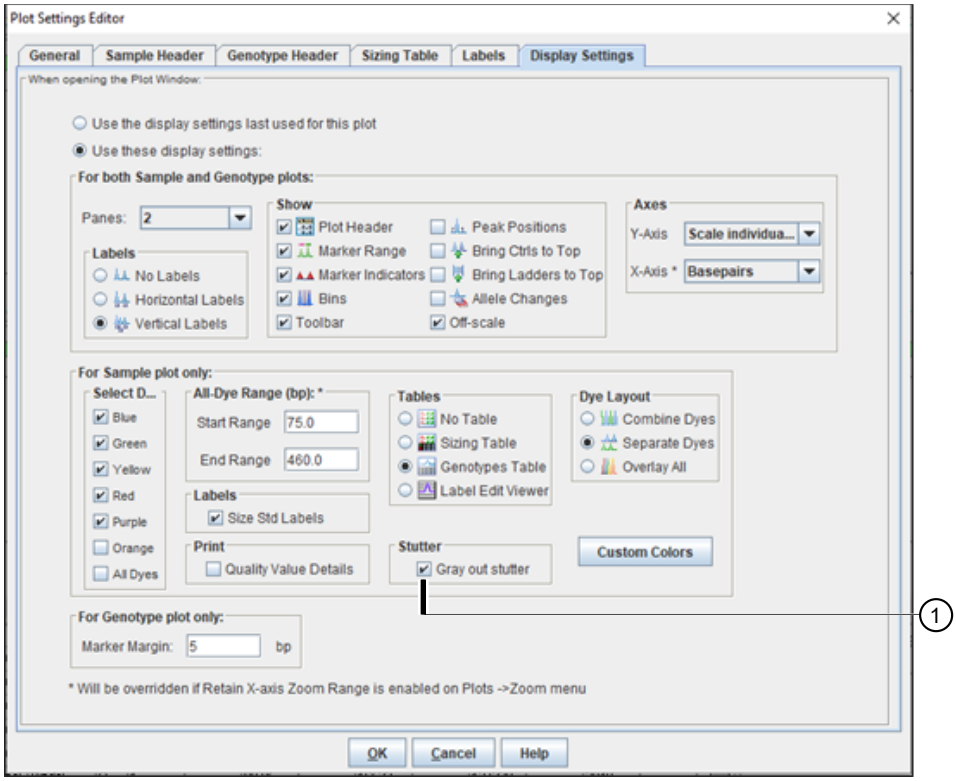


① Analytical threshold; example = **50 rfu**
② Analysis method; example = **MyAnalysisMethod**
③ Panel; example = **GlobalFiler_Panel_v1.1**
④ Size standard; example = **GS600_LIZ_(60-460)**

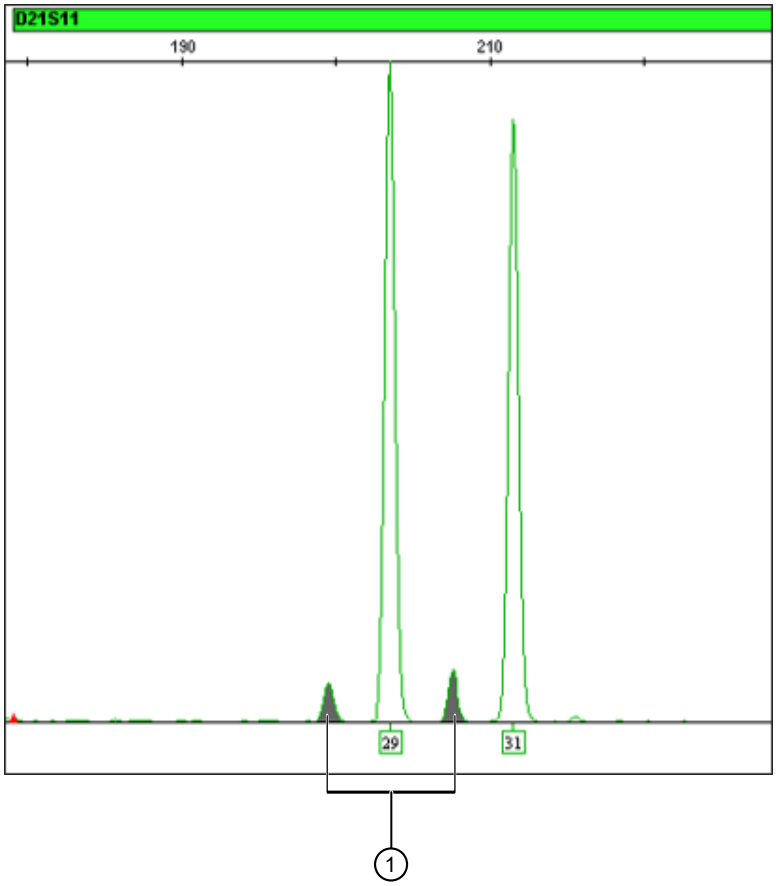
Gray out stutter peaks

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

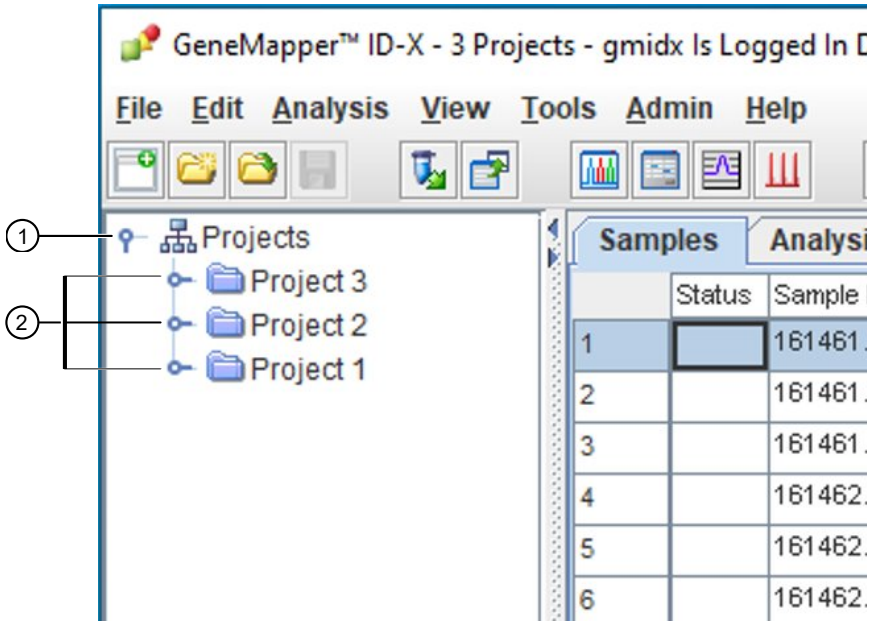
You can open and close multiple projects simultaneously.

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

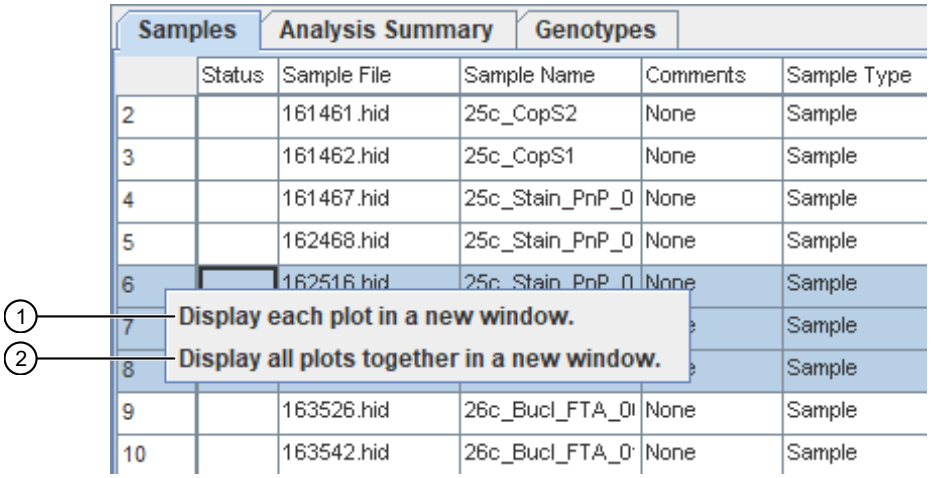
3. In the **View** menu, select one of the new display options.
   - **View ▸ Display plots** opens all samples simultaneously, replacing any other open plots.
   - **View ▸ Display all plots together in a new window** opens all samples simultaneously in a new plot, leaving any existing plot open
  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



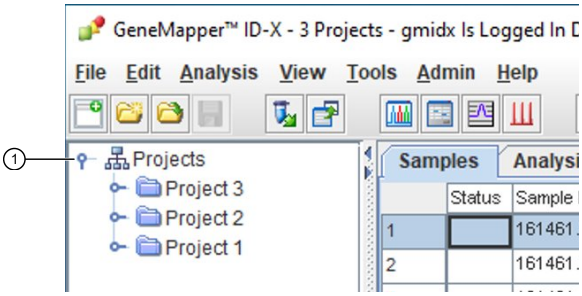
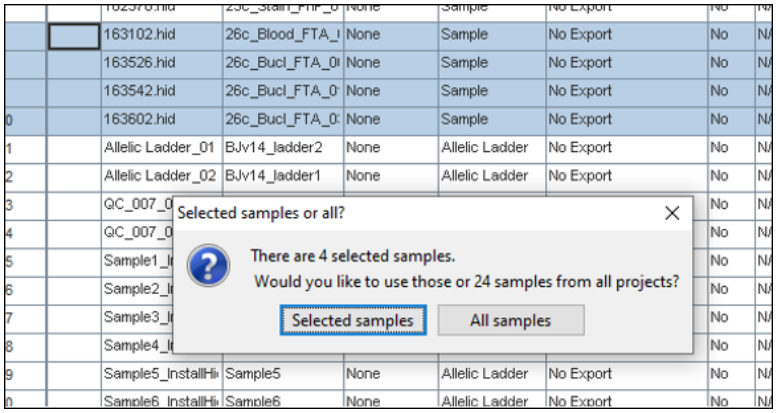
① Open a profile for the selected sample in its own plot
② Arrange the plot windows

Use new features in the Profile Comparison tool

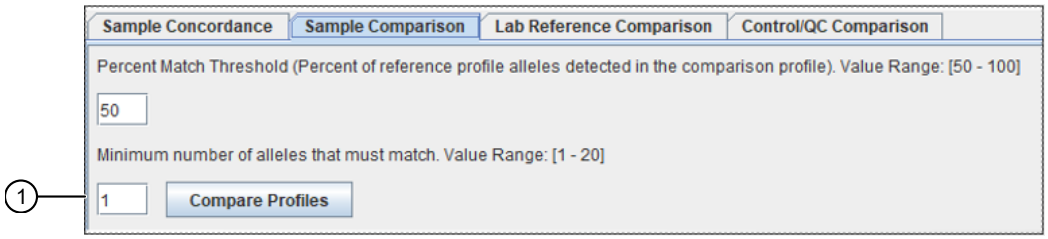
There are two new features available in the Profile Comparison tool:

- **Compare profiles in different projects**—The new ability to open multiple projects simultaneously (see "Open and close multiple projects" on page 18) 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.

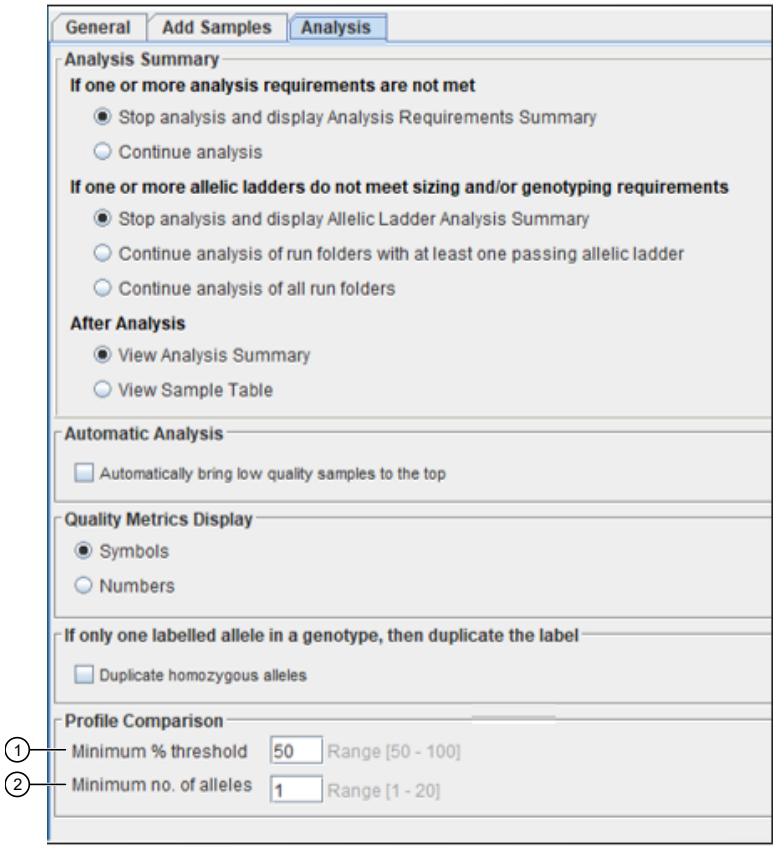
As needed, use the new features in the Profile Comparison tool.

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 26.
	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.
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	

(continued)

Test	Test description	Result	Comments
Data analysis and review	User can apply additive stutter filters.	Pass	All functions operate as expected.
	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	
	User can configure default values for the match percentage and the minimum number of alleles to match.	Pass	
	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. There was 100% concordance between v1.6 and v1.7 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.
- The features and updates introduced in 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.

GeneMapper™ *ID-X* Software v1.7 patches and software features

GeneMapper™ *ID-X* Software v1.7.1

GeneMapper™ *ID-X* Software v1.7.1 is a patch to the GeneMapper™ *ID-X* Software v1.7. This patch addresses several issues but does not include new features. For more information on GeneMapper™ *ID-X* Software v1.7.1, see “Related documentation” on page 53.

GeneMapper™ *ID-X* Software v1.7.1 includes the following updates:

- Vestigial Oracle function was corrected to address PostgreSQL function and resolve Client SQL errors to prevent potential data loss.
- PostgreSQL database connection limit was increased from 100 to 260 to improve client connection limits.
- Custom administrator accounts were created.
- Improved system performance for large project analysis by increasing memory allocation for both the application executable and database processes.

GeneMapper™ *ID-X* Software v1.7.2

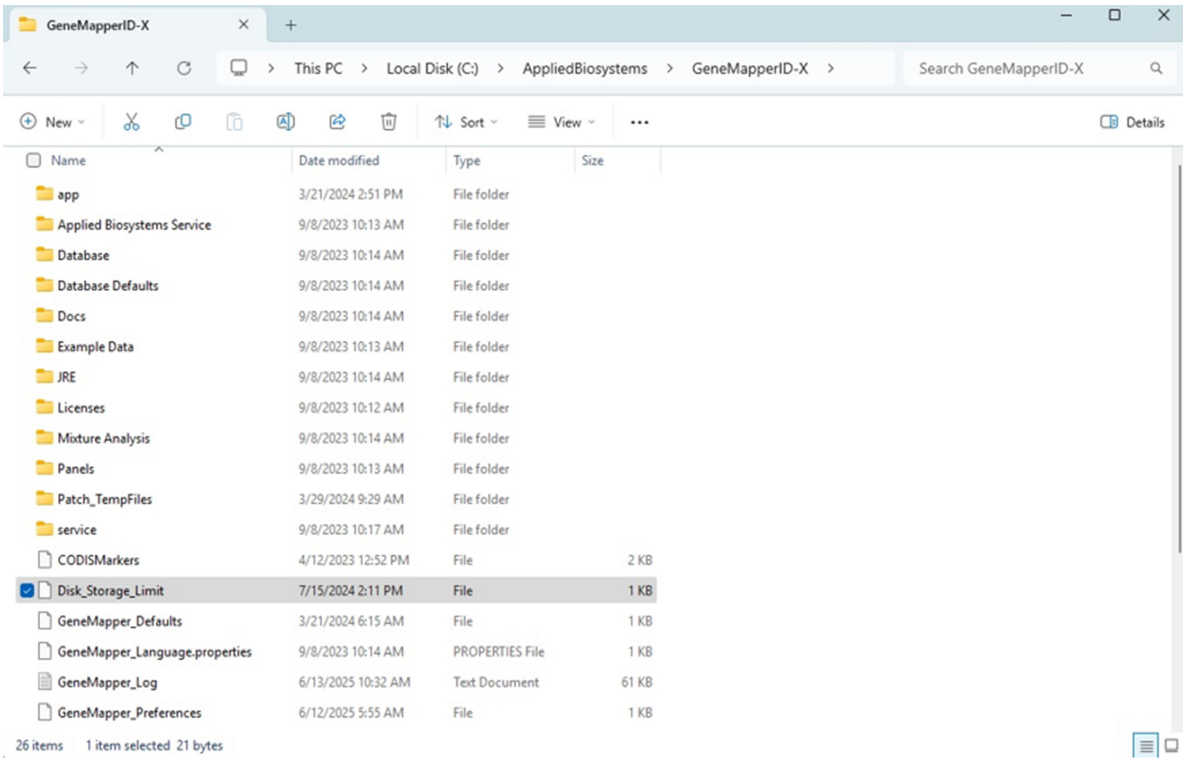
GeneMapper™ *ID-X* Software v1.7.2 is a patch to the GeneMapper™ *ID-X* Software v1.7 and GeneMapper™ *ID-X* Software v1.7.1. This patch addresses several issues but does not include new features. For more information on GeneMapper™ *ID-X* Software v1.7.2, see “Related documentation” on page 53.

Software features in GeneMapper™ *ID-X* Software v1.7.2

To customize the database storage limit notification (full installation only) perform the steps below.

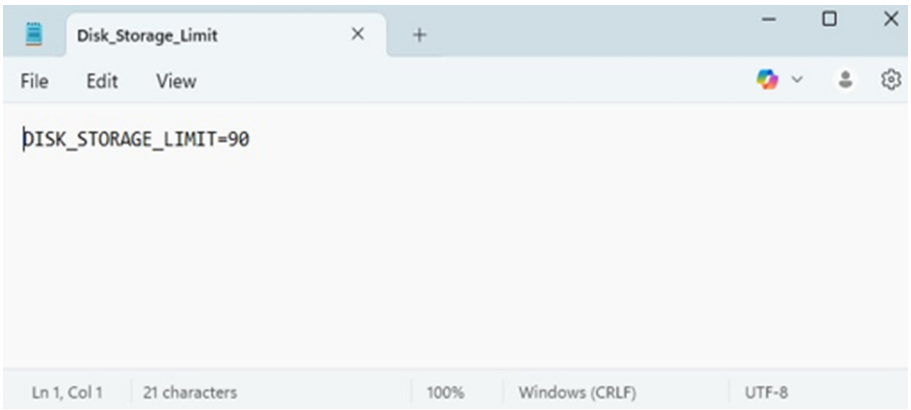
To adjust the database (full installation) storage limit notifications, update the percentage full value in the **Disk_Storage_Limit** text file.

1. Navigate to the **GeneMapperID-X folder**: `<installation drive>/AppliedBiosystems/GeneMapperID-X/`.



2. Open the file with a text editor application, such as **Notepad**.

Note: The default value of 90, indicates a notification will be presented to the user at time of software launch when the full installation computer Hard Disk Drive (HDD) has become 90% full.



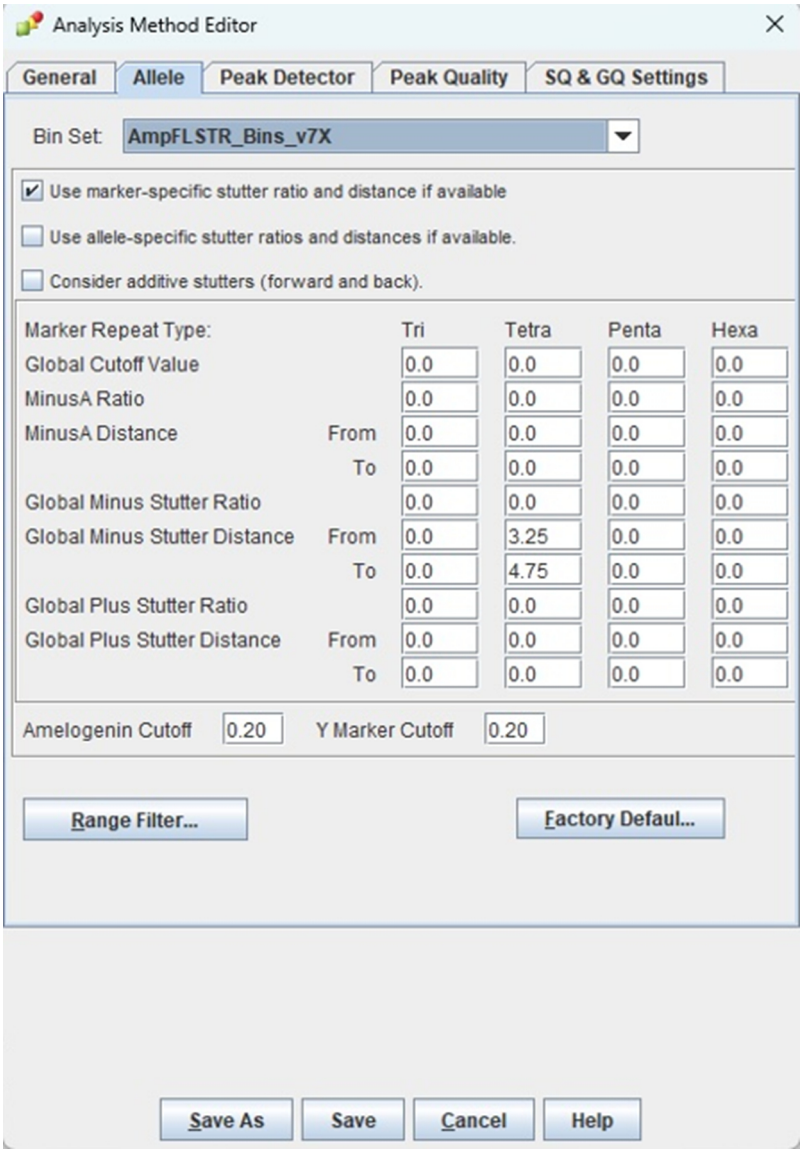
3. Adjust the value (percentage) lower or greater to adjust the notification.

Note: Disk storage limit notifications are displayed on the full installation computer only.

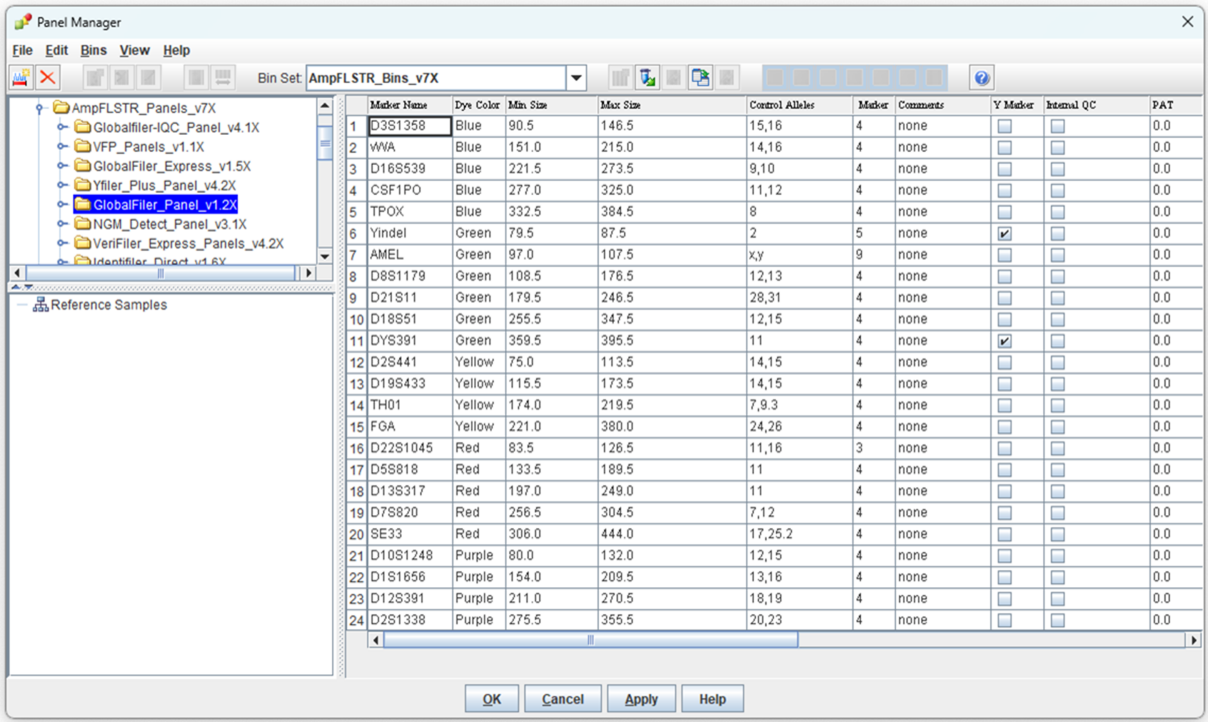
Configure a Y Marker Cutoff

The **Y Marker Cutoff** allows for the removal of non-allelic peaks from Y Markers in STR-PCR amplification results.

The parameter filters peaks at Y Markers (example = **Yindel** and **DYS391**) based on the peak height of the X allele at marker Amelogenin. The default **Y Marker Cutoff** value of 0.20 filters peaks below 20% of the Amelogenin X peak height.



The **Y Marker Cutoff** applies only to Y Markers as designated in the amplification kit panel definition (example = **GlobalFiler_Panel_V1.2x** showing checkmark in **Y Marker** column for **Yindel** and **DYS391**).



	Marker Name	Dye Color	Min Size	Max Size	Control Alleles	Marker	Comments	Y Marker	Internal QC	PAT
1	D3S1358	Blue	90.5	146.5	15,16	4	none			0.0
2	vWA	Blue	151.0	215.0	14,16	4	none			0.0
3	D16S539	Blue	221.5	273.5	9,10	4	none			0.0
4	CSF1PO	Blue	277.0	325.0	11,12	4	none			0.0
5	TPOX	Blue	332.5	384.5	8	4	none			0.0
6	Yindel	Green	79.5	87.5	2	5	none	✔		0.0
7	AMEL	Green	97.0	107.5	X,Y	9	none			0.0
8	D8S1179	Green	108.5	176.5	12,13	4	none			0.0
9	D21S11	Green	179.5	246.5	28,31	4	none			0.0
10	D18S51	Green	255.5	347.5	12,15	4	none			0.0
11	DYS391	Green	359.5	395.5	11	4	none	✔		0.0
12	D2S441	Yellow	75.0	113.5	14,15	4	none			0.0
13	D19S433	Yellow	115.5	173.5	14,15	4	none			0.0
14	TH01	Yellow	174.0	219.5	7,9.3	4	none			0.0
15	FGA	Yellow	221.0	380.0	24,26	4	none			0.0
16	D22S1045	Red	83.5	126.5	11,16	3	none			0.0
17	D5S818	Red	133.5	189.5	11	4	none			0.0
18	D13S317	Red	197.0	249.0	11	4	none			0.0
19	D7S820	Red	256.5	304.5	7,12	4	none			0.0
20	SE33	Red	306.0	444.0	17,25.2	4	none			0.0
21	D10S1248	Purple	80.0	132.0	12,15	4	none			0.0
22	D1S1656	Purple	154.0	209.5	13,16	4	none			0.0
23	D12S391	Purple	211.0	270.5	18,19	4	none			0.0
24	D2S1338	Purple	275.5	355.5	20,23	4	none			0.0

GeneMapper™ *ID-X* Software v1.7.3

GeneMapper™ *ID-X* Software v1.7.3 is a patch to the GeneMapper™ *ID-X* Software v1.7, GeneMapper™ *ID-X* Software v1.7.1, and GeneMapper™ *ID-X* Software v1.7.2.

Issues addressed in the GeneMapper™ *ID-X* Software v1.7.3

The issues listed below were addressed in the GeneMapper™ *ID-X* Software v1.7.3.

For a complete list of issues addressed in the GeneMapper™ *ID-X* Software v1.7.3, see the GeneMapper™ *ID-X* Software v1.7.3 and NOC v1.0 release notes.

- PostgreSQL database performance—Resolved database performance issues affecting project analysis and saving operations.
- Security Manager fixes—The following GeneMapper™ *ID-X* Software v1.7.2 Security Manager issues were fixed:
  - Assignment of incorrect **User Role** upon successive new user login.
  - Assignment of incorrect **Analyst Role** privileges.

Software features in GeneMapper™ *ID-X* Software v1.7.3

Software features included in the GeneMapper™ *ID-X* Software v1.7.3 are described in the following sections.

Note: Java SE was updated to version 1.8.0.202.

Trim (remove) tabs for blank fields in tab-delimited (TXT) exports

By default, tabs are maintained for blank fields in TXT exports of the **Samples** and **Genotypes** tables. You can trim (remove) tabs for blank fields by editing a section of the `GeneMapper_Defaults` configuration file.

1. Open the `GeneMapper_Defaults` configuration file located at:

   `<installation drive>:\AppliedBiosystems\GeneMapperID-X`

2. By default, the `EXPORT_TRIM_TABS` command line is set to `false` (tabs maintained). To trim tabs, set the command line to `true`: `EXPORT_TRIM_TABS=true` (see Figure 1).

   Note: The export process for CSV files is unaffected.

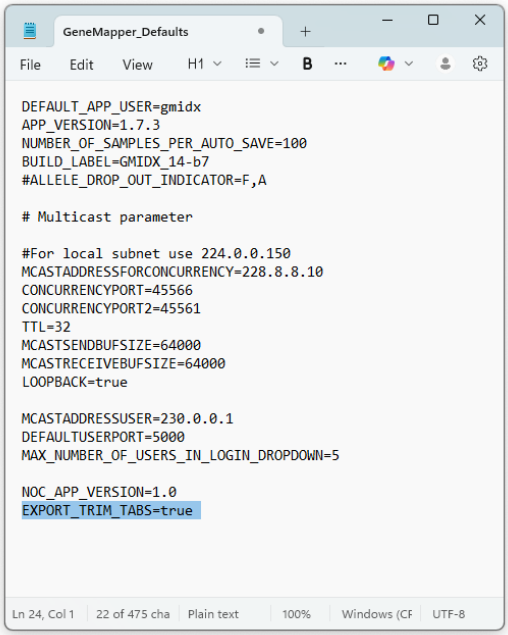


Figure 1 Configuration file: `EXPORT_TRIM_TABS=true`

3. Save the file, then start or restart the software to apply the export setting.

Number of Contributors (NOC) estimation (optional plugin)

The NOC v1.0 plugin is an optional plugin for GeneMapper™ *ID-X* Software v1.7.3 that estimates the number of contributors to a mixed DNA sample, aiding in the interpretation of mixed-contributor DNA profiles. Contributor estimation is important for accurate mixture resolution and can be used in downstream probabilistic genotyping (PG) analysis software, such as GeneMapper™ PG Software v1.0.

The NOC plugin can be installed during the setup of GeneMapper™ *ID-X* Software v1.7.3, whether you are performing a patch or a new installation. However, installing the NOC plugin is optional and not required for upgrading to or installing the software.

For more information about the installation of the software or NOC plugin, see the software release notes.

NOC v1.0 model

The NOC plugin uses a specific model that contains the necessary components to analyze data from the GlobalFiler™ STR amplification kit and enable accurate NOC analysis. The model characterizes DNA sample degradation, a critical factor for simulating DNA profiles.

Note: Models for more STR amplification kits may be included in future versions.

NOC model files are located at:
`<installation drive>:\AppliedBiosystems\GeneMapperID-X\app\plugins\panels`

The model includes the following definitions and settings:

- STR amplification kit panel, bin set, and stutter definitions
  - `GlobalFiler_Panel_v1.0.1`
  - `GlobalFiler_Bins_v1.0.1`
  - `GlobalFiler_Stutter_v1.0.1`
- Genetic analyzer base model settings
  - Peak amplitude threshold (PAT)
  - Allele-specific stutter values (n-8, n-4, n-2, n+2, and n+4)
  - Marker-specific peak shoulder and noise
  - Marker-specific peak height ratio (PHR)
  - Marker-specific allelic drop-out
- Population databases (allele frequencies)

Note:

- GlobalFiler™ STR amplification data used to build the model were generated using the Applied Biosystems™ 3500 Series and SeqStudio™ Flex Series genetic analyzers. Validation of the data during the development of GeneMapper™ PG Software v1.0 showed no significant difference between the genetic analyzer data. Therefore, the GeneMapper™ *ID-X* Software NOC plugin uses only the 3500-instrument base model for NOC analysis and the user interface does not allow selection of a base model instrument.
- Model-specific PATs (defaults) are replaced by the PAT designated in the sample **Analysis Method** in the GeneMapper™ *ID-X* Software. For any subsequent probabilistic genotyping analysis in separate software, such as GeneMapper™ PG Software, ensure the sample **Analysis Method** PAT is entered in the software where needed.

NOC v1.0 algorithms

The NOC plugin uses 4 algorithms for NOC estimation:

- Maximum Allele Count (MAC)
- Total Peaks
- Fixed Decision Tree
- TFSPlus Decision Tree

These algorithms are consistent with those used in the GeneMapper™ PG Software v1.0, except for the Height Distributions algorithm, which is not used by the GeneMapper™ *ID-X* Software v1.7.3 NOC plugin.

For more information about NOC v1.0 algorithms, see the following sections:

- “Maximum Allele Count (MAC) algorithm” on page 42
- “Total Peaks algorithm” on page 43
- “Decision tree algorithms” on page 44

For more information about the GeneMapper™ PG Software v1.0, see the *GeneMapper™ PG Software v1.0 Getting Started Guide* (Pub. No. MAN1000548).

Use of simulated samples

The NOC plugin uses simulated samples in the following analysis algorithms:

- Total Peaks
- Fixed Decision Tree
- TFSPlus Decision Tree

In these algorithms, the NOC plugin simulates 1,000 profiles based on the selected population, approximate amount of sample DNA (based on peak heights), model settings, and estimated DNA degradation. The accuracy of NOC results depends on how closely the simulated DNA profiles mimic the actual sample. Simulated profiles are created with 1, 2, 3, or 4 contributors.

Use the NOC plugin to perform NOC analysis

IMPORTANT! We recommend performing NOC analysis only on sample data without stutter filtering enabled. The NOC plugin model is complex and includes default allele-specific stutter filtering. Performing NOC analysis on stutter-filtered data can result in excessive stutter peak filtering and inaccurate NOC estimations.

1. To perform NOC analysis, select one or more samples in the **Samples** table, then in the menu bar, click **NOC** to select a NOC analysis option (see Figure 2).
   - Select **NOC for selected samples** to analyze only the samples selected in the **Samples** table.
   - Select **NOC for all samples** to analyze all samples in the project.

   Alternatively, samples can be shown in an active display plot and NOC analysis initiated using the **Predict NOC** option in the **NOC** menu (see Figure 3).

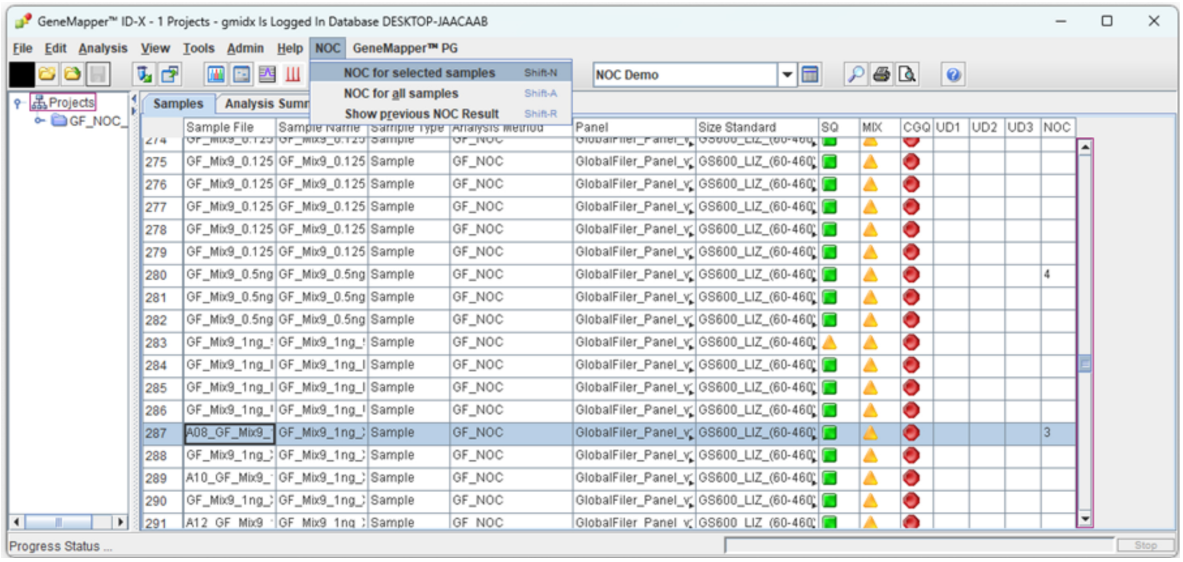


Figure 2 NOC analysis options

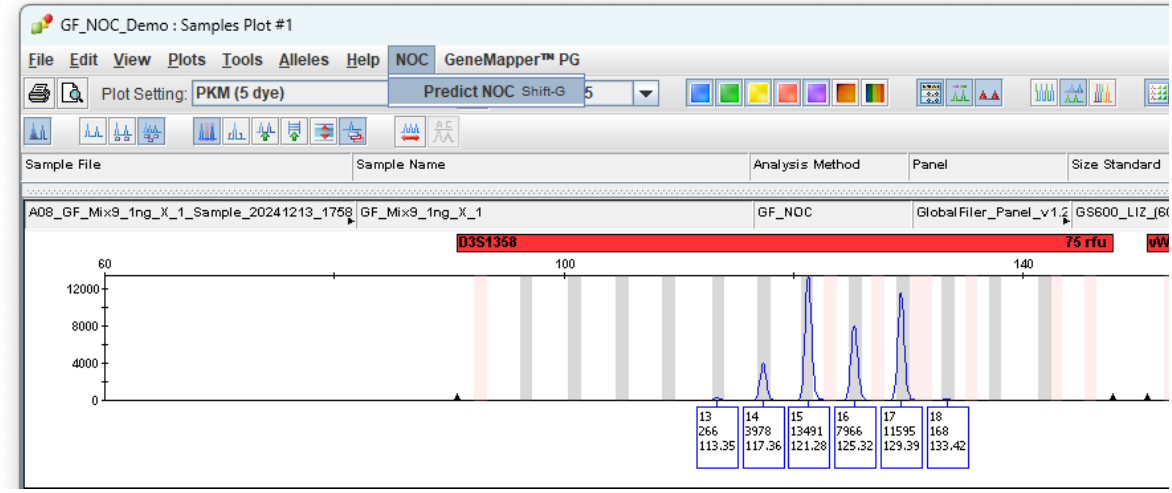


Figure 3 NOC analysis using the Predict NOC option

The **NOC Manager** window opens to the **NOC Analysis** tab. At this point, MAC NOC analysis has been completed for each sample selected (or open in the display plot window). **Mean Peak Height**, **Mean AT Value**, **Degradation**, **NOC Summary**, and **MAC NOC** are automatically calculated for each sample.

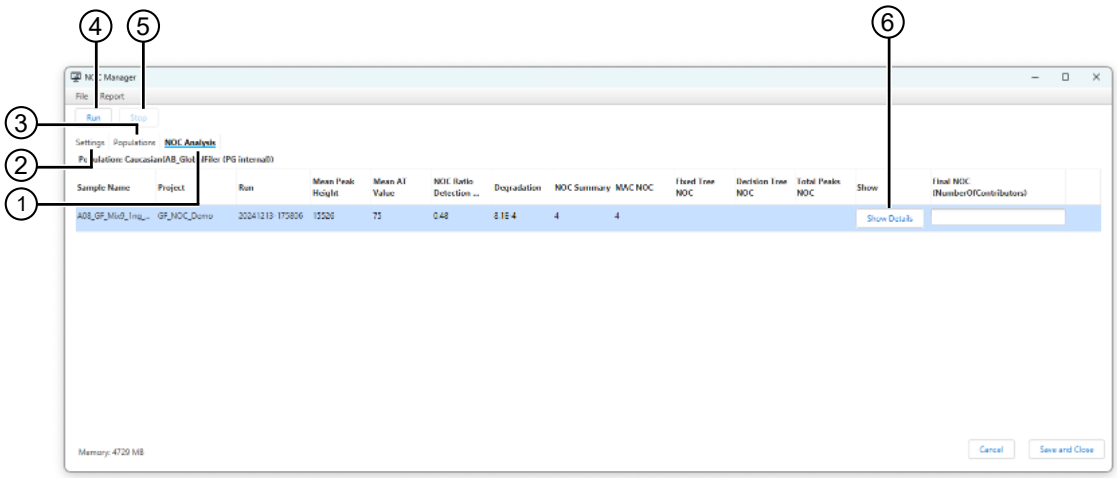


Figure 4 NOC Analysis tab in the NOC Manager window

① **NOC Analysis** tab
② **Settings** tab
③ **Populations** tab
④ **Run** button
⑤ **Stop** button
⑥ **Show Details** button (in **NOC Analysis** tab)

2. *(Optional)* Select the **Settings** tab to view the GMID-X and NOC algorithm settings.

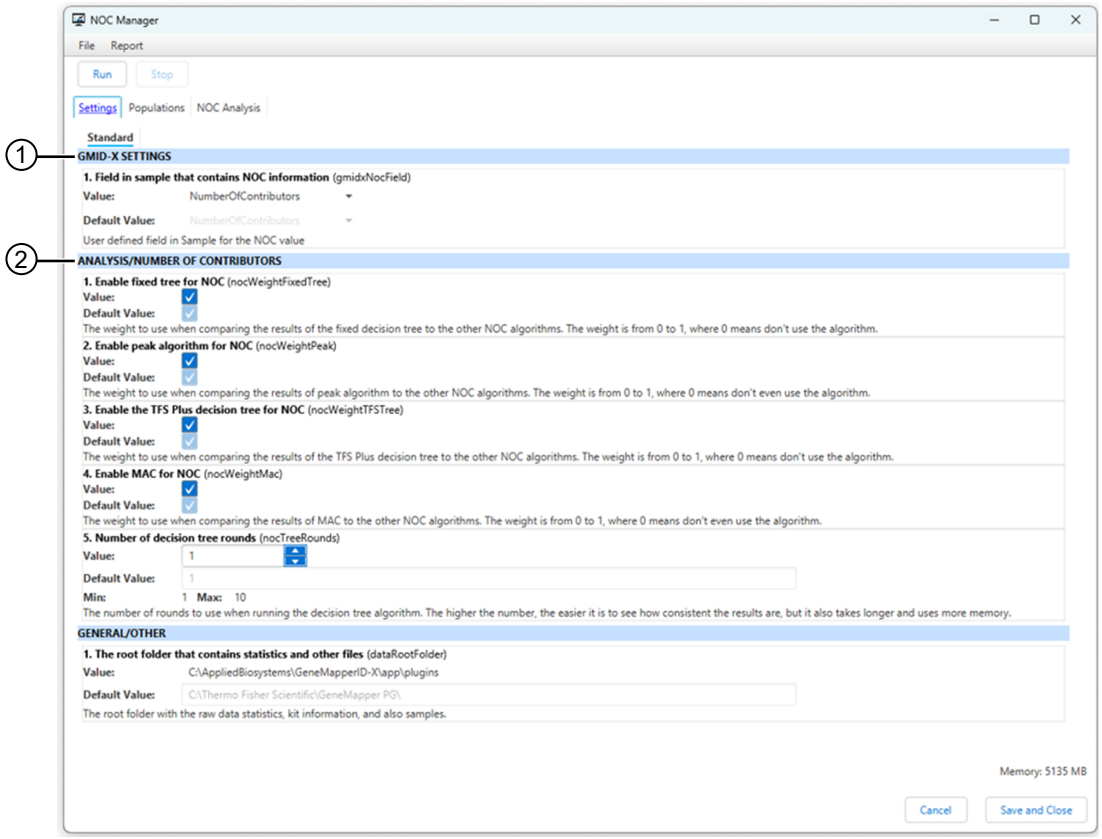


Figure 5 Settings tab in the NOC Manager window

① **GMID-X SETTINGS** pane
② **ANALYSIS/NUMBER OF CONTRIBUTORS** pane

Note: By default, the NOC estimate is displayed in the **NOC** column of the **Samples** table (setting: **NumberOfContributors**). To show the NOC estimate in another column, select a user-defined column (**UD1**–**UD9**) by choosing the setting: **UserDefinedColumn1**–**UserDefinedColumn9**. For more information about adding user-defined columns, see the instrument user guide.

---

3. *(Optional)* Select the **Populations** tab to view preloaded population databases. Click **Manage Population** to open, import, export, or delete a population database.

Note: Before importing a population database, ensure it is normalized: apply a minimum allele frequency (MAF) to underrepresented alleles and ensure that allele frequencies for each marker sum to 1.

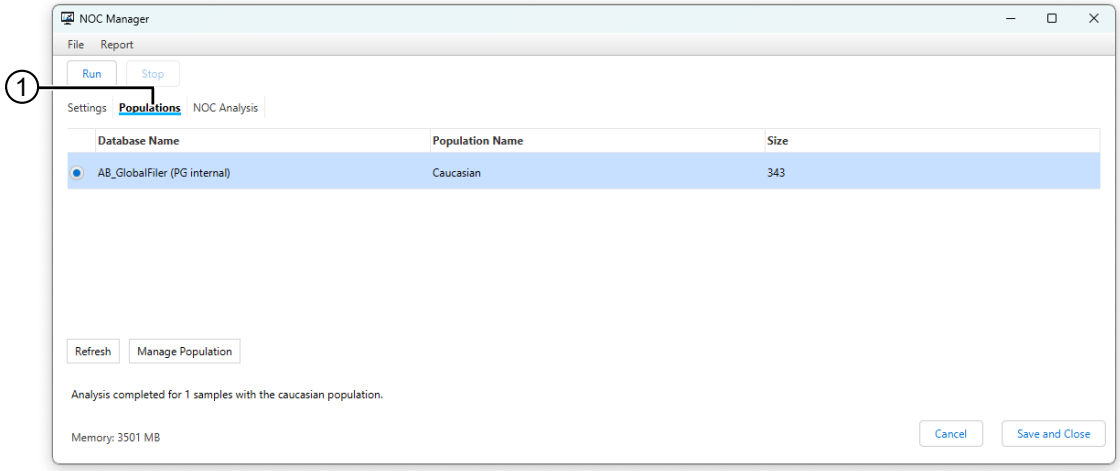
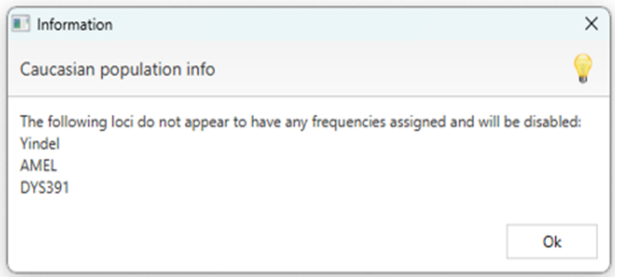


Figure 6 Populations tab in the NOC Manager window

① **Manage Population** button

4. To continue the NOC analysis, select the **NOC Analysis** tab, then click **Run**.

   If a dialog box pops up indicating that loci do not appear in the selected population database (typically YSTR or non-STR loci), click **Ok** to proceed.



NOC analysis begins and the status of each NOC algorithm displays as **Computing** (see Figure 7).

Note: Analysis time is approximately 1 minute per sample. Overall analysis time depends on the number of selected samples, DNA profile complexity, and system performance (processor, memory, and concurrent applications).

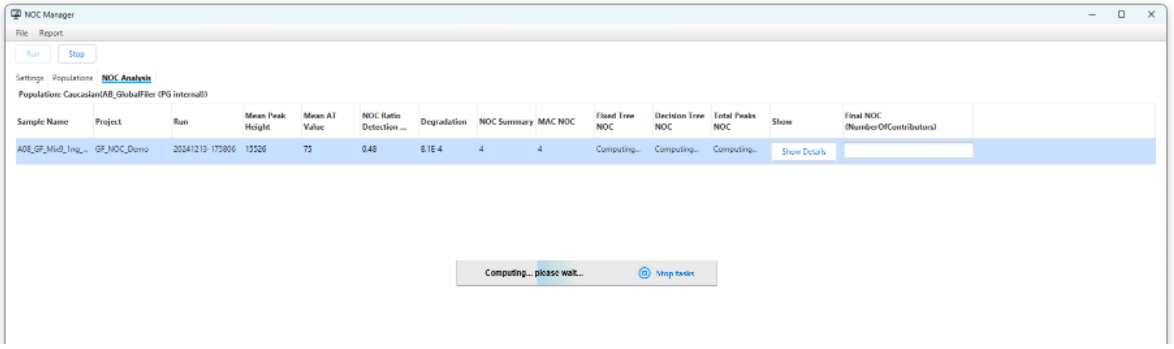


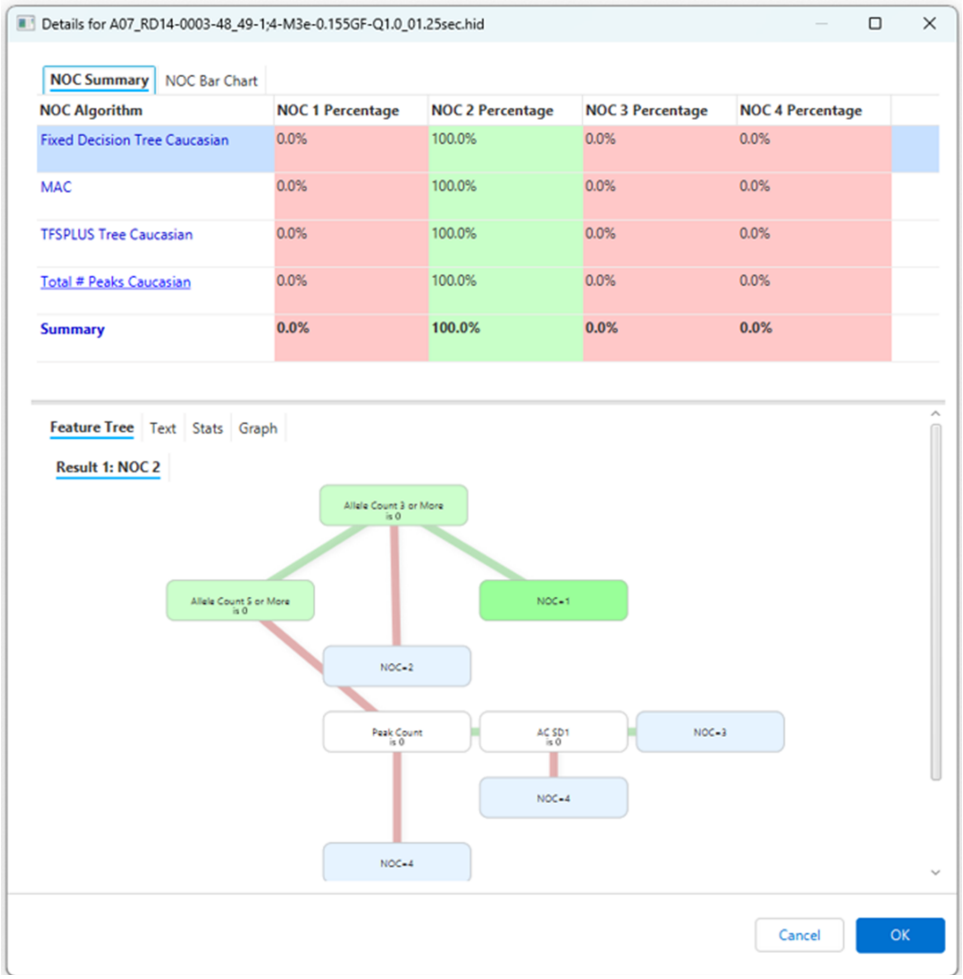
Figure 7 NOC algorithm status: Computing

When the analysis is complete, view results in the **NOC Manager** window. To view detailed results for each NOC algorithm and save a final NOC estimate, proceed to the next section.

View NOC results, then save a final NOC estimate

1. In the **NOC Analysis** tab, click **Show Details** (or the NOC value) to view detailed information for each NOC algorithm.

   To view individual algorithm results, click the hyperlinked algorithm name in the **Details** window. Alternatively, from the **NOC Manager** window, you can select the NOC estimate below the algorithm name.



2. After viewing the NOC analysis results, enter the final NOC estimate in the **Final NOC** field.

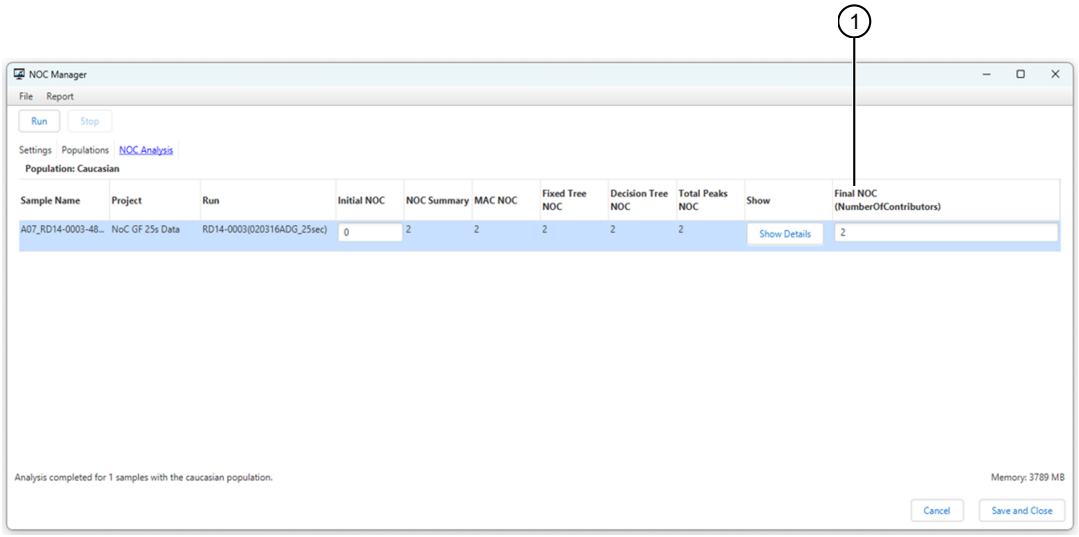


Figure 8 Final NOC estimate entered in the Final NOC field

① **Final NOC** field

3. Click **Save and Close** to commit the NOC value to the default **NOC** column (or custom column if chosen) of the **Samples** table.

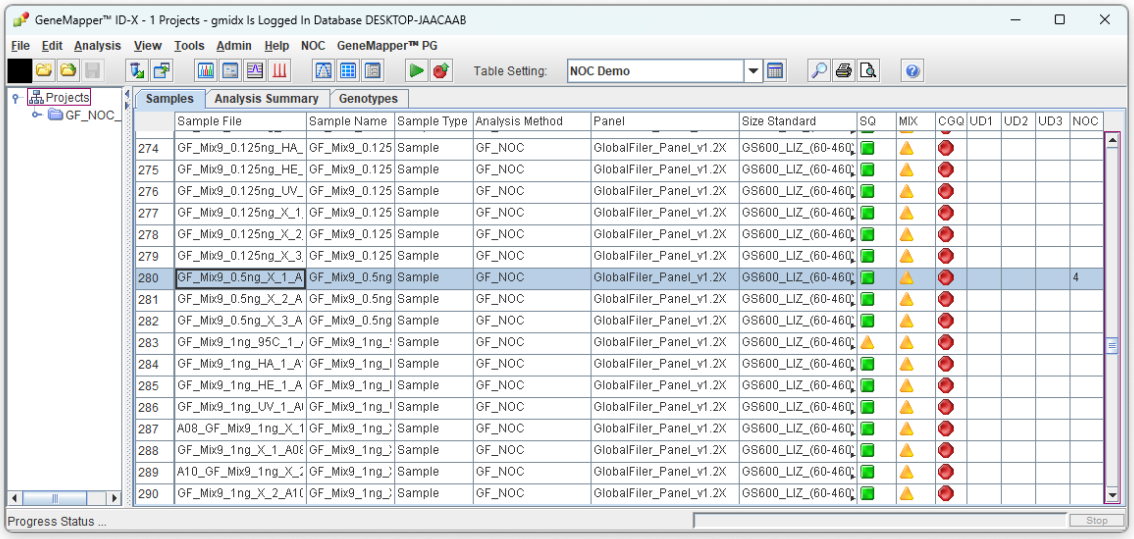


Figure 9 NOC value in the default NOC column of the Samples table.

4. Save the project to maintain the NOC value.

Maximum Allele Count (MAC) algorithm

The Maximum Allele Count (**MAC**) algorithm is the simplest method of estimating the number of contributors to a mixed DNA sample. Most individuals show either one peak at a locus (homozygous) or two peaks at a locus (heterozygous). The following general rules can be applied:

- At most, 2 alleles at a locus indicates a single source DNA profile (NOC = 1).
- At most, 4 alleles at a locus indicates a two-person DNA mixture (NOC = 2).
- More than 4 alleles at a locus indicates more than two (2) contributors to the mixture.

MAC analysis results are shown in 2 plots: **MAC vs ph** and **MAC vs %**.

- The **MAC vs ph** plot shows the maximum allele count observed at any locus versus peak height in relative fluorescence units (RFU) (see Figure 10).
- The **MAC vs %** plot shows the maximum allele count versus peak height, expressed as a percentage of the mean peak height for each locus (see Figure 11).

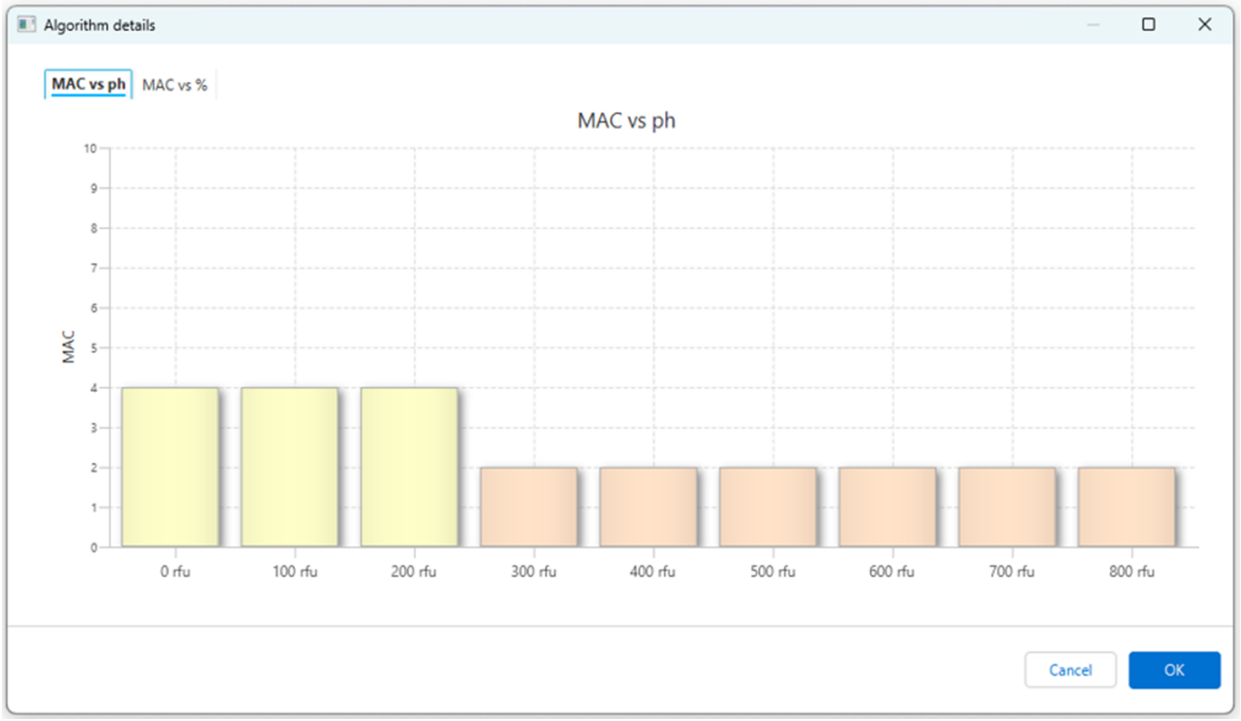


Figure 10 MAC vs ph plot

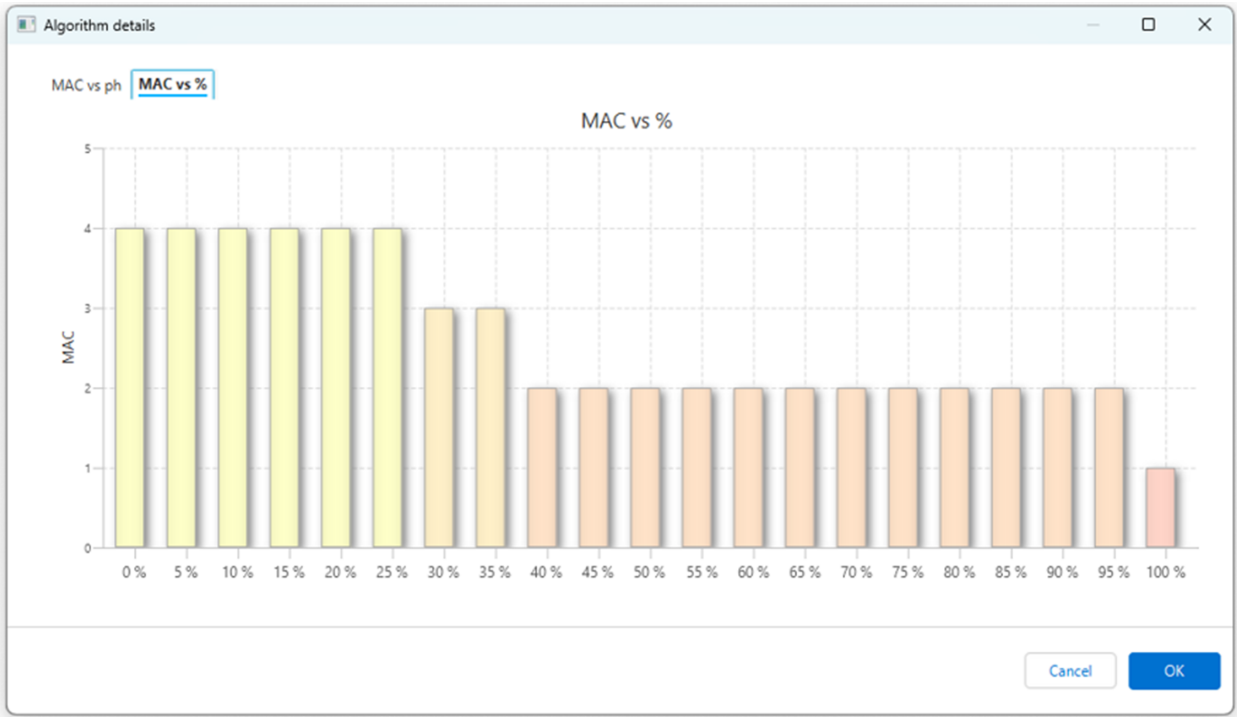


Figure 11 MAC vs % plot

Total Peaks algorithm

The **Total Peaks** algorithm assumes that mixed samples with more peaks are likely to have more contributors. The software simulates mixed samples (default: 1,000) with known 1, 2, 3, and 4 contributors and the following properties:

- The selected population
- The approximate amount of DNA in the sample (estimated by peak height)
- The selected stutter and drop-in/drop-out models
- The analytical threshold and other filter settings
- The level of degradation observed in the sample

The software then plots total peak count versus number of contributors for the simulated profiles. It overlays the actual peak count of the sample as a red line (known peaks, unknown contributors) and compares it to the simulated totals for each contributor count (see Figure 12).

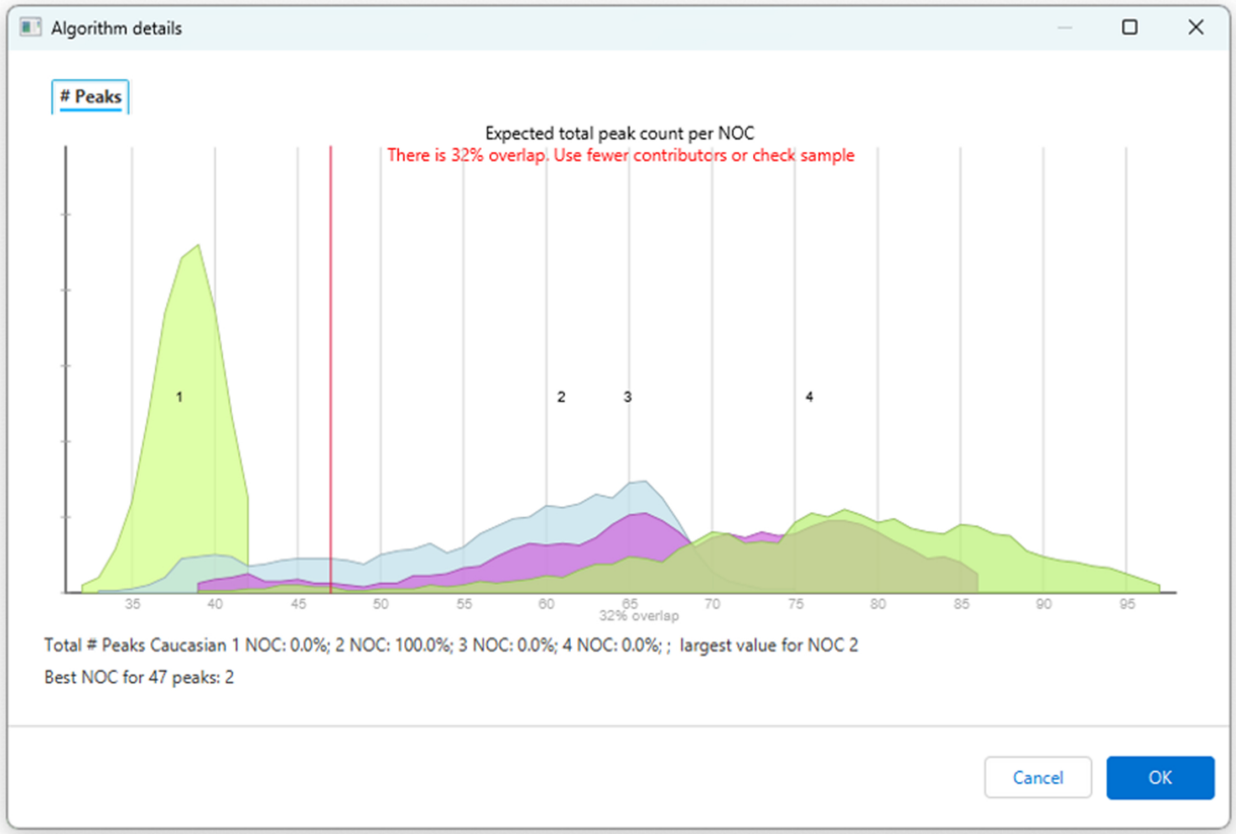


Figure 12 # Peaks plot

For more information about NOC estimation using the **Total Peaks** algorithm, see the *GeneMapper™ PG Software v1.0 Getting Started Guide* (Pub. No. MAN1000548).

Decision tree algorithms

Decision trees are a machine learning approach for classification—they identify unknowns by comparing their features to a large set of examples. In GeneMapper™ *ID-X* Software NOC v1.0, the classification task is to estimate the number of contributors (NOC) in an unknown sample.

The NOC plugin uses 2 decision tree approaches:

- **Fixed Decision Tree**
  - Always has the same structure (branches and features).
  - Based on a published method of NOC analysis recommended within the forensic community.
  - In some forensic data analysis software, it may be the only method of NOC analysis used.

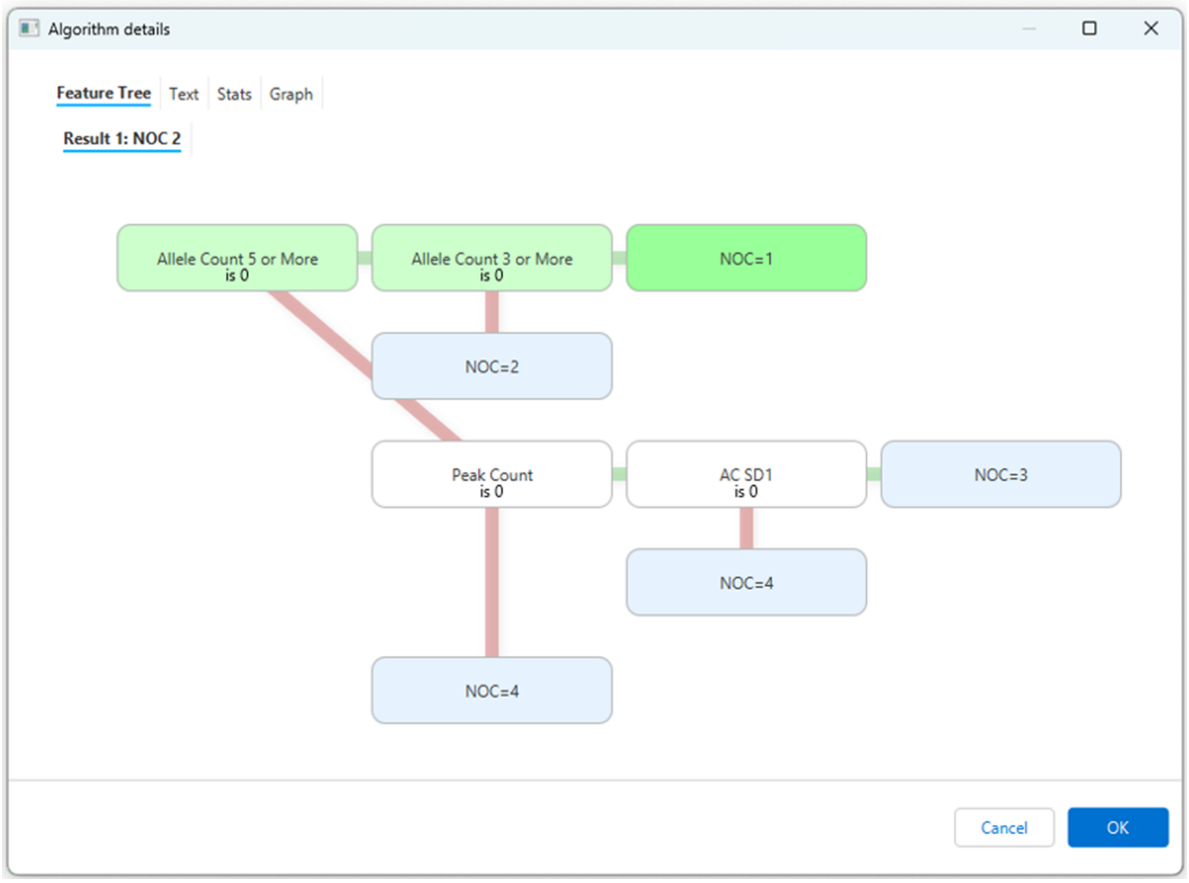


Figure 13 Fixed Decision Tree algorithm details The **Fixed Decision Tree** algorithm optimizes the thresholds of the fixed tree but leaves the tree structure as it is. A user can follow the branches and features to arrive at a classification.

- **TFSPlus Decision Tree**
  - Developed by Thermo Fisher Scientific.
  - Uses the NOC base model to simulate thousands of random samples that match the properties of the unknown sample, then builds a decision tree from these simulations.
  - Because it relies on simulated samples, the tree can be different for each run and each unknown sample.

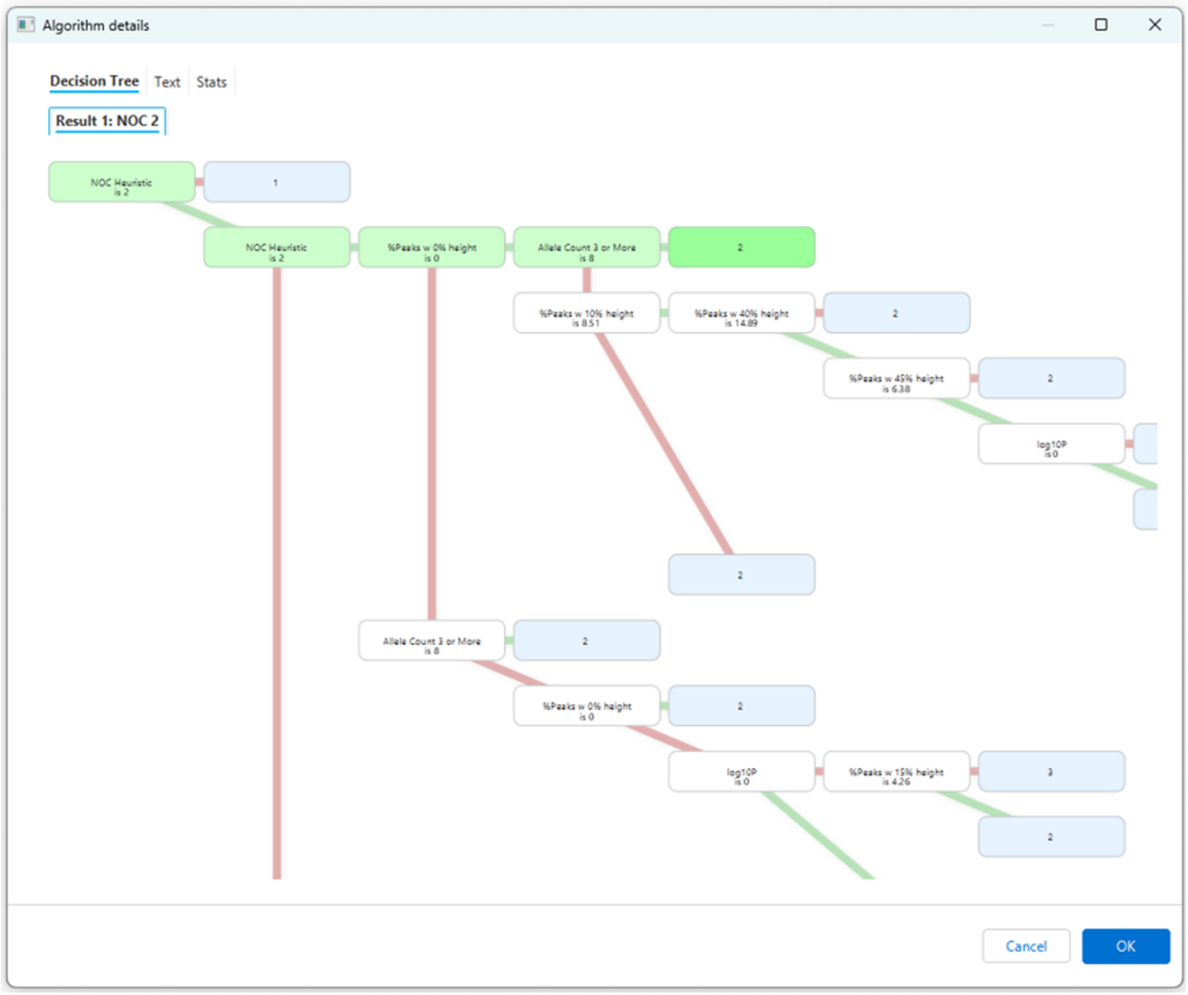


Figure 14 TFSPlus Decision Tree algorithm details The **TFSPlus Decision Tree** can change structure and is drawn based on the results of the simulated samples. A user can follow the branches and features to arrive at a classification.

GeneMapper™ *ID-X* Software v1.7.3 and NOC v1.0 verification

Table 3 Test cases performed

Test	Test description	Result
Software performance	The GeneMapper™ *ID-X* Software v1.7.3 patch will improve application performance for the following: • Sample/Project importing • Project opening • Saving and exporting • Sample analysis (analyze project) • Reanalysis • Editing	Pass

Table 3 Test cases performed *(continued)*

Test	Test description	Result
Software regression	Software regression testing[1]	Pass
NOC Analysis	User can perform NOC analysis on a selected sample, multiple selected samples, or all samples within a project.	Pass
NOC Concordance	User can generate NOC estimations equivalent to those produced by GeneMapper™ PG Software v1.0 for 2, 3, 4, and 5 contributor mixed DNA profiles.	Pass
NOC Consensus	Comparison of NOC estimation to the true number of contributors for the evaluated sample.	Pass

[1] For more information, see the GeneMapper™ *ID-X* Software v1.7.3 and NOC v1.0 release notes.

Table 4 Computers used for verification testing

Make/model	Operating System (OS)	Processor (CPU)	Memory	Testing type
Dell Latitude 9430	Windows™ 11 Enterprise	12th Gen Intel Core i7 1.80 GHz with 10 cores	16 GB	Software verification
Dell Latitude 5420	Windows™ 11 Enterprise	11th Gen Intel Core i7 3.0 GHz with 4 cores	32 GB	Software verification
Dell Latitude 5420	Windows™ 11 Enterprise	11th Gen Intel Core i7 3.0 GHz with 4 cores	32 GB	Software verification
Dell Latitude 5420	Windows™ 11 Enterprise	11th Gen Intel Core i7 3.0 GHz with 4 cores	32 GB	Software verification
Dell Precision 7560	Windows™ 10 Professional	10th Gen Intel Core i7 2.7 GHz with 6 cores	32 GB	Software and NOC verification
Dell Precision 5550	Windows™ 11 Enterprise	11th Gen Intel Core i7 2.5 GHz with 8 cores	16 GB	NOC verification

Verification testing results

Software performance

Large project sizes significantly affect system performance when you import samples, and open, save, export, and analyze projects with many samples. Database performance decreases as the number of samples increases. Comparisons between databases with 100,000 samples and 298,000 samples, and projects with 10 samples and 300 samples, show a significant performance improvement with GeneMapper™ *ID-X* Software v1.7.3 compared to GeneMapper™ *ID-X* Software v1.7. For more information, see the following table.

Table 5 GeneMapper™ *ID-X* Software v1.7 and GeneMapper™ *ID-X* Software v1.7.3 performance testing results

Samples in project	Software version	Import samples	Open project	Save as project	Export project	Import project	Analyze project
Database size (samples): 100,000							
10	1.7	1 second	5 seconds	15 seconds	5 seconds	20 seconds	28 seconds
	1.7.3	1 second	4 seconds	8 seconds	4 seconds	10 seconds	18 seconds
300	1.7	7 seconds	1 minute, 10 seconds	2 minutes, 32 seconds	1 minute, 55 seconds	5 minutes, 21 seconds	10 minutes, 15 seconds
	1.7.3	5 seconds	45 seconds	1 minute, 40 seconds	1 minute, 25 seconds	5 minutes, 5 seconds	5 minutes, 39 seconds
Database size (samples): 298,000							
10	1.7	1 second	10 seconds	20 seconds	10 seconds	25 seconds	2 minutes
	1.7.3	1 second	3 seconds	3 seconds	5 seconds	5 seconds	3 seconds
300	1.7	10 seconds	5 minutes	7 minutes	4 minutes	11 minutes	2 hours, 22 minutes
	1.7.3	5 seconds	4 minutes	30 seconds	2 minutes	5 minutes	4 minutes

Note: Testing was performed using a computer with 32 GB installed memory.

NOC v1.0 concordance and consensus

All NOC estimations were performed using the **AB_GlobalFiler** normalized Caucasian population database and default GeneMapper™ PG Software v1.0 parameters and built-in base model. The following NOC v1.0 estimation algorithms are present in GeneMapper™ PG Software and were tested for concordance:

- Maximum Allele Count (MAC)
- Total Peaks
- Decision Tree (TFSPlus Decision Tree)
- Fixed Decision Tree

The following data sets and analysis settings were used in the NOC v1.0 testing:

Table 6 Data sets and analysis settings used in the NOC v1.0 testing

GeneMapper™ *ID-X* Software and NOC version	GeneMapper™ PG Software version	STR kit	Data and formats	Analysis settings
1.7.3 and 1.0	1.0	GlobalFiler™	GMIDX: PG Developmental Validation .hid and .fsa files GMPG: PG Developmental Validation Genotype table with stutter Combined .csv for GMPG	GMIDX: Default plus AT:20 GMPG: Default

Concordance testing was performed between GeneMapper™ *ID-X* Software NOC v1.0 and GeneMapper™ PG Software v1.0. The shared NOC algorithms are identical in both software versions (GeneMapper™ PG Software also includes additional NOC algorithms). Algorithms that use simulation data can produce slightly different results each time the analysis is repeated due to variations in the profiles simulated.

Results of the NOC v1.0 validation testing showed concordance between NOC v1.0 for GeneMapper™ *ID-X* Software and GeneMapper™ PG Software, with exceptions noted for NOC algorithms employing simulated DNA profiles. NOC v1.0 consensus testing also showed concordance to the true number of contributors for all 2, 3, 4, and 5 contributor mixed DNA samples.

Only the **AB_GlobalFiler** normalized Caucasian allele frequencies (present in both GeneMapper™ *ID-X* Software and GeneMapper™ PG Software) were used during NOC v1.0 verification testing. Each mixture included at least one contributor of Caucasian ancestry.

Conclusions

- The features and updates introduced in GeneMapper™ *ID-X* Software v1.7.3 were successfully and correctly implemented without adverse effects on other software functionality.
- GeneMapper™ *ID-X* Software performance was improved with the v1.7.3 patch. For updated minimum and recommended computer specifications, see the GeneMapper™ *ID-X* Software v1.7.3 and NOC v1.0 release notes.
- GeneMapper™ *ID-X* Software v1.7.3 with the NOC plugin can be used to estimate the number of contributors (NOC) to mixed DNA profiles of 2, 3, 4, and 5 contributors. Concordance with GeneMapper™ PG Software NOC v1.0 was demonstrated.

Based on the nature of the modifications addressed in this update, and the testing performed, we recommend that you evaluate this software as it pertains to your 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.

Note: If validating GeneMapper™ *ID-X* Software v1.7.3 NOC v1.0 against GeneMapper™ PG Software, it is important to maintain analysis method settings between sample analyses to ensure consistency in peak height calculations and subsequent NOC analysis.

GeneMapper™ *ID-X* Software v1.7.4

GeneMapper™ *ID-X* Software v1.7.4 is a patch for GeneMapper™ *ID-X* Software v1.7.3.1.

Software features in GeneMapper™ *ID-X* Software v1.7.4

Data file integrity check

In GeneMapper™ *ID-X* Software v1.7.4, the software adds additional features to check for data file integrity. The software handles data files based on the instrument software version that created the files.

Table 7 File check behavior by instrument software version

Data file source		GeneMapper™ *ID-X* Software action
Instrument software	**Software version**	
SeqStudio™ Flex Series Instrument Software	v1.2.1	GeneMapper™ *ID-X* Software verifies data integrity by checking that the certificate in the data file is trusted. If the certificate in a data file matches a known certificate, the data file is imported. If a data file contains an unknown certificate or has a failed data integrity check, an administrator-level user can import the data.
SeqStudio™ Data Collection Software	v1.2.6	
3500 Series Data Collection Software	v4.0.3	
3730*xl* Data Collection Software	v5.0.3	
Any instrument software listed above	Files created with earlier software versions	The software prompts you to choose whether to import data with no certificate.

Add samples from sample files

In GeneMapper™ *ID-X* Software v1.7.4, the procedure to add samples includes an additional data file integrity check. Use the following steps to import data files. If applicable, you can choose whether to import files created with earlier versions of instrument software.

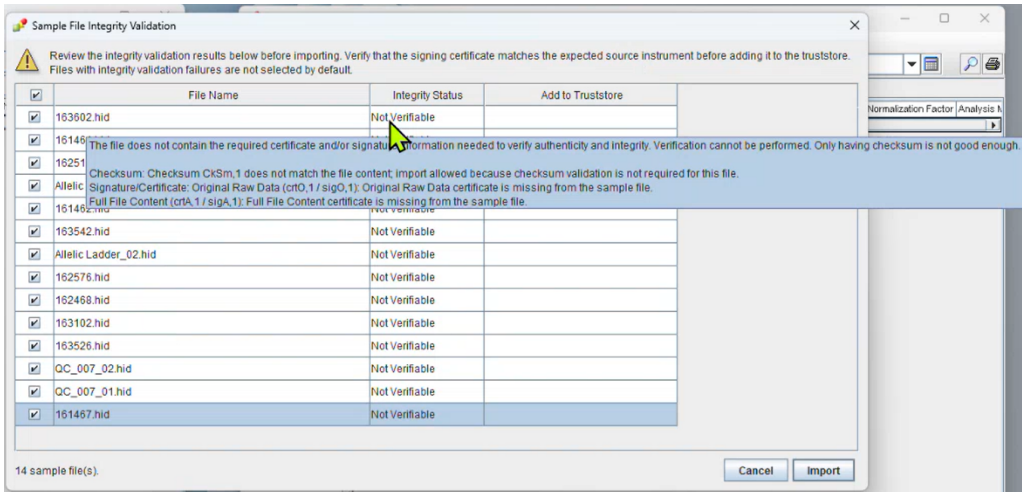
1. Click **(Add Samples to Project)**.
2. Select the **Files** tab (default selection), then navigate to the folder that contains the sample files.
3. Select a folder (or select individual files using **Ctrl+Click**), then click **Add To List**.
4. In the **Sample file Integrity Validation** window, you can view file certificates, if available, and determine whether to proceed with file import based on the file integrity status.

   The **Sample file Integrity Validation** appears if one of the following conditions is present:

   - The data files were created in an earlier instrument software version. See Table 7.
   - The certificate for the data file is absent.
   - The certificate for the data file has an integrity issue.

   a. Review the file integrity status.

   Tip: Place the pointer over the integrity status to view more information.



   b. If a file certificate is available, an administrator can view, then add the certificate to the truststore.

   c. Select the files you trust.

   d. Click **Import**.

5. Click **Add**.

Certificate status

Status	Description
Trusted	The signature is valid and the certificate is trusted.
Verified	The signature is valid and a certificate is present, but the certificate is not yet in the trust store.
Not Verifiable	No usable signature or certificate is present.
Integrity Failed	The signature, certificate, algorithm, configuration, or validation check fails.

GeneMapper™ *ID-X* Software v1.7.4 verification

GeneMapper™ *ID-X* Software v1.7.4 does not modify the analysis algorithms of the software.

Functional testing was performed to verify the changes implemented in GeneMapper™ *ID-X* Software v1.7.4. Test data was generated on the following genetic analyzers, then analyzed using GeneMapper™ *ID-X* Software v1.7.4:

- SeqStudio™ 8 Flex Genetic Analyzer
- SeqStudio™ 24 Flex Genetic Analyzer
- SeqStudio™ Genetic Analyzer—2 instruments
- 3500 Genetic Analyzer
- 3500xL Genetic Analyzer
- 3730*xl* DNA Analyzer—2 instruments

Testing included representative human identification workflows using samples prepared with the GlobalFiler™ IQC PCR Amplification Kit. The samples included no-template controls (NTCs), control DNA at an input amount of 1 ng, and allelic ladders. The results verified that the new security features and other functionality introduced in GeneMapper™ *ID-X* Software v1.7.4 operated as intended, with no adverse impact on existing features or workflows.

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 Software features, Verification, and Validation User Bulletin	MAN0029209
GeneMapper™ ID-X Software v1.7 and NOC v1.0 Release Notes	**A40007529**
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 1.7.3	NA

Customer and technical support

For support, use one of the contact methods listed below, depending on your location.

Location	Contact method
In North America	Send an email to: **HIDTechSupport@thermofisher.com**
	Call **888-821-4443**; select option **2**, say "Application Support", then say "HID" or "Human Identification".
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 its affiliates 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 questions, contact Life Technologies at **www.thermofisher.com/support**.

Life Technologies Corporation | 6055 Sunol Blvd | Pleasanton, California 94566 USA
For descriptions of symbols on product labels or product documents, go to thermofisher.com/symbols-definition.

Revision history: MAN0029209 C (English)

Revision	Date	Description
C	28 July 2026	Updated for GeneMapper™ *ID-X* Software v1.7.4.
B	26 September 2025	• Patches and new features were added for GeneMapper™ *ID-X* Software v1.7. • Minor updates were made for consistency of style and terminology.
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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