applied biosystems

GeneMapper™ PG Software v1.0

GETTING STARTED GUIDE

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Revision A

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

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Revision history: MAN1000548 A (English)

Revision	Date	Description
A	25 June 2025	New getting started guide for GeneMapper™ PG Software v1.0.

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

Contents

1 About the software

The purpose of the GeneMapper™ PG Software is to analyze multiple evidence and reference samples to find potential leads.

The software can be used to help answer the following questions:

- Is a person of interest (POI) part of this mixture?
- How does the likelihood ratio change if the POI is replaced by an unknown contributor?
- What are the individual profiles (deconvolution) of an evidence sample?
- How many contributors does this sample have?

For many evidence samples, there can be additional questions:

- Which evidence samples contain potential persons of interest (POIs)?
- Which POIs are promising leads?
- What do two samples have in common (that is, do they contain a common POI)?

Supported file types

GeneMapper™ PG Software v1.0 supports multiple file types. For example:

- SER project files from the GeneMapper™ *ID-X* Software
- XML files from CODIS
- CMF files from CODIS v3.3
- CSV and TXT files from a variety of applications, such as GeneMapper™ *ID-X* Software and Microsoft™ Excel™ Software

At a minimum, the files must include sample names, marker names, alleles, and peak heights.

Standard workflow

GeneMapper™ PG Software

Install the software

1. Install the software (“Install GeneMapper™ PG Software v1.0” on page 11).
2. Sign in the software (“Sign in the software the first time” on page 16).
3. Activate your license (“Activate a license before using the software” on page 17).

Set up the software

1. Configure electropherogram (EPG) settings (“Configure electropherogram (EPG) settings” on page 19).
2. Configure other software settings (see “Configure the software settings” on page 21).

Create a project

1. Import profiles (samples), and set the samples as reference or evidence profiles (“Import samples” on page 53).
2. *(Optional)* Tag samples (“Manage samples (Actions button)” on page 64). Tagging allows you to group samples, which can be helpful for running memory-intensive algorithms like automate, or for comparing specific kinds of samples.
3. Edit sample details; for example, edit the amount of DNA, initial NOC (“Edit sample summary (Sample Details tab)” on page 59).

Perform NOC analysis

1. Select a scenario and settings (see the software help).
2. Select and run the NOC algorithms (“Start the NOC analysis” on page 73).
3. View results (“View the NOC analysis results” on page 74).

Perform deconvolution

1. Select a scenario and settings (“Configure the deconvolution settings” on page 81). When you enter the NOC for the deconvolution, base it on the previous NOC analysis.
2. Run the deconvolution algorithm (“Start deconvolution” on page 82).
3. View results (“View the deconvolution results” on page 82).
4. Perform actions as needed (“Perform actions as needed” on page 85). For example:
   - Add derived profiles as reference or evidence profiles.
   - Find reference profiles based on the deconvoluted profiles.
   - Compare degradation charts of evidence with the extracted contributor profiles.

GeneMapper™ PG Software

Determine the likelihood ratio (LR)

1. Select a scenario and settings (“Configure the LR settings” on page 93).
2. Calculate the likelihood ratio (“Start or stop the LR calculation” on page 95).
3. View results (“View the LR results” on page 96).

Determine the robustness of the LR

1. Update the robustness parameters and/or select a new scenario and settings in the LR screen (“Update the parameters for robustness” on page 107 and/or “Configure the LR settings” on page 93).
2. Run the robustness algorithm (“Start or stop the robustness calculation” on page 107).
3. View results (“View the robustness results” on page 105).

2 Installation requirements

Requirements

Component	Minimum requirement	Recommended specification
Processor	1.8 GHz	3.0 GHz or greater
RAM	16 GB	32 GB or greater
Operating System	64-bit, x64-based processor	

Required time for full installation

The amount of time required to perform a full installation is approximately 15 minutes, depending on the speed of the computer.

Compatible instruments and software

GeneMapper™ PG Software supports data generated on the following Thermo Fisher Scientific instruments and corresponding Data Collection Software:

Instrument	Data Collection Software
SeqStudio™ Flex Series Genetic Analyzer	Data Collection Software v1.1.1
SeqStudio™ Genetic Analyzer	Data Collection Software v1.2.1
3500/3500xL Genetic Analyzer	3500 Data Collection v1.0, v2.0, v3.0, or v4.0

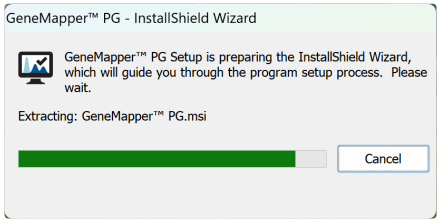
3 Installation overview

The following sections provides detailed instructions to install and set up GeneMapper™ PG Software v1.0.

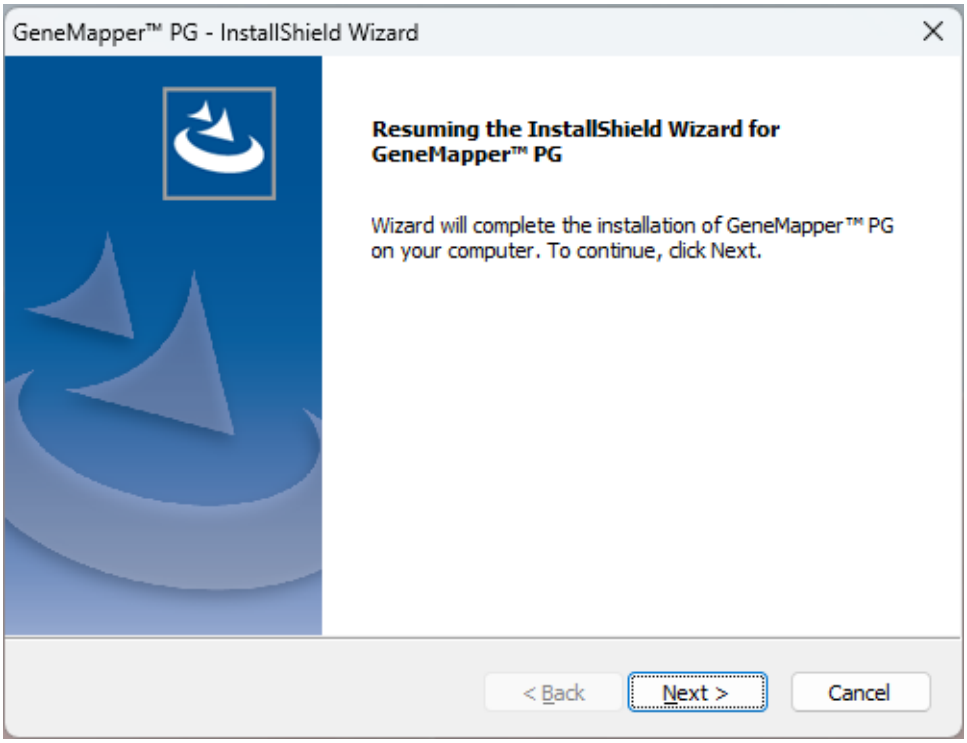
During installation, you can install an optional plugin which allows for seamless integration of the software with GeneMapper™ *ID-X* Software. With the optional plugin installed, you can export samples from GeneMapper™ *ID-X* Software version 1.7 or later directly to GeneMapper™ PG Software.

Install GeneMapper™ PG Software v1.0

1. Download and unzip the installer (`GeneMapper_PG.exe`).
2. Right-click the installer and select **Run as administrator**.

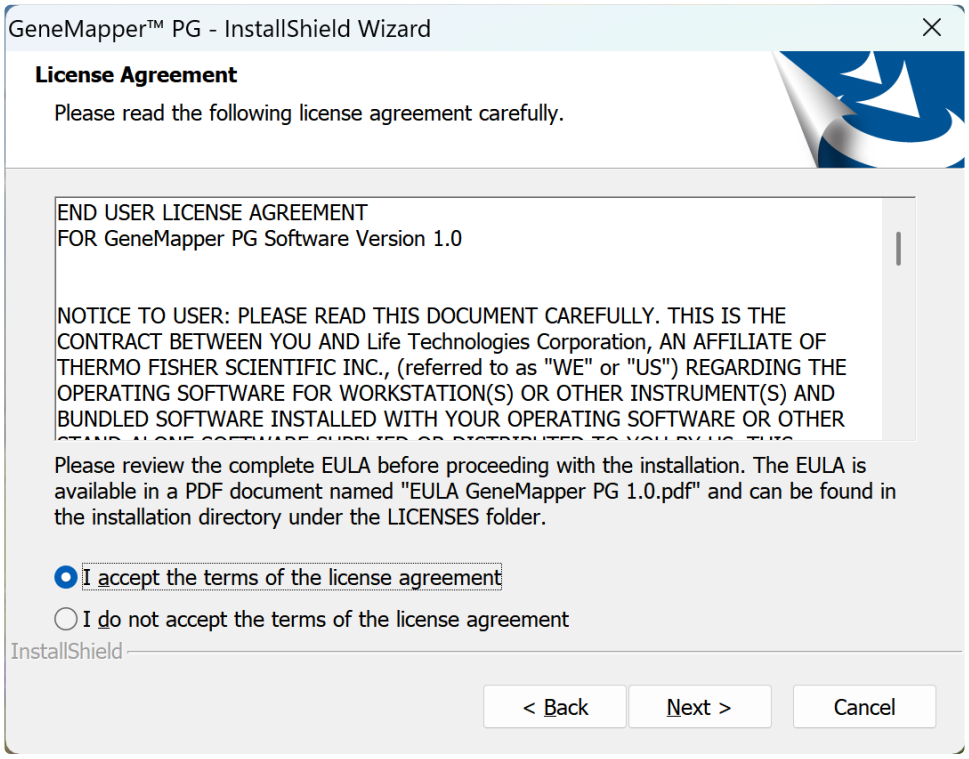


3. In the **Welcome** window, click **Next**.



4. In the **License Agreement** screen, perform the following actions.
   a. Read the agreement.
   b. Select **I accept the terms of license agreement**.

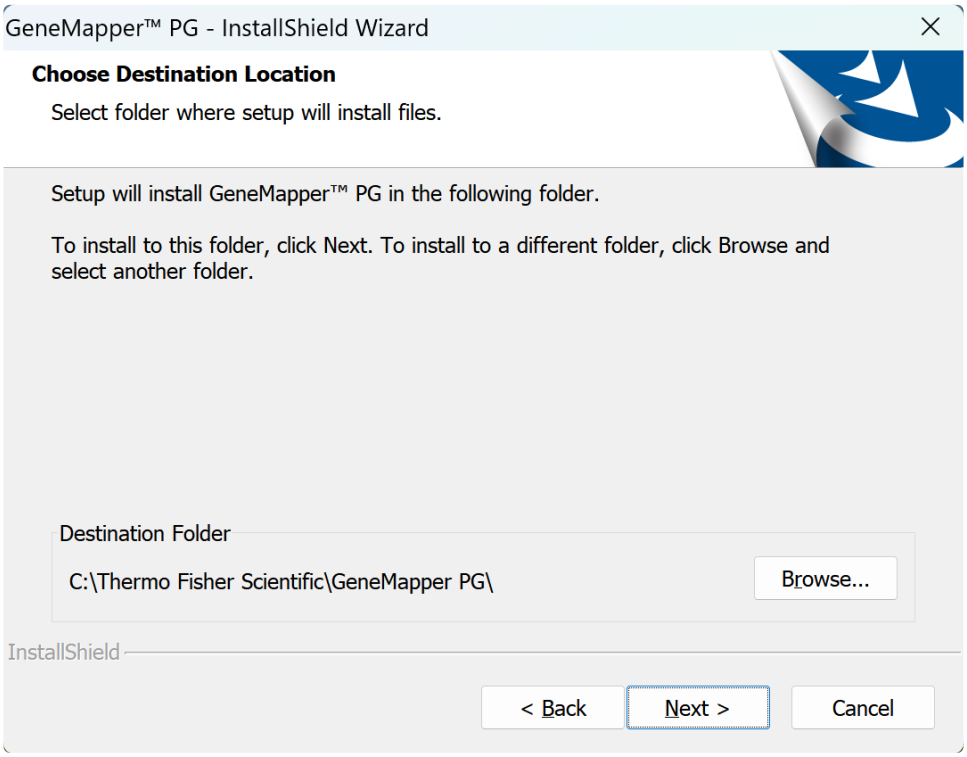
c. Click **Next**.



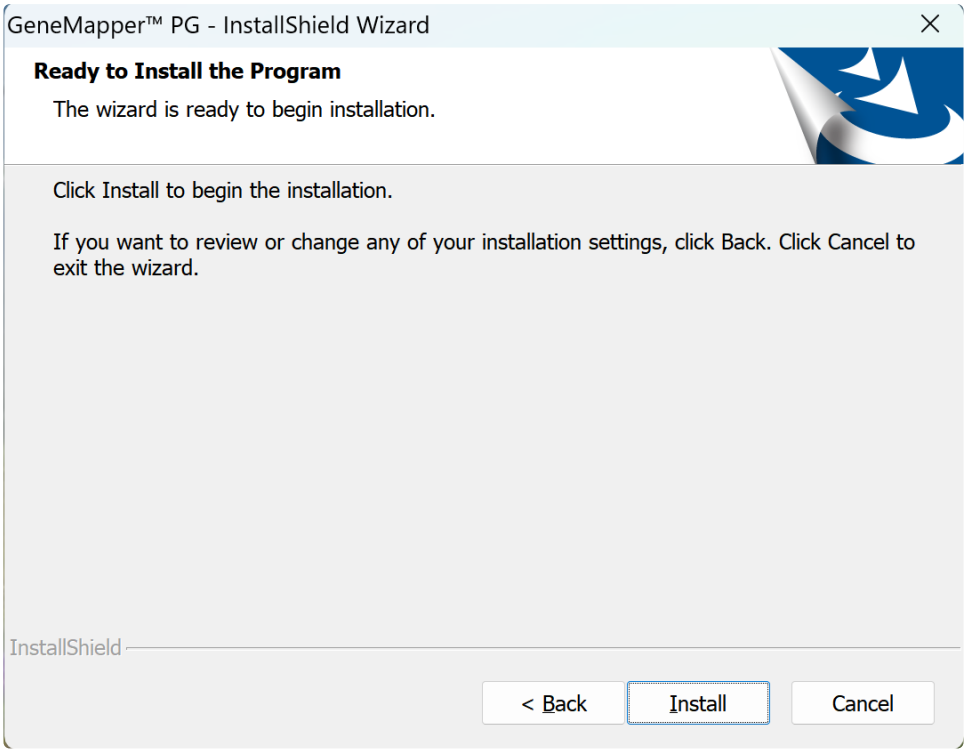
5. Click **Next** to install the software to the default location.

   To install the software to a drive different from the default drive, select a destination folder with ≥10 GB of free space, then click **Next**.

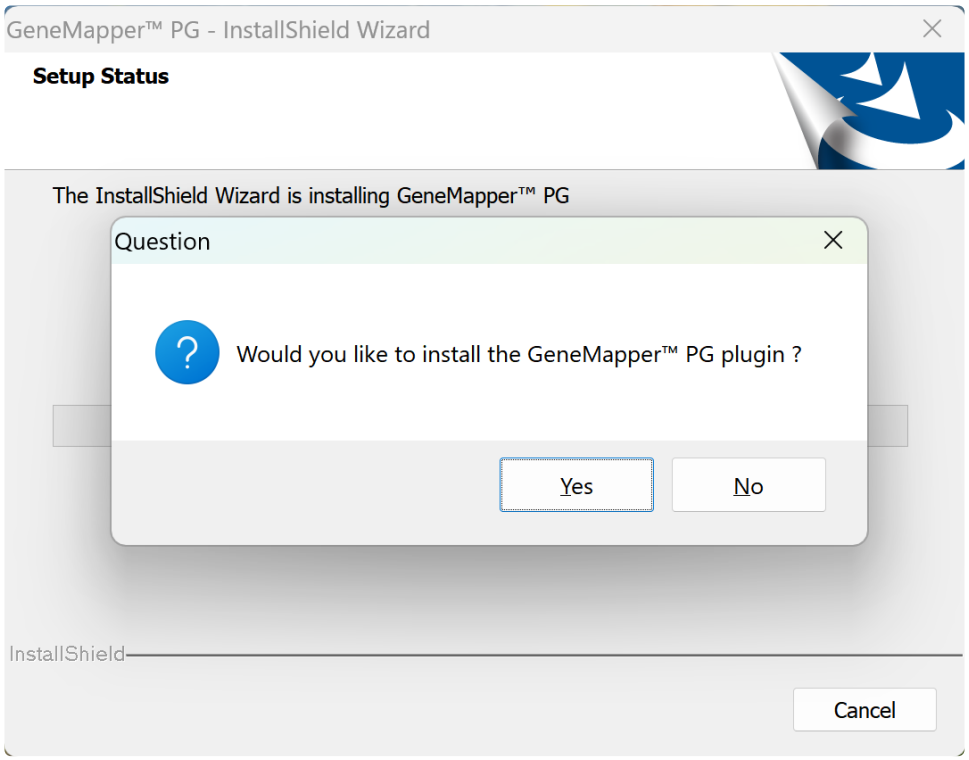
IMPORTANT! If you select an invalid destination (such as A: drive or CD-DVD ROM) and click **Next**, an invalid drive error message is displayed. When you click **OK**, the installation stops. To recover, click **Cancel**, then start the installation over again using a valid destination folder.



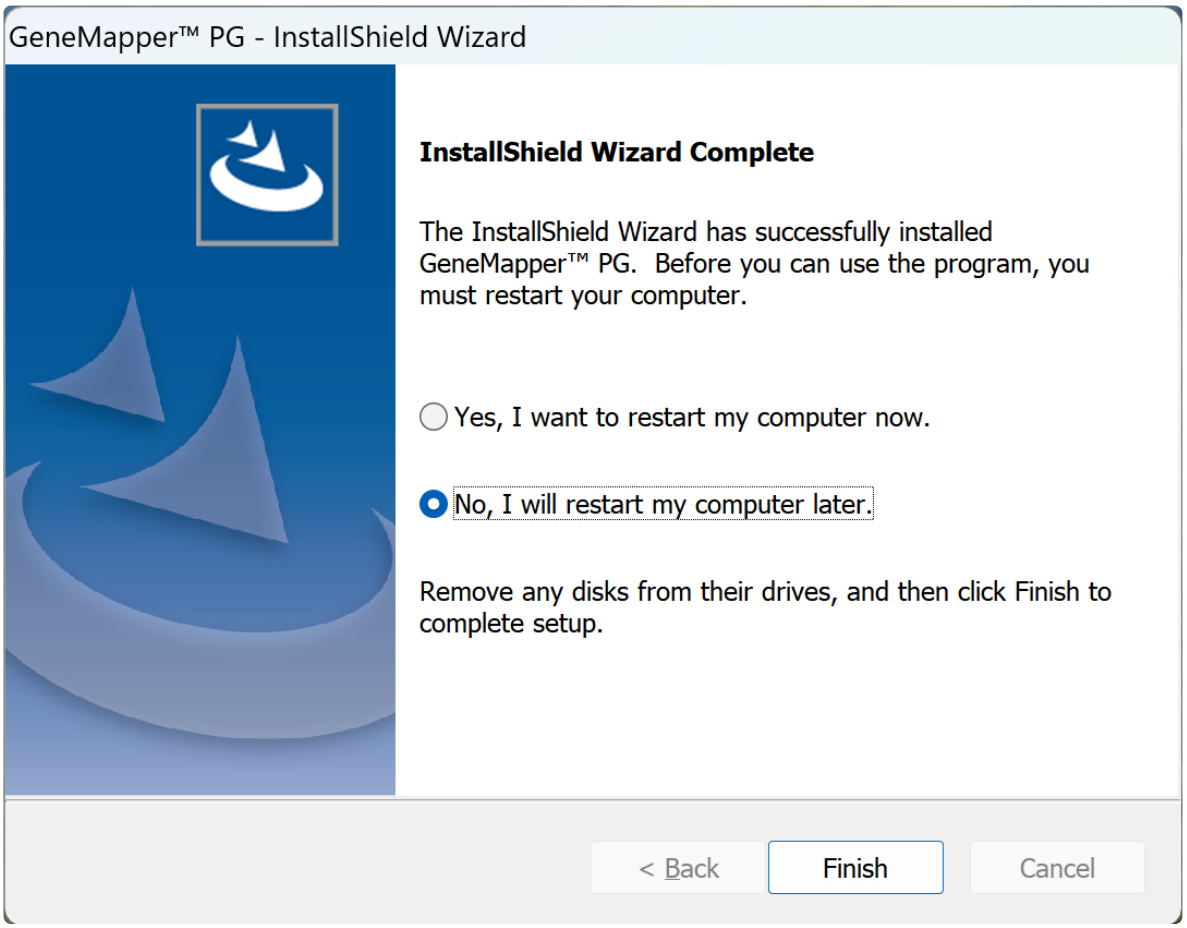
6. To begin the installation, click **Install**.



7. To install the optional plugin for exporting samples from GeneMapper™ *ID-X* Software directly to GeneMapper™ PG Software, click **Yes**.



8. In the **InstallShield Wizard Complete** window, select **Yes, I want to restart my computer now**, then click **Finish**.



Sign in the software the first time

1. On the desktop, double-click the software icon to start the software.
2. Select the desired user mode.

User modes and levels

The software provides different user modes and user levels that allow or prevent access to several software features. Users can select the user mode and user level that best suits their needs.

User modes

User mode	Description
User	Standard laboratory users.
Training	Users who are training on the software, or users who are testing software settings. Training mode settings are saved separately and do not affect User or Validation mode settings.
Validation	Advanced laboratory users. **IMPORTANT!** This document is written for the Validation mode. If you are signed into the software with a different user mode, the software screens may display different items or options.

User levels

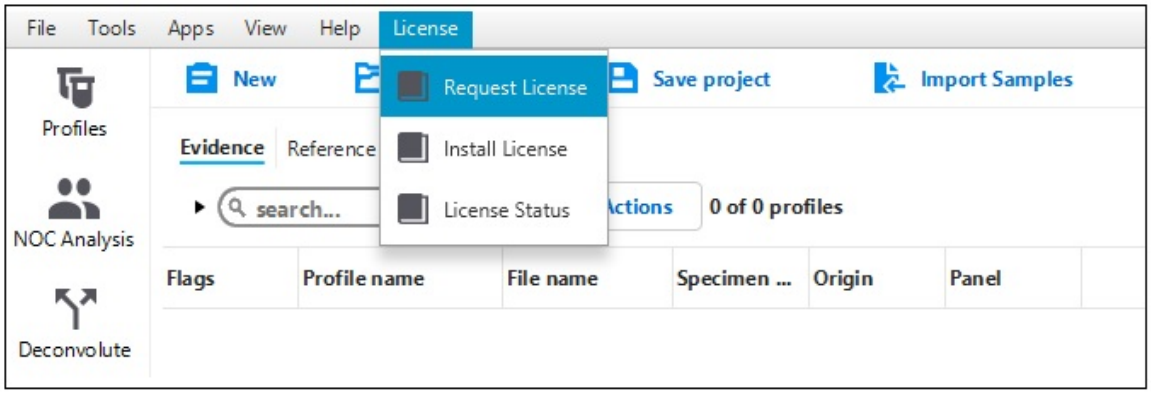
In the **Settings** screen, the user level that you select determines the settings that you can configure. The user levels are:

- **Standard**
- **Advanced**
- **Expert**

To view the settings that can be configured at each user level, see the software help system.

Activate a license before using the software

1. Start the software.
2. In the navigation pane, at the top of the screen, select **License** ▸ **Request license**.



3. In the Thermo Fisher Scientific Licensing Portal, enter the activation ID for the platform, then click **Download License Request File** to generate a license file.

4. If you are not using the default folders, move the response BIN file to the same folder as the request BIN file.

5. At the top of the screen in the software, select **License ▸ Install license**.

   Install the license file within 24 hours of generating the license file.

After the license is active, the full functionality of the software is available.

For help, email the license request and response files to **techsupport@thermofisher.com** or to your local Thermo Fisher Scientific representative.

4 Get started

Sign in the software

1. On the desktop, double-click the software icon to start the software.
2. Select the user mode.
3. If the software has been used before on the computer, select from the following options.

Option	Description
Continue from my last point	Reopen the project that was last open so that you can immediately continue working on the same samples.
Start with a clean slate	Open the software with a blank, empty project.

Configure electropherogram (EPG) settings

IMPORTANT! Not all EPG options are available in all screens.

1. Above the electropherogram, click **EPG Settings** to open the **EPG Settings** dialog box.
2. Select a peak style:
   - **EPG**—Standard electropherogram view, similar to the GeneMapper™ *ID-X* Software.
   - **BAR**—Bar graph view; this view can make it easier to see the relative fluorescence unit (RFU) of each peak.

3. *(For EPGs that show multiple contributors)* Select contributors and colors.
   a. Select (☑) or deselect (☐) the contributors to overlay in the EPG.
   b. To change the contributor color: Right-click the color square. In the dialog box, select a color from the dropdown list, then click **OK**.
4. Select (☑) or deselect (☐) the options to display in the EPG.
   - **Show AT** (analytical threshold)—Analytical threshold. The minimum RFU required to consider any peak (in addition to the locus-specific values). Signal greater than this value can indicate an allele or an artifact.
   - **Show Pop Freq** (population frequency)—The frequency at which an allele (the peak) is seen in a population.
   - **Show Dropin threshold**—The level below which a peak can reasonably "drop in" to the profile; that is, the peak will appear in the profile.
   - **Show Dropout threshold**—The level below which a peak can reasonably "drop out" of the profile; that is, the peak will not appear in the profile.
   - **Show PHR** (peak height ratio)—The ratio between a peak and the tallest peak in a locus.
   - **Show Nr Peaks**—The total number of peaks.
5. Select (☑) or deselect (☐) more details.
   - **Show detailed pane**
   - **Show Mean PH detail** (peak height)
   - **Show Dropin detail**
   - **Show Dropout detail**
   - **Show Nr Peaks detail** (number of peaks)
   - **Show Scores detail**
   - **Show Overall Scores detail**
   - **Show Peak/Allele details**
   - **Show AT detail** (analytical threshold)
   - **Show Contributor details**
6. Click **OK** to save the changes.
   Saved changes are applied to all EPGs in the software. Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

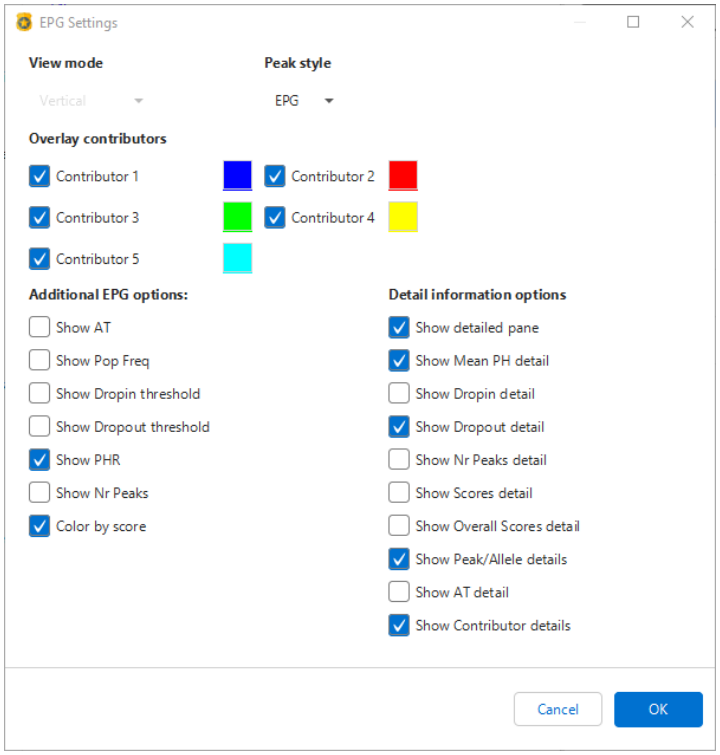


Figure 1 EPG example This is the **EPG Settings** dialog box that is displayed from the **Settings** screen. Not all EPG options are available in all screens.

Configure the software settings

IMPORTANT! The software settings are universal. That is, the same settings apply to all users and all projects in your laboratory.

Display the Settings screen

1. In the navigation pane, select **Configure** ▸ **Settings**.
2. *(Optional)* In the left pane, select a category of settings to display.
   - **All** (default selection)
   - **General**
   - **Model**
   - **Import and Export**
   - **Analysis**
   - **GMID-X Settings** (GeneMapper™ *ID-X* Software settings)
   - **Project Settings**
   - **GUI**

3. *(Optional)* In the **Settings** screen toolbar, select a view mode:
   - **Table View** (default selection)
   - **Forms View**

4. If you are signed into the software in Validation mode, you can access the items and tasks shown in the **Settings** screen.

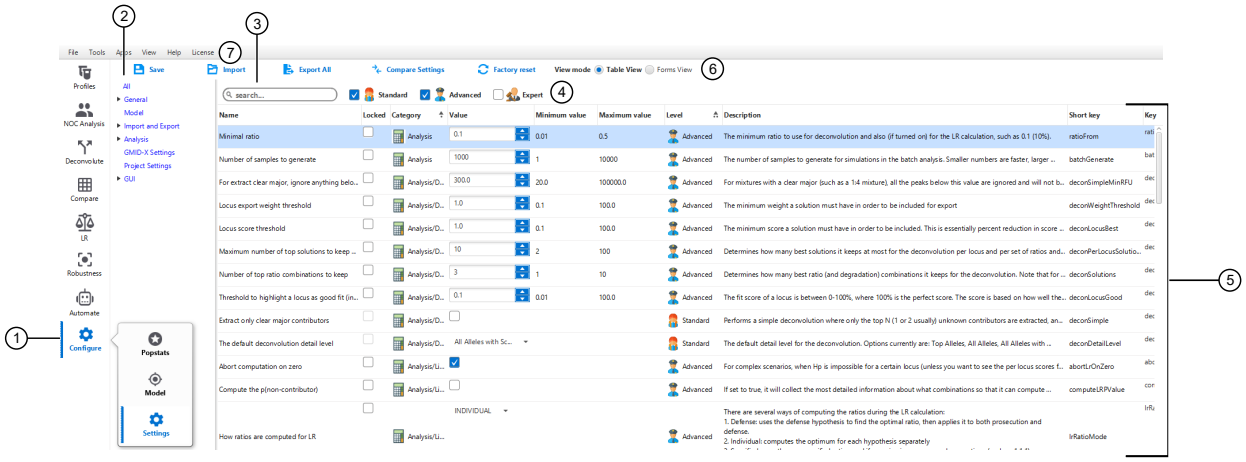


Figure 2 Settings screen

1. **Configure** app; select **Settings**
2. Select a category of settings to display; to configure the settings, see the following procedures:
   - "Configure general settings" on page 23
   - "Configure universal model settings" on page 26
   - "Configure import and export settings" on page 31
   - "Configure analysis settings" on page 36
   - "Configure GMID-X settings" on page 46
   - "Configure project settings" on page 48
   - "Configure GUI settings" on page 49
3. Search the settings table
4. Select a user level
5. Displays the current software settings; see "Settings table" on page 22
6. **Settings** screen toolbar.
7. Menu bar

Settings table

Item	Description	Editable field
Name	The setting name.	No
Locked	Determines whether the setting can be changed: • Enable (☑ 🔒) to prevent users from editing the **Value** column settings. • Disable (☐) to allow users to edit the **Value** column settings.	Yes
Category	The category of software functions that the setting applies to (for example, **Analysis** or **Model**).	No
Value	The setting value.	Yes
Minimum value	The minimum value that can be assigned to the setting.	No

(continued)

Item	Description	Editable field
Maximum value	The maximum value that can be assigned to the setting.	No
Level	The minimum user level required to view or make changes to the setting: **Standard**, **Advanced**, or **Expert**.	No
Description	A detailed description of the setting	No

Configure general settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
   By default, all settings are displayed in table view.

   Note: For a description of the settings table, see "Settings table" on page 22.

2. In the left pane, double-click **General** to show the general categories.

3. Select a category to configure.
   - **Other**
   - **Memory**
   - **Execution**

4. Select one or more user levels to determine the settings that are displayed.

   Note: The user mode that you selected at sign-in determines the user levels that are available for selection. For example, the **Expert** user level is not available if you signed in with the **User** user mode. For information about what settings levels are available for each user mode, see Table 1.

5. In the **Locked** column, lock or unlock the settings.
   - **Lock**—Select the checkbox (☑ 🔒) to lock the settings. To change locked settings, a user must be in validation mode.
   - **Unlocked**—Deselect the checkbox (☐) to unlock the settings. Any user can change unlocked settings.

6. In the **Value** column, edit the value for each setting as needed. For a description of each setting, see Table 1.

7. In the toolbar, click **Save**, then click **OK** to close the confirmation message.

8. To use the updated settings, run the affected algorithms.

Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

Table 1 General settings

Item	Description	Default value	Allowed value	User level
Other				
Information level	Determines the amount of information that is displayed. Greater levels show more information; greater levels are helpful for checking one particular locus. **Note:** A high information level significantly slows the processing time. At a level > 5, it can take several minutes for the software to update; the software may also freeze because levels >5 can result in thousands of lines of information.	0	0–10 levels After viewing the information of interest, we recommend that you change the value back to 0 or 1. **IMPORTANT!** To avoid freezing the software, we recommend that you do not select levels >3 for a full deconvolution or full likelihood ratio calculation.	Advanced
Minimum number of loci	The minimum number of loci expected of any reasonable profile. If a profile does not contain the minimum number of loci specified, the software prompts you to continue or cancel.	8 loci	0–50 loci	Advanced
Minimum profile mean RFU	The minimum RFU value for the mean peak height of a sample. If a peak height is less than the selected RFU value, the software prompts you to continue or cancel. If you continue, the peak will be ignored for the peak height distributions.	200.0 RFU	0.0–2,000.0 RFU	Advanced
The current folder that contains profile data	The default location for profile data.	File path: `C:\Thermo Fisher Scientific\GeneMapper PG\profiles\`	User-defined file path	Standard

Table 1 General settings *(continued)*

Item	Description	Default value	Allowed value	User level
The folder to store feature files and network files	The default location for all result files, including feature files and log files.	File path: `C:\Thermo Fisher Scientific\GeneMapper PG\output\`	User-defined file path	Standard
The root folder that contains statistics and other files	The default location for raw data statistics, kit information, samples, and settings.	File path: `C:\Thermo Fisher Scientific\GeneMapper PG`	User-defined file path	Standard
Memory				
Maximum number of samples stored in history	The maximum number of samples (profiles) that the software can temporarily store (similar to browser cache). If the maximum number is exceeded, the software may freeze.	10 files	10–1,000 files	Advanced
Minimum number of samples stored in history	The minimum number of samples (profiles) that the software can temporarily store (similar to browser cache).	2 files	2–10 files	Advanced
Minimum required memory in GB to store the sample result history	The minimum amount of memory (GB) required to temporarily store sample results.	2 GB	1–5 GB	Advanced
Execution				
Code to use for protection	A code that can be used to lock Microsoft™ Excel™ spreadsheets to prevent accidental editing. If a spreadsheet is locked, a user must enter this code to open or edit the spreadsheet. **IMPORTANT!** This code is not meant to provide security; it is only intended to prevent accidental editing.	PureGenius	User-defined code	Expert

Configure universal model settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
   By default, all settings are displayed in table view.

   Note: For a description of the settings table, see “Settings table” on page 22.

2. In the left pane, click **Model**.

3. Select one or more user levels to determine the settings that are displayed.

   Note: The user mode that you selected at sign-in determines the user levels that are available for selection. For example, the **Expert** user level is not available if you signed in with the **User** user mode. For information about what settings levels are available for each user mode, see Table 2.

4. In the **Locked** column, lock or unlock the settings.
   - **Lock**—Select the checkbox ( ) to lock the settings. To change locked settings, a user must be in validation mode.
   - **Unlocked**—Deselect the checkbox ( ) to unlock the settings. Any user can change unlocked settings.

5. In the **Value** column, edit the value for each setting as needed. For a description of each setting, see Table 2.

6. In the toolbar, click **Save**, then click **OK** to close the confirmation message.

7. To use the updated settings, run the affected algorithms.

Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

Table 2 Model settings

Item	Description	Default value	Allowed value	User level
Algorithmic dropout limit	*(Applies to the LR and deconvolution calculations)* If an EPG does not have a peak, but the computed profile does, the software does not consider this as a potential solution if the predicted peak is greater than this value. We recommend that you use the default value so that the software considers all reasonable solutions.	2,000.0	500.0–50,000.0	Advanced
Algorithmic limit of peak height for dropin	*(Applies to the LR and deconvolution calculations)* If an EPG has a peak, but the computed profile does not, the software does not consider this peak in a potential solution. If a peak is less than this value, the software considers this peak in a potential solution. We recommend that you use the default value so that the software considers all reasonable solutions.	800.0	200.0–10,000.0	Advanced
Analytical Threshold	Analytical threshold. The minimum RFU required to consider any peak (in addition to the locus-specific values). Signal greater than this value can indicate an allele or an artifact. To use the same analytical threshold for all loci, ensure that the **Use global AT** setting is active (☑).	20.0 RFU	1.0–10,000.0 RFU	Advanced
Consider dropin and dropout	Determines whether the software considers an evidence profile to have dropin peaks and dropout peaks. For example, if there is an unexplained peak in an EPG that is not an allele, shoulder, spike, pull-up, or stutter, then the peak could be dropin.	Active (☑)	• Inactive (☐) • Active (☑)	Advanced
Consider noise peaks	Determines whether the software considers an evidence profile to have noise peaks. For example, if there is an unexplained peak in an EPG that is not an allele, shoulder, spike, pull-up, or stutter, then the peak could be noise. **Note:** By default, this setting is active (☑). However, if you use a large AT value and remove all noise-related peaks, you may want to make this inactive (☐).	Active (☑)	• Inactive (☐) • Active (☑)	Advanced

Table 2 Model settings *(continued)*

Item	Description	Default value	Allowed value	User level
Consider that a sample may have stutter	During the LR computation and deconvolution, the software considers potential stutter peaks. This setting is also used during simulations (for example, for NOC).	Active (☑)	• Inactive (☐) • Active (☑)	Advanced
Default probability of dropin	The default probability that a peak of a certain height may have dropped in, if the continuous model is turned off. This setting is also used if the statistical model returns a probability that is less than the set default dropin probability.	5.0E-4	0.0–0.1	Expert
Default probability of dropin for a locus	The default probability that a peak dropped in when the continuous model is turned off. This setting is also used if the dropin probability of the model returns 0 and the peak height is less than the dropin threshold. This setting is per locus. For example, if the overall chance of seeing any dropin peak is 5%, this value is 5% divided by the number of loci. During the simulation, the software uses this value to determine if a noise peak should be generated, then uses the noise model to draw the peak height or the dropin model (which is a gamma function, used for allelic dropins).	0.15	1.0E-6–1.0	Advanced
Default probability of dropout	The default probability that an allele dropped out when the continuous model is turned off. This setting is also used if no other information is available (for example, if there is no locus information).	5.0E-4	0.0–0.1	Expert
Default theta for sub-population	Theta is part of the LR calculation and represents how closely related members of a population are. For subpopulation structures: If the contributors are related, increase the value. **Note:** For more information, see: **https://strbase-archive.nist.gov/pub_pres/NJSP2006_Statistics.pdf**	0.01	0.0–0.5	Standard

Table 2 Model settings *(continued)*

Item	Description	Default value	Allowed value	User level
Expected intralocus balance	The expected intralocus peak height balance. If the intralocus balance is outside of this range, the profile/locus is flagged.	0.65 **Note:** The default value is based on the quality control specification for intralocus balance for the GlobalFiler™ PCR Amplification Kit.	0.3–0.8	Advanced
Global peak filter in (%)	A global filter that removes low-level peaks based on a user-defined percentage of the tallest peak at a locus.	0.0%	0.0–20.0%	Expert
Maximum distance in bp for pullup to be considered	If pullup is active (☑), this is the maximum distance (in base pairs) for which peaks in other channels are considered to be pullup.	0.2 bp	0.1–1.0 bp	Advanced
Maximum distance in scan points for pullup to be considered	If pullup is active (☑), this is the maximum distance (in scan points) for which peaks in other channels are considered to be pullup. **Note:** Because scan points are not usually available, there is another setting that uses base pair distances. See **Maximum distance in bp for pullup to be considered**.	2.0 scan points	0.5–10.0 scan points	Advanced
Maximum pullup ratio	If pullup is active (☑), and the parent peak is below saturation, this is the maximum ratio of the potential pullup peak vs. the peak from the other channel.	0.05	0.01–0.3	Advanced
Maximum pullup saturated ratio	If pullup is active (☑), and if the parent peak is an OS peak (saturated), this is the maximum ratio of the potential pullup peak vs. the peak from the other channel. When the parent peak is saturated, the percent pullup can be much greater (because the true parent peak could be much larger).	0.2	0.01–0.3	Advanced

Table 2 Model settings *(continued)*

Item	Description	Default value	Allowed value	User level
Minimum average peak height	If the mean peak height for a sample is less than this value, the sample is flagged as having low DNA (⬇). This setting is also used to calculate scores (for example, comparing peak heights). If the peak heights are less than this value, the software allows more extreme variability. If the peak heights are greater than this value, the software uses the PHR based on the model variability (for example, 0.3 for a peak height of 2,000 RFU).	10.0	10.0–10,000.0	Advanced
Minimum number of different alleles	The minimum number of different possible alleles a locus or target must have to be included in any of the machine learning models.	6 alleles	2–100 alleles	Advanced
Model pullups	When active (☑), the software considers the possibility of pullup peaks (bleed through of other colors near a peak). In most cases, the analysis can remove pullup peaks. However, if there is a casework mixture where a potential pullup peak overlaps with a peak from a minor contributor, it can be inactive (☐). In that case, pullups are considered for both LR and deconvolution. **Note:** The simulator for NOC does *not* generate pullup peaks.	Inactive (☐)	• Inactive (☐) • Active (☑)	Advanced
Model shoulder probabilities	When active (☑), the software considers a certain probability of shoulder peaks near a parent allele peak. In most cases, the analysis can remove shoulder peaks. However, if there is a casework mixture where a potential shoulder peak may also contain a peak from a minor contributor, it can be inactive (☐). In that case, shoulders are considered for NOC, LR, and deconvolution. **Note:** Shoulder peaks are also known as "n–1" or "Minus A" peaks.	Active (☑)	• Inactive (☐) • Active (☑)	Advanced
Number of PCR cycles	The number of PCR cycles used during sample amplification. **Note:** We designed and tested only for the 29 cycle protocol.	29 cycles	28–30 cycles	Advanced

Table 2 Model settings *(continued)*

Item	Description	Default value	Allowed value	User level
Penalty when a POI allele drops out	The model computes the probability of dropout for a given peak height. This probability is then scaled with the dropout penalty. (Unless the dropout peak is less than the analytical threshold, in which case the probability for dropout is 1).	0.1	0.001–1.0	Expert
Standard deviation multiplier value	The multiplier for standard deviation (s.d.) to eliminate outliers with the help of standard deviation and mean. The software uses this value to remove outliers from distributions. For example, if you use the default value of 3, the software uses 3 × s.d. to exclude outliers. By definition, 99.7% of values lie within 3 standard deviations of a normally distributed population.	3.0	2.0–4.0	Expert
Use continuous model	The continuous model uses all information, including peak heights, stutter, noise (dropin), and dropout When inactive (☐), the software uses semi-continuous or binary methods to analyze the data. The semi-continuous model uses peak heights, but no stutter and a fixed dropin and dropout probability; see **Consider that a sample may have stutter**. The binary model only uses the fact that a peak is there or not; see **Consider dropin and dropout**.	Active (☑)	• Inactive (☐) • Active (☑)	Advanced
Use global AT	When active (☑), the software uses the same analytical threshold for all loci. When inactive (☐), the software uses the individual analytical thresholds of all the loci. To set a value for the global AT, see the **Analytical Threshold** setting.	Inactive (☐)	• Inactive (☐) • Active (☑)	Advanced

Configure import and export settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
   By default, all settings are displayed in table view.

   Note: For a description of the settings table, see “Settings table” on page 22.

2. In the left pane, double-click **Import and Export** to show the import and export categories.

3. Select a category to configure.
   - **Import**—Settings for files that are imported into the software
   - **Export**—Settings for files that are exported from the software
   - **Reports**—Settings for software reports
4. Select one or more user levels to determine the settings that are displayed.

   Note: The user mode that you selected at sign-in determines the user levels that are available for selection. For example, the **Expert** user level is not available if you signed in with the **User** user mode. For information about what settings levels are available for each user mode, see Table 3.
5. In the **Locked** column, lock or unlock the settings.
   - **Lock**—Select the checkbox (☑ 🔒) to lock the settings. To change locked settings, a user must be in validation mode.
   - **Unlocked**—Deselect the checkbox (☐) to unlock the settings. Any user can change unlocked settings.
6. In the **Value** column, edit the value for each setting as needed. For a description of each setting, see Table 3.
7. In the toolbar, click **Save**, then click **OK** to close the confirmation message.
8. To use the updated settings, run the affected algorithms.

Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

Table 3 Import and export settings

Item	Description	Default value	Allowed value	User level
Import				
Always ignore OL	When active (☑), the software ignores the OL (off ladder) column in the sample file and does not show an error or warning for OL samples.	Inactive (☐)	• Inactive (☐) • Active (☑)	Standard
Excluded drives for import	To avoid long wait times when importing files from network drives (especially drives that are not connected), you can list drives to exclude from the file tree that is shown on file import.	No default value (field is empty)	User-defined	Standard
Favorite folders for import	Specify default folders for importing profiles.	No default value (field is empty)	User-defined	Standard

Table 3 Import and export settings *(continued)*

Item	Description	Default value	Allowed value	User level
The default sample column name	The name of the column in the sample file that contains the sample names.	Sample Name	User-defined; any combination of lower- and uppercase alphanumeric characters is allowed	Standard
Export				
Local maximum number of alleles per locus	For the CODIS exporter[1], the software checks that no more peaks are exported than the specified maximum number for a particular locus. If a sample has more peaks at any locus, the software displays a warning message.	4	1–50	Standard
Local minimum weight % threshold (100%-risk)	For the CODIS exporter[1], the software checks that every allele to export has the minimum specified score/weight. For profiles with alleles that have no score or weight assigned, the software assumes that the allele would pass. If an allele does not qualify, the software displays a warning message.	98	0–100	Advanced
Local min threshold 1:xxxxx	For the CODIS exporter[1], the software checks that a profile does not occur more than once in the specified minimum threshold in the database by chance, based on the specified population. If a sample does not qualify, the software displays a warning message.	10,000	1–1,000,000,000	Advanced

Table 3 Import and export settings *(continued)*

Item	Description	Default value	Allowed value	User level
Minimum number of alleles in profile	For the CODIS exporter[1], the software checks that the number of alleles in an exported profile is equal to or greater than the specified minimum number. If a sample has less than the minimum number of alleles at any location, the software displays a warning message.	1	1–500	Advanced
National maximum number of alleles per locus	For the CODIS exporter[1], the software checks that no more peaks are exported than the specified maximum number for a particular locus. If a sample has more peaks at any locus, the software displays a warning message.	4	1–50	Advanced
National minimum weight % threshold (100%-risk)	For the CODIS exporter[1], the software checks that every allele to export has the minimum specified score/weight. For profiles with alleles that have no score or weight assigned, the software assumes that the allele would pass. If an allele does not qualify, the software displays a warning message.	98	0–100	Advanced
National min threshold 1:xxxxx	For the CODIS exporter[1], the software checks that a profile does not occur more than once in the specified minimum threshold in the database by chance, based on the specified population. If a sample does not qualify, the software displays a warning message.	10,000,000	1–1,000,000,000	Advanced

Table 3 Import and export settings *(continued)*

Item	Description	Default value	Allowed value	User level
State maximum number of alleles per locus	For the CODIS exporter[1], the software checks that no more peaks are exported than the specified maximum number for a particular locus. If a sample has more peaks at any locus, the software displays a warning message.	4	1–50	Advanced
State minimum weight % threshold (100%-risk)	For the CODIS exporter[1], the software checks that every allele to export has the minimum specified score/weight. For profiles with alleles that have no score or weight assigned, the software assumes that the allele would pass. If an allele does not qualify, the software displays a warning message.	98	0–100	Advanced
State min threshold 1:xxxxx	For the CODIS exporter[1], the software checks that a profile does not occur more than once in the specified minimum threshold in the database by chance, based on the specified population. If a sample does not qualify, the software displays a warning message.	1,200,000	1–1,000,000,000	Advanced
Reports				
A logo file	The file name and path for the logo (image file) that appears in the report header.	GMIDX_GIFs/ABIFullPrintLogo.jpg	The file name and path are user-defined; the file type must be JPG	Expert

Table 3 Import and export settings *(continued)*

Item	Description	Default value	Allowed value	User level
Software name	The software name that appears in the report header.	GeneMapper™ PG	User-defined; any combination of lower- and uppercase alphabetic characters is allowed	Expert
Software version	The software version number that appears in the report header.	1.0.0	User-defined; any combination of lower- and uppercase alphanumeric characters is allowed	Expert

[1] The CODIS exporter converts files to a file format that is accepted by CODIS. You can then upload the files into CODIS local, state, or national databases.

Configure analysis settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
   By default, all settings are displayed in table view.

   Note: For a description of the settings table, see “Settings table” on page 22.

2. In the left pane, double-click **Analysis** to show the analysis categories.

3. Select a category to configure.
   - **Deconvolution**
   - **Memory**
   - **Likelihood Ratios**
   - **Number of contributors**
   - **Search**
   - **Simulation**

4. Select one or more user levels to determine the settings that are displayed.

   Note: The user mode that you selected at sign-in determines the user levels that are available for selection. For example, the **Expert** user level is not available if you signed in with the **User** user mode. For information about what settings levels are available for each user mode, see Table 4.

5. In the **Locked** column, lock or unlock the settings.
   - **Lock**—Select the checkbox (☑ 🔒) to lock the settings. To change locked settings, a user must be in validation mode.
   - **Unlocked**—Deselect the checkbox (☐) to unlock the settings. Any user can change unlocked settings.
6. In the **Value** column, edit the value for each setting as needed. For a description of each setting, see Table 4.
7. In the toolbar, click **Save**, then click **OK** to close the confirmation message.
8. To use the updated settings, run the affected algorithms.

Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

Table 4 Analysis settings

Item	Description	Default value	Allowed value	User level
Deconvolution				
Determine ratios before deconvolution	When active (☑), the software performs a quick initial deconvolution to determine the best ratios before performing the full deconvolution. This is helpful when there are many unknown contributors, and a full deconvolution of all ratios may take a considerable amount of time. When inactive (☐), you can specify the ratios. When you run the deconvolution algorithm, the software displays a dialog box where you can enter ratios.	Inactive (☐)	• Inactive (☐) • Active (☑)	Expert
Extract only clear major contributors	When active (☑), the software performs a simple deconvolution where only the top (usually 1 or 2) unknown contributors are extracted, and the minor contributors are ignored. To determine the minor level, see: • **For extract clear major, ignore anything below that RFU value** • **For extract major, the ratio below which we ignore everything** In the deconvolution, the software ignores peaks below those thresholds.	Inactive (☐)	• Inactive (☐) • Active (☑)	Standard

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
For extract clear major, ignore anything below that RFU value	For mixtures with a clear major contributor (for example, a 1:4 mixture), the software ignores all peaks that are less than this value. The software does not consider these peaks to be part of the major contributor.	300.0 RFU	20.0–100,000.0 RFU	Advanced
For extract major, the ratio below which we ignore everything	For mixtures that clearly have 1–2 major contributors and mixture ratios that are clearly different from 1:1, the software ignores everything below this ratio.	0.3	0.1–0.8	Expert
Locus export weight threshold	The minimum weight that a locus must have to be included for export.	1.0	0.1–100.0	Advanced
Locus fit threshold	The minimum fit (%) that a locus must have to be included in the analysis. 0% is the worst possible fit between the computed and the evidence profile. 100% is a perfect fit (100% is possible only in rare cases).	0.0	0.0–100.0	Expert
Locus score threshold	The minimum score a solution must have to be included in the analysis. The software reports all values that are greater than or equal to the defined threshold. Decimal values are permitted. For example: • If you set the threshold to 90.00%, and a locus has scores of 99.00% and 98.00%, both results appear in the analysis. • If you set the threshold to 90.00%, and a locus has scores of 99.00% and 0.10%, only the 99.00% result appear in the analysis.	1.0	0.1–100.0	Advanced
Maximum amount of DNA	The maximum amount of DNA (ng) to use for the NOC identification (for example, when creating amount-specific models).	10.0 ng	0.005–10.0 ng	Expert

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
Maximum number of top solutions to keep per locus	The maximum number of best solutions to include for deconvolution, per locus and per set of ratios and degradation parameters. For example, if the best solution is 1:4, and this setting is 5, the software keeps ≤5 of the best solutions for that particular locus and that particular set of ratios. For ≥3 contributors, we recommend that you set a number less than or equal to the default value. The amount of memory required to keep all solutions can be very high, which may cause the software to slow down. **Note:** This setting does not affect the LR calculation. For the LR calculation, you can keep all solutions.	10 solutions	2–100 solutions	Advanced
Minimal ratio	The minimum ratio is used for the deconvolution and the LR calculation. To use this ratio for the LR calculation, you must select the **SPECIFIED** option in the **How ratios are computed for LR** setting.	0.1 (10%)	0.01–0.5	Advanced
Minimum amount of DNA	The minimum amount of DNA (ng) that is required for the NOC identification.	0.25 ng	0.001–10.0 ng	Expert
Number of samples to generate	The number of samples to generate for simulations in the batch analysis. The run time is faster for smaller numbers of samples. The run time is slower for larger numbers of samples, but the results are more accurate.	1,000 samples	1–10,000 samples	Advanced
Number of top ratio combinations to keep	The number of best ratio (and degradation) combinations to include for the deconvolution. Each set of ratio combinations has many solutions. For ≥3 contributors, we recommend that you use the default value (3 combinations). The amount of memory required to keep all solutions can be very high, which can increase the run time. **Note:** This setting does not affect the LR calculation. For the LR calculation, all solutions are included.	3 combinations	1–10 combinations	Advanced

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
The default deconvolution detail level	The default detail level for the deconvolution.	All Alleles with Scores	• **Top Alleles** • **All Alleles** • **All Alleles with Scores** • **All Alleles with All Details**	Standard
Threshold to highlight a locus as good fit (in %)	The threshold that determines if a locus is a good fit. The fit score of a locus is based on how well the calculated solution fits the actual evidence profile. The score ranges from 0–100%, where 100% is a perfect score. For example: • If the prediction for a peak is 100 RFU, and the actual peak is 100 RFU, then the score is 100%. • If the prediction for a peak is 100 RFU, and the actual peak is 50 RFU, the fit is determined by the height comparison method used: – DIST (distributions) method—The value is determined using the statistical model in all detail (such as the peak height variance). – Percent method—The percentage is the same as the RFU (for example, 50 RFU is 50%). – Binary method—The result is 0% if the peak is below the threshold or 100% otherwise.	0.1	0.01–100.0	Advanced
Memory				
Maximum # results in memory	The maximum number of analysis results that the software stores in memory.	10 results	0–100 results	Advanced
Maximum amount of DNA	The maximum amount of DNA (ng) to use for the NOC identification (for example, when creating amount-specific models).	10.0 ng	0.005–10.0 ng	Expert

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
Minimal ratio	The minimum ratio is used for the deconvolution and the LR calculation. To use this ratio for the LR calculation, you must select the **SPECIFIED** option in the **How ratios are computed for LR** setting.	0.1 (10%)	0.01–0.5	Advanced
Minimum amount of DNA	The minimum amount of DNA (ng) that is required for the NOC identification.	0.25 ng	0.001–10.0 ng	Expert
Number of samples to generate	The number of samples to generate for simulations in the batch analysis. The run time is faster for smaller numbers of samples. The run time is slower for larger numbers of samples, but the results are more accurate.	1,000 samples	1–10,000 samples	Advanced
Likelihood Ratios				
Abort computation on zero	For complex scenarios, when Hp is impossible for a certain locus (unless you want to see the per locus scores for the other loci), it saves time to stop the computation at that point. For example, if one locus has Hp = 0 (impossible for the hypothesis to explain the evidence), the LR = 0 no matter what the other loci values are. Therefore, it saves time to stop calculations after an Hp = 0 is found.	Active (☑)	• Inactive (☐) • Active (☑)	Advanced
Compute the p(non-contributor)	When active (☑), the software collects the most detailed information about possible combinations to calculate the probability that a non-contributor has a better or equal LR score than the person of interest (POI). The result is the sum of the Random Match Probability (RMP) of all profiles that would result in a better LR score. **Note:** For details, see: Dørum, Guro, Øyvind Bleka, Peter Gill, Hinda Haned, Lars Snipen, Solve Sæbø, and Thore Egeland. 2014. "Exact Computation of the Distribution of Likelihood Ratios with Forensic Applications." Forensic Science International: Genetics 9 (March):93–101. See: **https://doi.org/10.1016/j.fsigen.2013.11.008**	Inactive (☐)	• Inactive (☐) • Active (☑)	Advanced

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
How ratios are computed for LR	Determines the method for computing the ratios during the LR calculation. **Note:** Estimating the ideal ratios can take long time to calculate, in particular for complex scenarios. We recommend that you specify the ratios as much as possible. The logic of the calculation follows the standard approach described in *Forensic DNA Profiling: A Practical Guide to Assigning Likelihood Ratios*. This approach has been extended to a continuous model, including peak heights *and* stutter. (*Forensic DNA Profiling: A Practical Guide to Assigning Likelihood Ratios*, Jo-Anne Bright, Michael D. Coble)	INDIVIDUAL	• **DEFENSE**—Uses the Hd hypothesis to find the optimal ratio, then applies it to both Hp and Hd hypotheses. • **INDIVIDUAL**—Computes the optimum for each hypothesis separately. • **SPECIFIED**—Uses the user-specified ratios. If none are given, uses equal proportions (such as 1:1:1). • **INTEGRAL**—Uses the integral of all the scores for all ratios, such as 1:2:3, 1:3:5, and so on.	Advanced
Maximum amount of DNA	The maximum amount of DNA (ng) to use for the LR calculation.	10.0 ng	0.005–10.0 ng	Expert
Minimal ratio	The minimum ratio is used for the deconvolution and the LR calculation. To use this ratio for the LR calculation, you must select the **SPECIFIED** option in the **How ratios are computed for LR** setting.	0.1 (10%)	0.01–0.5	Advanced
Minimum amount of DNA	The minimum amount of DNA (ng) that is required for the LR calculation.	0.25 ng	0.001–10.0 ng	Expert
Minimum LR threshold for inclusive result	The minimum threshold that is required for a laboratory to consider a result inclusive. • **Inclusive result (Hp)**—The LR score is greater than this threshold. • **Inconclusive result (Hd)**—The Log(LR) is between 0 and this threshold. • **Exclusive result (Ho)**—The Log(LR) is <0.	3.0	0.0–100.0	Advanced

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
Number of samples to generate	The number of samples to generate for simulations in the batch analysis. The run time is faster for smaller numbers of samples. The run time is slower for larger numbers of samples, but the results are more accurate.	1,000 samples	1–10,000 samples	Advanced
Pick non-existing (dropout) alleles for unknowns ('Q')	When active (☑), dropouts are considered when comparing computed versus actual profiles. The software may also pick nonexisting peaks (dropouts) on purpose, depending on the expected peak height (if such a dropout is possible). This makes the computation slower, but can make sense for small minor contributors, where there is a reasonable probability that there was a different peak (Q) that has dropped out.	Active (☑)	• Inactive (☐) • Active (☑)	Advanced
Record detailed information during LR calculation	*(This options is intended only for training and validation modes.)* When active (☑), the software collects the most detailed information about the combinations and formulas used. **Note:** This setting works only for low-complexity scenarios with 2–3 contributors. Otherwise, the software may run out of memory.	Inactive (☐)	• Inactive (☐) • Active (☑)	Advanced
Number of contributors				
Apply stutter filter for NOC	When active (☑), the software applies a stutter filter to the sample before running any of the NOC algorithms.	Active (☑)	• Inactive (☐) • Active (☑)	Expert
Enable fixed tree for NOC	When enabled (1.0), fixed tree is considered along with other NOC algorithms. When inactivated (0.0), fixed tree is excluded.	Active (☑)		Advanced
Enable height distribution for NOC	When enabled (1.0), height distribution is considered along with other NOC algorithms. When inactivated (0.0), height distribution is excluded.	Inactive (☐)		Advanced
Enable Heuristic algorithm for NOC	When enabled (1.0), the heuristic algorithm is considered along with other NOC algorithms. When inactivated (0.0), the heuristic algorithm is excluded.	Active (☑)		Advanced

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
Enable MAC for NOC	When enabled (1.0), the maximum allele count (MAC) is considered along with other NOC algorithms. When inactivated (0.0), MAC is excluded.	Active (☑)	• Inactive (☐) • Active (☑)	Advanced
Enable peak algorithm for NOC	When enabled (1.0), the peak algorithm is considered along with other NOC algorithms. When inactivated (0.0), peak algorithm is excluded.	Active (☑)		Advanced
Enable the TFS Plus decision tree for NOC	When enabled (1.0), the TFS Plus decision tree is considered along with other NOC algorithms. When inactivated (0.0), the TFS Plus decision tree is excluded.	Active (☑)		Advanced
Maximum amount of DNA	The maximum amount of DNA (ng) to use for the NOC identification (for example, when creating amount-specific models).	10.0 ng	0.005–10.0 ng	Expert
Maximum number of contributors to consider	The maximum number of contributors that the software can recognize in any given profile. For example, if the maximum number is set to 4, the software only recognizes ≤4 contributors, even if there are more than 4 contributors.	4 contributors	1–8 contributors	Expert
Minimal ratio	The minimum ratio is used for the deconvolution and the LR calculation. To use this ratio for the LR calculation, you must select the **SPECIFIED** option in the **How ratios are computed for LR** setting.	0.1 (10%)	0.01–0.5	Advanced
Minimal simulation ratio	The minimum ratio to use for the simulation. This setting impacts the NOC estimation. It is important to set the appropriate value based on what you consider to be a mixture. For example: • If you set this value to 10%, the software cannot detect the 5% minor contributor. The result is NOC = 1 when it is an NOC = 2 mixture. • If you set a very small value, such as 0.1%, the software may generate a greater than expected NOC result due to the inclusion of very minor contributors.	0.01 (1%)	0.001–0.2	Advanced

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
Minimum amount of DNA	The minimum amount of DNA (ng) that is required for the NOC identification.	0.25 ng	0.001–10.0 ng	Expert
Minimum peak height for NOC	The minimum peak height to consider for the number of contributors. This value is used to calculate the following: limits for the number of contributors, the minimum percent of a minor contributor, and reasonable possible ratios. For example, if a sample has a mean peak height (per allele) of 200 RFU, and this value is set to 100 RFU, then no more than 2 contributors are reasonable.	150.0 RFU	10.0–5,000.0 RFU	Expert
Number of decision tree rounds	The number of times that the software runs the decision tree algorithm. The greater the number, the easier it is to see how consistent the results are; however, larger numbers user more memory and take longer to process.	1	1–10	Advanced
Number of samples to generate	The number of samples to generate for simulations in the batch analysis. The run time is faster for smaller numbers of samples. The run time is slower for larger numbers of samples, but the results are more accurate.	1,000 samples	1–10,000 samples	Advanced
Search				
Absolute minimum percent match	The absolute minimum percent match of a reference profile against an evidence profile required to consider the evidence profile in further processing.	30.0%	10.0–80.0%	Standard
Maximum amount of DNA	The maximum amount of DNA (ng) to use for the NOC identification (for example, when creating amount-specific models).	10.0 ng	0.005–10.0 ng	Expert
Minimal ratio	The minimum ratio is used for the deconvolution and the LR calculation. To use this ratio for the LR calculation, you must select the **SPECIFIED** option in the **How ratios are computed for LR** setting.	0.1 (10%)	0.01–0.5	Advanced
Minimum amount of DNA	The minimum amount of DNA (ng) that is required for the NOC identification.	0.25 ng	0.001–10.0 ng	Expert

Table 4 Analysis settings *(continued)*

Item	Description	Default value	Allowed value	User level
Minimum percent match	The minimum percent match of a reference profile against an evidence profile required to show the evidence profile in the heat map and match result list. **Note:** The absolute minimum required to process the evidence sample, see **Absolute minimum percent match**.	80.0%	10.0–100.0%	Standard
Number of samples to generate	The number of samples to generate for simulations in the batch analysis. The run time is faster for smaller numbers of samples. The run time is slower for larger numbers of samples, but the results are more accurate.	1,000 samples	1–10,000 samples	Advanced
Simulation				
Maximum amount of DNA	The maximum amount of DNA (ng) to use for the simulation.	10.0 ng	0.005–10.0 ng	Expert
Minimal ratio	The minimum ratio used for the simulation.	0.1 (10%)	0.01–0.5	Advanced
Minimum amount of DNA	The minimum amount of DNA (ng) that is required for the simulation.	0.25 ng	0.001–10.0 ng	Expert
Number of samples to generate	The number of samples to generate for simulations in the batch analysis. The run time is faster for smaller numbers of samples. The run time is slower for larger numbers of samples, but the results are more accurate.	1,000 samples	1–10,000 samples	Advanced

Configure GMID-X settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
   By default, all settings are displayed in table view.

   Note: For a description of the settings table, see “Settings table” on page 22.

2. In the left pane, click **GMID-X Settings**.

3. Select one or more user levels to determine the settings that are displayed.

   Note: The user mode that you selected at sign-in determines the user levels that are available for selection. For example, the **Expert** user level is not available if you signed in with the **User** user mode. For information about what settings levels are available for each user mode, see Table 5.

4. In the **Locked** column, lock or unlock the settings.
   - **Lock**—Select the checkbox (☑ 🔒) to lock the settings. To change locked settings, a user must be in validation mode.
   - **Unlocked**—Deselect the checkbox (☐) to unlock the settings. Any user can change unlocked settings.
5. In the **Value** column, edit the value for each setting as needed. For a description of each setting, see Table 5.
6. In the toolbar, click **Save**, then click **OK** to close the confirmation message.
7. To use the updated settings, run the affected algorithms.

Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

Table 5 GMID-X settings

Item	Description	Default value	Allowed value	User level
Analysis Method from GMID-X	The default name and location of the analysis method file (XML) from the GeneMapper™ *ID-X* Software.	File path: `C:\Thermo Fisher Scientific\GeneMapper PG\panels\ v1.7_AnalysisMethod.xml`	User-defined file path	Expert
Field in sample that contains NOC information	When importing samples from the GeneMapper™ *ID-X* Software, this is the field that contains the number of contributors.	No default value (field is empty)	User-defined file path	Expert
Location of CODIS(cmf/rcms) .xml files	The default location of the CODIS(cmf/rcms) files (XML).	File path: `C:\Thermo Fisher Scientific\GeneMapper PG\CODIS\`	User-defined file path	Expert
Location of GMID-X .ser files	The default location of the data files (SER) from the GeneMapper™ *ID-X* Software.	File path: `c:\Thermo Fisher Scientific\GeneMapper PG\profiles\gmidx\`	User-defined file path	Expert
Stutter file from GMID-X	The default name and location of the stutter file (TXT) from the GeneMapper™ *ID-X* Software.	File path: `C:\Thermo Fisher Scientific\GeneMapper PG\panels\GlobalFiler\ AmpFLSTR_Stutter_v7X.txt`	User-defined file path	Expert

Configure project settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
   By default, all settings are displayed in table view.

   Note: For a description of the settings table, see “Settings table” on page 22.

2. In the left pane, click **Project Settings**.

3. Select one or more user levels to determine the settings that are displayed.

   Note: The user mode that you selected at sign-in determines the user levels that are available for selection. For example, the **Expert** user level is not available if you signed in with the **User** user mode. For information about what settings levels are available for each user mode, see Table 6.

4. In the **Locked** column, lock or unlock the settings.
   - **Lock**—Select the checkbox ( ) to lock the settings. To change locked settings, a user must be in validation mode.
   - **Unlocked**—Deselect the checkbox ( ) to unlock the settings. Any user can change unlocked settings.

5. In the **Value** column, edit the value for each setting as needed. For a description of each setting, see Table 6.

6. In the toolbar, click **Save**, then click **OK** to close the confirmation message.

7. To use the updated settings, run the affected algorithms.

Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

Table 6 Project settings

Item	Description	Default value	Allowed value	User level
Default project save location	The default save location for projects.	File path: `C:\Users\<user name>\Documents\My_PG_Projects` where: `<user name>` is the name of the currently signed in user	User-defined file path	Standard
Project directory name limit	The maximum number of characters for the name of the directory where projects are saved; see **Default project save location**.	100 characters	1–256 alphanumeric characters	Expert
Recent project limit	The number of projects to show in the recent project list. See the **My recent project files** setting.	8 projects	1–20 projects	Expert
Set date format	The date format to display.	yyyy-dd-mm	Several date formats are available; select any option in the dropdown list.	Standard

Configure GUI settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
   By default, all settings are displayed in table view.

   Note: For a description of the settings table, see “Settings table” on page 22.

2. In the left pane, double-click **GUI** to show the GUI categories.

3. Select a category to configure.
   - **EPG**—Configure items that are displayed in the electropherograms (EPGs).
   - **Table Settings**—Configure items that are displayed in tables.

4. Select one or more user levels to determine the settings that are displayed.

   Note: The user mode that you selected at sign-in determines the user levels that are available for selection. For example, the **Expert** user level is not available if you signed in with the **User** user mode. For information about what settings levels are available for each user mode, see Table 7.

5. In the **Locked** column, lock or unlock the settings.
   - **Lock**—Select the checkbox (☑ 🔒) to lock the settings. To change locked settings, a user must be in validation mode.
   - **Unlocked**—Deselect the checkbox (☐) to unlock the settings. Any user can change unlocked settings.
6. In the **Value** column, edit the value for each setting as needed. For a description of each setting, see Table 7.
7. In the toolbar, click **Save**, then click **OK** to close the confirmation message.
8. To use the updated settings, run the affected algorithms.

Saved changes persist between sign-in sessions, whether you sign in with **Continue from my last point** or **Start with a clean slate**.

Table 7 GUI settings

Item	Description	Default value	Allowed value	User level
General				
Auto save feature	When active (☑), the software automatically saves changes to the settings at the specified time interval. To set the time interval, see the **How often to save** setting.	Active (☑)	• Inactive (☐) • Active (☑)	Standard
Condense the UI	When active (☑), the software displays the icons for most buttons, but not the labels.	Inactive (☐)	• Inactive (☐) • Active (☑)	Standard
Determines the heat map style	The color and style of the heat maps.	Red-Yellow-Green	• **Red-Yellow-Green** • **Red-White White-Blue** • **White-Green** • **White-Yellow-Green** • **5 colors**	Standard
GUI scaling	Determines the overall size of the software screens; the text and other screen elements automatically adjust.	1.0	0.5–3.0	Standard

Table 7 GUI settings *(continued)*

Item	Description	Default value	Allowed value	User level
How often to save	Determines how often the software automatically saves changes to projects. This requires the **Auto save feature** setting to be active.	5 minutes	0–360 minutes	Advanced
Maximum days to keep logs	The maximum number of days that log files are retained in the software. The software automatically deletes log files after the specified time.	30 days	1–365 days	Expert
More colorful UI	When active (☑), the software displays more icons and displays more colors for charts, table cells, and some other UI elements.	Active (☑)	• Inactive (☐) • Active (☑)	Standard
Name of the parameters/settings file	The default name for the exported settings file.	pgsettings.json	User-defined file name; must be a JSON file	Advanced
Show hints	When active (☑), the software displays popup hints for the current screen. The hints are usually displayed after 1–2 minutes of user inactivity.	Active (☑)	• Inactive (☐) • Active (☑)	Standard
Show the toolbar	When active (☑), the toolbar is shown on each screen.	Active (☑)	• Inactive (☐) • Active (☑)	Standard
The default log level	The information to include in the software log files.	Error	• **Debug** • **Info** • **Warning** • **Error**	Expert
Time to show tooltip	The amount of time that elapses before tooltips are displayed.	750 milliseconds	50–60,000 milliseconds	Standard

Table 7 GUI settings *(continued)*

Item	Description	Default value	Allowed value	User level
EPG				
All epg options	The software allows you to change display options for EPGs. Click **Edit** in the **Value** column to open the **EPG Settings** dialog box. For more information, see "Configure electropherogram (EPG) settings" on page 19.	No default value; click the **Edit** button to configure the EPG display options	User-selected display options	Standard
Color of contributor 1	The color displayed in graphs and tables for contributors 1–5.	RGBA scale: 0, 0, 255, 1	User-defined RGBA scale	Standard
Color of contributor 2		RGBA scale: 255, 0, 0, 1		
Color of contributor 3		RGBA scale: 0, 255, 0, 1		
Color of contributor 4		RGBA scale: 255, 255, 0, 1		
Color of contributor 5		RGBA scale: 0, 255, 255, 1		
Table Settings				
Show checkboxes in the samples table	When active (☑), checkboxes are displayed in the samples table. You can select a sample by selecting the checkbox (☑). When inactive (☐), checkboxes are not displayed in the samples table. You can select a sample by clicking the sample row.	Inactive (☐)	• Inactive (☐) • Active (☑)	Advanced

Save settings

1. In the navigation pane, select **Configure** ▸ **Settings**.
2. Configure the settings as needed.
   - "Configure general settings" on page 23
   - "Configure universal model settings" on page 26
   - "Configure import and export settings" on page 31
   - "Configure analysis settings" on page 36
   - "Configure GMID-X settings" on page 46
   - "Configure project settings" on page 48
   - "Configure GUI settings" on page 49
3. In the toolbar, click **Save**, then click **OK** to close the confirmation message.
4. To use the updated settings, run the affected algorithms.

Import samples

Import samples to:

- Create a new project
- Add samples to an existing project

When you import samples:

- You specify the location of the sample files on the hard drive or a network drive.
- The sample files are copied to the GeneMapper™ PG Software projects folder.
- The original sample files are not changed.

Table 8 Types of samples in the software

Sample type	Description	Usage
Evidence sample	Unknown samples, typically mixtures, that will be analyzed for NOC, deconvolution, and the LR in the software.	Used to identify the number of contributors and perform deconvolution to separate individual contributors.
Reference sample	Known single-source samples used for comparison to evidence samples or to identify a known contributor to a mixture.	Operate as a baseline for comparison against evidence samples to identify or confirm known contributors.

1. In the primary toolbar, click **Import Samples**.
2. In the **Files** tab, navigate to and open the folder that contains the sample files to import.

3. Select one or more sample files to import:
   - To add files one at a time, double-click each file.
   - To add multiple files at the same time, select individual files using **Ctrl+Click**, then click **Add file(s)**.

   The files are displayed in the **Selected files** pane. In the right-most pane, you can view details for each file.

4. *(If needed)* Remove files from the **Selected files** pane: Select one file, then click **Remove file**, or click **Clear list** to remove all the files.

5. Click **OK**.

6. In the **Samples from the selected files** dialog box, make the following changes as needed, then click **OK**.
   - Select (☑) the samples to include in the import; deselect (☐) the samples to exclude.
   - Set all samples as reference or evidence samples.
     Alternatively, in the **Type** column, set individual samples as reference or evidence samples.
   - In the **Specimen Type** column, assign a different specimen type to individual samples.

   The remaining fields in this dialog box are not editable.

7. If there are issues with any of the selected samples, the software displays the number of issues and provides solutions to address them. Make the following changes as needed, then click **OK**.
   - Select (☑) or deselect (☐) the solutions.
   - In the **Choice** column, select an option from the dropdown list for each sample. The options vary, depending on the sample issue.

   The imported samples are displayed in the **Profiles** screen. It may take ≤30 seconds for the samples to load.
   - Profiles for evidence samples are displayed in the **Evidence** tab, and contain peak height information.
   - Profiles for reference samples are displayed in the **Reference** tab, and do not contain any peak height information.

Display the Profiles screen

1. In the navigation pane, click **Profiles** (default selection).

2. If you are signed into the software in Validation mode, you can access the items and tasks shown in the Profiles screen.

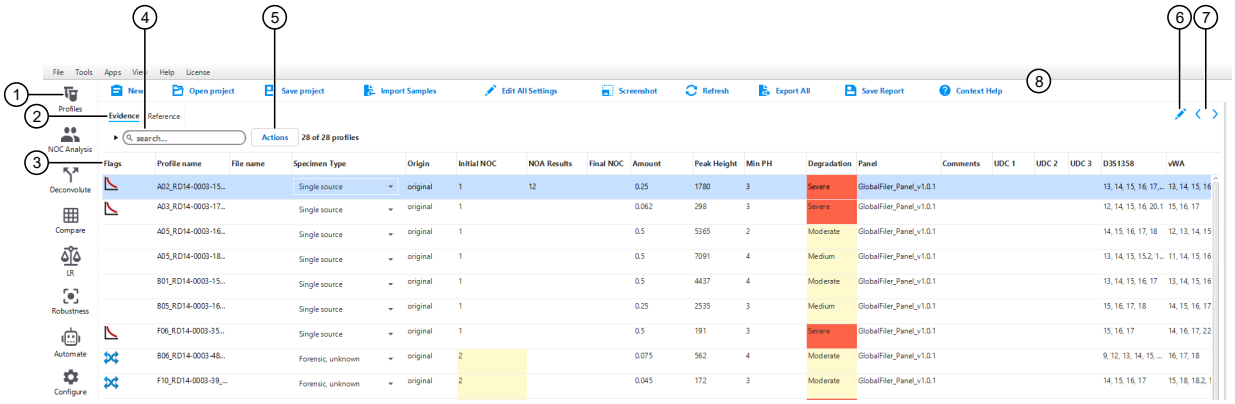


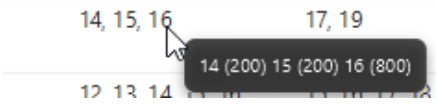
Figure 3 Profiles screen

1. **Profiles** app.
2. All evidence or reference profiles (samples) in the project.
3. Samples table.
4. Search and filter options.
5. **Actions** dropdown list.
6. Software settings.
7. Electropherograms and sample details.
8. Menu bar and primary toolbar.

Evidence samples table

Item	Description
Flags	Any flags assigned to the sample by the software. For a description of the flags, see “Review flags (Profiles screen)” on page 57.
Profile name	The name of the DNA profile (sample).
File name	The name of the file that the DNA profile was imported from.
Specimen Type	The specimen type assigned to the DNA profile (for example, **Biological Mother** or **Sibling**).
Origin	*(This field cannot be edited)* The origin of the sample, as determined by the software: • For evidence and reference profiles, the **Specimen Type** column is populated according to the imported sample file. However, if the sample file does not specify a specimen type, the software assigns a specimen type of **Unknown** to evidence profiles and **Reference** to reference profiles. • If you create an evidence profile from a reference profile, the software keeps the specimen type as **Unknown**. • If you create a reference profile from an evidence profile, the software changes the specimen type to **Deduced Reference**.
Initial NOC	The initial number of contributors for the sample, before running the software algorithms. The initial number of contributors may be known (as for a reference sample) or specified by a user. For more information, see “Edit sample summary (Sample Details tab)” on page 59.

(continued)

Item	Description
NOA Results	Number of analysis results. The total number of analyses performed on a sample. For example, if you run 3 NOC analyses, 2 deconvolution analyses, and 1 LR analysis on a sample, the column displays **6**. To see a list of the analyses performed and a summary of the results, click the value in the **NOA results** column.
Final NOC	The final number of contributors specified by the user, after running the software algorithms.
Amount	If known, the amount of DNA (ng) in the sample.
Peak Height	The mean peak height (RFU) of the sample (that is, the average of the peak heights for all alleles in the sample). For single-source samples, the height directly correlates to the amount of DNA in the sample.
Min PH	Minimum peak height (RFU). The smallest peak found in the sample, which can indicate the analytical threshold (AT).
Degradation	A description of the degradation level; for example, **Undegraded** or **Severe**. The level is determined by the beta value of the degradation curve. When beta is 0, there is no degradation; the larger beta is, the more degradation there is. The formula to calculate the degraded height for an allele is: undegraded height × 10^ (– bp size × beta) where: • **undegraded height** is the undegraded height of the specific allele • **bp** is the base pair size of the specific allele
Panel	The GeneMapper™ *ID-X* Software panel used for the sample.
Comments	Any comments made by a user for the DNA profile (sample).
UDC1, **UDC2**, and **UDC3**	User-defined. Users can define these columns in the CE instrument Data Collection Software or in the GeneMapper™ *ID-X* Software.
Locus columns	The alleles for each locus amplified in the sample. If you place the pointer over the locus name in the column heading, you can view the dye color, stutter percentages, and analytical threshold for the locus. If you place the pointer over the alleles listed for the sample, you can view the peak heights. This example shows the peak heights for alleles 14, 15, and 16. 

Review flags (Profiles screen)

Flags indicate the sample quality (for example, **Degraded**) or indicate a specific type of sample (for example, **Training**). For quality flag specifications, see

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see "Evidence samples table" on page 55 or "Reference samples table" on page 58.

3. Review the **Flags** column.

   A profile may show one or more of the flags that are listed in Table 9. You can place the pointer over a flag to view details.

Note: To flag a sample or remove a flag from a sample, see "Manage samples (Actions button)" on page 64.

Table 9 Flags in the Profiles screen

Flag	Description
(Degraded)	The sample appears to be degraded.
(Excluded)	(User-defined) The sample is excluded from the calculation.
(High DNA)	The sample contains the maximum amount of DNA and may not be suitable for analysis. The maximum amount of DNA is user-defined; the default value is 10 ng.
(Known reference)	The sample is from a known individual.
(Lead)	(User-defined) Sample for an investigative lead.
(Low DNA)	The sample contains the minimum amount of DNA and may not be suitable for analysis. The minimum amount of DNA is user-defined; the default value is 0.25 ng.
(Mixture)	The sample is a mixed-source sample. A sample is considered a potential mixture if it meets either of the following conditions: • **Condition 1**—Two or more loci contain three or more called alleles • **Condition 2**—One or more loci contain three or more called alleles *and* another two or more loci have the PHR flag.
(NOC unclear)	The DNA amount in the sample is too low to obtain a good result from the NOC algorithms. The flag also appears if the NOC algorithms do not generate acceptable confidence scores.
(OL)	The sample includes off-ladder alleles (alleles that size outside bins).
(PHR)	The peak height ratio between the lowest and highest peaks in a marker size range is less than the minimum peak height ratio.

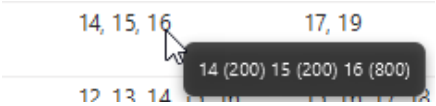
Table 9 Flags in the Profiles screen *(continued)*

Flag	Description
(Stochastic)	The sample has peak height imbalances <40% or allelic dropout. This analysis is based on the combined average peak height of a subset of larger STR loci (CSF1P0, D18S51, FGA, SE33, and D2S1338).
(Test)	(User-defined) Sample for testing.
(Training)	(User-defined) Sample for training.
(Truth)	(User-defined) Sample for the truth. The "truth" is a contributor who is known to be part of a mixture.
(Unknown)	(User-defined) Sample of unknown origin or unknown contributors.
(Unusable)	The sample cannot be interpreted. Do not trust analysis results from this sample.
(Validation)	(User-defined) Sample for validation.

Reference samples table

Column	Description
Flags	Any flags assigned to the sample by the software. For a description of the flags, see “Review flags (Profiles screen)” on page 57.
Profile name	The name of the DNA profile (sample).
File name	The name of the file that the DNA profile was imported from.
Specimen Type	The specimen type assigned to the DNA profile (for example, **Biological Mother** or **Sibling**). • For evidence and reference profiles, the **Specimen Type** column is populated according to the imported sample file. However, if the sample file does not specify a specimen type, the software assigns a specimen type of **Unknown** to evidence profiles and **Reference** to reference profiles. • If you create an evidence profile from a reference profile, the software keeps the specimen type as **Unknown**. • If you create a reference profile from an evidence profile, the software changes the specimen type to **Deduced Reference**.
Origin	*(This field cannot be edited)* The origin of the sample, as determined by the software: • For all profiles (evidence and reference), the software assigns **original** as the origin when the profile is imported into the software. • If you create an evidence profile from a reference profile, the software changes the origin to **hypothetical**. • If you create a reference profile from an evidence profile, the software changes the origin to **hypothetical**.
Panel	The GeneMapper™ *ID-X* Software panel used for the sample.

(continued)

Column	Description
Locus columns	The alleles for each locus amplified in the sample. If you place the pointer over the locus name in the column heading, you can view the dye color, stutter percentages, and analytical threshold for the locus. If you place the pointer over the alleles listed for the sample, you can view the peak heights. This example shows the peak heights for alleles 14, 15, and 16. 

Edit sample summary (Sample Details tab)

1. Display the sample details for the profile of interest.
2. Select the **Sample Details** tab, then select the **Summary** tab.
3. *(Optional)* At the top of the **Summary** tab, click an option, then perform the required actions.

Option	Action
Flag sample	In the **Flag Selection** dialog box, select one or more flags, then click **OK**. The selected flags are displayed in the **Flags** column of the **Profiles** screen.
Remove flag	In the **Flag Selection** dialog box, select one or more flags to remove, then click **OK**. The selected flags are removed from the **Flags** column of the **Profiles** screen.
Associate Truth	The "truth" is a contributor who is known to be part of a mixture. For example, in a case where the victim is known, the DNA of the victim is the "truth". • To add a contributor: In the **Associate Truth** dialog box, select a contributor, then click **OK**. The selected contributor is listed in the **Summary** tab under **Known contributors**. To add multiple contributors, repeat this step. **Note:** If the contributor that you want to add is not listed, click **Browse**, select a profile from the dropdown list, then click **OK**. The contributor is added to the list in the **Associate Truth** dialog box. • To remove all contributors: In the **Associate Truth** dialog box, click **Clear**, then click **OK**. All contributors are removed from the **Summary** tab. **Note:** You cannot select the contributors to remove. All contributors are removed when you click **Clear**.
Degradation chart	Opens the **Degradation Chart** window, which shows the estimated degradation level of the selected sample. For more information, see “Show a degradation chart for a sample” on page 70.

4. View or edit the fields as needed:
   - Editable fields are listed in Table 10
   - View-only fields are listed in Table 11

Table 10 Summary tab—Editable fields

Field	Description	*(Optional)* Action
Name	The name of the DNA profile (sample).	Enter a new name for the sample.
Specimen Type	The specimen type assigned to the DNA profile (for example, **Biological Mother** or **Sibling**). • For evidence and reference profiles, the **Specimen Type** column is populated according to the imported sample file. However, if the sample file does not specify a specimen type, the software assigns a specimen type of **Unknown** to evidence profiles and **Reference** to reference profiles. • If you create an evidence profile from a reference profile, the software keeps the specimen type as **Unknown**. • If you create a reference profile from an evidence profile, the software changes the specimen type to **Deduced Reference**.	Select a specimen type from the dropdown list.
Intimate sample	When selected (☑), specifies that a sample is an "intimate" sample. Intimate samples can be used to indicate whether the sample is likely to contain a mixture.	Select (☑) or deselect (☐) the checkbox.
Amount of DNA (ng)	If known, the amount of DNA (ng) in the sample.	Enter the amount of DNA in ng.
Initial NOC	The initial number of contributors for the sample, before running the software algorithms. The initial number of contributors may be known (as for a reference sample) or specified by a user.	Enter an initial estimate for the number of contributors. Base the initial NOC estimation on your interpretation of the filtered EPG. It is easier to estimate the initial NOC in the **Filtered EPG** tab because the artifact peaks are removed.
Final NOC	The final number of contributors specified by the user, after running the software algorithms.	Enter a final estimate for the number of contributors Enter the final NOC estimation after running the NOC algorithms.
Profile comments	Any comments made by a user for the DNA profile (sample).	Enter comments about the DNA profile. These comments are shown in the **Comments** column of the **Profiles** screen.
UDC1, **UDC2**, and **UDC3**	User-defined. Users can define these columns in the CE instrument Data Collection Software or in the GeneMapper™ *ID-X* Software.	Enter or replace the information about the DNA profile. The information is shown in **UDC 1**, **UDC 2**, and **UDC 3** columns in the **Profiles** screen.

Table 10 Summary tab—Editable fields *(continued)*

Field	Description	*(Optional)* Action
The remaining fields cannot be edited in the Summary tab, but can be edited elsewhere in the software, as indicated.		
Profile type	**Evidence** or **Reference**	To change the profile type, see "Turn an evidence profile into a reference profile" on page 69 or "Turn a reference profile into an evidence profile" on page 69.
Flags	Any flags assigned to the sample by the software. For a description of the flags, see "Review flags (Profiles screen)" on page 57.	To add or remove flags, see step 3.
Tags **Note:** The **Tags** field appears only if tags have been added to the sample.	You can use tags to create custom groups for your samples. For example, you can create a tag called "Complex mixtures", tag samples that fall into that group, then run algorithms only on that group.	To add or remove tags, see "Manage samples (Actions button)" on page 64.

Table 11 Summary tab—View-only fields

Field	Description
Origin	The origin of the sample, as determined by the software: • For all profiles (evidence and reference), the software assigns **original** as the origin when the profile is imported into the software. • If you create an evidence profile from a reference profile, the software changes the origin to **hypothetical**. • If you create a reference profile from an evidence profile, the software changes the origin to **hypothetical**.
CPI	The combined probability of inclusion for the currently selected population.
Nr markers with peaks	The number of loci with peaks.
Nr peaks (>AT)	The number of peaks that are above the analytical threshold (AT).
Smallest peak	Minimum peak height (RFU). The smallest peak found in the sample, which can indicate the analytical threshold (AT).
Mean peak height	The mean peak height (RFU) of the sample is calculated as the sum of all peak heights divided by the total number of expected alleles. The number of loci is multiplied by 2 for autosomal samples. For single-source samples, the height directly correlates to the amount of DNA in the sample.

Table 11 Summary tab—View-only fields *(continued)*

Field	Description
Degradation	A description of the degradation level; for example, **Undegraded** or **Severe**. The level is determined by the beta value of the degradation curve. When beta is 0, there is no degradation; the larger beta is, the more degradation there is. The formula to calculate the degraded height for an allele is: undegraded height × 10^ (– bp size × beta) where: • **undegraded height** is the undegraded height of the specific allele • **bp** is the base pair size of the specific allele
MAC	The maximum allele count for different peak heights.
Est Cont	The estimated number of contributors, based on matched samples and the maximum number of alleles.

View a sample electropherogram (EPG) in a new window

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see “Evidence samples table” on page 55 or “Reference samples table” on page 58.
3. In the profiles table, select one or more profiles of interest.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.
4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.
5. Click **View EPG of sample in a new window**.

The sample EPG is displayed in a new window. For more information about reviewing electropherograms, see “View the EPG and filtered EPG” on page 63 and “View sample details—Sample Details tab” on page 63.

Note: If you selected multiple samples, a new EPG window is opened for each sample. However, you can view only one EPG window at a time. Close the current EPG window to display the next one.

View the EPG and filtered EPG

1. View the electropherograms in the **EPG** and **Filtered EPG** tabs:

   Note: The **Filtered EPG** tab is available only for evidence profiles. It is not available for reference profiles.

   - **EPG** tab—Ensure that the sample EPG appears as expected (that is, it looks the same in GeneMapper™ *ID-X* Software).
   - **Filtered EPG** tab—The filtering is automatically applied and performs the following functions, based on the thresholds configured in the model settings:
     - **Stutter**—Removes stutter peaks with heights less than the threshold, then reduces stutter peaks with heights greater than the threshold.
     - **Noise**—Reduces noise peaks with heights greater than the threshold; removes noise peaks with heights less than the threshold.
     - **Shoulder**—*(If active)* Applies to peak heights in shoulder positions. Reduces peaks with heights greater than the threshold; removes peaks with heights less than the threshold.

2. *(If needed)* Adjust the EPG display:
   a. Click **+** to zoom in or click **-** to zoom out.
   b. Click **EPG Settings** to open the **EPG Settings** dialog box. For information on the EPG settings, see “Configure electropherogram (EPG) settings” on page 19.

View sample details—Sample Details tab

1. Display the sample details for the profile of interest.
2. Select the tab of interest:
   - **Summary**—Shows summary information for the selected sample.
   - **Analysis performed**—Lists any algorithms or calculations that have been run on the selected sample (for example, the NOC **Total Peaks** algorithm or the LR calculation).
   - **Height distribution**—Shows the height distributions of the selected sample. For more information, see “View NOC results: Height Distributions tab” on page 78.
   - **Filtered height distribution**—Shows the height distributions of the selected sample after the CAP filter is applied.
   - **Degradation chart**—Shows the estimated degradation level of the selected sample. For more information, see “Show a degradation chart for a sample” on page 70.
   - **Audit**—Lists auditable actions that are tracked by the software. Auditable actions include the following:
     - **Sample updates**—Tracks updates to any sample field, flags added or removed, and tags added or removed; tracks the user role that performed each update
     - **Profile analysis**—Tracks all analyses performed; tracks the user role that performed each analysis
     - **Exports**—Tracks all exports of profiles and results to files; tracks the user role that performed each export

- **NOC Heuristic**—Shows the estimated number of contributors for the selected sample, based on the maximum allele count and the number of loci with more than 2 peaks. It is not a complete NOC analysis.
- **NOC Summary**—This is the same information that is shown in the **NOC Analysis** screen. For more information, see "View NOC results: Contributor Analysis tool" on page 78.

Note: Data in the **Height distribution**, **Filtered height distribution**, **Degradation chart**, and **NOC Heuristic** tabs change after running calculations. The tabs do not continue to show data from the original profile (that is, the profile data that are displayed on import into the software).

Create a filtered sample

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see "Evidence samples table" on page 55 or "Reference samples table" on page 58.
3. In the profiles table, select one or more profiles of interest.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.
4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.
5. Click **Create filtered sample**.
6. To close the confirmation message, click **OK**.

The software applies the CAP filter to the selected sample, then creates another sample entry that contains only the peaks that pass filtering.

Perform actions as needed

Manage samples (Actions button)

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see "Evidence samples table" on page 55 or "Reference samples table" on page 58.

3. In the profiles table, select one or more profiles of interest.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.

   Note: Not all **Manage** options in step 5 can be applied to more than one profile at a time. In those cases, the option will be applied to the last profile that you selected.

4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.

5. Click **Manage** to show the edit menu, select an option, then perform the required actions.

Option	Action
Flag sample	In the **Flag Selection** dialog box, select one or more flags, then click **OK**. The selected flags are displayed in the **Flags** column of the **Profiles** screen.
Remove flag	In the **Flag Selection** dialog box, select one or more flags to remove, then click **OK**. The selected flags are removed from the **Flags** column of the **Profiles** screen.
Tag sample **Note:** You can use tags to create custom groups for your samples. For example, you can create a tag called "Complex mixtures", tag samples that fall into that group, then run algorithms only on that group.	In the **Sample Tag** dialog box, create or edit a tag: • **New tag**—Enter a name for the tag, then click **OK**. • **Existing tag**—Select a tag from the dropdown list, then click **OK**.
Remove tag	In the **Sample Tag** dialog box, select the tag to remove from the dropdown list, then click **OK**.
Set initial # contributors	1. In the **NOC** dialog box, enter an initial estimate for number of contributors. Base the initial NOC estimation on your interpretation of the filtered EPG. It is easier to estimate the initial NOC in the **Filtered EPG** tab because the artifact peaks are removed. 2. Click **OK**. The value is displayed in the **Initial NOC** column. **Note:** The **Filtered EPG** tab is available only for evidence profiles. It is not available for reference profiles. **Note:** The NOC estimation values in the **NOC Analysis** screen automatically synchronize with the values in the **Profiles** screen.
Set final # contributors	1. In the **NOC** dialog box, enter the final estimate for the number of contributors. Enter the final NOC estimation after running the NOC algorithms. 2. Click **OK**. The value is displayed in the **Final NOC** column. **Note:** The NOC estimation values in the **NOC Analysis** screen automatically synchronize with the values in the **Profiles** screen.

(continued)

Option	Action
View/Edit sample in new window	The **Edit sample** window opens: • The top pane shows the same information that is provided in the **Sample Details** tab. See "View sample details—Sample Details tab" on page 63. You can edit items in the **Summary** tab. • The bottom pane shows analytical threshold (AT), stutter, allele, and peak height information for each locus. You can edit values in the **Stutter**, **Forward Stutter**, and **Peak Height** fields. To save changes and close the window, click **OK**.

Compare sample electropherograms (EPGs)

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see "Evidence samples table" on page 55 or "Reference samples table" on page 58.
3. In the profiles table, select two or more samples to compare.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.
4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.
5. Click **Compare EPGs of selected samples**.
6. In the dialog box, select the **EPG Comparison** tab (default selection).
   For the selected samples, electropherograms are displayed for the first locus in the kit. To compare a different locus, use the search, select, or scroll tools at the top of the dialog box. To configure the electropherogram view, see "View the EPG and filtered EPG" on page 63.
7. Select the **Profile Comparison** tab.
   For the selected samples, the alleles for each locus are listed side-by-side.

Export selected samples to a file

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see "Evidence samples table" on page 55 or "Reference samples table" on page 58.

3. In the profiles table, select one or more profiles of interest.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.
4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.
5. Click **Export selected samples to file**.
6. In the dialog box, select a file format, then click **OK**.
7. Complete the required information, based on the file format that you selected.

Option	Action
Export without validation	
Standard CSV file with locus, allele, height	Select the columns to export, then click **OK**.
Standard TXT file with locus, allele, height	
Excel file with all sample information and one sheet per sample (.xlsx)	No further action required for this step.
Excel file sample summary table (.xlsx)	
Export with validation	
CODIS 3.3 XML file (with CoSTR validation)	1. Select a level for the law enforcement agency: **National**, **State**, or **Local**. 2. Enter the number of alleles and the threshold values. 3. Select the populations to consider for validation. 4. Click **OK** to open the **File validation** dialog box. 5. *(If needed)* Edit the fields at the top of the dialog box. These fields appear in the exported file and provide identifying information. The **Source lab** and **Destination lab** are required fields. 6. Review the results summary: • If the proposed export file is valid, the software displays **I found no issues**. • If the proposed export file is not valid, the software displays the number of issues, then provides details for each issue. 7. Click **OK** to export the file. Alternatively, you can click **Cancel**, fix one or more issues, then try exporting again.
RCMF file (Rapid CODIS file format, with CoSTR validation)	
DAT (.dat)	

8. Navigate to a save location, then click **OK** to export the selected samples to a file.

Note: If you selected multiple samples, all samples are exported in a single file. If you saved to the default location, the file is saved to the **Reports** folder for the last sample that you selected. For example, if the last sample you selected was **Sample_9**, the default location would be:
`<installation drive>:\Users\<user name>\Documents\My_PG_Projects\<project name>\Sample_9\Reports`

Combine replicate samples

You can combine replicate samples into one profile for further analysis. For example, to combine data from multiple PCR amplifications of the same low-level DNA extract into one composite profile for mixture analysis. This is helpful if different peaks are detected in the replicate runs.

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see “Evidence samples table” on page 55 or “Reference samples table” on page 58.

3. In the profiles table, select one or more profiles of interest.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.
4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.

5. Click **Combine replicate samples**.
6. In the dialog box, enter information for the combined sample:
   a. Enter a name, or accept the default name.
   b. Select a peak height option:
      - **Average**—Create a new sample with average peak heights. For each bin, the average peak height is taken.
      - **Majority**—Create a new sample with the majority peak heights. For each bin, a peak is taken if it is present in the majority of the samples.
   c. Click **OK**.
7. Click **OK** to close the confirmation message.

The combined sample is added to the profiles table in the **Evidence** or **Reference** tab.

Turn an evidence profile into a reference profile

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Evidence** tab (default selection).

   Note: For a description of the evidence samples table, see “Evidence samples table” on page 55.

3. In the profiles table, select one or more profiles of interest.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.
4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.

5. Click **Turn into reference**.
6. If the software determines that a selected evidence sample has stutter, select or deselect **This profile has stutter**.
   - When selected (☑), the software tries to remove the stutter peaks using the statistical model.
   - When deselected (☐), the software assumes that there is no stutter.
7. Click **Yes**.
   Each selected evidence sample (with stutter and noise peaks) is converted into a reference sample (with only alleles) by removing the stutter and noise peaks. The new reference samples are added to the **Reference** tab.

   Note: The selected evidence samples are not removed from the **Evidence** tab.

8. Click **OK** to close the confirmation message.

Turn a reference profile into an evidence profile

1. In the navigation pane, click **Profiles** (default selection).
2. Select the **Reference** tab.

   Note: For a description of the reference samples table, see “Reference samples table” on page 58.

3. In the profiles table, select one or more profiles of interest.
   - To select multiple, non-adjacent profiles, press **Ctrl+Click**.
   - To select multiple, adjacent profiles, press **Shift+Click**.
4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.

5. Click **Turn into evidence profile (with peak heights)**, then click **OK**.
   Each selected reference sample (with only alleles) is converted into an evidence sample by adding stutter and noise peaks based on the statistical model. The new evidence samples are added to the **Evidence** tab.

   Note: The selected reference samples are not removed from the **Reference** tab.

6. Enter an approximate peak height, then click **OK**.

7. Click **OK** to close the confirmation message.

Show a degradation chart for a sample

The software estimates how much a sample is degraded.

1. In the navigation pane, click **Profiles** (default selection).

2. Select the **Evidence** tab (default selection) or **Reference** tab.

   Note: For a description of each table, see “Evidence samples table” on page 55 or “Reference samples table” on page 58.

3. In the profiles table, select a profile of interest.

4. Click the **Actions** button to show a list of actions.

   Note: Alternatively, right-click any selected profile to show the list of actions.

5. Click **Show degradation chart**.
   The degradation chart opens in a new window, and provides the following information:
   - A determination of how degraded the sample is: **Undegraded**, **Mild**, **Moderate**, **Severe**, **Very Severe**
   - A plot of peak height vs. size for all dye channels
   - A best fit line for all dye channels (purple circles)
   - A best fit line for all dye channels excluding the yellow channel (red squares)

     Note: For the GlobalFiler™ PCR Amplification Kit, the yellow channel is known to be degradation resistant.

5 Perform NOC analysis

Number of contributors (NOC) analysis is a crucial step in resolving mixed profiles in forensic samples. Determining the number of contributors to a mixed sample is necessary for accurate mixture resolution.

Overview of NOC analysis

NOC analysis involves determining the number of contributors to a mixed sample. This can be straightforward for some samples but complex for others. There are several methods for NOC estimation that are available in the software.

Methods for estimating NOC

- Maximum allele count (MAC)
- Total peaks
- TFSPLUS trees
- Fixed Decision trees
- Height distributions

Use of simulated samples

Simulated samples are used to train the following NOC analysis algorithms:

- Total Peaks
- TFSPLUS Decision Tree
- Fixed Decision Tree
- Height distributions

Because many profile modeling parameters determine the simulation results, accuracy of the NOC results depends on how closely the simulated profiles mimic the actual casework sample. If a casework sample behaves differently, the results may not match.

For training these NOC algorithms, 1,000–2,000 simulated samples are sufficient. A greater number of simulated samples will result in smoother distributions and will generally produce more accurate results. However, >2,000 simulated samples takes longer to process and uses a significant amount of memory.

Display the NOC Analysis screen

1. In the navigation pane, click **NOC Analysis**.
   Data are displayed for the most recent profile that you selected in any screen.

2. If you receive a **Population not normalized** message, normalize the population before continuing with the NOC analysis. See “(If needed) Perform population normalization (LR and NOC Analysis screens)” on page 73.

3. To select a different profile:
   a. In the toolbar, click **Evidence**.
   b. In the **Profile Selection** dialog box, select a profile from the dropdown list, then click **OK**.

Note: Alternatively, you can scroll left (‹) or right (›) in the **Evidence** button to select a different profile.

---

4. If you are signed into the software in Validation mode, you can access the items and tasks shown in the NOC Analysis screen.

Figure 4 NOC Analysis screen

① **Profiles** app
② The currently selected profile (sample)
③ Configure settings.
④ Analysis tabs.
⑤ Contributor Analysis tool.
⑥ **NOC Analysis** screen toolbar.
⑦ Menu bar and primary toolbar.

(If needed) Perform population normalization (LR and NOC Analysis screens)

If you receive a **Population not normalized** message when you open the **NOC Analysis** screen or the **LR** screen, perform this procedure before continuing.

1. Click **OK** to close the **Population not normalized** message.
2. In the navigation pane, select **Configure** ▸ **Popstats**.
3. Select the tab for the population to normalize.
   Allele and frequency information is displayed for the selected population.
4. *(If needed)* Select a minimum allele frequency formula:
   - **1/(N+1)**
   - **5/(2N)**
   - **Custom**; if you select **Custom**, enter a value

   Note: The population size (N) represents the total number of samples in the population. You need to specify the value when import a population file. The value of N can be changed, if needed.

   Values are normalized to the selected formula.
5. Click fx **Normalize**.
6. To close the confirmation message, click **OK**.

Start the NOC analysis

You can run the NOC algorithms one at a time or run multiple algorithms at once.

Note: If your computer does not meet the minimum CPU and RAM requirements, you will not be able to run multiple algorithms at once. See “Requirements” on page 10.

1. Display the **NOC Analysis** screen for the sample of interest. See “Display the NOC Analysis screen” on page 72.
2. To run a single algorithm:
   a. Select a tab for the algorithm to run.
      - **MAC**
      - **Total Peaks**
      - **TFSPLUS Tree**
      - **Fixed Decision Tree**
      - **Height Distributions**

   b. Select **Enabled**  .

c. In the selected tab, click **Run**.

3. To run multiple algorithms at once:
   a. For each algorithm to run, select the algorithm tab, then select **Enabled**.
   b. In the toolbar, click **Run all algorithms**.

   The calculation can take several minutes. When complete, the results are displayed. See "View the NOC analysis results" on page 74.

View the NOC analysis results

This section provides information on each tab in the **NOC Analysis** screen. Click through each tab to view the results.

IMPORTANT! Use caution when interpreting the NOC analysis results. In general, the lower the AT and the greater the DNA amount, the more accurate the results are. NOC accuracy is calculated as a function of the analytical threshold (AT) and mean peak height (PH) of the profile for 1–4 contributors. Using the PROVEDIt dataset (~4,100 profiles) for 2 contributors, with a mean PH of 10,010 RFU and a mean AT (averaged across all loci) of 50 RFU, the NOC accuracy is ~95.45%. See "View NOC results: Contributor Analysis tool" on page 78.

View NOC results: EPG tab

1. Display the **NOC Analysis** screen for the sample of interest. See "Display the NOC Analysis screen" on page 72.
2. Click a population tab.
3. Select the **EPG** tab (default selection).
4. View the electropherograms in the **EPG** and **Filtered EPG** tabs:

   Note: The **Filtered EPG** tab is available only for evidence profiles. It is not available for reference profiles.

   - **EPG** tab—Ensure that the sample EPG appears as expected (that is, it looks the same in GeneMapper™ *ID-X* Software).
   - **Filtered EPG** tab—The filtering is automatically applied and performs the following functions, based on the thresholds configured in the model settings:
     - **Stutter**—Removes stutter peaks with heights less than the threshold, then reduces stutter peaks with heights greater than the threshold.
     - **Noise**—Reduces noise peaks with heights greater than the threshold; removes noise peaks with heights less than the threshold.
     - **Shoulder**—*(If active)* Applies to peak heights in shoulder positions. Reduces peaks with heights greater than the threshold; removes peaks with heights less than the threshold.

5. *(If needed)* Adjust the EPG display:
   a. Click **+** to zoom in or click **-** to zoom out.
   b. Click **EPG Settings** to open the **EPG Settings** dialog box. For information on the EPG settings, see “Configure electropherogram (EPG) settings” on page 19.
6. Enter your NOC estimations:
   - **Initial NOC estimation**—Base the initial NOC estimation on your interpretation of the filtered EPG. It is easier to estimate the initial NOC in the **Filtered EPG** tab because the artifact peaks are removed.
   - **Final NOC estimation**—Enter the final NOC estimation after running the NOC algorithms.

   Note: The NOC estimation values in the **NOC Analysis** screen automatically synchronize with the values in the **Profiles** screen.
7. *(Optional)* Enter comments in the **Analysis comments** field.

View NOC results: MAC tab

MAC is the maximum allele count for different peak heights.

Instead of computing the MAC for this sample using all peaks, the algorithm computes the MAC multiple times by choosing peaks above a specified height. This allows you to see if the MAC changes for larger peaks. Often, the MAC is large because of stutter or noise; these peaks will disappear for larger peak heights.

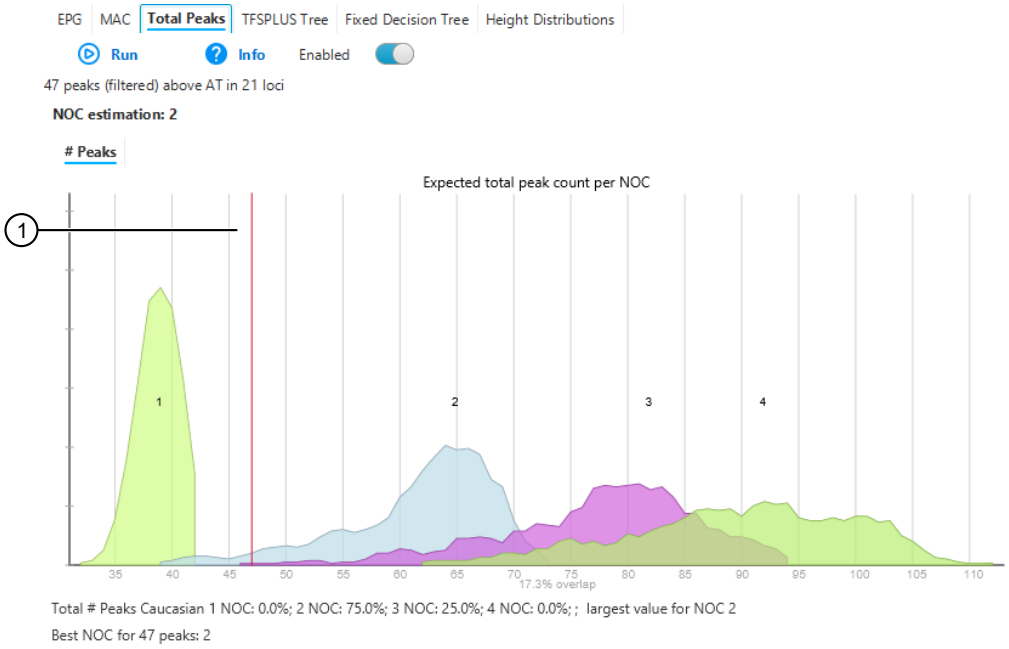
1. Display the **NOC Analysis** screen for the sample of interest. See “Display the NOC Analysis screen” on page 72.
2. Click a population tab.
3. Select the **MAC** tab.
4. View the following charts:
   - **MAC vs ph**—Shows the MAC for different peak heights.
   - **MAC vs %**—Shows the MAC for different peak heights as a percentage relative to the mean peak height per locus.

- For a robust single-source sample, most MAC values will be ~100% for 2 alleles per locus.
- For mixture samples, an example result could show maximum allele counts >2 at 15% of the peak height. For a sample that has maximum allelic peaks of 4,000 RFU, this corresponds to low-level peaks of ~600 RFU. Because such a high stutter is unlikely, the **MAC vs %** chart indicates that this may be a mixture. The software cannot determine if it is a mixture of more than two people because the MAC algorithm can underestimate the number of contributors due to shared alleles.

View NOC results: Total Peaks tab

The total peaks algorithm simulates samples of varying NOC, counts the total number of peaks seen, plots the resulting counts according to NOC, then shows the total peak count for the currently selected sample.

1. Display the **NOC Analysis** screen for the sample of interest. See “Display the NOC Analysis screen” on page 72.
2. Click a population tab.
3. Select the **Total Peaks** tab.
4. Under **# Peaks**, view the following:
   - The number of filtered peaks above the AT
   - The best NOC estimate for the sample
   - A chart that shows the expected total peak count per NOC for the simulated samples. The selected profile is the red vertical line.



(1) Selected profile

IMPORTANT! Because the algorithm is run on simulated samples, results are highly dependent on the selected settings. If the settings do not align well with the observed data, the results may be misleading. For more information, see “Use of simulated samples” on page 71.

View NOC results: TFSPLUS and Fixed Decision Tree tabs

Decision trees are machine learning algorithms that are commonly used for classification purposes.

The two decision tree algorithms in the GeneMapper™ PG Software use DNA profile features for classification. For example, some of the features used by the trees include the following:

- Total number of peaks
- Maximum allele count
- Number of loci with >3 peaks
- Variance of the peak count

Note: To see the full list of features for each tree: Select the tree tab of interest, then click **Info**.

- **TFSPLUS**—Runs the J48 decision tree algorithm with a specific set of features on a set of simulated samples, then displays the results for the currently selected sample.
- **Fixed Decision Tree**—Optimizes the thresholds of this fixed tree, but leaves the tree structure as it is.

1. Display the **NOC Analysis** screen for the sample of interest. See “Display the NOC Analysis screen” on page 72.
2. Click a population tab.
3. Select the **TFSPLUS Tree** tab to view the following information:

Tab	Description
Decision Tree	Displays the NOC result and the tree structure that produced the result. The tree structure is made of features (for example, mean peak height) at nodes with branches leading to a final NOC determination. For more information, see “View NOC results: TFSPLUS and Fixed Decision Tree tabs” on page 77.
Text	Displays the tree in text form (if/then statements).
Stats	Displays a bar chart that plots the NOC results vs. the score. The "score" is a percentage attributed to each estimated number of contributors. The highest bar in the chart indicates which NOC result is the best fit.

4. Select the **Fixed Decision Tree**—Displays the NOC result and the tree structure that produced the result. The tree structure is made of features (for example, mean peak height) at nodes with branches leading to a final NOC determination. For more information, see “View NOC results: TFSPLUS and Fixed Decision Tree tabs” on page 77.

Decision trees allow you to follow the logic of a complex algorithm as it was applied by the software. However, decision trees can be "overfitted". Overfitting occurs when the model is too complex—the tree fits the training data well, but cannot generalize to new, unseen data.

IMPORTANT! Because the algorithm is run on simulated samples, results are highly dependent on the selected settings. If the settings do not align well with the observed data, the results may be misleading. For more information, see “Use of simulated samples” on page 71.

View NOC results: Height Distributions tab

The height distributions algorithm plots the height distributions for random samples of different contributors and compares them to the height distributions of the current sample.

1. Display the **NOC Analysis** screen for the sample of interest. See “Display the NOC Analysis screen” on page 72.
2. Click a population tab.
3. Select the **Height Distributions** tab.
4. View the following charts:
   - **Frequency Charts**—Shows 2 bar charts for each NOC. Chart 1 (left) is the current sample; chart 2 (right) is many random samples. In the frequency charts, select different overlay views:
     - **Overlay target**—Overlay the observed profile distribution (target) with the expected distribution for NOC 1–4 to see which looks like the best match. As the NOC increases, expect to see a broader range of peak heights (a more spread-out distribution).
     - **Overlay diff**—Overlay the difference in peak height values between the current sample and the random sample.
     - **All in one view**—Vertically stacks chart 2 (the random sample) for each NOC on the same page, instead of displaying each chart in its own tab. In the **All in one view**, you may need to scroll down to view all of the charts.

     Look for how well the distribution of the current sample matches the distributions of random samples of different NOCs.
   - **Score Chart**—Displays a bar chart that plots the NOC results vs. the score. The "score" is a percentage attributed to each estimated number of contributors. The highest bar in the chart indicates which NOC result is the best fit.
5. *(If needed)* Adjust the size of the frequency charts: Click **+** to zoom in or click **-** to zoom out.

IMPORTANT! Because the algorithm is run on simulated samples, results are highly dependent on the selected settings. If the settings do not align well with the observed data, the results may be misleading. For more information, see “Use of simulated samples” on page 71.

View NOC results: Contributor Analysis tool

The Contributor Analysis tool provides:

- A summary of how well the algorithms agree
- The best result possible, assuming the observed data perfectly matches the simulated samples
- Limitations, based on the peak height and the minimum ratio selected for the simulation

1. Display the **NOC Analysis** screen for the sample of interest. See “Display the NOC Analysis screen” on page 72.
2. View the Contributor Analysis tool in the right pane. If needed, click-drag to expand the pane.
3. To view a summary of the results, select the **NOC Summary** tab (default selection). For each algorithm that was run, the table displays the accuracy percentage for each NOC.
4. To view the results as a graph, select the **NOC Accuracy Chart** tab. In the chart, you can adjust the AT and mean PH to see different outcomes. Accuracy values using the PROVEDIt dataset are provided below the graph.
5. To view the results as a bar chart, select the **NOC Bar Chart** tab.
6. To see all features used by the TFSPlus Tree algorithm, select the **TFSPlus List** tab.

Create a random example

Random examples can be useful for testing or exploration purposes.

1. Display the **NOC Analysis** screen for the sample of interest. See “Display the NOC Analysis screen” on page 72.
2. In the toolbar, click **Random**.
   The software displays a random sample in the **EPG** tab.
3. You can perform the same functions in the **NOC Analysis** screen for the random example as you can for any "real" sample. For example, you can adjust the number of contributors or run any NOC algorithm.
4. To create another random example, click **Random**.

Random examples do not persist in the software and cannot be saved. The random examples disappear if you create a new random example, select a different "real" sample, or close the software.

6 Perform deconvolution

Deconvolution is the process of analyzing mixed samples to establish the genotypes of individual contributors. The goal is to separate or deconvolute the mixture into constituent profiles.

Display the Deconvolute screen

1. In the navigation pane, click **Deconvolute**.
   Data are displayed for the most recent profile that you selected in any screen.

2. To select a different profile:
   a. In the toolbar, click **Evidence**.

   b. In the **Profile Selection** dialog box, select a profile from the dropdown list, then click **OK**.

   Note: Alternatively, you can scroll left (<) or right (>) in the **Evidence** button to select a different profile.

3. If you are signed into the software in Validation mode, you can access the items and tasks shown in the Deconvolute screen.

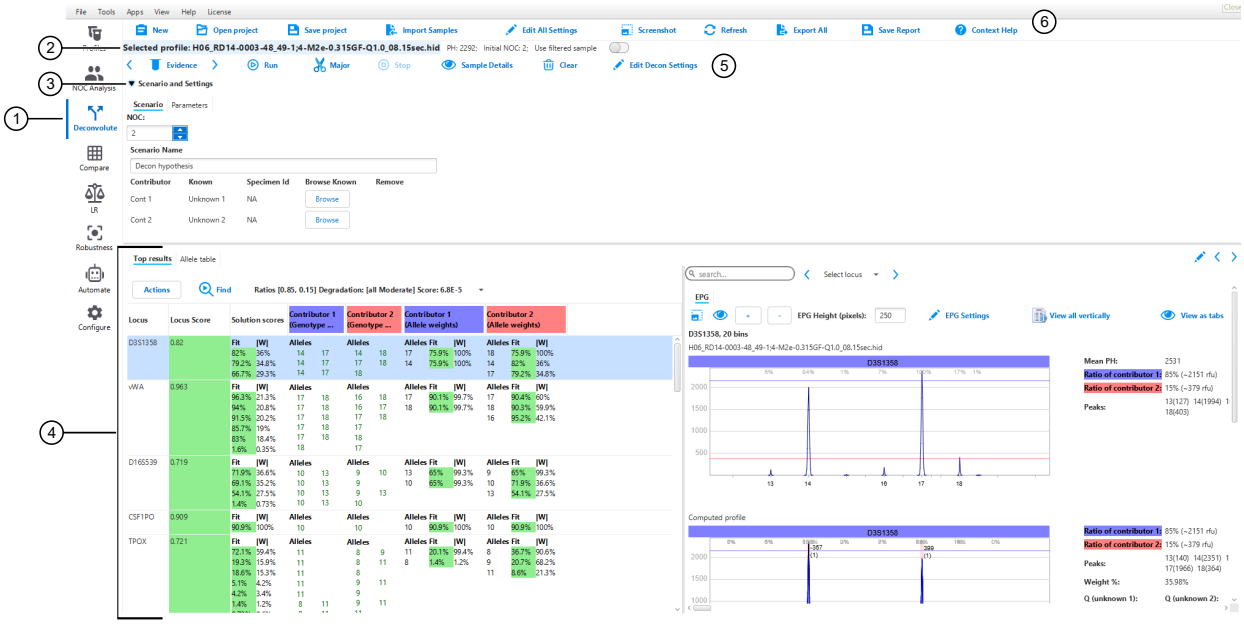


Figure 5 Deconvolute screen

1. **Deconvolute** app
2. The currently selected profile (sample)
3. Configure the deconvolution scenario and parameters; see “Configure the scenario and parameters (Deconvolute screen)” on page 81
4. Analysis tabs.
5. **Deconvolute** screen toolbar.
6. Menu bar and primary toolbar.

Configure the deconvolution settings

Configure the scenario and parameters (Deconvolute screen)

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Click the **Scenario and Settings** arrow to expand the pane.
3. Click the **Scenario** tab (default selection).
4. In the **NOC** field, select the number of contributors to deconvolute the profile into.
5. In the **Scenario Name** field, enter a name for the hypothesis.
6. To add a known profile to a contributor: In the **Browse Known** column, click **Browse**, then select a profile.

   Note: To remove a known profile, click **Remove**.
7. Click the **Parameters** tab, then configure the settings as needed.
8. To use the updated settings, run the deconvolution.

Edit the deconvolution settings

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. In the toolbar, click **Edit Decon Settings**.
3. In the **Parameters** dialog box, configure the settings as needed.
4. Click **OK** to save the settings and close the **Parameters** dialog box.
5. To use the updated settings, run the deconvolution.

Minimal ratio

The minimum ratio is used for the deconvolution and the LR calculation.

The minimal ratio defines the smallest mixture ratio that can be detected. At the default value of 0.1, the software can detect a minor contributor comprising 10% of the mixture. With this setting, lower values such as 0.01, 0.02, or 0.05 will not be considered by the software for minor contributors.

Start deconvolution

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. In the toolbar, click **Run**.
   The calculation can take several minutes. When complete, the results are displayed. See “View the deconvolution results” on page 82.

View the deconvolution results

Results will vary if you use different settings (for example, a different analytical threshold, dropin limit, or dropout limit). However, if you use the same settings, you will always get the same result because the algorithm is deterministic.

View deconvolution results: Top results tab—loci table

In the **Top results** tab, the loci table (left pane) displays the deconvolution results for each locus in the profile.

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Select the **Top results** tab (default selection).
3. Select a ratio.
4. Click **Find** to match the unknowns to references.

5. Select the level of detail to display in the loci table: Select **Actions ▸ Detail level**, then select an option:

Option	Description
Show just top alleles	Displays only the most likely alleles for each contributor, showing the simplest view of the results.
Show just alleles of all solutions	Displays the alleles and weights for the complete genotypes, but hides the column containing the scores (Fit and Weight).
Show all alleles with scores	Displays all considered alleles along with their Fit and Weight scores. This view includes: • All derived genotype combinations • Solution scores for each combination • Individual allele weights for each contributor.
Show all possible detail	In addition to the information shown for Show all alleles with scores, this option also displays peaks that were part of the solution but are not alleles. For example, stutter. Place the pointer over any of the peaks in the table for more detail on it, if needed.

6. In the loci table, review the results for each contributor. *The top row contains the best solution.*

Table 12 Loci table (with Show all possible detail selected)

Item	Description
Locus	Locus designation (the name of the locus).
Locus Score	The overall locus score that the software assigns to the unknowns that best explains the evidence (including any knowns). The score is the product of the individual fit scores per locus and is dependent on the model settings and ratios used. A perfect match is **1.000**.
Solution scores column	
Fit and **[W]**	The fit and weight of the locus for each possible solution. • **Fit**—The fit indicates how well the solution matched the evidence profile for the locus. The fit value includes dropins, dropouts, stutter, peak height imbalance, and so on. (A perfect score is 100%, which is usually not achievable.) • **[W]** (weight)—The weight is the normalized weight of the solutions compared to each other. The values add up to 100%. The weight can be useful as a relative comparison, but the fit indicates how well the solution fits the evidence profile. For example, there may be only one solution (weight 100%), but the fit to the profile can be poor (small fit value)—possibly due to incorrect conditioning or an incorrect number of contributors. On the other hand, there can be multiple solutions that are all good; in that case, the weight would be small, but the fit would be large.
Cont `<n>` **(Genotype weights) columns, where** `<n>` **is the contributor number (contributor 1, contributor 2, and so on)**	
Alleles	The alleles assigned to each contributor. Hover the pointer over the values to see a breakdown of solutions and corresponding scores.

Table 12 Loci table (with Show all possible detail selected) *(continued)*

Item	Description
Cont <n> (Allele weights) columns, where <n> is the contributor number (contributor 1, contributor 2, and so on)	
Alleles	The alleles assigned to each contributor. Hover the pointer over the values to see a breakdown of solutions and corresponding scores.
Fit and **[W]**	The fit and weight for each possible solution at a locus.

7. *(If applicable)* Review color-coding: If you associated the truth to the deconvolution, the following colors indicate which alleles were matched (for validation):
   - **Green**—The allele was in the truth.
   - **Red**—The allele was not in the truth.
   - **Pink plus "x"**—The truth includes this allele, but it was not part of the solution.

   Note: The "truth" is a contributor who is known to be part of a mixture. For more information, see "Associate truth" on page 90.

Perform a simple deconvolution (major contributor only)

Use this procedure to extract only the top/major contributor of a mixture sample.

1. Display the **Deconvolute** screen for the sample of interest. See "Display the Deconvolute screen" on page 80.
2. In the toolbar, click **Major**.
3. To import settings, click **Import**, navigate to the settings file (JSON) of interest, then click **Open**.
4. To export settings, click **Export All**, enter a file name, navigate to a save location, then click **Save** to save the settings as a JSON file.
5. To compare settings, click **Compare Settings**, navigate to the settings file (JSON or CSV) of interest, then click **Open**.
6. To use the factory default settings for deconvolution, click **Factory reset**.
7. Click **OK**.
   The software displays results for a possible major contributor and the largest minor contributor. For more information about deconvolution results, see "View the deconvolution results" on page 82.

Perform actions as needed

View additional information in a new screen

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Select the **Top results** tab (default selection).
3. Click the **Actions** button to display a list of actions.

   Note: Alternatively, in the loci table (left pane), right-click a locus to display the list of actions.

4. In the list, select **View**, then select an option:
   - **View solution details (alternatives) for selected locus**—Displays ratio details. Select the number of solutions to view, then click **OK**.
   - **View unknown profile <n>**—Displays the EPG and sample details for the selected unknown profile.

     Note: This view does not display filtered EPGs.

Add derived profiles

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Select the **Top results** tab (default selection).
3. Click the **Actions** button to display a list of actions.

   Note: Alternatively, in the loci table (left pane), right-click a locus to display the list of actions.

4. In the list, select an option:

Option	Action
Add TOP derived profiles	For top derived profiles, the software considers only the top alleles. 1. In the dialog box, select the unknowns, the minimum weight, and the minimum fit to add, then click **OK**. The derived profiles that meet the selected criteria are displayed. 2. Review the profiles, then click **OK**. 3. To close the confirmation message, click **OK**. The derived profiles are added to the **References** tab in the **Profiles** screen. The following columns are automatically populated: • **Profile name** column—The original sample name with the prefix **Minor** or **Major**; for example, **Minor_Test sample** or **Major_Test sample**. • **Specimen Type** column—**Deduced Suspect**. • **Origin** column—**derived**.
Add COMBINED derived profiles	For combined derived profiles, the software considers all possible allele combinations. 1. In the dialog box, select the unknowns, the minimum weight, and the minimum fit to add, then click **OK**. The derived profiles that meet the selected criteria are displayed. 2. Review the profiles, then click **OK**. 3. To close the confirmation message, click **OK**. The derived profiles are added to the **References** tab in the **Profiles** screen. The following columns are automatically populated: • **Profile name** column— **Combined_unknown_**<n>, where <n> depends on the number of profiles that were exported; for example **Combined_unknown_1**, **Combined_unknown_2**, and so on. • **Specimen Type** column—**Unknown**. • **Origin** column—**derived**.
Add derived evidence profiles (with peak heights)	For derived evidence profiles, the software considers alleles from the selected profiles. 1. In the dialog box, select the profiles to add to evidence, then click **OK**. 2. To close the confirmation message, click **OK**. The derived profiles are added to the **Evidence** tab in the **Profiles** screen. The following columns are automatically populated: • **Profile name** column—The original sample name with the prefix **Minor** or **Major**; for example, **Minor_Test sample** or **Major_Test sample**. • **Specimen Type** column—**Computed Unknown**. • **Origin** column—**derived**.

Export top derived profiles

For top derived profiles, the software considers only the top alleles.

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Select the **Top results** tab (default selection).
3. Click the **Actions** button to display a list of actions.

   Note: Alternatively, in the loci table (left pane), right-click a locus to display the list of actions.
4. In the list, select **Export TOP derived profiles**.
5. In the dialog box, select the unknowns, the minimum weight, and the minimum fit to export, then click **OK**.
   The derived profiles that meet the selected criteria are displayed.
6. Review the profiles, then click **OK**.
7. In the dialog box, select a file format, then click **OK**.
8. Complete the required information, based on the file format that you selected.

Option	Action
Export without validation	
Standard CSV file with locus, allele, height	Select the columns to export, then click **OK**.
Standard TXT file with locus, allele, height	
Excel file with all sample information and one sheet per sample (.xlsx)	No further action required for this step.
Excel file sample summary table (.xlsx)	
Export with validation	
CODIS 3.3 XML file (with CoSTR validation)	1. Select a level for the law enforcement agency: **National**, **State**, or **Local**. 2. Enter the number of alleles and the threshold values. 3. Select the populations to consider for validation. 4. Click **OK** to open the **File validation** dialog box. 5. *(If needed)* Edit the fields at the top of the dialog box. These fields appear in the exported file and provide identifying information. The **Source lab** and **Destination lab** are required fields.

(continued)

Option	Action
RCMF file (Rapid CODIS file format, with CoSTR validation)	**6.** Review the results summary: • If the proposed export file is valid, the software displays **I found no issues**. • If the proposed export file is not valid, the software displays the number of issues, then provides details for each issue. **7.** Click **OK** to export the file. Alternatively, you can click **Cancel**, fix one or more issues, then try exporting again.
DAT (.dat)	

9. Navigate to a save location, then click **OK** to export the profiles to a file.

Export combined derived profiles

For combined derived profiles, the software considers all possible allele combinations.

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Select the **Top results** tab (default selection).
3. Click the **Actions** button to display a list of actions.

   Note: Alternatively, in the loci table (left pane), right-click a locus to display the list of actions.

4. In the list, select **Export COMBINED derived profiles**.
5. In the dialog box, select the unknowns, the minimum weight, and the minimum fit to export, then click **OK**.
   The derived profiles that meet the selected criteria are displayed.
6. Review the profiles, then click **OK**.
7. In the dialog box, select a file format, then click **OK**.
8. Complete the required information, based on the file format that you selected.

Option	Action
Export without validation	
Standard CSV file with locus, allele, height	Select the columns to export, then click **OK**.
Standard TXT file with locus, allele, height	
Excel file with all sample information and one sheet per sample (.xlsx)	No further action required for this step.

(continued)

Option	Action
Excel file sample summary table (.xlsx)	No further action required for this step.
Export with validation	
CODIS 3.3 XML file (with CoSTR validation)	1. Select a level for the law enforcement agency: **National**, **State**, or **Local**. 2. Enter the number of alleles and the threshold values. 3. Select the populations to consider for validation. 4. Click **OK** to open the **File validation** dialog box. 5. *(If needed)* Edit the fields at the top of the dialog box. These fields appear in the exported file and provide identifying information. The **Source lab** and **Destination lab** are required fields. 6. Review the results summary: • If the proposed export file is valid, the software displays **I found no issues**. • If the proposed export file is not valid, the software displays the number of issues, then provides details for each issue. 7. Click **OK** to export the file. Alternatively, you can click **Cancel**, fix one or more issues, then try exporting again.
RCMF file (Rapid CODIS file format, with CoSTR validation)	
DAT (.dat)	

9. Navigate to a save location, then click **OK** to export the profiles to a file.

Match derived profiles to all references

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Select the **Top results** tab (default selection).
3. Click the **Actions** button to display a list of actions.

   Note: Alternatively, in the loci table (left pane), right-click a locus to display the list of actions.

4. In the list, select **Match derived profiles to all references**.
5. In the dialog box, select the **Matches with Alternatives** tab (default selection), then review any reference profiles that match the derived profiles.
6. Select the **Match List** tab to view any matches between the computed unknown contributors and the reference profiles. To be considered a match, the profiles must meet the specified match % threshold.
7. To close the dialog box, click **OK**.

Associate truth

The "truth" is a contributor who is known to be part of a mixture. For example, in a case where the victim is known, the DNA of the victim is the "truth".

To determine if there were any mismatches in the deconvolution, associate the truth to the solution.

1. Display the **Deconvolute** screen for the sample of interest. See “Display the Deconvolute screen” on page 80.
2. Select the **Top results** tab (default selection).
3. Click the **Actions** button to display a list of actions.

   Note: Alternatively, in the loci table (left pane), right-click a locus to display the list of actions.
4. In the list, select **Associate Truth**.
5. In the dialog box, pick a truth from the dropdown list, then click **OK**.
6. To determine how well the alleles of the contributor profiles match the associated truth, place the cursor over the contributor column header to view the percentage of alleles that were matched.
7. For each locus in the table, view the highlighted alleles.
   - If there are green highlighted alleles throughout the deconvoluted profile, the truth profile is likely a contributor to the mix. In this case, you can condition the likelihood ratio on the truth profile.
   - If there are alleles in the deconvoluted profile that are not highlighted in green, the truth profile is likely not a contributor to the mix. Note the following:
     - An allele preceded by an "x" indicates dropout in a potential solution.
     - A red allele indicates that the allele is in the derived solution, but not in the reference profile.

Save a report for the current screen

The data that are reported depends on the current screen.

1. In the primary toolbar, click **Save Report**.
2. Follow the prompts to perform the next steps. The steps differ, depending on the screen that you are currently in.

7 Determine the likelihood ratio (LR)

The likelihood ratio (LR) is a statistic used to provide weight for a given proposition explaining an observed evidence profile. The LR is a comparison of two conditional probabilities:

- The probability of the observed evidence profile given that a person of interest (POI) is a contributor to the DNA (generally denoted as "H_p" or "H_1").
- The probability of the observed evidence profile given that some other unknown, unrelated individual is the true contributor ("H_d" or "H_2").

Deconvolution vs. LR

Option	Description
Deconvolution	• Typically used for analyzing a mixed evidence sample in isolation. • The relevant population is not known; therefore, allele frequencies are not applied. • You can perform conditional deconvolution using a POI reference profile. For example, if you have a POI reference profile from the victim, you can use this information to isolate and deconvolute the DNA of other contributors.
LR	• LR analysis involves hypotheses that include a POI reference profile. • It is important to select the correct allele frequencies for this analysis. – The model uses allele frequencies to check how likely it is for a specific allele to appear by chance. This likelihood changes based on how common the allele is in the population. – Allele frequencies are also used for calculating match probabilities within the LR calculation. – The LR calculations use the Balding Nichols equations. These equations include allele frequencies and theta to find the probability of observing a specific genotype.

Display the LR screen

1. In the navigation pane, click **LR**.
   Data are displayed for the most recent profile that you selected in any screen.

2. If you receive a **Population not normalized** message, normalize the population before continuing with the LR calculation. See "(If needed) Perform population normalization (LR and NOC Analysis screens)" on page 73.

3. To select a different profile:
   a. In the toolbar, click **Evidence**.
   b. In the **Profile Selection** dialog box, select a profile from the dropdown list, then click **OK**.

Note: Alternatively, you can scroll left (<) or right (>) in the **Evidence** button to select a different profile.

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4. If you are signed into the software in Validation mode, you can access the items and tasks shown in Figure 6.

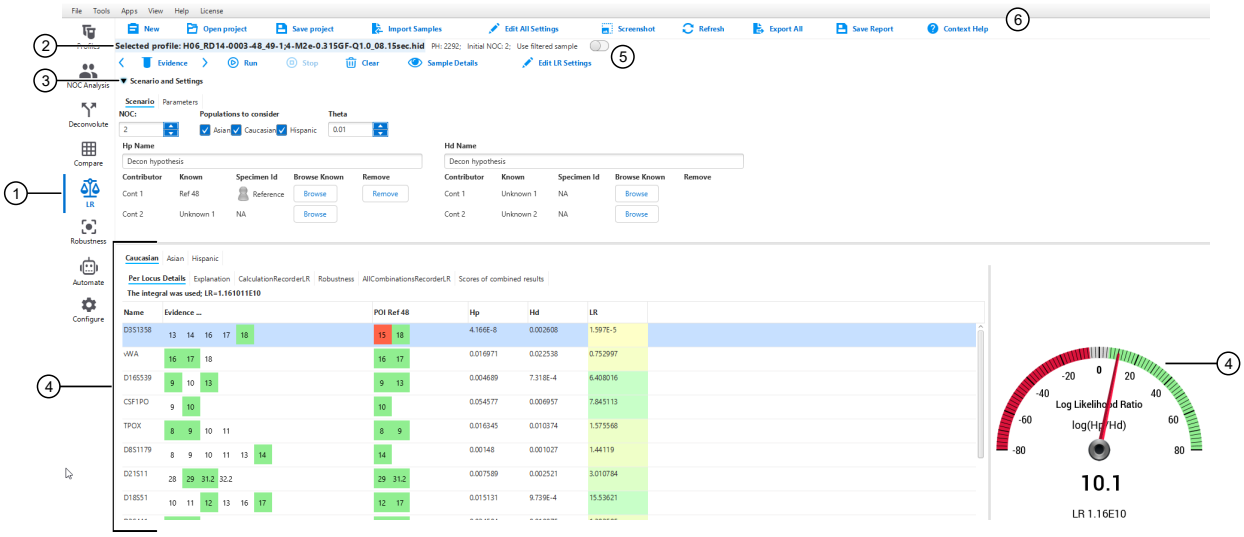


Figure 6 LR screen

1. **LR** app
2. The currently selected profile (sample)
3. Configure settings; see "Configure the scenario and settings for the LR calculation" on page 93
4. View results (population and analysis tabs); see:
   - "View LR results: Gauge (overall LR value)" on page 96
   - "View LR results: Per Locus Details tab" on page 97
   - "View LR results: Explanation tab" on page 99
   - "View LR results: Overall Log tab (information level)" on page 100
   - "View LR results: CalculationRecorderLR tab" on page 101
   - "View LR results: Robustness tab" on page 101
   - "View LR results: AllCombinationsRecorderLR tab" on page 102
   - "View LR results: Scores of combined results tab" on page 102
   - "Analyze a locus in detail (information level)" on page 95
5. **LR** screen toolbar:
   - Select a different profile
   - Start or stop the calculation; see "Start or stop the LR calculation" on page 95
   - Clear results.
   - Display the **Sample details** screen; see "View sample details—Sample Details tab" on page 63
   - Display the **Parameters** screen for the LR settings; see "Edit the LR settings" on page 95
6. Menu bar and primary toolbar.

Configure the LR settings

Configure the scenario and settings for the LR calculation

1. Display the **LR** screen for the sample of interest. See "Display the LR screen" on page 92.
2. Click the **Scenario and Settings** arrow to expand the pane.
3. Click the **Scenario** tab (default selection).
4. Enter or select the number of contributors (NOC).
5. Select (☑) the checkbox for one or more populations.

6. Enter a theta value. (The theta value is the inbreeding coefficient.)
7. Complete the Hp and Hd information:
   a. In the **Hp Name** and **Hd Name** fields, enter names for the hypotheses.
   b. To add a known profile to a contributor: In the **Browse Known** column, click **Browse**, then select a profile.

   IMPORTANT! For **Hp**, you must pick at least one known profile.

   Note: To remove a known profile, click **Remove**.
8. Click the **Parameters** tab, then configure the settings as needed.
9. To use the updated settings, run the LR calculation.

Theta

You can enter a specific value for theta or use the default value of 0.01. Theta, also known as the inbreeding coefficient, represents the level of relatedness in genetic analysis. It accounts for the fact that allele frequencies are not entirely random and independent, as individuals in a population are related to some extent.

A theta value of 0 represents no inbreeding, indicating complete genetic differentiation. A theta value of 1 represents complete inbreeding, meaning the populations are genetically identical. The software allows for theta values from 0.0–0.5.

Scenario	Explanation
Default Value	.01
Large populations	Low value, such as the default. For example, Caucasians in North America.
Small populations	Higher value (for example 0.03) for smaller, more isolated populations, For example, a population on a small island.

For more information, see page 8: **https://strbase-archive.nist.gov/pub_pres/NJSP2006_Statistics.pdf**.

How ratios are computed for LR

How ratios are computed determines the method for computing the LR.

Option	Description
SPECIFIED—Recommended	Uses a user-specified ratio. If none are given, uses equal proportions (such as 1:1:1).
DEFENSE	Uses the Hd hypothesis to find the optimal ratio, then applies it to both Hp and Hd hypotheses.
INDIVIDUAL	Calculates and applies the optimal ratio for each hypothesis individually.
INTEGRAL	Uses the integral of all the scores for all ratios, such as 1:2:3, 1:3:5, and so on.

Edit the LR settings

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. In the toolbar, click **Edit LR Settings**.
3. In the **Parameters** dialog box, configure the settings as needed.
4. Click **OK** to save the settings and close the **Parameters** dialog box.
5. To use the updated settings, run the affected algorithms.

Start or stop the LR calculation

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. In the toolbar, click **Run**.
   The calculation can take several minutes. When complete, the results are displayed. See “View the LR results” on page 96.
3. To stop the calculation, select an option:
   - In the **Computing** progress bar, click **Stop tasks**.
   - In the toolbar, click **Stop**.

Note: The stop options may not be available if the calculation completes quickly.

Analyze a locus in detail (information level)

This feature can help determine the cause of unexpected results (for example, a parameter that is not properly set). The information level that you select applies to only one locus.

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. Click a population tab.
3. Select the **Per Locus Details** tab (default selection).
4. Right-click the locus to analyze, then select **Analyze Locus in detail** to display the **Info Level** dialog box.
5. Select an information level to determine the amount of information that is displayed. Greater levels show more information, but can cause the software to run slowly.

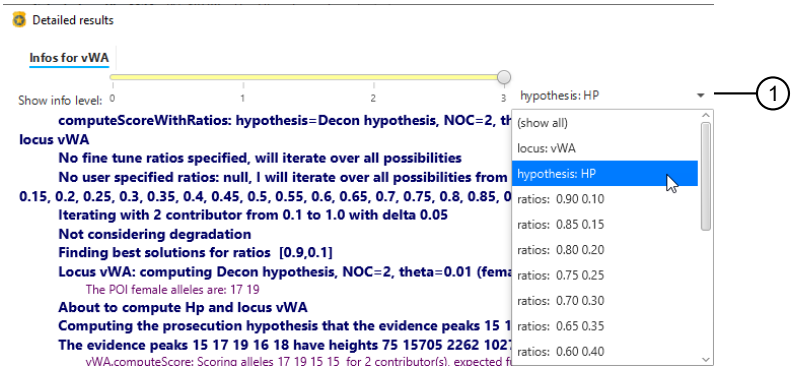
Note: A high information level significantly slows the processing time. At a level >5, it can take several minutes for the software to update; the software may also freeze because levels >5 can result in thousands of lines of information. After viewing the information of interest, we recommend that you change the value back to 0 or 1.

6. Click **OK**.
   After analysis, the **Detailed results** dialog box is displayed for the selected locus.

7. Select the **Info** tab (default selection), select an information level, then view the results.

   Note: The information level available in the **Detailed results** dialog box depends on the level that you selected in step 5. For example, if you selected **3**, you can select **0**, **1**, **2**, or **3** in the **Detailed results** dialog box. If you selected **1**, you can select only **0** or **1** in the dialog box.

8. To filter the information that is displayed, select an option in the dropdown list to the right of the **Show info level** slider. The default selection is **(show all)**.



① Dropdown list

9. *(Optional)* To export the log (TXT file), click **Export All**, navigate to a save location, then click **Save**.
   The TXT file is saved to the selected location, and automatically opens. To close, click **X**.

10. To close the dialog box, click **OK**.

View the LR results

The LR results that are displayed depend on the selected settings. For example, the analytical threshold, dropin limit, dropout limit, the population frequency file, the ratio computation method (whether integral or specified ratios), and so on.

View LR results: Gauge (overall LR value)

Note: The gauge values depend on the selected settings. For example, the analytical threshold, dropin limit, dropout limit, the population frequency file, the LR method (whether integral or specified ratios), and so on.

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.

2. Click a population tab.

3. In the right pane, view the gauge to see the LR score and the log of the LR score.

   The LR score is calculated as the ratio of two conditional, mutually exclusive probabilities:

   1. LR =

      $$\frac{P(E|Hp)}{P(E|Hd)}$$

      where **E** represents the observed evidence profile, $\mathbf{H_p}$ (or $\mathbf{H_1}$) represents the "prosecution" hypothesis that includes the POI as a contributor, and $\mathbf{H_d}$ (or $\mathbf{H_2}$) represents the "defense" hypothesis that some other unknown, unrelated individual is the true contributor.

   2. LRs can have a value between 0 and infinity; for easier understanding of potentially large values, scientific notation and/or the logarithm (log LR) may be used.

LR value	Conclusion	Notes
1	Inconclusive—There is equal support for both hypotheses	The closer the LR value is to 1, the less support there is for one proposition over the other. False positive and negative results are more likely around this value.
>1	Supports H_p (inclusion of POI)	The larger the value, the more support for the H_p proposition.
<1	Supports H_d (exclusion of POI)	The smaller the value (the closer to 0), the more support for the H_d proposition.

4. If the overall LR score is unexpected, check each locus in the table at left of the gauge for an unexpected result (for example, a rare allele or an exclusion relative to a known contributor). For more information, see "View LR results: Per Locus Details tab" on page 97.

View LR results: Per Locus Details tab

In the **Per Locus Details** tab, the loci table (left pane) displays the LR results for each locus in the evidence and selected contributor profiles. The individual ratios used are displayed above the table.

1. Display the **LR** screen for the sample of interest. See "Display the LR screen" on page 92.
2. Click a population tab.
3. Select the **Per Locus Details** tab (default selection).

4. In the loci table, review the results for the evidence profile and the selected contributors.

Item	Description
Name	Locus designation (the name of the locus).
Evidence `<sample>`[1]	The alleles (peaks) assigned to each locus in the evidence sample.
POI `<sample>`[1]	The alleles (peaks) assigned to each locus in the person of interest (POI) contributor sample.
Known `<sample>`[1]	The alleles (peaks) assigned to each locus in the known contributor sample. **Note:** This column is displayed only if there is a contributor in the **Hp** *and* **Hd** columns.
Hp	The likelihood calculated for the Hp hypothesis.
Hd	The likelihood calculated for the Hd hypothesis.
LR	The LR score is calculated as the ratio of two conditional, mutually exclusive probabilities: 1. LR = $\frac{P(E \mid Hp)}{P(E \mid Hd)}$ where **E** represents the observed evidence profile, $\mathbf{H_p}$ (or $\mathbf{H_1}$) represents the "prosecution" hypothesis that includes the POI as a contributor, and $\mathbf{H_d}$ (or $\mathbf{H_2}$) represents the "defense" hypothesis that some other unknown, unrelated individual is the true contributor. 2. LRs can have a value between 0 and infinity; for easier understanding of potentially large values, scientific notation and/or the logarithm (log LR) may be used.

LR value	Conclusion	Notes
0	POI exclusion	—
1	Inconclusive—There is equal support for both hypotheses	The closer the LR value is to 1, the less support there is for one proposition over the other. False positive and negative results are more likely around this value.
>1	Supports H_p (inclusion of POI)	The larger the value, the more support for the H_p proposition.
<1	Supports H_d (exclusion of POI)	The smaller the value (the closer to 0), the more support for the H_d proposition.

[1] Where: `<sample>` is the sample name.

5. To view an electropherogram for a locus: Right-click the locus, then select **View EPG**. For more information on EPGs, see "Configure electropherogram (EPG) settings" on page 19

6. To analyze a locus in detail: Right-click the locus, then select **Analyze Locus in detail**. For a detailed procedure, see "Analyze a locus in detail (information level)" on page 95.

View LR results: Explanation tab

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. Click a population tab.
3. Click the **Explanation** tab to read the results.

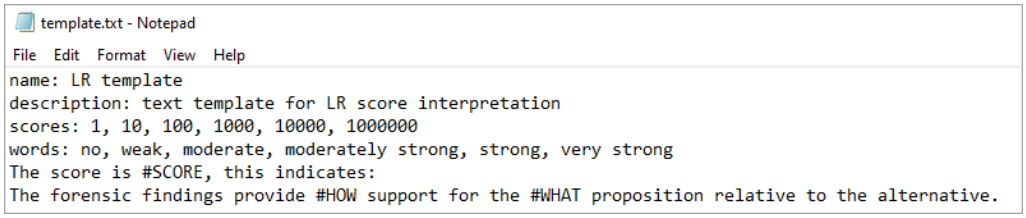
   The **Explanation** tab displays a written (English) version of the results, based on a template that can be customized.
4. *(Optional)* Customize the template for your laboratory:
   a. Navigate to the **LR** template folder, then open the **template.txt** file.

      The default file path is: `<installation drive>:\Thermo Fisher Scientific\GeneMapper PG\templates\LR\template.txt`

   b. Edit the text as needed, then save and close the file.

Item	Description
Name	The name of the template.
Description	A description of the template.
Scores	**Scores** and **Words** describe the strength of the LR value as supporting evidence. • **Scores** are numerical values, such as **1**, **10**, **100**, **1,000**, and so on. • **Words** are qualitative statements, such as **no**, **weak**, **moderate**, **moderately strong**, and so on. The **Scores** and **Words** should correspond to each other. For example, an LR score between **1,000** and **10,000** may be considered **moderately strong**. For more information, see: **https://www.justice.gov/olp/page/file/1095961/dl?inline**
Words	
Additional information	Any additional information that your laboratory would like to present. For example, what the score indicates or what hypotheses the findings support.

The text in the **Explanation** tab will be updated the next time the software is restarted.



View LR results: Overall Log tab (information level)

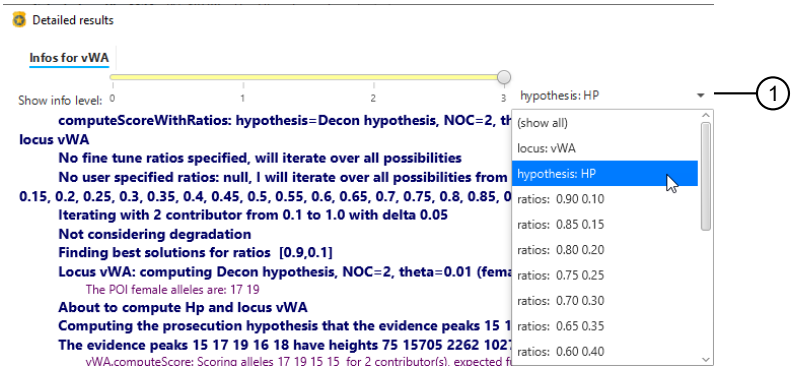
IMPORTANT! To see this tab in the **LR** screen, the information level (debug level) must be >0. See "Configure the LR settings" on page 93.

This feature can help determine the cause of unexpected results (for example, a parameter that is not properly set). The information level that you select applies to all loci.

1. Display the **LR** screen for the sample of interest. See "Display the LR screen" on page 92.
2. Click a population tab.
3. Select the **Overall Log** tab.
4. In the toolbar, click **Run**.
5. Select an information level to determine the amount of information that is displayed. Greater levels show more information, but can cause the software to run slowly.

   Note: A high information level significantly slows the processing time. At a level >5, it can take several minutes for the software to update; the software may also freeze because levels >5 can result in thousands of lines of information. After viewing the information of interest, we recommend that you change the value back to 0 or 1.

6. To filter the information that is displayed, select an option in the dropdown list to the right of the **Show info level** slider. The default selection is **(show all)**.



① Dropdown list

7. *(Optional)* To export the log (TXT file), click **Export All**, navigate to a save location, then click **Save**. The TXT file is saved to the selected location, and automatically opens. To close, click **X**.

View LR results: CalculationRecorderLR tab

IMPORTANT! To see this tab in the **LR** screen, you must enable **Record detailed information during LR calculation** in the LR settings. See “Configure the LR settings” on page 93.

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. Click a population tab.
3. Select the **CalculationRecorderLR** tab, then select a locus.
4. For the Hp and Hd hypotheses, view the score and combination results.

View LR results: Robustness tab

IMPORTANT! To see this tab in the **LR** screen, you must select (☑) **Compute the p(non-contributor)** (p-value) in the LR settings. See “Configure the LR settings” on page 93. Additionally, the tab will not be displayed if the log LR is not positive (>0) because exclusions are not admissible evidence.

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. Click a population tab.
3. Click the **Robustness** tab.
4. Change the settings as needed:
   - Enter the number of simulations to generate.
   - Select a relationship.
   - Select a contributor position.
     If a mixture has a dominant major (such as 1:4), the POI might be clearly in the major or minor position. In that case, you can select only that position for the simulation. However, if a mixture is closer to 1:1, any position is possible. In that case, it makes more sense not to select any position (that is, let the software simulate relatives in any position).
   - Select a locus.
5. Click **Simulate relatives**.

   Note: If the software does not generate a positive (>0) score, results are not displayed.

6. View the results for Hp and Hd.
   - **Results summary**—**Hp**, **Hd**, and **LR** scores, plausible combinations for the person of interest (POI), and the LR ratio.
   - **Positive Combinations** and **Negative Combinations**—Each entry is the Balding Nichols formula for each possible genotype that can be made with the evidence profile on a per-locus basis: the genotype combination, the equation probability of that genotype combination given the POI genotype, the number of combinations, the fit score, and the mixture ratio used.
   - **p-value**—Reflects the specificity of Hp. The probability that a simulated contributor, substituted for the POI, would result in a LR at least as large as the LR observed with the POI. In the plot, this is displayed as the Hp bar vs the simulated distribution
   - **Info**—Indicates whether positive scores were found.
   - **Comparison text**—Indicates the number of results that are better or the same compared to log(Hp).

View LR results: AllCombinationsRecorderLR tab

IMPORTANT! To see this tab in the **LR** screen, you must enable **Record detailed information during LR calculation** in the LR settings. See “Configure the LR settings” on page 93.

The **AllCombinationsRecorderLR** tab displays the detailed Balding Nichols formulas used.

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. Click a population tab.
3. Select the **AllCombinationsRecorderLR** tab, then select a locus.
4. Review the results for all combinations.

View LR results: Scores of combined results tab

IMPORTANT! To see this tab in the **LR** screen, you must select **INTEGRAL** for **How ratios are computed for LR** in the LR settings. See “Configure the LR settings” on page 93.

1. Display the **LR** screen for the sample of interest. See “Display the LR screen” on page 92.
2. Click a population tab.
3. Select the **Scores of combined results** tab.
4. View the results per ratio combination.
   - **Ratios**—Lists different ratio combinations for the possible contributors. For example, Contributor 1 = 10% and Contributor 2 = 90%, Contributor 1 = 20% and Contributor 2 = 80%, and so on.
   - **Hp, Hd, and LR**—For each ratio combination, provides the score and log values for Hp, Hd, and LR.

The LR score is calculated as the ratio of two conditional, mutually exclusive probabilities:

a. LR =

$$\frac{P(E \mid Hp)}{P(E \mid Hd)}$$

where **E** represents the observed evidence profile, $\mathbf{H_p}$ (or $\mathbf{H_1}$) represents the "prosecution" hypothesis that includes the POI as a contributor, and $\mathbf{H_d}$ (or $\mathbf{H_2}$) represents the "defense" hypothesis that some other unknown, unrelated individual is the true contributor.

b. LRs can have a value between 0 and infinity; for easier understanding of potentially large values, scientific notation and/or the logarithm (log LR) may be used.

LR value	Conclusion	Notes
0	POI exclusion	—
1	Inconclusive—There is equal support for both hypotheses	The closer the LR value is to 1, the less support there is for one proposition over the other. False positive and negative results are more likely around this value.
>1	Supports H_p (inclusion of POI)	The larger the value, the more support for the H_p proposition.
<1	Supports H_d (exclusion of POI)	The smaller the value (the closer to 0), the more support for the H_d proposition.

5. To export the results as a CSV file (Microsoft™ Excel™ spreadsheet): Click **Export to CSV**, navigate to a save location, then click **OK**.

6. To export the results as a Microsoft™ Excel™ spreadsheet (XLS or XLSX file): Click **Export to Excel with plots**, navigate to a save location, then click **OK**.

Save a report for the current screen

The data that are reported depends on the current screen.

1. In the primary toolbar, click **Save Report**.

2. Follow the prompts to perform the next steps. The steps differ, depending on the screen that you are currently in.

8 Determine the robustness of the LR

Use the **Robustness** screen to determine the how robust the likelihood ratio (LR) is by replacing the POI with an unknown individual or a relative.

Display the Robustness screen

IMPORTANT! Before starting the robustness calculation, you need to perform the LR calculation on the sample of interest, with the following LR setting selected (☑): **Compute the p(non-contributor)** (p-value). See "Configure the LR settings" on page 93 and "Start or stop the LR calculation" on page 95. Additionally, robustness data will not be displayed if the log LR is not positive (>0) because exclusions are not admissible evidence.

1. After running the LR calculation for the sample of interest, in the navigation pane, click **Robustness**.
   The **Robustness** screen is displayed for the selected sample.

2. If you are signed into the software in Validation mode, you can access the items and tasks shown in Figure 7.

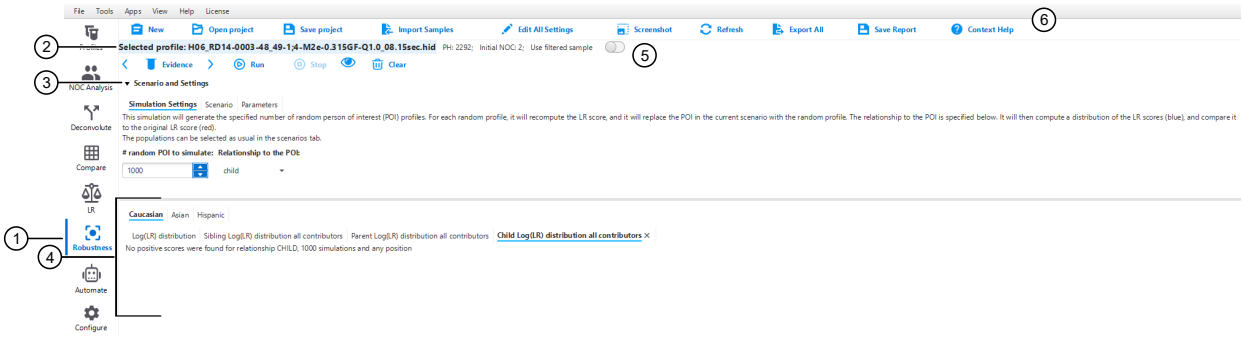


Figure 7 Robustness screen

1. **Robustness** app
2. The currently selected profile (sample)
3. Configure settings; see “Update the parameters for robustness” on page 107
4. View results (population tabs); see “View the robustness results” on page 105
5. **Robustness** screen toolbar:
   - Select a different profile
   - Start or stop the calculation; see “Start or stop the robustness calculation” on page 107
   - Display the **Log** dialog box (debug log)
   - Clear results; see “Clear the robustness results” on page 107
6. Menu bar and primary toolbar.

View the robustness results

1. Display the **Robustness** screen. See “Display the Robustness screen” on page 104.

   Note: The **Robustness** screen is pre-populated based on the most recent LR scenario and parameters that you ran in the **LR** screen. To change the scenario and parameters, see “Update the parameters for robustness” on page 107.

2. Click a population tab.

3. In the **Log(LR) distribution** tab, view the results:
   - **LR score distribution (p(non contributors))** and **Log(LR) value**—The LR score is calculated as the ratio of two conditional, mutually exclusive probabilities:
     a. LR =

$$\frac{P(E \mid Hp)}{P(E \mid Hd)}$$

     where **E** represents the observed evidence profile, $\mathbf{H_p}$ (or $\mathbf{H_1}$) represents the “prosecution” hypothesis that includes the POI as a contributor, and $\mathbf{H_d}$ (or $\mathbf{H_2}$) represents the “defense” hypothesis that some other unknown, unrelated individual is the true contributor.

     b. LRs can have a value between 0 and infinity; for easier understanding of potentially large values, scientific notation and/or the logarithm (log LR) may be used.

LR value	Conclusion	Notes
0	POI exclusion	—
1	Inconclusive—There is equal support for both hypotheses	The closer the LR value is to 1, the less support there is for one proposition over the other. False positive and negative results are more likely around this value.
>1	Supports H_p (inclusion of POI)	The larger the value, the more support for the H_p proposition.
<1	Supports H_d (exclusion of POI)	The smaller the value (the closer to 0), the more support for the H_d proposition.

- **Vertical red line in the graph**—The LR score for the currently selected sample.

4. Change the simulation settings as needed: At the top of the screen, click the **Scenario and Settings** arrow to expand the pane, then click the **Simulation Settings** tab (default selection).
   - Enter the number of simulations to generate.
   - Select a relationship.
   - Select a contributor position.

     If a mixture has a dominant major (such as 1:4), the POI might be clearly in the major or minor position. In that case, you can select only that position for the simulation. However, if a mixture is closer to 1:1, any position is possible. In that case, it makes more sense not to select any position (that is, let the software simulate relatives in any position).

5. Click **Run**.
   A new **Log(LR) distribution** tab is displayed based on your selections (for example, **Aunt Log(LR) distribution** tab). You can repeat this step as many times as you like.

   Note: If the software does not generate a positive (>0) score, results are not displayed.

6. To clear results:
   - **Individual tabs**—Click **X**.
   - **All results**—In the toolbar, click **Clear**.

Update the parameters for robustness

Note: In the **Robustness** screen, the **Scenario** tab is not editable. Instead, the **Scenario** tab is pre-populated with selections from the most recent LR scenario that you ran in the **LR** screen. If you need to make scenario changes, make the changes in the **LR** screen, re-run the LR calculation, then return to the **Robustness** screen. See "Configure the scenario and settings for the LR calculation" on page 93.

1. Display the **Robustness** screen. See "Display the Robustness screen" on page 104.
2. Click the **Scenario and Settings** arrow to expand the pane.
3. Click the **Parameters** tab, then configure the settings as needed.
4. To use the updated settings, run the affected algorithms.

Start or stop the robustness calculation

1. Display the **Robustness** screen. See "Display the Robustness screen" on page 104.
2. In the toolbar, click **Run**.
   The calculation can take several minutes. When complete, the results are displayed. See "View the robustness results" on page 105.
3. To stop the calculation, select an option:
   - In the **Computing** progress bar, click **Stop tasks**.
   - In the toolbar, click **Stop**.

   Note: The stop options may not be available if the calculation completes quickly.

Clear the robustness results

1. Display the **Robustness** screen. See "Display the Robustness screen" on page 104.
2. In the toolbar, click **Clear**.

9 Manage population statistics (popstats)

Multiple population data sets are provided in the software. Population data can be exported and imported in the software. Population files include allele frequency data for specific populations.

Display the Popstats screen

1. In the navigation pane, select **Configure** ▸ **Popstats**.
2. If you are signed into the software in Validation mode, you can access the items and tasks shown in Figure 8.

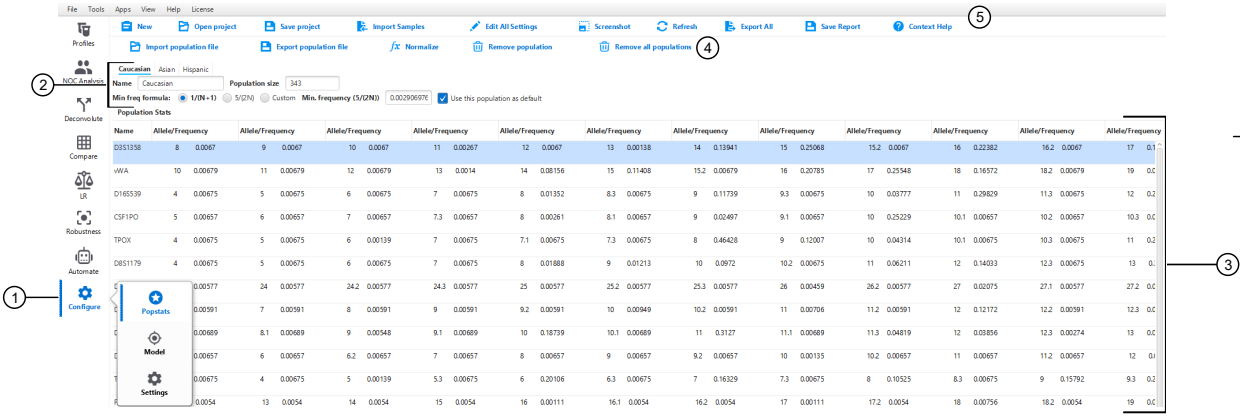


Figure 8 Popstats screen

① **Configure** app; select **Popstats**
② View or edit population information; see "Edit population statistics" on page 109
③ Allele and frequency data for each locus
④ **Popstats** screen toolbar
⑤ Menu bar and primary toolbar

Edit population statistics

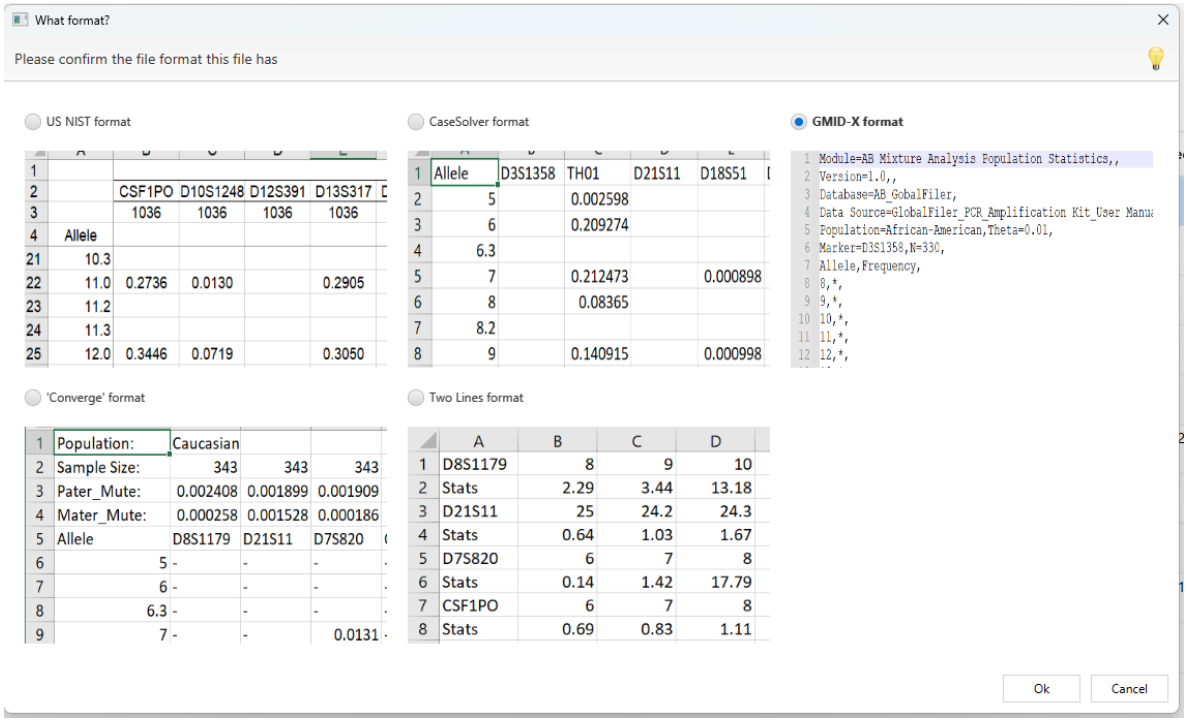
1. In the navigation pane, select **Configure** ▸ **Popstats**.
2. Select the tab for the population file to edit.
3. Enter a name and population size.
4. Select a minimum frequency formula, or enter a custom value.
5. *(Optional)* Select **Use this population as default**.

Import a population file

You can export a population file from one instance of the GeneMapper™ PG Software, then import the file into another instance.

Note: To export a population file, see "Export a population file" on page 110.

1. In the navigation pane, select **Configure** ▸ **Popstats**.
2. In the toolbar, click **Import population file**.
3. Navigate to the population file (CSV or TXT) to import, then click **Open**.
4. In the dialog box, select the appropriate format, then click **OK**.



5. To close the confirmation message, click **OK**.

6. If you receive a **Population not normalized** message, see "(If needed) Perform population normalization (Popstats screen)" on page 110.

A tab for the imported population file is added to the **Popstats** screen. The population will be available for selection in all screens where you can select a population.

Export a population file

You can export a population file from one instance of the GeneMapper™ PG Software, then import the file into another instance.

Note: To import a population file, see "Import a population file" on page 109.

1. In the navigation pane, select **Configure** ▸ **Popstats**.

2. Select the tab for the population file to export.

3. In the toolbar, click **Export population file**.

4. Enter a file name, navigate to a save location, then click **Save**.

   Note: You can export the population file only as a CSV file.

5. Enter a name for the population, then click **OK**.

   This is the name that will appear in the software, if the population file is imported into another instance of the GeneMapper™ PG Software.

The population file is exported to the selected save location.

(If needed) Perform population normalization (Popstats screen)

If you receive a **Population not normalized** message when you import a population file, perform this procedure.

1. Click **OK** to close the **Population not normalized** message.

2. Select the tab for the population file that you just imported.

3. *(If needed)* Select a minimum allele frequency formula:
   - **1/(N+1)**
   - **5/(2N)**
   - **Custom**; if you select **Custom**, enter a value

Note: The population size (N) represents the total number of samples in the population. You need to specify the value when import a population file. The value of N can be changed, if needed.

Values are normalized to the selected formula.

4. Click *fx* **Normalize**.
5. To close the confirmation message, click **OK**.

A Operate the software from a Command Line Interface

IMPORTANT! We support the use of the Command Line Interface only as it is explained in this appendix.

Note: If you are unfamiliar with Microsoft™ DOS, we do not recommend using the Command Line Interface. Use the Command Line Interface only if you are an advanced user (systems administrator, bioinformatician, network administrator).

About the Command Line Interface

The GeneMapper™ PG Software Command Line Interface can automate most software operations without using the graphic user interface. Commands can automate various operations such as likelihood ratio (LR) computations, deconvolution, and number of contributors (NOC) analysis. Scripts are written in simple text format and can be run using the provided runscript.bat command.

Set up command line interface

Confirm that GeneMapper™ PG Software is installed on the computer and contains these items:

Component	Description
`scripts/`	Contains example scripts.
`runscript.bat`	Batch file used to run scripts.

1. In the desktop, select **Start** ▸ **All Programs** ▸ **Accessories** ▸ **Notepad**.
2. In the **Notepad** window, enter one of the following options.

Option	Description
Run a script in the current folder.	• Go to the folder where the software is installed. For example, for the default installation folder, enter ***C:\Thermo Fisher Scientific\GeneMapper PG***. • Enter `runscript.bat scriptname.txt`.
Run a script from any location.	`runscript.bat C:\path\to\script.txt` Replace `scriptname.txt` or `C:\path\to\script.txt` with the actual script file name or path.

Command Line arguments

General commands

Control commands

Command	Description	Example
`help`	Displays available commands and usage information.	`help`
`interactive [on/off]`	Enables or disables interactive command input mode.	`interactive on`
`runStepByStep [on/off]`	Controls step-by-step execution with user confirmation.	`runStepByStep on`
`autoOpen [on/off]`	Controls automatic opening of output files.	`autoOpen on`
`quit` or `exit`	Terminates the current session.	`exit`

Parameter management

Command	Description	Example

`set [parameter]=[value]`	Assigns a value to a specified parameter.	`set evidence=sample1`
		`set dropin 0.01`
		`set dropout = 0.01`
		`set populationTheta  = 0.01`
		`set considerStutter= true`
		`set continuous = true`
		`set frequency locus=vWA allele=2 value=0.1`

`get [parameter]`	Retrieves the current value of a parameter.	`get populationTheta` `get dropout`

Load data

Command	Description	Example
`loadProject [folder]`	Imports a project from specified folder.	`loadProject C:/data/myproject`
`loadReferences [type] [file]`	Imports reference profile data.	`loadReferences csv references.csv`
`loadEvidence [type] [file]`	Imports evidence profile data.	`loadEvidence txt evidence.txt`
`loadModel [file]`	Imports a statistical model.	`loadModel model.xml`

Manage loci

Command	Description	Example
`disable [locus]`	Deactivates specified locus.	`disable AMEL`
`enable [locus]`	Activates specified locus	`enable DYS391`

`addAllele [locus] [allele]`	Adds allele to specified locus	`addAllele vWA 2`
		`addAllele vWA 2`
		`set frequency locus=vWA allele=2 value=0.1`

Display commands

Command	Description	Examples

`show [item]`	Displays detailed information about the specified item.	`show sample`
		`show hypothesis`
		`show scenario`
		`show parameters`
		`show profiles noc=2`

Loops

Command	Description	Examples
`FOR`	Iterates through specified items.	`FOR profiles NOC=2NOC MACENDFOR` This example runs the NOC MAC command for all profiles with 2 contributors.

		`FOR evidence`
		`  set sample=EVIDENCE_SAMPLE`
		`  lr h0=h0 h1=h1`
		`ENDFOR`
		This example will apply the LR calculation to all evidence samples in the dataset.

`IF`	A conditional loop that runs commands based on conditions.	`FOR profilesIF sampleName CONTAINS "Mix"NOC ALLENDIFENDFOR` The example starts a loop over profiles and checks the Number of Contributors (NOC) for all samples that contain "Mix" in the sample name.

Commands for LR and deconvolution

To calculate the LR for a given evidence sample under two hypotheses, use the following command:

```
lr h0=prosecution_hypothesis h1=defense_hypothesis
```

Table 13 More parameters

Parameter	Description	Example
`locus`	Calculates LR for a specific locus.	`lr locus=D3S1358 h0=h0 h1=h1`
`debug`	Sets debug level for detailed output.	`lr debug=3 h0=h0 h1=h1`
`min/max`	Defines expected LR range.	`lr min=0 max=1000000 h0=h0 h1=h1`
`ComputeLRPValue`	Enables computation of p-values.	`set computeLRPValue=true`

Example script

```
script C:\Thermo Fisher Scientific\PG\scripts\loadprovedit.txt
set evidence A02_RD14-0003-15d2U60-0.25GF-Q4.5_01.25sec.hid
show sample details
hypothesis h0 noc=2 prosecution known1=M3
hypothesis h1 noc=2 defense
print hypothesis
lr locus=D3S1358 debug=3 min=0 max=1000000  h0=h0 h1=h1
```

Deconvolution

To run a deconvolution algorithm for a given hypothesis, use the following command:

```
deconvolute hypothesis=h0 method=integral
```

Table 14 More parameters

Parameter	Description	Example
`poi`	Specifies the person of interest.	`deconvolute poi=Ref_49`
`truth`	Specifies a known truth reference for evaluation.	`deconvolute truth=Ref_50`
`locus`	Run deconvolution on a specific locus.	`deconvolute locus=D3S1358`
`debug`	Set debug level for detailed output.	`deconvolute debug=3`

Example script

```
script C:\Thermo Fisher Scientific\PG\scripts\loadprovedit.txt
hypothesis h0 noc=2 prosecution known1=Ref_49
deconvolute debug=1 ratio=1:4 poi=Ref_49 method=integral truth=Ref_49
locus=D3S1358
```

NOC commands

The basic command to estimate the number of contributors in the DNA mixture using all available methods is:

```
noc all
```

Table 15 More parameters

Parameter	Description	Example Syntax
`method`	Selects the NOC computation method (MAC, TAC, Tree, ANN, or ALL).	`noc method=MAC`
`debug`	Sets the debug level for detailed output.	`noc debug=3`
`featureSet`	Specifies the feature set to use.	`set featureSet=TFS`

Script

```
script C:\Thermo Fisher Scientific\PG\scripts\loadprovedit.txt
set sample GF-MX_Mix11_A1_29c_15s_07_G05_16.hid
set featureSet=TFS
noc all
```

Extract features

The basic command to compute statistical and forensic features from a DNA sample is:

```
features
```

Table 16 More parameters

Parameter	Description	Example Syntax
`debug`	Sets the debug level for detailed output.	`features debug=3`
`featureSet`	Specifies the feature set to use.	`set featureSet=TFS`

Script

```
script C:\Thermo Fisher Scientific\PG\scripts\loadprovedit.txt
set sample GF-MX_Mix11_A1_29c_15s_07_G05_16.hid
set featureSet=TFS
features
```

Simulations

The basic command to generate simulated profiles based on a statistical model is:

```
simulate noc=(number of contributors) ph=(mean peak height) ratio=(mixture
ratio)
```

Table 17 More parameters

Parameter	Description	Example Syntax
`noc`	Number of contributors.	`simulate noc=2`
`ph`	Specifies mean peak height.	`simulate ph=1200`
`ratio`	Specifies contributor ratios.	`simulate ratio=1:4`
`nr`	Number of profiles to generate.	`simulate nr=500`

Script

```
script C:\Thermo Fisher Scientific\PG\scripts\loadprovedit.txt
simulate noc=3 ph=1500 ratio=1:4 nr=100
```

Files

When running scripts or commands, various output files are generated and stored in a designated results folder. The output folder is specified in the application settings and can be changed using the `set outputFolder` command.

By default, results are stored in the output folder where the software is installed.

Change the output folder

```
setoutputFolder=C:\PG\Results
```

Automatically open output files

```
setautoOpen=true
```

Table 18 Types of generated files

File type	Description
Log files (.log)	Contain detailed execution logs and error messages.
CSV files (.csv)	Contain tabular results such as likelihood ratios and contributor estimates.
Excel files (.xlsx)	Contain Summary results, often used for reporting.
Text files (.txt)	Contain extracted hypothesis details, sample parameters, and execution results.

Run an LR calculation

```
lr h0=h0 h1=h1
```

Table 19 Example result files: LR calculation

File name	Description
LR_SampleName_log.txt	Contains debug information and detailed execution log.
LR_SampleName_results.csv	Contains LR values for each locus.
LR_SampleName_summary.xlsx	Summarized LR results in Excel format.

Run a deconvolution

```
deconvolute hypothesis=h0
```

Table 20 Example result files: Deconvolution

File name	Description
Deconvolution_SampleName_log.txt	Debug log of the process.
Deconvolution_SampleName_results.csv	Deconvoluted profiles.
Deconvolution_SampleName_summary.xlsx	Summarized results in an Excel report.

B Documentation and support

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**.