

STRyper User Guide



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License agreement

STRyper is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation, either version 3 of the License, or (at your option) any later version.

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The absence of warranty means that the author of this program cannot be held responsible for any data loss or undesired data alteration. Please see FAQ for instructions about data backup.

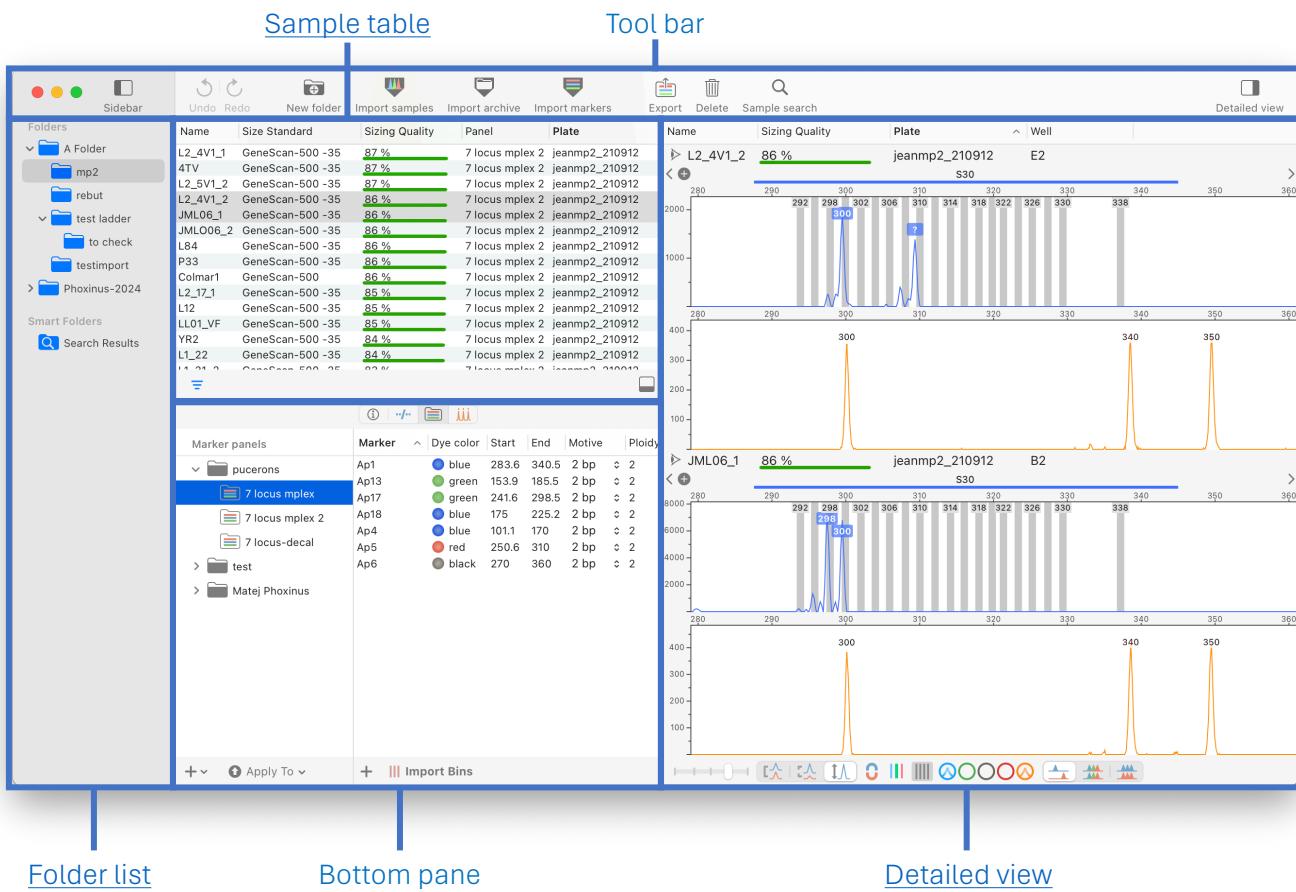
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Preliminary note

This guide explains how to use STRyper, but does not explain the biological principles of microsatellite genotyping. A user of this software must be already familiar with capillary sequencing, chromatograms, microsatellite markers, multiplexes, fluorescent dyes, molecular ladders, size standards, etc.

STRyper interface

STRyper is designed to analyze chromatograms generated by capillary sequencers for microsatellite genotyping. The application main window comprises several sections.

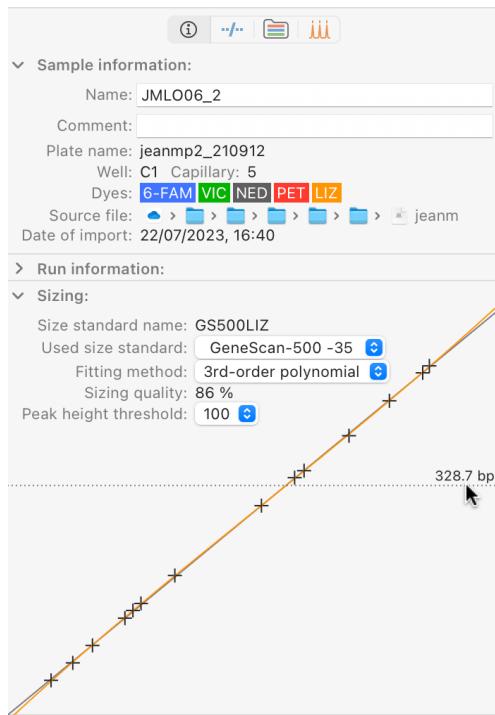


The **left sidebar** contains the **folder list**.

The **mid-section** contains:

- the sample table listing the **samples** (imported chromatogram files) in the selected folder,
- the bottom pane** with four **tabs**:

- o the sample inspector listing information about the selected sample(s),



- o **the genotype table**, listing genotypes for the sample displayed in the sample table (if any).

| Status | Sample | Panel | Marker | Size1 | Size2 | Allele1 | Allele2 |
|--------|-----------|----------------|--------|-------|-------|---------|---------|
| ● | 4TV | 7 locus mpl... | ● Ap2 | 417.5 | 431.6 | 416 | 430 |
| ● | 4TV | 7 locus mpl... | ● Ap2 | 417.4 | 431.6 | 416 | 430 |
| ● | Colmar1 | 7 locus mpl... | ● Ap2 | 427.7 | 427.7 | 426 | 426 |
| ● | Colmar1 | 7 locus mpl... | ● Ap2 | 428 | 428 | ? | ? |
| ● | JMLO6_1 | 7 locus mpl... | ● Ap2 | 417.3 | 419.3 | 416 | 418 |
| ● | JMLO6_1 | 7 locus mpl... | ● Ap2 | 417.4 | 419.4 | 416 | 418 |
| ● | JMLO0... | 7 locus mpl... | ● Ap2 | 417.4 | 419.4 | 416 | 418 |
| ● | JMLO0... | 7 locus mpl... | ● Ap2 | 417.4 | 419.4 | 416 | 418 |
| ● | L12 | 7 locus mpl... | ● Ap2 | 417.4 | 427.7 | 416 | 426 |
| ● | L12 | 7 locus mpl... | ● Ap2 | 417.5 | 427.7 | 416 | 426 |
| ∅ | L1_21_2 | 7 locus mpl... | ● Ap2 | | | | |
| ● | L1_21_2 | 7 locus mpl... | ● Ap2 | 429.6 | 431.3 | 428 | 430 |
| ● | L1_22 | 7 locus mpl... | ● Ap2 | 417.5 | 427.8 | 416 | 426 |
| ● | L1_22 | 7 locus mpl... | ● Ap2 | 417.4 | 427.8 | 416 | 426 |
| ● | L2_17_1 | 7 locus mpl... | ● Ap2 | 417.1 | 429.4 | 416 | 428 |
| ● | L2_4V1_1 | 7 locus mpl... | ● Ap2 | 417.3 | 417.3 | 416 | 416 |
| ● | L2_4V1_1 | 7 locus mpl... | ● Ap2 | 417.4 | 417.4 | 416 | 416 |
| ● | L2_4V1... | 7 locus mpl... | ● Ap2 | 417.5 | 417.5 | 416 | 416 |

- **the marker library**, listing panels of molecular markers, and molecular markers of the selected panel:

The screenshot shows the 'Marker panels' section of the software. On the left, a tree view shows a folder 'pucerons' containing a selected item '7 locus mplex'. Below it are '7 locus mplex 2', '7 locus-decal', 'Matej Phoxinus', and 'test'. On the right is a table titled 'Marker panels' with columns: Mar..., Dye color, Start, End, Motive, and Ploidy. The table lists markers Ap1 through Ap6, each with a specific dye color, start position, end position, motive, and ploidy.

| Marker panels | Mar... | Dye color | Start | End | Motive | Ploidy |
|---------------|--------|-----------|-------|--------|--------|--------|
| pucerons | Ap1 | blue | 283.6 | 340... | 2 bp | ◊ 2 |
| 7 locus mplex | Ap13 | green | 153.9 | 185.5 | 2 bp | ◊ 2 |
| | Ap17 | green | 241.6 | 298... | 2 bp | ◊ 2 |
| | Ap18 | blue | 175 | 225.2 | 2 bp | ◊ 2 |
| | Ap4 | blue | 101.1 | 170 | 2 bp | ◊ 2 |
| | Ap5 | red | 250.6 | 310 | 2 bp | ◊ 2 |
| | Ap6 | black | 270 | 360 | 2 bp | ◊ 2 |

Panel list Marker library

- **the size standard library**, listing available **size standards** and the **sizes** of the selected size standard:

The screenshot shows the 'Size Standards' section. On the left, a list of size standards is shown, with 'GeneScan-400HD' selected. On the right, a 'Sizes' list shows various sizes from 50 to 200. At the bottom, there are buttons for 'Duplicate' and 'Apply To ▾'.

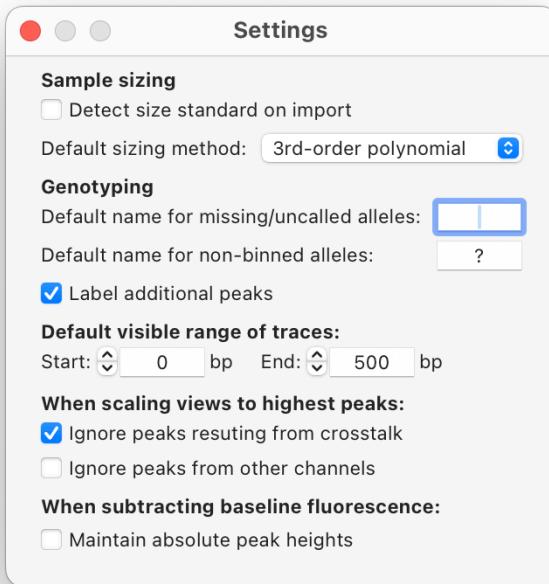
| Size Standards | Sizes |
|------------------|-------|
| GeneScan-400HD | 50 |
| GeneScan-1200 | 60 |
| GeneScan-350 | 90 |
| GeneScan-600 | 100 |
| Promega-ILS-600 | 120 |
| GeneScan-1000 | 150 |
| GeneScan-500 | 160 |
| GeneScan-500 -35 | 180 |
| | 190 |
| | 200 |

Size standard library Size list

The right pane contains the [detailed view](#) of the selected samples, genotypes, or markers.

The folder list, the bottom pane and the right pane **can be collapsed/expanded** by pressing the collapse buttons by dragging their separator, or via the View menu in the menu bar.

STRyper also has a **settings window** accessible from the menu bar via **STRyper > Settings**.



Managing samples

Sample folders

A **sample** refers to a chromatogram file that has been imported into the application.

A **folder** contains **samples** and/or other folders. You use folders to manage your samples by projects however you like. To create a folder, do one of the following:

- select **File > New Folder** from the menu bar,
- hover the mouse over the “Folders” section of the [folder list](#) and click the button:



- Click the “New Folder” button on the [toolbar](#).

To **add a subfolder to an existing folder** right-click or ctrl-click the folder and choose **Add Subfolder** from the contextual menu.

Folders can be dragged up or down, into, or out of, parent folders.

To rename a folder, you may either:

- click its name,

- right-click the folder and select the **Rename** contextual menu,
- selected the folder and hit the enter key,
- select the folder and select **Edit > Rename Folder** from the menu bar.

Note: folders in the same parent folder cannot have the same name.

To delete a folder, you can:

- right-click it and select **Delete Folder** from the contextual menu,
- select it and choose **Edit > Delete Folder** (⌘⌫) from the menu bar,
- select it and click the trash button  on the [toolbar](#).

Importing samples

STRyper imports chromatogram files following the ABIF specifications and ending with the “.fsa”, “.FSA”, “.hid” or “.HID” extensions. These files are imported as **samples** into [folders](#).

Note: HID file support is experimental as the specifications of this format are not public.

To import samples into a folder, this folder must be selected. Then do one of the following:

- click the **Import Samples** button  on the [toolbar](#),
- select **File > Import Samples...** from the menu bar,
- drag and drop FSA/HID files from the Finder into the sample table or onto a folder.

Note: you cannot import files by selecting or dropping their parent folder.

The sample table

Samples of the selected [folder](#) are listed in the [sample table](#). The sample table has a default set of columns showing sample metadata, including sample name, plate, run date...

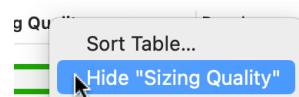
| Name | Size Standard | Sizing Quality | Panel | Plate |
|---------------|---------------------|----------------|------------------------|---------------------------|
| A10 | | | | 171218 |
| LADDER | GeneScan-500 | 76 % | | |
| IVC02f | GeneScan-500 | 84 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IMO03a | GeneScan-500 | 85 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IVC02a | GeneScan-500 | 85 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IVC02e | GeneScan-500 | 85 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IVC02b | GeneScan-500 | 85 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IMO03d | GeneScan-500 | 86 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| ILaP01c | GeneScan-500 | 86 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IMO03e | GeneScan-500 | 86 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IVC02d | GeneScan-500 | 86 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IOR03 | GeneScan-500 | 86 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| ILaP01b | GeneScan-500 | 86 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IMO03c | GeneScan-500 | 86 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| IOS05h | GeneScan-500 | 87 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |
| ILaP01a | GeneScan-500 | 87 % | 7 locus mplex 2 | jeanfinFHIJ_231007 |

Tip: the signification of each column is explained by a tooltip that appears when the column header is hovered.

To copy the textual content of the table, simply select rows, then **Edit > Copy (⌘C)** from the menu bar. The copied content can be pasted to a text editor or spreadsheet application.

To reorder columns, simply drag them with the mouse.

To show/hide columns, right-click or ctrl-click the table header. This pops up a contextual menu allowing to hide that column. Then check/uncheck the columns you want to show/hide.



To sort the table by a column, simply click its header.

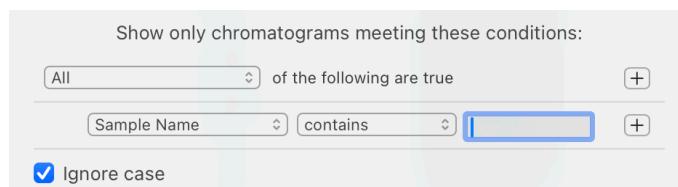
To sort the table by several columns, right-click or ctrl-click the table header and select **Sort Table...** from the contextual menu. This spawns a popover that lets you may change the priority of columns by dragging rows.



You may change the sorting order (ascending descending) by clicking the button with a chevron pointing down or up, and add remove sorting criteria using the "+" and "-" buttons:

Filtering the sample table

To filter samples and only display those meeting certain criteria, press the “filter” button below the [sample table](#). A popover will allow you to define filter criteria.



Note:

- a filter on samples is associated to a folder. If a folder has a filter applied to it, the “filter” button changes appearance:

- a [smart folder](#) (see below) cannot be filtered. You may instead modify its search criteria.
- A filter on samples is not dynamic. If samples are modified so that they meet or no longer meet filter criteria, you must reapply the filter by clicking the filter button, or select another folder and go back to the previous selection, to update the sample table.

Copying samples, moving samples between folders and deleting samples

To copy samples, select samples from the [sample table](#) and select **Edit > Copy (⌘C)** from the menu bar, or right-click samples and select **Copy** from the contextual menu.

You can then **paste copied samples** via **Edit > Paste (⌘V)**.

Notes:

- Copying also copies the textual data of selected rows to the pasteboard. This data can be pasted to a text editor or a spreadsheet.
- Upon pasting, the copied samples are duplicated in their current state, not in the state they had when you copied them. The sample's [genotypes](#) are copied as well.

To move samples between folders, select samples and drag them to the folder in the [folder list](#).

To delete samples, select them in the sample table and either: click the trash button  on the [toolbar](#), chose **File > Delete Sample(s) (⌘⌫)** from the menu bar or right-click samples and selected **Delete** from the contextual menu. This pops up an alert asking for your confirmation. **Note:** any deletion in STRyper can be undone.

Sample search and smart folders

To find samples according to different criteria among all samples of the database, press the search button  on the [toolbar](#) or select **File > Find Samples...** from the menu bar. This spawns a sheet allowing you do define the same criteria you would with the [filter popover](#).

Search results appear in a special folder called a **Smart Folder **. **A new smart folder is created upon each search.**

Smart folders in STRyper work similarly as smart folders in the Finder, which are created after a spotlight search is saved. This means that **samples meeting the search criteria will automatically be listed in the smart folder**. For certain search criteria however (folder name, size standard, panel name), the search results may not update immediately and will only update once the application saves its database (which occurs at most every 30 seconds).

You may also initiate a search by **adding a new smart folder**. To do so, hover the “Smart Folders” section in the folder list and click the  button: 

A smart folder can be renamed and moved just like a regular folder. However, you cannot drop any item (folder, samples) into a smart folder nor move a smart folder into another folder.

A smart folder is preserved between app launches, which means **you must delete a smart folder to discard search results**.

However, you need not create a new smart folder every time you want to find samples. **To modify the search criteria of an existing smart folder**, do one of the following:

- select the smart folder and click the  button at the below the sample table,
- right-click the smart folder and select **Modify Search Criteria** from the contextual menu,
- select the smart folder and select **Edit > Edit Smart Folder...** from the menu bar.

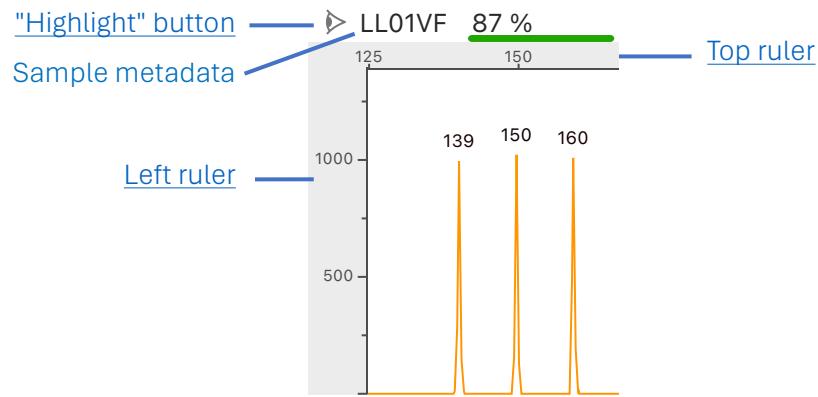
A smart folder does *not* contain copies of samples present in other folders. It just gathers samples meeting the search criteria, which means that **deleting samples from a smart folder removes them from the database**.

To reveal samples from a smart folder in their original folder, right-click or ctrl-click the sample(s) and select **Reveal in Parent Folder** from the contextual menu. **Note:** this item is disabled if clicked samples belong to multiple folders.

Visualizing samples

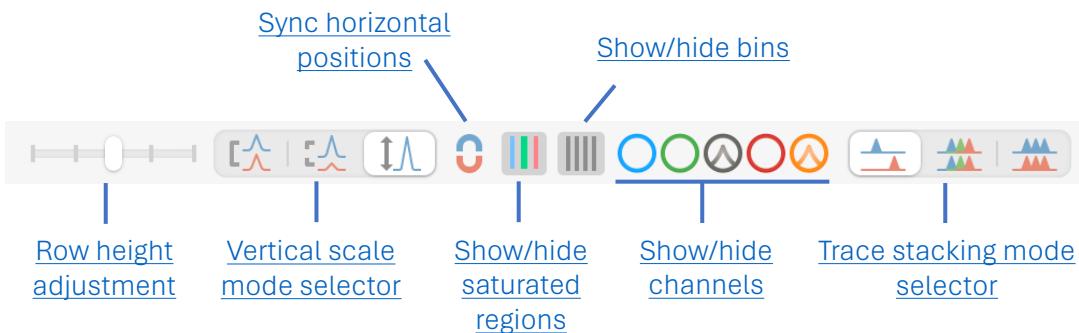
The detailed view

Chromatograms of samples that are selected in [the sample table](#) are immediately displayed in the detailed view on the [right pane](#).



If samples are not [stacked](#), the detailed view shows sample metadata in rows that are analogous to those of the [sample table](#) (with the same options for [hiding columns](#)), as well as rows showing **traces** (fluorescence curves).

When samples are displayed, the bottom of the right pane show this array of buttons:



Adjusting row height

The visible area of the detailed view can accommodate one to five rows showing traces. This number is set via the row height adjustment slider. Note: row height is constrained between 40 and 1000 pixels.

Showing/hiding channels

STRyper manages chromatogram file containing traces from four to five **channels** (colors, or emission wavelengths of fluorescent dyes).

To display or hide a channel, tick/untick the buttons with the corresponding color:

To display a channel and hide all others at the same time, click the colored button with the option key (⌘) pressed.

Note: when a row shows the chromatogram related to a [genotype](#), the channel of the genotype's marker is always visible.

Stacking curves in the same row

To display all traces in separate rows (which is the default), press the left segment  of the [stack trace mode selector](#). This mode is preferred to visualize amplicons and [molecular ladder](#) fragments individually.

To display all channels from each sample in a single row, press the middle segment  of the selector. This mode can be useful to compare samples with respect to the peaks they present at various channels.

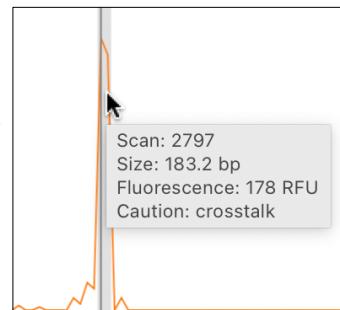
To display traces of the same channel from several samples in the same row, press the right segment  of the selector. In this mode, sample metadata is not displayed since each row can show several samples, and the header of the [detailed view](#) is replaced by a text indicating the number of samples stacked. This mode can help to [define bins](#) for molecular markers, among other uses.

Note: no more than 400 traces per row can be displayed in the detailed view.

Showing peak information

STRyper detects peaks in traces. If the [detailed view](#) shows a [single trace per row](#), hovering a peak with the mouse spawns a tooltip listing basic information about the peak:

- “Scan” is the number of data points that were recorded by the sequencer up to the peak tip (represented by a vertical line). It represents the time since the start of the fluorescence recording.
- “Size” is the estimated size of the DNA fragment that caused the peak and is inferred from the molecular ladder (see sample sizing).
- “Fluorescence” is the fluorescence intensity at the peak tip in Relative Fluorescence Units (RFU).
- “Caution: crosstalk” indicates that the peak likely results from crosstalk, i.e., it does not represent a DNA fragment from the channel that is visualized, but from another channel.



To show/hide peak information, select/deselect Traces > Peak Information Tooltips from the menu bar.

Adding peaks manually

STRyper does not detect peaks whose fluorescence level is less than 100. Adding a peak manually could be necessary if you consider that it represents an amplicon or a molecular ladder fragment.

To for the detection of a peak in a region where no peak is detected, you can:

- right-click below the tip of a peak and select **Add Peak here** from the contextual menu.
- If you use a trackpad with “force click” enabled, perform a force click (deep press) below the tip of the peak.

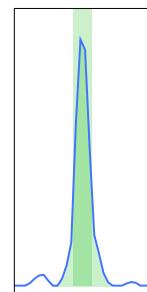
Either action will add the peak at the clicked location. If the clicked location does not appear to correspond to a peak, or if there is already a peak at the clicked point, the action will have no effect.

Showing saturated regions

To show/hide **regions where the fluorescence has saturated the sequencer's camera**, press the [Show/hide saturated regions button](#) .

Saturated regions are represented by rectangles which helps to identify a risk of **crosstalk** between channels. **The color of the rectangle representing a saturated region** corresponds to the channel that likely saturated the camera.

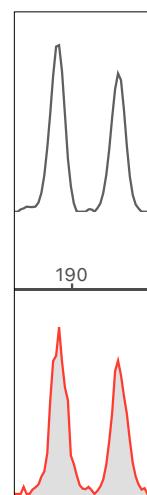
Note: saturated regions are not displayed if several chromatograms are stacked in the row.



Showing peaks resulting from crosstalk

Peaks in fluorescence curves may not represent DNA fragments but crosstalk between channels.

STRyper fills the area under such peaks with the color of the channel that likely induced crosstalk. These peaks are ignored by the application during automatic genotyping or determination of fragments in the DNA ladder.



To enable/disable the outlining of peaks resulting from crosstalk, activate/deactivate Traces > Outline Crosstalk Peaks from the menu bar.

Note: STRyper may occasionally consider legit peaks as resulting from crosstalk in case DNA fragment labelled with different dyes generated peaks at the same locations (in base pairs).

Subtracting baseline fluorescence level

By default, STRyper automatically subtract the baseline fluorescence level to make peaks stand out more. In that case, the curves shown on the [detailed view](#) do not represent raw fluorescence data.

To show raw fluorescence data, deselect **Traces > Subtract Baseline Fluorescence Level** from the menu bar. **Note:** curves are not smoothed by the application regardless of this setting.

By default, the absolute height of peaks is not affected by baseline fluorescence level subtraction, which therefore increases peak heights relative to the new baseline. If you want to maintain relative peak heights rather than absolute peak heights, uncheck the “Maintain absolute peak heights” checkbox in the [application settings](#).

Adjusting the vertical scale

The [left ruler](#), graduated in relative fluorescence units (RFU), indicates the intensity of peaks.

To change the vertical scale hence change the height of curves, click and drag vertically on the left ruler.

To adjust the scale such that the tip of the highest visible peak appears near the top of the row, double-click the left ruler. **Note:** this action has no effect if no peak is detected in the visible part of the trace(s).

There are three modes to adjust the vertical scale of rows:

To make all rows use the same vertical scale, press the left-hand button  of the [vertical scale mode selector](#) or select **Traces > Vertical Scales > Synchronized** from the menu bar. This action will have a effect only after you adjust the vertical scale of a row.

To adjust the vertical independently for each row, press the middle button  of the selector or select **Traces > Vertical Scales > Independent** from the menu bar. Any adjustment you make to the vertical scale will not affect other rows.

To make vertical scale adjust automatically to the highest visible peak, press the right-hand button  of the selector or select **Traces > Vertical Scales > Scale to Highest Peaks** from the menu bar. In this mode, you can still adjust the vertical scale by clicking and dragging the left ruler, but the row will rescale automatically upon scrolling. By default, this mode ignores peaks resulting from [crosstalk](#) and peaks in other channels when [visualising genotypes](#). This can be changed in the application [settings](#).

Horizontal positioning and zooming

For samples that have been [sized with a size standard](#), the [top ruler](#) shows graduations in base pairs to indicate the size of DNA fragments that induced peaks in traces. The ruler also show the current position of the mouse.

To zoom in/out horizontally, do one of the following:

- Place the mouse pointer over the traces and either:
 - pinch with two fingers, if this gesture is enabled in the trackpad setting.
 - double-tap with two fingers if this gesture is enabled in the trackpad setting. Hold the option key (⌥) while tapping to zoom out.
 - scroll vertically with the option key (⌥) pressed.
- click the [top ruler](#) where the cursor is a magnifying class. Press the option key while clicking the top ruler to zoom out.
- cover the area you wish to zoom to by clicking and dragging the mouse on the top ruler.



The default visible range of traces (by default, 0 to 550 base pairs) is specified in the application [settings](#). **Note:** the range must be at least 2 base-pair wide and is constrained to 0 – 1200 base pairs.

To zoom to the default range either:

- double-click the [top ruler](#) with the option key (⌥) pressed.
- right-click the top ruler and select **Zoom to Default Range** from the contextual menu.

To synchronize the horizontal scale and position across rows, press the [Sync horizontal positions button](#) such that it shows this symbol:  or select **Traces > Synchronize Positions** from the menu bar.

Note: positions are not synchronized upon activating the setting, but upon adjusting the scale or position of a particular row after the setting is active.

Highlighting an item in its source table

Sometimes, a sample or a genotype shown on the [detailed view](#) may not be visible in the [sample table](#) or [genotype table](#) if this table or the detailed view has been scrolled. In addition, the detailed view may show curves from different samples on the same row, and you may want to know to which sample a curve corresponds to.

To highlight a sample or genotype displayed on the detailed view in its source table:

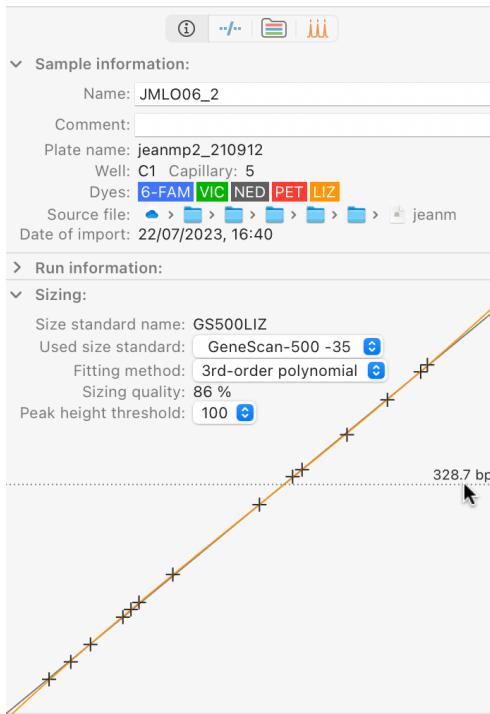
- click the Highlight button  at the top left of the traces.
- If the traces from several samples are [stacked in the same row](#), right-click or ctrl-click a curve and select **Highlight Source Sample** from the menu. You may alternatively perform a “deep press” on the curve on a Mac equipped with a force touch trackpad.



These actions highlight, with a white frame, the sample or genotype in its source table.

The sample inspector

The **sample inspector** displays information about selected samples. These pieces of information are organized in three sections: Sample information, Run information and Sizing.



To **show the sample inspector**, click the left button of the segmented control  of the bottom pane or select **View > Sample Inspector** from the menu bar.

To **collapse or expand a section**, click the triangle next to the section title.

Tip: to reveal the source file of a selected sample in the Finder, click the file icon in the “Sample information” section at the “Source file” field.



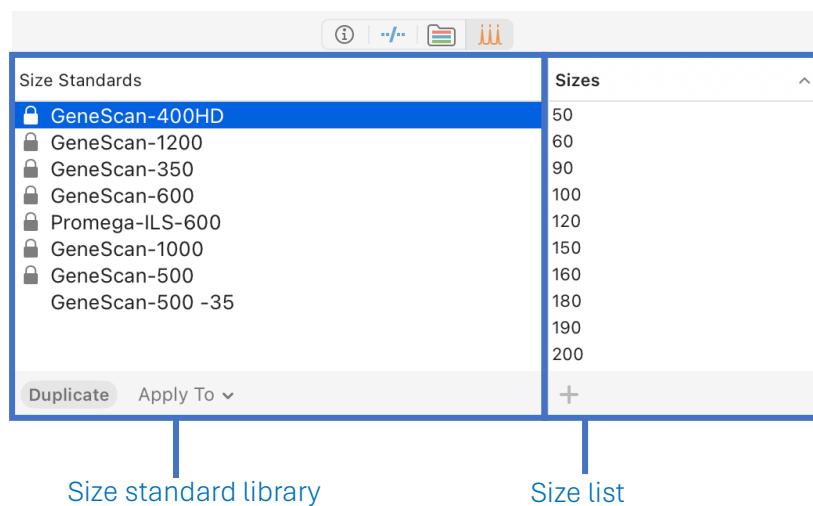
Sample sizing

To compute sizes in base pairs, a sample must contain fluorescence data from a **molecular ladder** composed of fragments of known sizes. These sizes are defined in a **size standard**. The name of this standard may be encoded in the FSA file, depending on the sequencing application. STRyper can read this name and apply a size standard whose name matches, if the “Detect size standard on import” option is enabled in the application [settings](#).

If no suitable size standard name was specified or found, an imported sample is not sized and cannot yet be genotyped. Sizes in base pairs do not appear in the top ruler above traces. You must *apply* a size standard manually. Applying a size standard triggers the detection of peaks for the appropriate channel and their assignment to fragment sizes listed in the standard.

Applying a size standard to samples

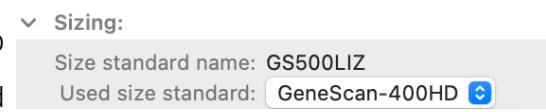
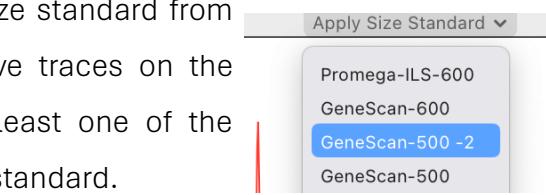
Available size standards are listed in the **size standard library**, which you access by clicking the right-hand button  of segmented control of the bottom pane or by selecting **View > Size Standard Library** in the menu bar. The sizes composing the selected standard appear in the **size list**.



To apply a size standard to samples, do one of the following:

- From the size standard library, drag and drop the row corresponding to a size standard onto the [sample table](#). This will apply the size standard to all samples from the table.
- Select a size standard from the list, click the “**Apply To**” button below the list and select the target samples from the contextual menu (either all samples listed in the table or only selected samples).

- Right-click samples from the [sample table](#) and chose the size standard from the **Apply Size Standard** contextual menu. This will apply the size standard to all clicked/selected samples.
- Select samples from the [sample table](#) and select a size standard from the “Apply Size Standard” button that is visible above traces on the [detailed view](#). Note: this button is not visible if at least one of the samples whose traces are displayed already has a size standard.
- Go to the [sample inspector](#) at the “Sizing” section and select an item from the “Used size standard” popup button. This will apply the size standard to all selected samples:

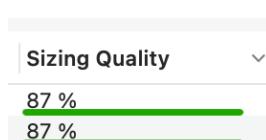


Tip: to assign peaks of the molecular ladder even if the correct size standard is already applied, just reapply the size standard.

The default fitting method specified in the application [settings](#) is used to compute the size in base pairs for each [scan](#).

Sizing quality

After applying a size standard, a score of **sizing quality** from 0 to 100% appears in the “Sizing Quality” column of the [sample table](#) (and the [detailed view](#)). Sizing quality is represented by a gauge whose color varies from red to green depending on the score.



This quality score is based on the difference between the size computed for each ladder fragment and its theoretical size defined in the size standard. This difference, referred to as “offset”, is then compared between adjacent fragments. The absolute difference in offset between nearby fragments is inversely proportional to the sizing quality.

Note: the sizing quality score is only an indication. Lower quality scores than other samples of the same run may indicate errors in size assignment or electrophoretic problems, but **high scores do not guarantee the absence of error** in assignment of peaks to sizes, and **intermediate scores may not necessarily indicate errors**. Molecular ladders must be [checked visually](#) regardless of the score.

Sizing quality can also be evaluated by checking the [fitting curve](#).

Sample sizing failure

Application of a size standard might not always result in the [top ruler](#) showing graduations in base pairs. This means that **sizing has failed** or that the **sizing quality score is too low** (0%). Sample

sizing fails if not enough peaks of the molecular ladder could be assigned to sizes of the size standard. This can be due to a fluorescence signal that is too weak for peak detection, electrophoretic problems, or application of an inappropriate size standard. This failure is indicated by:

- no value for the sizing quality score,
- “Sizing failed” indication in the “Sizing” section of [the sample inspector](#), in lieu of the fitting curve,
- “Sizing failed” indicated on the [top ruler](#).

When sizing quality is zero, the top ruler shows “Sizing too poor” instead of graduations.

Note: no [genotype calling](#) can be performed in these conditions.

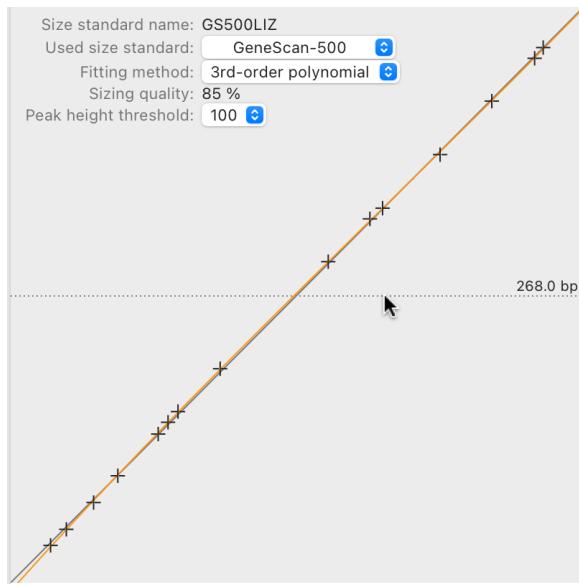
If you suspect that sizing failed because the fluorescence signal is too weak, you may lower the **peak height threshold** in the Sizing section of the [sample inspector](#). This threshold corresponds to the minimal fluorescence level a peak must have to be detected. The default value is 100. Changing this setting will affect all selected samples and trigger the detection of peaks of the ladder for these samples.

Peak height threshold: 100 

In case of sizing failure, inspect the trace of the molecular ladder in the [detailed view](#). A failure is often associated with electrophoretic problems that prevent the detection of molecular ladder fragments (peaks may be missing or have irregular shapes). In such cases, amplicons should be submitted to a another sequencer run.

The fitting curve

To display the **fitting curve** of a selected sample, go to the [sample inspector](#) and expand the “Sizing” section.



On the above image, each cross represents a molecular ladder fragment that was assigned a size of the size standard. Its horizontal position is the [scan number](#) at the tip of the peak caused by the fragment. Its vertical position is the fragment’s theoretical size in base pairs. Using these points, a [fitting method](#) estimates the size (in base pairs, Y axis) for every scan of the chromatogram. This relationship is represented by a curve whose color corresponds to the dye of the molecular ladder. The dark grey line represents the relationship inferred via [linear regression](#) (if linear regression is chosen as a fitting method, this line is not drawn).

The **curve should pass as close as possible to every point**. Points departing noticeably from the curve may indicate that a size was not attributed to the correct fragment of the ladder. In this case, size assignments to DNA fragments may be [corrected manually](#).

Choosing the appropriate fitting method

For each scan number (fluorescence data point), the corresponding size in base pairs is computed according to a **fitting method**. Three fitting methods are available:

- **The Linear regression** (1^{st} order polynomial) method assumes a linear relationship between scan number (n) and size (s): $s = an + b$.
- **The 2^{nd} order polynomial** method assumes a relationship of the form: $s = an^2 + bn + c$.
- **The 3^{rd} order polynomial** method (default) assumes a relationship of the form: $s = an^3 + bn^2 + cn + d$.

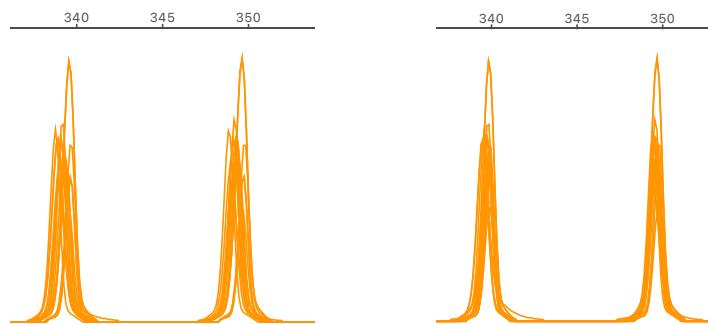
The coefficients a , b , c , d are computed by solving a system of equations by the Cholesky decomposition method.

To apply a fitting method to samples, do one of the following:

- Right-click samples from the [sample table](#) and choose a fitting method in the **Fitting Method** contextual menu.
- Select samples from the sample table, go to the [sample inspector](#), “Sizing” section and choose a value from the “Fitting method” popup button. 

Applying a fitting method triggers the recomputation of sizes. **The default fitting method** can be defined in the application [settings](#).

Which fitting method to choose depends on the consistency between estimated fragment sizes of different samples. To evaluate this consistency, you can [stack all samples](#) from the same run/plate in the same row and [show the channel](#) of the molecular ladder. Then, try different fitting methods and select the one for which peaks superimpose the most, as it is the case for the 3rd order polynomial on the right-hand image below. The lineage regression (left-hand image) estimates sizes that are less consistent.



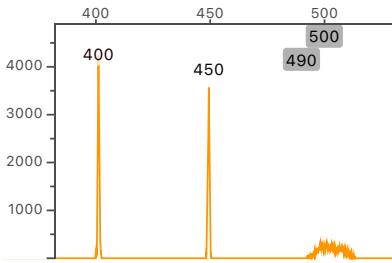
When in doubt, use the 3rd order polynomial, as this method better considers variations and anomalies in the electrophoresis efficiency. Anomalies have a more local influence on the sizing than with the linear regression method.

You must use the same fitting method for all samples analyzed at the same molecular marker, regardless of the run. This is because different fitting methods yield sizes differing by several base pairs for the same allele.

Checking and editing size assignment in molecular ladders

It is strongly recommended to check for errors in the assignment of peaks to sizes in the molecular ladder for each sample, regardless of the [sizing quality score](#).

To **visualize sizes attributed to ladder fragments**, select samples and display the channel corresponding to the ladder. Make sure to display [a single trace per row](#). The size attributed to each ladder fragment appears as a label above the corresponding peak. Sizes that were not assigned to fragments (because no suitable peaks were found) appear in grey under the top ruler.



To assign a size to a (different) peak, grab the corresponding size label and drop it onto the peak. If the peak already has a size assigned to it, this size will be replaced by the new size and will become unassigned.

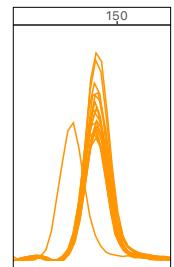
Note: the application enforces increasing sizes from left to right, e.g., you cannot assign size 200 to a peak that is at the right of another that has size 250. You must first remove size 250 from the other peak.

To remove a size from the sizing, perform one of the following:

- select the corresponding size label and either hit the delete key , select **Edit > Remove Ladder Size** from the menu bar, or click the trash icon on the [toolbar](#).
- double click the corresponding size label or the peak underneath,
- drag the corresponding size label above the row showing traces.
- Right-click the size label or the peak underneath and select **Remove Size** from the contextual menu.

After each change in size assignment, the sizing is automatically recomputed according to the fitting method applied to the sample and the fitting curve is updated.

Tip: to quickly check for errors in size assignments, or to assess if the chosen fitting method is the best, [stack all samples in the same row](#) and check whether peaks of the ladder superimpose neatly. If certain peaks appear off, as in the example on the right, this may indicate error in peak assignment for the corresponding sample(s). You may [highlight samples](#) corresponding to these peaks.



Defining custom size standards

STRyper includes the specifications of several commercial size standards, which cannot be modified nor deleted.

To define your own size standard, duplicate an existing one with the **Duplicate** button below the [size standard library](#). On this duplicate, sizes can be added, removed, or changed in the [size table](#).

To remove a size from the standard:

- select the size and select **Edit > Delete Size** or click the trash icon  on the [toolbar](#).
- Right-click the size and choose **Delete** from the contextual menu.

To add a size to the standard, select the size standard add click the  button below the [size table](#).

To change the value of a size in the standard, select its cell, click on the number and enter a new value. You may alternatively right-click the size and choose **Edit Size** from the contextual menu.

| |
|-----|
| 139 |
| 150 |
| 160 |
| 200 |

Note: a size must be at least 10 bp and cannot exceed 1500 bp. A size standard must have at least four sizes and cannot have duplicate sizes.

Genotyping

The samples you analyse in STRyper correspond to amplified **molecular markers**. These markers must be specified in STRyper and are grouped in **panels**. A panel corresponds to a multiplex of markers amplified together or pooled post-PCR. Even a marker amplified alone (not in multiplex) must belong to a panel, which therefore contains a single marker.

Panels are listed in **the panel list**, which is accessible by clicking the third button on the segmented control: ⓘ ⚡ 📁 ⓘ or by selecting **View > Marker Library** in the menu bar.

The screenshot shows the STRyper software interface with two main panels. On the left is the **Panel list**, which displays a tree view of marker panels. A panel named "7 locus mplex" is selected. On the right is the **Marker library**, which shows a table of markers with columns for Mar..., Dye color, Start, End, Motive, and Ploidy. The markers listed are Ap1, Ap13, Ap17, Ap18, Ap4, Ap5, and Ap6. Below the tables are buttons for "Apply To" and "Import Bins".

Creating marker panels

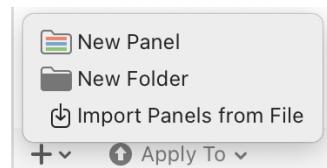
A **panel** is a folder containing molecular markers. If STRyper does not find any panel in the database, it creates one called “New Panel”. This panel contains no marker.

Like samples, panels can themselves be organized into folders.

To create a new panel or folder, click the **+** button below the [panel list](#).

Panels and folders can be renamed, deleted, and dragged like [sample folders](#).

You may also [import marker panels](#) exported from STRyper or GeneMapper.



To add a panel to an existing folder, click-click the folder and select **Add Panel** from the contextual menu.

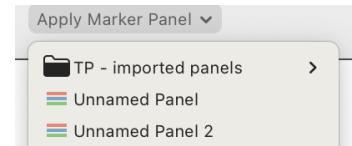
Associating a marker panel to samples

For genotyping, the panel corresponding to the multiplex of markers must be *applied* to samples amplified with this multiplex. A marker panel can be applied to samples before or after [molecular markers](#) are added to the panel.

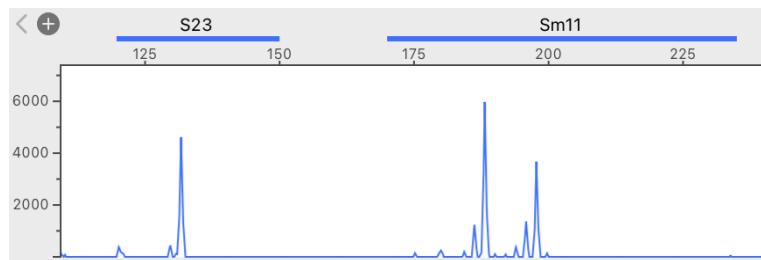
To apply a marker panel to samples, do one of the following:

- Drag the panel from the [panel list](#) onto the sample table. The panel will be applied to all listed samples.
- Select a panel from the list, click the “**Apply To**” button below the list and select the target samples from the contextual menu (either all listed samples or only selected samples).

- Right-click samples from the [sample table](#) and choose the panel from the **Apply Marker Panel** contextual menu. The panel will be applied to clicked/selected samples.
- Select samples from the [sample table](#) and select a marker panel from the “**Apply Marker Panel**” button that is visible above traces on the [detailed view](#). Note: this button is not visible if the sample(s) shown have no [size standard](#) or a [sizing quality](#) of 0%. Instead, a text indicates “Cannot apply marker panel”.



Upon applying a panel that contains [molecular markers](#) to samples, the [detailed view](#) displays the markers above the trace(s) of the corresponding channel. A marker range is presented as a horizontal segment whose color represents the marker’s dye, below the marker’s name.



If the panel does not contain any marker for the corresponding channel, this area of the detailed view remains blank, but the **+** button to [add a marker to the panel](#) is enabled.

Note: markers cannot be displayed on the detailed view if:

- traces from several channels are [stacked on the same row](#), unless the detailed view [displays genotypes](#).
- samples associated with different marker panels are stacked on the same row. In this case, a text indicating “Multiple marker panels” appears instead of markers.
- the sample sizing quality is 0% or the sample has no size standard applied. In this case, a text indicating “Marker panel not shown” is displayed instead of markers.

If the applied panel has markers, a blank **genotype** (with no allele called) will be added to each sample for each marker upon applying the panel. Genotypes appear in the [genotype table](#).

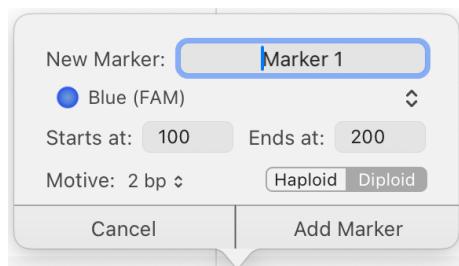
If the panel contains no marker, genotypes will be created for all samples on which the panel is applied only once you add molecular markers to the panel (see below).

Defining molecular markers

In STRyper, a **marker** specifies the **channel** (color) of the **fluorescent dye** that labels the primers used to amplify a microsatellite marker, and the **range** (in base pairs) where alleles are expected, the length of the **repeat motive**, as well as the **ploidy** of the locus, which defines the number of allele per individual. A marker also has a name.

To add a marker to a panel, do one of the following:

- select a panel from the [panel list](#) and click the **+** button below [the marker library](#). A popover will let you define the name, the color (dye), the range, the length of the repeat motive and the ploidy of the new marker.
- On the [detailed view](#) showing the appropriate channel of a sample that has the panel [applied to it](#), click the **+** button at the top left of the trace. Then, click and drag on the area where the mouse cursor shows a green ‘+’ sign to define the range of the new marker. Once you release the mouse button, the popover will let you define attributes of the marker, except its dye.



Note:

- Specifying the correct length of the repeat motive helps allele calling.
- The ploidy and channel of a marker cannot be changed after its creation.
- Adding a marker to panel automatically creates a blank genotype at this marker to each sample for which the panel has been applied. If some samples already associated with the panel were not amplified at this marker (i.e., if the multiplex used for these samples did not include this marker), you should create a new multiplex containing the new marker rather than adding the marker to the existing multiplex. For this, you may [copy markers between panels](#).

To change the range and name of a marker do one of the following:

- edit (click) the cell of the “Name,” “Start” or “End” column of the [marker library](#).
- double-click a marker label (rectangle) [above a trace](#) and enter new values in the popover.
- click the **⋮** button on the marker label, or right-click the label, and select **Edit Name and Range** from the contextual menu, which spawns the popover.



To resize a marker and therefore change its range, you can click and drag its edges.



To navigate between markers of the same channel in the [detailed view](#), you can:

- click a navigation button, **<** or **>**, above the [top ruler](#),

- place the cursor over the top ruler or the area showing markers and scroll left or right. Note: this requires a trackpad or an Apple mouse. This behavior can be disabled by unchecking **Traces > Allow Swipe between Markers** from the menu bar.
- perform a three-finger swipe, if this gesture is enabled in the trackpad preferences of macOS.

To zoom to the range of a marker, click the action button  on the marker label, or right-click it, and select **Zoom to Marker** from the contextual menu.

Copying markers between panels

If several multiplexes you use share molecular markers, copying markers between panels avoids defining the same marker several times. **Note:** copied markers are independent: changes made to a copied marker are not applied to the original marker, and reciprocally.

To copy markers between panels, first select the source panel and markers to be copied in the [marker library](#) and then, either:

- choose **Edit > Copy (⌘C)** from the menu bar, or right-click the markers and select **Copy** from the contextual menu. Then select the destination panel and choose **Edit > Paste (⌘V)**.
- Drag the rows corresponding to markers and drop them onto the destination panel.

Note: you cannot copy markers that overlap, or have the same name as, existing markers of the destination panel.

Defining bins

Once a marker is defined, STRyper can look for alleles by scanning peaks in the marker range. However, to attribute peaks to known alleles, **bins** must be defined. A bin corresponds to the range of expected sizes for amplicons of a given allele. A microsatellite marker typically include dozens of bins that are separated from each other by the length of the repeat motive. Like a marker, a bin has start and end coordinates in base pairs, and a name. During [genotype calling](#), any allele detected within a bin gets the bin's name, which will appear in the "Allele1" or "Allele2" column of the [genotype table](#).

To generate bins for a marker, first do one of the following:

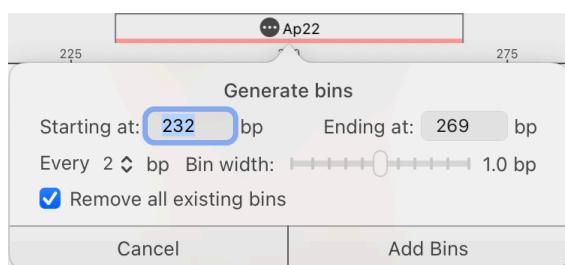
- If the marker's panel is [applied to samples](#), select one or several of these samples in the [sample table](#). In the detailed view, scroll the trace to the range of the marker. If you have selected several samples, you may stack them in the same row.

- Select a marker in the [marker library](#). The [detailed view](#) shows the whole marker's range. **However**, this does not display traces and therefore does not suggest where to place bins appropriately.

Then, you can either:

- click the action button  on the marker label, or right-click it, and select **Generate Bins** from the contextual menu. A popover will let you define the set of bins to add.
- Right-Click or ctrl-Click the view showing traces within the range of the marker and select **Generate Bins** from the contextual menu.

These actions spawn a popover allowing to define the set of bins to add. The spacing between bins represents the motive length of the marker.



New bins will be added at the specified positions, which correspond to their middle. In the example shown here, the first bin will start at 231.5 bp and end at 232.5 bp.

Note: Generating bins removes any existing bin that overlaps with new bins. You can remove all existing bins by ticking “Remove all existing bins” checkbox.

Tip: It is recommended to leave a margin of several base pairs (bp) between the edges of the marker and the first and last bins, to facilitate [moving bins](#), if necessary.

Bins are represented as vertical rectangles whose top section shows their names. Bin are named after the middle of their range in base pairs.

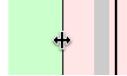
Some bin names are automatically hidden to avoid overlap. You may need to [zoom in](#) to see all bin names. Upon generating bins, the [detailed view](#) enters a mode allowing you to [move bins](#), as new bins rarely coincide well with the marker's alleles. This is because an amplicon and a ladder DNA fragment of the same lengths can migrate at different speeds during electrophoresis.



Moving bins

To move all bins of a marker together, click the action button  on the marker above trace, right-click the marker, or right-click in the area within the marker range, then select **Move all Bins** from the

contextual menu. The action button turns into a checkbox , the background of the trace in the marker's range takes a light pink color (see the [screen capture](#) below), and the mouse cursor becomes an open hand over this area to signify that bins can be moved. You may then move the bin set by dragging the mouse anywhere in the pink area. A green area appears underneath to represent the allowed range of the bin set, which ensures that bins remain in the marker's range. Upon clicking the pink area, a red vertical line with two converging black triangles appears at the click location. This line represents an **anchor** around which you may shrink/expand the bin set (see below). This position will not move during this process.




You may **expand/shrink the bin set** by dragging the left or right edge of the pink area. A green area and a black vertical line denote the range that the edge can take while avoiding overlap. This ensures that bins remain in the marker's range and do not overlap.

Note: When moving bins, genotypes [cannot be edited](#), and [saturated regions](#) and [peak information](#) cannot be displayed. This affects all rows in which the marker is visible.

Tip: [stacking many samples](#) (preferably from the same sequencer run or plate) in the same row helps to determine where bins should be. Peaks resulting from **stuttering** indicate the probable location of other alleles and can be used to add/adjust bins. You may [move the bin set](#) such that the appropriate bin sits right behind the peak that represents a given allele. If other bins are not located properly with respect to peaks, position the anchor point at the middle of the bin that is behind a peak (by clicking at that location), and move the edge of the pink area such that bin locations coincide with peak locations.



Note: certain alleles may have odd sizes due to mutations that do not correspond to indels of microsatellite motives. For such alleles, you may [add individual bins](#).

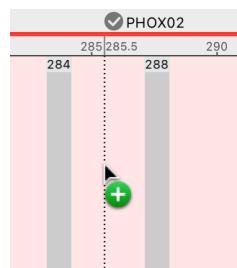
Editing bins individually

To **add/edit individual bins**, you can either:

- click the action button  on the marker label, or right/ctrl-click it, and select **Edit Bins**.

- Right-click or ctrl-click the [detailed view](#) in the range of a marker and select **Edit Bins Manually** the contextual menu.
- If a bin is already present and if you use a trackpad with force touch enabled, perform a force click on the bin. This will active the mode to edit individual bins and select the clicked bin.

The action button then turns into a checkbox , the background of the trace in the marker's range takes a light pink color, and the mouse cursor takes a green '+' sign over this area to signify that bins can be added. Genotypes cannot be edited, and saturated regions and peak information cannot be displayed while this area is visible. This affects all rows on which the marker is shown.



To add a bin, you may either:

- **click and drag** on the pink area (outside any exiting bin) to define the range of the new bin. The bin is added upon releasing the mouse button.
- **double click** in the pink area. A new bin will be created at the mouse location. **Note:** the bin width is 1 base pair, or less depending on available room between existing bins. No bin is added if there is not enough room.

Either action spawns a popover allowing to specify a name and range for the bin.

To change the name and range of a bin, double-click it, which spawns a popover allowing to specify a name and range.

To resize a bin, click and drag one of its edges. You may also **move a bin** by simply dragging it.

To exit bin editing, you can either: hit the escape key, click the checkbox on the marker label or click anywhere on the trace outside the pink area.

Hiding bins

You may wish to **hide bins** to make peaks more visible. To do so, click the [Show/hide bins button](#) or deselect **Traces > Bins** from the menu bar.

Note: bins stay visible while they are being edited or moved.

The genotype table

A **genotype** is a set of one or two alleles at a marker for a sample that has a panel of markers [applied to it](#). Each allele has a size in base pairs, and a name. The intensity of the peak it induced (in RFU) is also recorded.

[The genotype table](#) lists the genotypes of the samples listed in the sample table, for which a [panel of markers is applied](#). You can reorder, hide columns, and sort the genotype table like you can for the [sample table](#).

The screenshot shows a software interface for managing genetic data. At the top, there are several icons: a magnifying glass, a folder, and three orange bars. Below this is a table with the following columns: Status, Sample, Panel, Marker, Size1, Size2, Allele1, and Allele2. The table contains 20 rows of data, each representing a sample and its genotype information. The samples listed include 4TV, Colmar1, JML06_1, JMLOO..., L12, L1_21_2, L1_22, L2_17_1, L2_4V1_1, and L2_4V1_2. The 'Marker' column consistently shows 'Ap2'. The 'Size1' and 'Size2' columns show numerical values such as 417.5, 431.6, 416, and 430. The 'Allele1' and 'Allele2' columns show values like 416, 426, 418, and 428. The 'Status' column includes a small icon of a circle with a dot. At the bottom of the table, there are several blue icons: a magnifying glass, a double arrow, a refresh, a download, and a search bar.

| Status | Sample | Panel | Marker | Size1 | Size2 | Allele1 | Allele2 |
|--------|-----------|----------------|--------|-------|-------|---------|---------|
| ● | 4TV | 7 locus mpl... | ● Ap2 | 417.5 | 431.6 | 416 | 430 |
| ● | 4TV | 7 locus mpl... | ● Ap2 | 417.4 | 431.6 | 416 | 430 |
| ● | Colmar1 | 7 locus mpl... | ● Ap2 | 427.7 | 427.7 | 426 | 426 |
| ● | Colmar1 | 7 locus mpl... | ● Ap2 | 428 | 428 | ? | ? |
| ● | JML06_1 | 7 locus mpl... | ● Ap2 | 417.3 | 419.3 | 416 | 418 |
| ● | JML06_1 | 7 locus mpl... | ● Ap2 | 417.4 | 419.4 | 416 | 418 |
| ● | JMLOO... | 7 locus mpl... | ● Ap2 | 417.4 | 419.4 | 416 | 418 |
| ● | JMLOO... | 7 locus mpl... | ● Ap2 | 417.4 | 419.4 | 416 | 418 |
| ● | L12 | 7 locus mpl... | ● Ap2 | 417.4 | 427.7 | 416 | 426 |
| ● | L12 | 7 locus mpl... | ● Ap2 | 417.5 | 427.7 | 416 | 426 |
| ∅ | L1_21_2 | 7 locus mpl... | ● Ap2 | 429.6 | 431.3 | 428 | 430 |
| ● | L1_21_2 | 7 locus mpl... | ● Ap2 | 417.5 | 427.8 | 416 | 426 |
| ● | L1_22 | 7 locus mpl... | ● Ap2 | 417.4 | 427.8 | 416 | 426 |
| ● | L2_17_1 | 7 locus mpl... | ● Ap2 | 417.1 | 429.4 | 416 | 428 |
| ● | L2_4V1_1 | 7 locus mpl... | ● Ap2 | 417.3 | 417.3 | 416 | 416 |
| ● | L2_4V1_1 | 7 locus mpl... | ● Ap2 | 417.4 | 417.4 | 416 | 416 |
| ● | L2_4V1... | 7 locus mpl... | ● Ap2 | 417.5 | 417.5 | 416 | 416 |

Note:

- The size of an allele (in the “size1” and “size2” columns) is estimated via the molecular ladder and is not the true allele (amplicon) size, which is an integer.
- The intensity of the peak representing the allele (“height1” and “height2” columns, which are hidden by default) is taken from [raw fluorescence data](#).
- If no genotype is listed for a given sample at a marker, it means that the sample does not have a panel containing this marker applied to it.

If a panel of markers is [applied to samples](#), you can select their genotypes (and display traces on the detailed view) by right-clicking these samples on the [sample table](#) and choosing **Select Genotype(s)** from the contextual menu. If these samples have no applied panel or if all their genotypes are [filtered out](#), the menu item is disabled.

To identify the samples associated with genotypes, first select genotypes in the genotype table, and either:

- press the arrow button  below the table.
- right-clicking or ctrl-click the selecting genotypes and choose **Show Source Sample(s)** from the contextual menu.

Automatic genotype calling

Genotype calling consists of (i) detecting peaks that represent alleles, which determines allele sizes, and (ii) attributing names to alleles. Either operation can be done automatically or manually. When a genotype is called automatically, each allele is named after the bin that comprises the tip of its peak. Traditionally, bin names represent allele sizes in base pairs, but they may take any string of characters.

The **status** of genotype calling is represented in the [genotype table](#) by an icon in the **status column**:

- : The genotype has not been called nor [edited](#). Alleles have no size and have the name given to missing alleles, which is blank by default. This status is given to every genotype generated by [applying a marker panel](#) to samples.
- : The genotype has been automatically called.
- ∅: No suitable peak was found in the marker range during automatic genotype calling.
- ⊖: The genotype has been [edited manually](#).
- 🟡: The marker has been modified (range, bins) since genotype calling (either manual or automatic).
- ⚠: Sample sizing ([marker offset](#), molecular ladder, [fitting method](#)) has been modified since genotype calling. You may need to check the genotype.
- ❗: Sample [sizing quality is 0](#) or no size standard has been applied to the sample. In this case, the genotype cannot be called nor edited, alleles have no size and no name.

Note: genotype status does not represent the quality of genotype calling.

To automatically call genotypes, do one of the following:

- Click the **Find Alleles button**  below [the genotype table](#). This action calls genotypes, or re-calls genotypes that have not been edited manually (whose status is not ∅).
- Select and right-click genotypes from [the genotype table](#) and select **Find Alleles** from the contextual menu.
- Select and right-click samples from the sample table and select **Find Alleles** from the contextual menu (these samples must have a panel containing at least one marker applied to them). This action calls genotypes for markers of the panel.

Note:

- A genotype cannot be called nor edited manually if no size standard has been applied to the sample or if [sizing failed](#) (genotype status is).
- Automatic genotype calling is not required to attribute sizes and names to alleles. You may [edit genotypes manually](#), should you wish to.
- Automatic genotype calling removes allele names for a marker that has no bin. Allele sizes in base pairs will [appear above peaks](#) instead of their names.
- Alleles outside existing bins take the name attributed to out-of-bin alleles. By default, this name is a question mark "?". This name can be modified in the [settings](#).
- If no suitable peak was found in the marker range, alleles get the name attributed to missing alleles, by default a blank string. This name can be modified in the [settings](#).

To modify the default names for non-binned or missing alleles, display the application [settings](#) and enter the character chain of your choice in the appropriate fields. **Note:** These changes do not affect the names of alleles that have already been called.

Binning alleles automatically

You may want to (re-)bin alleles that were previously found if, for instance, you have modified bins or edited the molecular ladder (genotype status is or). Automatic binding does not find peaks that correspond to alleles, it only names alleles after bins that overlap peak tips. Therefore, it does not change your [manual assignments](#) of peaks to alleles.

To bin alleles, you can either:

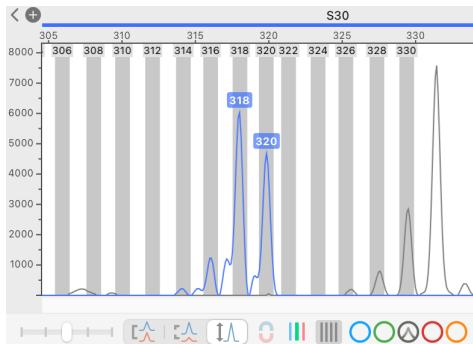
- Click the “Bin Alleles” button below [the genotype table](#). This action ignores genotypes that have been edited manually (whose status is).
- Select and right-click genotypes from [the genotype table](#) and select **Bin Alleles** from the contextual menu.

Note:

- This action has the effects of [automatic genotype calling](#) on allele names.
- This action also finds alleles for samples whose genotypes have not been called (genotype status is).

Displaying alleles on chromatograms

To view alleles as labels above peaks, select genotypes from [the genotype table](#). If necessary, click the left segment of [stack trace mode selector](#):  . The [detailed view](#) displays the corresponding traces at the marker's range, as shown below.



Alleles appear above peaks as rectangles indicating the allele names. The color of these labels corresponds to the dye of the marker. If no peak has been attributed to alleles in the marker range, alleles are not visible. In this viewing mode, each row of the detailed view corresponds to one selected row of the genotype table (in the same order) and you cannot stack several samples per row. **Note:** allele labels also appear when [viewing samples](#), unless several samples or channels are [stacked in the same row](#).

Tip: You may choose to [display several channels](#) (colors) per row. On the image above, the black channel is displayed for a genotype of a marker labelled with the blue dye (the blue curve thus shows even though the blue button is not ticked). Displaying several channels may be useful to determine if peaks are subject to [crosstalk between channels](#).

Note: when viewing genotypes, horizontal positions cannot be [synchronized between rows](#), as this would cause rows to display ranges that do not correspond to the markers. Each view can be scrolled horizontally and zoomed, but its visible range will be reset to that of the marker each time the genotype is selected in the genotype table.

Displaying alleles as dots

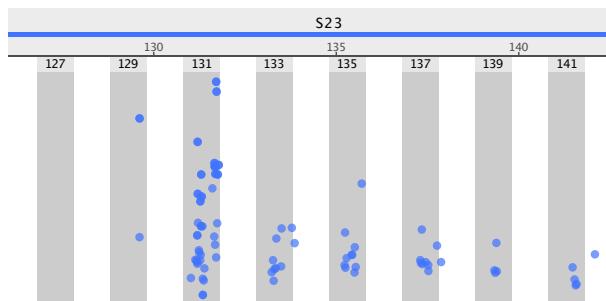
STRyper can represent alleles as dots in the [detailed view](#). In this mode, all alleles of a marker appear on the same row. This mode helps comparing allele sizes and spotting rare/unusual alleles.

To visualize alleles of the same marker as dots on a single row, first selected genotypes in the [genotype table](#), then:

- click the right-hand segment of the [stack trace mode selector](#):  or

- select **Traces > Stack Genotypes per Marker** from the menu bar.

The detailed view shows alleles as colored dots whose vertical positions represent the heights of corresponding peaks. No trace is shown.



Tip: you may [zoom in](#) to reduce the overlap between dots.

To highlight the genotype of a given allele, click the dot representing the allele. The row corresponding to the genotype in [the genotype table](#) will be highlighted with a white frame.

To display the chromatogram associated with an allele, right-click or ctrl-click the dot representing the allele and select **View Chromatogram** from the popup menu. The corresponding genotype will be selected and the chromatogram will appear on the detailed view. For this, the visualisation mode changes, as shown on the segmented control: .

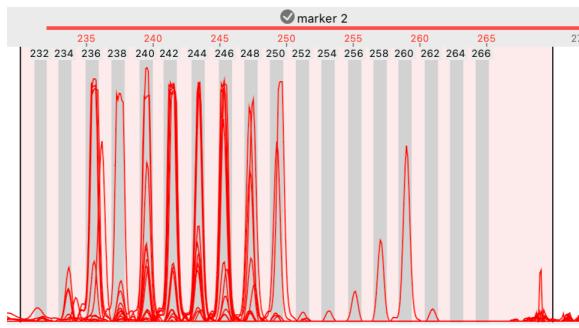
Defining marker offsets

Amplicons and ladder DNA fragments often react differently to variations in electrophoretic conditions. Hence, the computed size of the same allele may slightly vary between sequencer runs, even on the same sequencer. Such variations can shift the location of alleles with respect to bins, defeating the purpose of bins. [Moving bins](#) does not address the issue as this action affects all samples genotyped at the marker.

STRyper's solution to this issue is to **adjust the offset of the marker** of specific samples, that is, to adjust the *computed sizes of peaks* within the marker range *for these samples* without modifying bins.

A **marker offset** is composed of two numbers that correspond to terms a and b of the formula $y = a + bx$, where x is the size of a peak computed thanks to the molecular ladder, and y is the actual size used in the marker's range. If there is no offset, $a = 0$ and $b = 1$. b is constrained to the interval [0.9, 1.1]. Thankfully, you do not have to determine these numbers.

To **adjust the offset of a marker** for specific samples of known genotypes, selected them from the [sample table](#) and [stack them in the same row](#). Then select **Adjust Offset** from the marker contextual menu (accessed via right-clicking the marker or by clicking the action button ⓘ). Then, [move bins](#) such that their positions match those of peaks. Changing the offset does not modify bins. Indeed, sizes of the [top ruler](#) move in sync with bins (and become red to denote the offset). The marker offset is represented by the difference between its range appearing above traces and the pink area behind traces.



To exit offset adjustment, either hit the escape key, click the checkbox ⓘ on the marker label, click anywhere on the trace outside the pink area, or select other samples.

Because offset the offset of a marker is specific to samples, it is an attribute of the samples' genotypes for the marker. This offset therefore appears in the **Offset** column of the [genotype table](#). The numbers in parentheses are terms a and b of the offset.

| Offset |
|--------------|
| (6.2, 0.978) |
| (6.2, 0.978) |
| (6.2, 0.978) |
| (6.2, 0.978) |

To remove offsets applied to genotypes, select these genotypes on the [genotype table](#), right-click the selection and select **Remove Offset(s)** from the contextual menu. You may alternatively select one or several samples in the [sample table](#), click the action button ⓘ on the marker label above traces, or right-click it, and select **Reset Offset**.

Note:

- Offset adjustment is not available for a marker that has no bins.
- If samples with different offsets for the same marker are [stacked in the same row](#), the offset that is represented by the position of bins and by sizes on the top ruler will be that of a random sample in the selection.
- Peaks that are outside the marker range (above traces) cannot be considered as alleles even if they are covered by the pink area representing the marker range with its offset. This is because this area may overlap that of another marker (see below).
- A marker offset may make bins appear outside their marker's range. Bins from different markers that are very close to each other may thus visually overlap. To avoid it, leave sufficient space

between bins of different markers of the same dye. If overlapping bins do correspond to existing alleles, you should redefine primers to change amplicons sizes such that alleles can be unambiguously attributed to the correct marker.

- When you [move bins](#) of a marker that has an offset for the sample(s) shown, bins are positioned as if the marker had no offset, during the operation.

Copy and paste marker offsets

You can copy and paste marker offsets between samples/genotypes that are analyzed at the same marker panel. This way, you may define a marker offset for one reference sample and apply it to others.

To **copy the offset of a single marker** to the pasteboard, you can either:

- Select the sample(s) or genotype and [display the marker](#) on the detailed view. Then click the marker's action button  and select **Copy Offset** from the contextual menu. Note: this action is not available if the marker has no offset or if alleles are [displayed as dots](#).
- Select a single genotype from the [genotype table](#) and select **Edit > Copy** from the menu bar (**⌘C**), or right-click the genotype on the table and select **Copy** from the contextual menu. **Note:** if several genotypes are selected or if the genotype has no offset, no marker offset will be copied.

To **copy the offsets of all the markers analyzed on a sample** to the pasteboard, select the sample in the [sample table](#) and either:

- select **Edit > Copy** (**⌘C**) from the menu bar,
- right-click the sample and select **Copy** from the contextual menu.

Note:

- if several samples are selected, no marker offset will be copied.
- This action only copies the offset of markers that have offsets.
- Any copy operation from STRyper or another app removes any previously copied offset from the pasteboard.

To **apply a copied marker offset to other samples or genotypes**, select these samples or genotypes from the [sample table](#) or [genotype table](#) respectively. Then either:

- right-click the sample(s) or genotype(s) and select **Paste Offset(s)** from the contextual menu.

Note:

- This action is not available if none of the selected samples or genotypes has been analyzed at a marker whose offset has been copied.

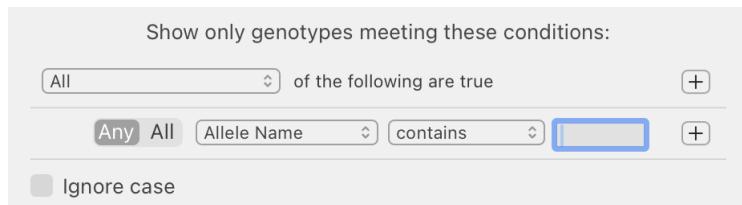
- If you copy & paste marker offsets between samples (not genotypes), you may choose to paste the offsets of all markers or just one, via a submenu.
- [Display a marker](#) in the detailed view, click the marker's action button ⓘ and select **Paste Offset** from the contextual menu.

Note:

- this action is not available if the pasteboard does not contain a copied offset for this marker.
- This action applies the offset to the genotype(s) or sample(s) displayed at the row. To apply the offset to all selected samples or genotypes, samples must be [stacked in the same row](#) or genotypes must be [displayed as dots](#).

Filtering genotypes

To **filter genotypes** and only display those meeting your criteria, press the “filter” button 🔍 below the [genotype table](#). A popover will allow you to define filter criteria. You may filter according to the name, the size or the intensity (height) of alleles. If *both* alleles of a diploid genotype must meet the condition you define, select the **All** on the segmented button. If only one of the alleles must meet the condition, select **Any**. This button has no effect on haploid genotypes.



Note:

- A filter on genotypes is associated to a [folder](#) and is recorded between app launches. If a folder has a filter applied to it, the “filter” button changes appearance: 🔍.
- A filter on genotypes is not dynamic. If genotypes are modified so that they meet or no longer meet filter criteria, you must reapply the filter or select another folder and go back to the previous folder, to update the genotype table.

To **remove a filter on genotypes**, press the “filter” button 🔍 below the genotype table and select **Remove Filter** from the popover.

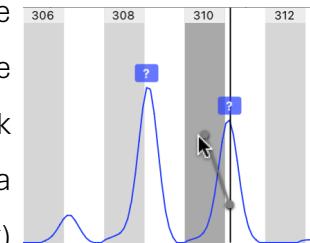
Tip: you can maintain a list of all genotypes meeting certain criteria. For this, create a [smart folder](#) that contains all samples of the database (for instance, by setting an import date that is more recent than 2020) and apply a filter to the genotypes on that folder.

Editing genotypes

STRyper allows manual assignment of peaks to alleles and modifications of alleles on the [detailed view](#).

To assign a peak to an allele in the marker range, you can either:

- Double-click the peak, or right-click it and select **Add Allele** from the contextual menu. If the peak has no allele, it will get one (possibly using an allele assigned to another peak). Note: if the peak already has an allele, double-clicking it will remove the allele, which may move to another peak if that other peak already has an allele (thereby creating a homozygote).
- Click the peak and drag the mouse. If the marker has [bins](#), a handle starting at the position corresponding to the peak tip will appear. Drag the other end of the handle to the bin and release the mouse button. The peak will take an allele named after the bin. If you release the mouse outside a bin, the allele will get the “out of bin” name (by default, a question mark) unless you release the handle above or below the view showing the sample, in which case the action will have no effect.
- Drag an allele label from another peak to the desired peak. The allele will be named after the bin present at the peak’s tip, or the “out of bin” name if there is no such bin.



Note: none of the above is possible for peaks that are outside the marker range. If a peak outside the marker range should be considered as an allele, you must [expand the marker range](#).

If a peak that should be an allele was not detected (probably because its fluorescence level is less than 100 units), you may [insert a peak manually](#).

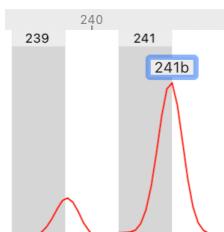
To remove an allele (without creating a homozygote if the marker is diploid) you can:

- select the allele label and either hit the delete key, select **Edit > Remove Allele** from the menu bar, or click the trash icon  on the [toolbar](#).
- drag the allele label above the top edge of the row showing traces.

This allele will lose its size and will get the name of missing alleles (by default, an empty string).

To give an allele a custom name, do one of the following:

- Enter the name in the “allele1” or “allele2” column of the [genotype table](#).
- Double-click the allele label above the peak and type the name.

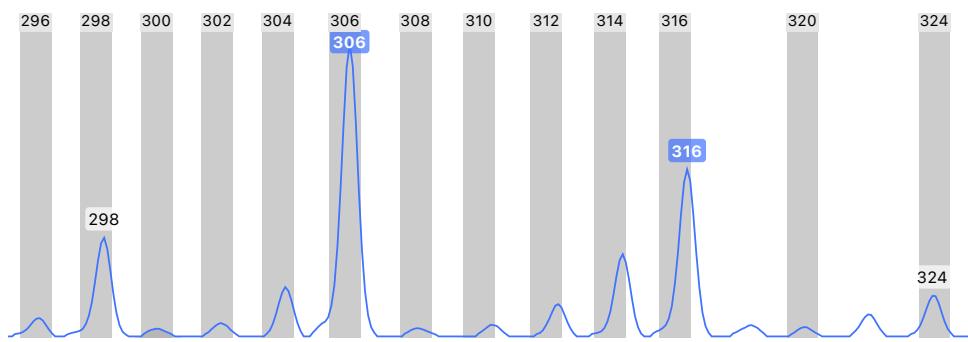


Note: if you delete an allele name, its size in base pairs will appear above its peak instead.

Tip: to quickly review genotypes, [sort](#) the genotype table by marker, allele1 and allele2 in ascending order (assuming allele names correspond to sizes). Then, view genotypes from top to bottom. This method helps detecting errors in allele call.

Additional peaks

In addition to alleles, STRyper may annotate other peaks found in a marker range if they meet certain criteria. These peaks are labelled like alleles, except that their names appear in black over a white background. Additional peaks can be helpful to identify contamination between samples, insufficient specific of the PCR or polyploidy.



Additional peaks can be [edited](#) like alleles: their labels can be moved between peaks and renamed by double-clicking, and they can be deleted by the “delete” key. In addition, they can be deleted by double-clicking their peak. These actions have no effect on the sample’s genotype as defined by the “Allele1” and “Allele2” columns of the genotype table.

Note: an additional peak label cannot be moved to a peak that has an allele. The allele must be removed first.

If you consider an additional peak as a real allele:

- Drag an allele label onto the peak. This will remove the additional peak label.
- If no allele label is present at the marker, first remove the additional peak label from the peak (by double-clicking the peak or removing the label with the delete key), then double click the peak, which will attach an allele to it.

To label a peak as an additional peak right-click the peak and **Add Label** from the contextual menu. This menu is not available if the peak has an allele.

To remove an additional peak, you can:

- select the peak label and either hit the delete key, select **Edit > Delete Label** from the menu bar, or click the trash icon  on the [toolbar](#).
- drag the peak label above the top edge of the row showing traces,

- double-click the peak.

To remove all additional peaks from several genotypes, select these genotypes on the [genotype table](#), right-click them and select **Remove Additional Peaks** from the contextual menu.

Information on additional peaks appear in the “Additional Peaks” column of the genotype table. For each peak, the column shows the size (in base pairs, rounded to the nearest decimal) of the additional peak and its name, separated by a colon.

| Additional Peaks |
|---------------------|
| 248.7:248 264.0:264 |

Data from different peaks are separated by spaces and are sorted by increasing size. This column is not editable.

To disable the annotation of additional peaks during automatic genotype calling, untick the corresponding checkbox in the [settings window](#).

Exporting genotypes

To export genotypes as a tab-delimited text file, you can:

- go the [genotype table](#) and click the [toolbar](#) “Export” button, which should look like this:  If it does not, click anywhere in the genotype table. Alternatively, click the export button  below the genotype table. A window will let you choose to export the whole table or only the selected rows, if any.
- Right-click or ctrl-click selected genotypes from the [genotype table](#) and choose **Export to Text File...** from the contextual menu. This will spawn a window allowing to export selected/ clicked genotypes.

Note: the exported file comprises all the columns that are visible in the genotype table, and only these columns. You must [change the column visibility](#) if you want to change the data to be exported.

To add sample metadata to the exported genotypes, tick the **Add Sample-related Columns** checkbox in the export panel. Each visible field in the [sample table](#) will be added to each genotype.

You can copy rows of genotypes to the pasteboard via **Edit > Copy**, and paste them to a spreadsheet or text editor. **Note:** this does not copy sample metadata and column headers.

Export/import

Exporting marker panels

STRyper can **export marker panels to a text file** for archiving, editing some properties with a text editor, or transferring the panels to colleagues. This text file describes all markers and bins of the

panel. You can export a single panel, or all panels contained in a folder. For this, do one of the following:

- select the panel/folder from the [panel list](#) and click the “Export” button  on the [toolbar](#).
- select the panel/folder and select **File > Export Panel(s)...**
- right-click the panel/folder and select **Export to Text File...** from the contextual menu.

Note: if the folder does not contain any panel, these actions are not available.

The exported file is a UTF-16 text file formatted as this example:

```
panel panel_name
# an optional comment line that can be added anywhere
marker      marker1    154.92     180.73     red   2       4
bin    167    166.75    167.40
bin    164    163.57    164.45
bin    165    164.70    165.44
bin    163    162.60    163.32
bin    166    165.60    166.46
bin    168    167.64    168.63
bin    162    161.55    162.35
bin    161    160.54    161.31
bin    176    176.03    176.91
marker      marker2    242    275.65     red   2       3
bin    253    252.31    253.03
bin    255    254.14    255.05
bin    270    269.44    270.42
panel new_panel 2
marker      marker2    155    180     black  2       4
bin    167    166.75    167.40
bin    164    163.57    164.45
```

- Fields are delimited by **tabulations**.
- Lines starting with “#” can be used to add comments.
- The first uncommented line starts with the keyword “panel” followed by the panel name.
- The next line defines the first marker. The line starts with the keyword “marker”. The following fields represent in this order: the marker name, the start coordinate, the end coordinate, the channel color (either “blue”, “green”, “red”, “black” or “orange”), the ploidy (either 1 or 2) and the motive length (2 to 7).
- The subsequent lines define the marker bins. Bins of a marker, and markers of a panel, can be described in any order, but all bins of a marker must be described before the next marker. Each row must start with the keyword “bin”. The following fields specify the bin name, start and end coordinates.
- Decimal separators are periods.

Note: STRyper allows most Unicode characters (excluding tabs) in panel, marker and bin names. However, for compatibility with other applications, roman characters are recommended.

Importing marker panels

STRyper can **import panels from text files** conforming to the above [specifications](#), as well as panel files exported by GeneMapper (version 4). Here is an example of such file:

```
# This a Genemapper v4 panel file
Version      GM v 4.0(not checked)
Kit type:   MICROSATELLITE(ignored)
Chemistry Kit (Ignored) none
Panel new_panel none
marker1    Red  154.92   180.73   -     4     0     none  none  false
marker2    Red  242    275.65   -     3     0     none  none  false
Panel new_panel 2
marker3    Yellow 155  180   -     4     0     none  none  false
```

You may refer to the GeneMapper user guide for a description of this format. Elements in grey can be omitted, as there are ignored during import. It is however *crucial* that the keyword “Version” appears in the first column before the first panel, as this is used to determine the file format.

Important: files must end with the extension “.txt”.

Note:

- markers imported from a GeneMapper file are considered diploid.
- This type of file does not contain bin information, you must therefore [import bins](#) separately.

To import marker panels from a text file, do one of the following:

- click the “Import markers” button  on the [toolbar](#) or select **File/Import Marker Panel(s)...** from the menu bar. The imported panel(s) will appear at the bottom of the [panel list](#).
- Click the “+” button at the bottom of the panel list and choose **Import Panels from File** in the contextual menu.
- right-click a folder in the [panel list](#) and select **Import Panels from File...** from the contextual menu. The panel(s) will be imported into that folder.

Note: if several panels are imported from one file, they will be gathered in a new folder named after the file.

During import, any blank line from the text file is skipped, leading and trailing spaces are removed from fields and lines starting with “#” are ignored. If the imported file does not conform to the specifications,

or if markers/bins overlap, are too short, or exceed the allowed range, an error message will describe the issue(s).

Importing bins

If you imported markers from a genemapper file, these markers will contain no bin. You may thus need to import bins from another file generate by GeneMapper: a binset description file. The GeneMapper 4 binset format looks as follows:

```
# This is a comment line
Version      GM v 4.0 (not checked)
Chemistry Kit (ignored)
BinSet Name (ignored)
Panel Name a_panel
Marker Name marker1
383 363.825 0.5 0.5 dark gray
386 367.65 0.5 0.5 dark gray mutant
392 373.18 0.5 0.5 dark gray
395 375.605 0.5 0.5 dark gray
398 379.095 0.5 0.5 dark gray mutant
401 382.235 0.5 0.5 dark gray
404b 385.395 0.5 0.5 dark gray
Marker Name marker2
193 173.72 0.46 0.47 dark gray
196? 176.93 0.43 0.43 dark gray
203 183.19 0.5 0.5 dark gray
207 186.93 0.5 0.5 dark gray
209 188.95 0.5 0.5 dark gray
```

You may refer to the GeneMapper user guide for a description of this format. Elements shown in grey are ignored and can be omitted.

You may also import bin descriptions from a file [exported by STRyper](#). This could be useful to transfer bins between panels containing the same markers. For instance, you may have added new bins to account for rare/irregular alleles, and you may wish to use this set of bins on another computer. For this, you may [export the panel](#), then import the bins from the exported file into the equivalent panel on the other computer. Importing the file [as a new panel](#) would not replace bins from the existing panel, it would create a new panel that is not associated with any sample.

By contrast, importing bins into a marker panel replaces existing bins. This updates the [detailed view](#) with the new bins for every sample already analysed at the panel. Every called genotype of these samples will get [status](#) 🟡, to denote the fact that bins have changed.

To import bins for markers of a panel, do one of the following:

- select the panel in the [panel list](#) and click the button “Import Bins” below [marker table](#),
- right-click or ctrl-click the panel and select **Add Bins from File** from the contextual menu, then choose the file to import.

Note:

- These actions are disabled if the panel to import bins into does not contain any marker.
- The import will fail if bins of the same marker overlap, if a bin falls outside the range of its marker, or if the file does not refer to the panel or its markers by their exact names.
- The file need not define bins for all markers of the panel. For the markers named in the file, all existing bins will be replaced by the bins described in the file. Other markers of the panel will not be modified.

To import bins for only certain makers of a panel, you have two options:

- make sure that all lines related to the other markers of the panel, and their bins, are absent from the file you import.
- in the file, rename any marker you want to leave untouched, using a name that does not match any marker of the panel. The application skips markers whose names do not match those of markers listed in the [marker library](#).

Exporting and importing folders

A [folder](#), with all its samples and subfolders (including subfolders of subfolders) can be exported as a single file and imported afterward or into a different instance of the application. The exported archive contains all genotypes, size standards and marker panels (including markers and bins) applied to the samples contained in the folder. An archive has the following icon:



To export a sample folder, do one of the following:

- Select the folder in the [folder list](#) and click the export button  on the [toolbar](#).
- Select the folder and choose **File > Export Folder...** from the menu bar.
- Right-click the folder and select **Export to Archive...** in the contextual menu.

Note: If the exported folder is a [smart folder](#), it is exported as a regular folder. Its search criteria are not encoded in the file.

To import a folder from an archive, do one of the following:

- drag and drop an archived folder into the [folder list](#). **Note:** you can only drop one archive at a time.
- click the “Import archive” button  on the [toolbar](#) and chose the folder to import.
- select **File > Import Archived Folder...** from the menu bar and chose the folder to import.

The last two methods place the imported folder at the bottom of the [folder list](#).

Note:

- Any marker panel applied to samples in that folder is imported and placed in a new folder named after the imported folder, in the [panel list](#), unless this panel is already present in the database (i.e., has the same name, markers and bins, with the exact same attributes: name, start, end, etc.).
- Any size standard not already present in the database (with the same name and ladder fragment sizes) is imported as well and the string “-imported” is appended to its name.

FAQ

Where is my data stored?

Your data is stored in `~/Library/Application support/STRyper/`. You may access this folder from the Finder by selecting **Go > Go To Folder... (⇧⌘G)** and pasting this path into the field.

Can I change the location of the database?

No. STRyper looks for its database in `~/Library/Application support/STRyper/`. Moving the database elsewhere will make the application recreate a blank database in this folder. However, you may replace the database folder with a symbolic link named identically and pointing to another folder.

Is my data backed up?

STRyper saves its database every 30 seconds, if necessary, but it does make backup copies. We recommend using a backup solution, such as Time Machine, to back up the database.

Does STRyper do database versioning?

No, STRyper does not maintain different versions of the database. For this, you must use your own backup/versioning solution.

What if STRyper could not load the database?

There is nothing you can do to fix a corrupt database beyond replacing it with a backup. If the app cannot load the database and therefore cannot be used, you may delete or move the folder `~/Library/Application support/STRyper/` to another location and relaunch the application. You may additionally report the issue.

How can I work on the same project on different computers?

You can [export and import folders](#) between computers. Transferring/synchronizing the whole database has not been tested. If you which to do so, you must make sure that the database is fully transferred before opening STRyper.

Is there an equivalent to GeneMapper's bin sets?

You may define panels with different sets of bins for the same markers, but STRyper has a more flexible solution: defining the [offset of a marker](#) for specific samples.

Why don't the size standards listed in the library have dyes names?

The [size standard library](#) lists, for instance, “GeneScan 500” rather than “GeneScan 500 **LIZ**”, “LIZ” being the dye used. This is because the dye is irrelevant to sizing, only the size of fragments matter. Simply ignore the dye used by your size standard, just make sure to apply one with appropriate sizes.

Can I use allelic ladders?

STRyper does not allow specifying allelic ladders for markers. An allelic ladder, also called “inter-lane standard”, contains a mixture of known alleles for one or several markers. STRyper considers a chromatogram file obtained from such mixture as a regular sample. You may however use this sample to efficiently [adjust the offset](#) of a marker for all samples analyzed in the same conditions.

Why was this peak not attributed to an allele?

This may be because the peak is considered by the application as resulting from crosstalk, i.e., it does not represent a DNA fragment from the channel that is visualized, but from another channel. You can check this by showing peak tooltips. You can still [assign an allele](#) manually to the peak.

Alternatively, the peak may be too faint to be detected if its fluorescence level is less than 100. In this case, hovering it with the mouse does not make a vertical line appear at its tip. You can still [force the detection of the peak](#) and assign it to an allele.

Can I use STRyper for forensics or diagnostics?

STRyper **must not** be used for forensics or diagnostics. STRyper comes with no guarantee whatsoever and is only intended for research use.

Does STRyper assess genotype quality?

No. Genotype quality must be assessed by the user. In our experience, genotyping quality computed by applications is poorly informative.

Is there a history of changes applied to genotypes?

STRyper does not maintain a history of manual changes applied to genotypes, as this is not important to most researchers. You may still add notes to a genotype in the “Notes” column of the [genotype table](#).

How can I export genotypes with only one row per individual for all markers?

You cannot. This is because samples from the same folder can be analyzed at different panels, hence markers (this is especially true for smart folders). However, if samples are analyzed at the same markers in the exported genotype file, you can achieve what you want with [R](#):

```
requires(data.table)
genotypes <- fread("genotypes.txt", header = TRUE, sep = "\t") # use the appropriate path for
"genotypes.txt"

# if you wish to paste allele names into genotype strings:

genotypes[,genotype := paste(Allele1, Allele2, sep = "")]
genotypesPerIndividual <- dcast(genotypes, Sample ~ Marker, value.var = "genotype")

# if not:
genotypesPerIndividual <- dcast(genotypes, Sample ~ Marker, value.var = c("Allele1","Allele2"))
# you may use c("Allele1","Allele2","Size1","Size2") if required

# You may include more columns in the formula, e.g.: Sample + Panel + Well ~ Marker, assuming
these columns are present in the table
```

Can I analyze polyploid individuals?

STRyper only manages haploid and diploid markers. At a polyploid marker, the genotype cannot directly be determined from the number of peaks. However, you may use [additional peaks](#) to annotate additional alleles. This could be a solution to genotype polyploid individuals.

Can I use STRyper for other markers than microsatellites, such as AFLPs?

You should probably not. STRyper was designed for microsatellite markers.

How can STRyper be used in a multi-user environment?

As for any regular app, the user of STRyper is the user logged in the operating system. If several users must use the app on the same computer and work on different projects, the computer administrator must create a user account for each.

Different users can of course separate their projects into different [folders](#), but these folders will be accessible to everyone using the app from the same user account.

Where can I report bugs?

Please, report bugs at <https://github.com/jeanlain/STRyper/issues>.

Will STRyper be ported to Windows?

The author of STRyper does not have the resources to port the application to other platforms. To make porting a reality, direct a Windows developer to <https://github.com/jeanlain/STRyper>.