

“Future trends in
forensic DNA technology”
seminar series

ThermoFisher
SCIENTIFIC

GMID_X Helpful Tips and Tricks

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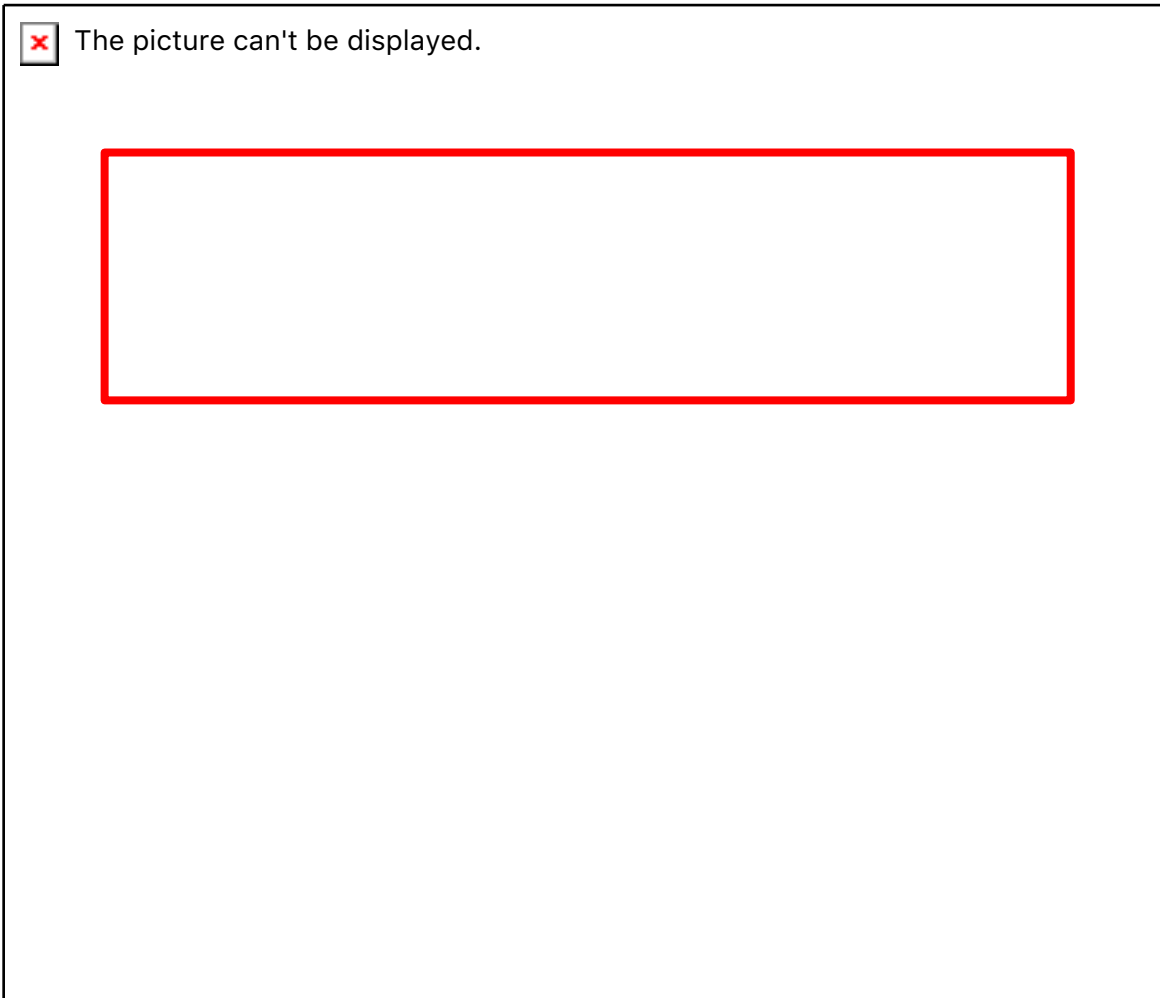
What you may not know GMID_X can do...

- Printing Features
- Command Line Interface
- Profile Comparison Tool:
 - Searching for Employee Database Profiles and Checking for Contamination/Duplicate Profiles
- Scaling Y Axis
- Raw Data View for Spikes
- Calculating Peak Height Ratios
- Calculating % Pull Up
- Shortcut Keys



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Tip #1: *How Can I Print 5 Dyes on 1 Page?*



To print with allele call, size (bp), and height (RFU):

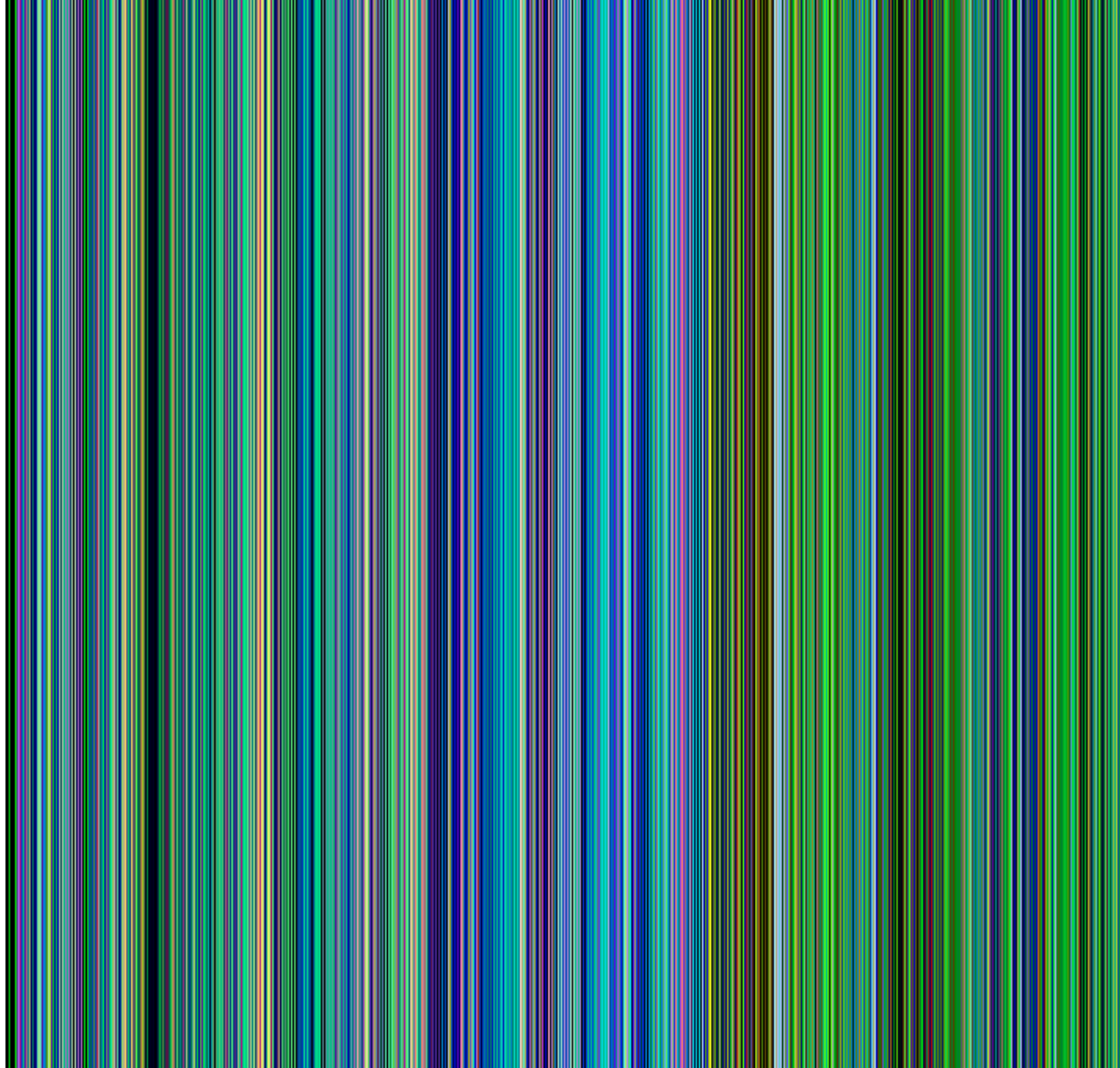
1. Create a new **Plot Setting** or open up a previously made **Plot Setting** in **Plot Setting Editor**.
2. Click on the **Labels** tab.
3. Modify labels as shown.
4. Click **ok**.

Tip #1: Printing Options



4. Click on **Print**.
5. Click on **Page Setup** tab
6. Choose **A2 (ISO/DIN & JIS)** option under Size.

Tip #1: Printing Options



Tip #2: *Is there a way to print a whole bunch of samples/ projects at once?*

- Command Line Interface allows user to perform software tasks without opening up the GMID_X software.
- Some of these features include:
 - Exporting 1 or more projects
 - Exporting 1 or more size standard and/or analysis methods
 - Export sample plot data into individual PDF's
 - Export data for selected samples in a project

Tip #2: Command Line Interface: Exporting Sample Plot Data Example



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Tip #3: *Is there an easy way to check my samples against our employee profiles?*

Key features include:

1. Import profiles into a Reference/Custom Control Database and/or Employee Database
 - Profiles can be imported via .txt or analyzed data upload.
2. Tool can search any analyzed data against profiles uploaded into the database for full and partial matches.
3. Ability to export comparison results for further analysis and reporting

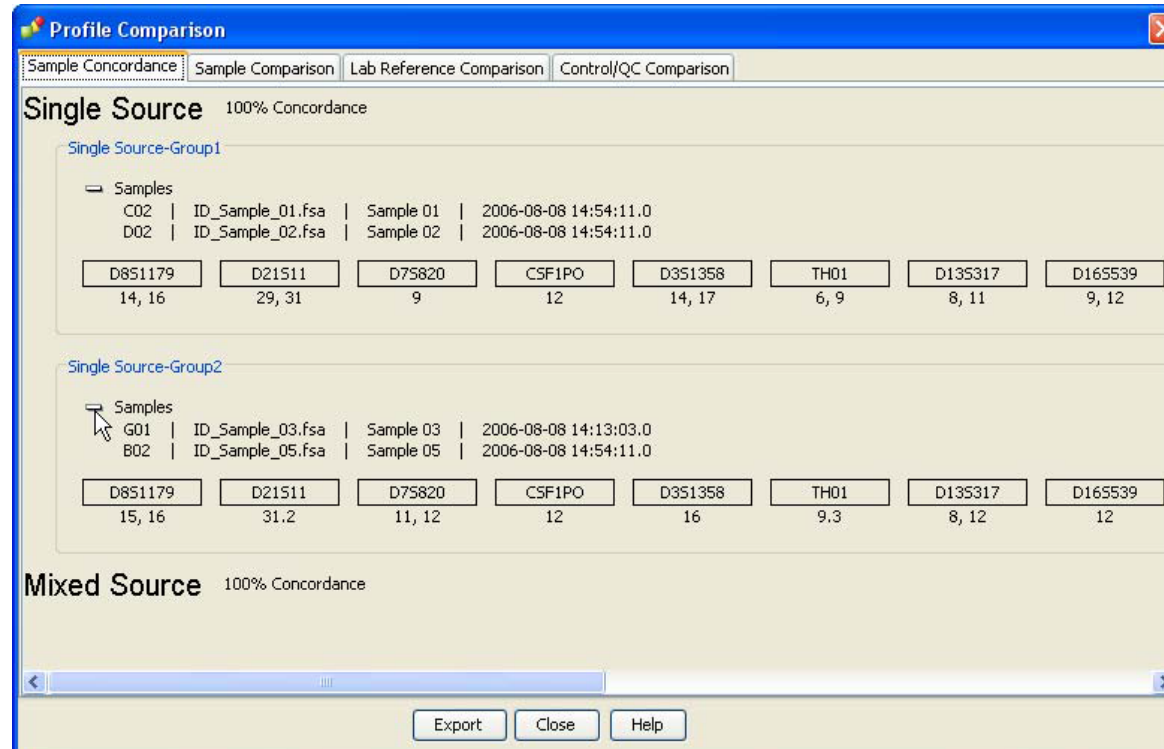
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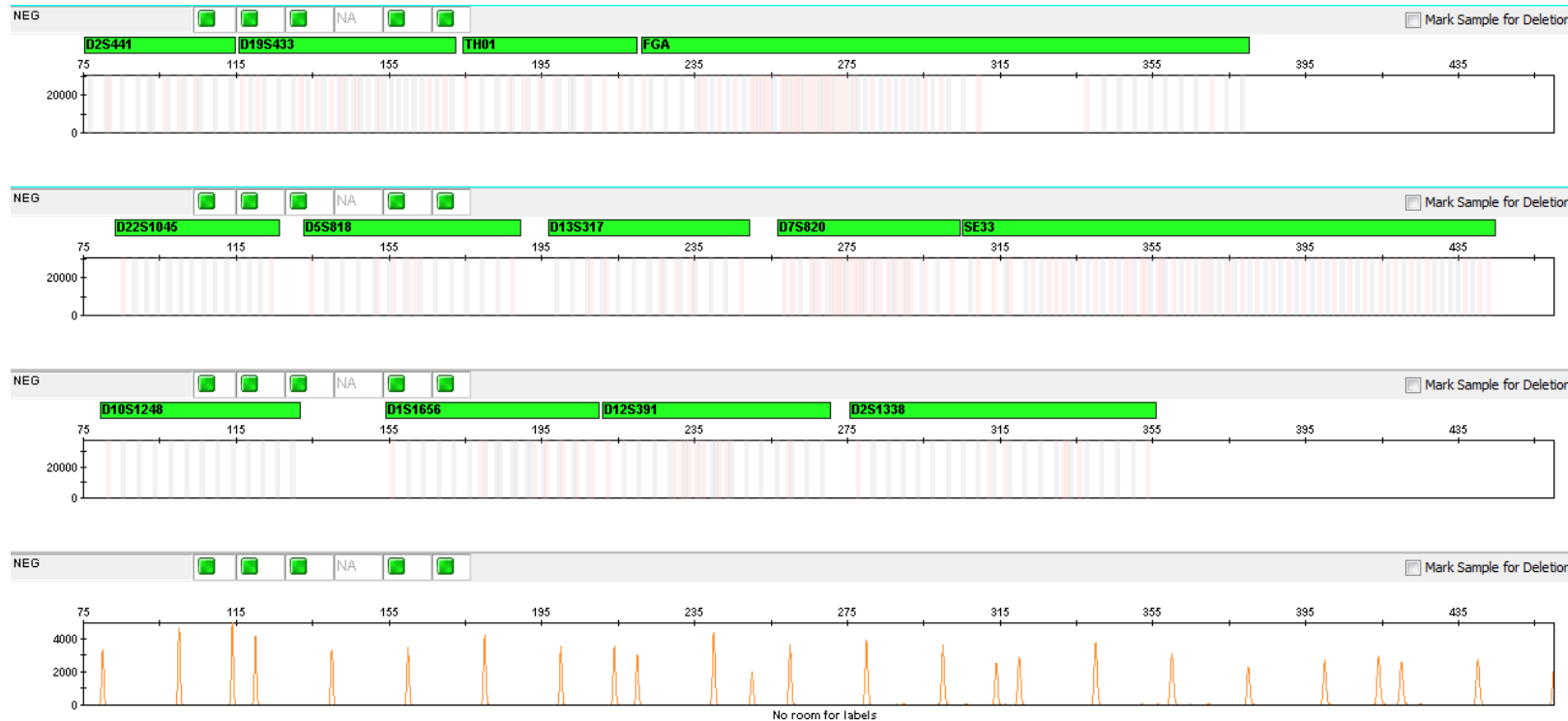
Tip #3: Profile Comparison Tool

Features of the Profile Comparison Tool:

- Compares all samples within the project to one another.
- Compares all samples within the project to any imported lab reference profiles.
- Compares all samples within the project to imported custom control and QC sample profiles.
- Has user definable percent match thresholds



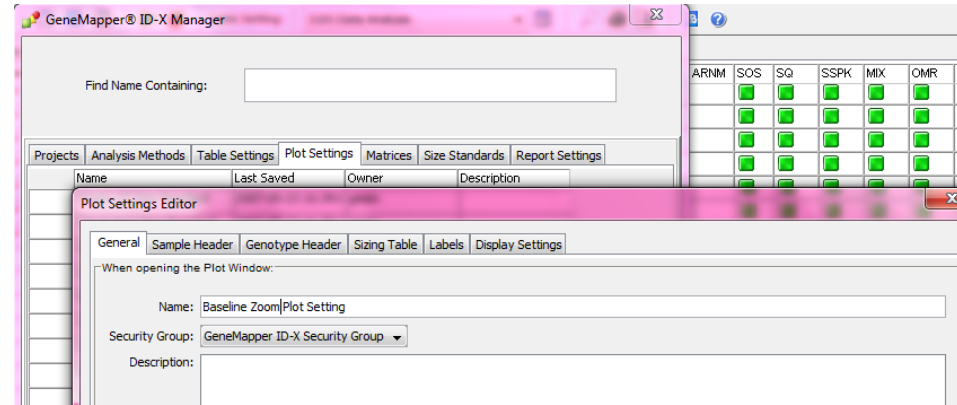
Tip #4: How can I change the scaling range for different dye panes?



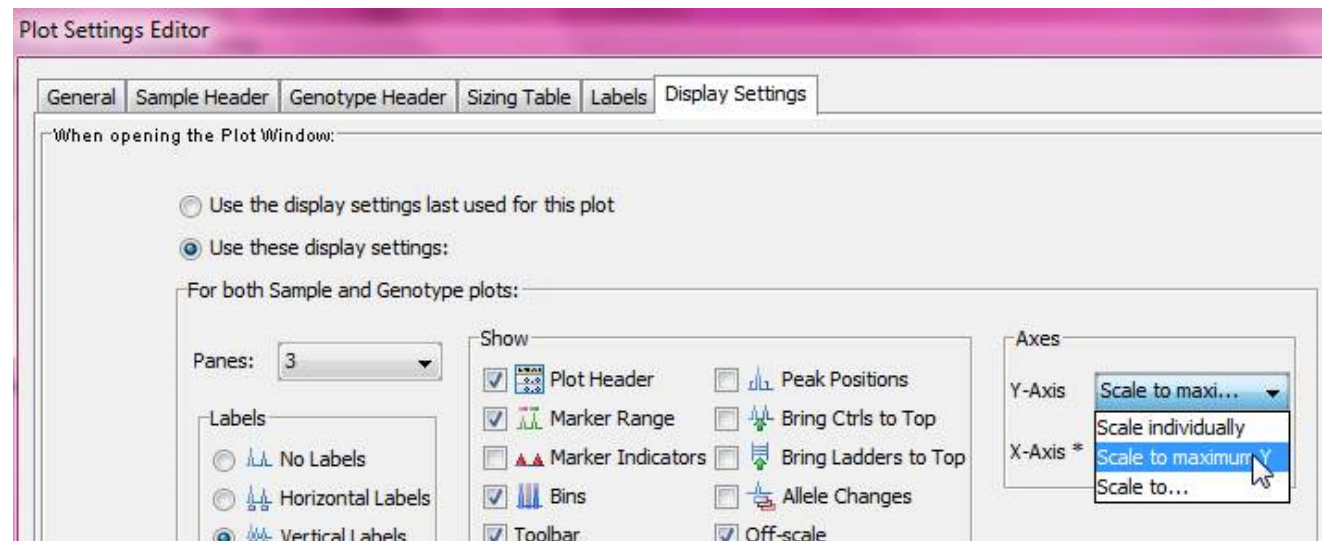
Issue: Trying to review/print NEG's but GMID_X I need to zoom into each dye channel independently and as soon as I hit print or the down key the zoom goes away. Is there a fix?

Tip #4: Y Scale Axis Zooming

1. Open up **Plot Setting Editor** or create **New Plot Setting** in GeneMapper ID_X Manager.

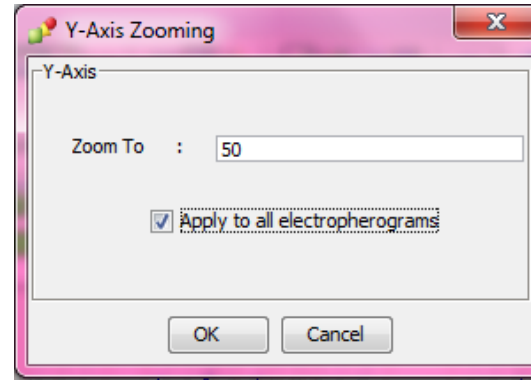


2. Under Display Setting set the scale for the Y Axis to “Scale to maximum Y”.



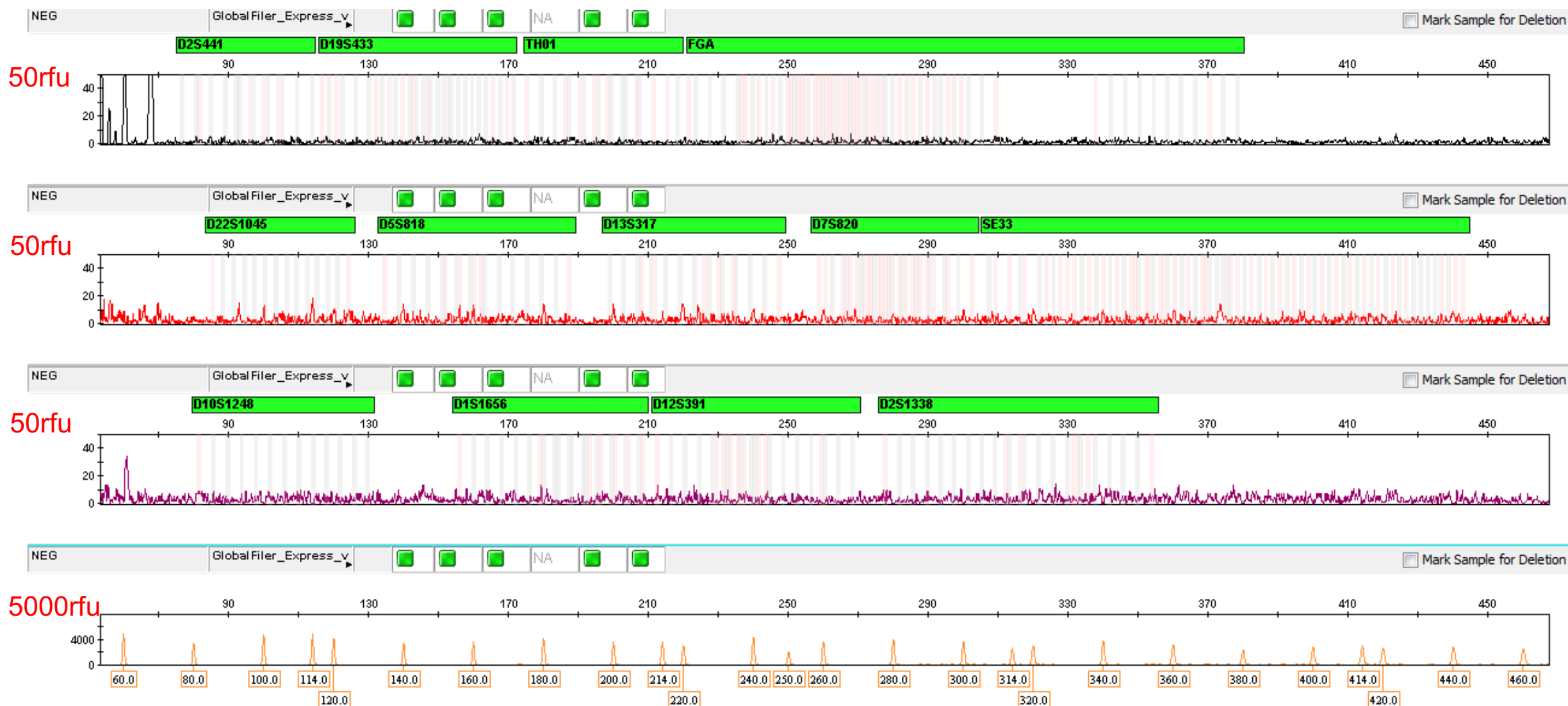
Tip #4: Y Scale Axis Zooming Continued...

3. **Right click** on a specific dye and **choose a value** that you would like all dye channels zoomed in to (i.e. 50 rfu). Make sure to **check** “Apply to all electropherograms”.



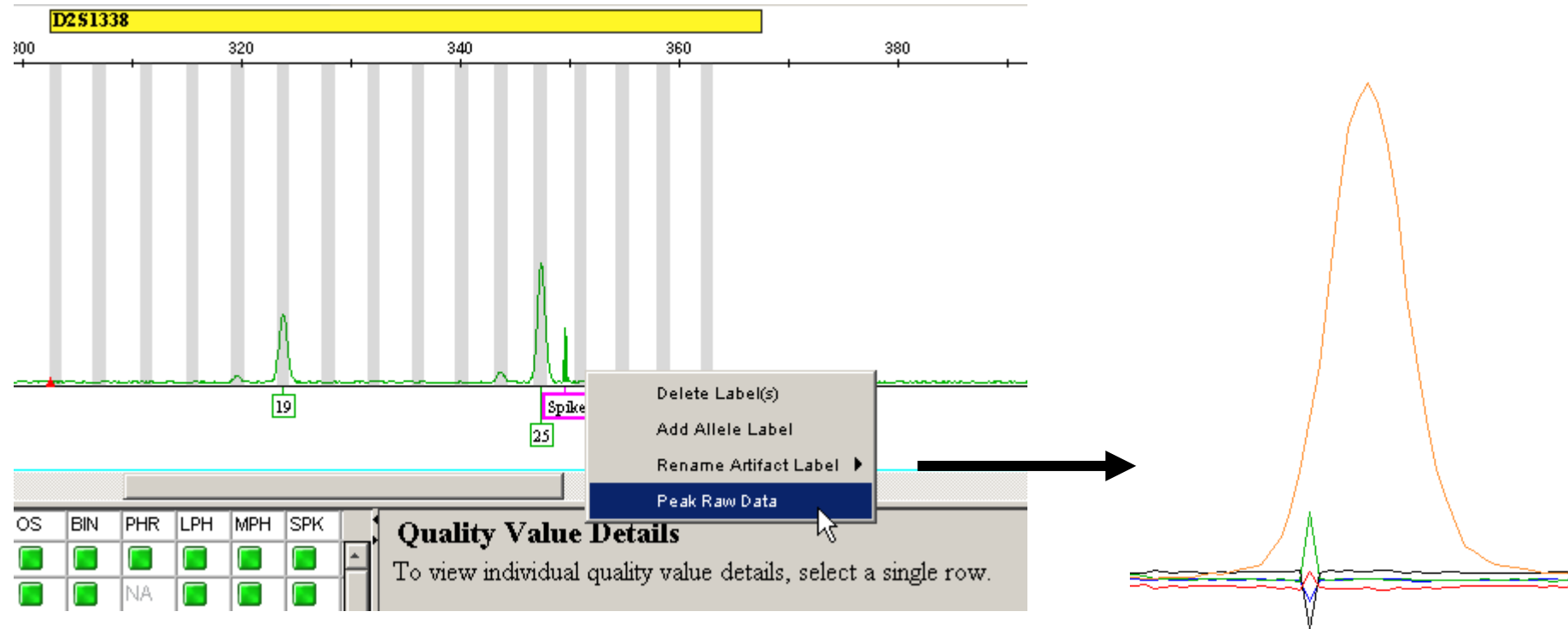
4. Hold down the Shift key and double click on a specific dye channel (i.e. the ILS dye channel) that you would like to modify without affecting the others and modify the scale. Still holding down the shift key- drag to the appropriate scale if necessary.

Tip #4: Y Scale Axis Zooming Continued...



Tip #5: *Is there an easier way to determine if a Spike is truly a Spike?*

If a spike is suspected, **right click** on the suspected peak and choose **Peak Raw Data**.

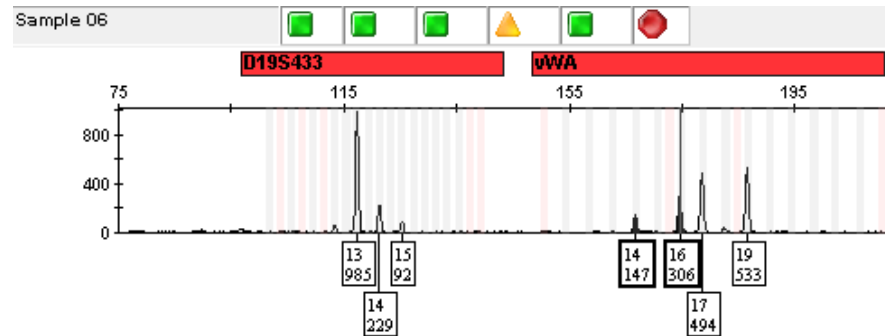


A new window opens up with the specific peak. All that is needed is to **zoom in** on the Y axis. Tab over to go back to your EPG.

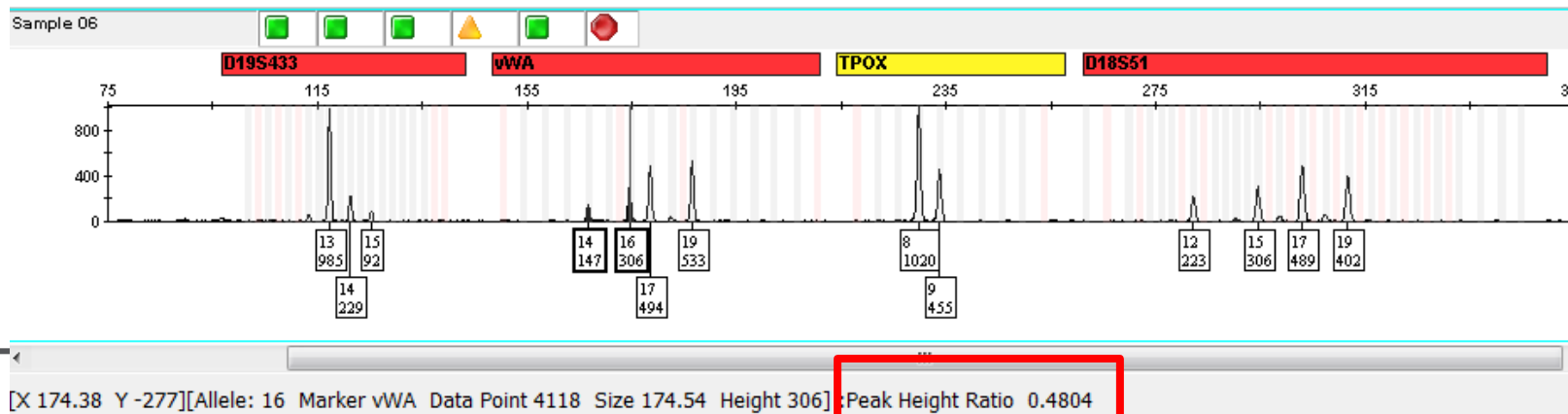
Tip #6: *I wish there was an easier way to figure out peak height ratios...*

GMID_X can calculate your peak height ratios for any peak within a same dye channel!

1. Holding down the Shift key click on the two peaks in question. In example below user clicked on the 14 and 16 alleles at vWA.



2. The Peak Height Ratio is displayed on the bottom of the screen.



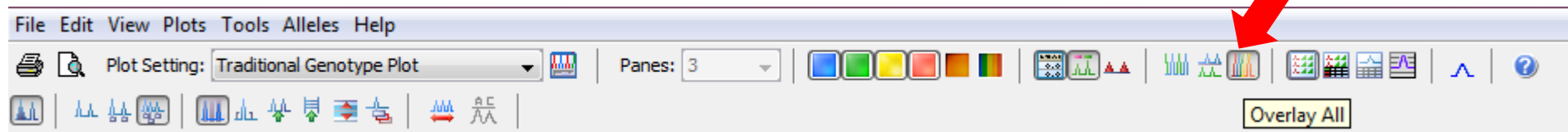
Tip #7: *OK that's great, but can it determine my % pull up too?*

GMID_X can also calculate your % pull up!

1. **Select the two peaks** (i.e. parent peak and suspected pull up peak)

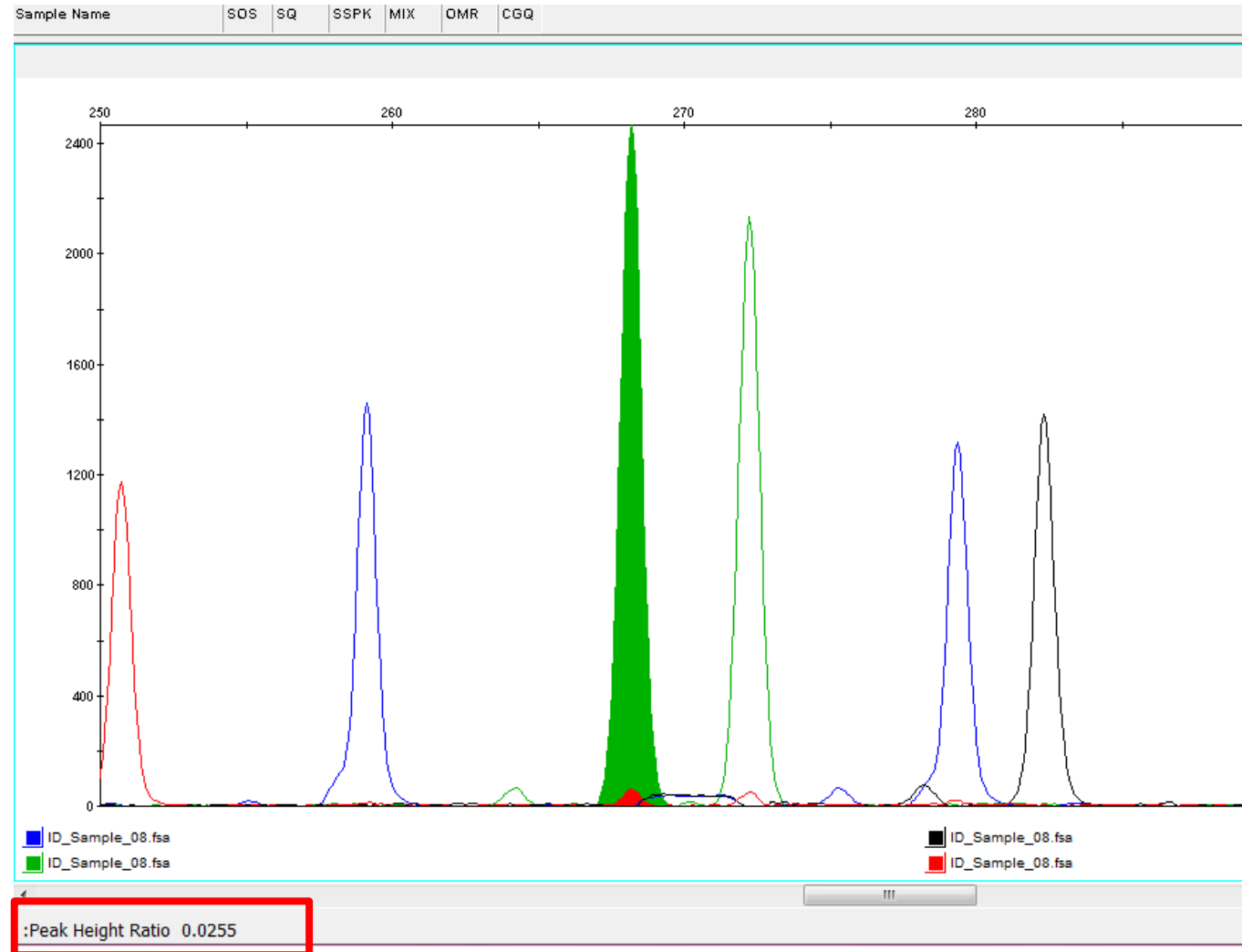


2. Click on **Overlay All** on toolbar



Tip #7: Calculating % Pull Up

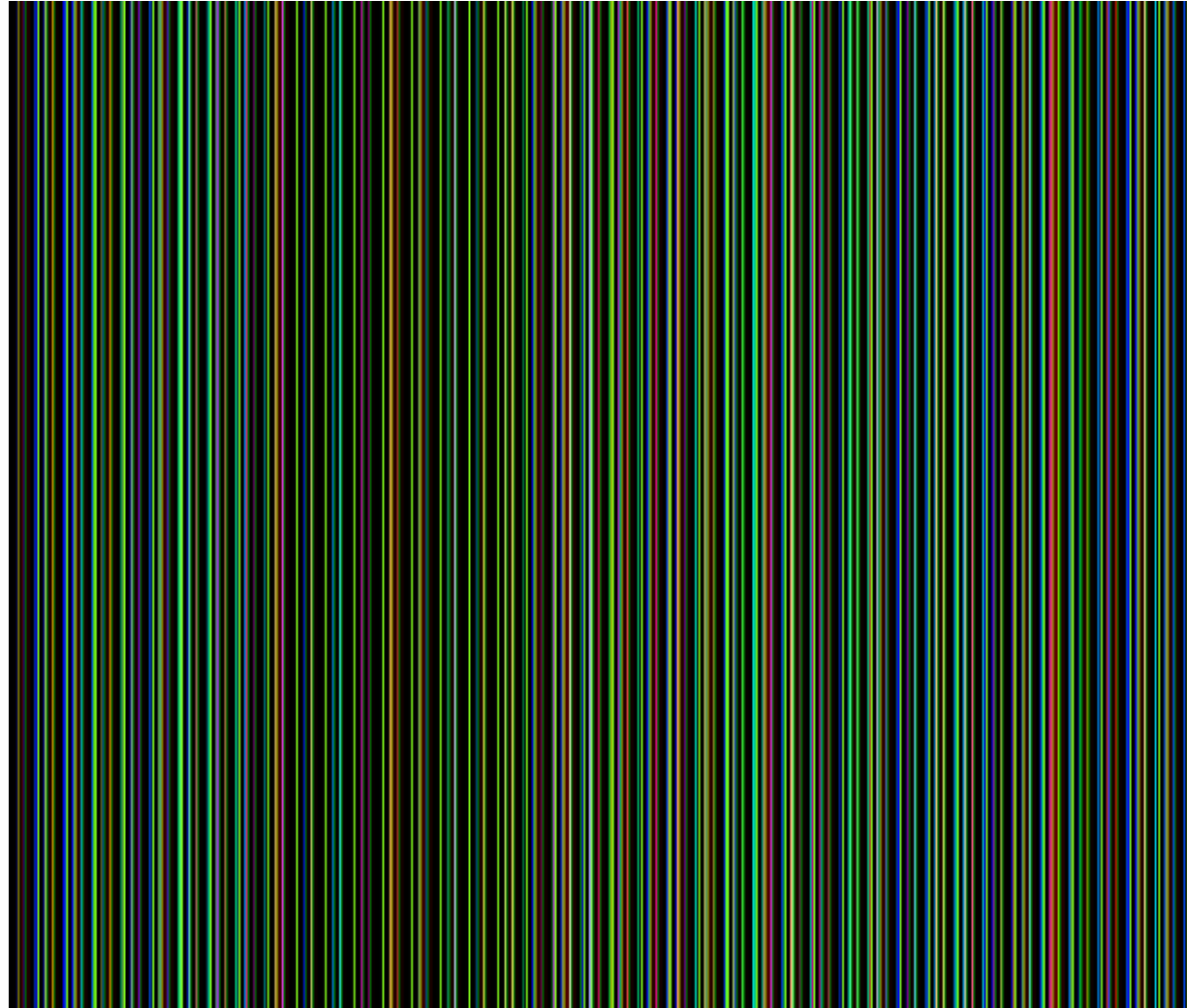
3. The Peak Height Ratio of the two highlighted peaks is shown on the bottom of the EPG.



Tip #8: Shortcut Keys

Name	Icon	Shortcut	Description
Project Window Toolbar			
New Project		Ctrl + N	Creates a new project.
Open Project		Ctrl + O	Opens a saved project.
Save Project		Ctrl + S	Saves the current project.
Add Samples to Project		Ctrl + K	Adds samples to a project.
Export Table		Ctrl + E	Exports the contents of the currently selected table in a .txt file.
Display Plots		Ctrl + L	Displays either the Samples plot for samples selected in the Samples table, or the Genotypes plot for markers selected in the Genotypes table.
Report Manager		Ctrl + Q	Generates a table-formatted report using user-defined report settings.
Label Edit Viewer		Alt+V+T	Contains a detailed list of edits made to allele and artifact labels in a Sample s plot, with reasons for change.
Size Match Editor		Alt+T+E	Provides views of the size standard definition and size calling curve for each sample highlighted in the project.
Analysis Method Editor		Alt+T+O	Allows you to edit the parameters of new and existing analysis methods.
Panel Manager		Ctrl + J	Displays the markers and bins used to allele-call samples.
GeneMapper ID-X Manager		Ctrl + M	Allows you to edit the parameters of new and existing GeneMapper ID-X files (analysis methods, table settings, plot settings, matrices, size standards, report settings and projects).
Analyze		Ctrl + R	Analyzes the project currently open.
Low Quality to Top		Ctrl + B	Sorts the data in the Samples or Genotypes tab so samples or markers with lower PQV scores are at the top of the table.
Table Setting menu		No shortcut	Lists available table settings.
Table Setting Editor		Ctrl + T	Allows you to edit the parameters of new and existing table settings.
Find		Ctrl + F	Allows you to search the Samples tab or Genotypes tab columns.
Fill down	No icon	Ctrl + D	Fills down the selected column in the Samples table.

Tip #8: Shortcut Keys Continued...



- Holding down **Shift** and clicking on any header in software also sorts that column.



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