

## How do I add a plot?

- You can drag and drop any BAM, BED, IDF, TSF or VCF file directly into the Plot View. Additionally, if a BED or VCF file is bgzipped you can drag and drop the BED.GZ or VCF.GZ file into the Plot View as well. GenomeBrowse also supports many other file formats.
- You can also stream BAM and TSF files by clicking on the Add button (  Add ) in the top-left corner of GenomeBrowse. From here you can stream TSF annotation tracks from the cloud, add BAM files from your EA Pipeline account, or add example data. Data from the cloud can also be downloaded to your local computer.
- You can also do the same as above by right-clicking in empty space in either the Plot Tree or the Plot View and selecting the Add button.
- You can change the default visible plots for Read Alignment (BAM) files by opening the **Options...** dialog in the **Tools** menu or by clicking on the Gear icon in the toolbar (  ) and checking or unchecking the **Coverage** or **Pile-up** options.
- You can change where new plots are added in the **Options** dialog. By default new plots are added to the **Top** of the plot view, this can be changed to have plots added to the **Bottom** of the view.

## How do I navigate?

- There are two navigation modes in GenomeBrowse:
  - In Navigation Pointer Mode (  ), you can pan any plot or axis by holding down the left mouse button. Dragging with the right mouse button scales the plot.
  - Zoom Mode (  ) will give you access to the rubber band zoom feature.
- You can use the scroll wheel to zoom in and out in any mode.
- By default, all plots have y-axis fit-data or auto zoom enabled. To change the y-axis zoom mode, hover over a plot and click the zoom mode button on the right edge (labeled with a letter).
- You can jump to a specific region or gene by typing it into the Zoom Toolbar. This includes typing in a gene or transcript name. If there are multiple options, the first 10 results from each searchable track will be displayed in a drop down list.
- There is a zoom slider for the x-axis in the toolbar between the - and + buttons. These controls scale the x-axis on all plots.
- There are left and right arrows framing the Domain Scale. These controls pan the x-axis on all plots.
- Keyboard shortcuts:
  - Arrow keys allow you to pan on the current plot.
  - + and - zoom in and out.
  - Shift + scroll wheel lets you zoom on just the y-axis.

- Ctrl + Shift + scroll wheel lets you zoom on both axes.
- Double-click on the y-axis to zoom to y-extents.
- Double-click on the x-axis (or on a chromosome in the Domain View) to zoom to x-extents or the current chromosome.
- Right-click before you complete a zoom selection to cancel.

## How do I see my previous view?

- Clicking the Back and Forward arrows (  ) allows you to traverse zoom history.
- Right-clicking or holding the mouse button down on one of the buttons for a few seconds gives you a list of recent zoom history states, so that you can jump back by multiple steps.
- Keyboard shortcuts: Alt+left and Alt+right.

## How do I change the species and/or genome build?

- You can choose a new build from the drop down menu in the Genome Toolbar.

## How do I move and resize plots?

- You can drag plots around in the Plot View using their handles (at the left of a plot) or drag-and-drop nodes in the Plot Tree.
- To resize the plot, you can mouse over the handle (at the bottom of a plot) and drag up or down.

## How do I change how my data is displayed in a plot?

- In some plots, a gear icon will appear in the top-left corner when view options are available. Click on this gear icon to view plot-type specific options.
- If the control panel is already open, you just need to select a plot to have the control options update with those relevant to that plot type.
- To open the control panel, right-click on a plot and choose **Controls...**
- In pile-up plots, you can choose to **Emphasize Strand** or **Emphasize Mismatches** and **Stack Above Axis**, **Stack Split by Strand** or **Stack Paired-ends**. Multi-mapped alignments can be filtered by clicking on **Filter Multi-Mapped Alignments**. More controls are available by clicking on the **More Controls...** button. This brings up more display and filtering options.
- In a gene track, you can view regions in **Compact** or **Expanded** mode. **Auto** blends the two modes to adjust based on plot height.
- In variant maps, variant, interval and value plots, you can hide and show the **Feature labels** and change the label field.
- Value plots have the additional feature of being able to change the **Value** displayed based on the values available from the source.

### How do I edit plot labels?

- Double-click on any plot title or axis label to edit the text.
- Right-click on any plot title or axis label and select **Edit...**
- Right-click on a Plot Tree node and choose **Edit Title**.
- Double-click any Plot Tree node's text.

### How do I change the colors?

- Choose **Options...** in the **Tools** menu and click on the **Color** tab.
- **Reference Mismatch** defines the color of variant plots when zoomed out.

### How do I delete a plot?

- Select the plot and press the delete key.
- Right-click on the plot in either the Plot Tree or the Plot View and choose **Delete**.

### How do I change the Domain View (default is a cytoband)?

- Right-click on any plot in the Plot Tree or Plot View and choose **Set As Domain View Plot**.
- To change back to a cytoband, right-click on the Domain View and choose **Restore Cytoband Plot**.

### What can I do with the mouse anchor?

- Right-click anywhere in a plot and choose **Place Mouse Anchor** to mark a location.
- Keyboard shortcuts: Ctrl+` to set, Alt+` to remove, and ` to center the view on it.

### How do I save my project?

- By default, the project is saved on close. To disable this feature, open **Options...** dialog in the **Tools** menu and uncheck **Save projects on close** on the **General** tab.
- Similarly, the project settings are saved on close. To disable this feature, uncheck **Save program settings on close** in the **Options** dialog.
- Click **Save Program Settings Now** to save GenomeBrowse in its current state.

### How do I manage downloads from Public Data Sources?

- Once files are selected for download the **Download** window will open indicating progress of downloads. If GenomeBrowse is closed while files are being downloaded the Download manager will be minimized to the tray and downloads will continue.
- The **Download** manager can be accessed from the **Tools** menu.

### How do I view a list of features or find features in a sparse annotation track?

- If you hover over the upper-left corner of a plot view, a table icon will appear (). If you click on this icon the **Feature List** will open. By default up to 1000 features from the current zoom will be displayed.
- You can jump to the start of the genome by clicking on the **Start** button, and then back to the current zoom by clicking on the **Zoom** button.
- Features can be sorted by clicking on the field names (column headers). Once for ascending order, twice for descending order.
- Click on a feature to jump (zoom) to that feature in the plot view.
- Selected row(s) can be copied to the clipboard. Click on a row or use Ctrl+click or Ctrl+A to select multiple or all rows. Then right-click and select **Copy Selected Row(s) to Clipboard** or **Copy Selected Row(s) with Headers**. This table can then be pasted into a spreadsheet program or text file.
- A mouse anchor can be set at any of the features in the list by right clicking on a row and selecting **Set Mouse-Anchor At...**
- If there are more than 1000 features you can click on the **Read More...** link in the lower left corner to add more features to the list.

### How do I create a new project, save or open a recent project?

- In the **File** menu there are options to create a new project, open a recent project, open a project by browsing the file system, save or save as a new project. When you create a new project you will be prompted to select the project genome assembly and to download the reference sequence if you do not already have it locally.

### How do I know when there is an update available?

- There will be an **Update Available** message and a download icon () in the lower-right corner of the GenomeBrowse window indicating that there is a newer version available. Click on the message to open the download page in a web browser to obtain the latest version. NOTE: This feature is only available in version 1.06 and later.

**For more help, visit:**

[goldenhelix.com/GenomeBrowse/online\\_help](http://goldenhelix.com/GenomeBrowse/online_help)



## Mouse

Double-click on a title, scale, or node label to edit it in-place

Use the scroll wheel to zoom in or out

- On canvas—affects x-axis only unless auto-zoom is on or a modifier key is used
- On scale—affects the scale axis only unless auto-zoom is on or a modifier key is used

Double-click on the domain view or an x-axis scale:

- Zoom to target chromosome
- If already zoomed to a chromosome, zooms out to full data extents

Double-click on a y-axis scale to zoom to full data extents

Double-click on a plot feature to zoom to the feature extents

### Pointer Navigation Mode

Left-drag to pan canvas or scale

Right-drag to stretch canvas or scale

Click the other mouse button to cancel a drag-to-zoom operation in progress

### Zoom Box Mode

Left-drag to zoom into selected area

Right-drag to zoom out, fitting the previous view in the selected area

Click the other mouse button to cancel a drag-to-zoom operation in progress

*Zoom modifiers remain restricted while y-axis auto-zoom is enabled. When both axes are enabled, dragging in a straight line affects only the axis parallel to the drag line.*

## Keys

Alt+[Key]	Menu access
Ctrl+J	Show download window
Alt+Left	Previous view (back)
Alt+Right	Next view (forward)
F1	GenomeBrowse Manual
F2	Edit title of current node (Plot Tree)
Del	Delete selected nodes (Plot Tree or Plot View)
Ctrl+A	Select all (Plot Tree or Plot View)
Ctrl+C	Copy selected text (Console or Plot Tree or Editor)
Ctrl+Z	Undo (in any text box)
Ctrl+N	Create new project
Ctrl+O	Open project
Ctrl+S	Save project
Ctrl+Shift+S	Save project as...
Ctrl+Shift+T	Show/Hide Plot Tree
Ctrl+Shift+C	Show/Hide Controls
Ctrl+Shift+O	Show/Hide Console
Ctrl+Shift+F	Show/Hide Feature List
Ctrl+Shift+N	Show/Hide Note Editor
A or P	Switch to pointer navigation mode
Z	Switch to zoom box mode
Q	Set y-axis auto zoom mode on selected plots
F or W	Set y-axis fit-data zoom mode on selected plots
H or E	Set y-axis hold zoom mode on selected plots
M or R	Set y-axis manual zoom mode on selected plots
F5	Reload selected plots
Arrow keys +/-	Pan current plot Zoom current plot
Back tick (`) Ctrl+' Alt+'	Jump to mouse anchor Place/move mouse anchor Clear mouse anchor

Zoom with mouse wheel or keyboard (+/-)	
Shift+	Apply to opposite axis (e.g. y instead of x over canvas)
Ctrl+Shift	Apply to both axes (over canvas only)
Right-hold	Apply to both axes (scroll wheel only over canvas)
Double-click domain view or x-axis scale	
Shift+	Zoom to full data extents regardless of current zoom

## General Use

Left-drag to move a plot group by dragging its move handle (left side)

Left-drag to resize a plot by dragging its size handle (bottom edge)

Right-click on a specific target (such as the title) to get a list of relevant options

Left-drag on the funnel in the Domain Plot to pan the selection in the Plot View

Left-drag on the edge of the funnel to resize it  
Left-drag outside of the current funnel to jump to new location

Drag the zoom slider or use adjacent +/- buttons to zoom in/out on the x-axis

To change the y-axis zoom mode, hover over a plot and click the zoom mode button on the right edge (labeled with a letter).

### Search Box/Location Bar

Click once to select all text in the search box

Double-click to select a portion of the search box value

With a cursor in the search box, triple-click to select all text

Type to replace selection with new chromosomes, coordinates, or feature name

- Zoom to a specific range by entering two end points
- Jump to a small surrounding area by entering one position
- Jump to a gene by typing in the gene name

While typing, the search box will search all tracks that are set as "searchable"

To set a track as searchable, right-click on it (Plot Tree or Plot View). Searchable data will show a "searchable" option. If checked, it is already searchable. If not, check it.

The link button to the right of the search box includes quick links to the current zoom for a few online genome browsers

The link button also includes a copy function for the current zoom in a format compatible with most genome browsers

## Modifiers

Click to select plot or Plot Tree node

Ctrl+ Multiple selection  
Shift+ Select range between first selected and target

Ctrl+Mouse Wheel Scroll the plot view instead of zooming

*Zoom modifiers remain restricted in some y-axis zoom modes*

*Note: Use the Cmd key on Macs instead of Ctrl*

Mode Toolbar      Genome Toolbar      Location Toolbar

Menu

Plot Toolbar

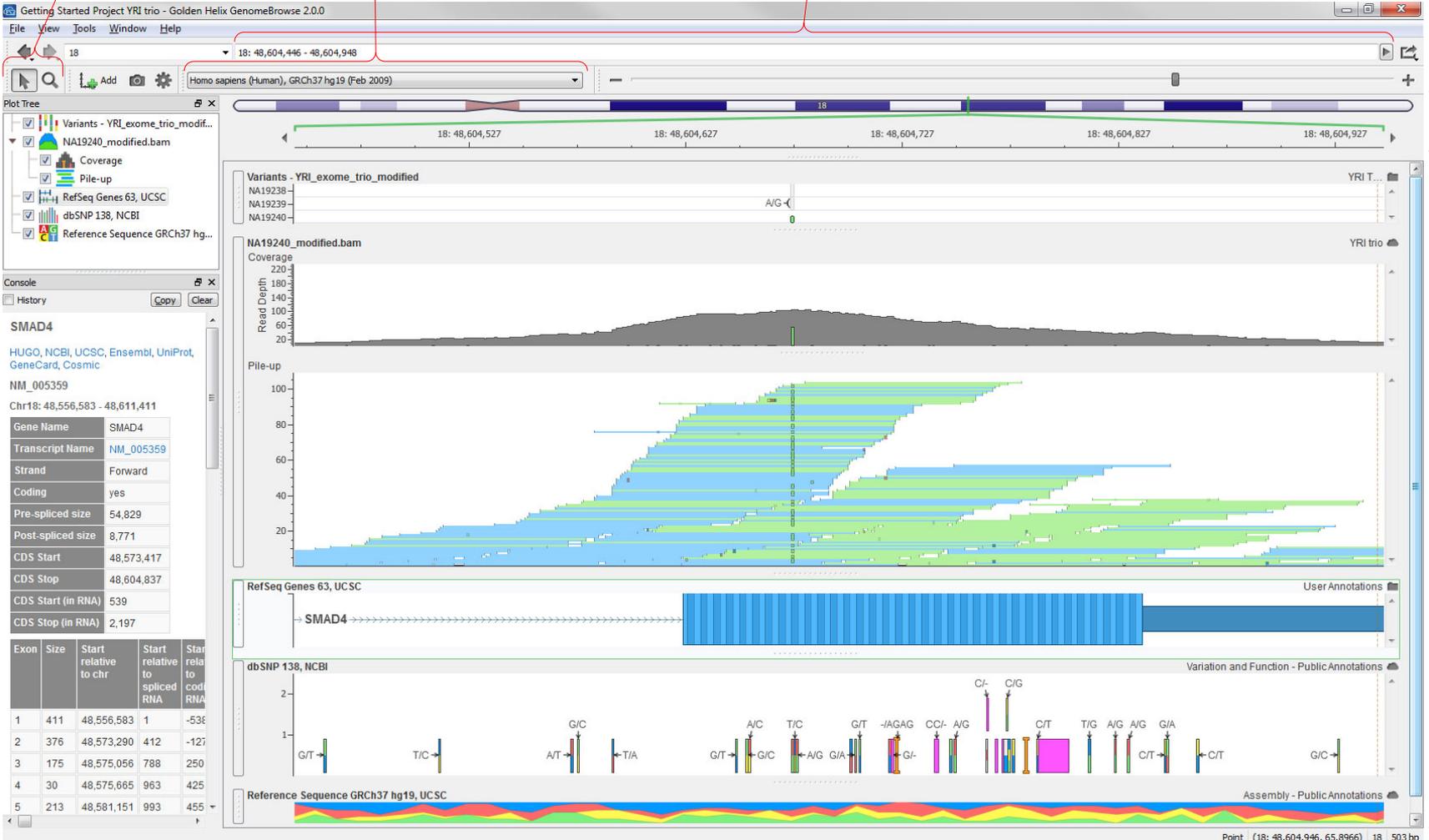
Plot Tree Window

Console Window

Zoom Toolbar

Domain View  
Domain Funnel  
Domain Scale

Plot View



Getting Started Project YRI trio - Golden Helix GenomeBrowse 2.0.0

File View Tools Window Help

18 18: 48,604,446 - 48,604,948

Homo sapiens (Human), GRCh37 hg19 (Feb 2009)

Plot Tree

- Variants - YRI\_exome\_trio\_modif...
- NA19240\_modified.bam
- Coverage
- Pile-up
- RefSeq Genes 63, UCSC
- dbSNP 138, NCBI
- Reference Sequence GRCh37 hg...

Console

History Copy Clear

**SMAD4**

HUGO, NCBI, UCSC, Ensembl, UniProt, GeneCard, Cosmic

NM\_005359

Chr18: 48,556,583 - 48,611,411

Gene Name	SMAD4
Transcript Name	NM_005359
Strand	Forward
Coding	yes
Pre-spliced size	54,829
Post-spliced size	8,771
CDS Start	48,573,417
CDS Stop	48,604,837
CDS Start (in RNA)	539
CDS Stop (in RNA)	2,197

Exon	Size	Start relative to chr	Start relative to spliced RNA	Start relative to cod RNA
1	411	48,556,583	1	-538
2	376	48,573,290	412	-127
3	175	48,575,056	788	250
4	30	48,575,665	963	425
5	213	48,581,151	993	455

Variants - YRI\_exome\_trio\_modified

NA19238  
NA19239  
NA19240

NA19240\_modified.bam

Coverage

Read Depth

Pile-up

RefSeq Genes 63, UCSC

dbSNP 138, NCBI

Reference Sequence GRCh37 hg19, UCSC

Point | (18: 48,604,946, 65.8966) | 18 | 503 bp