# Customizing the View

Controls

Chromosome view can be customized by using the control panel on the left (Figure 1). The *Attribute* and *Order By* controls show options depending on the current project, while the content of the *Annotate amino acids* control depends on the annotation files associated with the current genome build in the *Library File Management*. In order for any change to take place, push the **Apply** button.

Figure 1. Control panel (an example is shown)

Group data by

The first option, *Group data by*, specifies the number of *Alignments* tracks (Figure 2). *All* will result in only one track, with all the samples on it. *Sample* creates one track per sample, while *Attribute* produces one *Alignments* track per level of the *Attribute* (i.e. one track per group).

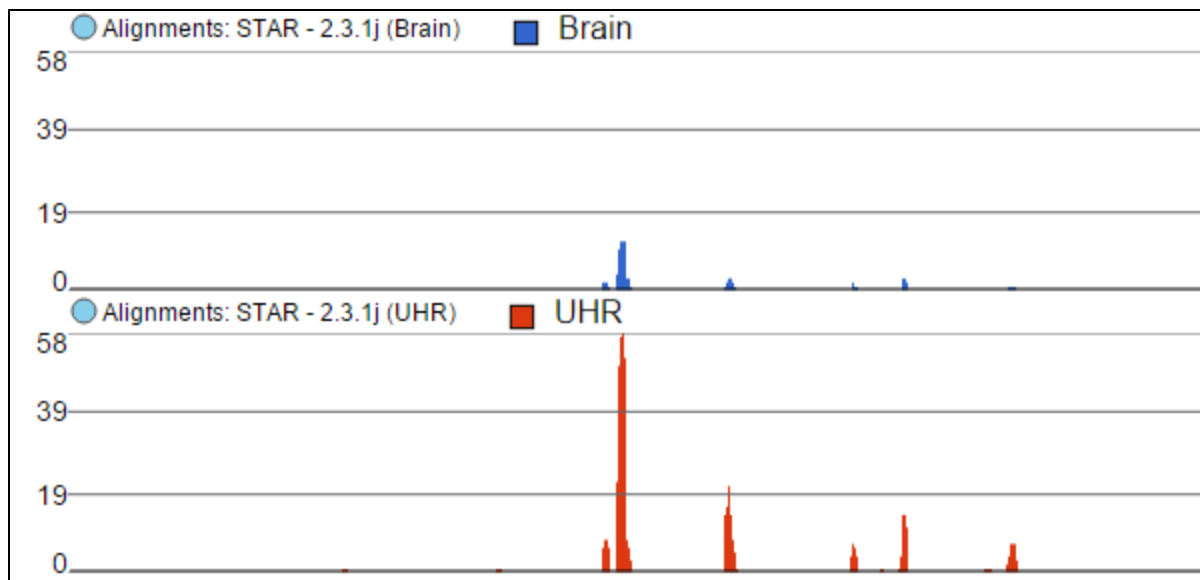**All**
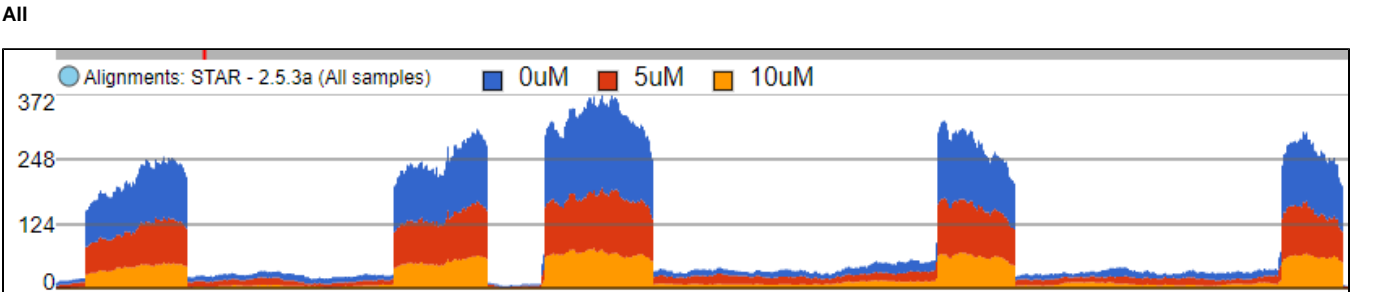
Sample

Attribute

Figure 2. Group data by: All creates one Alignments track for the entire project, Sample creates one Alignments track for each sample, Attribute creates one Alignments track for each group (an example is shown)

Annotate amino acids by

Annotate amino acids by controls the appearance of the *Amino acids* track and allows you to pick the transcript database that will be used to plot codons (Figure 3). The drop down list shows the databases currently available for the selected genome (additional databases can be added via *Library File Management*).
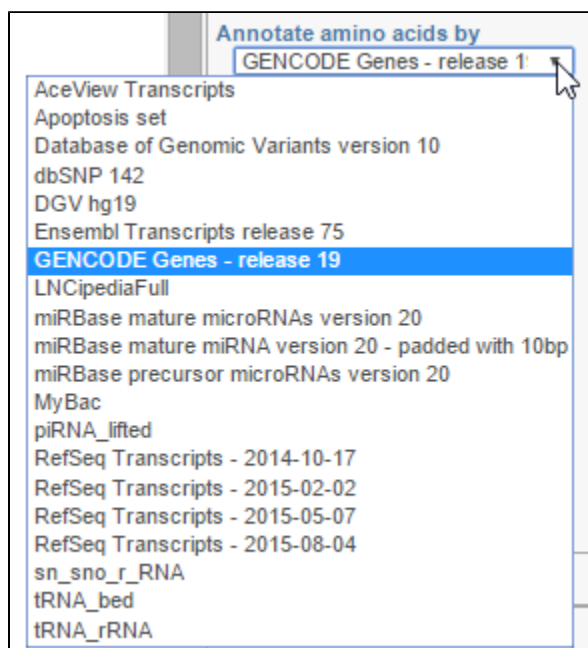

Figure 3. Annotate amino acids by: transcript models currently associated with the chosen genome are displayed in the drop-down list and can be used to plot Amino acids track (an example is shown)

Color by

Color by option affects the colouring of the *Alignments* track and *Isoform proportion* track. When *Sample* is selected from the drop-down list, individual samples will be shown on the aforementioned tracks, each sample being given a different colour. If attributes were assigned to samples, they will also be visible in the *Color by* drop-down (Figure 4) and you will be able to highlight levels of the selected attribute (Figure 5).
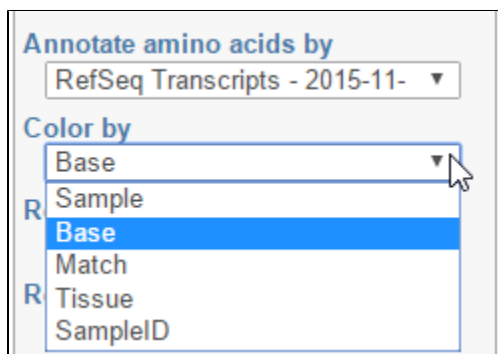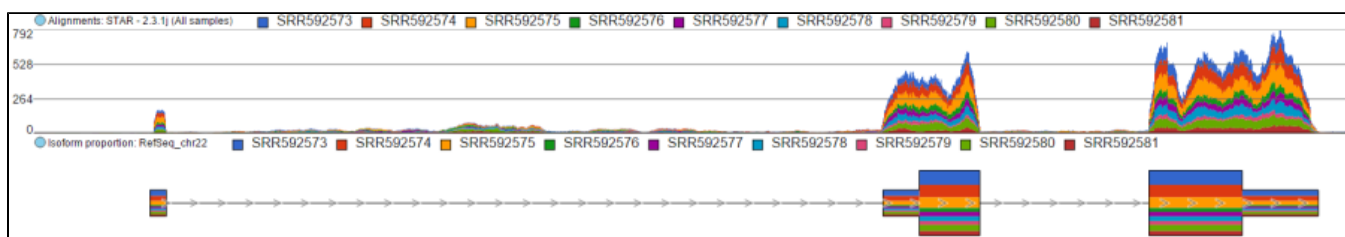
Figure 4. Color by: the options control colouring of Alignments and Isoform proportion tracks. Sample, Base, and Match options are present by default. If attributes have been assigned to samples, they will appear in the drop-down list. In this example, that is the "Tissue" attribute

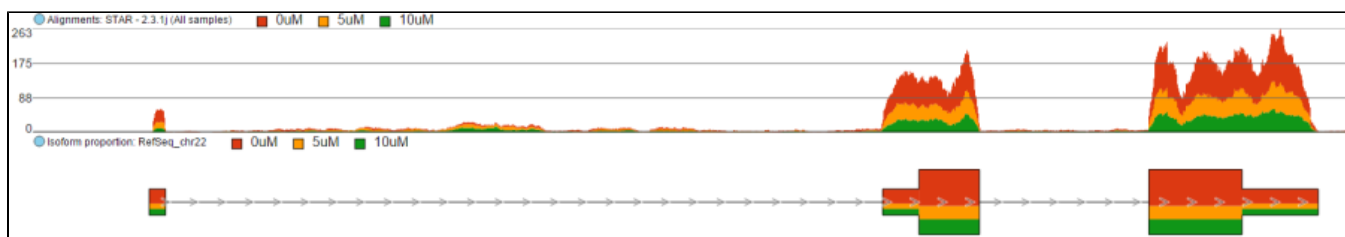**Color by Sample**

Color by <Attribute>

Figure 5. Difference between Color by Sample and Color by . Color by Sample uses different colours to depict individual samples; Color by uses different colours to depict levels of the selected sample attribute (as present in the Data tab). Alignments and Isoform proportion tracks are shown (an example)

The effect of the option to *Color by Base* can be seen with high power magnification (Figure 6). Individual base calls are highlighted by different colours. When that option is chosen at low power magnification, all the bases are shown in grey.


Figure 6. Color by Base highlights the base calls by colours. Different colours are visible with high power magnification; otherwise all the bases are shown in gray (an example)

Finally, *Color by Match* can be used to quickly identify mismatches against the reference genome. A matching base is coloured in blue, while mismatch bases are shown in yellow.

Read histogram Y-axis max

The maximum of the y-axis of *Alignments* tracks is set by *Read histogram Y axis scales* option (Figure 7). When using *Project max*, the y-axis for each track is set individually, based on the maximum within that sample. On the other hand, *Track max* uses the maximum across all the samples and uses that value as the maximum for all.
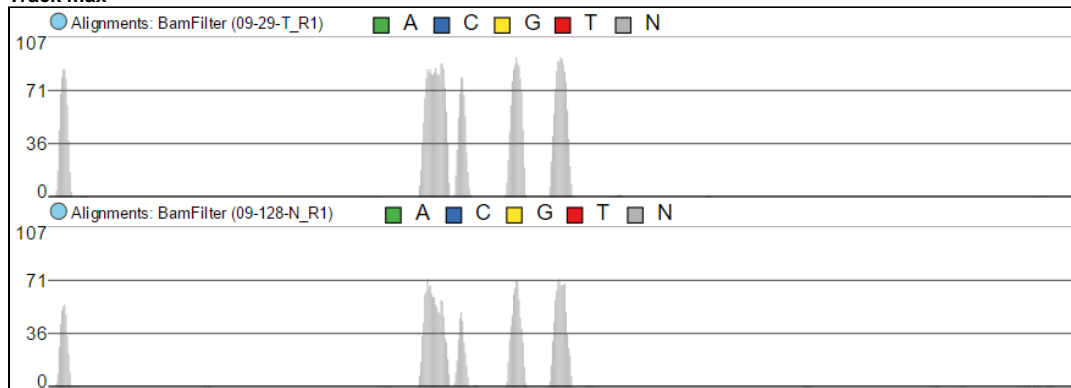
Project max
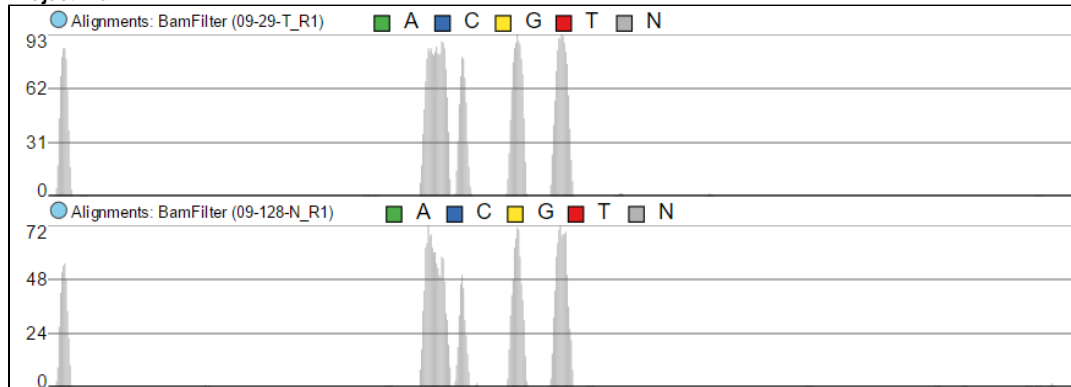
Track max

Figure 7. Read histogram Y axis scales. When set to Linked, all the tracks have the same Y axis maximum, which depends on the sample with the highest coverage. Using Independent sets Y axis maximum independently for each sample.

Read histogram type

Read histogram type changes the presentation of the *Alignments* track and should be used in conjunction with the *Group data by* and *Color by* tracks to get the desired visualisation.

When set to *Sum*, the *Read histogram type* shows the sum of base calls at each position, i.e. total coverage per position. Figure 8 shows an *Alignments* track with three samples. With the *Sum* option, the number of reads at each base in each sample is added and displayed. The contribution of individual samples is not visible since the track is *Colored by Group* (but that would make sense in this example).
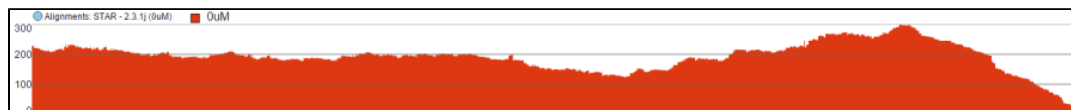

Figure 8. Alignments track: total coverage per locus is shown by using "Read histogram type" set to "Sum" and "Group data by" set to

To show the average coverage per locus, switch *Read histogram type* to *Average* and leave *Color by* as is (i.e. by group) (Figure 9). With this setting, *Chromosome view* will calculate the average by dividing the total coverage per locus by the number of samples. Note that using *Color by Sample* would not make sense here. Although Figure 8 looks quite like Figure 7, the y-axis range is different.
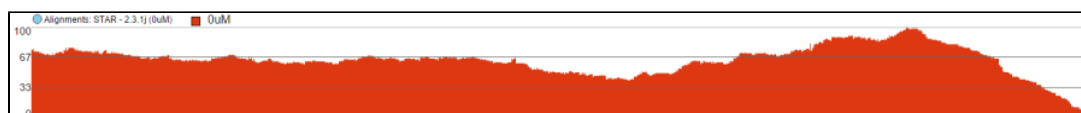

Figure 9. Alignments track: average coverage per locus is shown by using "Read histogram type" set to "Average", "Group data by" set to "Attribute", and "Color by" set to

Finally, the option *Overlay* is useful if you want to directly compare base counts over several samples (or groups) as each will be represented by a line (i.e. no stacking). The example in Figure 10 is based on microarray data, showing three groups on the same *Alignments* track. The red group has the highest base counts, while the counts in the blue group are much lower.
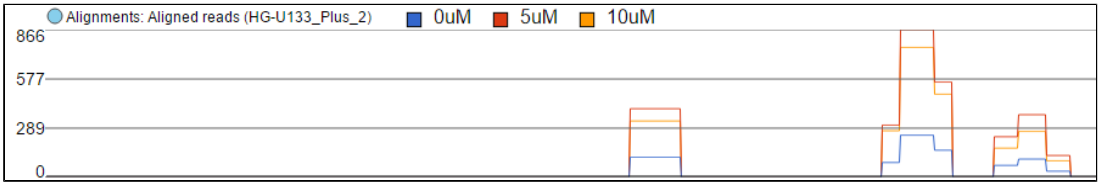

Figure 10. Alignments track: coverage per locus is shown by using "Read histogram type" set to "Overlay". Each plot is a single experimental condition ("Group data by" set to "Attribute", "Color by" set to). Lines are rectangular since microarray data is used (an example)

Split read histogram by strand

To view the reads histogram grouped by the specific strand that they've mapped to, click the *Split read histogram by strand* checkbox. This displays the forward reads at the top half of the track and the reverse reads on the bottom half of the track (Figure 11). This track can be helpful in studies such as ChIP-Seq, where strand-specific read distributions can display hallmarks of DNA-protein interactions.
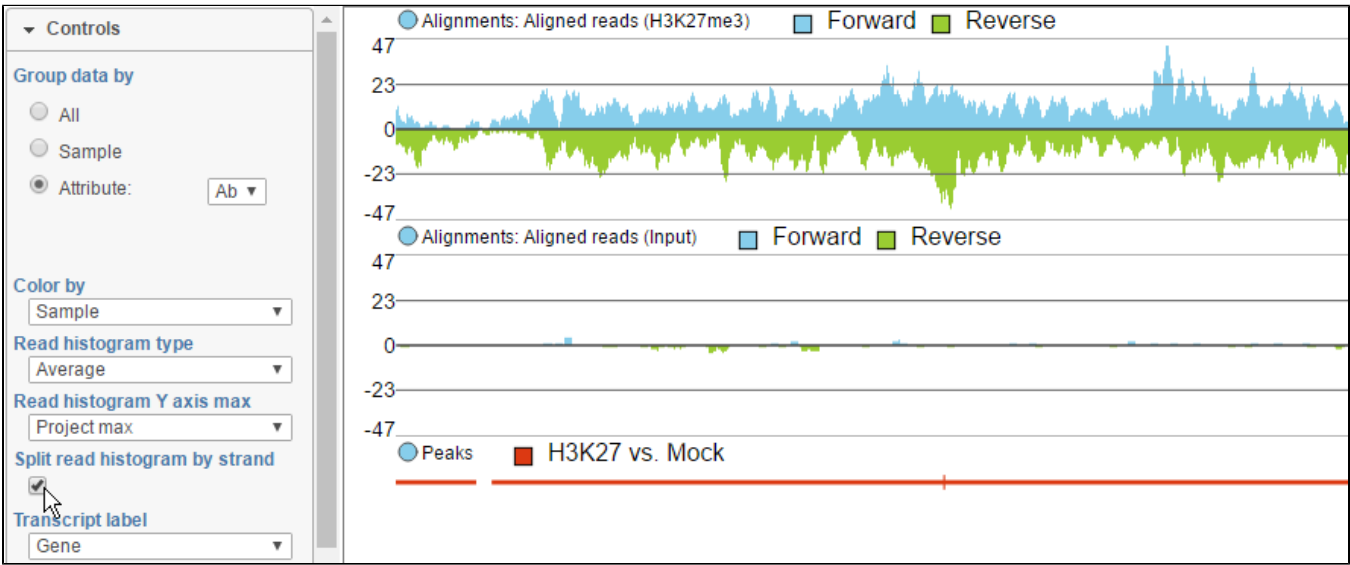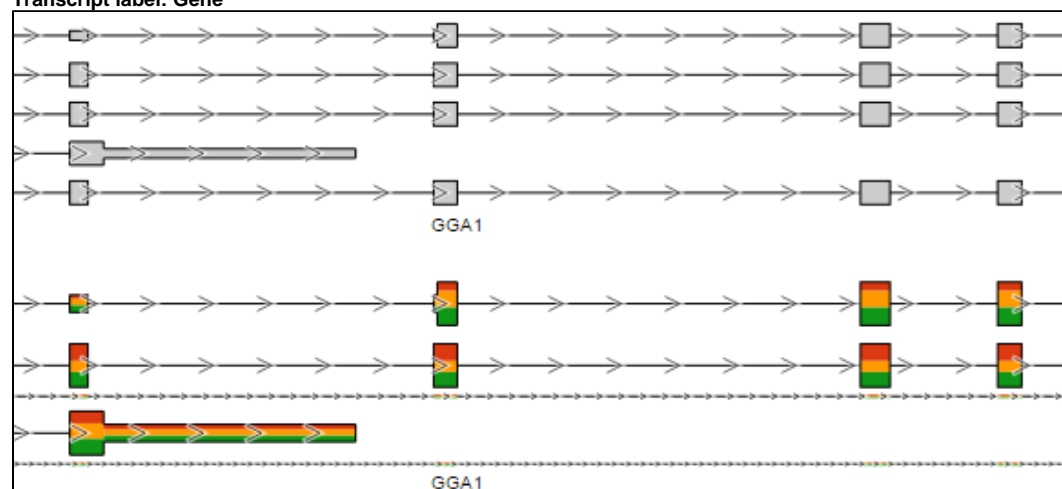

Figure 11. Viewing reads by strand along the reads histogram

Transcript label

You can use the *Transcript label* selector to specify labels on the reference transcript track and *Isoform proportion* track (Figure 12).

Transcript label: Gene

Transcript label: Transcript

Figure 12. ranscript label: setting the control to Gene shows only gene label, while Transcript shows transcript labels. Both transcript database and Isoform proportion tracks are affected Short sequencing reads can be coloured by strand (Reads pileup color: Strand) or by base (Reads pileup color: Base).

Reads pileup and probe color

Reads pileup color: Strand
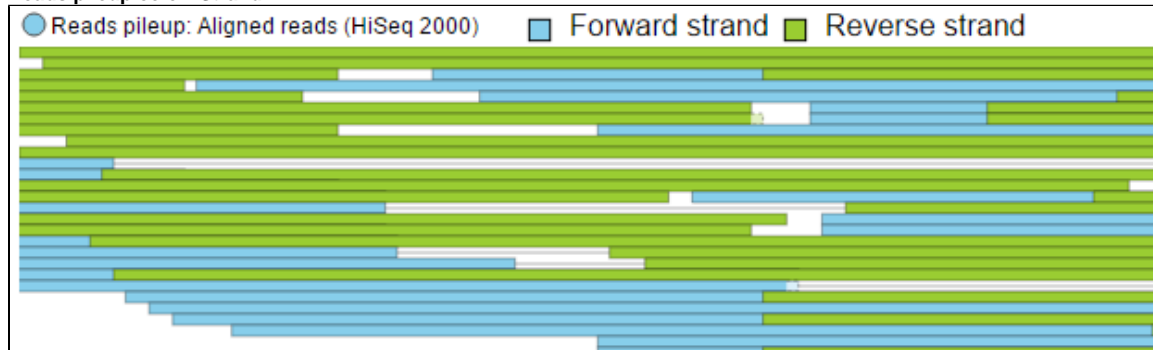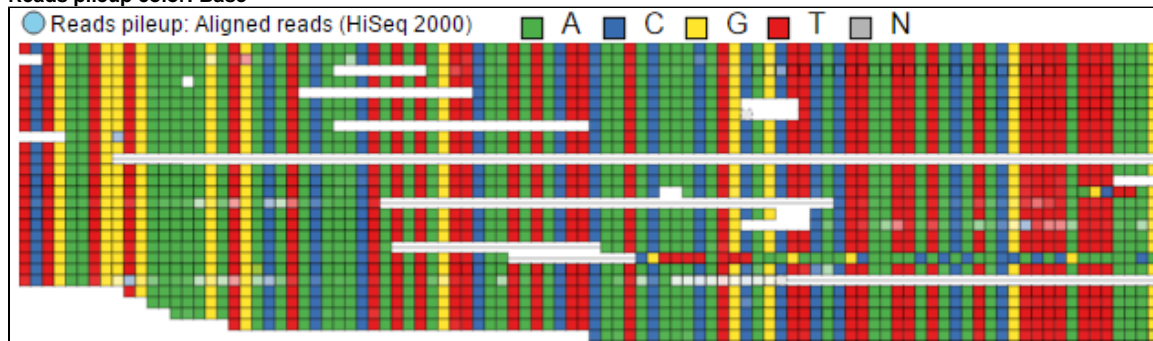

Reads pileup color: Base

Figure 13. Reads pileup color: colouring of the short sequencing reads by Strand or by Base

Probe color control customizes the appearance of Probe intensities track (Figure 14). When set to *Intensity*, the color of a probe reflects its intensity, using a color gradient from white (low) to admiral (high). Alternatively, when *Strand* is turned on, probes on the reverse strand are in parakeet green, while probe on the forward strand is in sky blue.

Probe color: Intensity

Probe color: Strand

Figure 14. Probe color: "intensities" colors probes proportionally to their intensity, "strand" uses colors to indicate probe positioning (an example is shown)

If a variant database is available for the current genome, the variants can be added to the *Reference genome* track. To show the variants, point the *Variant database* control to the database of your choice.

To change any of the colors on the canvas, use the *Customize track colors* tool. A resulting dialog will help you to pick another color (**drop-down** button opens the color-picker) (Figure 15).
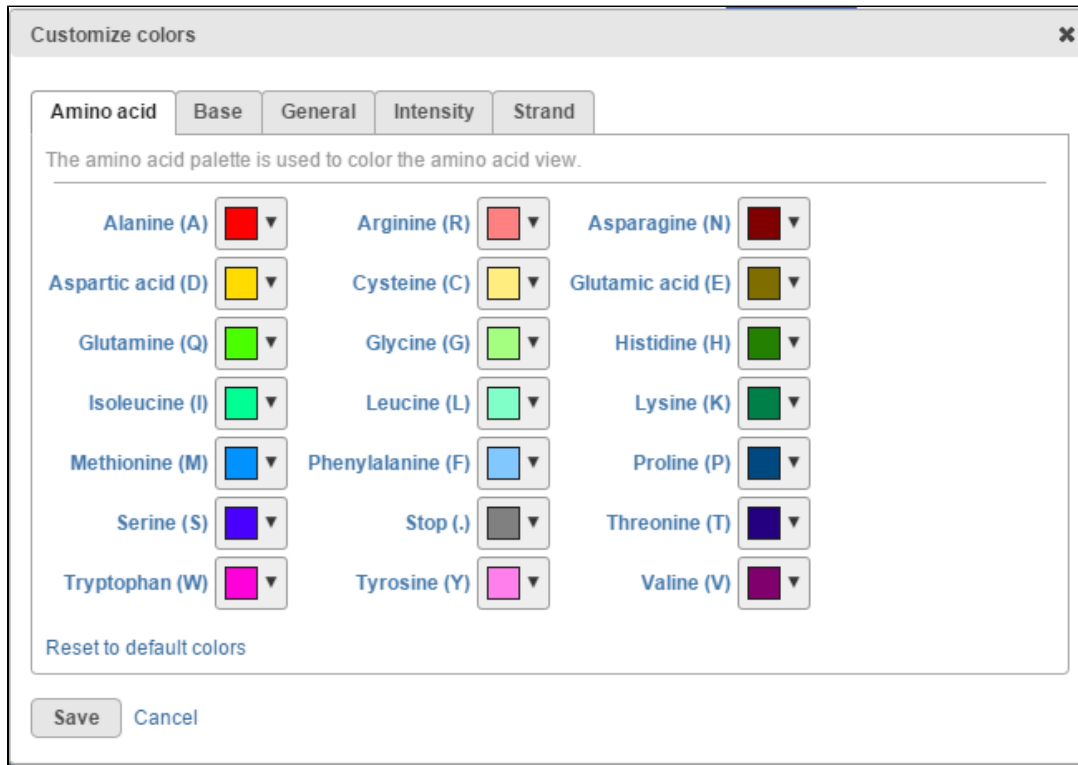
Figure 15. Customize colors dialog: selecting a drop-down arrow opens the color-picker tool

Track Order

The position of the tracks on canvas can be controlled by using the *Track order* tool. If you want a track to be visible all the time, i.e. while scrolling up or down, pin it to the top or to the bottom. Below shows the *Cytoband* track pinnned to the top of the canvas and *Reference genome* track pinned to the

bottom of the canvas. To unpin a track, click on the **pin icon** ( ). The track will be unpinned and a message *No tracks are pinnned to the top / bottom*

will appear. To pin a track, **drag** the track name to the *No tracks…* message. Alternatively, you can use the green arrows ( ) to pin a track. When you mouse over an arrow, the new position of the track will be highlighted on the canvas; click on the **arrow** to accept.

A track can be hidden (meaning it will not be visible) by selecting the **red minus**, or unhidden by selecting the **green plus** icon.

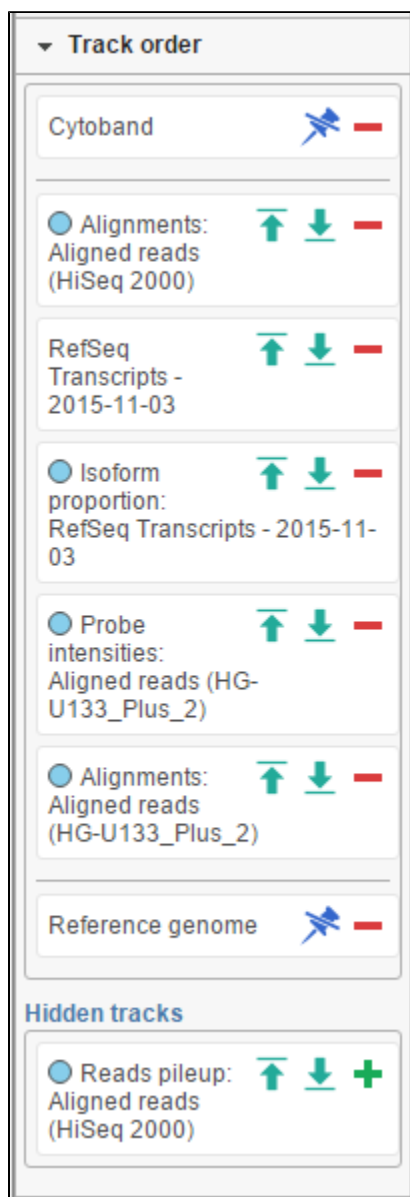The tracks can be reordered by **drag and drop**.

Figure 16. Track order tool: To change the position of a track drag and drop to the new position. To pin a track to the top / bottom of the canvas, use the up and down arrows. To unpin a track, select the pin icon. A track can be hidden by clicking on the red minus symbol and unhidden by selecting the green plus. Coloured dot by a track names indicates the layers to which the track belongs (an example is shown)

Selection Details

At the bottom of the control panel you will find the *Selection details* section (Figure 17). It is used to display information on the element selected on the canvas (using the *Pointer mode*).

Figure 17. Selection details showing information on the element selected on the canvas. The example shows details of a microarray probe. Note the two link-outs ("Browse on UCSC" and "BLAST this sequence")

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

Your Rating: ☆☆☆☆☆   Results: ★★★★★ 35 rates