
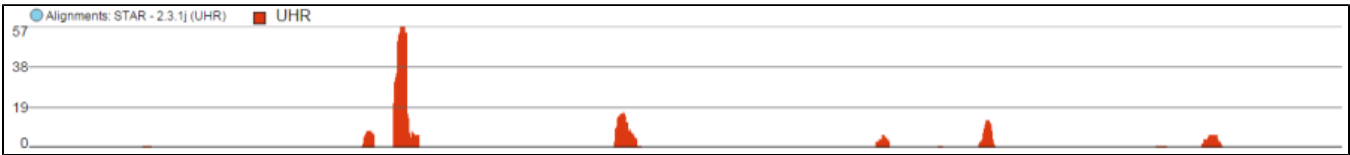


Visualizing the Results Using Data Tracks

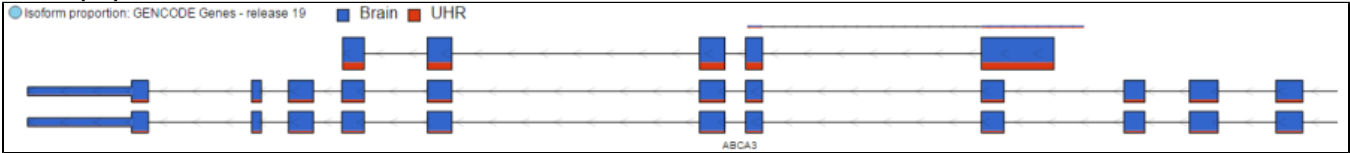
Data tracks section of the *Select tracks* dialog enables you to specify the tracks for visualization on the canvas. An overview of the available track types is provided in Figure 1. Note that not all tracks are visible at all times and that their presence depends whether specific data types are present in the project as well as the zoom level. The tracks can be customized and their appearance changed by using the control panel on the left. Different track also has it own specific configuration settings which allow you to pin the track to move the track, pin the track, change the styles of the track and hide the track using

the settings options on the left of each track ()

Alignments track



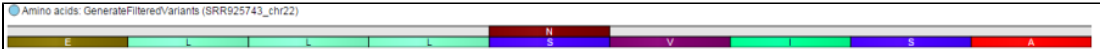
Isoform proportion track



Variants track



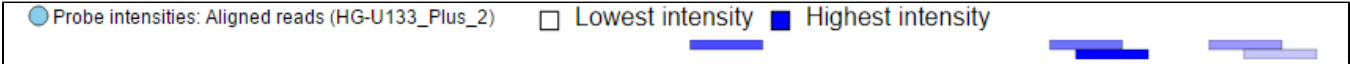
Amino acids track



Reads pileup track



Probe intensities track



Peaks track



Figure 1. Data tracks in Chromosome view (examples)

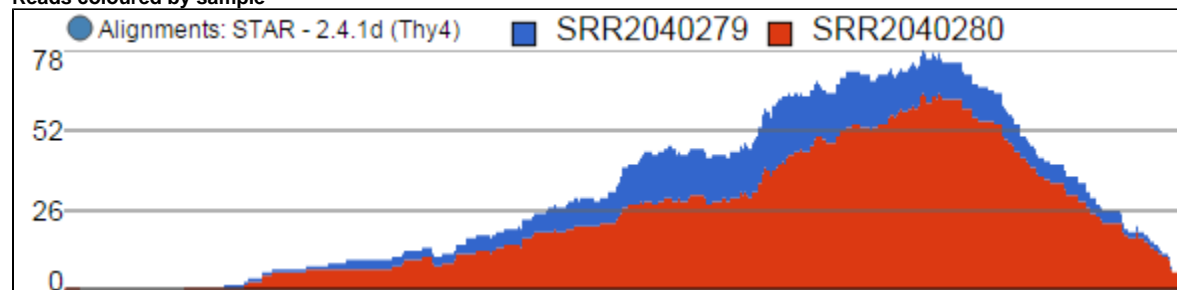
Alignments Track

Alignments track displays a histogram view of alignments present in .bam files in a stacked histogram fashion (similar to Partek® Genomics Suite®). The y-axis shows number of (raw) base calls per position. By default, reads are coloured by sample. Variations on the track are displayed below. They can be configured in the following ways:

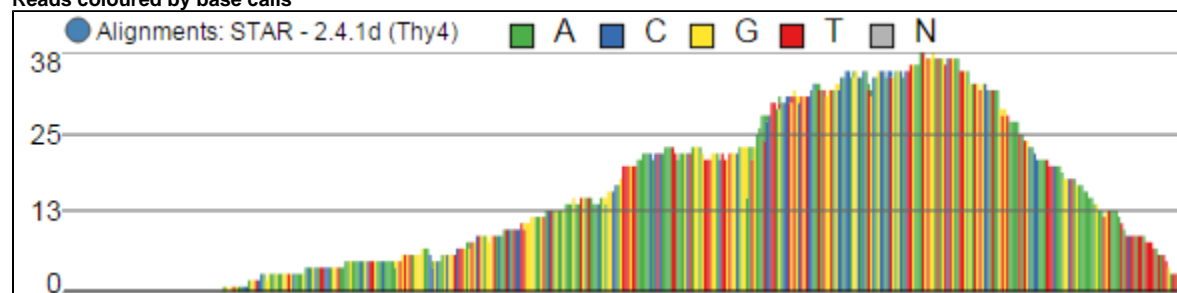
- The histogram can be colored by sample, attribute groups or by base call. By default, it is colored by sample except when the chromosome viewer is invoked from a variant data table.
- When colouring reads by sample, the reads are stacked (on top of each other), i.e. in the example below there are more reads in the red sample than in the blue sample. This is an example of a *Sum* histogram type. This can also be configured to display overlays or averages.
- Reads can be split into two tracks corresponding to the strand that they map to. This can be invoked by clicking the *Split read histogram by strand* checkbox.
- Y-axis can be scaled for all samples to have the same max or each sample has its own specific max

For more information on configuring tracks see our page on [Customizing the chromosome viewer](#)

Reads coloured by sample



Reads coloured by base calls



Reads split by strand

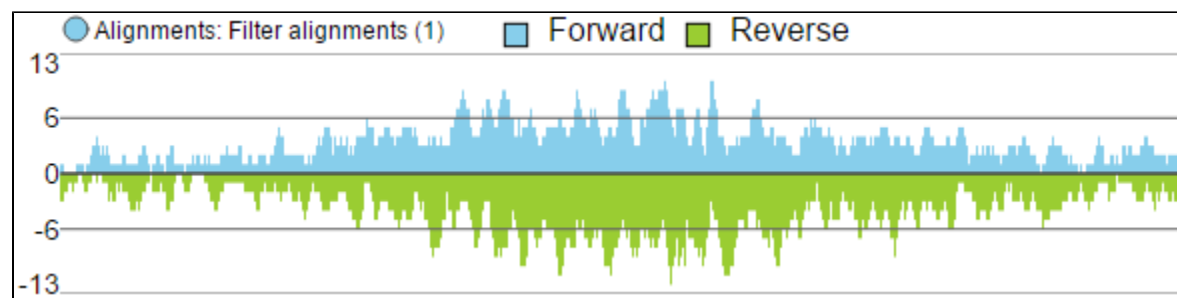


Figure 2. Various configurations of the Alignments track

Isoform Proportion Track

The *Isoform proportion* track displays the reads mapped to transcripts and helps to visualize differential expression and alternative splicing, this track is only available on the feature list data node which is generated from differential expression analysis. It uses standard symbols for exons (boxes) and introns (lines connecting the boxes). The height and color of each transcript is proportional to its LS mean value. Figure 3 shows a gene with two transcripts in RefSeq database; the top transcript is more abundant than the bottom transcript and is preferentially expressed in the "blue" condition (labeled as 0 uM). The bottom transcript, on the other hand, seems to be expressed at the same level across all three conditions (i.e. 0 uM, 5 uM, 10 uM). The number and structure of transcripts on the plot depend on the transcript model that was used for mapping.

For more information on configuring tracks see our page on [Customizing the chromosome viewer](#)

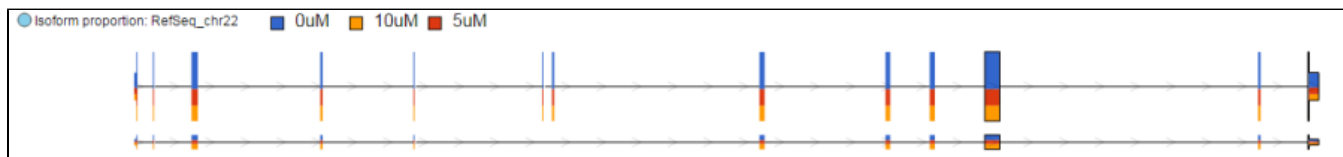


Figure 3. Isoform proportion track: the transcripts are shown as present in the transcript model that was used for mapping. Exons are depicted as boxes. The size of each transcript is proportional to the number of reads mapping to it. Colors indicate samples to which the reads belong

Variants Track

Variant tracks show single nucleotide variants (SNVs) and indels, and appear in the *Select track* dialog if *Detect variants* task has been performed. Presentation of variants depends on the level of zoom. With low power magnification, SNVs are seen as purple columns and indels are bars (insertions: green bars; deletions: red bars) (Figure 4).



Figure 4. Variants track at low power magnification: SNVs are symbolized by purple columns and an insertion is presented as a green bar (an example is shown). A deletion is presented as a red bar (none is visible on the figure)

Upon zoom-in, SNVs are drawn as pie charts, representing the proportion of each base call at that locus (Figure 5)

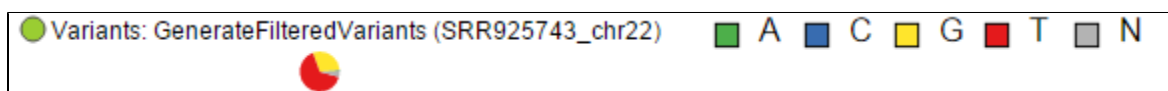


Figure 5. Variants track at high power magnification: each SNV is presented as a pie chart and each slice symbolises the relative frequency of each base call (an example is shown). Base call colour codes are given by the track name

At higher modification, insertions are seen as green boxes, with individual inserted bases presented using a pie chart, while deletions look like red boxes and the affected bases are also presented by a pie (Figure 6).

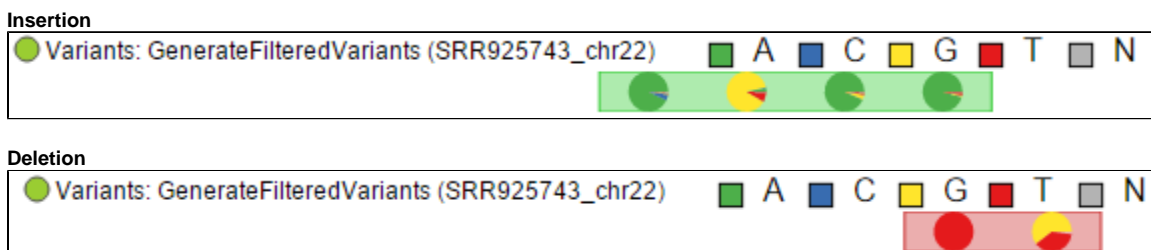


Figure 6. Variants track at high power magnification: insertion is presented as a green box, deletion is presented as a red box. An example is shown.

Amino Acids Track

Amino acids track becomes available in the *Select tracks* dialog after completing the *Annotate variants* task. The actual appearance of the track depends on the zoom level. With low-power magnification, you will see a message *View not available at this zoom level, Please zoom in to view amino acids*.

When you zoom closer to the genome, all the amino acids become visible as colored boxes (Figure 7) and labeled using the single-letter amino acid code. Alternative amino acids are depicted as additional box on the top of the consensus sequence.



Figure 7. Amino acids track at high power magnification: consensus amino acid sequence is at the bottom of the track, while a variant is shown on the top (change from Threonine to Proline is shown)

If an amino acid spans two exons, its box will be truncated and the line connecting the exons will be dashed. An example is in Figure 8.

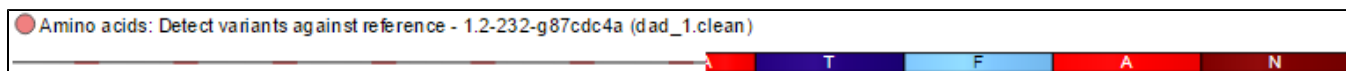


Figure 8. Amino acids track: exon-spanning amino acids indicated by truncated boxes (i.e. Alanine on the left) (an example is shown)

An empty gray box on the top of consensus sequence is used to indicate a STOP codon, which is a consequence of a mutation (Figure 9).



Figure 9. Amino acids track: A variant which is in fact a STOP codon is represented by an empty box, as seen on the top of the G (an example is shown)

Untranslated bases, such as ones downstream of a STOP codon are depicted by lighter shades. Figure 10 shows two transcripts in an amino acid track; the direction is from left to right, so amino acids downstream of a STOP codon (P > G > L) are lightly shaded.



Figure 10. Amino acids track: amino acids downstream of a STOP codon are depicted by lighter shades. STOP codon is represented by "." in the middle, direction is from right to left (an example is shown)

Reads Pileup Track

Reads pileup track plots the short sequencing reads, as present in the .bam file. The track is not on by default (go to **Select tracks** to turn it on) and its appearance depends on the magnification; if you are zoomed out a message - *Zoom in to view individual reads* - will be displayed.

Forward strand reads are in sky blue, while reverse strand reads are in parakeet green. If paired-end chemistry was used, the paired reads will be depicted as half reads within a gray rectangle encompassing the pair (Figure 11). Singletons will be depicted as thicker reads.

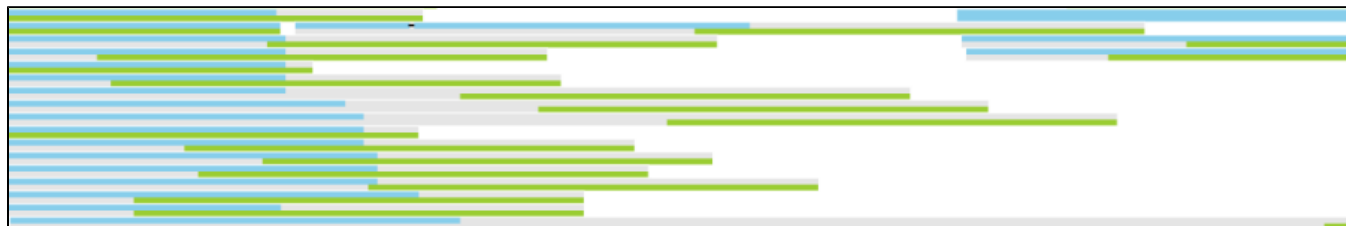


Figure 11. Reads pileup track: short sequencing reads are represented as bars. Paired-end reads are located within a gray box encompassing both pairs. Singletons, such as that on the top right, are depicted as thicker reads (an example is shown)

If you used a junction-aware aligner (such as TopHat or STAR), the junction reads will be depicted using dashed lines, which connect exon-spanning parts of the same read (Figure 12).

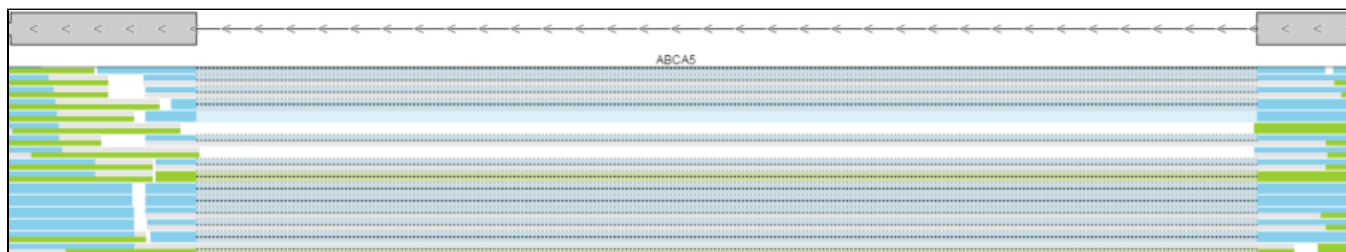


Figure 12. Reads pileup track: junction reads are depicted using dashed lines. A RefSeq track is added at the top, to visualise the exons (an example is shown)

Deleted bases can also be seen on a Reads pileup track, as fat black lines (Figure 13).



Figure 13. Reads pileup track: deleted bases depicted using fat black lines (an example is shown)

Probe Intensities Track

Microarray probes are visualised by the *Probe intensities* track. The probes are shown as bars and their colour depends on the probe intensity, ranging from white (low) to admiral blue (high) (Figure 14).

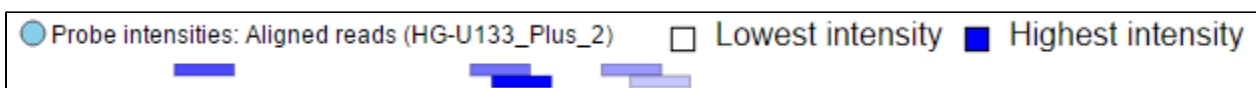


Figure 14. Probe intensities track: probes are depicted as bars and their colour reflects the intensity (an example is shown)

As with the *Reads pileup* track, probes may not be visible with low power magnification and you will see a message - *Zoom in to view individual microarray probes*.

Peaks Track

The Peaks track displays the results of [peak caller](#) tasks. It displays a bar that spans genomic location of each peak call. If *summits* are identified by the peak caller, such as the MACS2 algorithm, then its genomic location is marked by a vertical line. The color marks either the pair being compared by the peak caller or, if present, the sample attribute associated with the sample.

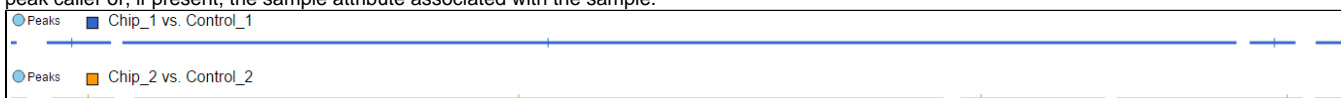


Figure 15. Peaks track shown for two different pairs

Additional Assistance

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

[« Selecting Data Tracks for Visualization](#) [Annotating the Results](#) »



Your Rating:      Results:      34 rates