

# Visualizing differential isoform expression

*Chromosome View* in the Partek Genomics Suite software enables visualization of differential expression and alternative splicing results in RNA-Seq data.

- Select **New Track**
- Select **Add a track from spreadsheet** and select **1/transcripts (RNA-Seq\_results.transcripts)** from the drop-down menu
- Select **Next >** (Figure 1)

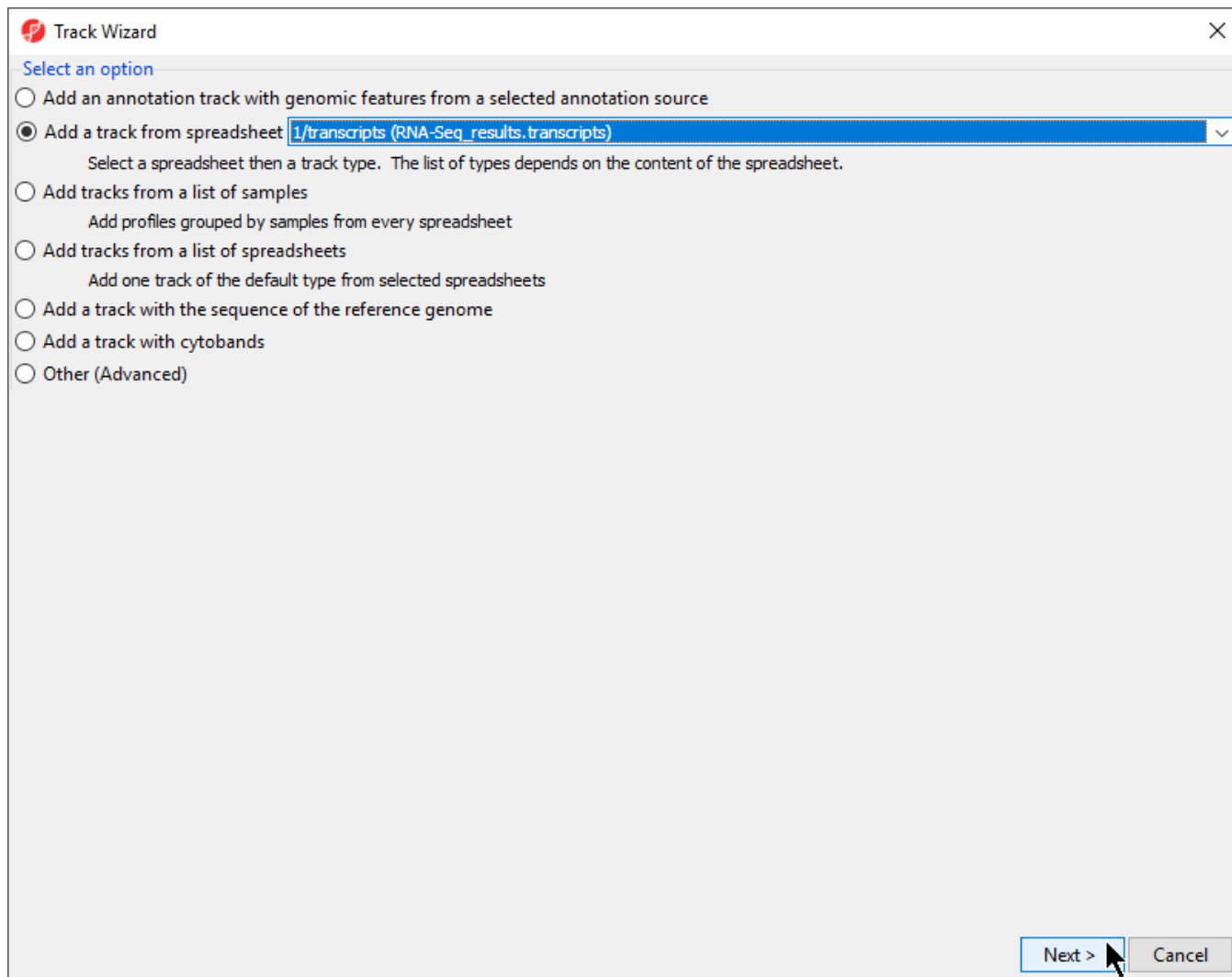


Figure 4. Adding a new track to *Chromosome View*

The new track will be added to *Chromosome View* (Figure 2).

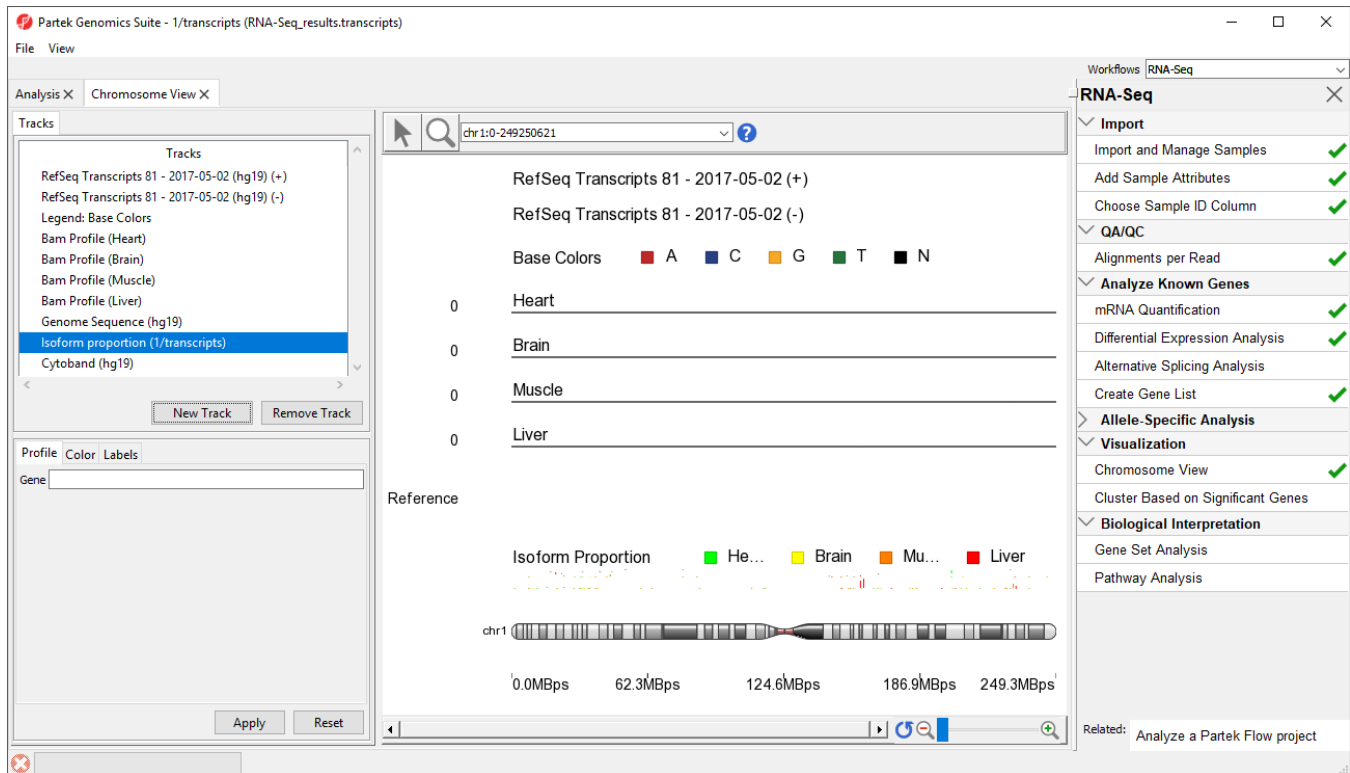


Figure 5. Viewing isoform proportion track in Chromosome View

At this point, you may find it useful to alter track properties. Each track can be individually configured. For example, isoform information will be easier to visualize if we remove a few tracks.

- Select *Cytoband (hg19)* in the *Tracks* panel
- Select **Remove Track** to remove it from the viewer
- Repeat for *Genomic Label*, *RefSeq Transcripts - 2017-05-02 (hg19) (-)*, *Legend: Base Colors*, and *Genome Sequence*

Next, we are going to view a single gene, SLC25A3, with differentially expressed isoforms.

- Type **SLC25A3** in the *Plot Position* bar at the top of the window and hit **Enter**. The browser will browse to the gene

To further improve our visualization of SLC25A3 isoforms, we can modify the remaining tracks.

- Select *RefSeq Transcripts - 2014-01-03 (hg19) (+)* from the *Tracks* panel
- Change *Track height* to 60 using the slider
- Select **Apply** to change track height
- Repeat steps to set each *Bam Profile* track to a height of 40 to complete our changes
- Move the *Isoform proportion* track to below the *RefSeq Transcripts* track by selecting and dragging it up the list (Figure 3)

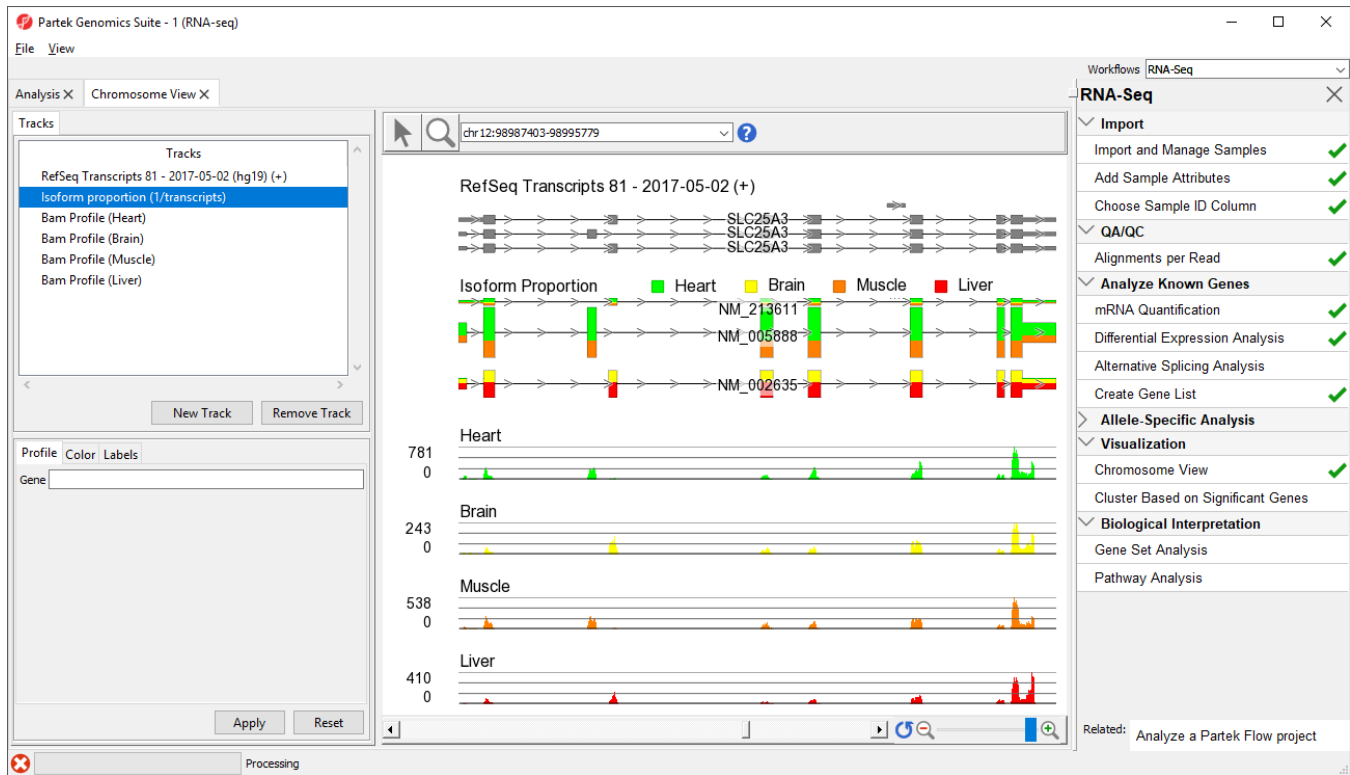


Figure 6. Changing tracks in Chromosome View to facilitate visual analysis of isoform proportions

The *Muscle*, *Brain*, *Heart*, *Liver*, and genomic label tracks were described in a previous section. Here, the focus is on the *Isoform proportion* track, which visualizes differential expression and alternative splicing. The reads that are mapped to a certain sample and the proportion of the transcript expressed in that sample are colored to match the *Bam Profile* track of that sample. In this screenshot, *Brain* is yellow, *Heart* is green, *Liver* is red, and *Muscle* is orange.

SLC25A3 was reported by Wang, et al., (Nature, 2008) to have “mutually exclusive exons (MXEs)”. The reads mapped to the 3 transcripts of this gene in each of the tissue samples are shown in the *Genome Viewer* in the isoform proportion track. The relative abundances of the individual transcripts of this gene are shown by the height of the color coded bars on each transcript in the *isoform proportion* track. Note transcript NM\_213611 has low expression while transcripts NM\_005888 and NM\_002635 have higher expression. Also note that NM\_005888 is expressed primarily in the heart and muscle, indicated by the primarily green and orange bars, while NM\_002635 is expressed primarily in the brain and liver, indicated by the primarily yellow and red bars.

For additional tips on using the *Chromosome View*, refer to [Visualizing mapped reads with Chromosome View](#).

## References

Wang, E.T., Sandberg, R., Luo, S., Khrebtkova, I., Zhang, L., Mayr, C., Kingsmore, S.F., Schroth, G.P., & Burge, C.B. Alternative isoform regulation in human tissue transcriptomes. *Nature*, 2008; 456: 470-6.

« [Visualizing mapped reads with Chromosome View](#) [Gene Ontology \(GO\) Enrichment](#) »

## Additional Assistance

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



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