## 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)

Prack Wizard		×
Select an option		
O Add an annotation track with genomic features from a selected annotation source		
Add a track from spreadsheet 1/transcripts (RNA-Seq_results.transcripts)		~
Select a spreadsheet then a track type. The list of types depends on the content of the spreadsheet.		
○ Add tracks from a list of samples		
Add profiles grouped by samples from every spreadsheet		
O Add tracks from a list of spreadsheets		
Add one track of the default type from selected spreadsheets		
O Add a track with the sequence of the reference genome		
○ Add a track with cytobands		
O Other (Advanced)		
	Next >	Cancel
Figure 4. Adding a new track to Chromosome View		

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

🤣 Partek Genomics Suite - 1/transcripts (RNA-Seq_results.trans	ripts)	- 🗆 X
File View		
		Workflows RNA-Seq
Analysis X Chromosome View X	1	-RNA-Seq X
Tracks	hr 1:0-249250621	└─ Import
Tracks		Import and Manage Samples 🗸
RefSeq Transcripts 81 - 2017-05-02 (hg19) (+)	RefSeq Transcripts 81 - 2017-05-02 (+)	Add Sample Attributes 🗸
RefSeq Transcripts 81 - 2017-05-02 (hg19) (-)	RofSeg Transcripts 81 - 2017-05-02 (_)	Choose Sample ID Column 🗸
Legend: Base Colors		✓ QA/QC
Bam Profile (Brain)	Base Colors 📕 A 🔳 C 📕 G 🔳 T 🔳 N	Alignments per Read
Bam Profile (Muscle)		✓ Analyze Known Genes
Bam Profile (Liver)	0 Heart	mRNA Quantification
Genome Sequence (hg19)	Dunin	Differential Expression Analysis
Cytoband (hg19)		Alternative Splicing Analysis
<	o Muscle	Create Gene List
New Track Remove Track	0	
	0 Liver	Visualization
Profile Color Labels		Chromosome View
Gene	Deferrer	Olustes Based on Circliferent Corner
	Reference	
		<ul> <li>Biological Interpretation</li> </ul>
	Isoform Proportion 🗧 He 📃 Brain 📕 Mu 📕 Liver	Gene Set Analysis
		Pathway Analysis
	0.0MBps 62.3MBps 124.6MBps 186.9MBps 249.3MBps	
Apply Reset		Related
		Analyze a Partek Flow project

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 form 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 porportions

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., Khrebtukova, 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.



Your Rating: ☆☆☆☆☆ Results: ★★★★ 34 rates