

Visualizing reads and enriched regions

We can visualize the reads and enriched regions using the Partek *Genome Viewer*:

- Select **ChIP-Seq** from the spreadsheet tree
- Select **Chromosome View** from the *Visualization* section of the *ChIP-Seq* workflow

The *Chromosome View* tab will open. The default tracks are the transcript tracks, the sequence visualization tracks, and the cytoband track (Figure 1).

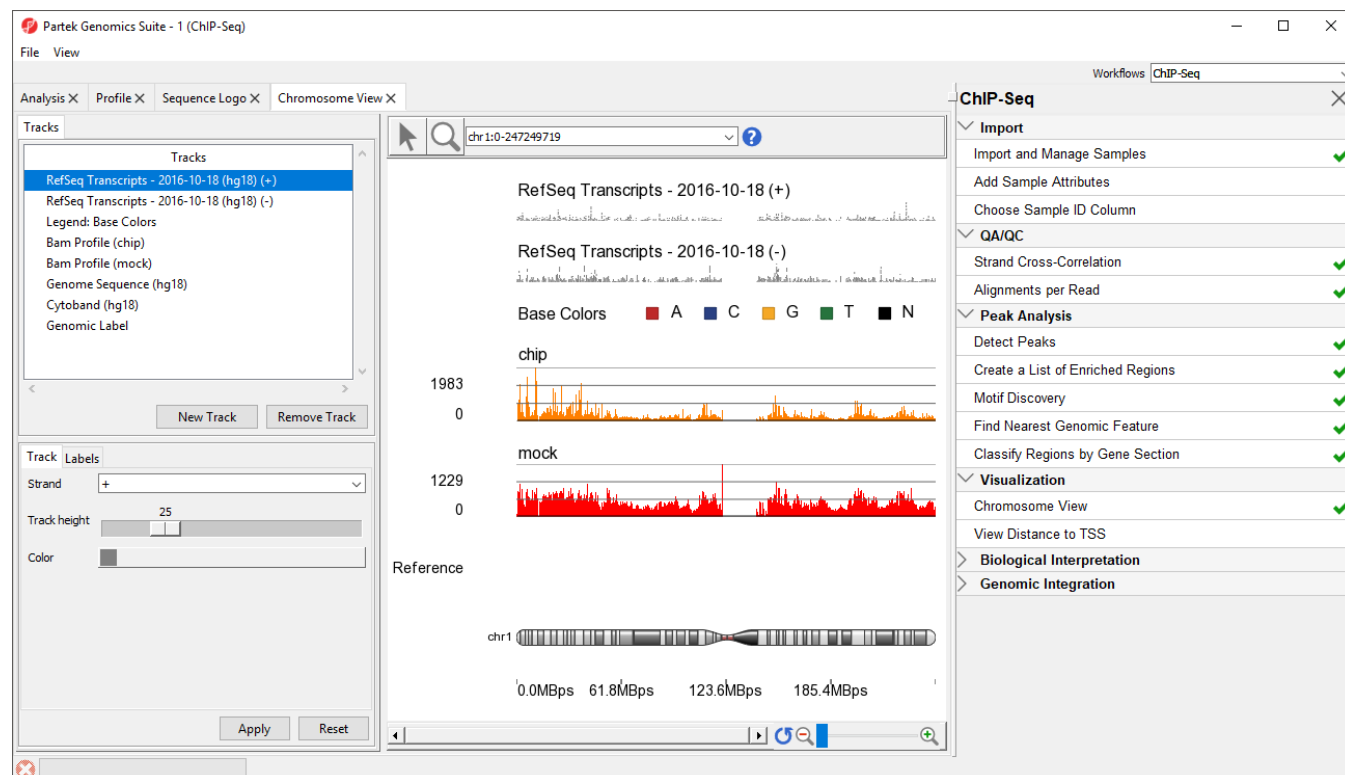


Figure 10. Viewing ChIP-Seq data in Chromosome View

We can add additional tracks to view the results of our analysis.

- Select **New Track** from the left-hand side of the *Tracks* tab
- Select **Add tracks from a list of spreadsheets**
- Select **Next >**
- Select the **p-value_filtered.txt** and **Motifs_instances.txt** tracks on the *Tracks* panel
- De-select **Aligned Reads**
- Select **Create** (Figure 2)

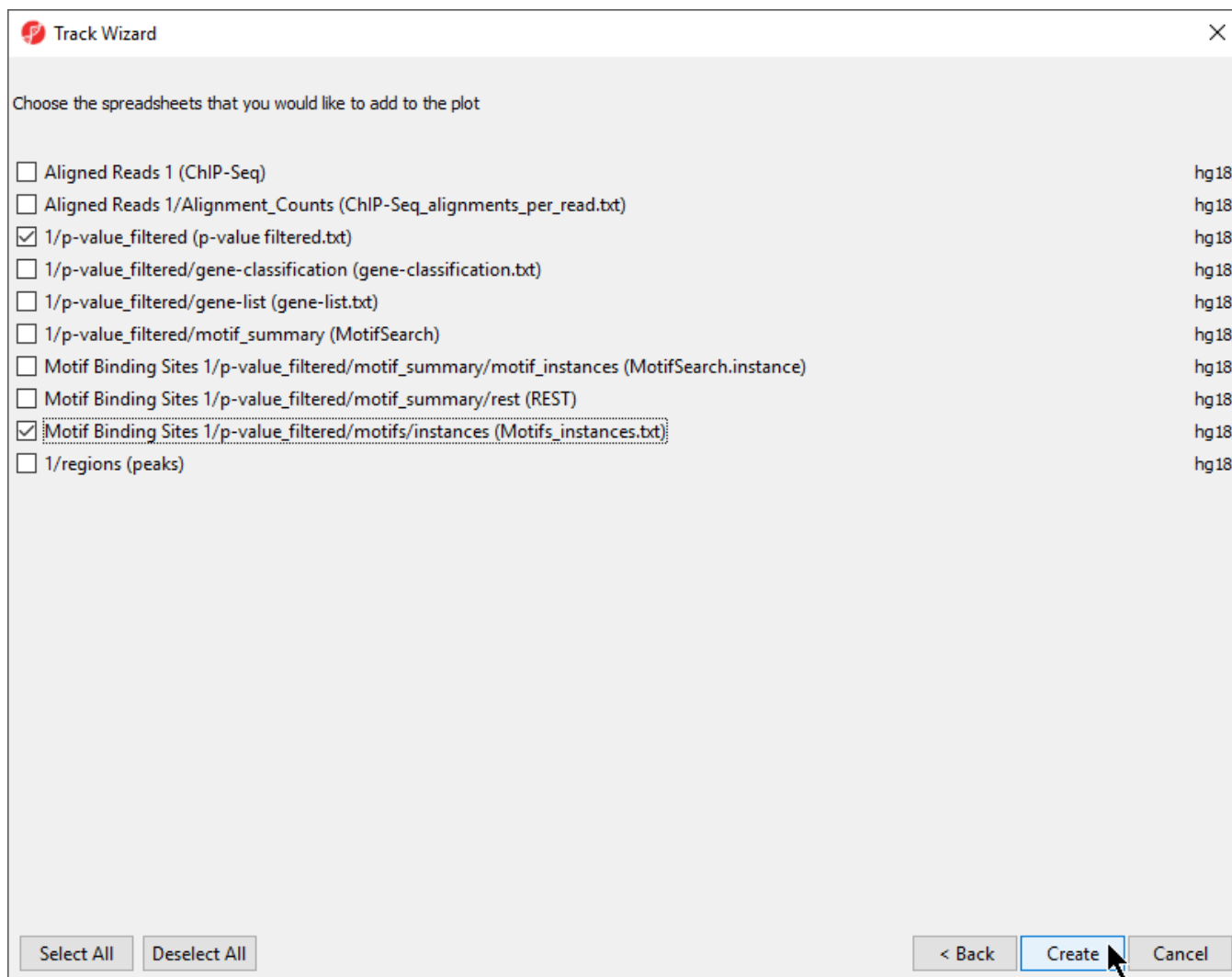


Figure 11. Adding spreadsheet tracks to Genome Viewer

This will display the enriched regions found in the samples and the locations of the motif instances from the *de novo* motif discovery (Figure 3).

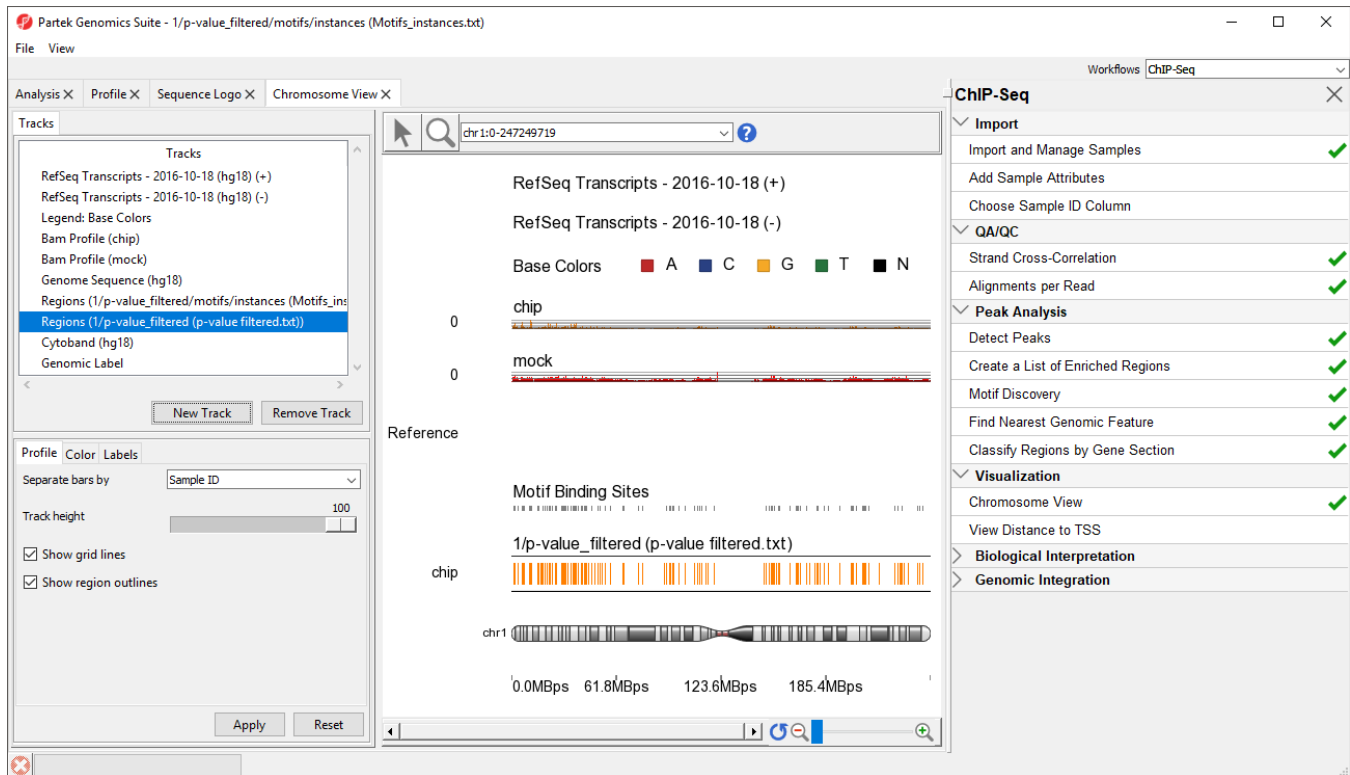


Figure 12. Adding *p*-value and motif binding tracks

The two tracks display the detected regions at each location on the chromosome for the NRSF-enriched sample, *chip*, and aligned them to the *de novo* discovered motif binding sites. If you have not gone through the steps for peak detection and motif discovery, these tracks will not be available.

To facilitate analysis, we will consolidate the tracks. To select a track, either left-click it in the *Tracks* panel or activate Selection Mode by selecting the () icon and left-click the track in the viewer. Selecting a track opens its configuration options in the track properties panel below the *Tracks* panel.

- Select **RefSeq Transcripts - 2016-10-18 (hg18) (+)** on the *Tracks* panel
- Set *Strand* to **Both** using the drop-down menu in the Track section of the track properties panel
- Select **Apply**

The *RefSeq Transcripts* track now shows transcripts from both strands. We can remove the dedicated (-) strand track.

- Select **RefSeq Transcripts - 2016-10-18 (hg18) (-)** on the *Tracks* panel
- Select **Remove Track**

Several other tracks will not be used in our analysis; we can remove them as well.

- Select **Legend: Base Colors**, **Genome Sequences (hg18)**, and **Cytoband (hg18)** on the *Tracks* panel by left clicking on each while holding the **Ctrl** key on your keyboard
- Select **Remove Track**

The height of many tracks can be adjusted by changing the *Track height* setting in the *Profile* tab.

- Select **Regions (1/p-value_filtered (p-value filtered.txt))** on the *Tracks* panel
- Set *Track height* to **25** using the slider
- Select **Apply**
- Repeat for **Regions (1/p-value_filtered/motifs/instances (Motifs_instances.txt))**

This view clearly shows the *Bam Profile* tracks for *chip* and *mock* samples alongside smaller track indicating motif binding sites, significant peaks, and RefSeq transcripts (Figure 4).

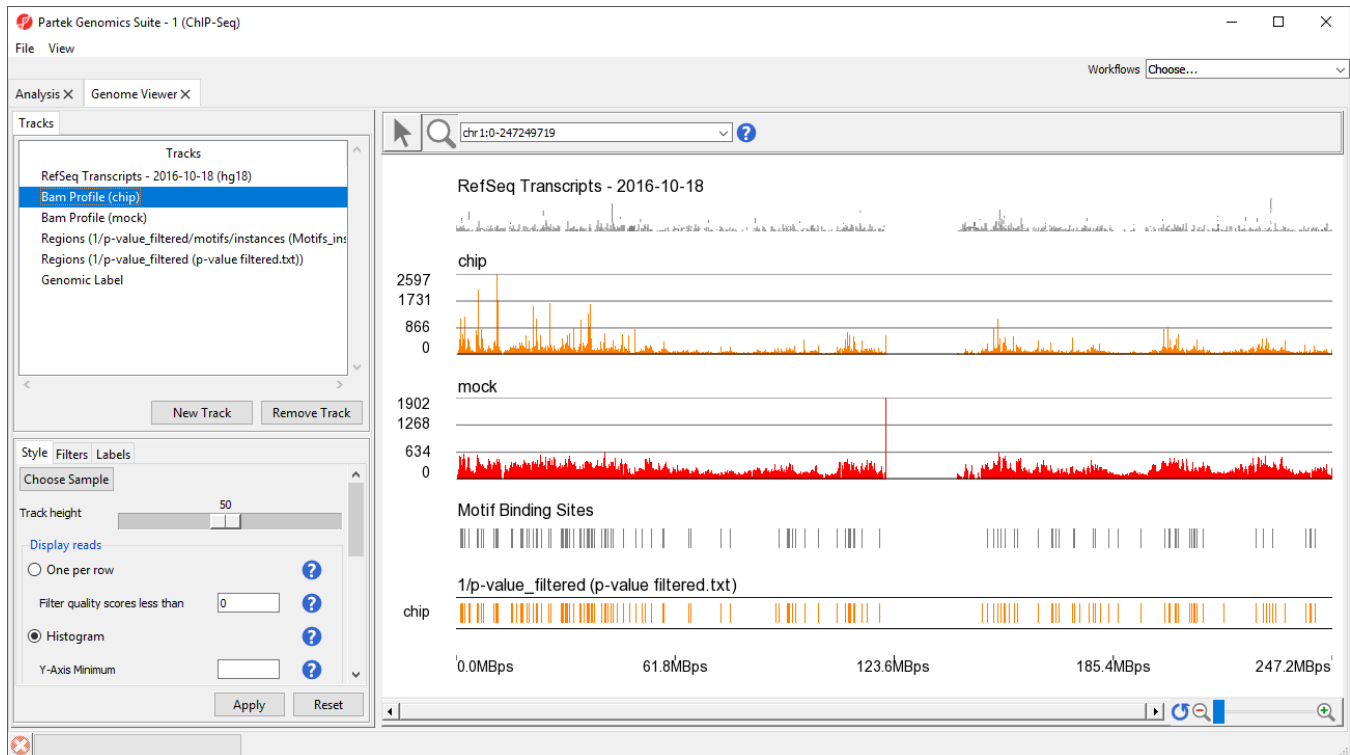


Figure 13. Genome Viewer tracks can be modified to facilitate data exploration and analysis

We can also see strand-specific information by color-coding forward and reverse strand read information on the *Bam Profile (chip)* track.

- Select **Bam Profile (chip)** on the *Tracks* panel
- Select **Alignments** in the *Display Color Options* section of the *Style* tab
- Select **Strands** under *Color by*
- Select **Apply**

A legend track will be added at the bottom of the viewer showing that forward strand reads are colored green and reverse strand reads are colored red. We can move this track to below *Bam Profile (chip)*.

- Left-click **Legend: strands** in the *Tracks* panel and drag it up the list to below *Bam Profile (chip)* (Figure 5)

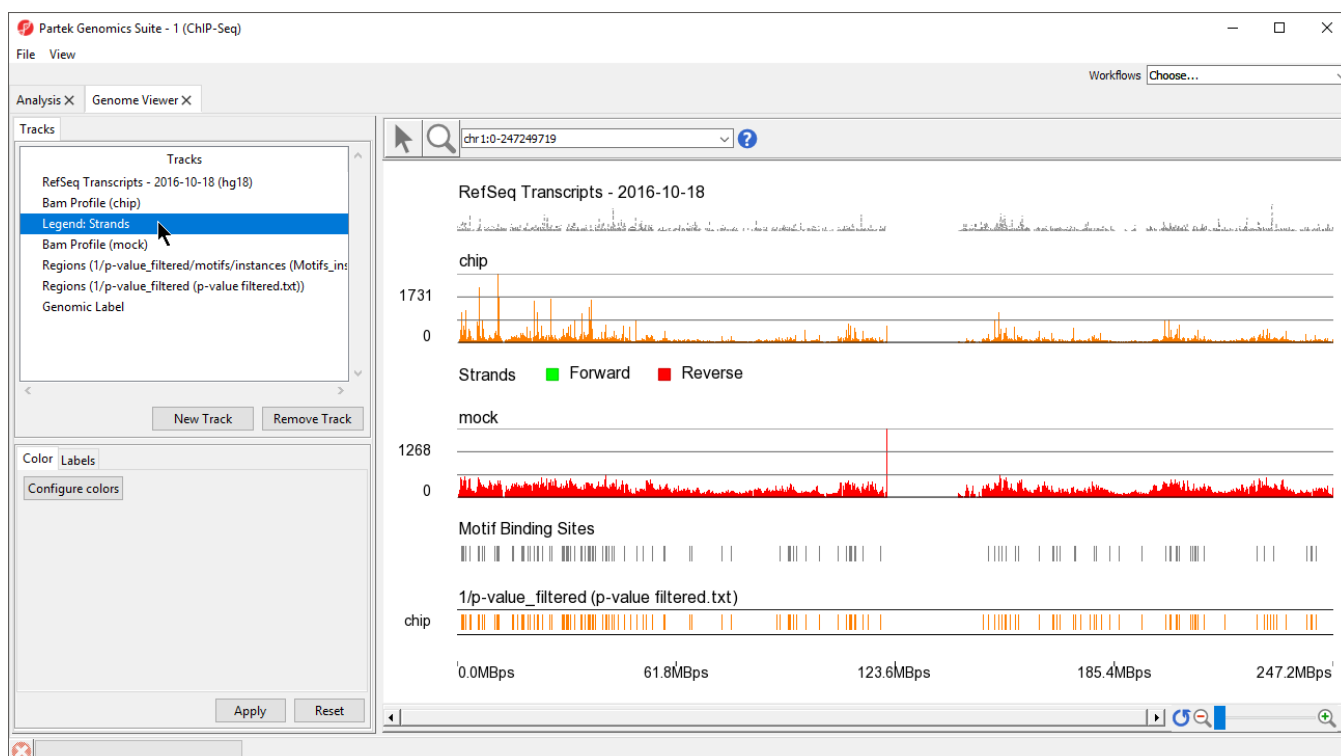


Figure 14. Move tracks by left-clicking and dragging them in the Tracks panel

Chromosome View opens to a whole-chromosome view of chromosome 1. To analyze the data we can zoom in on the data (Figure 6).

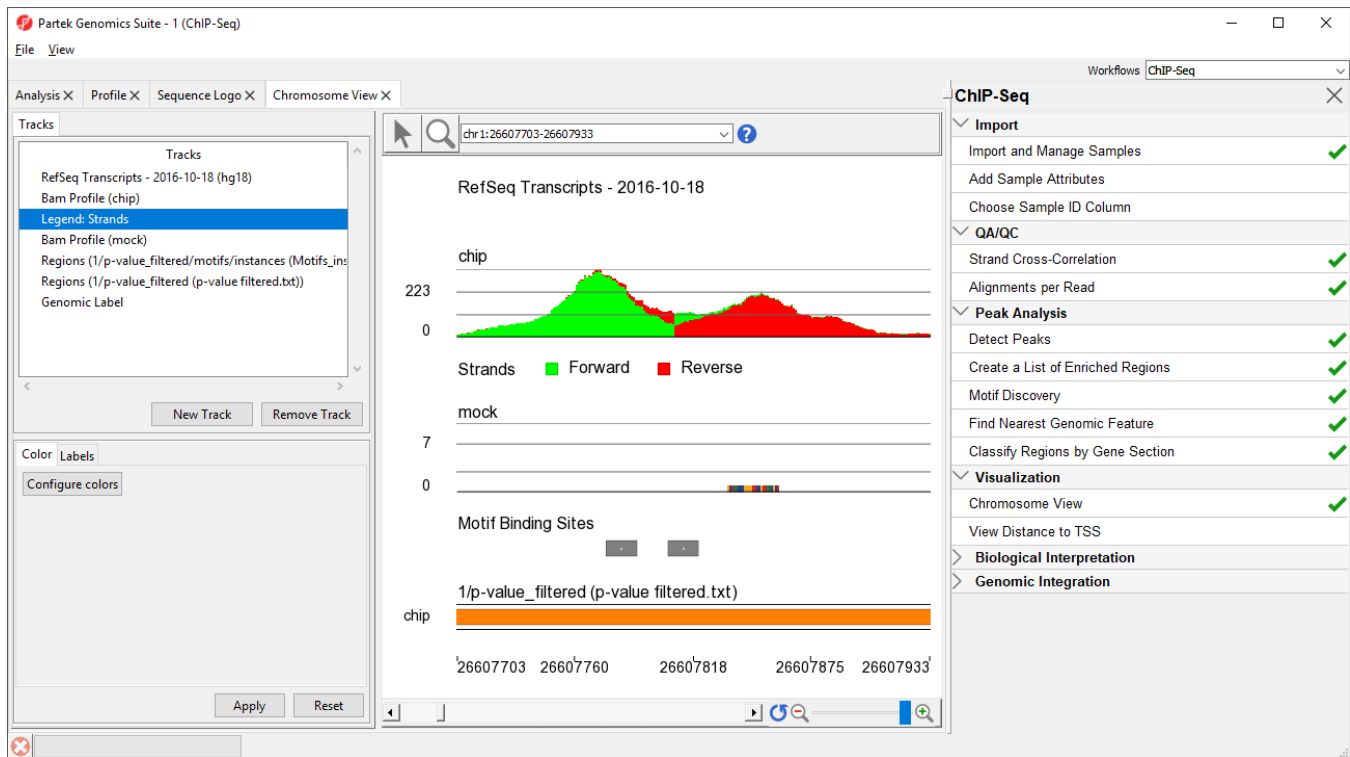


Figure 15. Viewing the zoomed-in view of an enriched region showing two possible binding sites at the location

There are four methods for zooming in and out in *Chromosome View*. (1) Select (🔍) to activate Zoom/Navigate Mode. With this mode selected, left-clicking and drawing a box on a track will zoom to the region in the box. (2) Use the mouse scroll wheel (3) Select the zoom in (🔍) and zoom out (🔍) on the zoom controls (🔍). Selecting (🔄) resets the zoom to whole chromosome. (4) Use the slider on the zoom controls (🔍). (5) Zoom to a location or gene by typing the coordinates or gene name in the Navigation bar (chr1:26607703-26607934) and pressing Enter on your keyboard. (5) Starting on a spreadsheet, right-click a row with region information, and select **Browse to Location**.

We can practice this using a gene highlighted in the paper describing this data set, NEUROD1.

- Type **NEUROD1** in the navigation bar
- Select **Enter** on your keyboard to navigate to NEUROD1 (Figure 7)

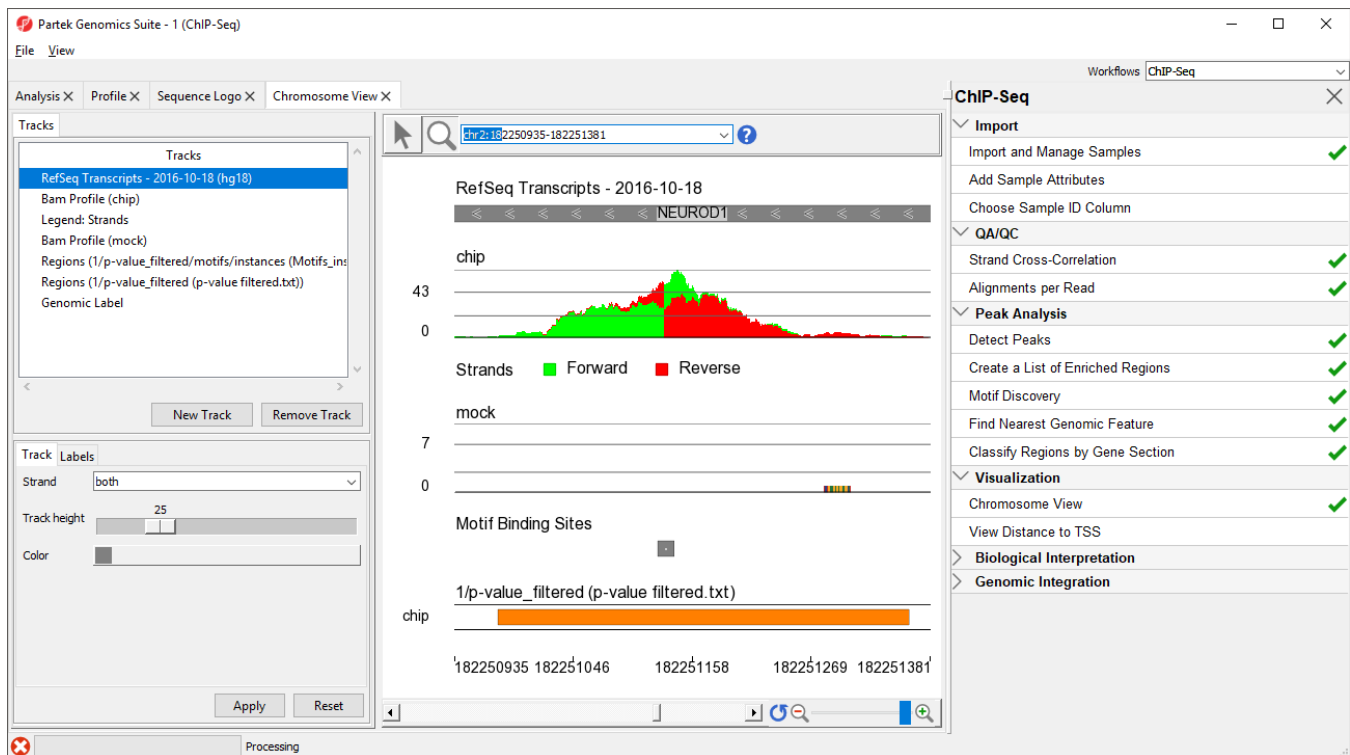



Figure 18. Zoomed-in view of NEUROD1 binding site for NRSF

You can save the reads shown in the visible genome browser window by selecting (), right-clicking in the peak area on the *Bam Profile* track, and selecting **Dump Displayed Reads to Spreadsheet** from the pop-up menu.

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:        37 rates