Visualize methylation at each locus

Partek Genomics Suite enables you to visualize each probe and compare the methylation between the groups at a single CpG site level.

- Right click row 5. *SBNO2* in the *LCLs_vs_B_Cells_CpG_Islands* spreadsheet
- Select **Browse to Location** from the pop-up menu

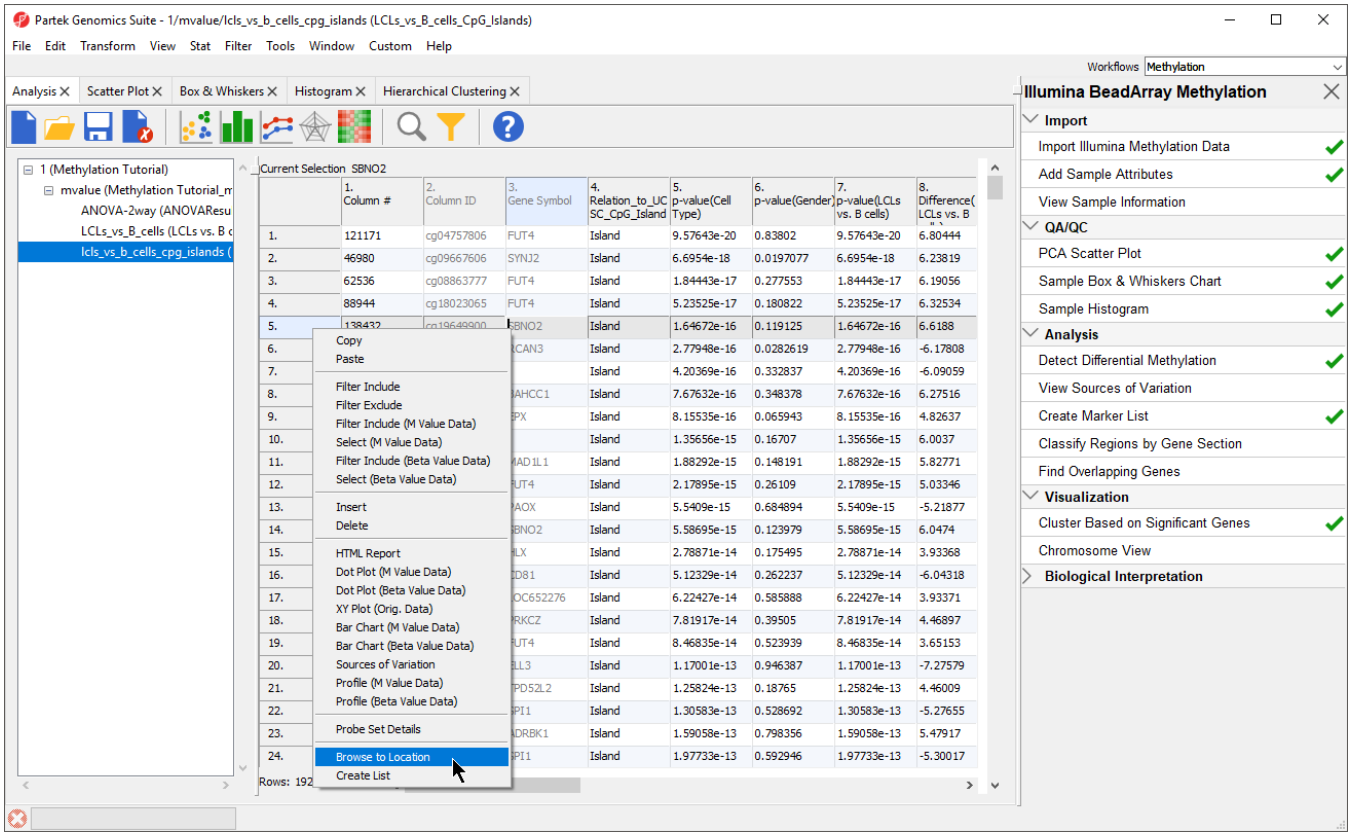


Figure 4. Browsing to location from spreadsheet with differentially expressed genes

The *Chromosome View* tab will open, zoomed in to the selected CpG locus in SBNO2 (Figure 2).

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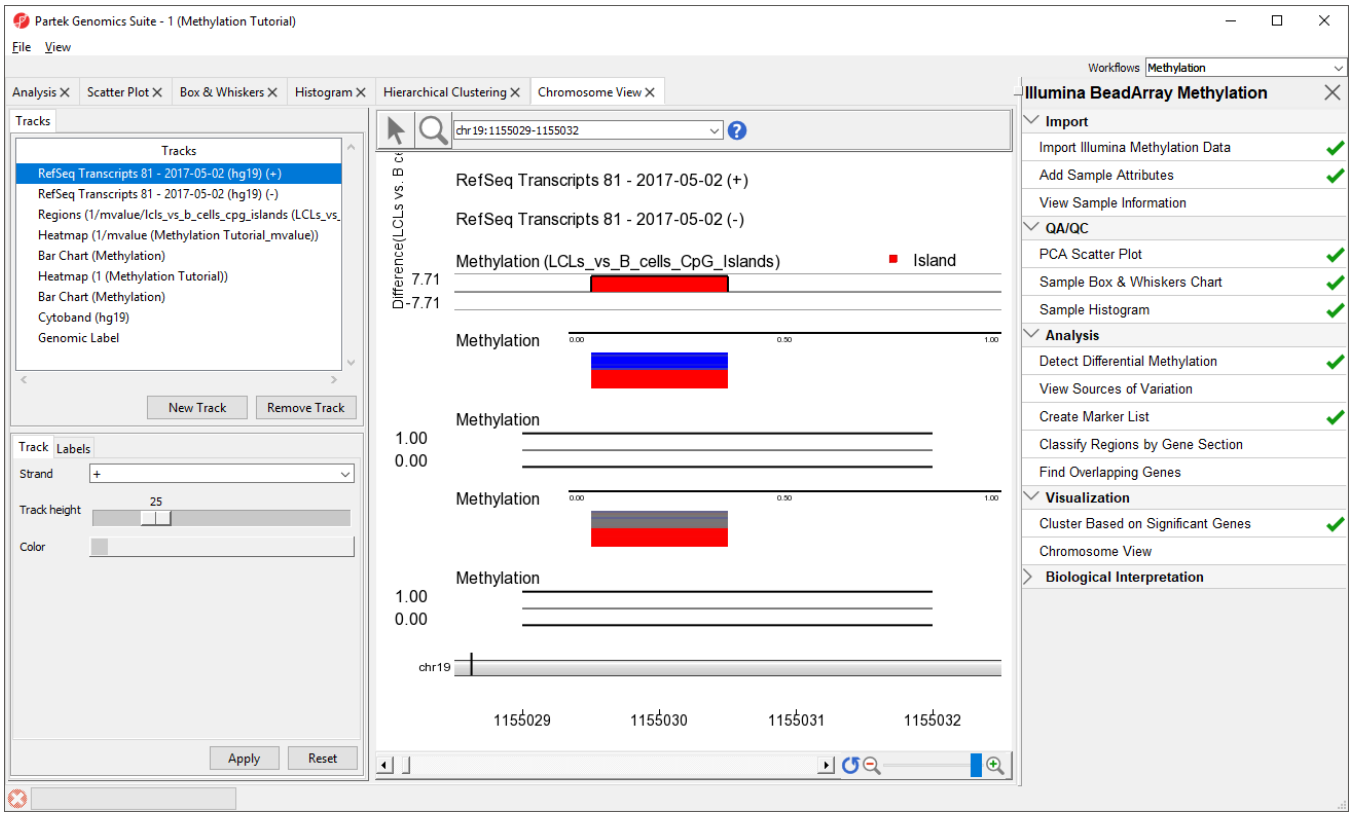


Figure 5. Viewing location in Genome Viewer

The *Chromosome View* visualization is composed of a series of tracks corresponding to annotation files and data files.

- *RefSeq Transcripts 2017-05-02 (hg19) (+)*: transcripts coded by the positive strand
- *RefSeq Transcripts 2017-05-02 (hg19) (-)*: transcripts coded by the negative strand
- *Regions*: by default, difference in methylation (M-value) between the groups
- *Heatmap (1/mvalue)*: M values for all the samples
- *Barchart (Methylation)*: methylation level in M value of the selected sample (to select a sample, click on a heat map)
- *Heatmap (Methylation Tutorial)*: Beta values for all the samples
- *Barchart (Methylation)*: methylation level in Beta value of the selected sample (to select a sample, click on a heat map)
- *Cytoband*: cytobands of the current chromosome
- *Genomic Label*: coordinates on the current chromosome

To modify a track, select it in the *Tracks* panel to bring up its configuration options panel below the *Tracks* panel. Let's modify a few tracks to improve our visualization of the data.

- Select the *Regions* track, opens to *Profile* tab
- Select *Color* tab
- Set *Color bars by* to **Difference (LCLs vs. B cells) (Description)**
- Select **Apply** to change

This will color regions by up or down methylated.

- Select the *Heatmap (1/mvalue)*
- Select **Remove Track**
- Select *Bar Chart (Methylation)* located directly below the *Regions* track
- Select **Remove Track**

We can now more clearly see the Difference in M values for the region in the *Regions* track, the heatmap of beta values in the *Heatmap* track, and the beta value for the loci of the selected sample in the *Bar Chart* track.

- Select a sample on the heatmap to view its beta value in the *Bar Chart* track (Figure 3)

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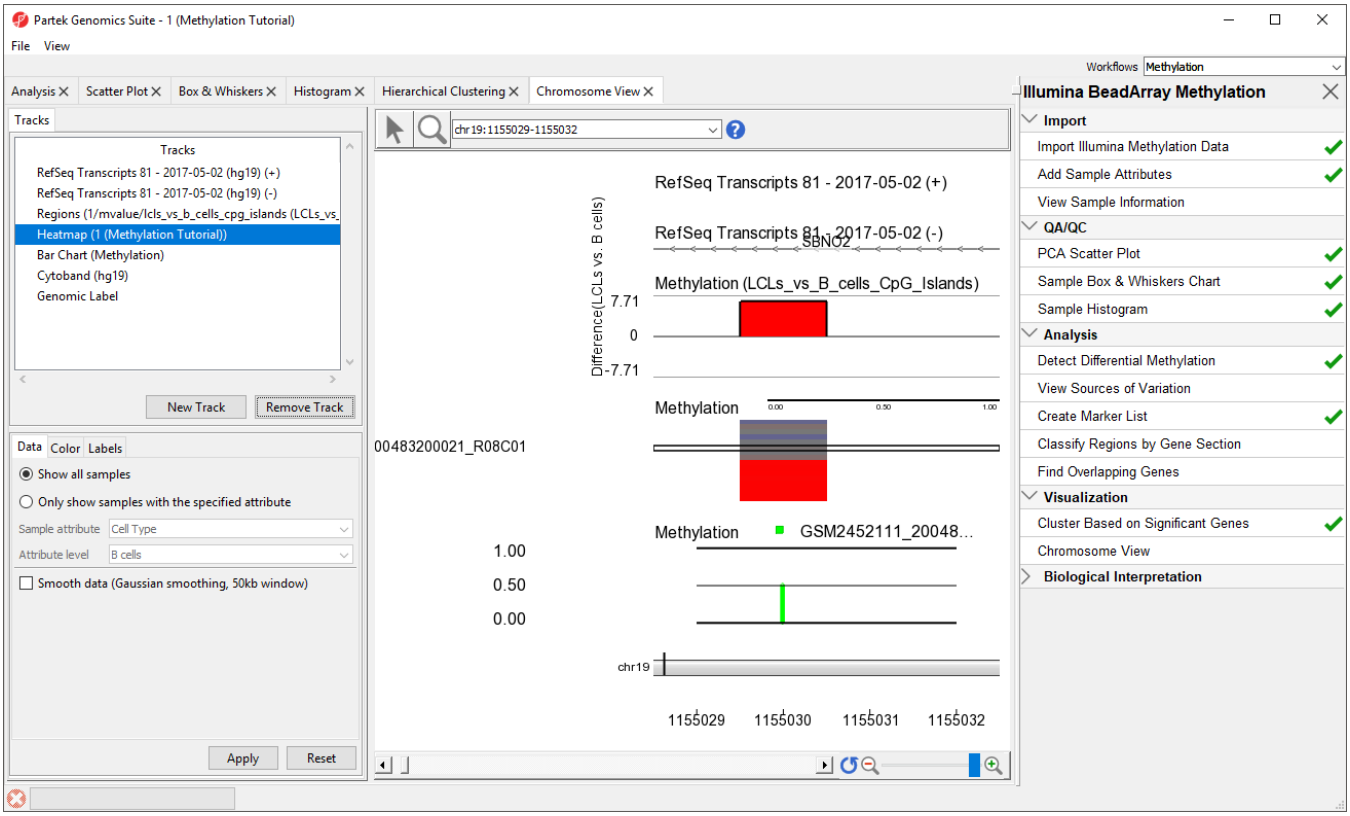
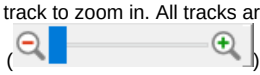


Figure 6. Modify the tracks of the Genome Viewer to facilitate visual analysis

The **New Track** button allows new tracks to be added to the viewer, while the **Remove Track** button removes the selected track from the viewer. Tracks can be reordered by selecting a track in the *Tracks* panel and dragging it up or down to move it in the list. In the *Chromosome View*, select () for selection mode and () for navigation mode. In navigation mode, left-click and draw a box on any track to zoom in. All tracks are synced and will zoom together. Zooming can also be controlled using the interface in the lower right-hand corner of the tab (). View can be reset to the whole chromosome level using reset zoom (). Searching for a gene or transcript in the position box will also zoom directly to its location.

The available tracks can be supplemented with a special annotation file that can be built using a UCSC annotation file as the basis. Building and viewing the UCSC annotation file is available as an optional section of the tutorial, Optional: Add UCSC CpG island annotations.

« Obtain methylation signatures Perform gene set and pathway analysis »

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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