

# 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

Partek Genomics Suite - 1/mvalue/lcls\_vs\_b\_cells\_cpG\_islands (LCLs\_vs\_b\_cells\_CpG\_Islands)

File Edit Transform View Stat Filter Tools Window Custom Help

Analysis X Scatter Plot X Box & Whiskers X Histogram X Hierarchical Clustering X

1 (Methylation Tutorial)

- mvalue (Methylation Tutorial)
- ANOVA-2way (ANOVA Results)
- LCLs\_vs\_B\_cells (LCLs vs. B cells)
- LCLs\_vs\_b\_cells\_cpG\_islands (LCLs vs. B cells CpG Islands)**

Current Selection: SBNO2

|     | 1. Column # | 2. Column ID | 3. Gene Symbol | 4. Relation_to_UC<br>SC_CpG_Island | 5. p-value(Cell<br>Type) | 6. p-value(Gender) | 7. p-value(LCLs<br>vs. B cells) | 8. Difference(LCLs<br>vs. B cells) |
|-----|-------------|--------------|----------------|------------------------------------|--------------------------|--------------------|---------------------------------|------------------------------------|
| 1.  | 121171      | cg04757806   | FUT4           | Island                             | 9.57643e-20              | 0.83802            | 9.57643e-20                     | 6.80444                            |
| 2.  | 46980       | cg09667606   | SYNJ2          | Island                             | 6.6954e-18               | 0.0197077          | 6.6954e-18                      | 6.23819                            |
| 3.  | 62536       | cg08863777   | FUT4           | Island                             | 1.84443e-17              | 0.277553           | 1.84443e-17                     | 6.19056                            |
| 4.  | 88944       | cg18023065   | FUT4           | Island                             | 5.23525e-17              | 0.180822           | 5.23525e-17                     | 6.32534                            |
| 5.  | 138432      | cg19649900   | SBNO2          | Island                             | 1.64672e-16              | 0.119125           | 1.64672e-16                     | 6.6188                             |
| 6.  |             |              | UCAN3          | Island                             | 2.77948e-16              | 0.0282619          | 2.77948e-16                     | -6.17808                           |
| 7.  |             |              |                | Island                             | 4.20369e-16              | 0.332837           | 4.20369e-16                     | -6.09059                           |
| 8.  |             |              | HAHCC1         | Island                             | 7.67632e-16              | 0.348378           | 7.67632e-16                     | 6.27516                            |
| 9.  |             |              | EPX            | Island                             | 8.15535e-16              | 0.065943           | 8.15535e-16                     | 4.82637                            |
| 10. |             |              |                | Island                             | 1.35656e-15              | 0.16707            | 1.35656e-15                     | 6.0037                             |
| 11. |             |              | ADIL1          | Island                             | 1.88292e-15              | 0.148191           | 1.88292e-15                     | 5.82771                            |
| 12. |             |              | FUT4           | Island                             | 2.17895e-15              | 0.26109            | 2.17895e-15                     | 5.03346                            |
| 13. |             |              | AOX            | Island                             | 5.5409e-15               | 0.684894           | 5.5409e-15                      | -5.21877                           |
| 14. |             |              | SBNO2          | Island                             | 5.58695e-15              | 0.123979           | 5.58695e-15                     | 6.0474                             |
| 15. |             |              | ILX            | Island                             | 2.78871e-14              | 0.175495           | 2.78871e-14                     | 3.93368                            |
| 16. |             |              | CD81           | Island                             | 5.12329e-14              | 0.262237           | 5.12329e-14                     | -6.04318                           |
| 17. |             |              | OC652276       | Island                             | 6.22427e-14              | 0.585888           | 6.22427e-14                     | 3.93371                            |
| 18. |             |              | PRKC2          | Island                             | 7.81917e-14              | 0.39505            | 7.81917e-14                     | 4.46897                            |
| 19. |             |              | FUT4           | Island                             | 8.46835e-14              | 0.523939           | 8.46835e-14                     | 3.65153                            |
| 20. |             |              | ILL3           | Island                             | 1.17001e-13              | 0.946387           | 1.17001e-13                     | -7.27579                           |
| 21. |             |              | PD52L2         | Island                             | 1.25824e-13              | 0.18765            | 1.25824e-13                     | 4.46009                            |
| 22. |             |              | PI1            | Island                             | 1.30583e-13              | 0.528692           | 1.30583e-13                     | -5.27655                           |
| 23. |             |              | DRBK1          | Island                             | 1.59058e-13              | 0.798356           | 1.59058e-13                     | 5.47917                            |
| 24. |             |              | PI1            | Island                             | 1.97733e-13              | 0.592946           | 1.97733e-13                     | -5.30017                           |

Rows: 192

Context Menu for Row 5 (SBNO2):

- Copy
- Paste
- Filter Include
- Filter Exclude
- Filter Include (M Value Data)
- Select (M Value Data)
- Filter Include (Beta Value Data)
- Select (Beta Value Data)
- Insert
- Delete
- HTML Report
- Dot Plot (M Value Data)
- Dot Plot (Beta Value Data)
- XY Plot (Orig. Data)
- Bar Chart (M Value Data)
- Bar Chart (Beta Value Data)
- Sources of Variation
- Profile (M Value Data)
- Profile (Beta Value Data)
- Probe Set Details
- Browse to Location**
- Create List

Workflows: Methylation

**Illumina BeadArray Methylation**

- Import
  - Import Illumina Methylation Data ✓
  - Add Sample Attributes ✓
  - View Sample Information
- QA/QC
  - PCA Scatter Plot ✓
  - Sample Box & Whiskers Chart ✓
  - Sample Histogram ✓
- Analysis
  - Detect Differential Methylation ✓
  - View Sources of Variation
  - Create Marker List ✓
  - Classify Regions by Gene Section
  - Find Overlapping Genes
- Visualization
  - Cluster Based on Significant Genes ✓
  - Chromosome View
- Biological Interpretation

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).

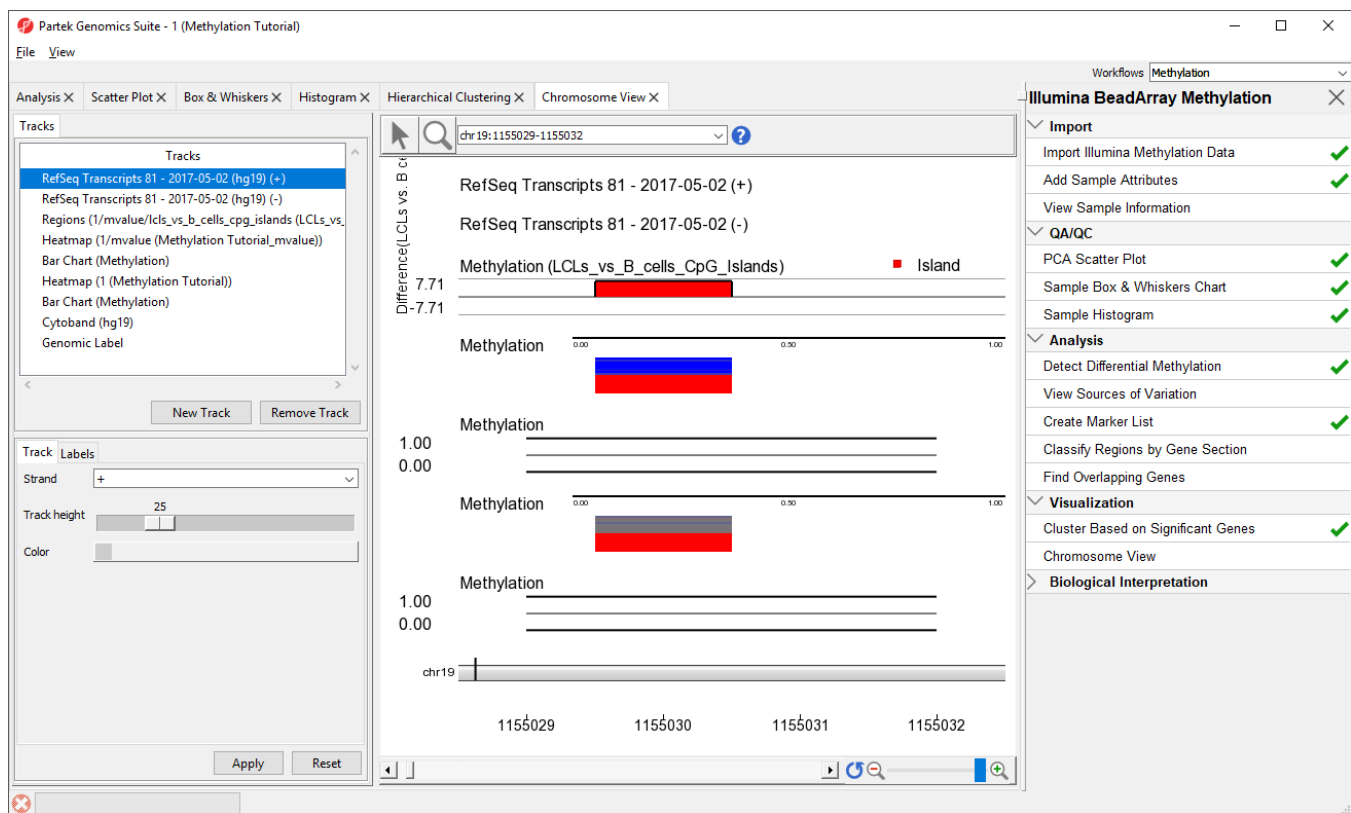


Figure 5. Viewing location in Genome Viewer

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
- *Bar Chart (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
- *Bar Chart (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)

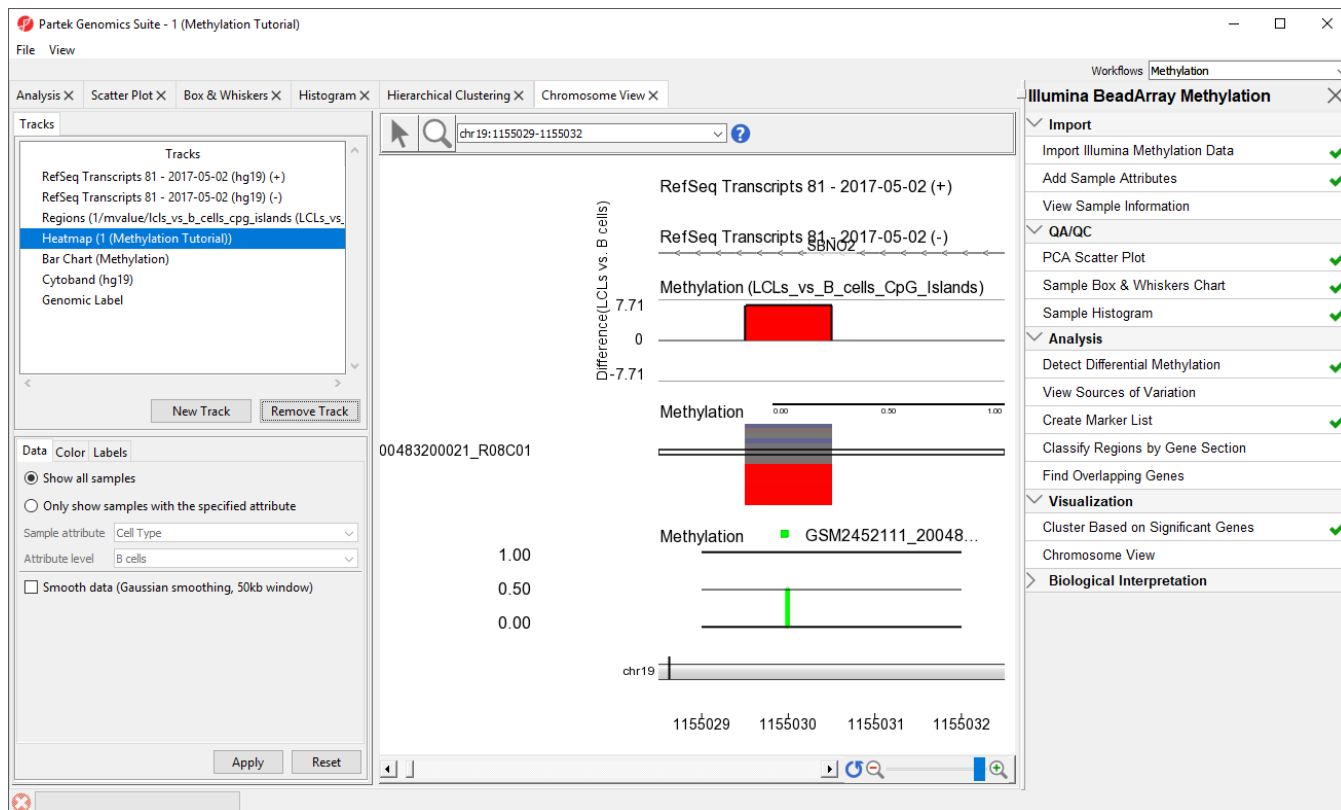


Figure 6. Modify the tracks of the Genome Viewer to facilitate visual analysis

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.



Your Rating:  Results:  34 rates