

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 SC CpG Island	5. p-value (Cell Type)	6. p-value (Gender)	7. p-value (LCLs vs. B cells)	8. Difference (LCLs 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).

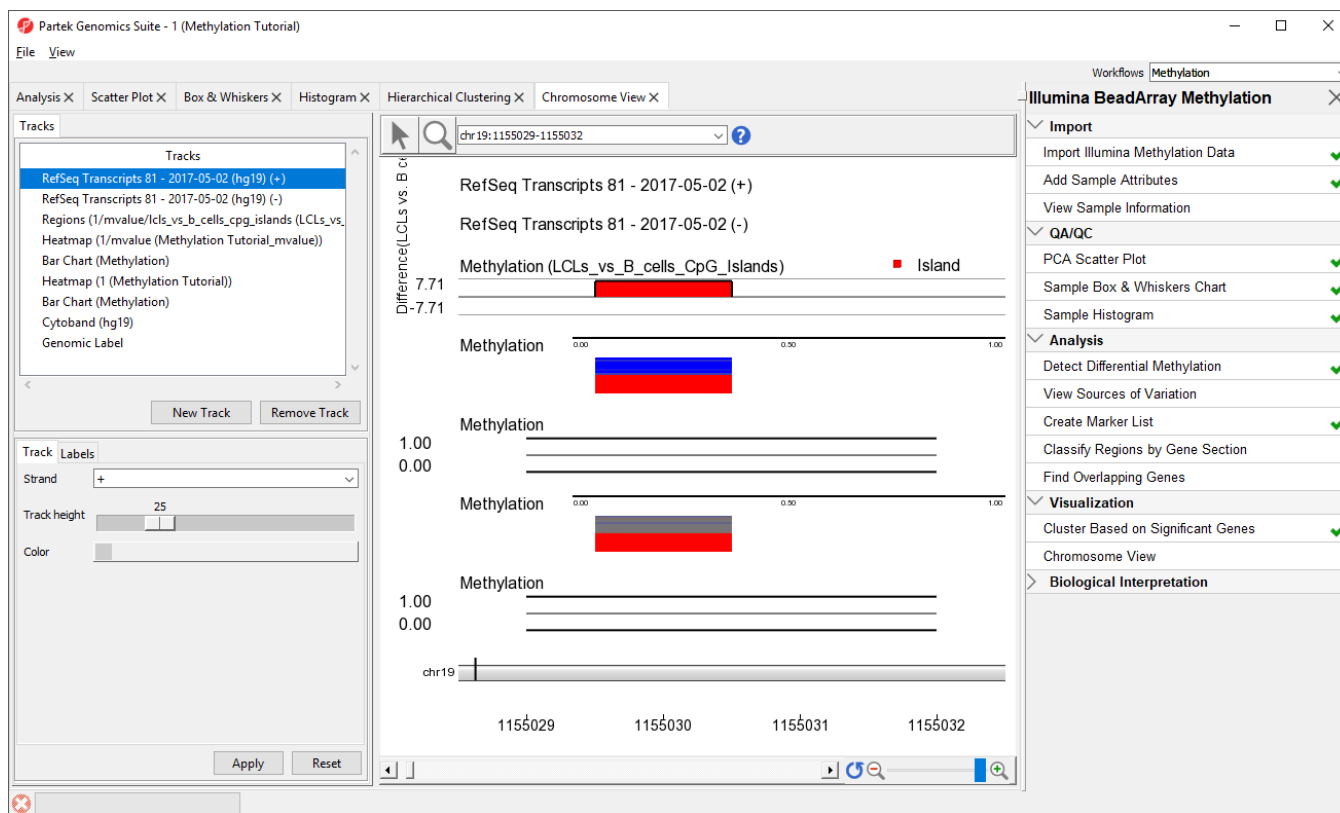


Figure 5. Viewing location in Genome Viewer

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)

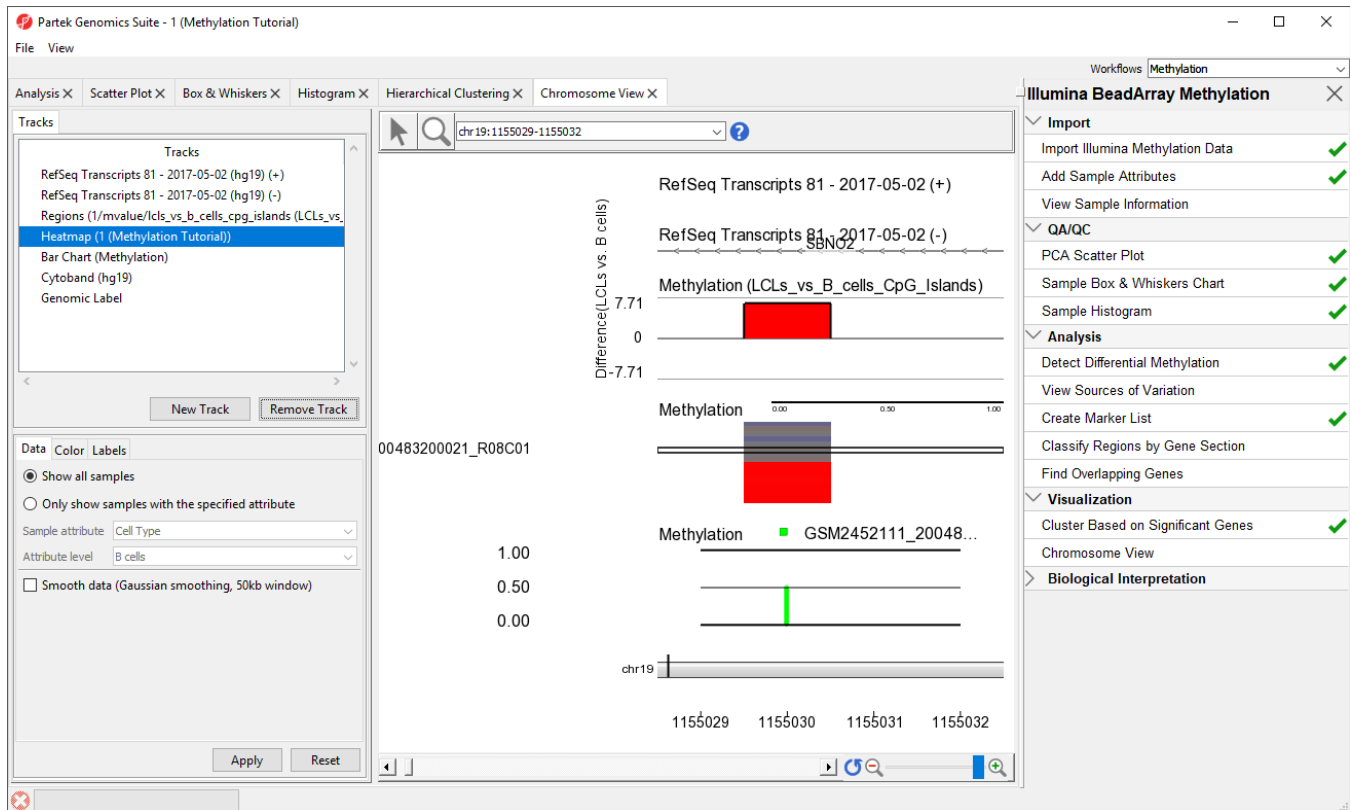


Figure 6. Modify the tracks of the Genome Viewer to facilitate visual analysis

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