

Obtain methylation signatures

The significant CpG loci detected in the previous step actually form a methylation signature that differentiates between LCLs and B cells. We can build and visualize this methylation signature using clustering and a heat map.

- Select the *LCLs_vs_Bcells_CpG_Islands* spreadsheet in the spreadsheet pane on the left
- Select **Cluster Based on Significant Genes** from the *Visualization* panel of the *Illumina BeadArray Methylation* workflow
- Select **Hierarchical Clustering** for *Specify Method* (Figure 1)

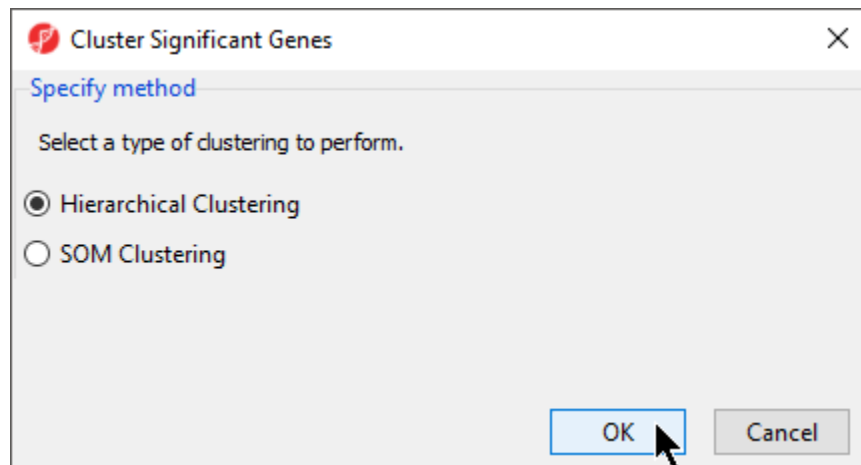


Figure 1. Selecting Hierarchical Clustering for clustering method

- Select **OK**
- Verify that **LCLs_vs_Bcells_CpG_Islands** is selected in the drop-down menu
- Verify that **Standardize** is selected for *Expression normalization* (Figure 2)

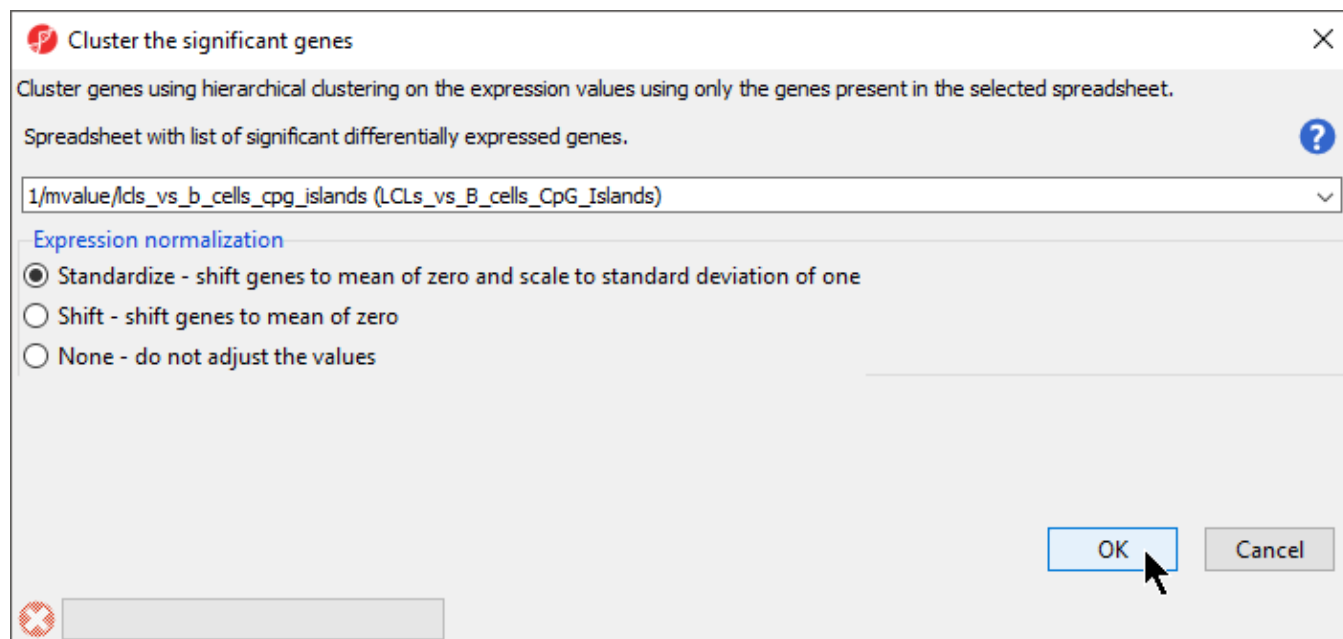


Figure 2. Selecting spreadsheet and normalization method for clustering

- Select **OK**

The heat map will be displayed on the Hierarchical Clustering tab (Figure 3).

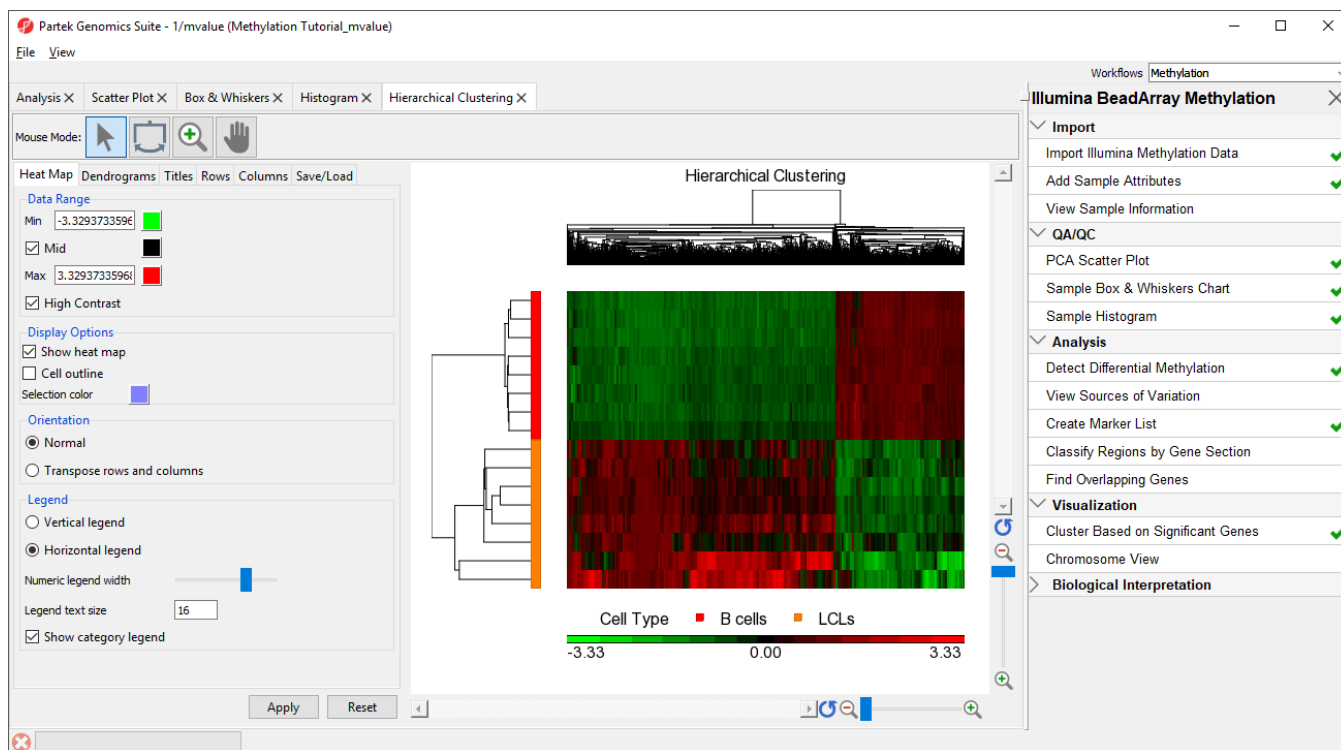


Figure 3. Hierarchical clustering with heat map invoked on a list of significant CpG loci

The experimental groups are rows, while the CpG loci from the *LCLs vs B cells* spreadsheet are columns. Methylation levels are compared between the LCLs and B cells groups. CpG loci with higher methylation are colored red, CpG loci with lower methylation are colored green. LCLs samples are colored orange and B cells samples are colored red in the dendrogram on the left-hand side of the heat map.

« [Filter loci with the interactive filter](#) [Visualize methylation at each locus](#) »

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

