


Hierarchical clustering using a gene list

- Opening a gene list as a child spreadsheet
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Opening a gene list as a child spreadsheet

Gene lists can be visualized and their ability to distinguish samples evaluated using a hierarchical clustering heat map. Because of the batch effect in this data set, we will perform hierarchical clustering using batch-corrected intensity values. To do this, we need to open the *fourtreatments* list of differentially expressed genes as a child spreadsheet of the *batch-remove* spreadsheet

- Select **fourtreatments** from the spreadsheet tree
- Select  to close the spreadsheet
- Select **1-removeresult (batch-remove)** from the spreadsheet tree
- Select **File** from the main tool bar
- Select **Open as child...**
- Select **fourtreatments** using the file browser

The *fourtreatments* spreadsheet will open as a child spreadsheet of *batch-remove* (Figure 1).

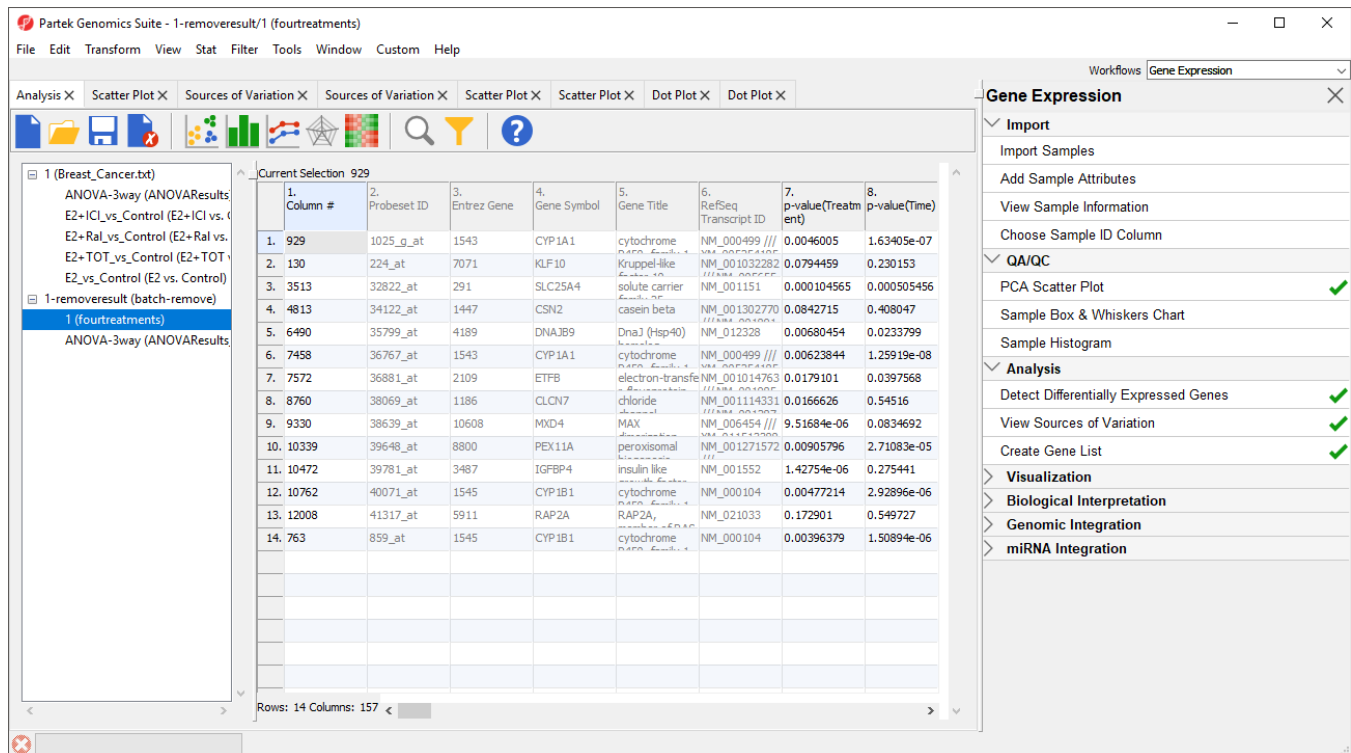


Figure 4. The *fourtreatments* spreadsheet is open as a child spreadsheet of *batch-remove*. Visualizations performed using *fourtreatments* will pull intensity values from *batch-remove*.

Visualizations performed using the *fourtreatments* spreadsheet will now use intensity values from the *batch-remove* spreadsheet.

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To invoke hierarchical clustering, follow the steps below.

- Select **Cluster Based on Significant Genes** from the *Visualization* section of the *Gene Expression* workflow
- Select **Hierarchical Clustering**
- Select **OK**
- Select **1-removeresult/1 (fourtreatments)** from the drop-down menu
- Select **Standardize** for *Expression normalization* (Figure 2)

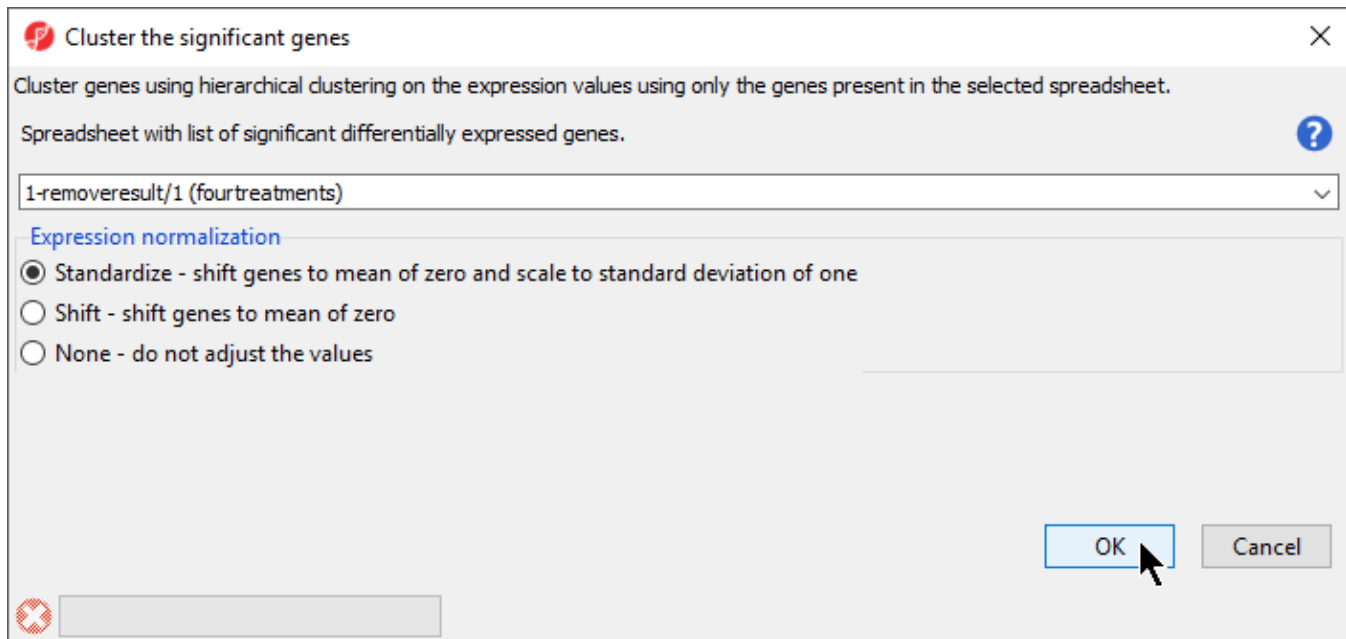


Figure 5. Configuring the Cluster the significant genes dialog

- Select **OK**

The hierarchical clustering heat map will open in a new tab (Figure 3).

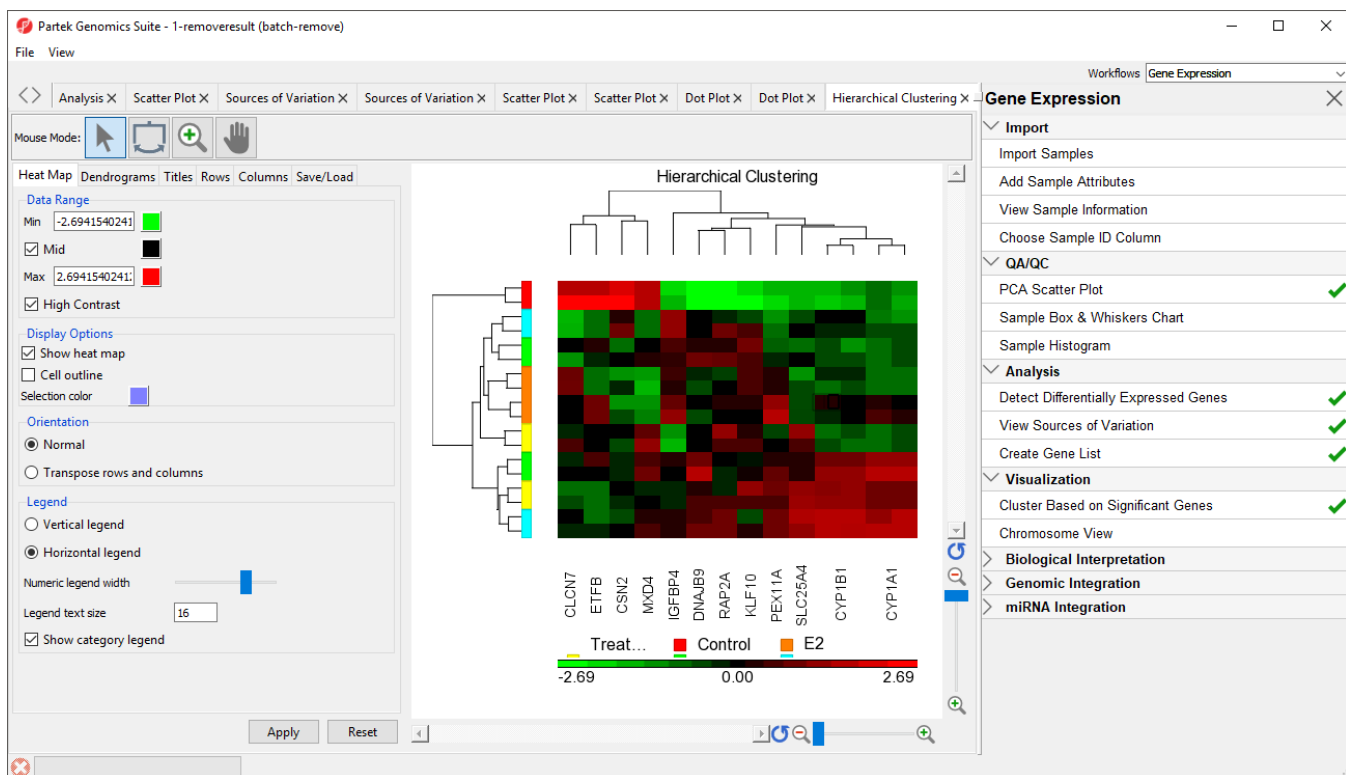


Figure 6. Hierarchical clustering of genes with significantly different expression across the treatment groups

Genes without changes in expression are given a value of zero and are colored black. Up-regulated genes have positive values and are displayed in red. Down-regulated genes have negative values and are displayed in green. Each sample is represented in a row while genes are represented as columns. Dendrograms illustrate clustering of samples and genes. To learn more about configuring the hierarchical clustering heat map, see the [Hierarchical Clustering Analysis](#) user guide.

For detailed information about the methods used for clustering, refer to the Partek Manual **Chapter 8: Hierarchical & Partitioning Clustering**.

[« Creating a gene list using the Venn Diagram](#) [GO enrichment using a gene list »](#)

Additional Assistance

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