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 (2) 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 ٠

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

									Workflows Gene Expression	
lysis X Scatter Plot X Sources of V	Variation × Sour	ces of Variation :	× Scatter Plo	t × Scatter P	lot × Dot Plot	× Dot Plot >	<		Gene Expression	
								✓ Import		
								Import Samples		
1 (Breast_Cancer.txt)								Add Sample Attributes		
ANOVA-3way (ANOVAResults	1. Column #	2. Probeset ID	3. Entrez Gene	4. Gene Symbol	5. Gene Title	6. RefSea	7. p-value(Treatm	8. p-value(Time)	View Sample Information	
E2+ICI_vs_Control (E2+ICI vs. (Column #	FIODESCLID	Lifez dene	Gene Symbol	Gene nue	Transcript ID	ent)	p-value(nine)		
E2+Ral_vs_Control (E2+Ral vs.	1. 929	1025 <u>g</u> at	1543	CYP1A1	cytochrome	NM_000499 ///	0.0046005	1.63405e-07	Choose Sample ID Column	
E2+TOT_vs_Control (E2+TOT)	2. 130	224_at	7071	KLF10	Kruppel-like	NM_001032282	0.0794459	0.230153	∼ qa/qc	
E2_vs_Control (E2 vs. Control)	3. 3513	32822_at	291	SLC25A4	solute carrier	NM_001151	0.000104565	0.000505456	PCA Scatter Plot	
1 (fourtreatments)	4. 4813	34122_at	1447	CSN2	casein beta	NM_001302770	0.0842715	0.408047	Sample Box & Whiskers Chart	
ANOVA-3way (ANOVAResults	5. 6490	35799_at	4189	DNAJB9	DnaJ (Hsp40)	NM_012328	0.00680454	0.0233799	Samala Histogram	
	6. 7458	36767_at	1543	CYP1A1	cytochrome	NM_000499 ///	0.00623844	1.25919e-08	Sample Histogram	
	7. 7572	36881_at	2109	ETFB	electron-transfe	NM_001014763	0.0179101	0.0397568	✓ Analysis	
	8. 8760	38069_at	1186	CLCN7	chloride	NM_001114331	0.0166626	0.54516	Detect Differentially Expressed Genes	
	9. 9330	38639_at	10608	MXD4	MAX	NM_006454 ///	9.51684e-06	0.0834692	View Sources of Variation	
	10. 10339	39648_at	8800	PEX11A	peroxisomal	NM_001271572	0.00905796	2.71083e-05	Create Gene List	
	11. 10472	39781_at	3487	IGFBP4	insulin like	NM_001552	1.42754e-06	0.275441	> Visualization	
	12. 10762	40071_at	1545	CYP1B1	cytochrome	NM_000104	0.00477214	2.92896e-06	Biological Interpretation	
	13. 12008	41317_at	5911	RAP2A	RAP2A,	NM_021033	0.172901	0.549727		
	14. 763	859_at	1545	CYP1B1	cytochrome	NM_000104	0.00396379	1.50894e-06		
					DAPO Lander 4					

igure 4. The fourtreatments spreadsheet is open as a child spreadsheet of bath-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 hiearchical 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.

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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

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

