Performing pathway enrichment

- Creating a list of significant genes
- Performing pathway enrichment analysis

Before performing pathway enrichment, we need to create a gene list from the ANOVA results.

Creating a list of significant genes

- Select Gene Expression from the workflows drop-down menu
- Select the ANOVAResults gene spreadsheet
- Select Create Gene List from the Analysis section of the Gene Expression workflow
- · Select Brain vs. Heart from the List Manager dialog (Figure 1) leaving the other options as defaults
- Select Create

🥵 List Manager					×
List	Spreadsheet Name	List Info Venn Diagram	ANOVA Streamlined	Advanced	
A	1 (Affy_miR_BrainHeart_ir	ainHeart_in Single factor: find genes that vary across all samples upon single factor			
В	2 (Affy_HuGeneST_BrainH	Name		Setting	# Pass
C	2/1 (ANOVAResults gene)	 Tissue 			
		Replicate			
		0			
		Contrast: find genes that change between two categories			
		Name	-	Setting	# Pass
		Brain vs. Heart		Have Any Change	✓ 420
		Configuration for "Brain	/s. Heart"		# Pass: 420
		Include size of the	hange Fol	d change > 2 OR Fold change < -2	2
		Include significance	of the change p-v	alue with FDR V < 0.05	
		420 genes passed the specified criteria. You are about to create a list of genes that Have Any Change in Brain relative to Heart with fdr (step up) < 0.05, Fold change > 2 or Fold change < - 2			
<	×	Save list as: Brain v	s. Heart Br	owse Create	Configure
				-	Close

Figure 3. Configuring the list manager dialog

A new list of 420 genes will be created as a child spreadsheet of 1 (ANOVAResults gene).

• Select Close to exit the List Manager dialog

Performing pathway enrichment analysis

- Select the new gene list, Brain vs. Heart
- Select Pathway Analysis from the Biological Interpretation section of the Gene Expression workflow
- Select Next > to continue with *Pathway Enrichment*

Pathway Enrichment is the only option available for a gene list. To learn more about the other option, Pathway ANOVA, see the Gene Ontology ANOVA tutorial, which follows the same procedure as Pathway ANOVA.

- Select Next > to continue with the Brain vs. Heart spreadsheet
- Select Next > to continue with default settings for Fisher's Exact test
- Select Next > to continue with Homo sapiens and 4. Gene Symbol as parameters

Partek Pathway will now open. If this is your first time using Partek Pathway on the selected species, Partek Pathway will automatically download the KEGG information needed for the analysis. Once the pathway enrichment calculation has been performed, a new spreadsheet, *Pathway-Enrichment.txt*, will be added as a child spreadsheet of *Brain vs. Heart* and Partek Pathway will launch (Figure 2).

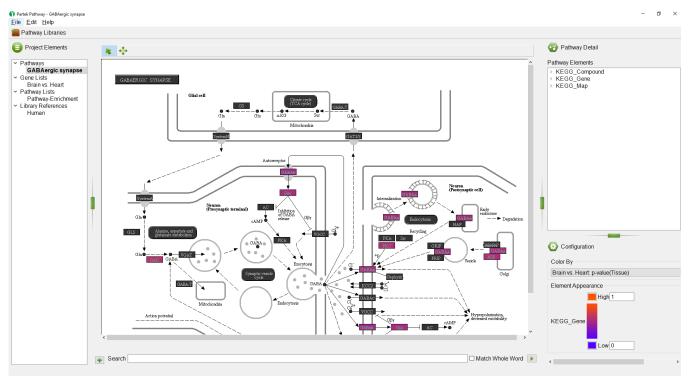


Figure 4. Partek Pathway displaying the most significantly enriched pathway from the gene list

The pathway currently displayed has the highest enrichment score. Both Partek Genomics Suite and Partek Pathway offer options for analyzing the results of pathway enrichment analysis. The next two sections of the user guide will show the options for analyzing the results of pathway enrichment in each program.

« Partek Pathway Analyzing pathway enrichment in Partek Genomics Suite »

Additional Assistance

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

