Gene Ontology (GO) Enrichment

With the GO Enrichment feature in Partek Genomics Suite, you can take a list of significantly expressed genes/transcripts and find GO terms that are significantly enriched within the list. For a detailed introduction to GO Enrichment, refer to the GO Enrichment User Guide (Help > On-line Tutorials > User Guides).

- Select the Diff_Exp_and_Alt_Splice spreadsheet from the spreadsheet tree
- Select Gene Set Analysis in the Biological Interpretation section of the RNA-Seq workflow (Figure 1)

Partek Genomics Suite - 1/Diff_Exp_and	_Alt_Splice (Diff E	xp and Alt Spli	ce.txt)							- 🗆 X
File Edit Transform View Stat Filter	Tools Wind	ow Custom	Help							
										Workflows RNA-Seq
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				•						Import and Manage Samples
🗉 1 (RNA-seq)	Current Selection	n 1								Add Sample Attributes
Alignment_Counts (RNA-seq_ali		1. Chromosome	2. Start	3. Stop	4. Strand	5. Transcript	6. Gene	7. chisq(DiffExpr)	8. 9. p-value(DiffExpr chi	Choose Sample ID Column
exon_reads (RNA-Seq_results.exc	1.	1	762971	794827	+	NR 047519	LINC01128	228.523	0 11	✓ QA/QC
exon_rpkm (RNA-Seq_results.exc	2.	1	762971	794827	+	NR 047521	LINC01128	27,4808	4.66763e-06 11	Alignments per Read
gene_reads (RNA-Seq_results.ge	3.	1	762971	794827	+	NR 047523	LINC01128	56,2006	3.80667e-12 11	✓ Analyze Known Genes
gene_rpkm (RNA-Seq_results.ge	4,	1	762971	778985	+	NR 047526	LINC01128	41.632	4.80245e-09 11	mRNA Quantification
ANOVA-1way (ANOVAResul	5.	1	910579	917498	-	 NM_001291366	PERM1	3734.54	0 91	Differential Expression Analysis
mapping_summary (RNA-Seq_re	6.	1	910579	917498	-	NM_001291367	PERM1	257.338	0 91	Differential Expression Analysis
transcript_reads (RNA-Seq_result	7.	1	934342	935553	-	NM_021170	HES4	20.7877	0.000116521 88	Alternative Splicing Analysis
transcripts (RNA-Seg results.tran	8.	1	934344	935553	-	NM_001142467	HES4	99.7966	1.71885e-21 88	Create Gene List
unexplained_regions (RNA-Seq_i	9.	1	1017198	1051737	-	NM_001330306	C1orf159	15.0462	0.00177761 10	Allele-Specific Analysis
	10.	1	1017198	1051737	-	NM_017891	C1orf159	14.9806	0.00183327 10	\sim Visualization
	11.	1	1109286	1133314	+	NM_001130045	TTLL 10	8.79841	0.0320947 6.5	Chromosome View
	12.	1	1138888	1142090	-	NM_004195	TNFRSF18	9.49271	0.023409 18	Cluster Based on Significant Genes
	13.	1	1152288	1167448	-	NM_016176	SDF4	876.451	0 17	
	14.	1	1152288	1167448	-	NM_016547	SDF4	129.146	8.2635e-28 17	
	15.	1	1189292	1209235	-	NM_058167	UBE2J2	12.1468	0.00689678 94	Gene Set Analysis
	16.	1	1189292	1209235	-	NM_194457	UBE2J2	59.968	5.97151e-13 94	Pathway Analysis
	17.	1	1189292	1209235	-	NM_194458	UBE2J2	59.9745	5.95234e-13 94	
	18.	1	1243960	1247058	+	NM_153339	PUSL1	54.3018	9.67473e-12 50	
	19.	1	1246965	1260068	-	NM_001256456	INTS11	15.0457	0.00177799 12	
	20.	1	1246965	1260068	-	NM_001256460	INTS11	129.706	6.25886e-28 12	
< > > <	Rows: 25384 C	olumns: 27 _K	1						>	✓ Related: Analyze a Partek Flow project
😮 Pr	ocessing									

Figure 7. Selecting Gene Set Analysis

• Select GO Enrichment in the Gene Set Analysis dialog (Figure 2)

• Select Next >

🤣 Gene Set Analysis	×
-Select the method of analysis	
○ Gene Set ANOVA	0
O Gene Set Enrichment Analysis (GSEA)	0
GO Enrichment	0
	Next > Cancel
	.:

Figure 8. Selecting the method of analysis

- Select the spreadsheet 1/Diff_Exp_and_Alt_Splice (Diff Exp and Alt Splice.txt) from the drop-down menu (Figure 3)
- Select Next >

🤣 Gene Set Analysis		×
-Select the spreadsheet that contains the genes you want to	test	
1/Diff_Exp_and_Alt_Splice (Diff Exp and Alt Splice.txt)		~
n.		
	< Back Next >	Cancel
		``
Figure 9. Selecting the spreadsheet that contains the genes you want to	test	

- Select Use Fisher's Exact test
 Select Invoke gene ontology browser on the result
 Set Restrict analysis to functional groups with more than _ genes to 2 (Figure 4)
 Select Next >

🤣 Gene Set Analysis	×
- Configure the parameters of the test	
Our State	
○ Use Chi-Square test	
Invoke gene ontology browser on the result	
Restrict analysis to functional groups with more than 2 genes	
Restrict analysis to functional groups with fewer than genes	0
-Result File	
GO-Enrichment.txt	Browse
< Back Next >	Cancel

Figure 10. GO Enrichment options

- Select Default mapping file (Figure 5)
 Select Next >

🤣 Gene Set Analysis	×
Select the method of mapping genes to gene sets	
Default mapping file	0
O Custom mapping file kegg_library.hsa	~
O Create a new mapping file from a spreadsheet	0
O Specify a Gene Matrix Transposed (GMT) file	0
O Specify a Gene Annotation (GAF) file	0
	< Back Next > Cancel
	•
rigure 11. Selecting the mapping file	

A *GO-Enrichment* spreadsheet, as well as a browser (Figure 6), will be generated with the enrichment score shown for each GO term. Browse through the results to find a functional group of interest by examining the enrichment scores. The higher the enrichment score, the more over represented this functional group is in the input gene list. Alternatively, you may use the Interactive filter on the GO-Enrichment spreadsheet to identify functional groups that have low p-values and perhaps a higher percentage of genes in the group that are present.



Figure 12. Viewing the Gene Ontology Browser

« Visualizing differential isoform expression Analyzing the unexplained regions spreadsheet »

Additional Assistance

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



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