

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)

The screenshot displays the Partek Genomics Suite interface. The main window shows a spreadsheet titled '1/Diff_Exp_and_Alt_Splice (Diff Exp and Alt Splice.txt)'. The spreadsheet has columns for '1. Chromosome', '2. Start', '3. Stop', '4. Strand', '5. Transcript', '6. Gene', '7. chisq(DiffExpr)', '8. p-value(DiffExpr)', and '9. chi sq'. The data is organized into rows, with the first row highlighted. The left sidebar shows a tree view of the RNA-Seq workflow, with 'Diff_Exp_and_Alt_Splice (Diff Exp)' selected. The right sidebar shows the 'RNA-Seq' workflow steps, including 'Import', 'QA/QC', 'Analyze Known Genes', 'Allele-Specific Analysis', 'Visualization', and 'Biological Interpretation'. The 'Biological Interpretation' section is expanded, showing 'Gene Set Analysis' and 'Pathway Analysis'. A mouse cursor is pointing at 'Gene Set Analysis'.

	1. Chromosome	2. Start	3. Stop	4. Strand	5. Transcript	6. Gene	7. chisq(DiffExpr)	8. p-value(DiffExpr)	9. chi sq
1.	1	762971	794827	+	NR_047519	LINC01128	228.523	0	11
2.	1	762971	794827	+	NR_047521	LINC01128	27.4808	4.66763e-06	11
3.	1	762971	794827	+	NR_047523	LINC01128	56.2006	3.80667e-12	11
4.	1	762971	778985	+	NR_047526	LINC01128	41.632	4.80245e-09	11
5.	1	910579	917498	-	NM_001291366	PERM1	3734.54	0	91
6.	1	910579	917498	-	NM_001291367	PERM1	257.338	0	91
7.	1	934342	935553	-	NM_021170	HES4	20.7877	0.000116521	88
8.	1	934344	935553	-	NM_001142467	HES4	99.7966	1.71885e-21	88
9.	1	1017198	1051737	-	NM_001330306	C1orf159	15.0462	0.00177761	10
10.	1	1017198	1051737	-	NM_017891	C1orf159	14.9806	0.00183327	10
11.	1	1109286	1133314	+	NM_001130045	TLL10	8.79841	0.0320947	6.5
12.	1	1138888	1142090	-	NM_004195	TNFRSF18	9.49271	0.023409	18
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
16.	1	1189292	1209235	-	NM_194457	UBE2J2	59.968	5.97151e-13	94
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

Figure 7. Selecting Gene Set Analysis

- Select **GO Enrichment** in the *Gene Set Analysis* dialog (Figure 2)
- Select **Next >**

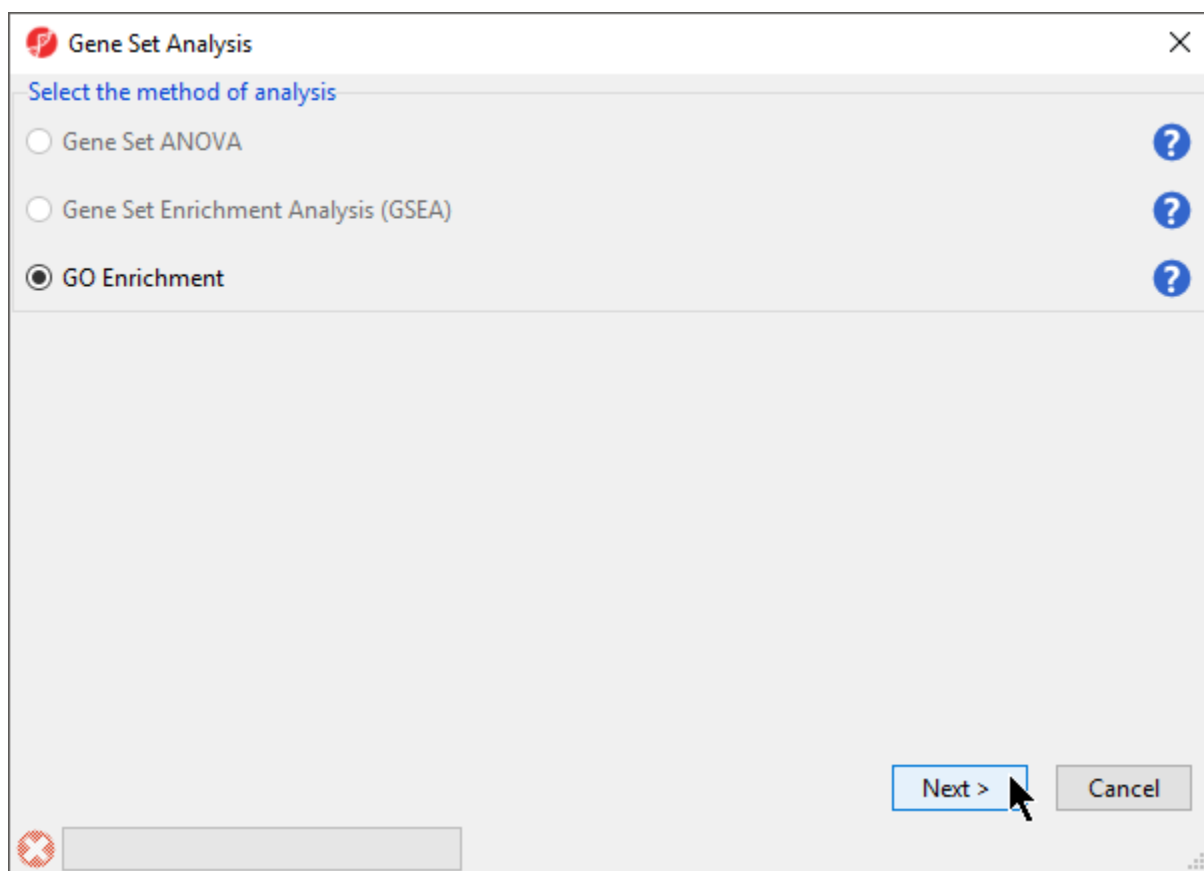


Figure 8. Selecting the method of analysis

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

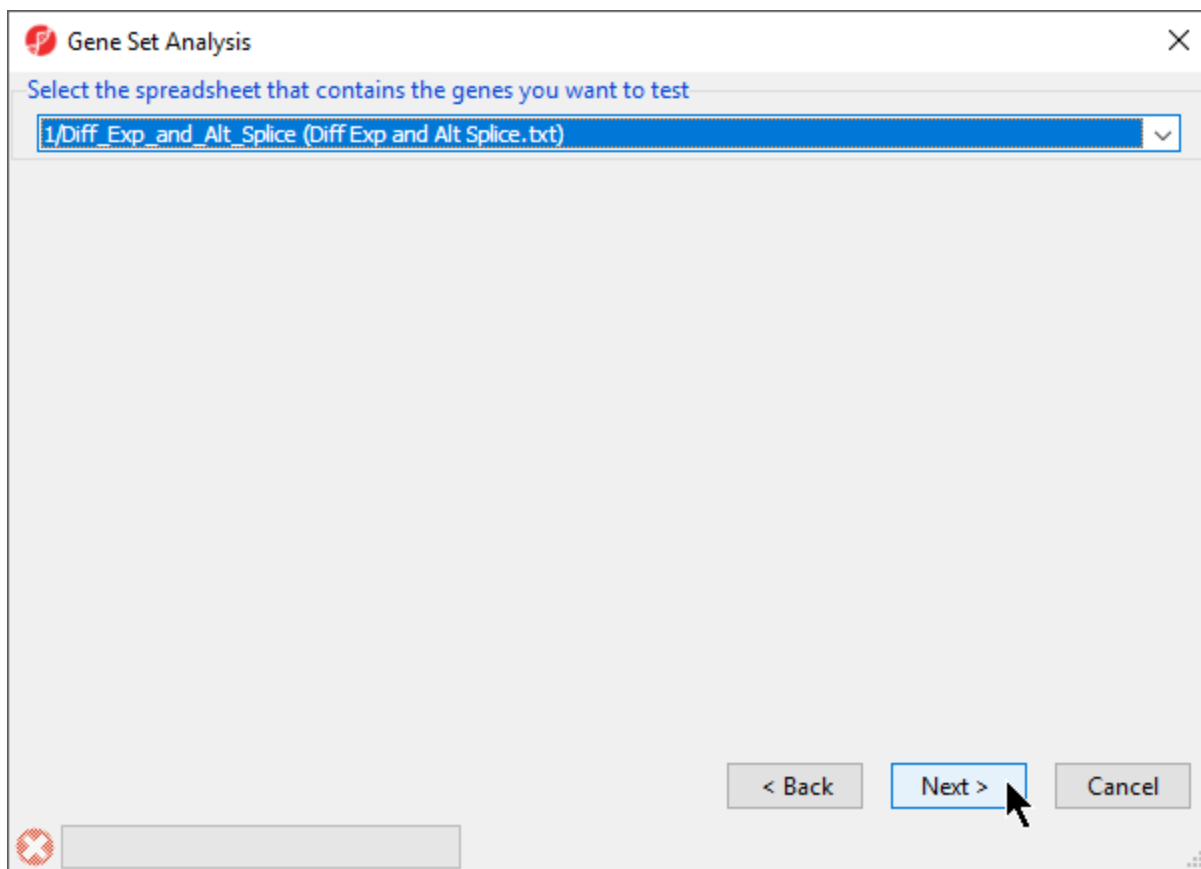
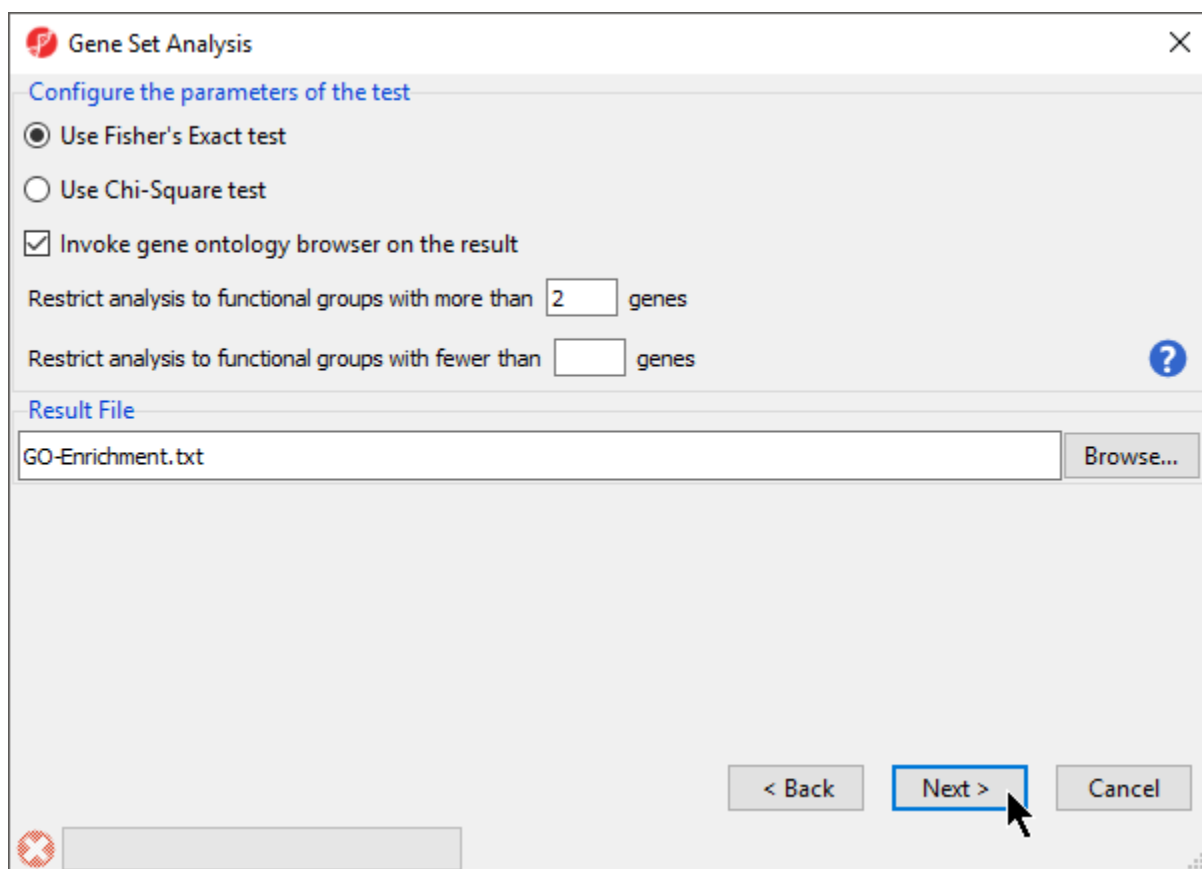


Figure 9. Selecting the spreadsheet that contains the genes you want to test

- 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 >**



The image shows a 'Gene Set Analysis' dialog box with a title bar containing a red circular icon with a white 'P' and a close button. The dialog is divided into two main sections. The top section, titled 'Configure the parameters of the test', contains two radio buttons: 'Use Fisher's Exact test' (selected) and 'Use Chi-Square test'. Below these is a checked checkbox labeled 'Invoke gene ontology browser on the result'. There are two input fields: 'Restrict analysis to functional groups with more than 2 genes' and 'Restrict analysis to functional groups with fewer than' followed by an empty field. A blue question mark icon is to the right of the second field. The bottom section, titled 'Result File', has a text field containing 'GO-Enrichment.txt' and a 'Browse...' button to its right. At the bottom of the dialog are three buttons: '< Back', 'Next >' (highlighted with a blue border and a mouse cursor), and 'Cancel'. A status bar at the very bottom shows a red 'X' icon in a square and a small help icon.

Gene Set Analysis

Configure the parameters of the test

☒ Use Fisher's Exact test

☐ Use Chi-Square test

☒ Invoke gene ontology browser on the result

Restrict analysis to functional groups with more than genes

Restrict analysis to functional groups with fewer than genes

Result File

GO-Enrichment.txt

Figure 10. GO Enrichment options

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

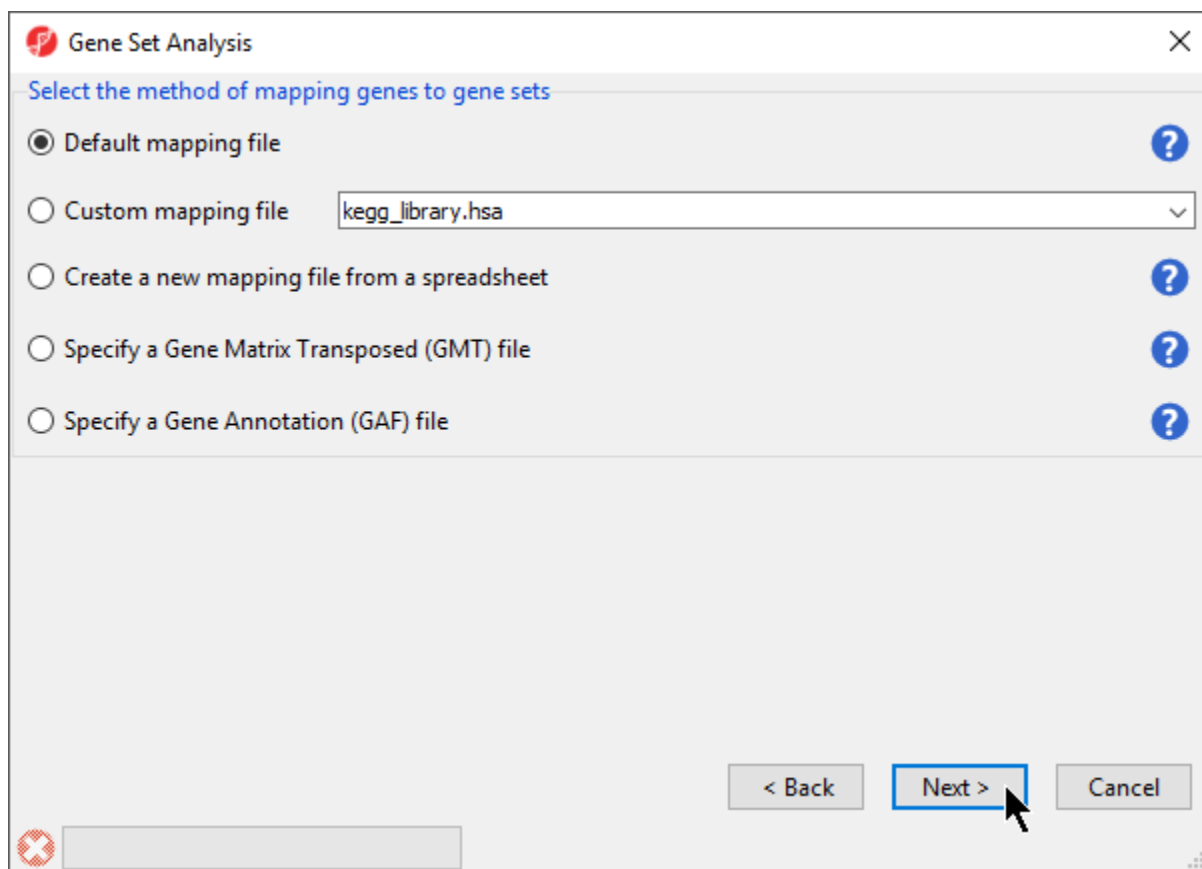


Figure 11. Selecting the mapping file

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.

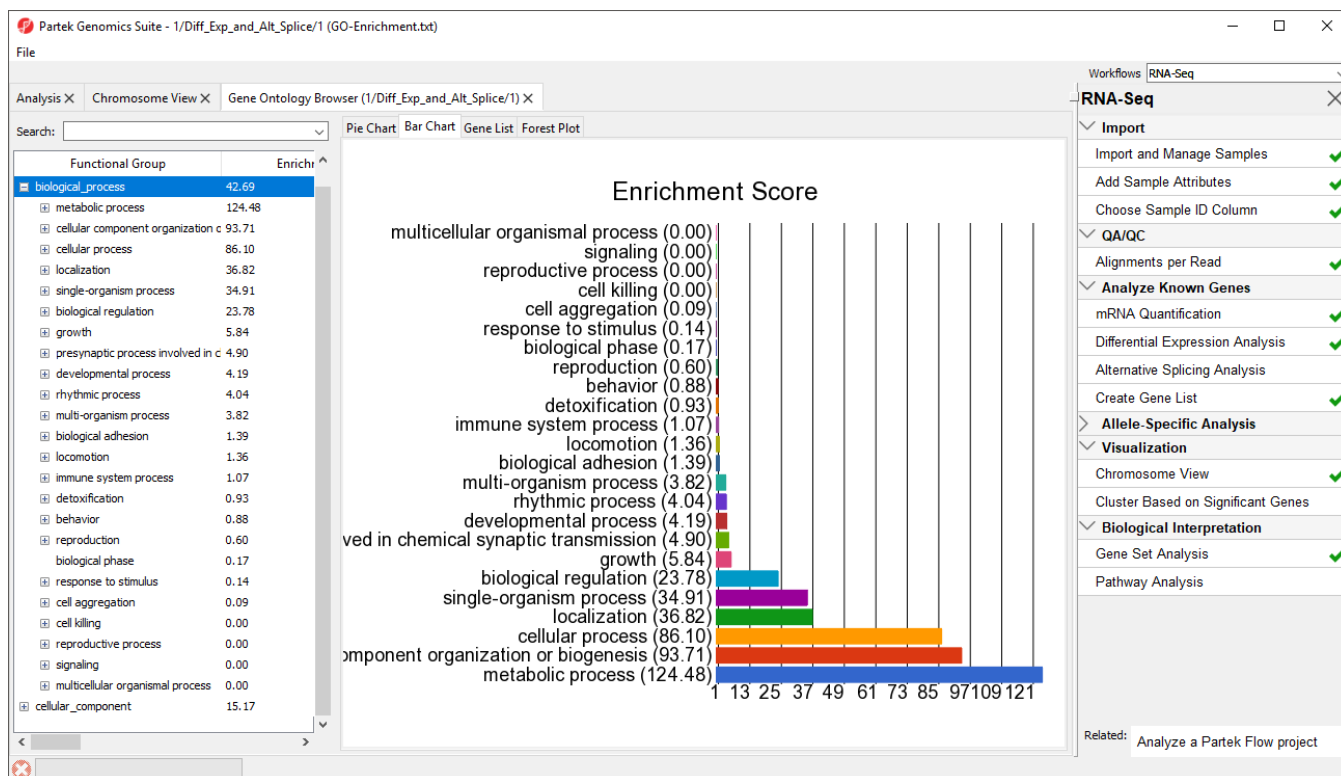


Figure 12. Viewing the Gene Ontology Browser

« 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.



★

Your Rating: ★★★★★

Results: ★★★★★ 33 rates

