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)

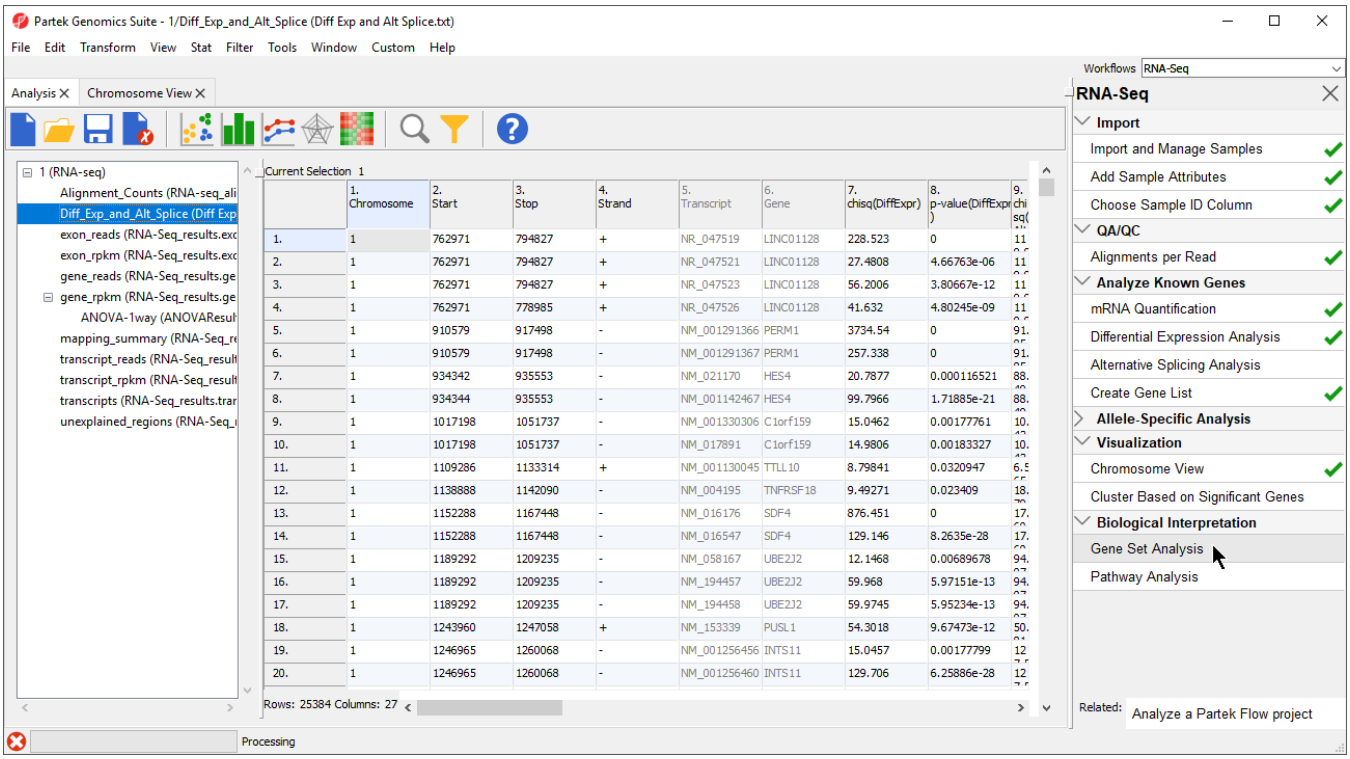

Figure 7. Selecting Gene Set Analysis

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

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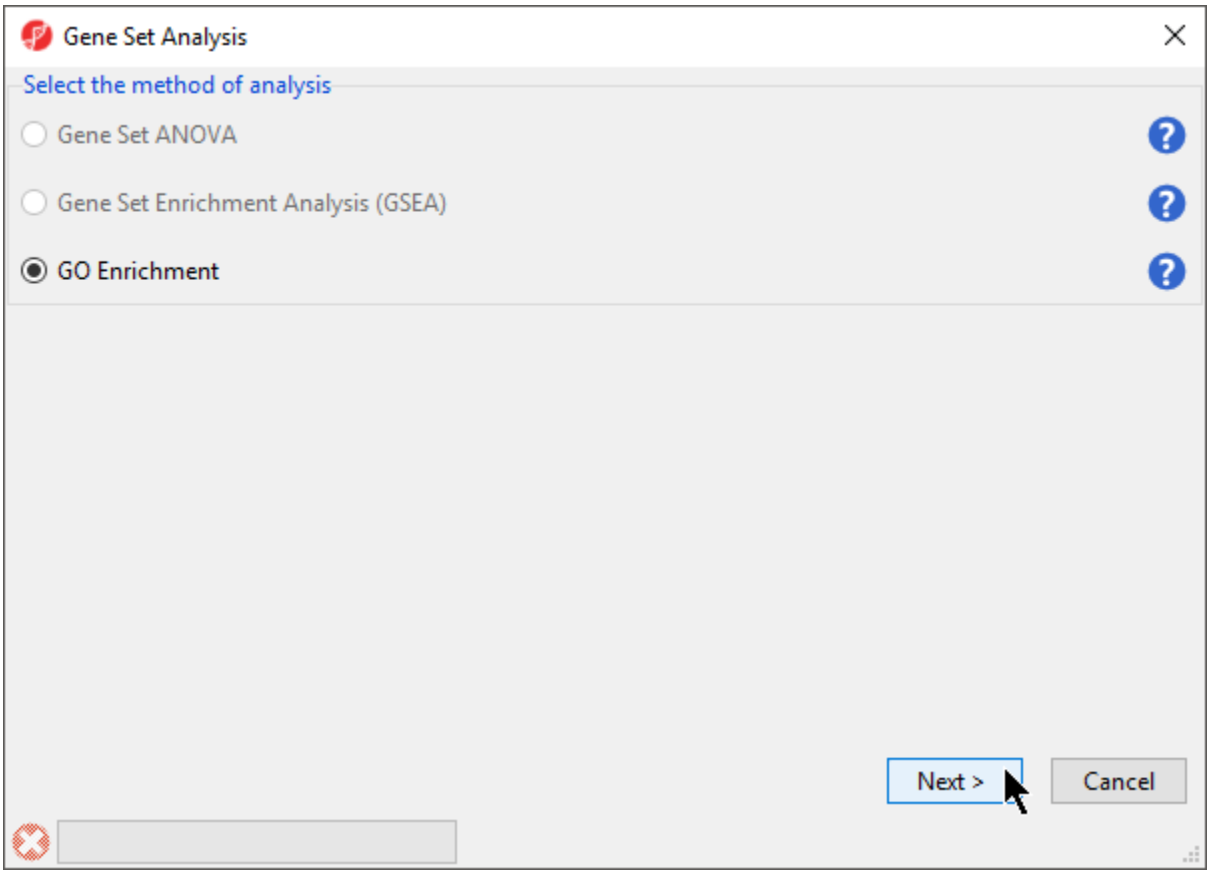

Figure 8. Selecting the method of analysis

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

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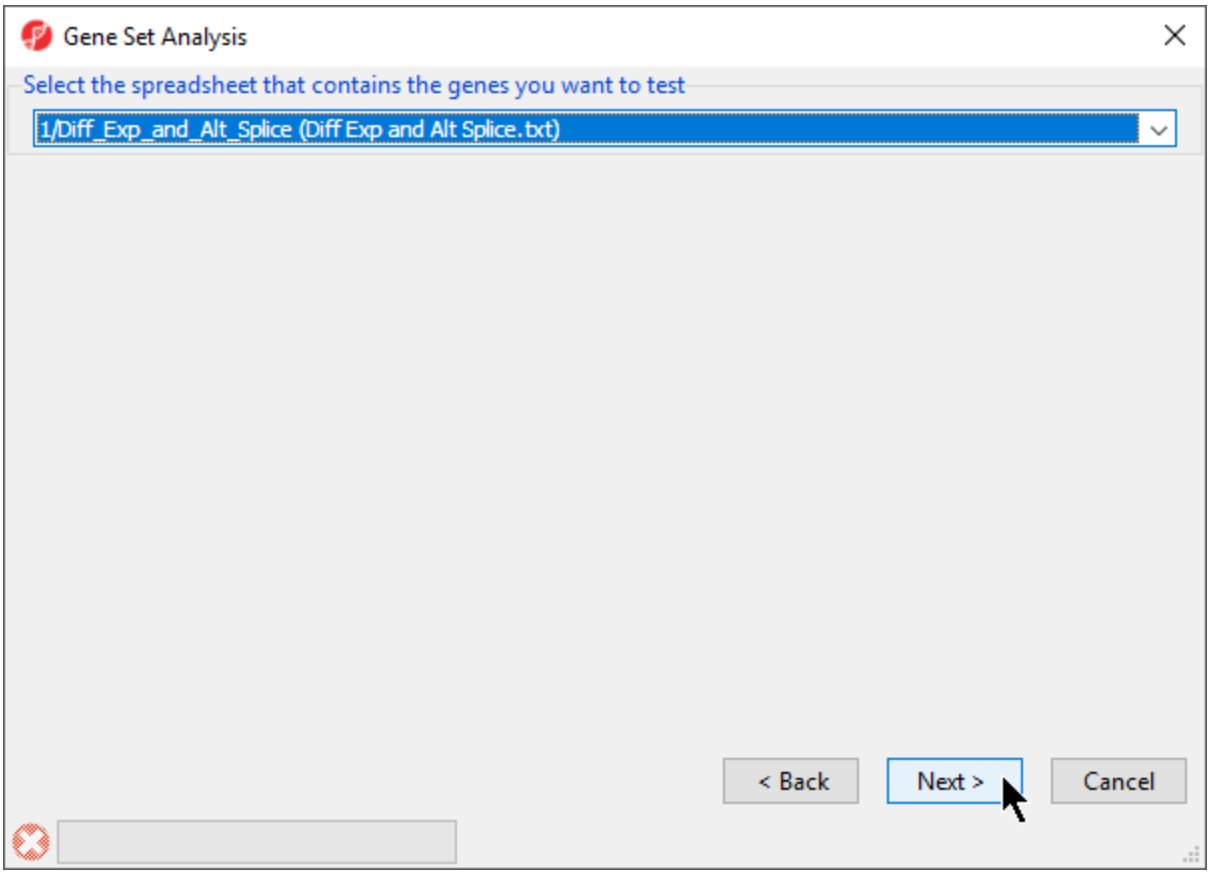

Figure 9. Selecting the spreadsheet that contains the genes you want to test

- 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 >**

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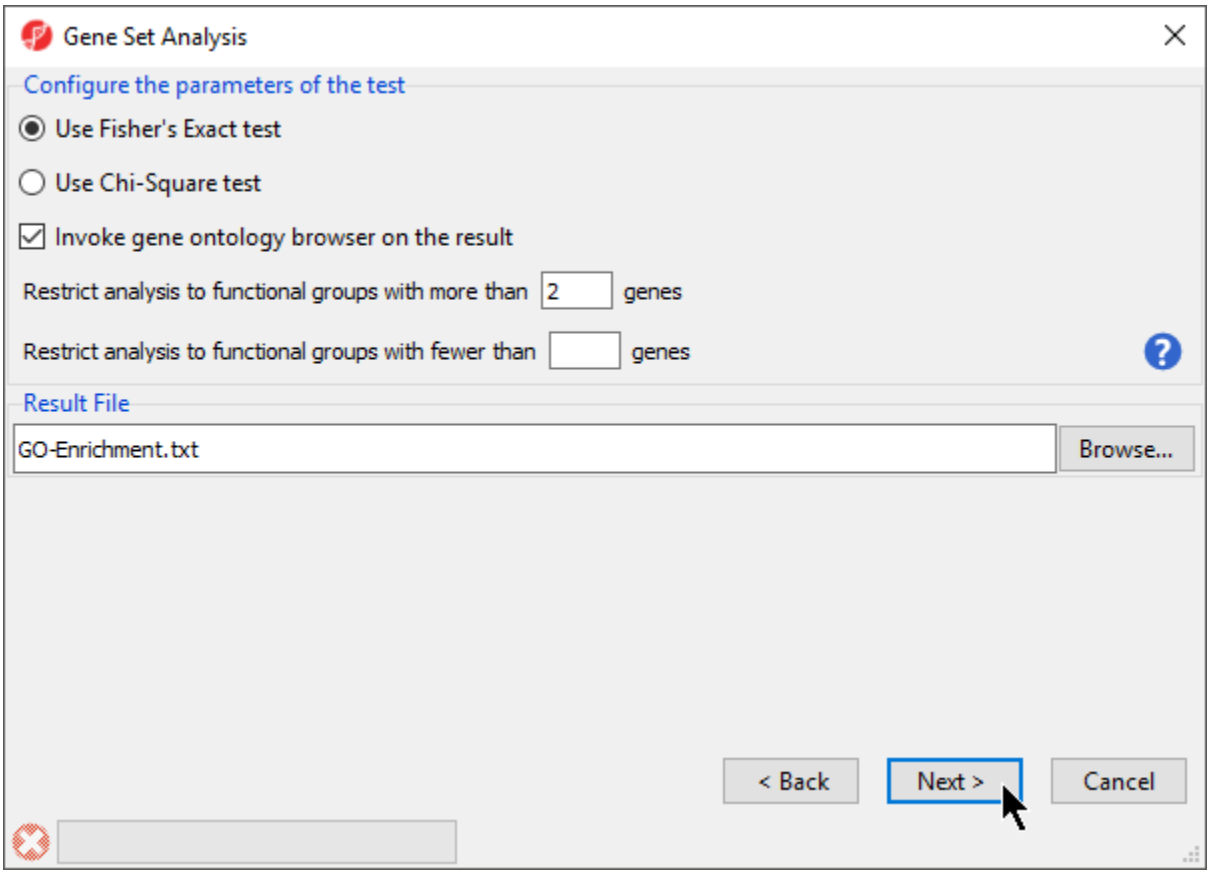

Figure 10. GO Enrichment options

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

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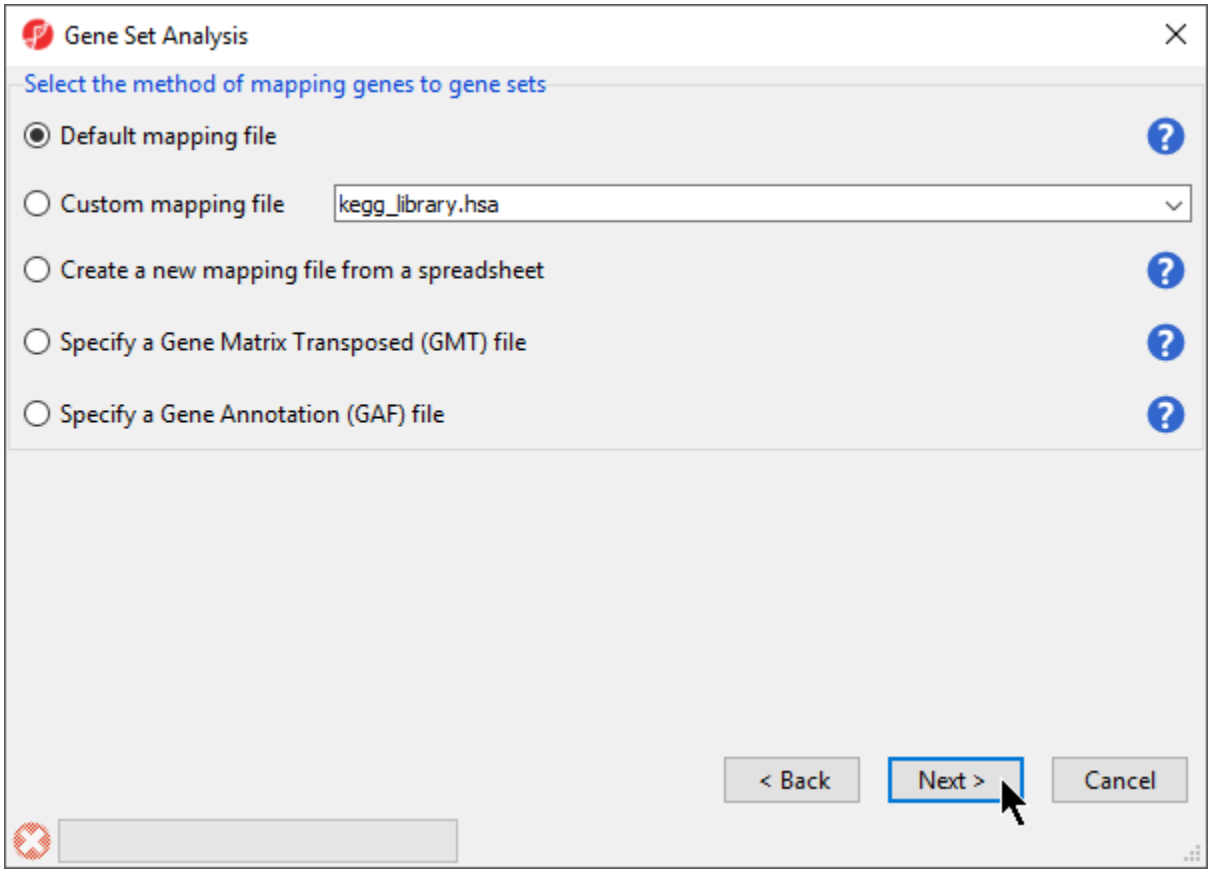

Figure 11. Selecting the mapping file

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.

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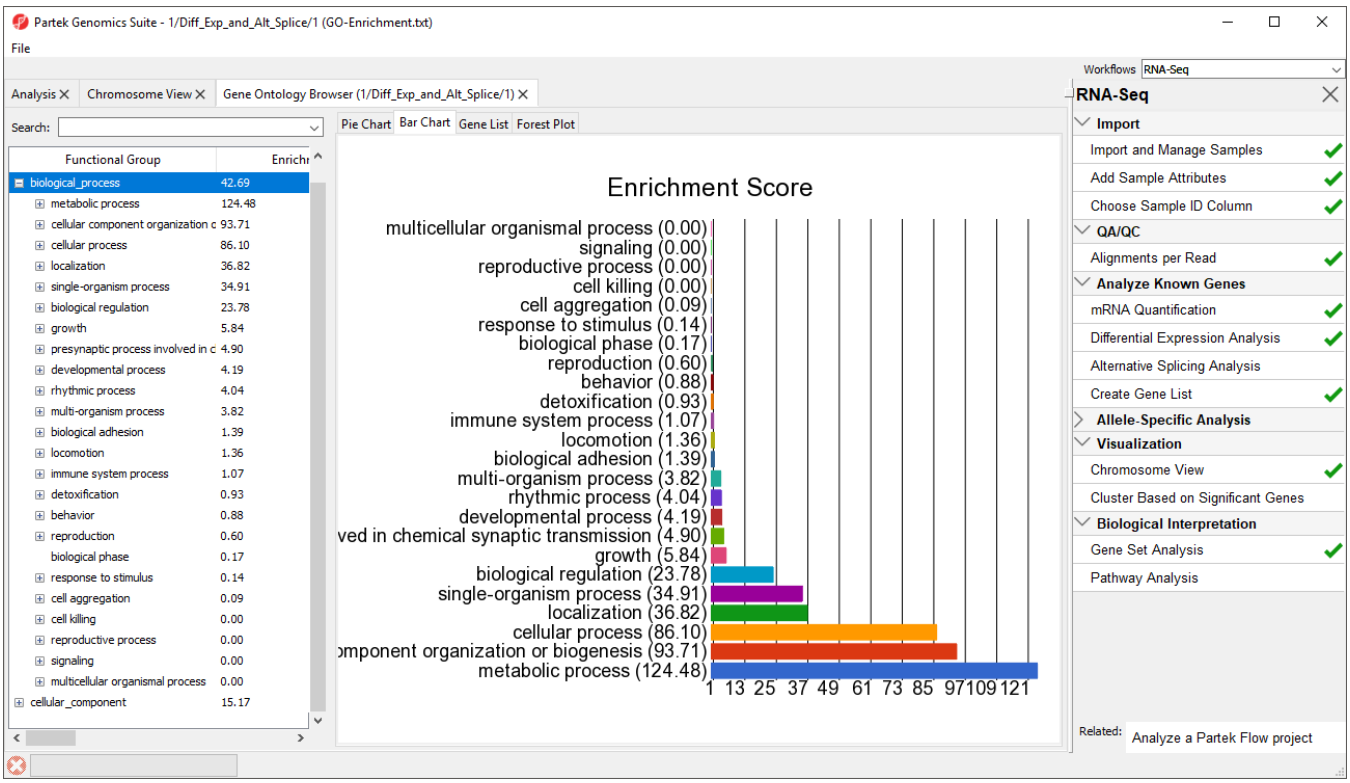

Figure 12. Viewing the Gene Ontology Browser

« Visualizing differential isoform expression Analyzing the unexplained regions spreadsheet »

Additional Assistance

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