

Gene Ontology analyser

RaNA-seq

2026-10-08 02:54:06.58930420875549

Functional enrichment analysis was performed with the goseq R package (Young, Wakefield, and Smyth 2010). 1303 genes with the lower p-value in the Differential Expression analysis were taken as input for this enrichment analysis. 157 Gene Ontology categories and 49 molecular pathways were statistically significant with a p-value cutoff less than 0.01.

References

Young, Matthew D, Matthew J Wakefield, and Gordon K Smyth. 2010. “goseq : Gene Ontology testing for RNA-seq datasets Reading data.” *Gene*, 1–21. <http://cobra20.fhcrc.org/packages/release/bioc/vignettes/goseq/inst/doc/goseq.pdf>.