Next-generation sequencing - analysis with DESeq2

Comparison of gene expression in DSCs compared to melanocytes - functional analysis

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# Resources and introduction

This document includes the functional analysis for the comparison of RNASeq data from dermal stem cells (DSCs) and Melanocytes. The exploratory data analysis and differential expression analysis are included in separate files. Statistical methods are described in a separate .docx file.

For additional info on analysis workflows check: DESEQ workflow: <https://www.bioconductor.org/packages/release/bioc/vignettes/DESeq2/inst/doc/DESeq2.html> <https://bioconductor.org/packages/release/workflows/vignettes/rnaseqGene/inst/doc/rnaseqGene.html>  
<https://www.bigbioinformatics.org/r-and-rnaseq-analysis> <https://github.com/bigbioinformatics/r-programming-and-rnaseq-workshop> ClusterProfiler: <https://pubmed.ncbi.nlm.nih.gov/34557778/>

# Overrepresentation analysis

## GO Terms

Gene sets that contain genes annotated by the same ontology term.

### GO: biological process

#### Top5 enriched pathways

