

The GEO2R analysis

ncbi.nlm.nih.gov/geo/geo2r?acc=GSE224758

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Use GEO2R to compare two or more groups of Samples in order to identify genes that are differentially expressed across experimental conditions. Results are presented as a table of genes ordered by significance. [Full instructions](#) [YouTube](#)

GEO accession **Set** Gene expression profiling of colon biopsies from ulcerative colitis patients and healthy volunteers RNA-seq Series analysis **BETA**

Samples Define groups Selected 17 out of 22 samples

GEO2R Options Profile graph R script

Apply adjustment to the P-values. [More...](#)

☐ Benjamini & Hochberg (False discovery rate)

☐ Benjamini & Yekutieli

☒ Bonferroni

☐ Hochberg

☐ Holm

☐ Hommel

Plot displays. [More...](#)

Significance level cut-off (enter number between 0 and 1)

Log 2 fold change threshold

Volcano and Mean-difference plot contrasts (select up to 5)

0 selected (clear)

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Reanalyze if you changed any options.

Visualization

GSE224758: UC vs Healthy

GSE224758: UC vs Healthy

Top differentially expressed genes

[Download full table](#) [Select columns](#)

Genes	padj	pvalue
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Venn diagram

Explore and download

GSE224758: DESeq2, Padj<0.01

UC vs Healthy

492

Total: 19671

GSE224758: Frequency of padj values

GSE224758: MA

Mean Symbol Description