Select contrasts to see results for

Choose an adjusted *p*-value cutoff

Choose a $\log_2$ fold-change cutoff

See more info and download data using the buttons

Search with gene attributes, e.g. gene symbols or annotations

Click to see exact $\log_2$ fold-changes in heatmap

Greater colour intensity means larger absolute $\log_2$ fold-change

Download all statistics

Select a gene and a contrast to visualise at Ensembl

Click to see MA plot and gene set enrichment summaries

Coloured boxes mean genes differentially expressed. Mouseover a box to see statistics for a gene.

Mouseover a gene to see GO and Interpro terms. Click a gene for more detailed information.