01_README.pdf

02_Summary_Table_*organism*.csv: GDS summary table for selected organism and keyword.

03_Results_sig_genes.csv: Summary table with number of significant studies per gene.

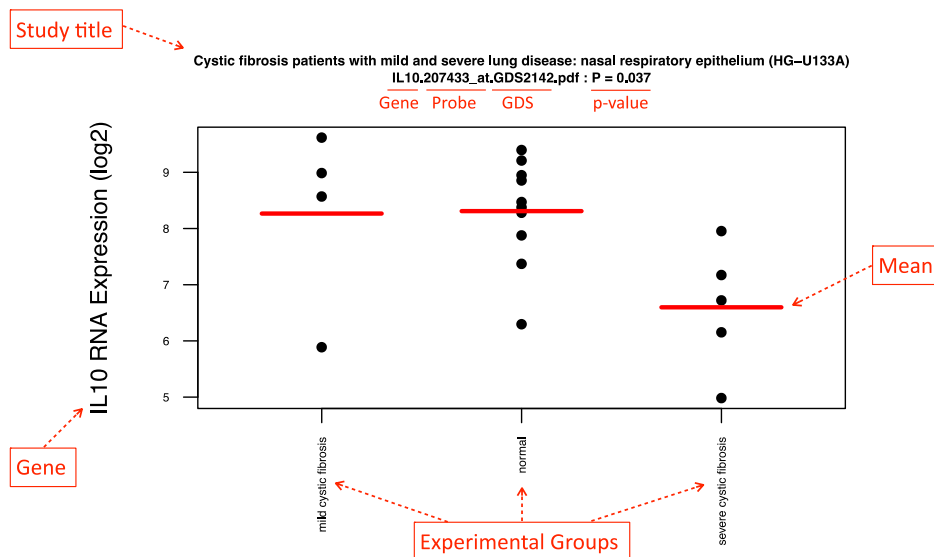04_Results_sig_studies.csv: Summary table with number of significant genes per study.

05_pValues_summary.csv: Unadjusted p-values for all mapped genes in studies with at least two samples per group. For genes with multiple probes the lowest p-value is shown. NA = gene was not mapped to a GDS or GDS had fewer than 2 Ns per group.

06_max_log2FC_summary.csv: Summary of largest absolute log2 fold change between the experimental groups for a mapped gene in a study with at least two samples per group. NA = gene was not mapped to a GDS or GDS had fewer than 2 Ns per group.

PDF files: Dot plots for probes that reached significance in ANOVA based on user-specified alpha level (default = 0.05). Red lines = mean.

CSV files: Expression values that were used to generate dot plots for significant probes.

Example output plot:

Cystic fibrosis patients with mild and severe lung disease: nasal respiratory epithelium (HG–U133A)
IL10.207433_at.GDS2142.pdf : P = 0.037

If these results are advancing your research, please cite our related publication:
https://academic.oup.com/bioinformatics/article-abstract/doi/10.1093/bioinformatics/btx452/3965322/ScanGEO-parallel-mining-of-highthroughput-gene