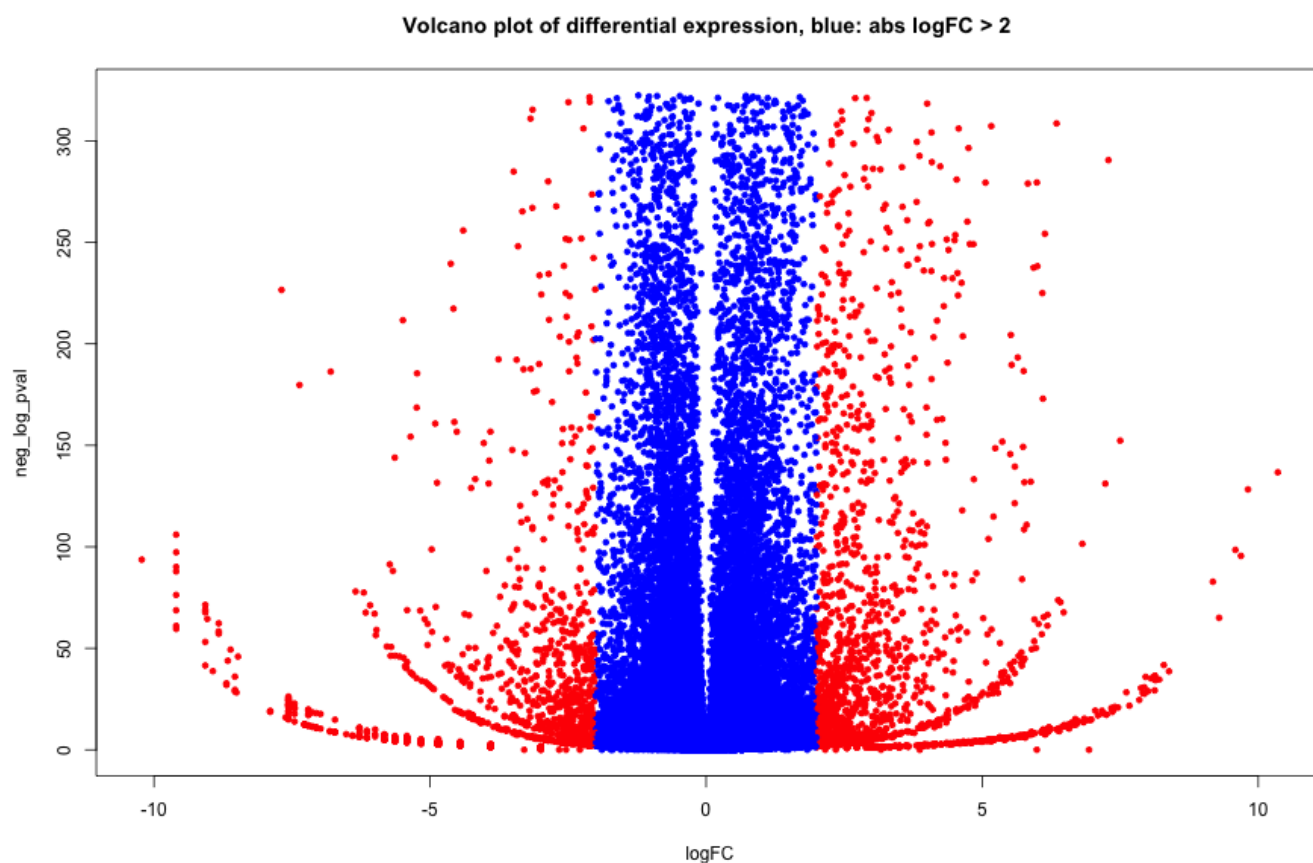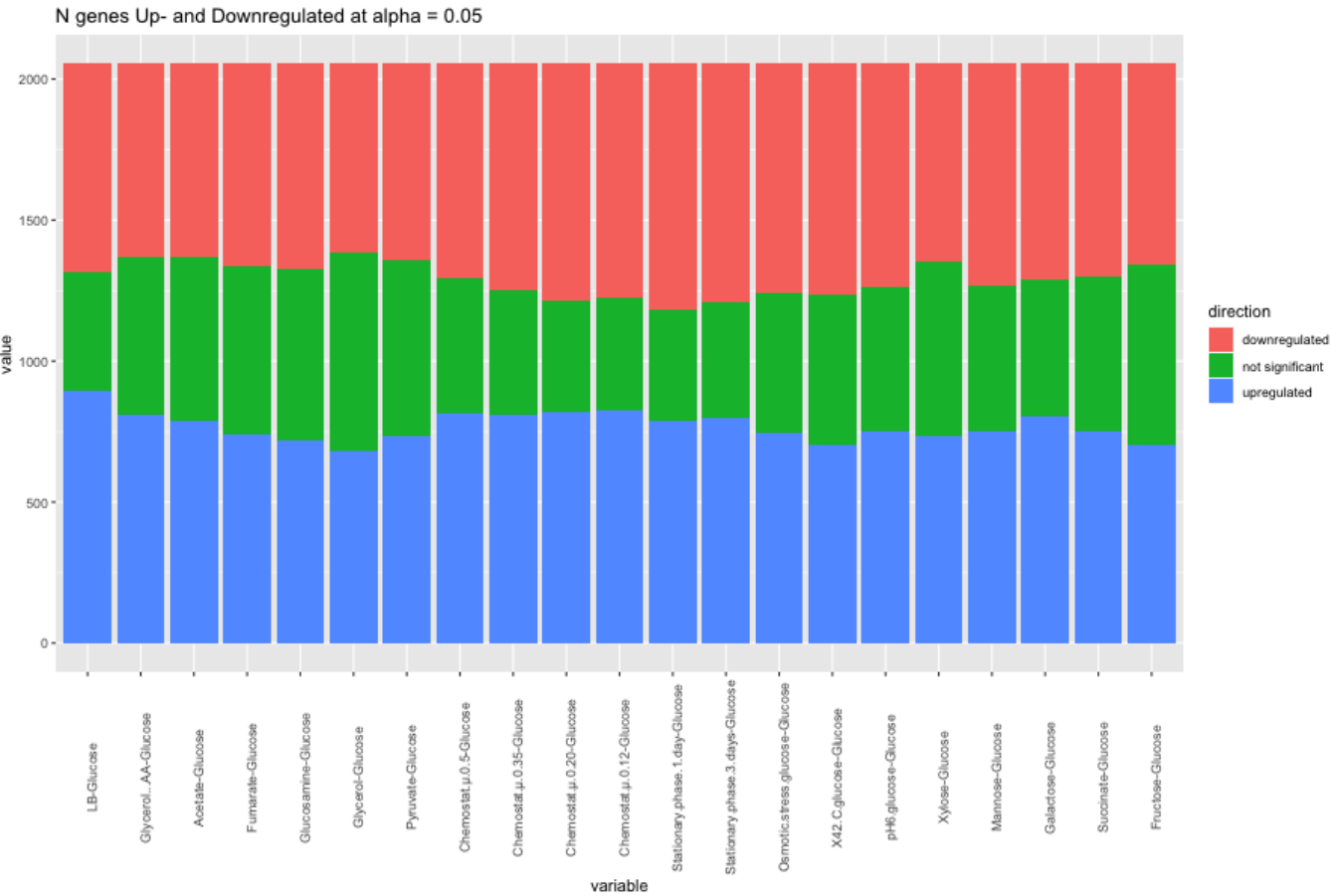# Differential expression analysis

Data

The data used in this notebook comes from the supplementary material of this paper: blabla It is resampled from counts that represent means and standard deviations.

Why EdgeR?

- Uses count data
- Normalization suited for count data, no between probe normalization as for

Results

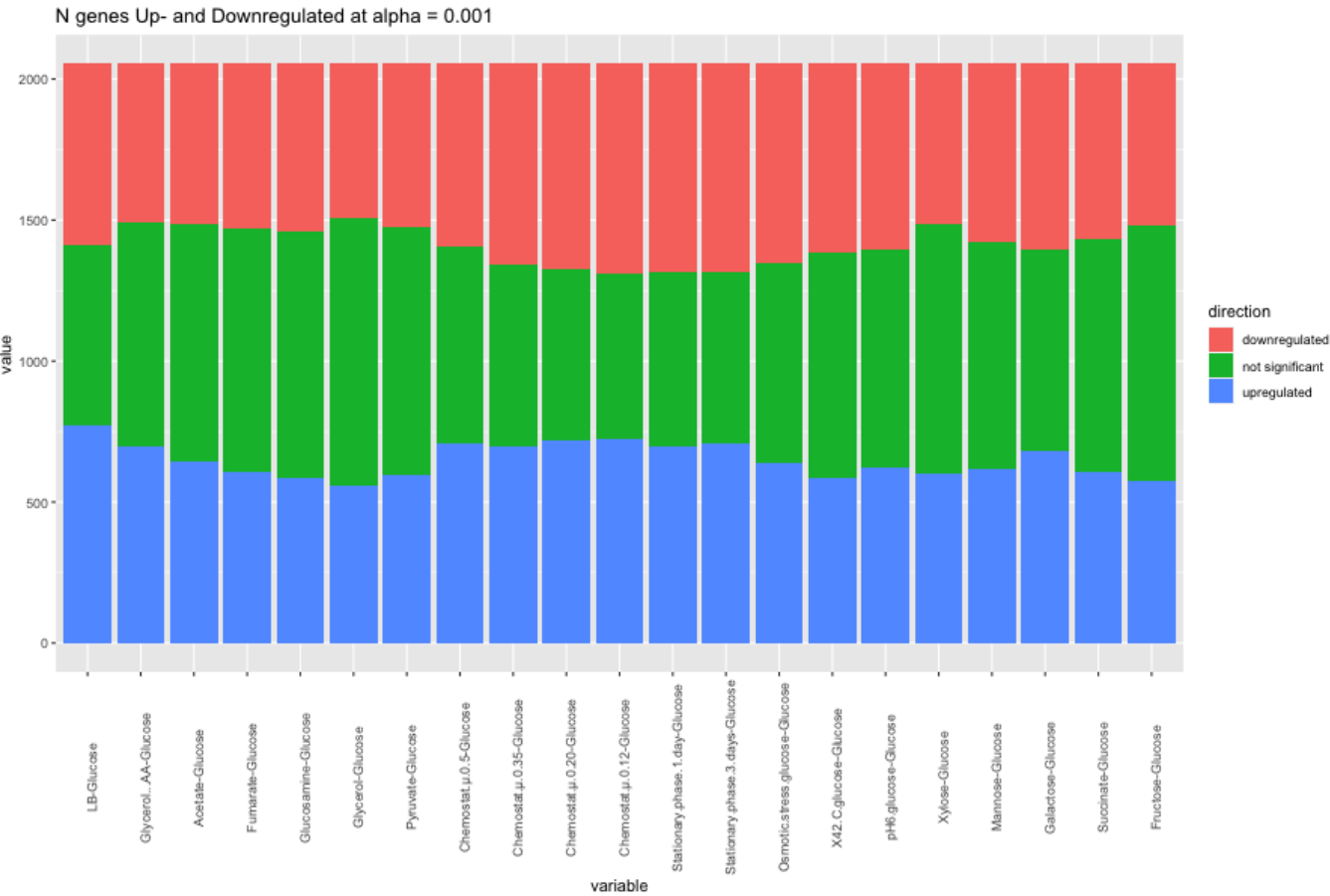Volcano plot of differential expression, blue: abs logFC > 2

Number of up- and downregulated genes decided by fishers combined method with an alpha cutoff of 0.05

Number of up- and downregulated genes decided by fishers combined method with an alpha cutoff of 0.01
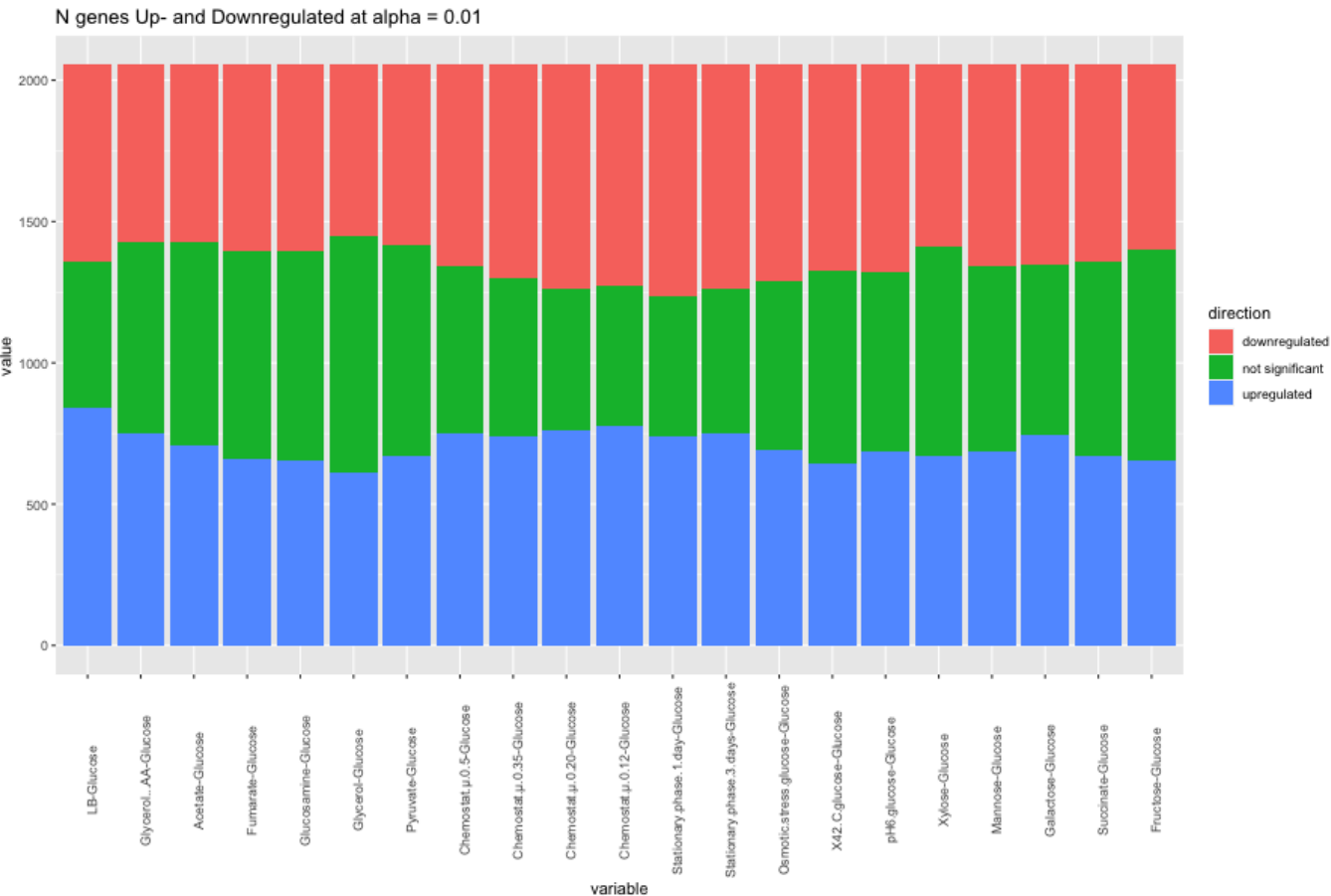
N genes Up- and Downregulated at alpha = 0.001

Number of up- and downregulated genes decided by fishers combined method with an alpha cutoff of 0.001

Go term analysis with piano

Why the given parameters?

- fishers combined test: includes the p-values found by differential expression analysis
-

Results

Significantly upregulated GO terms alpha = 0.05, log2fch = 2

Significantly downregulated GO terms alpha = 0.05, log2fch = 2

Significantly up-and downregulated GO terms alpha = 0.01, log2fch = 2