

# Differential expression analysis

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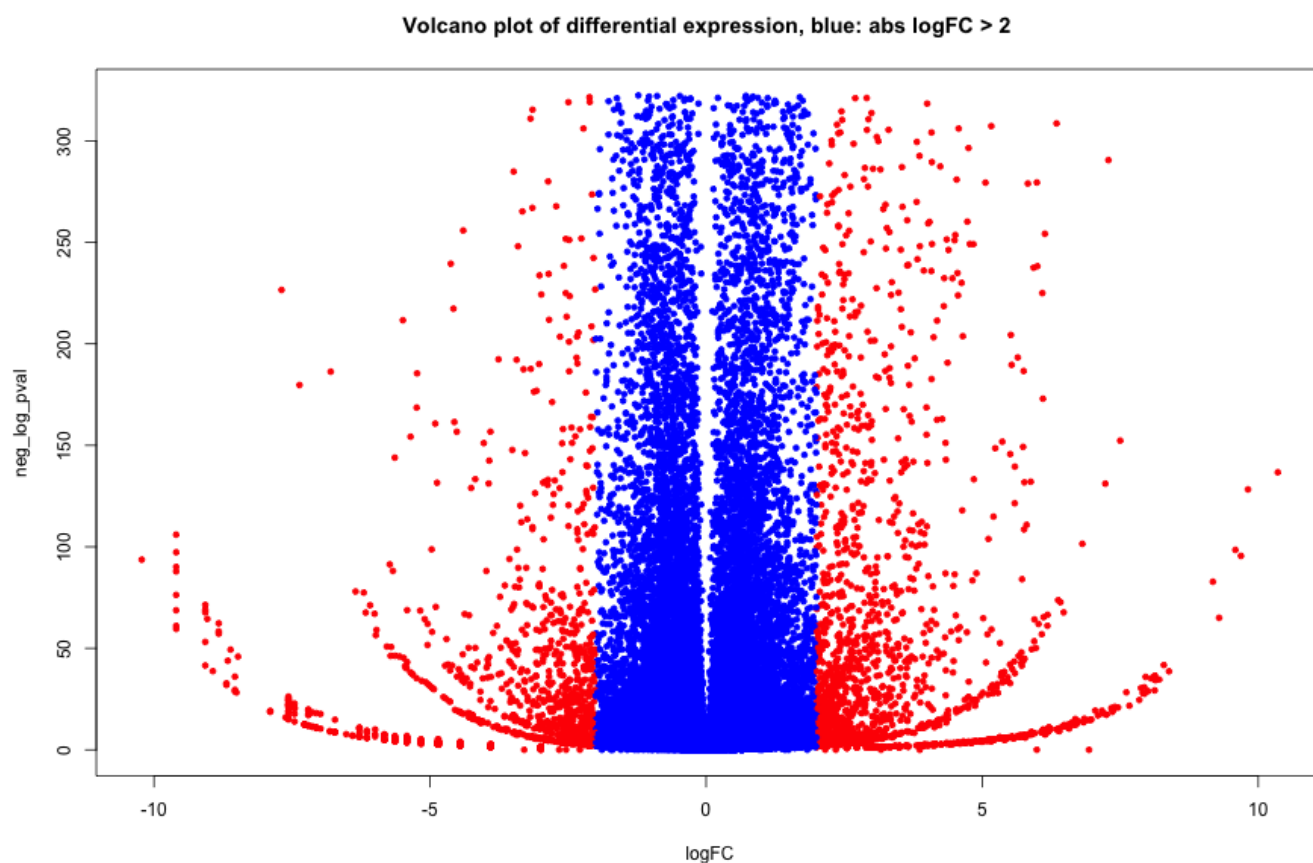
## Data

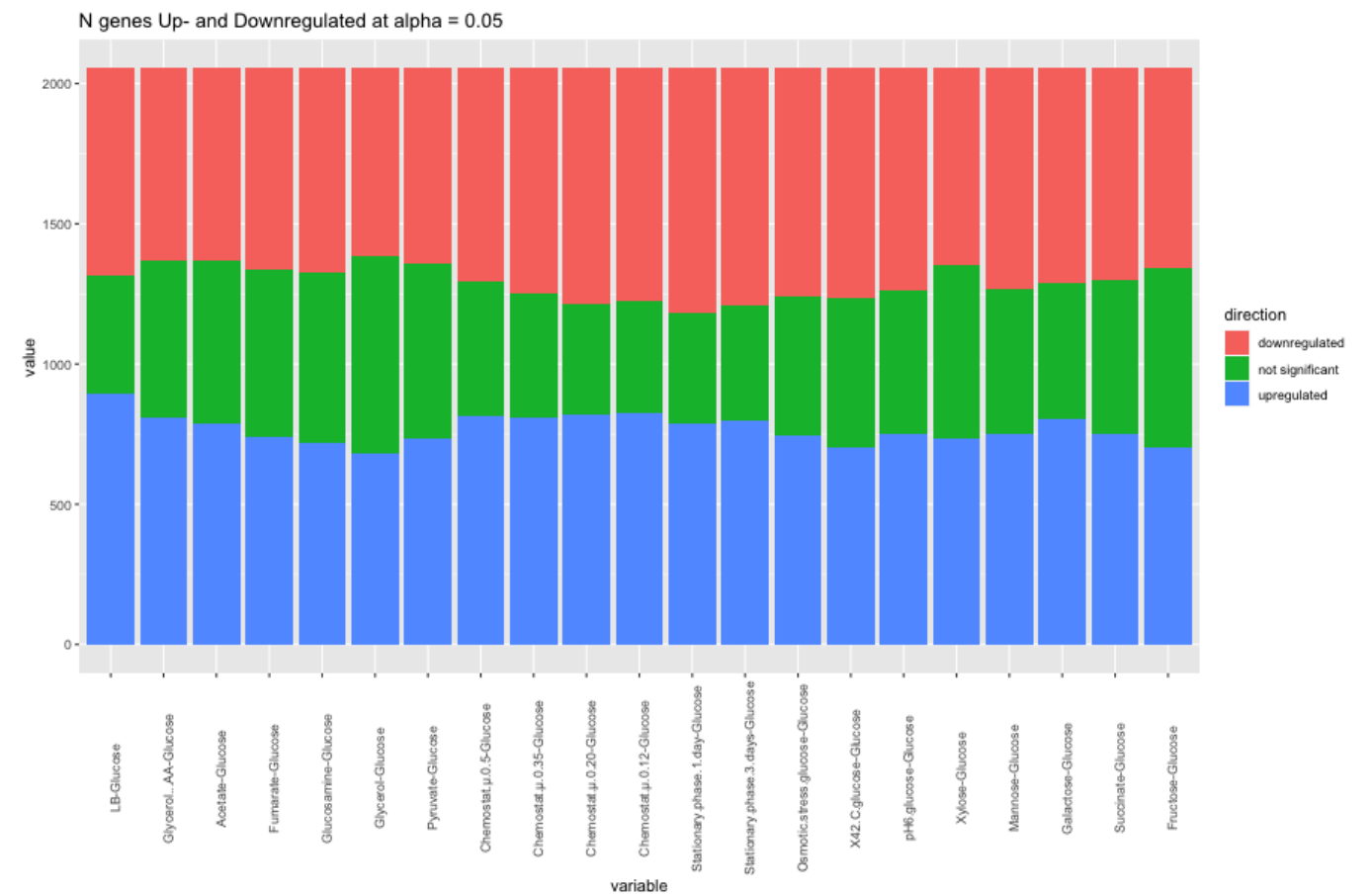
The data used in this notebook comes from the supplementary material of this paper: blabla It is resampled from counts that represent means and standard deviations.

## Why EdgeR?

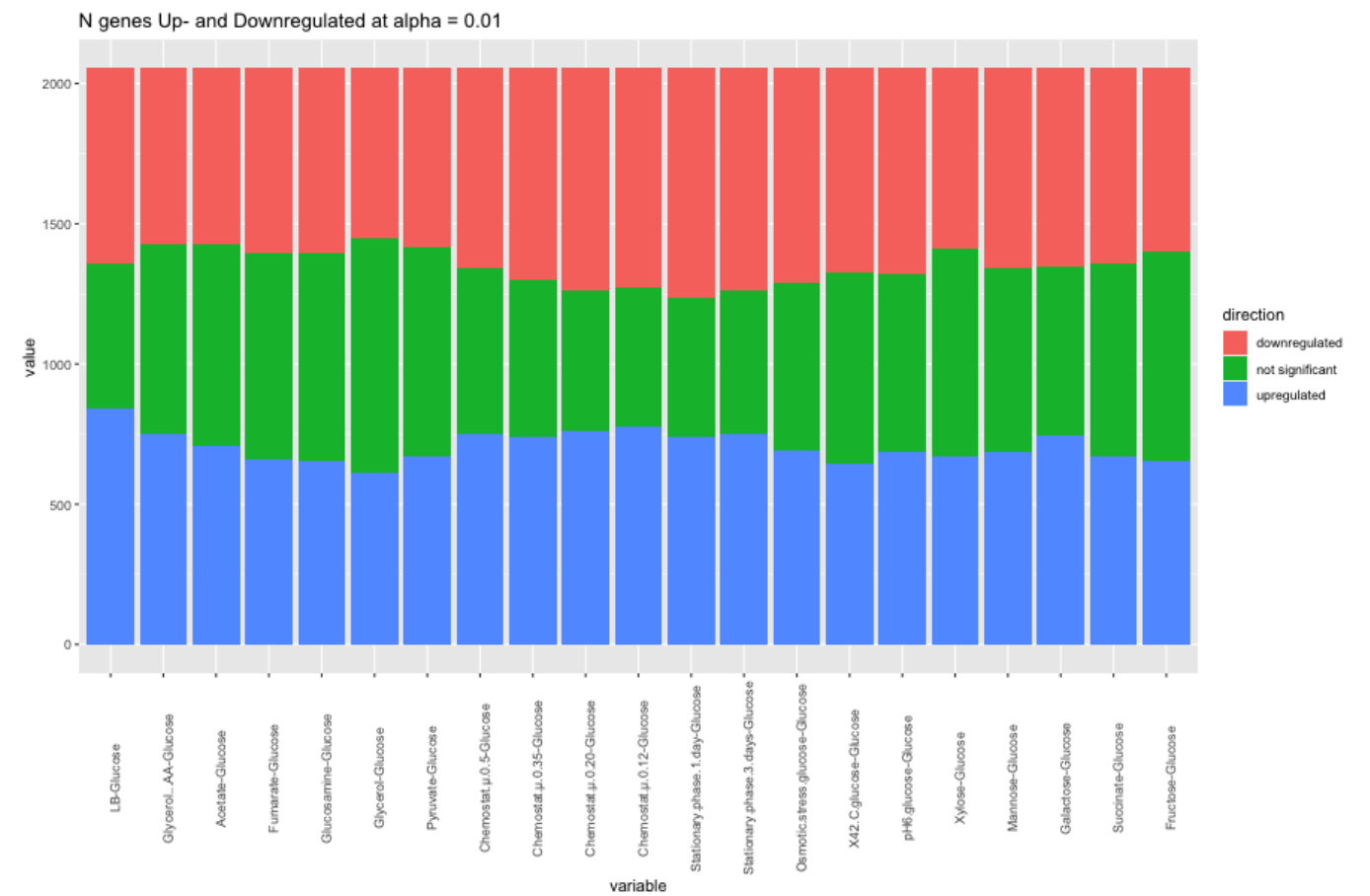
- Uses count data
- Normalization suited for count data, no between probe normalization as for

## Results

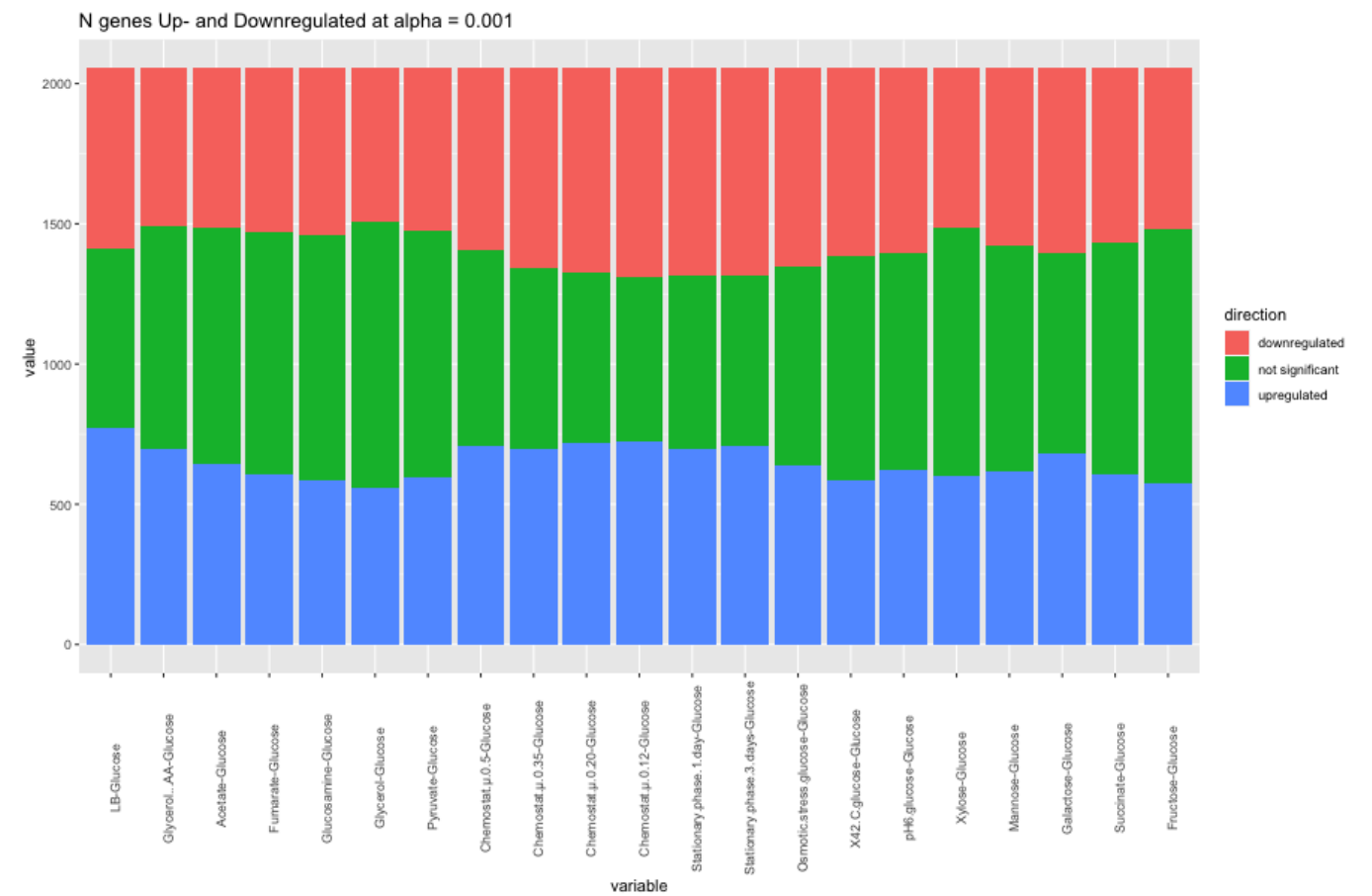




Number of up- and downregulated genes decided by fishers combined method with an alpha cutoff of 0.05



Number of up- and downregulated genes decided by fishers combined method with an alpha cutoff of 0.01



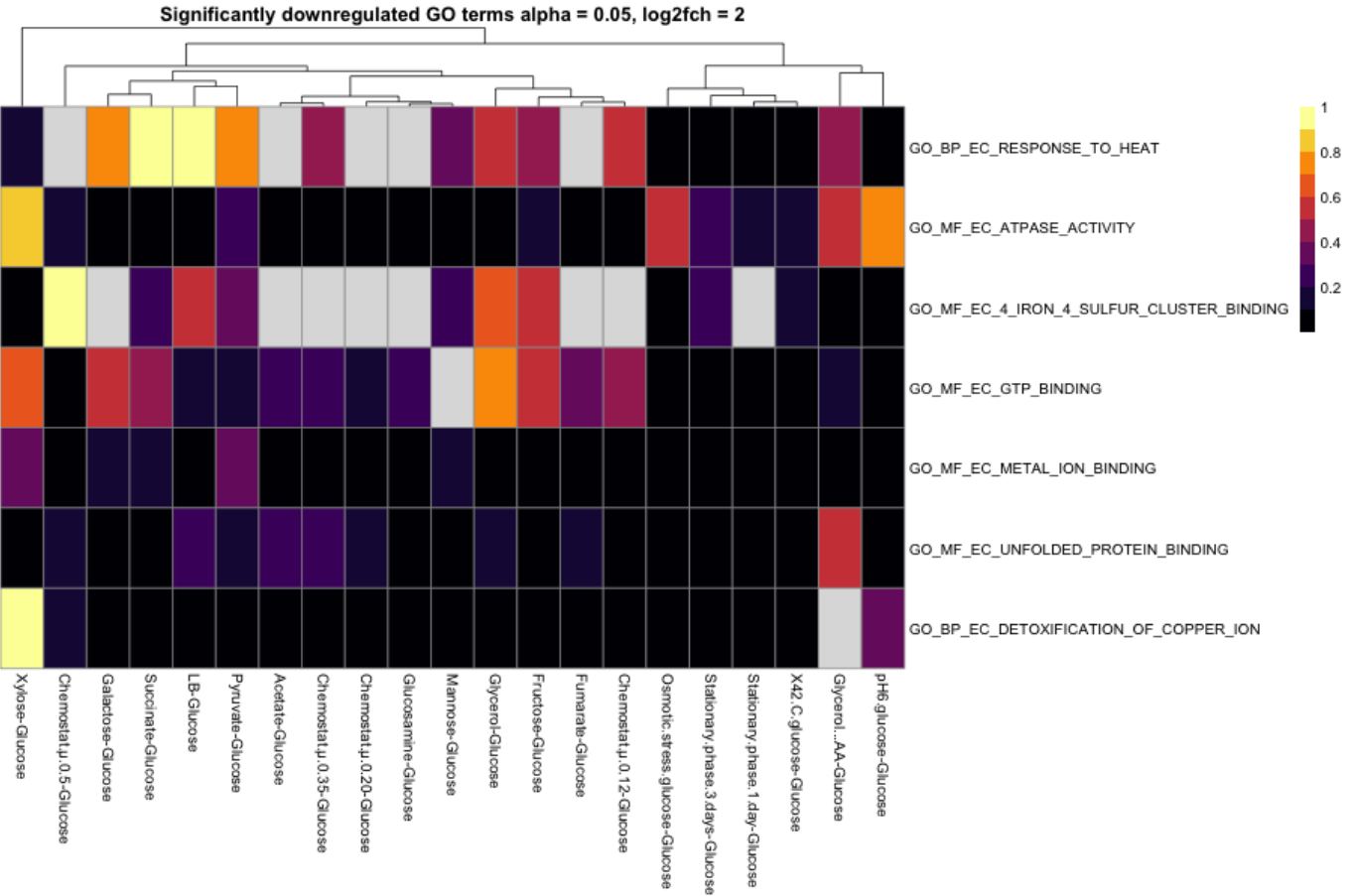
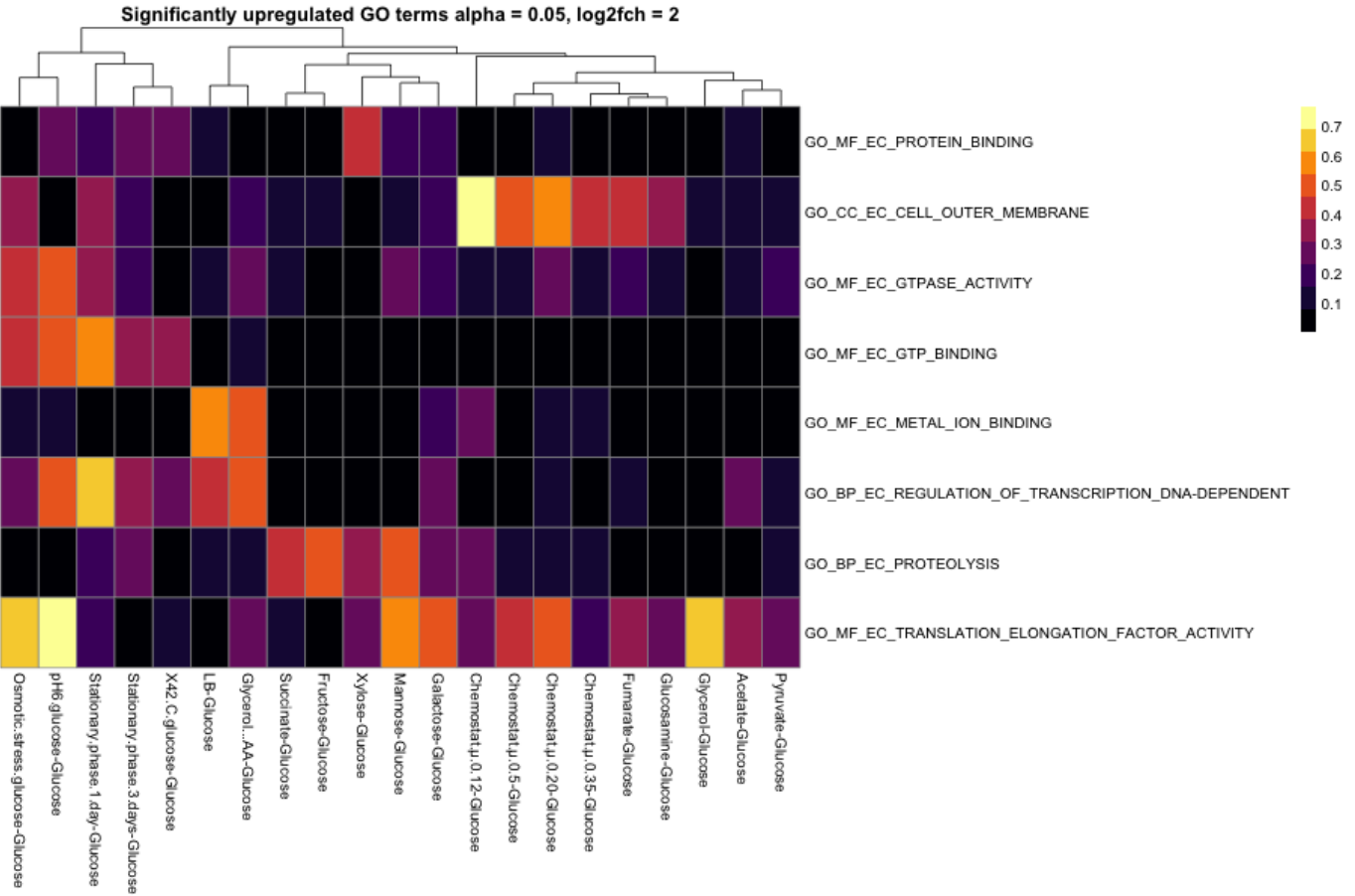
Number of up- and downregulated genes decided by fishers combined method with an alpha cutoff of 0.001

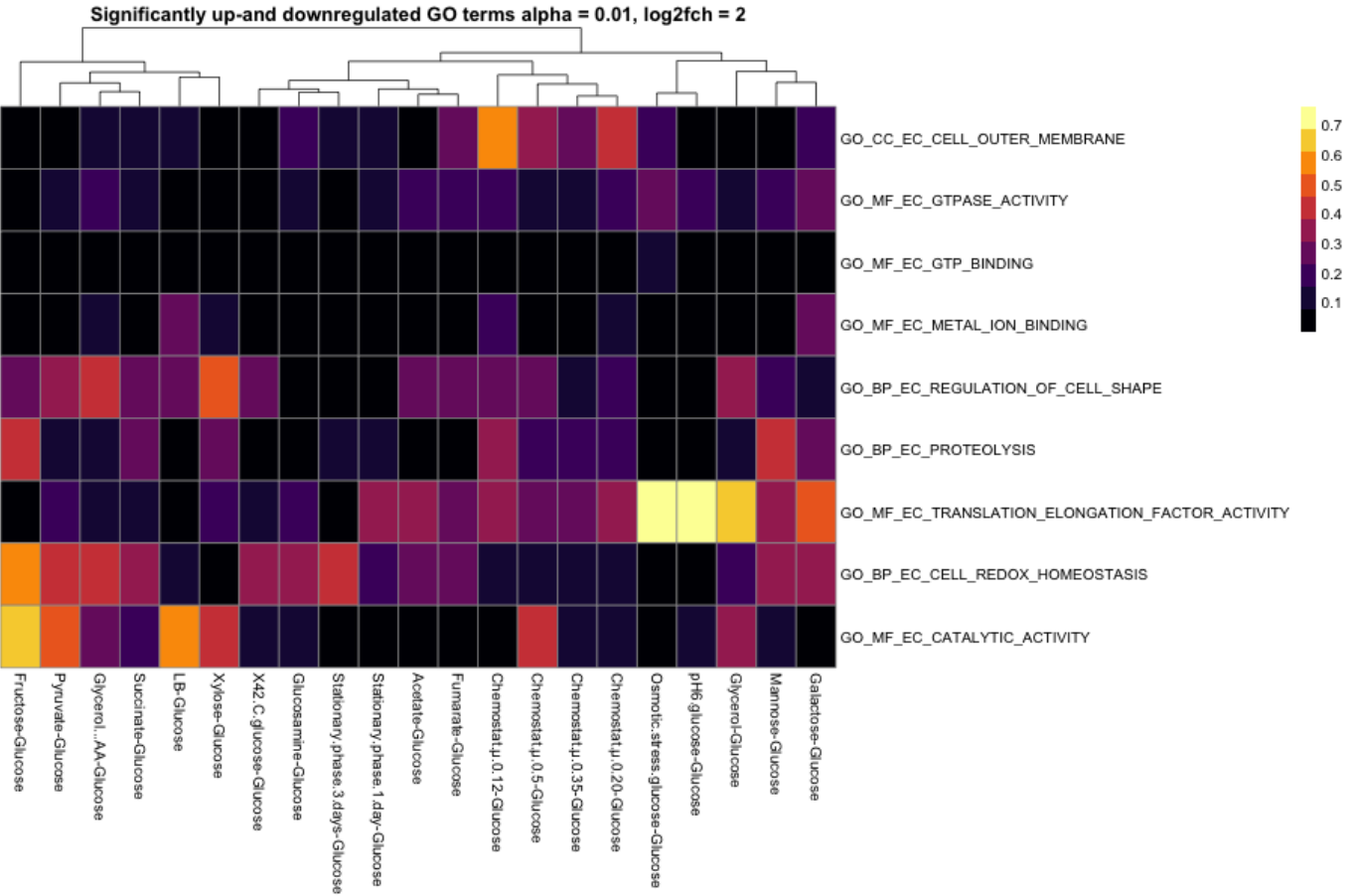
# Go term analysis with piano

## Why the given parameters?

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





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