

# Differential expression analysis

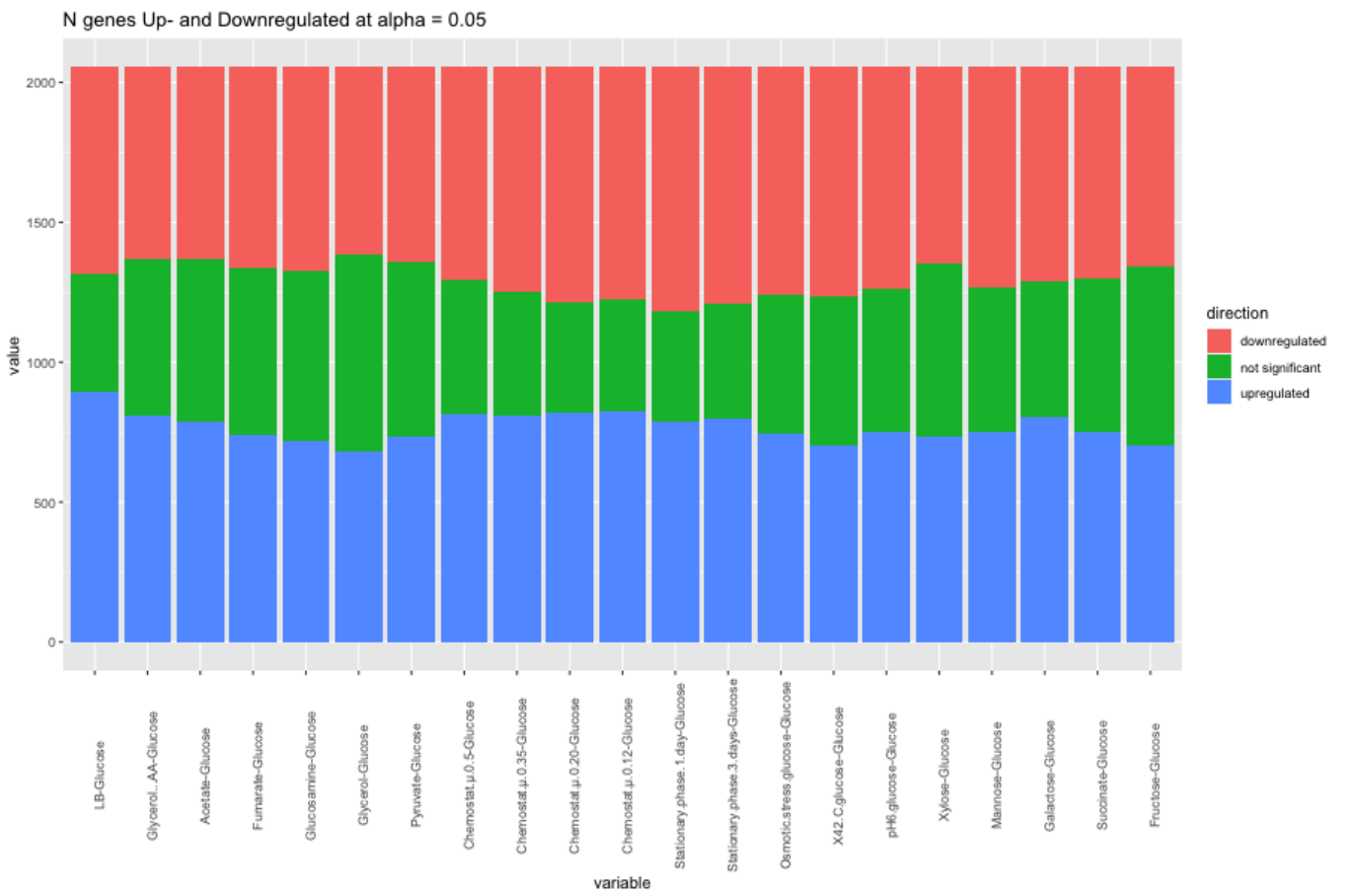
## Data

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.

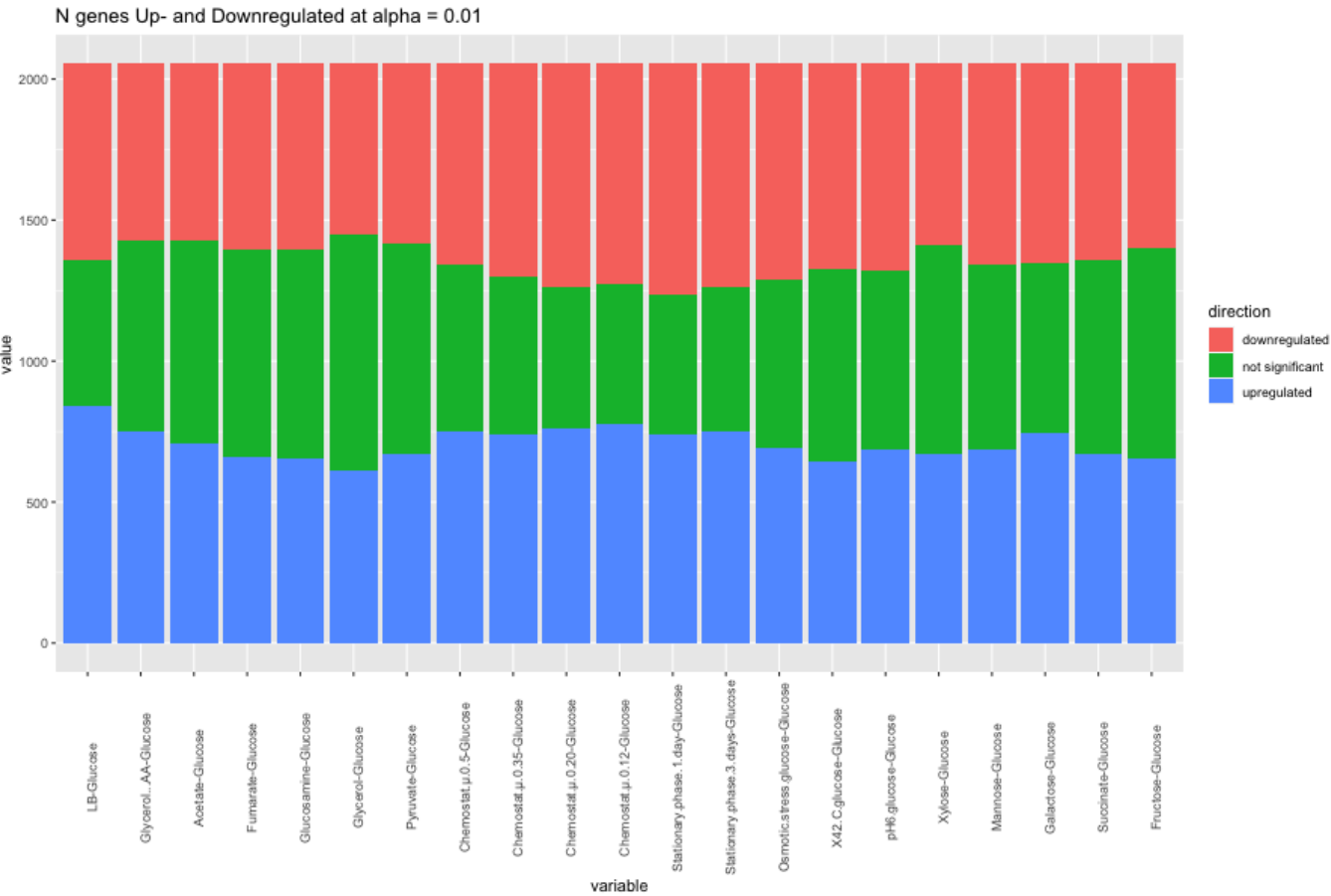
## Why EdgeR?

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

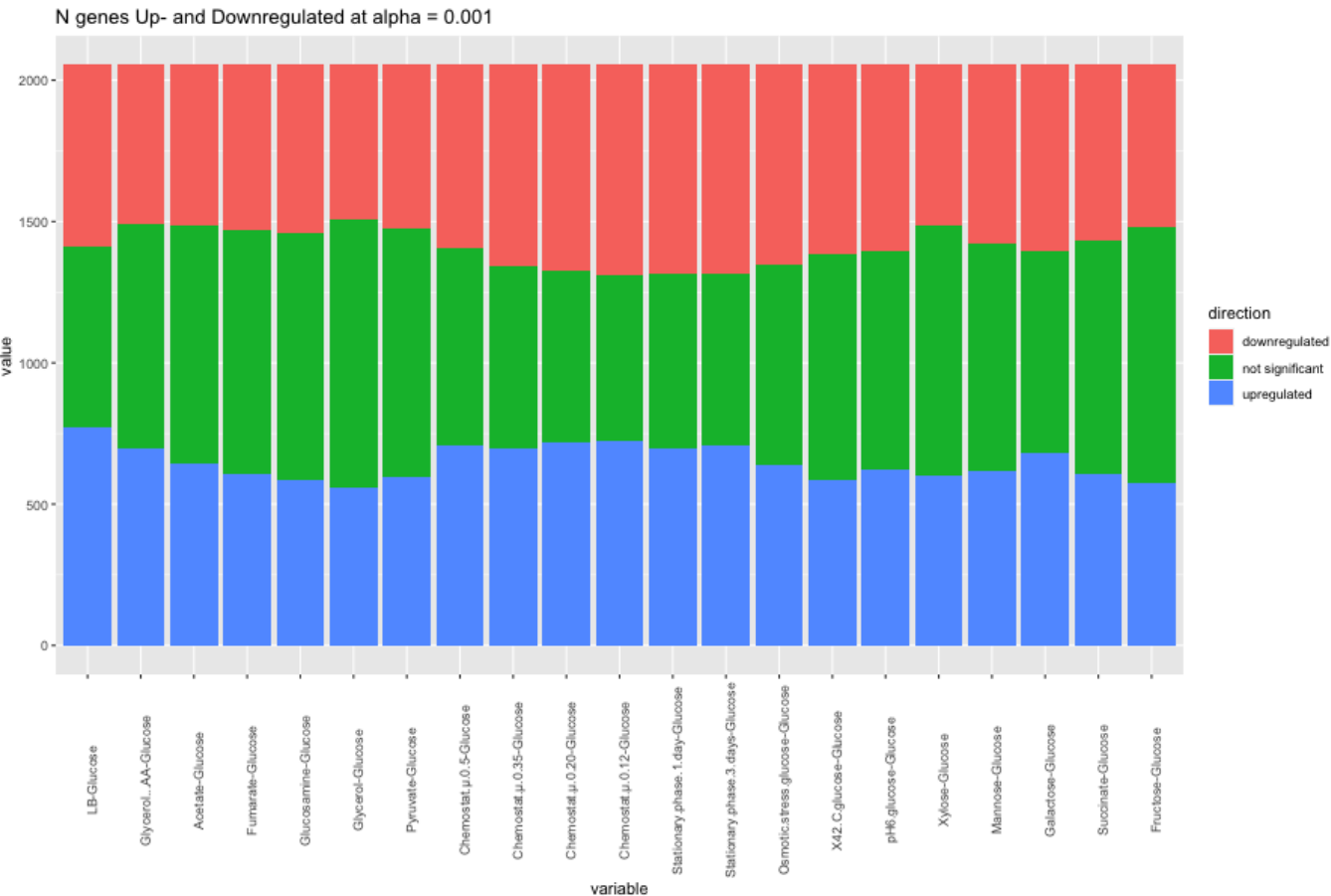
## Results



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

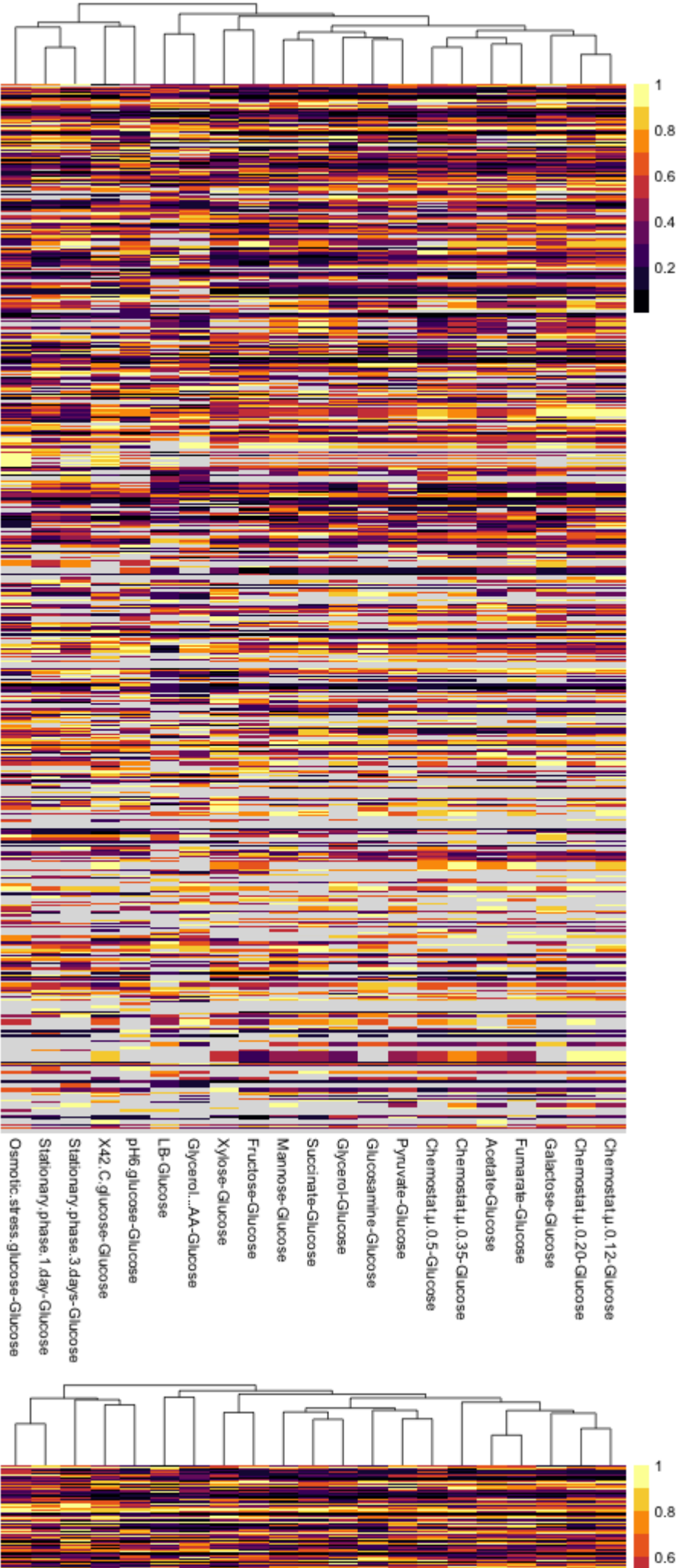
# Go term analysis with piano

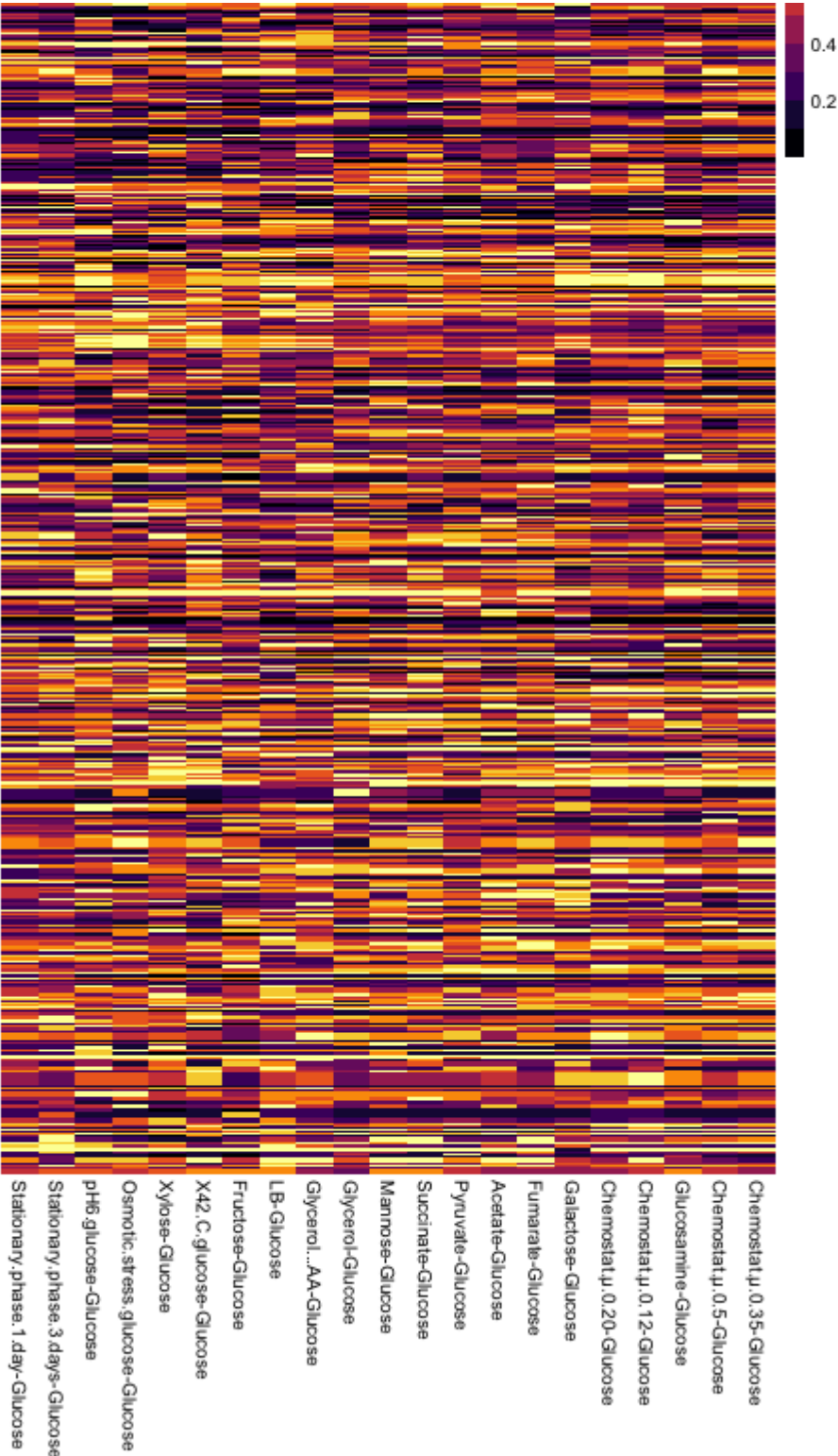
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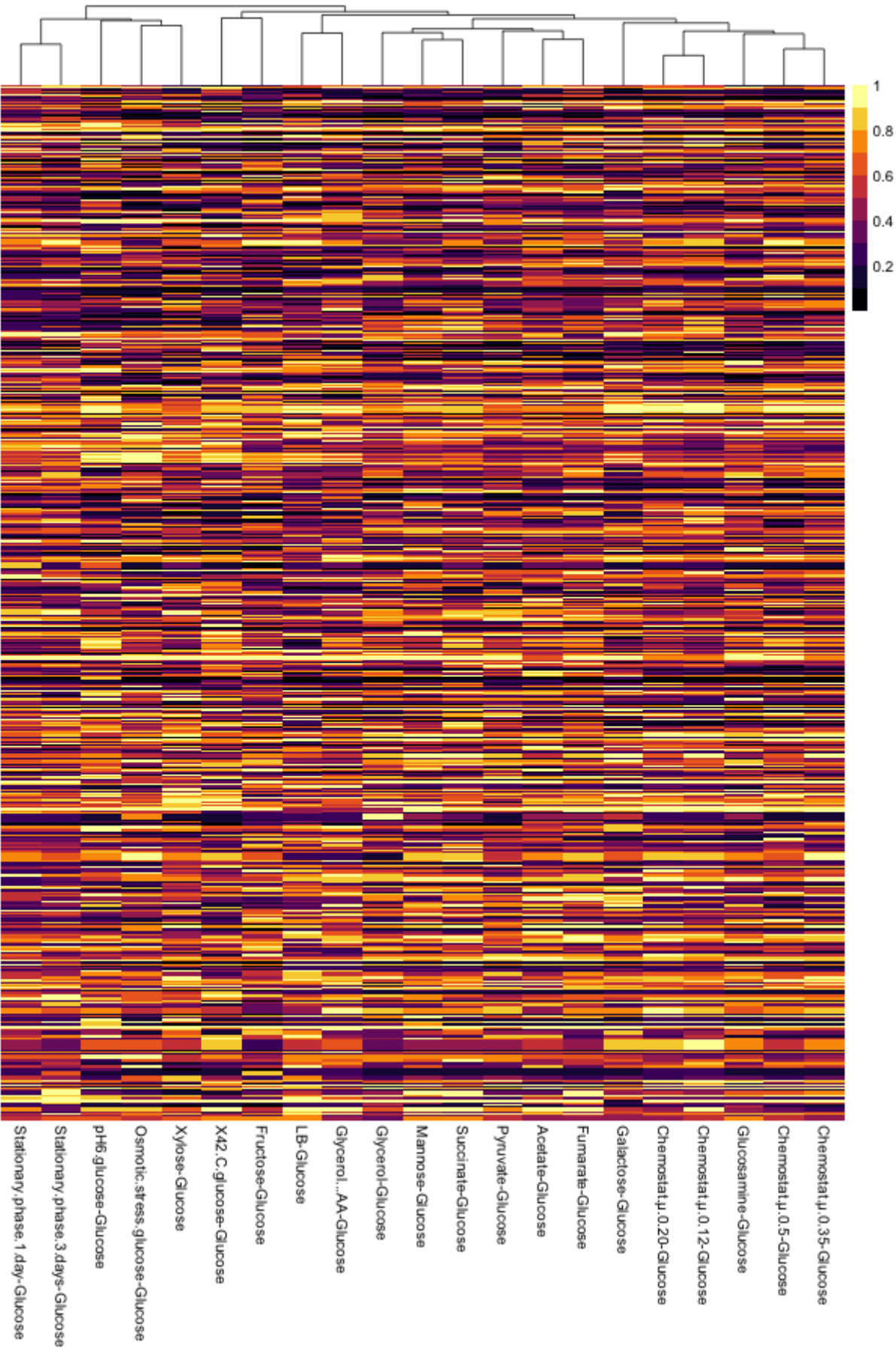
Why the given parameters?

- fishers combined test: includes the

Results







# Go term analysis with Goatools