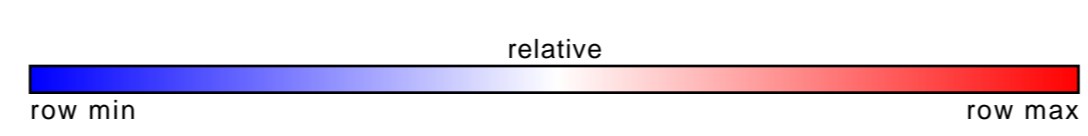


160P, 169P, 186P, 19P, 206P, 231P, 240P, 25P, 41P vs. 160M, 169M, 186M, 19M, 206M, 231M, 240M, 25M, 41M



160P, 169P, 186P, 19P, 206P, 231P, 240P, 25P, 41P vs. 160M, 169M, 186M, 19M, 206M, 231M, 240M, 25M, 41M

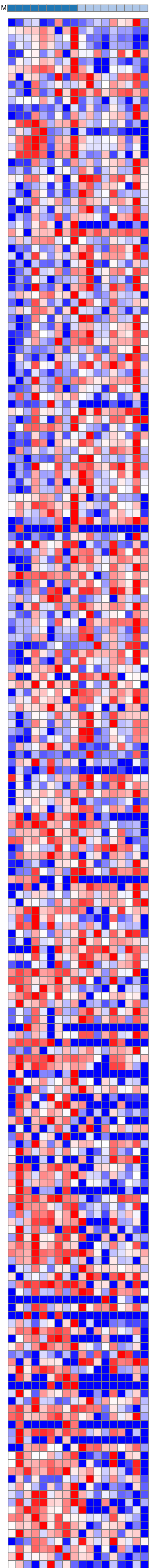


Table with columns: Description, Signal to noise, Rank, p-value, FDR(BH), Bonferroni, k, p-value low, p-value high, FWER, maxT, Fold Change. Lists genes like FTH1, DES, MYH11, etc.

1. Import File
File: Clipboard
2. Adjust
Flooring: 0.01
Log: true
Inverse log: false
Subtract mean from each row: false
Subtract median from each row: false
Divide each row by standard deviation: false
Divide each row by median absolute deviation: false
Subtract mean from each column: false
Subtract median from each column: false
Divide each column by standard deviation: false
Divide each column by median absolute deviation: false
Quantile normalization: false
Rank normalization: false
3. Marker Selection
Comparison(s): 160P, 169P, 186P, 19P, 206P, 231P, 240P, 25P, 41P vs. 160M, 169M, 186M, 19M, 206M, 231M, 240M, 25M, 41M
Permutations: 1000
Markers: 100
Include all columns in result dataset: false
Data is in log scale (used for fold change calculation): false
Compute: Permutation p-values
Test statistic: Signal to noise
Use median instead of mean: false
Ensure standard deviation is at least 5% of the class mean/median: false
Random number seed: 779948224
Save permuted scores: false
Test direction: Two sided