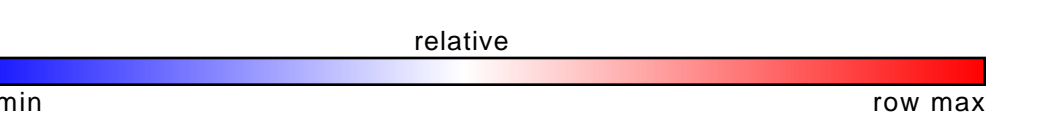


19N, 25N, 41N vs. 160M, 160P, 169M, 169P, 186M, 186P, 19M, 19P, 206M, 206P, 231M, 231P, 240M, 240P, 25M, 25P, 41M, 41P



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

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 various genes and their expression data across conditions.

1. Import File
File: Clipboard
2. Marker Selection
Comparison(s): 19N, 25N, 41N vs. 160M, 160P, 169M, 169P, 186M, 186P, 19M, 19P, 206M, 206P, 231M, 231P, 240M, 240P, 25M, 25P, 41M, 41P
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 directed: Two sided