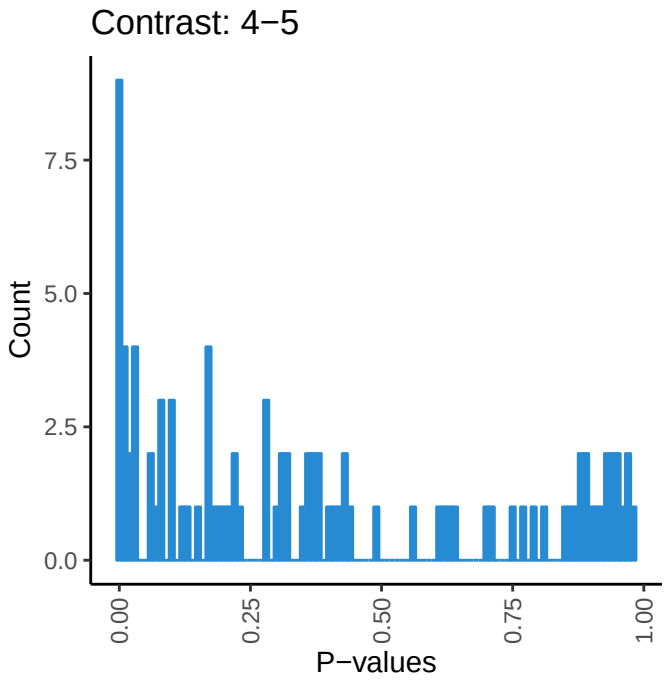
Project Name: multiple_comps

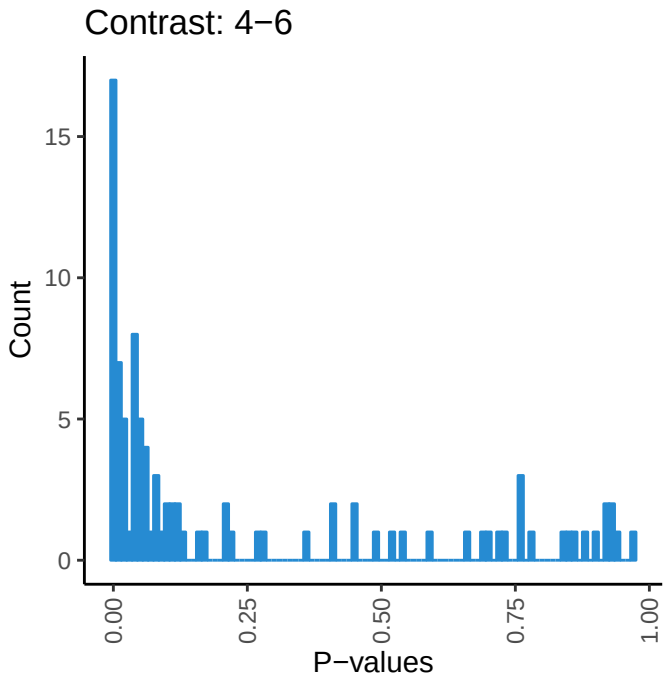
Normalyzer (ver (version not found))

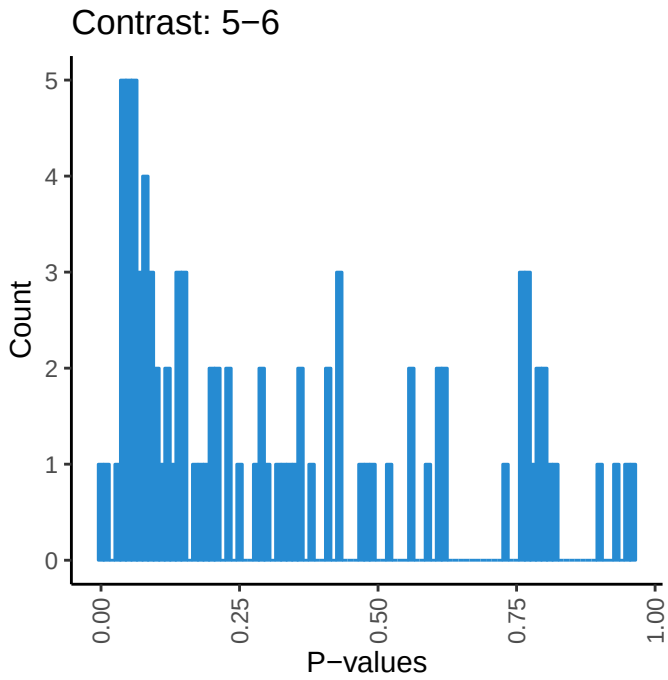
Report created on: 2018−12−12

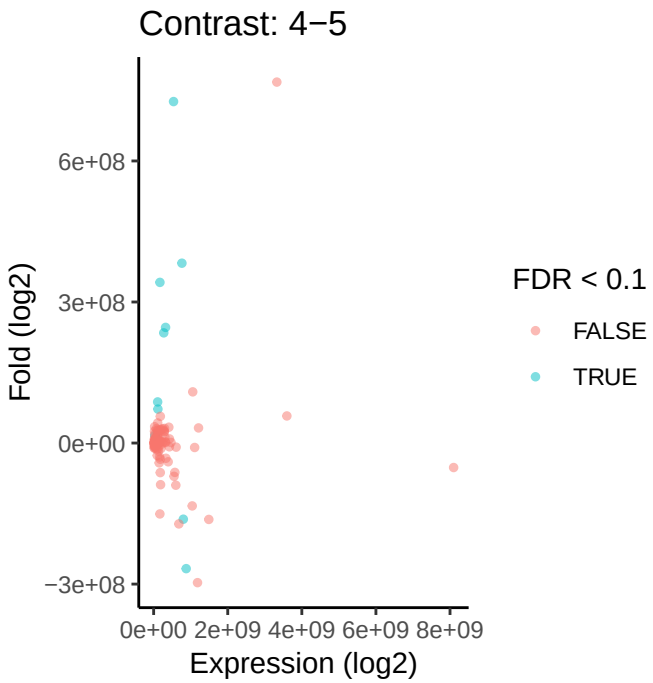
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High−Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

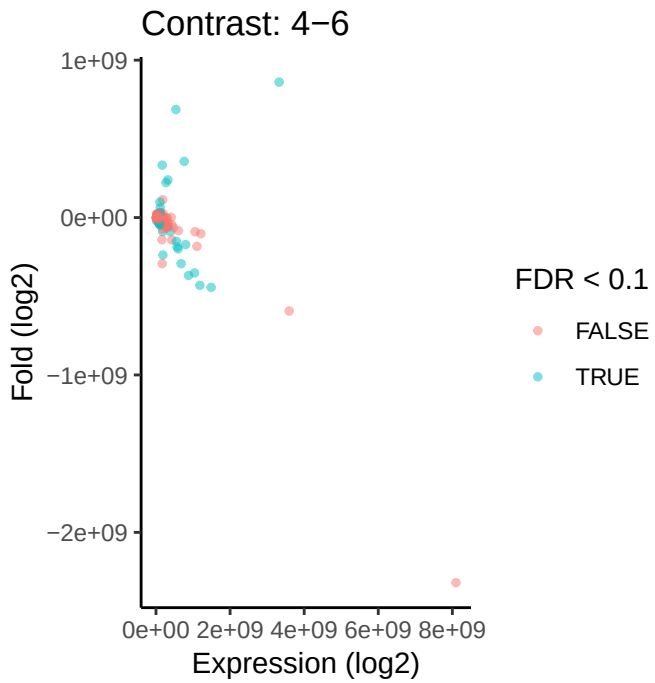
Documentation for analyzing this report can be found at http://quantitativeproteomics.org/normalyzer/help.php

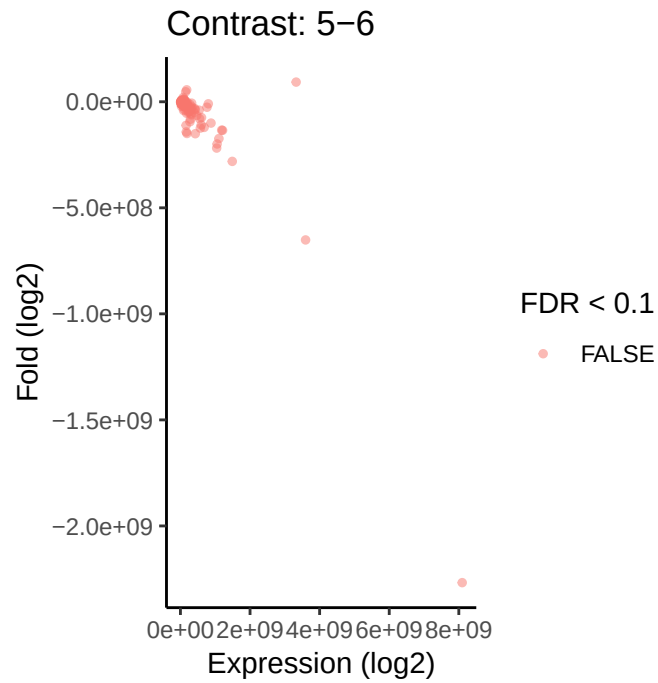

Contrast: 4−5
Count
P−values
0.0
2.5
5.0
7.5
0.00
0.25
0.50
0.75
1.00

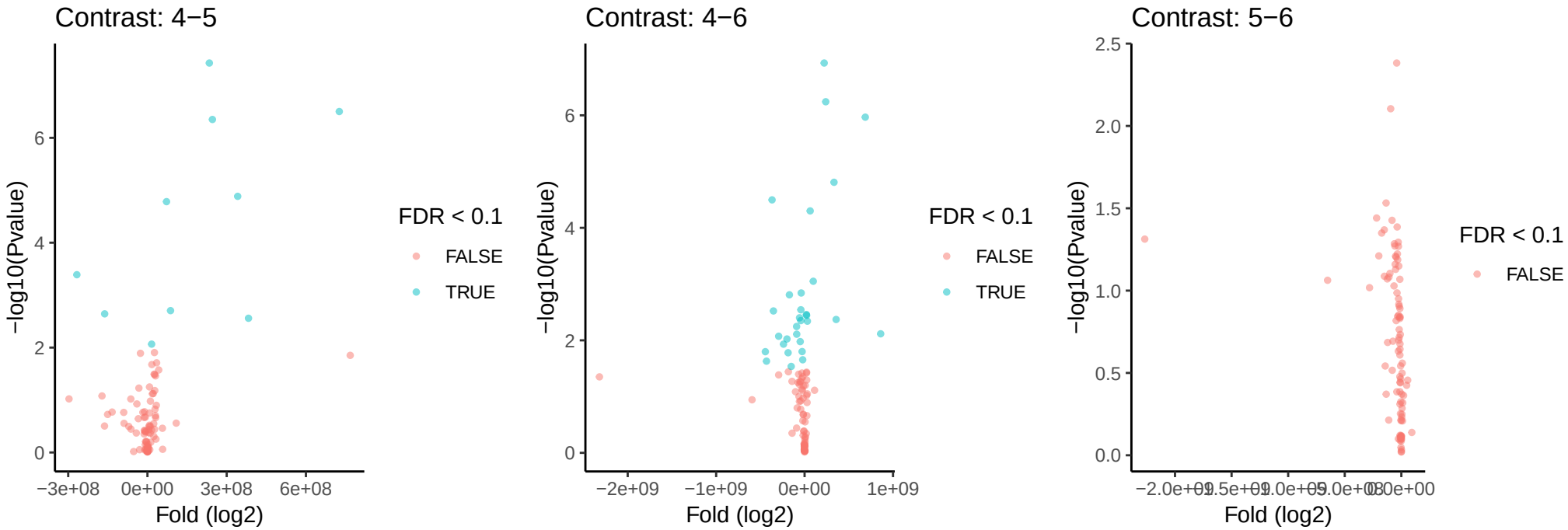

Contrast: 4−6
Count
P−values
0
5
10
15
0.00
0.25
0.50
0.75
1.00


Contrast: 5−6
Count
P−values
0
1
2
3
4
5
0.00
0.25
0.50
0.75
1.00


Contrast: 4−5
Fold (log2)
6e+08
3e+08
0e+00
−3e+08
0e+00 2e+09 4e+09 6e+09 8e+09
Expression (log2)
FDR < 0.1
FALSE
TRUE


Contrast: 4−6
Fold (log2)
1e+09
0e+00
−1e+09
−2e+09
0e+00 2e+09 4e+09 6e+09 8e+09
Expression (log2)
FDR < 0.1
FALSE
TRUE


Contrast: 5−6
Fold (log2)
0.0e+00
−5.0e+08
−1.0e+09
−1.5e+09
−2.0e+09
0e+00 2e+09 4e+09 6e+09 8e+09
Expression (log2)
FDR < 0.1
FALSE


Contrast: 4−5
−log10(Pvalue)
Fold (log2)
FDR < 0.1
FALSE
TRUE
Contrast: 4−6
−log10(Pvalue)
Fold (log2)
FDR < 0.1
FALSE
TRUE
Contrast: 5−6
−log10(Pvalue)
Fold (log2)
FDR < 0.1
FALSE