

SwipProteomics

Comparison: ‘Control-Mutant’

Method = MSstatsTMT

FDR < 0.05
657

Method = edgeR + Sum + IRS

FDR < 0.05
686

MSstatsTMT Top 5 significant proteins:

Symbol	log2FC	PValue	PAdjust	Tstatistic	SE	DF
Washc5	-1.3012495	0	0	-29.97081	0.0434172	34.00003
Washc1	-1.8735855	0	0	-22.25587	0.0841839	34.00001
Washc4	-1.5169269	0	0	-21.75455	0.0697292	34.00001
Washc2	-1.0677318	0	0	-21.67245	0.0492668	34.00003
Rab21	-0.5450661	0	0	-16.81386	0.0324177	34.00004

Comparison: ‘Intra-fraction’

Method = MSstats

F10	F4	F5	F6	F7	F8	F9
22	26	24	20	27	30	34

Total number of unique proteins (FDR < 0.05): 78

Method = edgeR

F10	F4	F5	F6	F7	F8	F9
7	12	21	20	25	36	19

Total number of unique proteins ($\text{FDR} < 0.05$):

Commonly significant sig prots:

Gene	UniProt
Rab21	P35282
Washc4	Q3UMB9
Washc2	Q6PGL7
Washc5	Q8C2E7
Washc1	Q8VDD8

Rank-Correlation of PValues

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cor(edger,msstats,method="spearman",use="pairwise.complete")
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Control.F#-Mutant.F#	Control-Mutant
0.6424383	0.7921496

Rank-Correlation of log2fc:

Control.F#-Mutant.F#	Control-Mutant
0.8554378	0.929861