

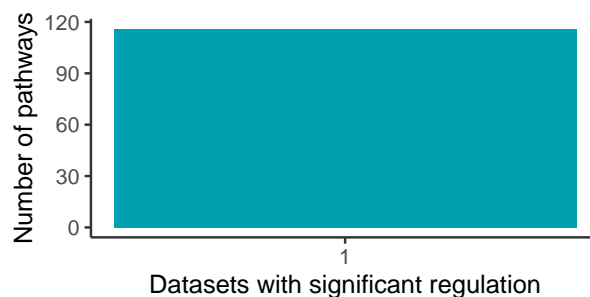
Reactome Analysis Result

17 August, 2022

Introduction

This report summarizes the pathway analysis result created by the **Reactome Analysis Service**. For more information, visit <https://www.reactome.org>.

In this reports, pathways found differentially expressed at an adjusted p-value ≤ 0.05 are considered to be significantly regulated.



Analysis Overview

- Number of datasets analysed: 3
- Reactome version: 81
- Disease pathways were included

Dataset summaries

RNASEQ_NORM_1:

- 2398 pathways
- 9636 fold changes for genes / proteins

PROTEOMICS_INT_2:

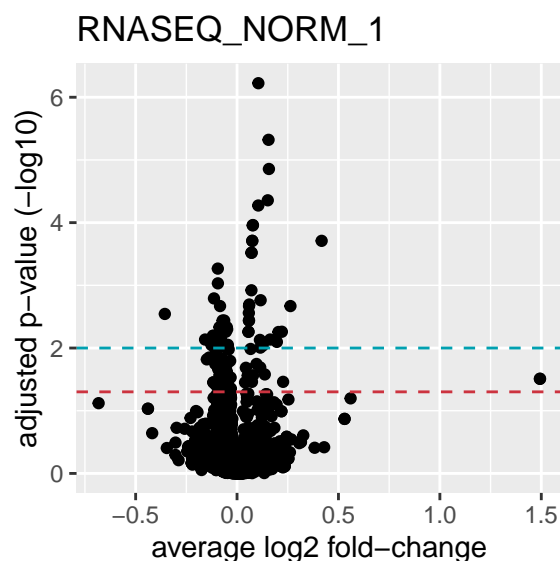
- 2096 pathways
- 4553 fold changes for genes / proteins

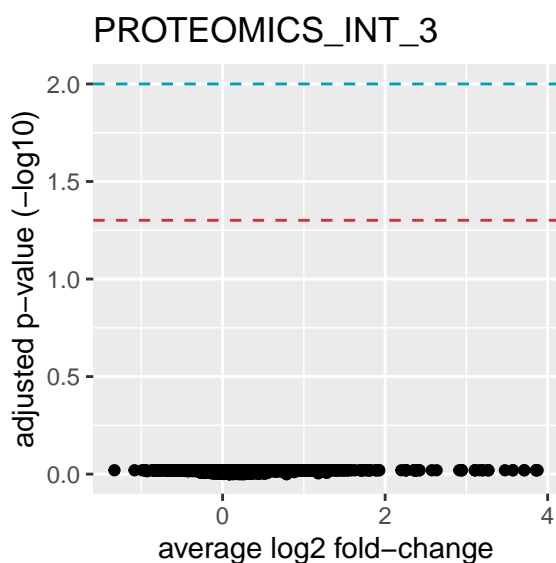
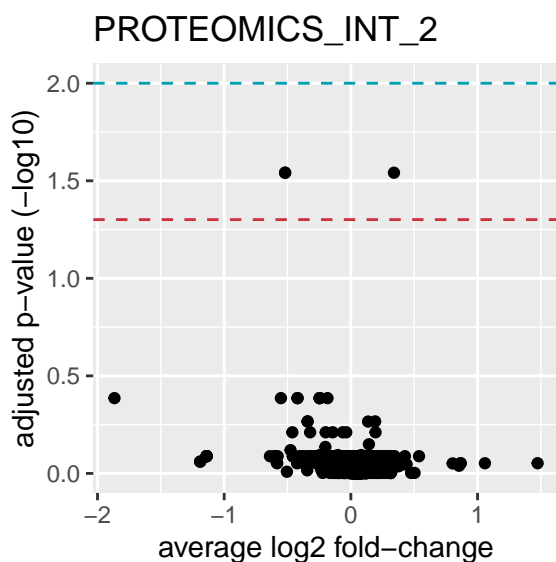
PROTEOMICS_INT_3:

- 1683 pathways
- 1987 fold changes for genes / proteins

Number of datasets the different pathways were found to be significantly regulated in:

Pathway analysis



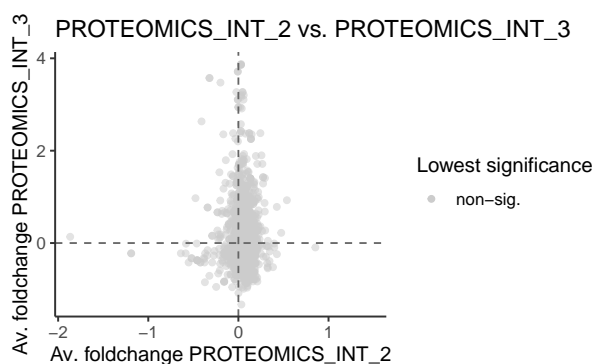
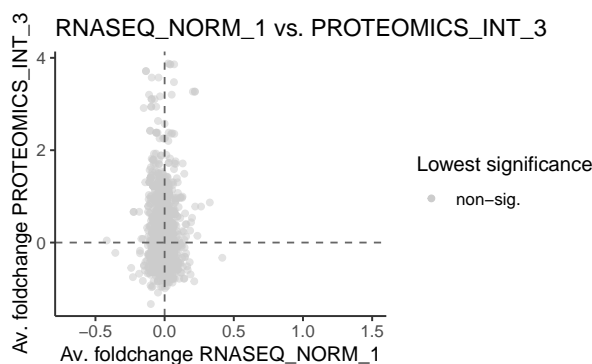
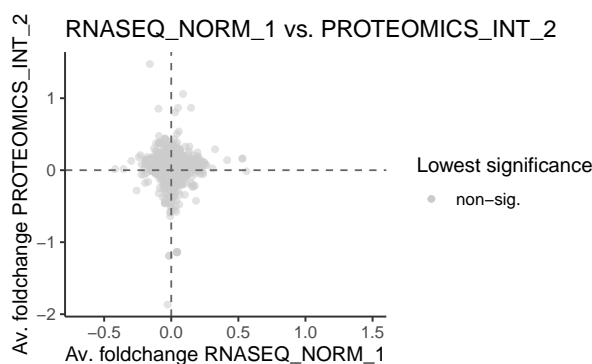


These volcano plots summarize the pathway results for every dataset. Every point is one pathway. The x-axis represents the average fold-change of all genes / proteins within that pathway. The y-axis represents the p-value where “higher” values are more significant ($-\log_{10}$ transformation). The red line represents $p = 0.05$, and the blue line $p = 0.01$.

Pathway correlation

Correlation between all datasets (if more than one). Every point represents one pathway, with the x-axis showing the average fold-change of one dataset and the y-axis the average fold-change of the other dataset. Only pathways that were observed in both

datasets are shown. Points are colored based on the lowest observed significance.



Similar regulated pathways

Pathways that show the same direction on all of the datasets. The direction of regulation is only assessed for significantly regulated pathways.

SRP-dependent cotranslational protein targeting to membrane (R-HSA-1799339)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.899	0.955
Av. FC	0.105	0.025	0.005
N Genes	99	90	24

Unfolded Protein Response (UPR) (R-HSA-381119)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	< 0.001	0.936	0.966
Av. FC	0.155	0.051	0.132
N Genes	84	52	16

IRE1alpha activates chaperones (R-HSA-381070)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	< 0.001	0.96	0.955
Av. FC	0.157	0.043	0.396
N Genes	48	27	10

XPB1(S) activates chaperone genes (R-HSA-381038)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	< 0.001	0.964	0.955
Av. FC	0.151	0.043	0.396
N Genes	46	26	10

Response of EIF2AK4 (GCN2) to amino acid deficiency (R-HSA-9633012)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.87	0.955
Av. FC	0.105	0.02	-0.052
N Genes	87	75	25

Eukaryotic Translation Elongation (R-HSA-156842)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.816	0.955
Av. FC	0.078	0.011	-0.025
N Genes	80	73	25

Peptide chain elongation (R-HSA-156902)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.816	0.955
Av. FC	0.077	0.01	-0.028
N Genes	76	70	22

Response of EIF2AK1 (HRI) to heme deficiency (R-HSA-9648895)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Down
FDR	< 0.001	0.887	0.955
Av. FC	0.417	0.139	-0.33
N Genes	14	5	3

Viral mRNA Translation (R-HSA-192823)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.816	0.955
Av. FC	0.075	0.009	0.015
N Genes	76	70	21

Selenocysteine synthesis (R-HSA-2408557)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.816	0.955
Av. FC	0.075	-0.001	0.015
N Genes	80	71	22

Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) (R-HSA-975956)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.829	0.955
Av. FC	0.07	0.013	0.036
N Genes	81	75	25

Eukaryotic Translation Termination (R-HSA-72764)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	0.816	0.955
Av. FC	0.072	0.012	0.03
N Genes	79	72	22

Selenoamino acid metabolism (R-HSA-2408522)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.001	0.829	0.955
Av. FC	0.071	0.011	-0.071
N Genes	98	88	26

Maturation of spike protein (R-HSA-9694548)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.002	0.994	0.955
Av. FC	0.116	0.03	0.979
N Genes	33	19	3

Formation of a pool of free 40S subunits (R-HSA-72689)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.002	0.816	0.955
Av. FC	0.06	0.01	0.131
N Genes	88	82	29

ATF6 (ATF6-alpha) activates chaperone genes (R-HSA-381183)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.002	0.93	0.955
Av. FC	0.263	0.072	0.78
N Genes	10	6	2

L13a-mediated translational silencing of Ceruloplasmin expression (R-HSA-156827)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.002	0.816	0.955
Av. FC	0.059	0.014	0.089
N Genes	98	92	33

GTP hydrolysis and joining of the 60S ribosomal subunit (R-HSA-72706)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.003	0.816	0.966
Av. FC	0.058	0.015	0.167
N Genes	99	93	34

Eukaryotic Translation Initiation (R-HSA-72613)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.004	0.835	0.988
Av. FC	0.059	0.018	0.215
N Genes	106	99	37

Cap-dependent Translation Initiation (R-HSA-72737)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.004	0.835	0.988
Av. FC	0.059	0.018	0.215
N Genes	106	99	37

DNA strand elongation (R-HSA-69190)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.001	0.994	0.955
Av. FC	-0.095	0.049	1.014
N Genes	30	27	11

G1/S-Specific Transcription (R-HSA-69205)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.001	0.816	0.955
Av. FC	-0.094	0.032	-0.102
N Genes	28	18	13

Lagging Strand Synthesis (R-HSA-69186)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.002	0.994	0.955
Av. FC	-0.114	0.042	1.03
N Genes	18	16	5

Activation of ATR in response to replication stress (R-HSA-176187)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.002	0.887	0.988
Av. FC	-0.084	0.023	0.178
N Genes	35	27	16

Phosphorylation of proteins involved in G1/S transition by active Cyclin E:Cdk2 complexes (R-HSA-69200)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.003	0.928	0.955
Av. FC	-0.356	0.017	-0.224
N Genes	4	3	2

Extension of Telomeres (R-HSA-180786)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Down
FDR	0.004	0.994	0.955
Av. FC	-0.071	0.048	0.219
N Genes	47	35	16

Chromosome Maintenance (R-HSA-73886)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Down
FDR	0.004	0.999	0.955
Av. FC	-0.063	0.059	0.123
N Genes	106	72	32

Formation of tubulin folding intermediates by CCT/TriC (R-HSA-389960)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.005	0.91	0.955
Av. FC	-0.087	0.019	-0.374
N Genes	16	15	2

G1/S Transition (R-HSA-69206)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.005	0.87	0.966
Av. FC	-0.05	0.036	0.224
N Genes	125	99	34

Telomere Maintenance (R-HSA-157579)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Down
FDR	0.005	0.887	0.966
Av. FC	-0.07	0.093	0.27
N Genes	79	55	20

DNA Replication (R-HSA-69306)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.005	0.964	0.955
Av. FC	-0.056	0.046	0.409
N Genes	141	113	27

Mitotic G1 phase and G1/S transition (R-HSA-453279)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.005	0.876	0.955
Av. FC	-0.049	0.037	0.253
N Genes	142	103	36

Telomere C-strand (Lagging Strand) Synthesis (R-HSA-174417)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.006	0.948	0.995
Av. FC	-0.084	0.058	0.448
N Genes	31	24	10

G2/M Checkpoints (R-HSA-69481)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.006	0.887	0.955
Av. FC	-0.055	0.034	0.214
N Genes	137	108	49

Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding (R-HSA-389958)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.006	0.994	0.955
Av. FC	-0.08	0.052	-0.212
N Genes	23	22	5

Prefoldin mediated transfer of substrate to CCT/TriC (R-HSA-389957)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.006	0.994	0.955
Av. FC	-0.082	0.054	-0.212
N Genes	22	21	5

Polymerase switching (R-HSA-69091)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.006	0.96	1
Av. FC	-0.118	0.048	0.787
N Genes	12	11	3

Leading Strand Synthesis (R-HSA-69109)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.006	0.96	1
Av. FC	-0.118	0.048	0.787
N Genes	12	11	3

Processing of DNA double-strand break ends (R-HSA-5693607)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.007	0.816	0.986
Av. FC	-0.08	0.003	0.056
N Genes	68	48	31

Removal of the Flap Intermediate (R-HSA-69166)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.007	0.974	0.955
Av. FC	-0.102	0.034	0.99
N Genes	14	12	3

Keratinization (R-HSA-6805567)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.982	0.029	0.955
Av. FC	0.001	-0.519	-0.328
N Genes	13	15	2

Formation of the cornified envelope (R-HSA-6809371)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.982	0.029	0.955
Av. FC	0.001	-0.519	-0.328
N Genes	13	15	2

Differently regulated pathways

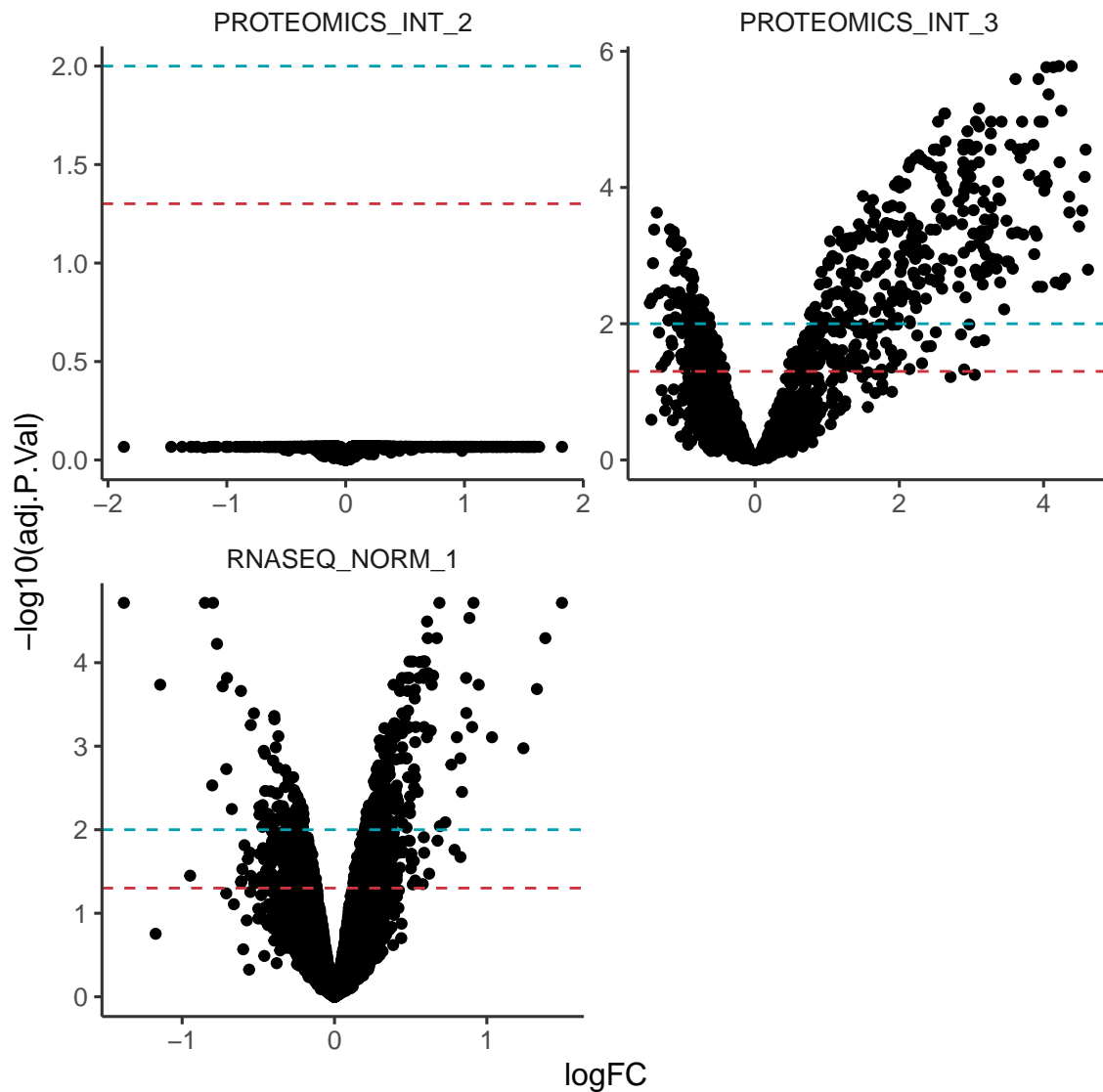
Alpha-oxidation of phytanate (R-HSA-389599)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	
FDR	0.785	0.029	
Av. FC	-0.025	0.34	
N Genes	6	2	

Protein / Gene level results

Classical differential expression analysis performed on the genes / proteins of every dataset.

Note: Depending on the gene set analysis method used, the approach used to assess differential expression at the gene / protein level may vary to the approach used for the pathway level.



Top up-regulated protein/genes

RNASEQ_NORM_1

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
WARS	0.9127108	7.3830977	20.55279	0e+00	1.92e-05	10.708669
INHBE	1.4935321	1.4746356	20.34346	0e+00	1.92e-05	10.636527
SEC24D	0.6890348	6.9290240	20.08397	0e+00	1.92e-05	10.545545
ATF3	0.8858805	0.7445957	18.23071	0e+00	2.92e-05	9.841656

SSR4	0.6079477	6.6608662	17.75591	0e+00	3.22e-05	9.644704
ULBP1	1.3843754	1.9205121	16.48171	1e-07	5.09e-05	9.078377
SEC61A1	0.6122315	7.6375592	16.31893	1e-07	5.09e-05	9.001792
PHGDH	0.6721849	7.9382805	16.24238	1e-07	5.09e-05	8.965426
VIMP	0.5936056	5.1398395	14.51234	2e-07	9.68e-05	8.079351
SEC61B	0.5138707	7.1872224	14.39181	2e-07	9.68e-05	8.012694

PROTEOMICS_INT_2

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
BBS12	0.6369868	4.274366	6.088638	0.0002734	0.8571405	-2.422128
ALDH3A2	0.4399406	6.134150	4.833531	0.0012365	0.8571405	-2.735696
HACL1	0.2406534	7.208473	3.889957	0.0044575	0.8571405	-3.076210
MAP2K4	0.3785861	5.987610	3.797769	0.0050877	0.8571405	-3.115488
KMT2C	1.8205498	1.832925	3.711435	0.0057646	0.8571405	-3.153322
NEMP1	0.2406242	7.037131	3.670797	0.0061159	0.8571405	-3.171486
KIF14	0.2780431	6.936317	3.636846	0.0064269	0.8571405	-3.186837
ALDH6A1	0.3154636	7.964080	3.604435	0.0067395	0.8571405	-3.201641
BCAR3	0.4854898	3.663056	3.450007	0.0084671	0.8571405	-3.274200
ACAP1	0.3369269	6.214799	3.367837	0.0095722	0.8571405	-3.314179

PROTEOMICS_INT_3

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
PSMA3	4.389080	9.685077	27.90504	0	1.7e-06	12.684784
DDX24	4.213921	7.411492	26.58060	0	1.7e-06	12.350785
SH2B2	4.037655	6.618130	24.70068	0	1.7e-06	11.831759
BRD7	4.135186	8.214070	24.37473	0	1.7e-06	11.735917
CXorf38	3.929237	7.637680	22.46349	0	2.6e-06	11.135205
MYH9	3.611049	11.473918	22.15010	0	2.6e-06	11.029948
HYPK	4.069224	7.941210	20.44364	0	4.3e-06	10.419579
SLC12A4	3.106126	3.764943	19.00637	0	6.9e-06	9.851530
LEO1	4.245468	9.354114	18.56905	0	7.5e-06	9.667798
BAG4	2.633677	4.081694	18.06237	0	8.2e-06	9.448088

Top down-regulated protein/genes

RNASEQ_NORM_1

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
TRAC	-0.8502672	6.092586	-21.94101	0.0e+00	0.0000192	11.160239
HBEGF	-0.7970655	5.041363	-19.51775	0.0e+00	0.0000192	10.340821
HIVEP3	-1.3824587	3.251268	-19.45548	0.0e+00	0.0000192	10.317775
IL7R	-0.7712773	3.780107	-15.79291	1.0e-07	0.0000596	8.747271
CD72	-0.7058058	4.946547	-13.15417	4.0e-07	0.0001525	7.286519
FMO1	-1.1441867	2.564377	-12.35308	6.0e-07	0.0001837	6.772227
TLR10	-0.7343332	6.702297	-12.17367	7.0e-07	0.0001920	6.651832
CCNE2	-0.6138968	6.467762	-11.80431	9.0e-07	0.0002183	6.397608
MSI2	-0.5286707	7.463337	-10.83839	1.9e-06	0.0004036	5.689501
SP110	-0.3953733	4.360343	-10.69798	2.1e-06	0.0004352	5.581009

PROTEOMICS_INT_2

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
EEFSEC	-0.6553507	4.237252	-4.080452	0.0034048	0.8571405	-2.998637
DCAF5	-0.2891843	4.366958	-4.002588	0.0037987	0.8571405	-3.029768
RPS6KA4	-0.2229728	6.592079	-3.746316	0.0054802	0.8571405	-3.137913
CDC34	-0.2457036	4.712287	-3.609208	0.0066925	0.8571405	-3.199452
FAM208B	-0.2693789	5.587487	-3.397871	0.0091516	0.8571405	-3.299456
BCL6	-0.2532270	6.515906	-3.267740	0.0111275	0.8571405	-3.364166
ALB	-1.8662077	8.659308	-3.119172	0.0139433	0.8571405	-3.440952
CENPN	-1.0107899	4.813357	-3.023611	0.0161407	0.8571405	-3.491959
FBXO38	-0.3303652	6.163447	-3.009826	0.0164863	0.8571405	-3.499419
TSPYL1	-0.2225277	6.418255	-2.920145	0.0189307	0.8571405	-3.548578

PROTEOMICS_INT_3

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
PCYT1A	-1.3622039	10.130308	-9.052827	1.16e-05	0.0002337	3.735319
NCAPD3	-1.1787434	9.919328	-8.218272	2.46e-05	0.0004108	2.941052
RPL12	-1.3987514	10.121600	-8.180597	2.55e-05	0.0004150	2.903591
UBA1	-1.1260208	9.603754	-8.016240	2.98e-05	0.0004458	2.738470
MS4A1	-1.1198977	13.309124	-7.732532	3.91e-05	0.0005362	2.446759

RAD18	-1.1552187	9.802763	-7.497380	4.94e-05	0.0006290	2.198339
SUV39H1	-1.0339943	10.921183	-7.477022	5.04e-05	0.0006379	2.176543
PPP2R5D	-1.0837983	11.320913	-7.458558	5.13e-05	0.0006457	2.156734
CUL4A	-1.0806264	10.936518	-7.310358	5.97e-05	0.0007231	1.996325
ITPR3	-0.9560508	9.609685	-6.986914	8.35e-05	0.0009453	1.637329
