

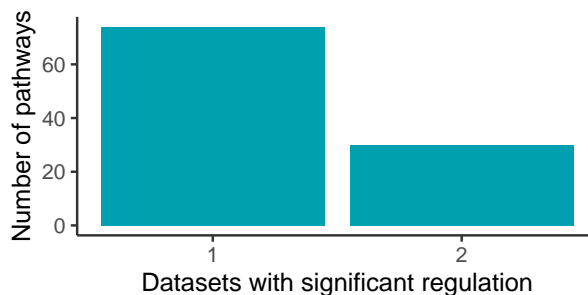
Reactome Analysis Result

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:

- 2397 pathways
- 9635 fold changes for genes / proteins

PROTEOMICS_INT_2:

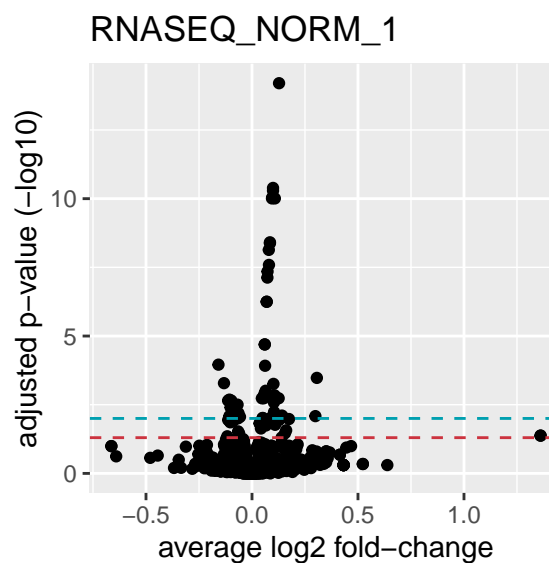
- 2096 pathways
- 4553 fold changes for genes / proteins

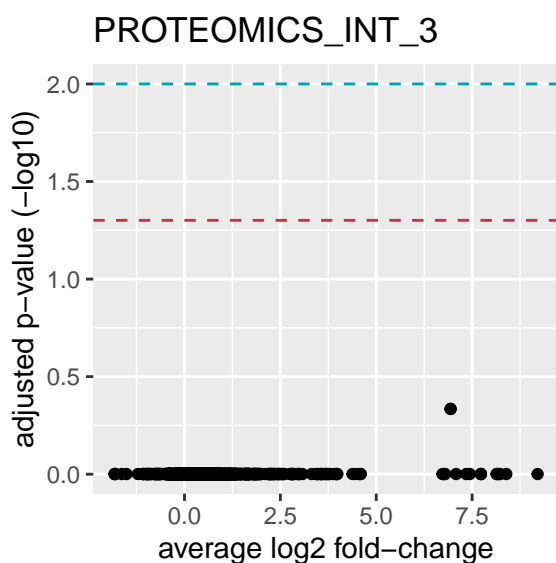
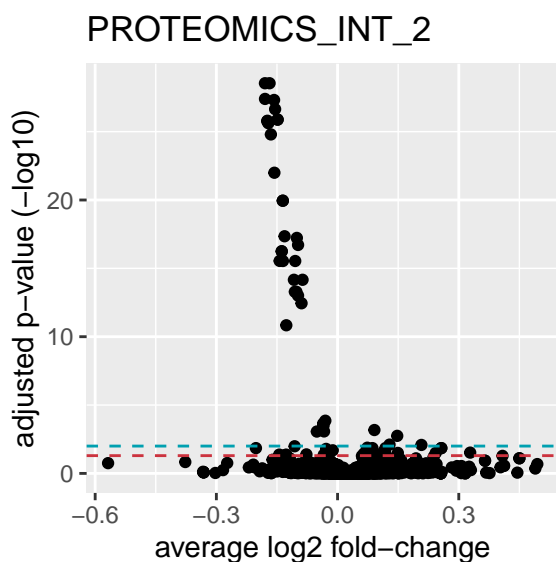
PROTEOMICS_INT_3:

- 1683 pathways
- 1987 fold changes for genes / proteins

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

Pathway analysis



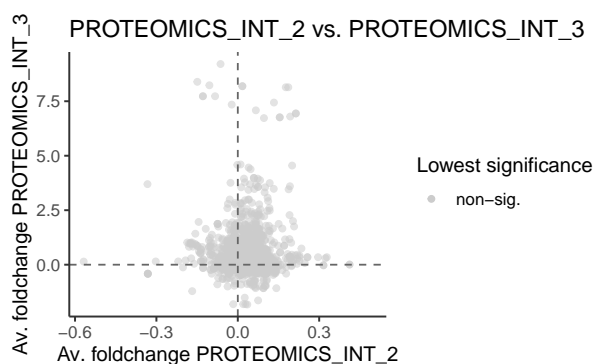
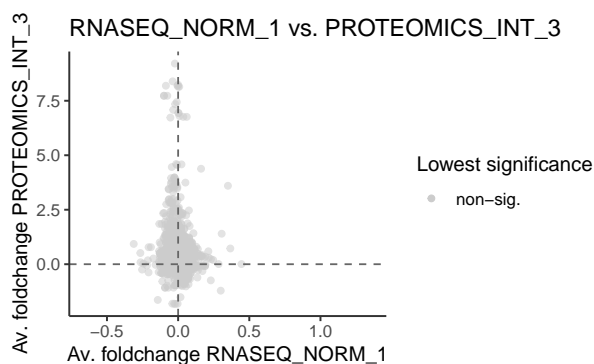
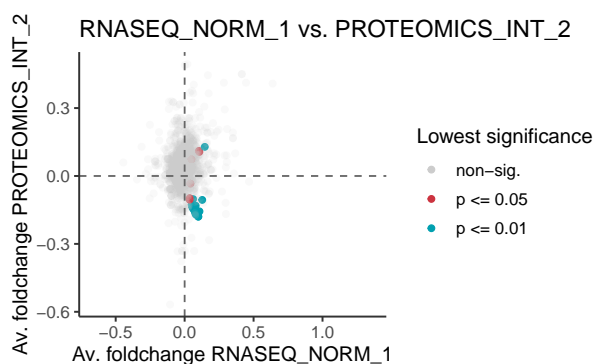


These volcano plots summarize the pathway results for every dataset. Every point is one pathway. The x-axis represents the average fold-change of all genes / proteins within that pathway. The y-axis represents the p-value where “higher” values are more significant ($-\log_{10}$ transformation). The red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

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.

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

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	< 0.001	0.855	0.998
Av. FC	0.306	0.061	1.399
N Genes	14	5	3

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

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Down
FDR	0.001	0.2	0.998
Av. FC	0.101	0.068	0.674
N Genes	84	52	16

Attenuation phase (R-HSA-3371568)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	< 0.001	0.275	0.998
Av. FC	-0.158	-0.052	-0.03
N Genes	21	14	8

HSF1-dependent transactivation (R-HSA-3371571)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.001	0.635	0.998
Av. FC	-0.132	-0.014	0.085
N Genes	27	18	12

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

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.002	0.746	0.998
Av. FC	-0.107	0.001	0.444
N Genes	22	21	5

HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand (R-HSA-3371497)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.002	0.781	0.998
Av. FC	-0.098	-0.001	0.588
N Genes	41	36	10

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

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.002	0.555	0.998
Av. FC	-0.113	-0.025	0.588
N Genes	16	15	2

Resolution of Sister Chromatid Cohesion (R-HSA-2500257)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.003	0.29	0.998
Av. FC	-0.068	-0.013	0.273
N Genes	112	95	45

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	Up
FDR	0.004	0.69	0.998
Av. FC	-0.101	-0.002	0.444
N Genes	23	22	5

RHO GTPases Activate Formins (R-HSA-5663220)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.006	0.368	0.998
Av. FC	-0.064	-0.007	0.755
N Genes	122	98	46

EML4 and NUDC in mitotic spindle formation (R-HSA-9648025)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.008	0.449	0.998
Av. FC	-0.065	-0.006	0.26
N Genes	103	86	39

E2F mediated regulation of DNA replication (R-HSA-113510)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.008	0.186	0.998
Av. FC	-0.106	-0.058	0.296
N Genes	21	17	5

Mitotic Prometaphase (R-HSA-68877)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.009	0.692	0.998
Av. FC	-0.057	0.003	0.431
N Genes	187	147	75

Amplification of signal from the kinetochores (R-HSA-141424)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.01	0.302	0.998
Av. FC	-0.067	-0.012	0.277
N Genes	91	76	36

Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal (R-HSA-141444)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.01	0.302	0.998
Av. FC	-0.067	-0.012	0.277
N Genes	91	76	36

HSF1 activation (R-HSA-3371511)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.011	0.646	0.998
Av. FC	-0.112	-0.025	0.671
N Genes	24	18	9

RHOBTB GTPase Cycle (R-HSA-9706574)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.013	0.548	0.998
Av. FC	-0.091	-0.018	0.243
N Genes	31	29	12

RHOBTB2 GTPase cycle (R-HSA-9013418)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Down
FDR	0.013	0.513	0.998
Av. FC	-0.104	-0.026	0.221
N Genes	22	20	10

Folding of actin by CCT/TriC (R-HSA-390450)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.014	0.323	0.998
Av. FC	-0.102	-0.057	1.2
N Genes	9	9	2

Anchoring of the basal body to the plasma membrane (R-HSA-5620912)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.03	0.855	0.998
Av. FC	-0.065	0.014	0.507
N Genes	95	56	35

AURKA Activation by TPX2 (R-HSA-8854518)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.035	0.713	0.998
Av. FC	-0.061	0.005	0.567
N Genes	71	51	31

Platelet sensitization by LDL (R-HSA-432142)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Down	Up
FDR	0.045	0.95	0.998
Av. FC	-0.117	-0.011	0.397
N Genes	15	13	3

Fatty acid metabolism (R-HSA-8978868)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Down
FDR	0.848	0.001	0.998
Av. FC	0.002	0.091	0.628
N Genes	116	60	9

Gluconeogenesis (R-HSA-70263)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.009	0.008	0.998
Av. FC	0.146	0.129	0.344
N Genes	27	18	7

HDMs demethylate histones (R-HSA-3214842)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.403	0.008	0.998
Av. FC	0.081	0.208	1.752
N Genes	22	16	10

Asparagine N-linked glycosylation (R-HSA-446203)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.01	0.013	0.998
Av. FC	0.05	0.074	1.071
N Genes	253	157	35

The citric acid (TCA) cycle and respiratory electron transport (R-HSA-1428517)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Down
FDR	0.763	0.014	0.998
Av. FC	-0.006	0.086	0.239
N Genes	169	118	9

Erythrocytes take up carbon dioxide and release oxygen (R-HSA-1237044)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.805	0.014	0.998
Av. FC	-0.054	0.257	0.344
N Genes	5	5	1

O2/CO2 exchange in erythrocytes (R-HSA-1480926)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.805	0.014	0.998
Av. FC	-0.054	0.257	0.344
N Genes	5	5	1

Pyruvate metabolism and Citric Acid (TCA) cycle (R-HSA-71406)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Down
FDR	0.876	0.014	0.998
Av. FC	0.011	0.119	0.05
N Genes	47	38	6

ER to Golgi Anterograde Transport (R-HSA-199977)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.158	0.025	0.998
Av. FC	0.041	0.074	1.314
N Genes	127	95	28

Respiratory electron transport (R-HSA-611105)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Down
FDR	0.708	0.028	0.998
Av. FC	-0.016	0.087	0.127
N Genes	103	69	2

COPI-mediated anterograde transport (R-HSA-6807878)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.386	0.029	0.998
Av. FC	0.033	0.078	2.319
N Genes	82	64	15

Erythrocytes take up oxygen and release carbon dioxide (R-HSA-1247673)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Down	Up	Up
FDR	0.627	0.03	0.998
Av. FC	-0.113	0.328	0.344
N Genes	2	3	1

Glycosphingolipid metabolism (R-HSA-1660662)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Down
FDR	0.688	0.032	0.998
Av. FC	0.026	0.149	0.153
N Genes	34	12	1

Branched-chain amino acid catabolism (R-HSA-70895)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.937	0.032	0.998
Av. FC	0.002	0.118	2.482
N Genes	21	15	3

XBP1(S) activates chaperone genes (R-HSA-381038)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Down
FDR	0.003	0.034	0.998
Av. FC	0.103	0.111	0.675
N Genes	46	26	10

Transport to the Golgi and subsequent modification (R-HSA-948021)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.104	0.034	0.998
Av. FC	0.043	0.072	1.314
N Genes	149	101	28

Metabolism of lipids (R-HSA-556833)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.8	0.034	0.998
Av. FC	0.004	0.066	0.838
N Genes	520	245	91

Mitochondrial Fatty Acid Beta-Oxidation (R-HSA-77289)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	Up
FDR	0.843	0.034	0.998
Av. FC	0.018	0.11	3.075
N Genes	31	20	2

Major pathway of rRNA processing in the nucleolus and cytosol (R-HSA-6791226)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.104	< 0.001	0.998
Av. FC	0.025	-0.101	0.859
N Genes	169	156	48

rRNA processing in the nucleus and cytosol (R-HSA-8868773)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.146	< 0.001	0.998
Av. FC	0.022	-0.098	0.802
N Genes	179	164	53

Differently 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	< 0.001	0.998
Av. FC	0.128	-0.106	0.8
N Genes	99	90	24

Peptide chain elongation (R-HSA-156902)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	< 0.001	0.998
Av. FC	0.099	-0.18	0.973
N Genes	76	70	22

Eukaryotic Translation Elongation (R-HSA-156842)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	< 0.001	0.998
Av. FC	0.099	-0.18	0.819
N Genes	80	73	25

Viral mRNA Translation (R-HSA-192823)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	< 0.001	0.998
Av. FC	0.095	-0.174	1.015
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	< 0.001	0.998
Av. FC	0.094	-0.174	0.972
N Genes	80	71	22

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

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Up
FDR	< 0.001	< 0.001	0.998
Av. FC	0.108	-0.156	1.422
N Genes	87	75	25

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	< 0.001	0.998
Av. FC	0.085	-0.165	0.831
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	< 0.001	0.998
Av. FC	0.085	-0.171	0.959
N Genes	79	72	22

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	< 0.001	< 0.001	0.998
Av. FC	0.079	-0.168	1.02
N Genes	88	82	29

Selenoamino acid metabolism (R-HSA-2408522)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	< 0.001	0.998
Av. FC	0.08	-0.131	0.811
N Genes	98	88	26

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

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	< 0.001	0.998
Av. FC	0.073	-0.157	0.949
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	< 0.001	< 0.001	0.998
Av. FC	0.073	-0.155	0.917
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	< 0.001	< 0.001	0.998
Av. FC	0.069	-0.148	0.857
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	< 0.001	< 0.001	0.998
Av. FC	0.069	-0.148	0.857
N Genes	106	99	37

Nonsense-Mediated Decay (NMD) (R-HSA-927802)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	< 0.001	0.998
Av. FC	0.06	-0.136	0.698
N Genes	100	93	31

Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) (R-HSA-975957)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	< 0.001	< 0.001	0.998
Av. FC	0.06	-0.136	0.698
N Genes	100	93	31

Cellular response to starvation (R-HSA-9711097)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Up
FDR	< 0.001	< 0.001	0.998
Av. FC	0.062	-0.102	1.226
N Genes	139	98	32

Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S (R-HSA-72662)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.001	< 0.001	0.998
Av. FC	0.064	-0.138	0.521
N Genes	56	54	22

Peroxisomal lipid metabolism (R-HSA-390918)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	
FDR	0.867	0.002	
Av. FC	0	0.148	
N Genes	25	10	

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

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Up	
FDR	0.72	0.032	
Av. FC	0.033	0.243	
N Genes	6	2	

Translation initiation complex formation (R-HSA-72649)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.002	< 0.001	0.998
Av. FC	0.056	-0.138	0.535
N Genes	55	54	21

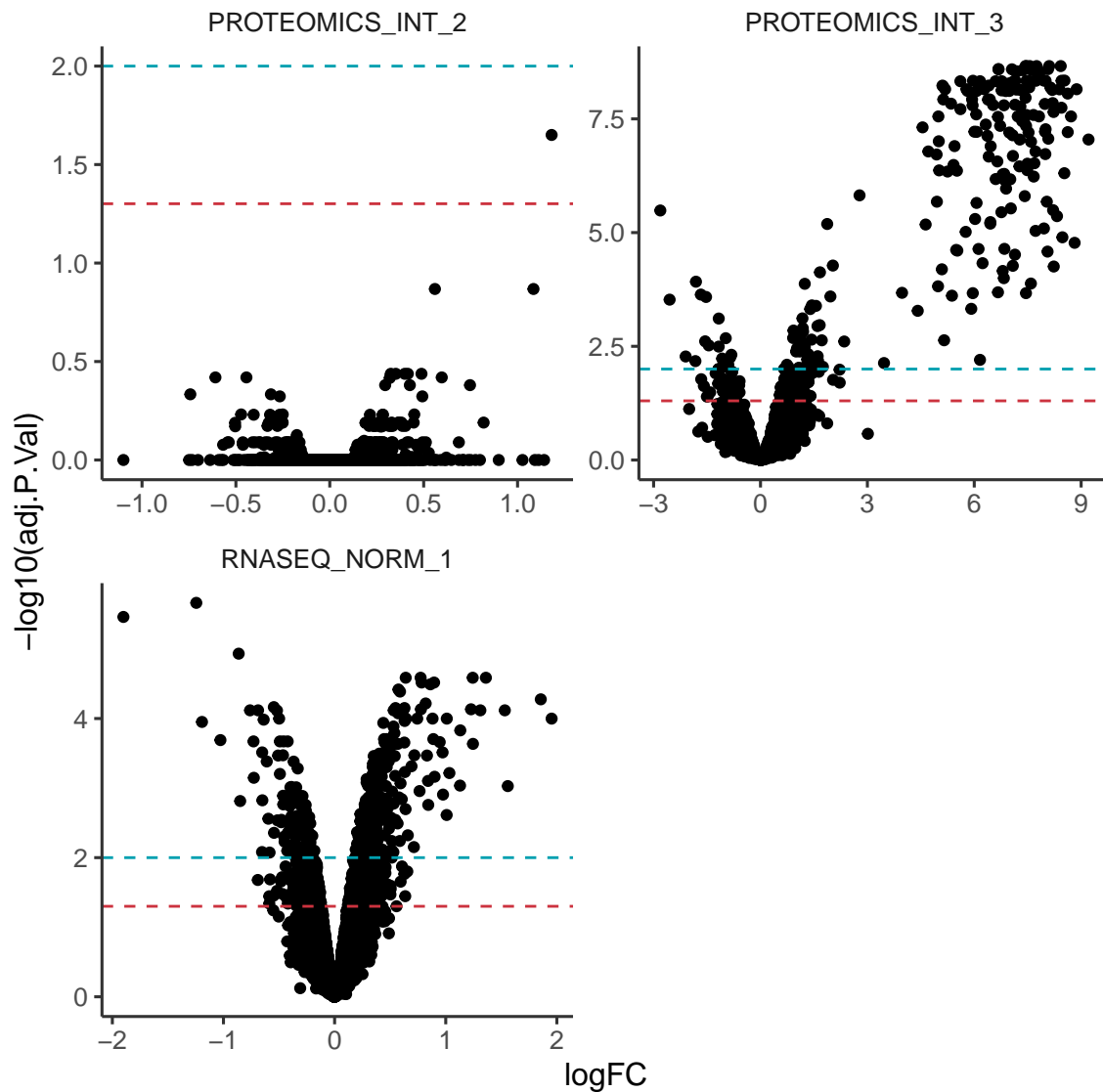
Formation of the ternary complex, and subsequently, the 43S complex (R-HSA-72695)

	RNASEQ_NORM_1	PROTEOMICS_INT_2	PROTEOMICS_INT_3
Regulation	Up	Down	Down
FDR	0.002	< 0.001	0.998
Av. FC	0.06	-0.143	0.606
N Genes	48	47	18

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
BNIP3	1.2427625	6.666911	19.28203	0e+00	2.59e-05	10.348714
SEC24D	0.6398932	6.929024	18.64700	0e+00	2.59e-05	10.095921
INHBE	1.3613345	1.474636	18.54210	0e+00	2.59e-05	10.053016
HK2	0.7739812	8.063837	18.47567	0e+00	2.59e-05	10.025672

P4HA1	0.8952833	6.416131	17.69588	0e+00	3.04e-05	9.694363
WARS	0.7830369	7.383098	17.63031	0e+00	3.04e-05	9.665610
LSP1	0.8618299	6.497991	17.30090	0e+00	3.23e-05	9.518977
SSR4	0.5746453	6.660866	16.77911	0e+00	3.83e-05	9.279021
SEC61B	0.5886769	7.187222	16.48316	1e-07	4.10e-05	9.138560
LRRC32	1.8553619	2.540811	15.85869	1e-07	5.30e-05	8.831288

PROTEOMICS_INT_2

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
BNIP3	1.1814335	7.095424	10.570358	0.0000049	0.0223701	2.2934506
PFKFB1	1.0848575	4.237815	7.311704	0.0000759	0.1354340	1.0059610
CYP51A1	0.5598672	8.613711	7.148307	0.0000892	0.1354340	0.9148148
SDHB	0.3250245	8.961145	5.634463	0.0004605	0.3650219	-0.1041238
ATP6V0A1	0.3992999	4.494340	5.570446	0.0004967	0.3650219	-0.1550398
HK2	0.4156871	11.404262	5.500468	0.0005399	0.3650219	-0.2115019
PCK2	0.3516007	9.592376	5.411571	0.0006008	0.3650219	-0.2844544
ALDOC	0.4882969	9.790111	5.357668	0.0006414	0.3650219	-0.3293650
FAM162A	0.5963219	7.819647	5.099026	0.0008824	0.3807273	-0.5520980
STAT2	0.3194455	6.956504	4.991894	0.0010099	0.3831570	-0.6479329

PROTEOMICS_INT_3

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
TULP4	8.427462	5.776730	60.73663	0	0	16.97889
PER1	8.102803	5.699838	55.00517	0	0	16.59636
COPA	7.749832	4.994465	53.27123	0	0	16.46311
KAT8	7.556984	5.268666	51.21708	0	0	16.29298
KIAA1328	7.463462	5.036851	51.06115	0	0	16.27948
BAG4	7.439379	4.081694	51.02099	0	0	16.27599
RTEL1	7.572201	5.136767	48.89557	0	0	16.08298
PQBP1	6.679322	4.693230	48.03592	0	0	16.00001
RPL23A	8.072335	5.540185	47.77731	0	0	15.97446
MAPRE2	7.057584	4.206044	47.07278	0	0	15.90346

Top down-regulated protein/genes

RNASEQ_NORM_1

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
HBEGF	-1.2444479	5.041363	-30.46771	0e+00	0.0000022	13.395315
HIVEP3	-1.9003565	3.251268	-26.74282	0e+00	0.0000035	12.614251
TRAC	-0.8630870	6.092586	-22.26763	0e+00	0.0000117	11.394708
GPR18	-0.5467458	5.160644	-15.14328	1e-07	0.0000686	8.460012
CD72	-0.7607923	4.946547	-14.17771	2e-07	0.0000763	7.923390
IL7R	-0.6886743	3.780107	-14.09995	2e-07	0.0000763	7.878276
SP110	-0.5184055	4.360343	-14.02405	2e-07	0.0000768	7.833957
IKZF1	-0.4989903	8.312841	-13.33832	3e-07	0.0001004	7.420393
MSI2	-0.6381131	7.463337	-13.08064	4e-07	0.0001039	7.258603
FMO1	-1.1932337	2.564377	-12.88241	4e-07	0.0001120	7.131652

PROTEOMICS_INT_2

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
HMGCR	-0.6090163	5.263031	-5.164688	0.0008130	0.3807273	-0.4944042
CHKA	-0.4438984	6.852022	-5.065900	0.0009198	0.3807273	-0.5815047
CDC34	-0.3135711	4.712287	-4.606131	0.0016642	0.4638571	-1.0108703
JCHAIN	-0.7426979	8.702611	-4.576017	0.0017320	0.4638571	-1.0403963
RPS6KA4	-0.2663223	6.592079	-4.474660	0.0019829	0.4751627	-1.1410577
UBE2T	-0.4721240	8.594440	-4.256525	0.0026668	0.5869069	-1.3644296
RPL21	-0.2504983	9.640674	-4.211907	0.0028359	0.5869069	-1.4112507
UBE2S	-0.4052257	8.105481	-4.128781	0.0031825	0.5889594	-1.4995067
RPL37A	-0.3179965	9.939984	-4.072322	0.0034438	0.5889594	-1.5602055
KPNA2	-0.2668472	10.712666	-4.050660	0.0035501	0.5889594	-1.5836568

PROTEOMICS_INT_3

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
SRPK1	-2.811971	8.311077	-14.814316	0.0000002	0.0000033	7.8311715
CLTA	-1.811336	6.090622	-9.263430	0.0000097	0.0001200	3.8858127
PPP1R2	-1.673190	9.555277	-8.464242	0.0000196	0.0002306	3.1386990
CDK12	-1.528140	9.039439	-8.313926	0.0000225	0.0002601	2.9914457
GMPS	-2.550105	9.018591	-8.161085	0.0000260	0.0002981	2.8394118

CHAMP1	-1.171488	10.565311	-7.152468	0.0000702	0.0007750	1.7738538
FLI1	-0.975170	9.650450	-6.200357	0.0001986	0.0020993	0.6581888
SAP130	-1.553133	8.724277	-6.045810	0.0002376	0.0024588	0.4660601
ESS2	-1.452025	8.105474	-5.857576	0.0002967	0.0030236	0.2276819
ABCF1	-1.172273	9.924015	-5.802776	0.0003168	0.0032120	0.1573698
