

Reactome Analysis Result

11 July, 2024

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

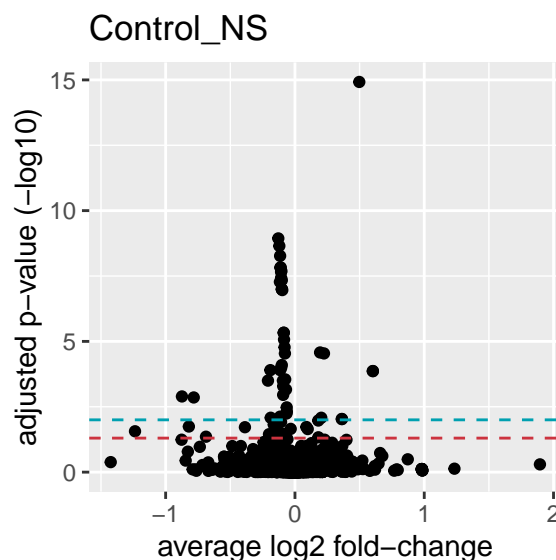
- Number of datasets analysed: 1
- Reactome version: 88
- Disease pathways were included

Dataset summaries

Control_NS:

- 2572 pathways
- 12299 fold changes for genes / proteins

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 $p = 0.01$.

Note

Since this result only contains a single datasets, some analyses are not included in this report.

Top-regulated pathways

Cholesterol biosynthesis (R-HSA-191273)

	Control_NS
Regulation	Up
FDR	< 0.001
Av. FC	0.497
N Genes	26

Regulation of cholesterol biosynthesis by SREBP (SREBF) (R-HSA-1655829)

	Control_NS
Regulation	Up
FDR	< 0.001
Av. FC	0.195
N Genes	56

Activation of gene expression by SREBF (SREBP) (R-HSA-2426168)

	Control_NS
Regulation	Up
FDR	< 0.001
Av. FC	0.224
N Genes	43

Cholesterol biosynthesis via desmosterol (R-HSA-6807047)

	Control_NS
Regulation	Up
FDR	< 0.001
Av. FC	0.603
N Genes	4

Cholesterol biosynthesis via lathosterol (R-HSA-6807062)

	Control_NS
Regulation	Up
FDR	< 0.001
Av. FC	0.603
N Genes	4

tRNA processing in the mitochondrion (R-HSA-6785470)

	Control_NS
Regulation	Up
FDR	0.008
Av. FC	0.204
N Genes	42

Virus Assembly and Release (R-HSA-168268)

	Control_NS
Regulation	Up
FDR	0.009
Av. FC	0.363
N Genes	2

Assembly of Viral Components at the Budding Site (R-HSA-168316)

	Control_NS
Regulation	Up
FDR	0.009
Av. FC	0.363
N Genes	2

FASTK family proteins regulate processing and stability of mitochondrial RNAs (R-HSA-9837092)

	Control_NS
Regulation	Up
FDR	0.011
Av. FC	0.181
N Genes	19

COPI-independent Golgi-to-ER retrograde traffic (R-HSA-6811436)

	Control_NS
Regulation	Up
FDR	0.019
Av. FC	0.088
N Genes	46

Metabolism of steroids (R-HSA-8957322)

	Control_NS
Regulation	Up
FDR	0.023
Av. FC	0.099
N Genes	123

rRNA processing in the mitochondrion (R-HSA-8868766)

	Control_NS
Regulation	Up
FDR	0.047
Av. FC	0.181
N Genes	38

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.129
N Genes	91

Eukaryotic Translation Elongation (R-HSA-156842)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.121
N Genes	83

Peptide chain elongation (R-HSA-156902)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.115
N Genes	79

Eukaryotic Translation Termination (R-HSA-72764)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.11
N Genes	83

Selenocysteine synthesis (R-HSA-2408557)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.112
N Genes	83

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.105
N Genes	91

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.107
N Genes	85

Viral mRNA Translation (R-HSA-192823)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.107
N Genes	79

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.102
N Genes	101

Selenoamino acid metabolism (R-HSA-2408522)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.116
N Genes	105

Eukaryotic Translation Initiation (R-HSA-72613)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.101
N Genes	109

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.101
N Genes	109

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.098
N Genes	102

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.087
N Genes	105

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.087
N Genes	105

Influenza Viral RNA Transcription and Replication (R-HSA-168273)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.084
N Genes	125

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.08
N Genes	171

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.078
N Genes	181

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

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.102
N Genes	49

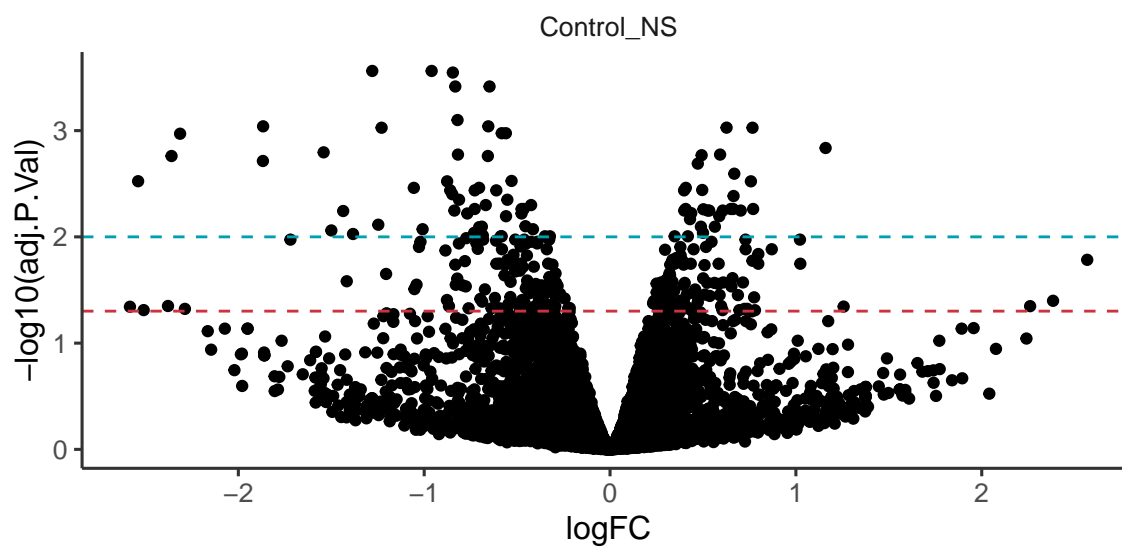
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S (R-HSA-72662)

	Control_NS
Regulation	Down
FDR	< 0.001
Av. FC	-0.107
N Genes	57

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

Control_NS

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
STARD4	0.6269767	5.855519	10.325053	7.0e-07	0.0009376	6.531139
HSD17B7	0.7665604	4.145393	10.212590	8.0e-07	0.0009392	6.311632

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
FGF1	1.1599173	2.610482	9.360287	1.8e-06	0.0014571	5.133912
OTUD1	0.5922230	6.363517	9.047698	2.5e-06	0.0016812	5.289344
PPL	0.4928045	6.922342	8.983472	2.6e-06	0.0017047	5.218036
DPYSL2	0.4722407	7.259081	8.637866	3.8e-06	0.0020435	4.844040
TM7SF2	0.6684746	6.756545	8.401344	5.0e-06	0.0025437	4.587652
MAP3K7CL	0.7579712	3.899901	8.122379	6.8e-06	0.0030015	4.274503
TUBA1A	0.4077416	9.394441	7.930915	8.5e-06	0.0034562	4.034652
TGFBR1	0.4958749	6.726674	7.842555	9.4e-06	0.0036203	3.944711

Top down-regulated protein/genes
Control_NS

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
PSG1	-1.2795536	6.669333	-14.429719	0.0e+00	0.0002745	9.671383
NR2F1	-0.9599362	5.967708	-13.577149	0.0e+00	0.0002745	9.074079
PTGIS	-0.8459189	9.437413	-12.999894	1.0e-07	0.0002841	8.742560
PVR	-0.6484618	7.964049	-12.104053	1.0e-07	0.0003845	8.064760
GPX1	-0.8326514	5.761857	-11.989130	2.0e-07	0.0003845	7.920132
CYP24A1	-0.8206274	9.721705	-10.941612	4.0e-07	0.0007951	7.099960
CAMK2A	-0.6550722	4.582633	-10.621915	5.0e-07	0.0009116	6.719940
ELF3	-1.8668112	3.602457	-10.479898	6.0e-07	0.0009116	6.348448
AKAP12	-1.2292902	6.630273	-10.113167	8.0e-07	0.0009394	6.343191
CAPN5	-0.5606533	7.089405	-9.839732	1.1e-06	0.0010583	6.083384