

Reactome Analysis Result

14 April, 2021

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

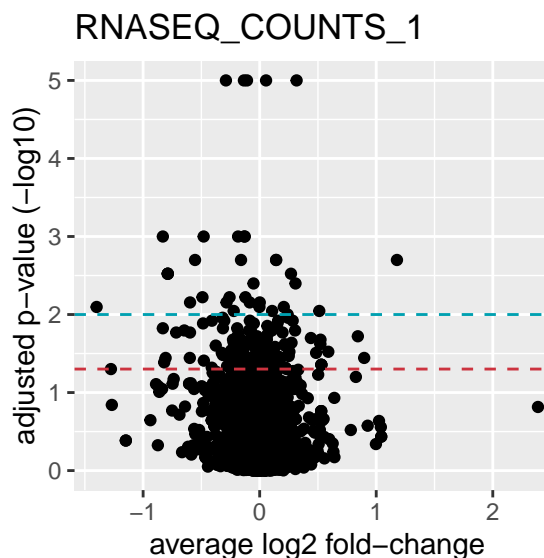
- Number of datasets analysed: 1
- Reactome version: 75
- Disease pathways were included

Dataset summaries

RNASEQ_COUNTS_1:

- 2464 pathways
- 13230 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

CD209 (DC-SIGN) signaling (R-HSA-5621575)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	< 0.001
Av. FC	0.055
N Genes	20

IkBA variant leads to EDA-ID (R-HSA-5603029)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	< 0.001
Av. FC	0.317
N Genes	7

Defective ABCC2 causes DJS (R-HSA-5679001)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.002
Av. FC	1.178
N Genes	1

Formation of apoptosome (R-HSA-111458)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.002
Av. FC	0.141
N Genes	10

Regulation of the apoptosome activity (R-HSA-9627069)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.002
Av. FC	0.141
N Genes	10

Regulation of FOXO transcriptional activity by acetylation (R-HSA-9617629)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.003
Av. FC	0.268
N Genes	11

NF-κB is activated and signals survival (R-HSA-209560)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.004
Av. FC	0.308
N Genes	13

Regulation of localization of FOXO transcription factors (R-HSA-9614399)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.007
Av. FC	0.001
N Genes	13

p75NTR signals via NF-κB (R-HSA-193639)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.008
Av. FC	0.207
N Genes	16

Deletions in the AXIN genes in hepatocellular carcinoma result in elevated WNT signaling (R-HSA-5467345)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.009
Av. FC	0.511
N Genes	1

Lagging Strand Synthesis (R-HSA-69186)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.009
Av. FC	0.107
N Genes	18

NFG and proNGF binds to p75NTR (R-HSA-205017)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.01
Av. FC	0.24
N Genes	3

RUNX2 regulates bone development (R-HSA-8941326)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.011
Av. FC	0.243
N Genes	30

AKT phosphorylates targets in the nucleus (R-HSA-198693)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.012
Av. FC	0.283
N Genes	10

Processive synthesis on the lagging strand (R-HSA-69183)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.012
Av. FC	0.159
N Genes	15

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

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.013
Av. FC	0.153
N Genes	14

TRAF6 mediated NF-kB activation (R-HSA-933542)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.014
Av. FC	0.146
N Genes	24

Termination of translesion DNA synthesis (R-HSA-5656169)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.014
Av. FC	0.066
N Genes	30

Cohesin Loading onto Chromatin (R-HSA-2470946)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.016
Av. FC	0.304
N Genes	10

NADE modulates death signalling (R-HSA-205025)

	RNASEQ_COUNTS_1
Regulation	Up
FDR	0.016
Av. FC	0.105
N Genes	6

CREB1 phosphorylation through the activation of Adenylate Cyclase (R-HSA-442720)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	< 0.001
Av. FC	-0.109
N Genes	11

Activated NTRK2 signals through PLCG1 (R-HSA-9026527)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	< 0.001
Av. FC	-0.289
N Genes	3

ERKs are inactivated (R-HSA-202670)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	< 0.001
Av. FC	-0.135
N Genes	12

MECP2 regulates transcription of neuronal ligands (R-HSA-9022702)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.001
Av. FC	-0.481
N Genes	8

Signaling by NTRK1 (TRKA) (R-HSA-187037)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.001
Av. FC	-0.133
N Genes	115

Toxicity of botulinum toxin type C (botC) (R-HSA-5250971)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.001
Av. FC	-0.831
N Genes	3

Negative regulation of MAPK pathway (R-HSA-5675221)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.001
Av. FC	-0.127
N Genes	43

Pyruvate metabolism (R-HSA-70268)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.001
Av. FC	-0.185
N Genes	30

Acetylcholine Neurotransmitter Release Cycle (R-HSA-264642)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.002
Av. FC	-0.554
N Genes	15

Nuclear Events (kinase and transcription factor activation) (R-HSA-198725)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.002
Av. FC	-0.16
N Genes	61

Defective F8 accelerates dissociation of the A2 domain (R-HSA-9672387)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.003
Av. FC	-0.788
N Genes	1

Defective F8 binding to the cell membrane (R-HSA-9672395)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.003
Av. FC	-0.788
N Genes	1

Defective F8 secretion (R-HSA-9672397)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.003
Av. FC	-0.788
N Genes	1

Organelle biogenesis and maintenance (R-HSA-1852241)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.004
Av. FC	-0.053
N Genes	285

NGF-independant TRKA activation (R-HSA-187024)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.006
Av. FC	-0.258
N Genes	5

GABA synthesis, release, reuptake and degradation (R-HSA-888590)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.006
Av. FC	-0.491
N Genes	19

Signaling by NTRKs (R-HSA-166520)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.006
Av. FC	-0.122
N Genes	133

ERK/MAPK targets (R-HSA-198753)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.007
Av. FC	-0.085
N Genes	21

Defective GSS causes GSS deficiency (R-HSA-5579006)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.007
Av. FC	-0.597
N Genes	1

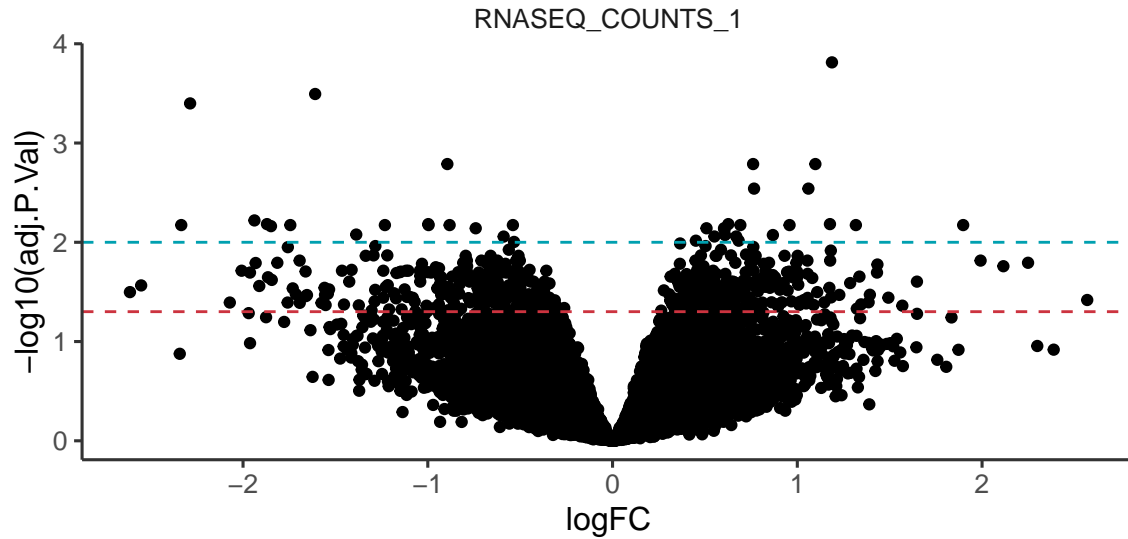
Activation of TRKA receptors (R-HSA-187015)

	RNASEQ_COUNTS_1
Regulation	Down
FDR	0.007
Av. FC	-0.284
N Genes	6

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_COUNTS_1

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
KLF15	1.1876134	6.128648	8.419573	0.00e+00	0.0001539	9.971708
SLC38A2	1.0977907	7.326535	6.656697	7.00e-07	0.0016284	6.119948
NFKBIA	0.7606894	6.270888	6.609032	7.00e-07	0.0016284	6.009144
MPST	0.7659132	4.604686	6.294975	1.60e-06	0.0028788	5.282425
PRKX	1.0600816	4.846126	6.255829	1.70e-06	0.0028788	5.190578
ANAPC16	0.6266283	5.111104	5.726933	6.40e-06	0.0065579	3.930552
GAS2L3	1.1767592	1.571442	5.758456	6.00e-06	0.0065579	3.729979
STARD10	0.6917483	5.309208	5.532717	1.05e-05	0.0067078	3.458752
P2RX7	0.9580860	6.817063	5.490586	1.17e-05	0.0067078	3.355297
GNRH1	1.3170009	1.665583	5.517319	1.09e-05	0.0067078	3.233341

Top down-regulated protein/genes

RNASEQ_COUNTS_1

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
RPH3A	-1.6096090	7.392365	-7.775647	0.00e+00	0.0003207	8.595577
VGF	-2.2864063	5.631175	-7.501807	1.00e-07	0.0003988	8.010642

DUSP6	-0.8941082	4.751211	-6.662364	6.00e-07	0.0016284	6.132025
PCSK1	-1.9383007	4.423736	-5.908751	4.10e-06	0.0060218	4.377887
DHRS11	-0.9972759	3.535037	-5.777225	5.70e-06	0.0065579	4.063501
ADCYAP1	-1.8703040	2.506895	-5.779866	5.60e-06	0.0065579	3.985109
KCNF1	-0.8819307	5.713793	-5.627806	8.30e-06	0.0067078	3.684884
PCYOX1L	-0.9957895	4.083952	-5.577294	9.40e-06	0.0067078	3.593012
NRN1	-1.2321810	6.004137	-5.563289	9.70e-06	0.0067078	3.530333
TRAPPC1	-0.5393978	4.978865	-5.535362	1.04e-05	0.0067078	3.470017
