

Reactome Analysis Result

26 August, 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

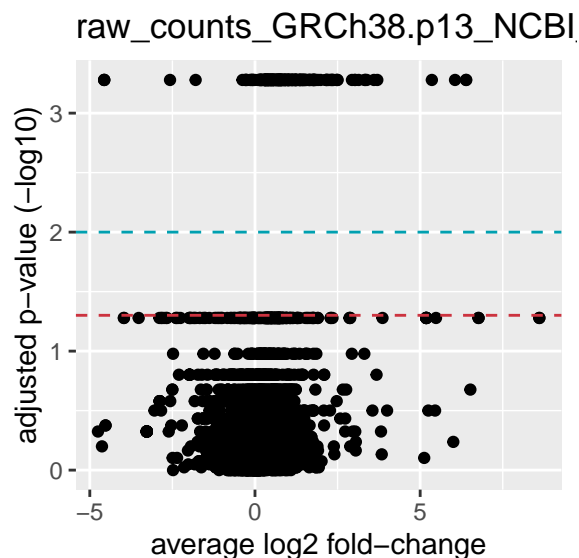
- Number of datasets analysed: 1
- Reactome version: 88
- Disease pathways were included

Dataset summaries

raw_counts_GRCh38.p13_NCBI_UNvsWT:

- 2636 pathways
- 10695 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 (-log10 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

Interleukin-6 signaling (R-HSA-1059683)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	1.77
N Genes	11

MAPK3 (ERK1) activation (R-HSA-110056)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.591
N Genes	10

BH3-only proteins associate with and inactivate anti-apoptotic BCL-2 members (R-HSA-111453)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	1.805
N Genes	9

RAF-independent MAPK1/3 activation (R-HSA-112409)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	1.691
N Genes	23

MAPK1 (ERK2) activation (R-HSA-112411)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.785
N Genes	9

SOS-mediated signalling (R-HSA-112412)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	1.539
N Genes	7

Cytokine Signaling in Immune system (R-HSA-1280215)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	1.047
N Genes	709

Signaling by Activin (R-HSA-1502540)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.761
N Genes	17

Disease (R-HSA-1643685)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.195
N Genes	1668

Signaling by EGFR in Cancer (R-HSA-1643713)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	1.008
N Genes	25

MyD88-independent TLR4 cascade (R-HSA-166166)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.74
N Genes	108

Signaling by NTRKs (R-HSA-166520)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.859
N Genes	129

Toll Like Receptor 9 (TLR9) Cascade (R-HSA-168138)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.854
N Genes	105

Toll Like Receptor 10 (TLR10) Cascade (R-HSA-168142)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.795
N Genes	94

Toll Like Receptor 3 (TLR3) Cascade (R-HSA-168164)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.798
N Genes	104

Toll Like Receptor 5 (TLR5) Cascade (R-HSA-168176)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.795
N Genes	94

Toll Like Receptor 7/8 (TLR7/8) Cascade (R-HSA-168181)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.871
N Genes	102

NOD1/2 Signaling Pathway (R-HSA-168638)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	1.101
N Genes	36

Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways (R-HSA-168643)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.981
N Genes	56

TICAM1, RIP1-mediated IKK complex recruitment (R-HSA-168927)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Up
FDR	0.001
Av. FC	0.922
N Genes	19

Recognition of DNA damage by PCNA-containing replication complex (R-HSA-110314)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.271
N Genes	30

Assembly Of The HIV Virion (R-HSA-175474)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.075
N Genes	16

Diseases associated with glycosaminoglycan metabolism (R-HSA-3560782)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.062
N Genes	38

Phase 1 - inactivation of fast Na⁺ channels (R-HSA-5576894)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-1.797
N Genes	6

TP53 Regulates Transcription of Genes Involved in G1 Cell Cycle Arrest (R-HSA-6804116)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.278
N Genes	14

DNA Damage Bypass (R-HSA-73893)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.127
N Genes	48

NR1H2 & NR1H3 regulate gene expression to limit cholesterol uptake (R-HSA-9031525)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.378
N Genes	5

Defective Base Excision Repair Associated with NTHL1 (R-HSA-9616333)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-4.564
N Genes	1

Defective NTHL1 substrate processing (R-HSA-9630221)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-4.564
N Genes	1

Defective NTHL1 substrate binding (R-HSA-9630222)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-4.564
N Genes	1

NFE2L2 regulates pentose phosphate pathway genes (R-HSA-9818028)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.081
N Genes	8

Translesion synthesis by POLK (R-HSA-5655862)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.013
N Genes	17

Inhibition of TSC complex formation by PKB (R-HSA-165181)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.138
N Genes	3

Myogenesis (R-HSA-525793)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.24
N Genes	25

Signaling by LTK in cancer (R-HSA-9842640)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-0.296
N Genes	7

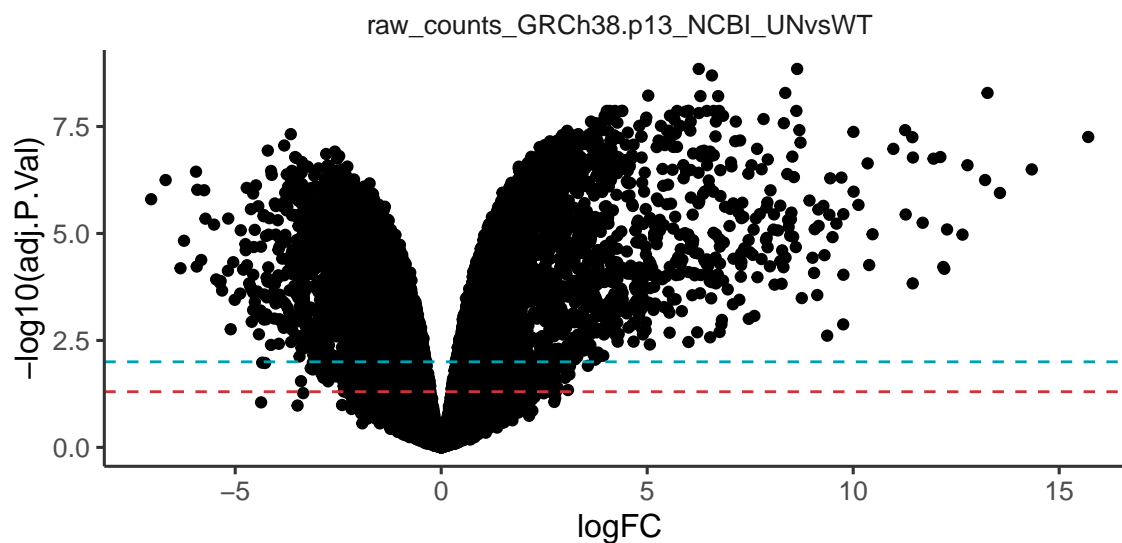
Defective SLC1A1 is implicated in schizophrenia 18 (SCZD18) and dicarboxylic aminoaciduria (DCBXA) (R-HSA-5619067)

	raw_counts_GRCh38.p13_NCBI_UNvsWT
Regulation	Down
FDR	0.001
Av. FC	-2.571
N Genes	1

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

raw_counts_GRCh38.p13_NCBI_UNvsWT

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
6648	8.640060	10.743271	61.58430	0	0	20.84098
4790	6.251164	8.750970	59.82359	0	0	20.58342

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
80149	6.571283	7.066217	55.12423	0	0	19.62698
7128	8.351622	8.787048	47.10008	0	0	18.71579
3576	13.260963	7.147679	47.81562	0	0	16.77721
84879	5.025525	11.137953	45.46615	0	0	18.60694
6385	6.293095	7.157872	44.57944	0	0	18.20094
11182	6.722913	7.564311	43.93286	0	0	18.12525
283149	4.220240	7.153010	39.04257	0	0	17.27189
4792	6.447821	8.918350	38.80355	0	0	17.25303

Top down-regulated protein/genes

raw_counts_GRCh38.p13_NCBI_UNvsWT

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
64170	-3.650811	5.894628	-28.24456	0	0e+00	14.41687
8986	-3.809817	5.260786	-24.60575	0	1e-07	13.17045
5055	-4.209348	4.600760	-23.33071	0	1e-07	12.64844
328	-2.580516	6.946197	-23.10388	0	1e-07	12.59876
10235	-2.792460	6.276486	-22.67676	0	1e-07	12.44009
2242	-2.476278	7.408913	-22.30853	0	2e-07	12.26075
863	-3.545401	4.057215	-21.93610	0	2e-07	12.09702
3417	-3.519782	5.268256	-21.75259	0	2e-07	12.07512
339559	-2.521299	6.165952	-21.59519	0	2e-07	11.98559
10613	-3.382260	5.803734	-20.93586	0	2e-07	11.71785