

Reactome Analysis Result

31 October, 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

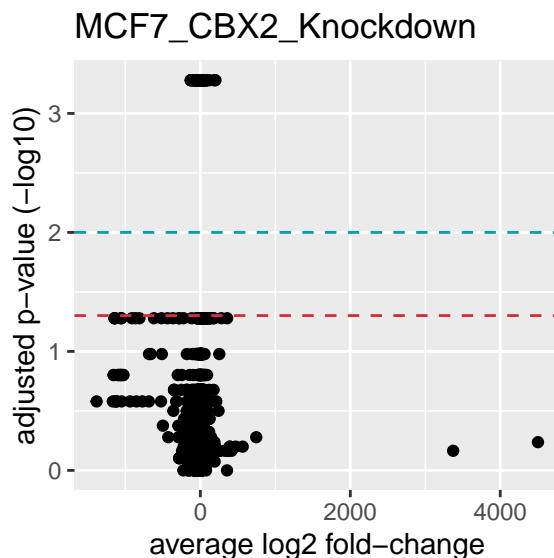
- Number of datasets analysed: 1
- Reactome version: 82
- Disease pathways were included

Dataset summaries

MCF7_CBX2_Knockdown:

- 2215 pathways
- 3763 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

PKA-mediated phosphorylation of CREB (R-HSA-111931)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	12.263
N Genes	5

PAOs oxidise polyamines to amines (R-HSA-141334)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	6.722
N Genes	1

Translocation of SLC2A4 (GLUT4) to the plasma membrane (R-HSA-1445148)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	19.463
N Genes	19

Acyl chain remodelling of PC (R-HSA-1482788)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	16.611
N Genes	11

Acyl chain remodelling of PG (R-HSA-1482925)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	27.232
N Genes	7

PKA activation (R-HSA-163615)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	17.687
N Genes	4

Abortive elongation of HIV-1 transcript in the absence of Tat (R-HSA-167242)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	8.735
N Genes	4

Adenylate cyclase activating pathway (R-HSA-170660)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	33.707
N Genes	2

Adenylate cyclase inhibitory pathway (R-HSA-170670)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	33.707
N Genes	2

Interactions of Tat with host cellular proteins (R-HSA-176034)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	43.86
N Genes	2

Retrograde neurotrophin signalling (R-HSA-177504)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	25.39
N Genes	4

Organelle biogenesis and maintenance (R-HSA-1852241)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	4.454
N Genes	118

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

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	13.188
N Genes	47

Ubiquinol biosynthesis (R-HSA-2142789)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	11.306
N Genes	3

Interconversion of polyamines (R-HSA-351200)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	6.722
N Genes	1

DSCAM interactions (R-HSA-376172)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	8.516
N Genes	4

CTLA4 inhibitory signaling (R-HSA-389513)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	37.583
N Genes	7

Defective GFPT1 causes CMSTA1 (R-HSA-4085023)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	19.698
N Genes	1

Platelet homeostasis (R-HSA-418346)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	7.34
N Genes	22

G alpha (z) signalling events (R-HSA-418597)

	MCF7_CBX2_Knockdown
Regulation	Up
FDR	0.001
Av. FC	11.021
N Genes	9

Synthesis of PS (R-HSA-1483101)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-69.87
N Genes	1

Macroautophagy (R-HSA-1632852)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-1.952
N Genes	40

PP2A-mediated dephosphorylation of key metabolic factors (R-HSA-163767)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-20.448
N Genes	1

Pausing and recovery of Tat-mediated HIV elongation (R-HSA-167238)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-5.98
N Genes	7

Tat-mediated HIV elongation arrest and recovery (R-HSA-167243)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-5.98
N Genes	7

HIV elongation arrest and recovery (R-HSA-167287)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-5.98
N Genes	7

Pausing and recovery of HIV elongation (R-HSA-167290)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-5.98
N Genes	7

ARMS-mediated activation (R-HSA-170984)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-17.528
N Genes	2

Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane (R-HSA-190840)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-35.751
N Genes	7

vRNP Assembly (R-HSA-192905)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-15.159
N Genes	1

Axonal growth inhibition (RHOA activation) (R-HSA-193634)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-32.494
N Genes	4

p75NTR regulates axonogenesis (R-HSA-193697)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-32.494
N Genes	4

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

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-21.317
N Genes	12

Olfactory Signaling Pathway (R-HSA-381753)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-50.244
N Genes	5

Post-chaperonin tubulin folding pathway (R-HSA-389977)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-38.07
N Genes	8

Passive transport by Aquaporins (R-HSA-432047)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-45.542
N Genes	1

Activation of NMDA receptors and postsynaptic events (R-HSA-442755)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-20.303
N Genes	25

Signaling by AXIN mutants (R-HSA-4839735)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-6.465
N Genes	4

Signaling by CTNNB1 phospho-site mutants (R-HSA-4839743)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-6.465
N Genes	4

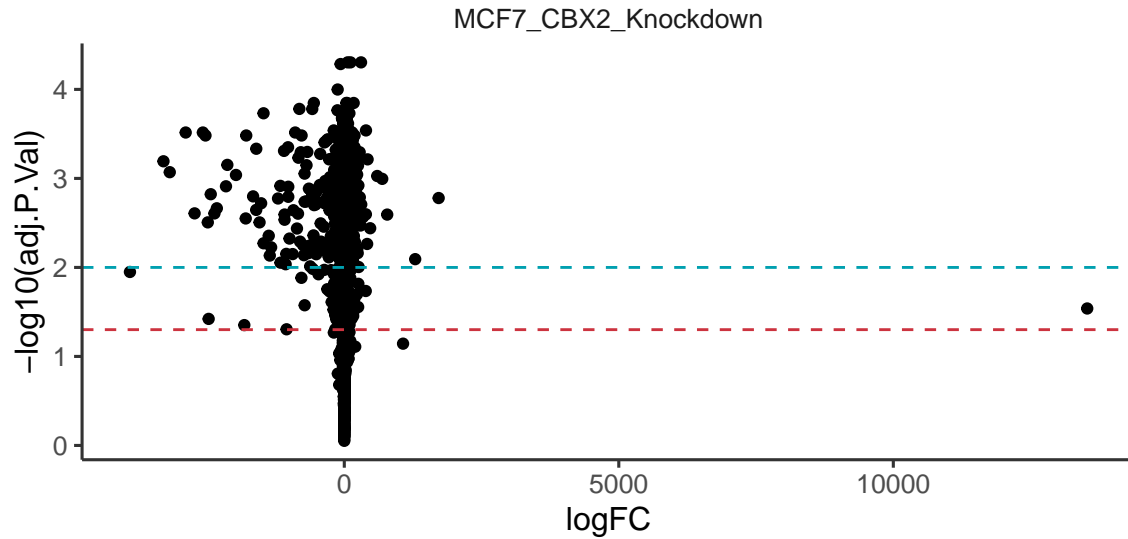
Signaling by APC mutants (R-HSA-4839744)

	MCF7_CBX2_Knockdown
Regulation	Down
FDR	0.001
Av. FC	-6.465
N Genes	4

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

MCF7_CBX2_Knockdown

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
ENSA	305.22446	294.85798	73.54608	0.0e+00	0.0000497	2.665433
FBP1	113.39127	142.16464	66.40942	0.0e+00	0.0000497	2.653692
HIST1H2AE	61.54871	39.53415	64.72573	0.0e+00	0.0000497	2.650351
BTBD6	37.69091	34.89619	42.52402	3.0e-07	0.0001421	2.563979
KIF9	49.89677	29.60996	41.89431	3.0e-07	0.0001421	2.559456
CERCAM	170.99839	120.54338	40.97598	3.0e-07	0.0001421	2.552498
RAP2C	41.46238	43.72748	35.38822	7.0e-07	0.0001854	2.498458
CDK9	93.34508	89.65361	34.45092	8.0e-07	0.0001854	2.486877
RGS19	35.03275	30.64962	31.81770	1.1e-06	0.0002103	2.449051
MRFAP1L1	43.73138	78.06631	31.79838	1.1e-06	0.0002103	2.448741

Top down-regulated protein/genes

MCF7_CBX2_Knockdown

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
PRDX6	-67.39595	220.90649	-60.32961	1.0e-07	0.0000519	2.640297
RTN4	-120.55664	191.00638	-50.00869	1.0e-07	0.0001003	2.605705

OST4	-554.72784	407.22789	-44.59789	2.0e-07	0.0001421	2.577593
RPL27	-818.52050	1715.53674	-38.78314	4.0e-07	0.0001656	2.533929
RPL27A	-583.51867	1038.86445	-37.98763	5.0e-07	0.0001659	2.526422
PDHA1	-124.12719	159.39725	-37.02118	5.0e-07	0.0001717	2.516677
RPL32	-1470.71694	1824.68562	-34.81318	7.0e-07	0.0001854	2.491458
PPP2R1B	-20.44768	21.17044	-34.25421	8.0e-07	0.0001854	2.484332
RDH11	-38.99037	36.00134	-32.48419	1.0e-06	0.0002103	2.459445
PPP3R1	-42.54210	49.56396	-32.22284	1.1e-06	0.0002103	2.455441
