

Reactome Analysis Result

01 May, 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

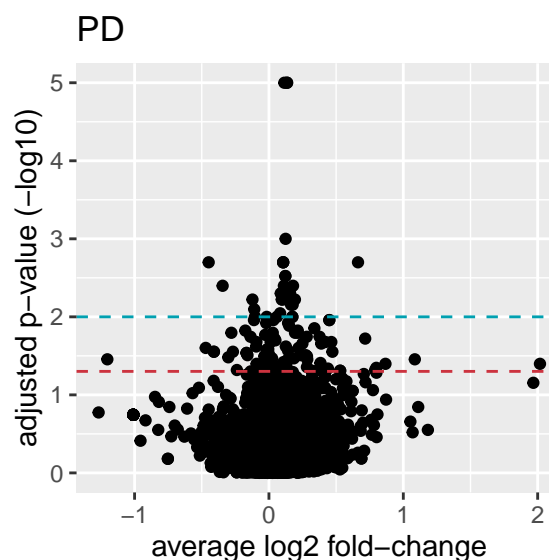
- Number of datasets analysed: 1
- Reactome version: 76
- Disease pathways were included

Dataset summaries

PD:

- 2458 pathways
- 12881 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

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

	PD
Regulation	Up
FDR	< 0.001
Av. FC	0.115
N Genes	93

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

	PD
Regulation	Up
FDR	< 0.001
Av. FC	0.135
N Genes	89

MyD88 dependent cascade initiated on endosome (R-HSA-975155)

	PD
Regulation	Up
FDR	< 0.001
Av. FC	0.135
N Genes	89

TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation (R-HSA-975138)

	PD
Regulation	Up
FDR	0.001
Av. FC	0.124
N Genes	88

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

	PD
Regulation	Up
FDR	0.002
Av. FC	0.106
N Genes	83

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

	PD
Regulation	Up
FDR	0.002
Av. FC	0.106
N Genes	83

Defective SLC7A7 causes lysinuric protein intolerance (LPI) (R-HSA-5660862)

	PD
Regulation	Up
FDR	0.002
Av. FC	0.663
N Genes	2

MyD88 cascade initiated on plasma membrane (R-HSA-975871)

	PD
Regulation	Up
FDR	0.002
Av. FC	0.106
N Genes	83

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

	PD
Regulation	Up
FDR	0.003
Av. FC	0.122
N Genes	96

TRIF(TICAM1)-mediated TLR4 signaling (R-HSA-937061)

	PD
Regulation	Up
FDR	0.003
Av. FC	0.122
N Genes	96

Toll-like Receptor Cascades (R-HSA-168898)

	PD
Regulation	Up
FDR	0.004
Av. FC	0.179
N Genes	148

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

	PD
Regulation	Up
FDR	0.004
Av. FC	0.111
N Genes	92

Toll Like Receptor TLR1:TLR2 Cascade (R-HSA-168179)

	PD
Regulation	Up
FDR	0.005
Av. FC	0.157
N Genes	100

Toll Like Receptor 2 (TLR2) Cascade (R-HSA-181438)

	PD
Regulation	Up
FDR	0.005
Av. FC	0.157
N Genes	100

Disease (R-HSA-1643685)

	PD
Regulation	Up
FDR	0.005
Av. FC	0.088
N Genes	1471

SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription (R-HSA-2173796)

	PD
Regulation	Up
FDR	0.006
Av. FC	0.193
N Genes	31

Early Phase of HIV Life Cycle (R-HSA-162594)

	PD
Regulation	Up
FDR	0.006
Av. FC	0.095
N Genes	14

Infectious disease (R-HSA-5663205)

	PD
Regulation	Up
FDR	0.006
Av. FC	0.099
N Genes	777

TNF signaling (R-HSA-75893)

	PD
Regulation	Up
FDR	0.006
Av. FC	0.13
N Genes	44

Toll Like Receptor 4 (TLR4) Cascade (R-HSA-166016)

	PD
Regulation	Up
FDR	0.007
Av. FC	0.176
N Genes	128

Defective Mismatch Repair Associated With MSH3 (R-HSA-5632927)

	PD
Regulation	Down
FDR	0.002
Av. FC	-0.449
N Genes	2

Diseases of Mismatch Repair (MMR) (R-HSA-5423599)

	PD
Regulation	Down
FDR	0.004
Av. FC	-0.345
N Genes	6

Mismatch repair (MMR) directed by MSH2:MSH3 (MutSbeta) (R-HSA-5358606)

	PD
Regulation	Down
FDR	0.006
Av. FC	-0.123
N Genes	15

Retrograde transport at the Trans-Golgi-Network (R-HSA-6811440)

	PD
Regulation	Down
FDR	0.008
Av. FC	-0.109
N Genes	49

Synthesis of IP2, IP, and Ins in the cytosol (R-HSA-1855183)

	PD
Regulation	Down
FDR	0.01
Av. FC	-0.104
N Genes	13

Endosomal Sorting Complex Required For Transport (ESCRT) (R-HSA-917729)

	PD
Regulation	Down
FDR	0.01
Av. FC	-0.017
N Genes	29

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

	PD
Regulation	Down
FDR	0.011
Av. FC	-0.011
N Genes	69

Mismatch Repair (R-HSA-5358508)

	PD
Regulation	Down
FDR	0.011
Av. FC	-0.111
N Genes	16

Uptake and function of anthrax toxins (R-HSA-5210891)

	PD
Regulation	Down
FDR	0.012
Av. FC	-0.02
N Genes	11

Assembly of the ORC complex at the origin of replication (R-HSA-68616)

	PD
Regulation	Down
FDR	0.015
Av. FC	-0.176
N Genes	6

Defective Mismatch Repair Associated With MSH2 (R-HSA-5632928)

	PD
Regulation	Down
FDR	0.016
Av. FC	-0.28
N Genes	3

Diseases of DNA repair (R-HSA-9675135)

	PD
Regulation	Down
FDR	0.017
Av. FC	-0.028
N Genes	13

Regulation of pyruvate dehydrogenase (PDH) complex (R-HSA-204174)

	PD
Regulation	Down
FDR	0.018
Av. FC	-0.137
N Genes	15

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

	PD
Regulation	Down
FDR	0.021
Av. FC	-0.093
N Genes	49

Mismatch repair (MMR) directed by MSH2:MSH6 (MutSalph) (R-HSA-5358565)

	PD
Regulation	Down
FDR	0.024
Av. FC	-0.095
N Genes	15

5-Phosphoribose 1-diphosphate biosynthesis (R-HSA-73843)

	PD
Regulation	Down
FDR	0.025
Av. FC	-0.47
N Genes	2

HIV Life Cycle (R-HSA-162587)

	PD
Regulation	Down
FDR	0.026
Av. FC	-0.005
N Genes	147

Budding and maturation of HIV virion (R-HSA-162588)

	PD
Regulation	Down
FDR	0.026
Av. FC	-0.013
N Genes	27

G beta:gamma signalling through CDC42 (R-HSA-8964616)

	PD
Regulation	Down
FDR	0.027
Av. FC	-0.016
N Genes	18

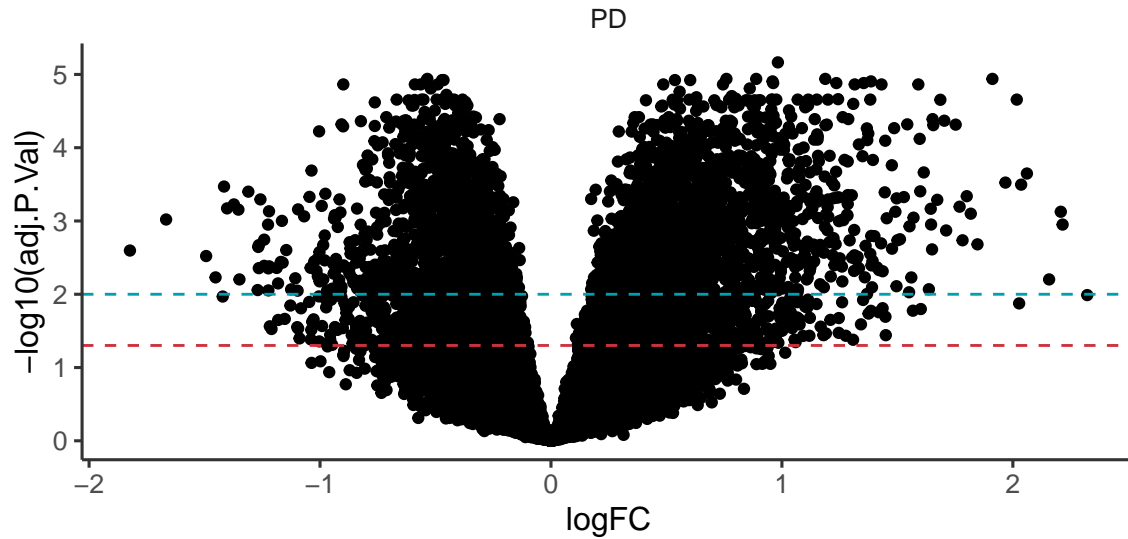
Synthesis of PIPs at the late endosome membrane (R-HSA-1660517)

	PD
Regulation	Down
FDR	0.028
Av. FC	-0.268
N Genes	11

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

PD

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
SLC6A12	0.9825957	5.145813	7.130456	0	6.80e-06	12.587668
ADAM33	1.1878063	4.528631	6.796827	0	1.15e-05	11.205818
EPOR	0.7597852	3.792112	6.621734	0	1.15e-05	10.463268
ISYNA1	0.8886739	4.805224	6.611507	0	1.15e-05	10.455898
HSPB1	1.9115185	7.574656	6.592483	0	1.15e-05	10.364440
SLC3A2	0.6029919	7.126062	6.496148	0	1.19e-05	9.986821
TRIM8	0.5367830	7.125815	6.457508	0	1.19e-05	9.830891
SMOX	0.9592588	5.911144	6.402872	0	1.24e-05	9.611292
SMTN	1.3856837	5.211364	6.392057	0	1.24e-05	9.568070
TRIP10	1.2356391	3.824521	6.330367	0	1.31e-05	9.302228

Top down-regulated protein/genes

PD

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
MSH2	-0.5352177	5.113783	-6.628472	0	1.15e-05	10.525032
MED14	-0.4718217	5.143853	-6.472945	0	1.19e-05	9.894637

HERC1	-0.4651456	7.458897	-6.442366	0	1.19e-05	9.768710
AKAP6	-0.5380794	7.591714	-6.441186	0	1.19e-05	9.762843
HACL1	-0.5893280	3.764473	-6.291771	0	1.37e-05	9.125784
GPCPD1	-0.8991474	5.708420	-6.250770	0	1.37e-05	8.999252
DDHD2	-0.5642909	7.000835	-6.218963	0	1.37e-05	8.872738
ATR	-0.4904745	4.667666	-6.214338	0	1.37e-05	8.853558
LRPPRC	-0.5203778	7.075826	-6.165760	0	1.55e-05	8.660389
MTCH2	-0.4525815	5.967504	-6.100593	0	1.90e-05	8.396758
