

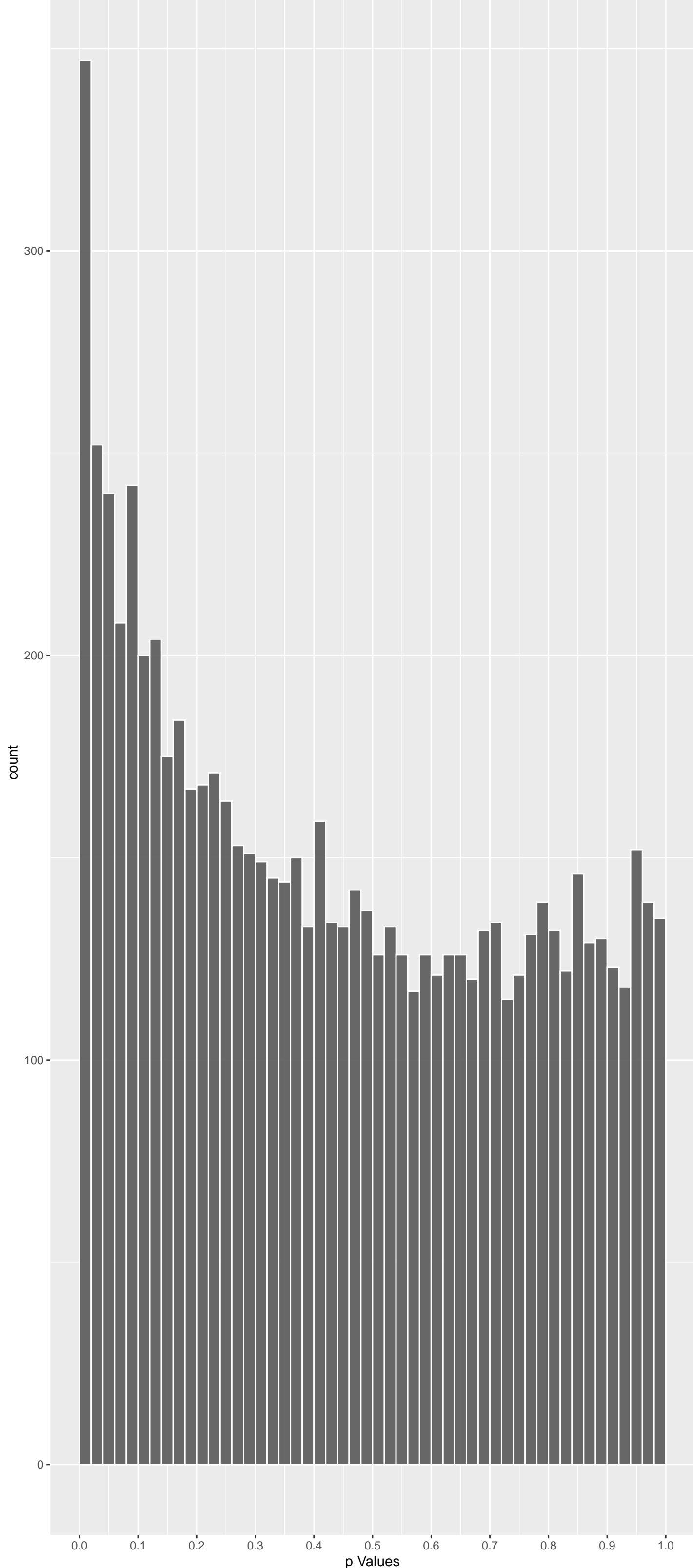
Top genes by P-value Permulated

Gene	Rho	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PPFIA3	-5.484826	1.241630e-07	5.382e-05	0.000e+00	0.000e+00	2.295e-02	0.000e+00
CHMP1B	0.000000	1.000000e+00	1.000e+00	0.000e+00	0.000e+00	1.000e+00	0.000e+00
ANKRD35	6.627095	1.027075e-10	2.377e-07	1.944e-05	1.944e-05	5.502e-04	9.733e-02
RAB8A	-3.921970	2.634834e-04	1.274e-02	3.444e-05	3.444e-05	6.049e-01	1.076e-01
DNAH2	8.123462	1.359214e-15	2.202e-11	3.583e-05	3.583e-05	3.568e-07	1.076e-01
ABCB1	-4.422030	2.933337e-05	2.898e-03	4.486e-05	4.486e-05	2.845e-01	1.112e-01
C1QTNF8	4.770376	5.516465e-06	8.714e-04	5.892e-05	5.892e-05	1.371e-01	1.112e-01
HAS2	-4.641299	1.038676e-05	1.389e-03	5.919e-05	5.919e-05	1.844e-01	1.112e-01
RGPD8	-4.769531	5.539656e-06	8.714e-04	9.069e-05	9.069e-05	1.371e-01	1.514e-01
OVOL1	4.076234	1.373129e-08	8.240e-03	1.179e-04	1.179e-04	4.923e-01	1.539e-01
TACR2	5.843973	1.529109e-08	1.032e-05	1.314e-04	1.314e-04	6.969e-03	1.539e-01
SDS	-4.446206	2.622010e-05	2.639e-03	1.417e-04	1.417e-04	2.655e-01	1.539e-01
CFAP45	5.595518	6.598918e-08	3.449e-05	1.471e-04	1.471e-04	1.790e-02	1.539e-01
FNBP4	-5.508997	1.082651e-07	4.873e-05	1.484e-04	1.484e-04	2.193e-02	1.539e-01
UBR2	-4.881997	3.150512e-06	5.867e-04	1.654e-04	1.654e-04	1.089e-01	1.539e-01
PROM1	-6.306251	8.576256e-10	1.390e-06	1.666e-04	1.666e-04	1.910e-03	1.539e-01
ARHGEF12	5.174211	6.866275e-07	2.139e-04	1.901e-04	1.901e-04	6.666e-02	1.539e-01
ABHD11	-5.146905	7.944563e-07	2.384e-04	2.050e-04	2.050e-04	7.132e-02	1.539e-01
HSD17B6	-4.274801	5.739255e-05	4.629e-03	2.183e-04	2.183e-04	3.682e-01	1.539e-01
ELL	-5.398452	2.016556e-07	7.969e-05	2.272e-04	2.272e-04	3.149e-02	1.539e-01
SLC10A6	-4.962615	2.086510e-06	4.448e-04	2.329e-04	2.329e-04	9.483e-02	1.539e-01
ADAM2	-5.354728	2.570561e-07	9.916e-05	2.346e-04	2.346e-04	3.825e-02	1.539e-01
VPS11	4.185160	8.548963e-05	5.894e-03	2.437e-04	2.437e-04	4.051e-01	1.539e-01
CLCNKA	-5.287575	3.718461e-07	1.339e-04	2.459e-04	2.459e-04	4.820e-02	1.539e-01
ZNF446	-4.475458	2.287432e-05	2.376e-03	2.713e-04	2.713e-04	2.467e-01	1.588e-01

Top genes by Q-Value Permulated

Gene	Rho	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PPFIA3	-5.484826	1.241630e-07	5.382e-05	0.000e+00	0.000e+00	2.295e-02	0.000e+00
CHMP1B	0.000000	1.000000e+00	1.000e+00	0.000e+00	0.000e+00	1.000e+00	0.000e+00
ANKRD35	6.627095	1.027075e-10	2.377e-07	1.944e-05	1.944e-05	5.502e-04	9.733e-02
RAB8A	-3.921970	2.634834e-04	1.274e-02	3.444e-05	3.444e-05	6.049e-01	1.076e-01
DNAH2	8.123462	1.359214e-15	2.202e-11	3.583e-05	3.583e-05	3.568e-07	1.076e-01
ABCB1	-4.422030	2.933337e-05	2.898e-03	4.486e-05	4.486e-05	2.845e-01	1.112e-01
HAS2	-4.641299	1.038676e-05	1.389e-03	5.919e-05	5.919e-05	1.844e-01	1.112e-01
C1QTNF8	4.770376	5.516465e-06	8.714e-04	5.892e-05	5.892e-05	1.371e-01	1.112e-01
RGPD8	-4.769531	5.539656e-06	8.714e-04	9.069e-05	9.069e-05	1.371e-01	1.514e-01
ABHD11	-5.146905	7.944563e-07	2.384e-04	2.050e-04	2.050e-04	7.132e-02	1.539e-01
SDS	-4.446206	2.622010e-05	2.639e-03	1.417e-04	1.417e-04	2.655e-01	1.539e-01
ELL	-5.398452	2.016556e-07	7.969e-05	2.272e-04	2.272e-04	3.149e-02	1.539e-01
FNBP4	-5.508997	1.082651e-07	4.873e-05	1.484e-04	1.484e-04	2.193e-02	1.539e-01
ADAM2	-5.354728	2.570561e-07	9.916e-05	2.346e-04	2.346e-04	3.825e-02	1.539e-01
SLC10A6	-4.962615	2.086510e-06	4.448e-04	2.329e-04	2.329e-04	9.483e-02	1.539e-01
CLCNKA	-5.287575	3.718461e-07	1.339e-04	2.459e-04	2.459e-04	4.820e-02	1.539e-01
OVOL1	4.076234	1.373129e-08	8.240e-03	1.179e-04	1.179e-04	4.923e-01	1.539e-01
CFAP45	5.595518	6.598918e-08	3.449e-05	1.471e-04	1.471e-04	1.790e-02	1.539e-01
UBR2	-4.881997	3.150512e-06	5.867e-04	1.654e-04	1.654e-04	1.089e-01	1.539e-01
TACR2	5.843973	1.529109e-08	1.032e-05	1.314e-04	1.314e-04	6.969e-03	1.539e-01
ARHGEF12	5.174211	6.866275e-07	2.139e-04	1.901e-04	1.901e-04	6.666e-02	1.539e-01
PROM1	-6.306251	8.576256e-10	1.390e-06	1.666e-04	1.666e-04	1.910e-03	1.539e-01
HSD17B6	-4.274801	5.739255e-05	4.629e-03	2.183e-04	2.183e-04	3.682e-01	1.539e-01
VPS11	4.185160	8.548963e-05	5.894e-03	2.437e-04	2.437e-04	4.051e-01	1.539e-01
PDCL	4.634848	1.071601e-05	1.412e-03	3.080e-04	3.080e-04	1.859e-01	1.588e-01

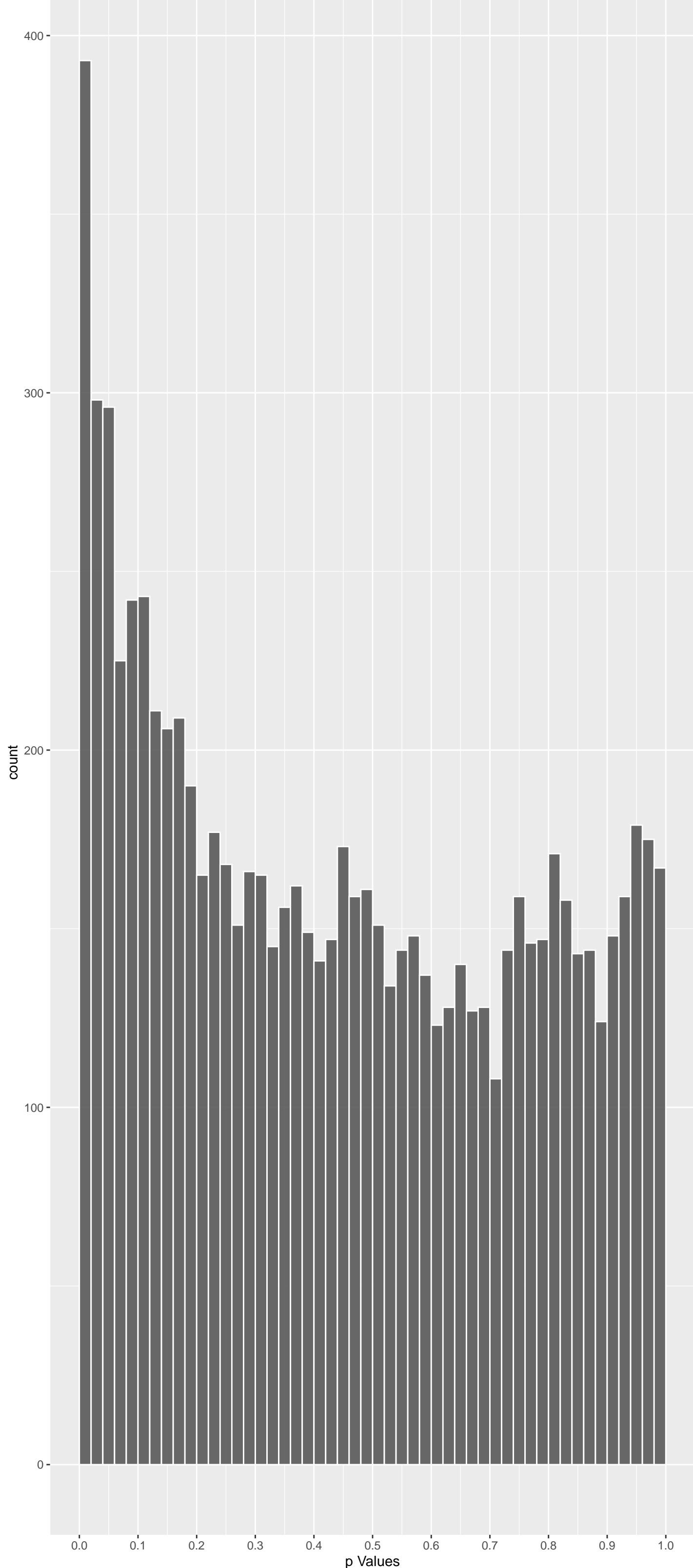
Positive Rho Permulated



Top Positive genes by P-value Permulated

Gene	Rho	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
ANKRD35	6.627095	1.027075e-10	2.377e-07	1.944e-05	1.944e-05	5.502e-04	9.733e-02
DNAH2	8.123462	1.359214e-15	2.202e-11	3.583e-05	3.583e-05	3.568e-07	1.076e-01
C1QTNF8	4.770376	5.516465e-06	8.714e-04	5.892e-05	5.892e-05	1.371e-01	1.112e-01
OVOL1	4.076234	1.373129e-08	8.240e-03	1.179e-04	1.179e-04	4.923e-01	1.539e-01
TACR2	5.843973	1.529109e-08	1.032e-05	1.314e-04	1.314e-04	6.969e-03	1.539e-01
CFAP45	5.595518	6.598918e-08	3.449e-05	1.471e-04	1.471e-04	1.790e-02	1.539e-01
ARHGEF12	5.174211	6.866275e-07	2.139e-04	1.901e-04	1.901e-04	6.666e-02	1.539e-01
VPS11	4.185160	8.548963e-05	5.894e-03	2.437e-04	2.437e-04	4.051e-01	1.539e-01
SFTPA1	4.345771	4.163610e-05	3.627e-03	3.058e-04	3.058e-04	3.159e-01	1.588e-01
PDCL	4.634848	1.071601e-05	1.412e-03	3.080e-04	3.080e-04	1.859e-01	1.588e-01

Negative Rho Permulated



Top Negative genes by P-value Permulated

Gene	Rho	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PPFIA3	-5.484826	1.241630e-07	5.382e-05	0.000e+00	0.000e+00	2.295e-02	0.000e+00
RAB8A	-3.921970	2.634834e-04	1.274e-02	3.444e-05	3.444e-05	6.049e-01	1.076e-01
ABCB1	-4.422030	2.933337e-05	2.898e-03	4.486e-05	4.486e-05	2.845e-01	1.112e-01
HAS2	-4.641299	1.038676e-05	1.389e-03	5.919e-05	5.919e-05	1.844e-01	1.112e-01
RGPD8	-4.769531	5.539656e-06	8.714e-04	9.069e-05	9.069e-05	1.371e-01	1.514e-01
SDS	-4.446206	2.622010e-05	2.639e-03	1.417e-04	1.417e-04	2.655e-01	1.539e-01
FNBP4	-5.508997	1.082651e-07	4.873e-05	1.484e-04	1.484e-04	2.193e-02	1.539e-01
UBR2	-4.881997	3.150512e-06	5.867e-04	1.654e-04	1.654e-04	1.089e-01	1.539e-01
PROM1	-6.306251	8.576256e-10	1.390e-06	1.666e-04	1.666e-04	1.910e-03	1.539e-01
ABHD11	-5.146905	7.944563e-07	2.384e-04	2.050e-04	2.050e-04	7.132e-02	1.539e-01

GO_Biological_Process_2023 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cilium Movement Involved In Cell Motilit	0.4327000	7	7.355e-05	9.907e-03	TEKT2:243 GAS8:333 TEK1:397 TEKT4:832 TEK75:1091 TEK73:2070
RIG-I Signaling Pathway (GO:0039529)	0.4066986	4	4.845e-03	1.450e-01	TRIM25:86 RNF135:683 OAS3:2142 PHB2:3254 NA NA
snRNA Modification (GO:0040031)	-0.3982016	4	5.811e-03	1.630e-01	NHP2:664 MEPC1:1041 METTL4:2120 METTL16:2700 NA NA
Striated Muscle Hypertrophy (GO:0014897)	0.3974506	4	5.904e-03	1.631e-01	HTR2B:174 MYOC:1067 TCAP:2410 RYR2:3117 NA NA
snRNA Transcription By RNA Polymerase II	-0.3933399	4	6.438e-03	1.660e-01	SNAPC5:205 ICE2:540 ZC3H8:2547 SNAPC1:3569 NA NA
Glucocorticoid Biosynthetic Process (GO: -0.3930256	3	1.838e-02	2.845e-01	CYP17A1:643 CYP11A1:1144 CYP21A2:3366 NA NA NA	
Negative Regulation Of Leukocyte Prolife	-0.3909163	5	2.467e-03	1.099e-01	IL33:138 LYN:264 ENPP3:440 GREM1:1056 TNFAIP3:6899 NA
SA Node Cell Action Potential (GO:008601	0.3895723	5	2.554e-03	1.106e-01	SCN3B:70 SCN5A:315 CACNA1G:909 CACNA1D:1118 HCN4:6695 NA
Hepoxilin Biosynthetic Process (GO:00511	0.3894269	4	6.986e-03	1.729e-01	ALOX15B:393 ALOXE3:871 ALOX15:873 ALOX12B:5173 NA NA
Hepoxilin Metabolic Process (GO:0051121)	0.3894269	4	6.986e-03	1.729e-01	ALOX15B:393 ALOXE3:871 ALOX15:873 ALOX12B:5173 NA NA
Negative Regulation Of Gene Expression V	-0.3824887	5	3.056e-03	1.160e-01	USP7:410 HELLS:1164 UHRF2:1205 UHRF1:2635 ZNF445:4002 NA
Intracellular Sequestering Of Iron Ion (-0.3736859	3	2.498e-02	3.109e-01	SRI:1130 FTH1:1336 FTHF:3594 NA NA NA	
Cellular Response To Leptin Stimulus (GO -0.3723909	6	1.583e-03	7.973e-02	UGCG:655 STAT3:795 SIRT1:995 LEPR:1091 NR4A3:4201 LEP:4562	
Regulation Of Endonoxylribonuclease Acti	-0.3713529	7	6.679e-04	4.443e-02	HMGB1:921 SIRT1:995 GZMA:1536 PRKCD:1678 RPS3:2046 DDX11:2091
Cellular Response To UV-A (GO:0071492)	0.3706472	9	1.179e-04	1.444e-02	MME:362 TIMP1:420 MMP9:548 MMPK3:596 OPN15W:1300 OPN3:2066
Positive Regulation Of Mast Cell Activat	-0.3663043	4	1.117e-02	2.249e-01	TSLP:116 SPHK2:505 NECTIN2:3754 NRA4A3:4201 NA NA
Chitin Catabolic Process (GO:0006032)	0.3658710	2	7.310e-02	4.439e-01	CTBS:1703 CHIT1:2715 NA NA NA NA
Chitin Metabolic Process (GO:0006030)	0.3658710	2	7.310e-02	4.439e-01	CTBS:1703 CHIT1:2715 NA NA NA NA
Serine Family Amino Acid Biosynthetic Pr	-0.3651139	10	6.391e-05	8.830e-03	SRR:68 SEPHS2:275 SERINC3:278 CTH:407 SERINC5:874 PSPH:1373
Positive Regulation Of Toll-Like Recepto	0.3548468	3	3.328e-02	3.448e-01	PTPN22:424 RSAD2:2707 SLC15A4:4075 NA NA NA
Regulation Of Toll-Like Receptor 7 Signa	0.3548468	3	3.328e-02	3.448e-01	PTPN22:424 RSAD2:2707 SLC15A4:4075 NA NA NA
Regulation Of Heterochromatin Formation	-0.3547256	7	1.154e-03	6.757e-02	SAMD1:1252 L3MBTL3:1732 CDK2:2002 TPR:2108 KDM1A:2776 MACROH2A1:2838
Cellular Response To Caffeine (GO:007131	0.3535853	5	6.177e-03	1.658e-01	RYR3:229 CASQ2:1175 RYR2:3117 RYR1:3384 SLC8A1:4212 NA
Response To Caffeine (GO:0031000)	0.3535853	5	6.177e-03	1.658e-01	RYR3:229 CASQ2:1175 RYR2:3117 RYR1:3384 SLC8A1:4212 NA
Regulation Of Monoatomic Anion Transport	-0.3533639	5	6.210e-03	1.658e-01	CA2:242 RAB1B:343 STC1:689 PDZK1:4901 ATP8B1:5660 NA
TRAIL-activated Apoptotic Signaling Path	-0.3528443	3	3.428e-02	3.456e-01	ZDHHC3:1612 SPI1:1683 FADD:3761 NA NA NA
Organic Hydroxy Compound Catabolic Proce	-0.3503321	6	2.960e-03	1.160e-01	HSD17B6:11 HGF23:742 LCT:1677 CYP24A1:2502 LDHD:3551 PDXP:5920
Negative Regulation Of CD8- positive, Alp	0.3503057	6	2.962e-03	1.160e-01	SOC3:361 ZBTB7B:831 DAPL1:2341 VSIR:3468 SLC4A2:3855 HFE:4005
Regulation Of Relaxation Of Muscle (GO:1 -0.3483387	3	3.664e-02	3.571e-01	SRI:1130 NEUROG1:2456 TIFAB:3684 NA NA NA	
Peptide Transport (GO:0015833)	0.3465613	4	1.637e-02	2.641e-01	CDH17:1053 DISP1:1441 TAP2:2377 TAP1:5277 NA NA
Membrane Lipid Catabolic Process (GO:004 -0.3426956	7	1.690e-03	8.355e-02	ENPP2:102 PPT1:71 SMDPD:2321 MGST2:2544 NAGA:2701 SGPL1:3481	
Axonemal Central Apparatus Assembly (GO: -0.3419322	6	5.098e-03	1.895e-01	DNAJB13:626 SPAG17:1473 SPEF1:2508 RSPH9:2838 HYDIN:5615 NA	
Inositol Metabolic Process (GO:0006020)	-0.3413715	5	3.782e-03	1.316e-01	MIOX:234 PPIP5K1:266 IMPA2:1082 ISYNA1:1658 SLC5A3:5213 PPIP5K2:6860
Glucocorticoid Metabolic Process (GO:000 -0.3400190	5	8.460e-03	1.914e-01	CYP17A1:643 CYP11A1:1144 HSD11B2:3099 CYP21A2:3366 YWHAH:4567 NA	
Transmembrane Receptor Protein Tyrosine	0.3333004	4	2.096e-02	2.949e-01	PTPRD:1284 PTN:2579 PTPRF:3200 TRIO:3947 NA NA
Leptin- Mediated Signaling Pathway (GO:00 -0.3298298	7	2.511e-03	1.106e-01	UGCG:655 STAT3:795 SIRT1:995 LEPR:1091 MKKS:3718 LEP:4562	
Cilium- Dependent Cell Motility (GO:00602	0.3282355	17	2.802e-06	9.437e-04	DNAH2:2 DNAH17:15 TEK72:243 GAS8:333 TEK1:397 TEKT4:832
Valine Metabolic Process (GO:0006573)	-0.3272274	5	1.127e-02	2.250e-01	HIBCH:428 BCAT1:481 BCAT2:556 IYBLB:6110 HIBADH:6319 NA
Copper Ion Import (GO:0015677)	0.3264548	6	5.618e-03	1.620e-01	STEAP4:922 STEAP2:1762 SLC31A2:2338 ATP7B:2734 SLC31A1:3544 STEAP3:5878
Negative Regulation Of cAMP--dependent Pr	-0.3252161	6	5.802e-03	1.630e-01	PRKARIA:465 SIRT1:995 PRKAR2A:1524 PKIB:2753 PRKAR2B:3870 PRKAR1B:7211

EnrichmentHsSymbolsFile2 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA	-0.39772802	6	7.509e-04	1.988e-02	HSPB1:231 CALU:282 PGAM1:289 AKR1B1:2689 OAT:3241 CTSD:3245
REACTOME_TRAIL_SIGNALING	-0.3684706	5	4.218e-03	5.962e-02	CASP8:345 TNFSF10:370 CASP10:2968 CFLAR:3103 FADD:3761 NA
SASAL_TARGETS_OF_CXCR6_AND_PTCH1_DN	-0.3639744	7	8.529e-04	2.145e-02	OTX1:513 ADAM28:1687 PIP5K1A:2141 APOD2:179 DAZL:2229 MDK:2358
NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	0.3553845	14	4.142e-06	3.347e-04	COL6A1:125 SPATC1L:676 PCB3P:905 PCNT:949 DIP2A:1306 POFUT2:1574
REACTOME_MET_ACTIVATES_PTN11	-0.3543166	5	6.069e-03	7.617e-02	PTPN11:714 GRB2:907 MET:1880 GAB1:3365 HGF:4918 NA
WP_DUAL_HIJACK_MODEL_OF_VIF_IN_HIV_INFE	-0.3440852	7	1.617e-03	3.209e-02	RBX1:805 CUL5:1319 CBFβ:2475 ELOC:2721 ELOB:2922 RUNX1:3128
WP_AFLATOXIN_B1_METABOLISM	0.3425762	2	9.332e-02	3.664e-01	EPHX1:1261 CYP1A2:3875 NA NA NA NA
BIOCARTA_TERT_PATHWAY	-0.3370366	8	9.623e-04	2.312e-02	MZF1:24 SP3:44 MYC:601 WT1:2000 TP53:2447 MAX:2480
SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP	0.3360426	6	4.361e-03	6.053e-02	TENM3:111 CHN2:124 TPPP3:2531 GJA1:2632 SYNGR3:4611 CXCL14:6009
BERGER_MBD2_TARGETS	0.3316365	2	1.043e-01	3.863e-01	CELA2A:2328 TFF2:3162 NA NA NA NA
NIKOLSKY_BREAST_CANCER_17P11_AMPLICON	0.3310199	10	2.891e-04	1.008e-02	SLC47A1:40 ALDH3A2:715 ULK2:921 MAPK7:1307 EPN2:1956 RNF112:2616
REACTOME_LEUKOTRIENE_RECEPTORS	0.3305484	5	1.047e-02	1.071e-01	CYSLTR2:41 LTBR4:244 LTBR4R2:1460 CYSLTR1:3033 GPR17:8999 NA
REACTOME_ERYTHROCYTES_TAKE_UP_OXYGEN_AND	-0.3283365	6	5.346e-03	6.999e-02	CGA:1616 HSD3B2:2812 LHB:3323 CYP21A2:3366 NA NA
REACTOME_MINERALOCORTICOID_BIOSYNTHESIS	-0.3279629	4	2.310e-02	1.751e-01	ABCB1:3 ALB:29 HSD11B1:54 HSD11B2:3099 SERPINB6:10826 NA
REACTOME_PREDNISONE_ADME	0.3267535	5	1.139e-02	1.127e-01	CHRN6:485 CHRN2:819 CHRNA4:1131 CHRN2B:2625 CHRN2A:3070 CHRNA3:3732
GARGALOVIC_RESPONSE_TO_OXIDIZED_POSTPHOL	-0.3231802	11	2.059e-04	7.859e-02	USP12:141 UGDH:542 ABHD3:991 SIRT1:995 RBBP6:1015 PIM1:1329
REACTOME_CHOLINE_CATABOLISM	-0.3219376	6	6.312e-03	8.757e-02	SLC44A1:368 DMGBD:1590 BHMT:1764 CHDH:3901 SARDH:4095 ALDH7A1:5563
REACTOME_TYPE_I_HEMIDESMOSOME_ASSEMBLY	0.3194070	11	2.442e-04	9.032e-03	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 KRT14:507 LAMB3:2108
WP_LNCRNAMEDIATED_MECHANISMS_OF_THERAPEU	-0.3149905	6	7.536e-03	8.778e-02	ABCB1:3 TP53:2447 HIF1A:2449 BCL2L1:3568 CDKN1A:4590 WNT6:4885
HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER	-0.3136956	7	4.049e-03	5.795e-02	MDM2:311 CCND2:480 FGF23:742 TSPAN31:2725 STK38L:3900 CDK4:4301
REACTOME_ESTABLISHMENT_OF_SISTER_CHROMAT	-0.3094044	11	3.802e-04	1.233e-02	STAG1:165 WAPL:653 STAG2:748 PDSN:585:1430 SMC3:1839 ESCO1:1944
WP_NICOTINE_EFFECT_ON_CHROMAFFIN_CELLS	0.3092904	4	3.215e-02	1.212e-01	CACNA1G:909 CHRNA4:370 CHRNA3:3732 CACNA1C:4724 NA NA
TURJANSKI_MAPK11_TARGETS	-0.3083739	5	1.693e-02	1.461e-01	MEF2C:1534 ELK1:1907 FOS:2213 FLMN:4838 ATF2:5001 NA
WIEMANN_TELOMERE_SHORTENING_AND_CHRONIC_	-0.3064893	3	6.596e-02	3.096e-01	HMGCR:1194 NR1D2:2832 CCFL5:5363 NA NA NA
REACTOME_MAPK1_ERK2_ACTIVATION	0.3048755	9	1.538e-03	3.139e-02	MAP2K2:92 PTN11:714 IL6:845 IL6ST:1603 JAK1:2874 TYK2:3793
REACTOME_CONJUGATION_OF_BEANZOATE_WITH_GL	0.2996712	2	1.421e-01	4.413e-01	GLYATL3:1919 ACSMB2:4606 NA NA NA NA
WP_NIPBL_ROLE_IN_DNA_DAMAGE_CORNELIA_DE	-0.2972222	7	6.461e-03	8.031e-02	CBX3:177 NIPBL:801 H2AX:1383 RNF8:2309 RNF168:3290 ATR:4070
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.2947028	34	2.746e-09	5.848e-07	SCAMP3:321 THBS3:356 EFNA3:412 DCST1:538 RUSC1:587 PBXIP1:630
NIKOLSKY_BREAST_CANCER_19P13_AMPLICON	-0.2945734	5	2.253e-02	1.726e-01	NR2F6:1417 OCB1:1659 MYO9B:1715 USHBP1:3229 USE1:8590 NA
WALLACE_PROSTATE_CANCER_DN	0.2916514	5	2.390e-02	1.783e-01	LAMA4:912 GJA1:2632 GPM6B:3142 RAP1B:4034 CAV2:6253 NA
BIOCARTA_RANMS_PATHWAY	-0.2915412	10	1.410e-03	2.970e-02	TPX2:217 NUMA1:922 GPNB1:1217 KPNNA2:1908 KIF15:2464 RANBP1:2783
KORKOLA_CHORIOCARCINOMA	-0.2865071	4	4.718e-02	2.555e-01	CGA:1616 LHB:3323 TPFI:4300 LEP:4562 NA NA
REACTOME_GLUCCORTICOID_BIOSYNTHESIS	-0.2855682	6	1.541e-02	1.577e-01	HSD11B1:54 CYP17A1:643 HSD3B2:2812 HSD11B2:3099 CYP21A2:3366 SERPINA6:10826
MYLLYKANAGAS_AMPLIFICATION_HOT_SPOT_1	-0.2851768	3	8.711e-02	3.543e-01	GATA1:579 TFE3:2600 WAS:7245 NA NA NA
REACTOME_ANDROGEN_BIOSYNTHESIS	-0.2851019	9	3.067e-03	4.876e-02	CYP17A1:643 HSD17B3:1092 CGA:1616 HSD3B2:2812 HSD17B12:3031 LHB:3323
WP_METHIONINE_METABOLISM_LEADING_TO_SULF	-0.2837163	11	1.120e-03	2.550e-02	GNMT:223 CTH:407 AHCY:903 CSA4:975 BHMT:1764 CDO1:4088
REACTOME_ELECTRIC_TRANSMISSION_ACROSS_GA	0.2836064	5	2.806e-02	1.965e-01	GJA10:38 PANX1:1629 PANX2:3760 GJC1:5773 GJD2:6420 NA
REACTOME_INTERLEUKIN_35_SIGNALLING	-0.2834042	12	6.861e-04	1.855e-02	IL12RB2:338 STAT3:795 IL6ST:1603 CANX:2437 IL27RA:2647 JAK1:2874
CHOI_ATL_ACUTE_STAGE	-0.2811314	4	5.148e-02	2.691e-01	MBD1:1719 MET:1880 ETV1:4778 LHX2:5785 NA NA

DisGeNET Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Diabetes--deafness syndrome maternally tr	-0.4540079	2	2.615e-02	3.330e-01	GCG:320 RAPGEF5:1120 NA NA NA NA
Color Blindness, Red	0.4388124	5	6.782e-04	6.460e-02	GNAT2:115 TEX28:423 OPN1LW:709 ATF6:1719 PDE6H:1964 NA
Spondylitis	-0.4303827	4	2.871e-03	1.461e-01	TNF:99 IL6:845 IL4:1133 VCAN:2299 NA NA
Congenital pyloric atresia	0.4246018	5	1.008e-03	8.912e-02	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 COL17A1:5471 NA
Junctional split	0.4224851	6	3.385e-04	4.427e-02	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 LAMB3:2108 LAMA3:4764
Localized vitiligo	-0.4203061	2	3.951e-02	3.887e-01	TNF:99 RBM45:2418 NA NA NA NA
Valvular disease	0.4129687	4	4.229e-03	1.700e-01	TIMP1:420 MMP9:548 TIMP2:2106 MMP2:2505 NA NA
Heritiz Disease	0.4071440	5	1.616e-03	1.117e-01	ITGB4:50 ITGA6:267 LAMC2:272 LAMB3:2108 LAMA3:4764 NA
Monilethrix	0.4042668	2	4.767e-02	4.079e-01	KRT80:303 DSG4:2753 NA NA NA NA
NOONAN SYNDROME 3	-0.4020566	5	1.848e-03	1.148e-01	SHOC2:459 SOS1:554 PTPN11:714 RAF1:835 KRAS:5235 NA
Neonatal alloimmune thrombocytopenia (NA	0.4008118	4	5.497e-03	1.909e-01	POU2F3:678 ITGB3:1325 PLA2G6:1975 PLA2G1B:2387 NA NA
Deficiency of monooxygenase	-0.4002087	2	4.995e-02	4.146e-01	CYP17A1:643 CYP2A41:2502 NA NA NA NA
X-Linked Infantile Nystagmus	0.3994022	3	1.657e-02	2.960e-01	FRMD17:179 CASK:885 GPR143:3782 NA NA NA
Angiokeratoma	-0.3980826	5	2.050e-03	1.221e-01	MANBA:259 VEGFA:482 GLA:720 DCAAF:1640 PTEN:5008 NA
T--lymphocyte immunodeficiency	0.3974587	6	7.472e-04	7.035e-02	SFTPA1:9 RAG1:43 CD3E:1166 SMARCAT1:1223 LBR:1624 SIPA1:5855
Chronic iridocyclitis	-0.3968144	2	5.204e-02	4.152e-01	IL6:845 RBM45:2418 NA NA NA NA
Bulla of lung	0.3949525	2	5.303e-02	4.152e-01	EPHX1:1261 TIMP2:2106 NA NA NA NA
Unilateral primary pulmonary dysgenesis	-0.3897480	5	2.542e-03	1.379e-01	TBX1:710 DGCR8:963 DGCR2:1105 DGCR6:1160 ESS2:4827 NA
Profound sensorineural hearing impairmen	0.3844221	4	7.748e-03	2.172e-01	RDX:391 CIB2:907 TRIOBP:2685 MYO15A:3438 NA NA
C3 Glomerulonephritis	0.3812874	3	2.217e-02	3.178e-01	CFHR5:1077 C3:1835 CFB:2798 NA NA NA
Papillary transitional cell carcinoma	-0.3810012	4	8.312e-03	2.198e-01	EGF:263 VEGFA:482 TP53:2447 ERBB2:4396 NA NA
Chilblain lupus 1	-0.3801020	3	2.259e-02	3.199e-01	GZMA:1536 TREX1:1848 SAMHD1:2257 NA NA NA
Small anterior fontanelle	-0.3793805	3	2.285e-02	3.199e-01	ORC1:736 MYCN:959 ATR:4070 NA NA NA
Focal Dermal Hypoplasia	-0.3769939	7	5.521e-04	5.616e-02	ALB:29 CYP26C1:245 TWIST2:820 GC:938 HCCS:2312 WNT3A:3778
Sore Throat	-0.3717820	4	1.002e-02	2.426e-01	TNF:99 SFI1:1220 CNOT1:2158 SMN2:4694 NA NA
Ineffective erythropoiesis	-0.3687181	5	4.298e-03	1.721e-01	GATA1:579 RPL26:1309 KLF11:1767 COX4I2:2797 SEC23B:3947 NA
Melanoma--Associated Retinopathy	0.3686096	3	2.701e-02	3.359e-01	RCVRN:1409 TRPM1:2432 IMMT:2456 NA NA NA
Plantar hyperkeratosis	0.3665791	6	1.768e-03	1.143e-01	PLEC:18 ITGB4:50 LAMC2:272 LAMB3:2108 LAMA3:4764 COL17A1:5471
Phosphorus measurement	-0.3659644	4	1.125e-02	2.554e-01	IP6K3:236 ENPP3:440 RGS14:1270 CSTA:6643 NA NA
Microcystic stromal tumor	0.3650379	5	4.700e-03	1.812e-01	MME:362 DICER1:814 VIM:2228 CTNNB1:3599 FOXL2:3873 NA
Chorioretinitis	-0.3602289	5	5.276e-03	1.885e-01	TNF:99 IL6:845 IFNG:1322 IL12:4283 IL10:4620 NA
Exudative age--related macular degenerati	-0.3592301	3	3.116e-02	3.541e-01	VEGFA:482 KDR:1230 FLT1:5021 NA NA NA
Hypomagnesuria	-0.3587335	6	2.341e-03	1.335e-01	CASR:34 CNM2:154 EGF:263 CLDN16:360 GNA11:5146 CLDN19:7703
Human metapneumovirus infection	-0.3576929	5	5.605e-03	1.909e-01	TNF:99 TSLP:116 PIP5K1:266 ISYNA1:1658 NCR1:9347 NA
Laryngismus	0.3575184	4	1.327e-02	2.702e-01	LAMC2:272 UBE3B:1999 LAMB3:2108 LAMA3:4764 NA NA
Female Pseudo--Turner Syndrome	-0.3556192	10	9.862e-05	2.546e-02	MAP2K2:92 MAP2K1:208 SHOC2:459 SOS1:554 PTPN11:714 RAF1:835
Rheumatoid Vasculitis	-0.3530058	2	8.370e-02	4.853e-01	CD28:2220 RBM45:2418 NA NA NA NA
Vitamin D--resistant rickets	-0.3519870	5	6.414e-03	2.015e-01	PTH:402 FGF23:742 RELB:2415 CYP2A41:2502 VDR:5749 NA
Myelitis	0.3518942	5	6.428e-03	2.015e-01	LAMC2:272 POU2F3:678 S100B:818 CSF2:2535 AQP4:7666 NA
Acute inflammatory demyelinating polyneu	-0.3516468	5	6.465e-03	2.020e-01	ALB:29 TNF:99 RBM45:2418 PMP22:2472 PTGDS:6593 NA