

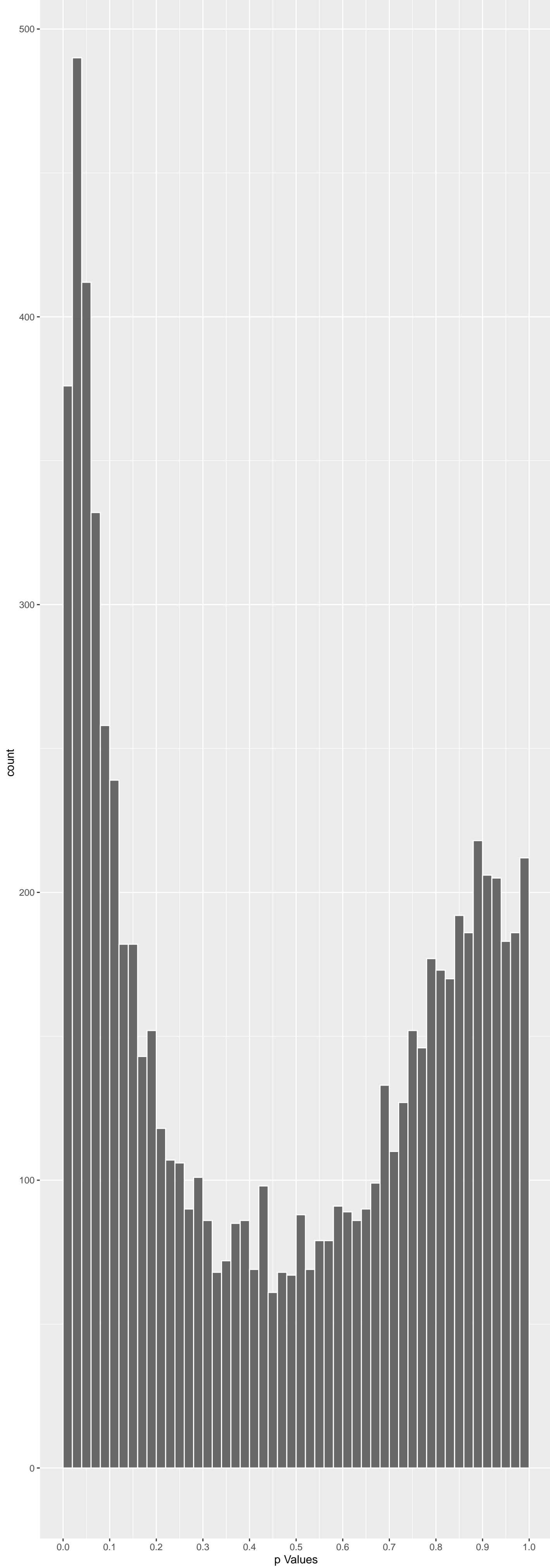
Top genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
AC010255	0.2862415	46	1.999e-02	1.496e-01	2.233e-03	1.000e+00	4.918e-01
CEP19	0.2620941	57	1.725e-02	1.375e-01	2.257e-03	1.000e+00	4.918e-01
TMEM216	0.2968999	54	8.714e-03	9.321e-02	2.456e-03	9.946e-01	4.918e-01
MARCHF4	0.2118844	91	1.435e-02	1.238e-01	2.460e-03	1.000e+00	4.918e-01
COPZ2	0.2881240	57	8.849e-03	9.938e-02	2.887e-03	9.946e-01	4.918e-01
SLC14A2	-0.3020572	118	6.757e-05	4.309e-03	3.069e-03	2.748e-01	4.918e-01
DZIP1	0.3280493	110	2.970e-05	2.450e-03	3.186e-03	2.007e-01	4.918e-01
FXYP6	0.2185245	68	2.965e-02	1.860e-01	3.372e-03	1.000e+00	4.918e-01
FNDC11	0.3917569	98	2.582e-06	5.228e-04	3.602e-03	1.055e-01	4.918e-01
RAB3B	0.3379367	42	8.814e-03	9.382e-02	3.634e-03	9.946e-01	4.918e-01
SAV1	-0.4623103	42	3.395e-04	1.278e-02	3.692e-03	4.731e-01	4.918e-01
RASL11B	0.2680241	54	1.789e-02	1.400e-01	3.851e-03	1.000e+00	4.918e-01
ZHX2	0.2551538	97	2.318e-03	4.210e-02	3.878e-03	7.622e-01	4.918e-01
PHLDB1	0.2122769	111	6.637e-03	7.982e-02	3.909e-03	9.423e-01	4.918e-01
SLC8A3	0.3213759	94	1.595e-04	7.762e-03	3.952e-03	3.777e-01	4.918e-01
CADPS2	0.3171220	100	1.204e-04	6.312e-03	4.016e-03	3.307e-01	4.918e-01
CD84	0.2108018	112	6.769e-03	8.044e-02	4.021e-03	9.423e-01	4.918e-01
ADARB2	-0.2328861	94	6.217e-03	7.642e-02	4.040e-03	9.385e-01	4.918e-01
SORCS1	0.2396231	102	3.335e-03	5.239e-02	4.160e-03	8.229e-01	4.918e-01
CMTR1	-0.2243401	65	2.916e-02	1.838e-01	4.175e-03	1.000e+00	4.918e-01
APCDD1	-0.2857765	91	9.589e-04	2.473e-02	4.234e-03	6.377e-01	4.918e-01
PROKR1	0.2288249	88	9.342e-03	9.681e-02	4.278e-03	1.000e+00	4.918e-01
SPIRE1	-0.1793261	101	2.885e-02	1.628e-01	4.335e-03	1.000e+00	4.918e-01
TNFRSF11B	0.2931201	98	4.351e-04	1.466e-02	4.353e-03	4.935e-01	4.918e-01
DNAH11	0.2388423	137	6.764e-04	1.968e-02	4.364e-03	5.727e-01	4.918e-01

Top genes by Q-Value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
M6PR	0.2756626	59	1.078e-02	1.047e-01	3.329e-02	1.000e+00	4.918e-01
CFTR	0.3181211	116	3.179e-05	2.561e-03	8.017e-03	2.062e-01	4.918e-01
YBX2	0.3897005	72	6.496e-05	4.251e-03	1.467e-02	2.733e-01	4.918e-01
ITGA3	0.2007961	112	9.895e-03	9.978e-02	1.937e-02	1.000e+00	4.918e-01
KRT33A	-0.2106784	74	2.854e-02	1.818e-01	2.146e-02	1.000e+00	4.918e-01
PGLYRP1	-0.2817490	74	3.405e-03	5.309e-02	1.622e-02	8.263e-01	4.918e-01
MGST1	-0.2914512	76	2.132e-03	3.984e-02	4.142e-02	7.426e-01	4.918e-01
UBR7	0.2715188	93	1.511e-03	3.272e-02	4.486e-03	7.076e-01	4.918e-01
RTN4R	-0.2022418	88	2.160e-02	1.567e-01	1.797e-02	1.000e+00	4.918e-01
CLDN11	0.1635836	41	2.106e-01	5.177e-01	2.880e-02	1.000e+00	4.918e-01
PKP2	0.1337284	103	9.973e-02	3.537e-01	4.710e-02	1.000e+00	4.918e-01
TRIB2	0.1997584	39	1.364e-01	4.186e-01	2.753e-02	1.000e+00	4.918e-01
LMCD1	0.1953246	78	3.699e-02	2.087e-01	5.943e-02	1.000e+00	4.918e-01
ANOS	-0.1701267	92	4.805e-02	2.399e-01	2.950e-02	1.000e+00	4.918e-01
KRT14	0.2076997	88	1.831e-02	1.422e-01	6.174e-02	1.000e+00	4.918e-01
KRT20	0.3226627	93	1.631e-04	7.885e-03	3.515e-02	3.797e-01	4.918e-01
NTN1	0.2406358	36	8.546e-02	3.258e-01	4.412e-02	1.000e+00	4.918e-01
TIGAR	-0.2470831	91	4.301e-03	6.180e-02	4.876e-02	8.822e-01	4.918e-01
FAM107B	-0.1255388	106	1.169e-01	3.851e-01	3.958e-02	1.000e+00	4.918e-01
CDK13	-0.0946497	95	2.636e-01	5.768e-01	4.993e-02	1.000e+00	4.918e-01
FAP	0.1289521	97	1.237e-01	3.961e-01	2.008e-02	1.000e+00	4.918e-01
DMRT3	0.2640984	72	6.795e-03	8.054e-02	5.706e-02	9.423e-01	4.918e-01
PLOD1	0.1822955	95	3.129e-02	1.911e-01	2.888e-02	1.000e+00	4.918e-01
MOGAT2	-0.2664729	98	1.364e-03	3.079e-02	1.693e-02	6.847e-01	4.918e-01
DIMT1	0.1037822	57	3.457e-01	6.490e-01	5.564e-02	1.000e+00	4.918e-01

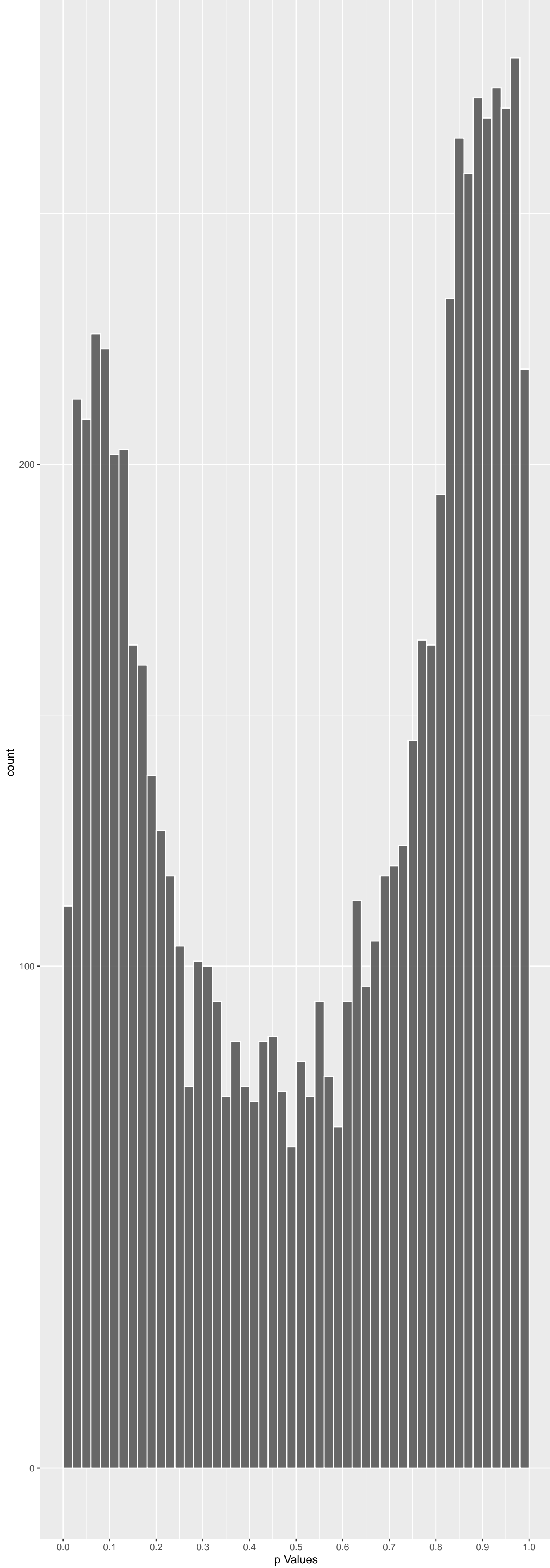
Positive Rho Permulated



Top Positive genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
AC010255	0.2862415	46	1.999e-02	1.496e-01	2.233e-03	1.000e+00	4.918e-01
CEP19	0.2620941	57	1.725e-02	1.375e-01	2.257e-03	1.000e+00	4.918e-01
TMEM216	0.2968999	54	8.714e-03	9.321e-02	2.456e-03	9.946e-01	4.918e-01
MARCHF4	0.2118844	91	1.435e-02	1.238e-01	2.460e-03	1.000e+00	4.918e-01
COPZ2	0.2881240	57	8.849e-03	9.938e-02	2.887e-03	9.946e-01	4.918e-01
DZIP1	0.3280493	110	2.970e-05	2.450e-03	3.186e-03	2.007e-01	4.918e-01
FXYP6	0.2185245	68	2.965e-02	1.860e-01	3.372e-03	1.000e+00	4.918e-01
FNDC11	0.3917569	98	2.582e-06	5.228e-04	3.602e-03	1.055e-01	4.918e-01
RAB3B	0.3379367	42	8.814e-03	9.382e-02	3.634e-03	9.946e-01	4.918e-01
RASL11B	0.2680241	54	1.789e-02	1.400e-01	3.851e-03	1.000e+00	4.918e-01

Negative Rho Permulated



Top Negative genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
SLC14A2	-0.3020572	118	6.757e-05	4.309e-03	3.069e-03	2.748e-01	4.918e-01
SAV1	-0.4623103	42	3.395e-04	1.278e-02	3.692e-03	4.731e-01	4.918e-01
ADARB2	-0.2328861	94	6.217e-03	7.642e-02	4.040e-03	9.385e-01	4.918e-01
CMTR1	-0.2243401	65	2.916e-02	1.838e-01	4.175e-03	1.000e+00	4.918e-01
APCDD1	-0.2857765	91	9.589e-04	2.473e-02	4.234e-03	6.377e-01	4.918e-01
SPIRE1	-0.1793261	101	2.885e-02	1.628e-01	4.335e-03	1.000e+00	4.918e-01
IQGAP2	-0.1877200	123	1.143e-02	1.089e-01	4.458e-03	1.000e+00	4.918e-01
PRODH	-0.2070884	110	8.388e-03	9.150e-02	4.640e-03	9.946e-01	4.918e-01
SLC26A3	-0.2552085	107	1.359e-03	3.050e-02	4.656e-03	6.825e-01	4.918e-01
COMT	-0.2792737	95	9.707e-04	2.495e-02	4.764e-03	6.397e-01	4.918e-01

EnrichmentHsSymbolsFile2 Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.05987105	1101	3.658e-11	2.372e-07	SAV1:2 IQGAP2:7 COMT:10 CCT6A:20 HADHB:24 TBCB:25
DODD_NASOPHARYNGEAL_CARCI	0.05090702	1409	3.131e-10	8.542e-07	CEP19:2 MARCFH4:4 FND01:18 DNAH11:19 ANKRD35:26 DNAI2:36
SCHLOSSER_SERUM_RESPONSE_DN	-0.07905333	542	3.952e-10	8.542e-07	CMTR1:4 NAGPA:12 EPB42:42 CD2AP:69 LRP1:91 CDK7:118
PUJANA_BRCA1_PCC_NETWORK	-0.05260838	1222	1.072e-09	1.738e-06	SLC14A2:1 CARM1:18 CCT6A:20 SLC6A6:53 NUP62:63 CD2AP:69
JOHNSTONE_PARVB_TARGETS_3_DN	-0.06812868	667	2.613e-09	3.098e-06	MIS18BP1:29 SLC6A6:53 ATG3:59 CENPE:74 BUB1:76 WDH01:88
STARKE_HYPOCAEMIA_22Q11_DELETION_DN	-0.38364159	20	2.866e-09	3.098e-06	PROD18:8 COMT:10 ARVCF:32 TRMT2A:62 RTN4R:102 TANG02:251
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	-0.06289883	735	8.587e-09	7.748e-06	WDFY3:17 CD2AP:69 CENPE:74 WDH01:88 GTF2I:81 ARG1:125
BUYTAERT_PHOTOYNAMIC_THERAPY_STRESS_UP	-0.06524128	676	9.558e-09	7.748e-06	WDFY3:17 KDM4B:21 DNAJB4:52 SLC6A6:53 GTF2I:81 ARG1:125
RODRIGUES_THYROID_CARCI	-0.07044644	570	1.121e-08	8.078e-06	SPIRE1:8 CCT6A:20 MCOLN3:23 ELOVL6:55 CENPE:74 WDH01:88
WP_22Q112_COPY_NUMBER_VARIATION_SYNDROME	-0.16862472	95	1.389e-08	8.564e-06	PROD18:8 COMT:10 ARVCF:32 TRMT2A:62 SLC7A4:87 RTN4R:102
ZHANG_BREAST_CANCER_PROG	-0.08766323	357	1.453e-08	8.564e-06	MIS18BP1:29 CNOT6:58 RIDA:65 ARPP19:66 CD2AP:69 BUB1:76
RODRIGUES_THYROID_CARCI	-0.07163072	521	2.670e-08	1.443e-05	SPIRE1:6 CCT6A:20 ADAM9:47 ELOVL6:55 WDH01:88 CUL4B:96
NIKOLSKY_BREAST_CANCER_12Q	0.40594170	15	5.230e-08	2.609e-05	NOC4L:116 GALNT9:313 POLE:580 SFSWAP:595 ULK1:660 CHFR:712
SENGUPTA_NASOPHARYNGEAL_CARCI	0.09500764	273	7.177e-08	3.324e-05	ANKRD35:26 DNAI2:36 TOGARAM2:73 CDC08:130 IFT172:131 CFAP45:132
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	-0.09500764	400	1.232e-07	5.327e-05	CD2AP:69 CENPE:74 MGLL:99 GINS1:105 EHPA1:109 WASP:123
DAZARD_RESPONSE_TO_UV_NHEK_DN	-0.07340417	258	1.475e-07	5.978e-05	WDFY3:17 WDH01:88 WAPL:123 DST:188 MTCL1:110 CASP8:191
HSIAO_LIVER_SPECIFIC_GENES	-0.10049184	196	1.294e-06	4.937e-04	TM4SF4:16 TAT:33 SLC38A3:38 ITH2:49 RIDA:65 ALB:80
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.06969136	409	1.484e-06	5.345e-04	COMT:10 WDFY3:17 TBCB:25 CD2AP:69 CLU:114 ACOT13:140
DODD_NASOPHARYNGEAL_CARCI	-0.04315541	1082	2.225e-06	7.596e-04	CCT6A:20 NUP62:63 RIDA:65 ARPP19:66 CENPE:74 BUB1:76
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.24114948	32	2.356e-06	7.639e-04	TRIM46:71 SCMP3:152 HCN3:311 TDRKH:323 FLAD1:538 TBHS3:1093
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.05688001	556	2.590e-06	7.998e-04	IQGAP2:7 MIS18BP1:29 ADAM9:47 ZNF654:61 CENPE:74 WDH01:88
ENK_UV_RESPONSE_KERATINOCYTE_DN	-0.06929358	392	2.756e-06	8.123e-04	CD2AP:69 BCAT2:101 RXYLT1:108 RARS1:166 PFKM:194 IMPA1:208
HOUNKPE_HOUSEKEEPING_GENES	-0.04844210	821	2.996e-06	8.447e-04	SAV1:2 CMTR1:4 COMT:10 KDM4B:21 TBCB:25 ATG3:59
OSMAN_BLADDER_CANCER_UP	-0.07550291	320	3.708e-06	9.945e-04	PTGER2:137 ATP11B:139 GZEB3:186 KBTBD6:240 APPL1:310 FAM107B:320
SENESE_HDAC3_TARGETS_UP	-0.06932866	380	3.834e-06	9.945e-04	SAV1:2 SPIRE1:6 IQGAP2:7 PTPRR3:34 SLC6A6:53 CUL4B:96
DEURIG_T_CELL_PRAVIMYCOTIC_LEUKEMIA_DN	-0.08404865	243	6.184e-06	2.645e-03	KLHL2:97 ADGRG3:1770 ABCB1:209 HES1:261 SFT1:315 PTPRR3:353
REACTOME_METABOLISM_OF_LIPIDS	-0.05190381	647	7.773e-06	1.967e-03	CYP11A1:14 CARM1:18 HADHB:24 ME1:37 CB2A:45 ELOVL6:55
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.07699113	283	8.676e-06	2.056e-03	PROD18:8 TAT:33 RIDA:65 NAGS:77 BCAT2:101 ARG1:125
IBRAHIM_NRF2_UP	-0.06153676	438	1.114e-05	2.491e-03	CCT6A:20 ME1:37 DNAJB4:52 MTMR12:64 FTH1:89 RXYLT1:108
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	0.07394779	295	1.331e-05	2.877e-03	PROKR1:17 RFXP3:35 GNHR1:106 DRD2:170 ADRB3:200 GPR37:226
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.06650115	363	1.464e-05	2.902e-03	ELOVL6:55 NUP62:63 ARPP19:66 CENPE:74 BUB1:76 WDH01:88
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO	0.11555900	118	1.476e-05	2.902e-03	FND01:18 PTK6:122 CHRNA4:143 ABHD16B:249 CAS5A:467 TCF15:540
MTSIADES_RESPONSE_TO_APLIDIN_DN	-0.08721012	207	1.592e-05	3.129e-03	BUB1:76 GINS1:105 EIF2AK2:183 AHCY:195 ATP13A3:210 SUGP2:233
IVANOVA_HEMATOPOIESIS_MATURE_CELL	-0.07987326	245	1.753e-05	3.343e-03	CMTR1:4 TM4SF4:16 SLC4A1:27 RHAG:75 PGLYRP1:83 SPTB:85
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.06444975	377	1.881e-05	3.420e-03	CEP19:2 DZIP1:6 DNAH11:19 TOGARAM2:73 CFAP45:132 CEP41:138
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-0.06336575	390	1.898e-05	3.420e-03	DNAJB4:52 ARPP19:66 CD2AP:69 BUB1:76 CUL4B:96 CISP2:164
WP_METHIONINE_METABOLISM_LEADING_TO_SULF	-0.36689445	11	2.514e-05	4.406e-03	BHMT:153 AHCY:195 CSAD:494 CBS:621 MAT1A:666 GNMT:868
SHEN_SMARCA2_TARGETS_UP	-0.06604083	335	3.491e-05	5.958e-03	WDFY3:17 ATG3:59 CUL4B:96 EIF2AK2:183 RAB23:238 VPS13C:364
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CA	0.14689327	66	3.716e-05	6.025e-03	CACNG4:85 EMD-104 DMD-228 CACNA2D3:346 ITGA3:358 ACTN1:405
WP_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARD	0.14689327	66	3.716e-05	6.025e-03	CACNG4:85 EMD-104 DMD-228 CACNA2D3:346 ITGA3:358 ACTN1:405

DisGeNET Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Ciliary Motility Disorders	0.20709555	55	1.109e-07	1.023e-03	DNAH11:19 DNAI2:36 CDC06:526 DNAH5:435 DNAH5:728 SPEG2:820
DiGeorge Syndrome	-0.19898041	57	2.088e-07	1.023e-03	PROD18:8 COMT:10 ARVCF:32 ALB:80 SPECTCL1:51 NDS1:1327
Impaired T cell function	-0.35315601	17	4.649e-07	1.519e-03	COMT:10 ARVCF:32 TNFRSF13B:258 UFD1:383 UMPS:428 CD19:565
Posterior embryotoxon	-0.25495313	31	9.072e-07	2.223e-03	COMT:10 ARVCF:32 UFD1:383 PEK2:407 JAG1:993 HIRA:1025
Seborrheic dermatitis	-0.31300806	20	1.267e-06	2.484e-03	COMT:10 ARVCF:32 SLC02A1:46 UFD1:383 HIRA:1025 TBX1:1600
Embryotoxon	-0.25222446	30	1.758e-06	2.873e-03	COMT:10 ARVCF:32 UFD1:383 PEK2:407 JAG1:993 HIRA:1025
Polynesians Bronchiectasis	0.23541034	34	2.054e-06	2.876e-03	DNAH11:19 DNAI2:36 CDC06:526 DNAH5:728 STK36:928 RSPH3:1118
Tetany	-0.30203645	20	2.939e-06	3.602e-03	COMT:10 ARVCF:32 UFD1:383 CASR:265 UFD1:383 TRPM6:904
22q11 Deletion Syndrome	-0.31090120	18	4.979e-06	5.424e-03	PROD18:8 COMT:10 ARVCF:32 UFD1:383 CXCR4:425 ZDHHC4:434
22q11 partial monosomy syndrome	-0.38897459	11	7.942e-06	7.788e-03	COMT:10 ARVCF:32 UFD1:383 PKAIXA:789 HIRA:1025 TKT1:1600
Thyrosy	-0.10341521	156	8.794e-06	7.837e-03	LPL67 ALB:80 PAX5:231 MDM2:345 IL6:430 LTB4:454
Small sarfobe	-0.33504955	13	2.886e-05	2.357e-02	COMT:10 ARVCF:32 UFD1:383 KCTD1:694 HIRA:1025 TBX1:1600
Shprintzen syndrome	-0.21873424	30	3.401e-05	2.498e-02	PROD18:8 COMT:10 ARVCF:32 UFD1:383 HIRA:1025 DGCRL6:1305
Dysseborrhic dermatitis	-0.30832704	15	3.567e-05	2.498e-02	COMT:10 ARVCF:32 SLC02A1:46 UFD1:383 HIRA:1025 TBX1:1600
Hereditary spherocytosis	-0.24775670	23	3.924e-05	2.565e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 SDS:167
Reticulocyte count (procedure)	-0.09306753	160	5.113e-05	3.022e-02	IQGAP2:7 SLC4A1:27 CD2AP:69 SPTB:85 ANK1:119 SPTA1:135
Occipital myelomeningocele	-0.38935050	9	5.241e-05	3.022e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
Abnormality of the tonsils	-0.34467567	11	7.557e-05	4.116e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
Anemia, Sickle Cell	-0.08760053	169	8.976e-05	4.543e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
Ewings sarcoma	-0.06934227	271	9.268e-05	4.543e-02	PAK3:39 LRP1:91 CASP8:191 ABCB1:209 LDX2:27 FCGR1:291
Kartagener Syndrome	0.11965410	88	1.072e-04	4.956e-02	DNAH11:19 DNAI2:36 CFTR:81 DNAH3:232 CDC06:526 DNAH9:435
Anemia, hereditary spherocytic hemolytic	-0.49417932	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Spherocytosis	-0.49417932	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Congenital atresia of nasopharynx	0.34929518	10	1.310e-04	4.956e-02	DNAH11:19 DNAH5:728 GAS8:1163 DRC1:1213 ARMC4:1815 DNAI1:2131
Other specified congenital malformations	0.34929518	10	1.310e-04	4.956e-02	DNAH11:19 DNAH5:728 GAS8:1163 DRC1:1213 ARMC4:1815 DNAI1:2131
Mental deficiency	-0.03846442	890	1.314e-04	4.956e-02	PROD18:8 TAT:33 PAK3:39 CLCNKB:50 CLCNKA:51 GTF2IRD1:54
Poor school performance	-0.03912154	849	1.415e-04	5.126e-02	PROD18:8 TAT:33 PAK3:39 CLCNKB:50 CLCNKA:51 GTF2IRD1:54
Upward slant of palpebral fissure	-0.10595977	108	1.464e-04	5.126e-02	COMT:10 ARVCF:32 EHMT1:273 UFD1:383 PEK2:407 CDK13:417
Solid Neoplasm	-0.04382415	658	1.536e-04	5.194e-02	TAT:33 LPL:67 BUB1:76 ALB:80 PGLYRP1:83 ANK1:119
Liver neoplasms	-0.03547721	1006	1.916e-04	6.261e-02	IQGAP2:7 COMT:10 KDM4B:21 TAT:33 LPL:67 ALB:80
Hepatocarcinogenesis	-0.05426389	395	2.393e-04	7.355e-02	KDM4B:21 NUP62:63 ALB:80 CLU:114 PTGES:117 ARG1:125
Increased variability in muscle fiber di	0.21663236	24	2.402e-04	7.358e-02	TCAP:145 ITGA7:555 SELENON1:829 TWNK:1469 SOSTM1:2146 COL6A1:2205
Pain, Postoperative	-0.22973681	21	2.688e-04	7.770e-02	COMT:10 TRPV1:133 ABCB1:209 LIF:566 SCN9A:735 AP3B1:962
Bilateral cataracts (disorder)	-0.10549628	100	2.737e-04	7.770e-02	ADAM8:47 PAX5:231 CASR:265 MGST1:333 IFNGR3:1341 GSTO1:389
Breast adenocarcinoma	-0.08948599	139	2.798e-04	7.770e-02	CASP8:191 ABCB1:209 GCLC:215 HSPB1:301 MDM2:345 VEGFA:446
Fabry Disease	-0.16580585	40	2.874e-04	7.770e-02	MANBA:142 ABCB1:209 NAGA:287 VCAIM1:305 IL6:430 VEGFA:446
Leukemia, Myelocytic, Acute	-0.03105901	1265	2.970e-04	7.770e-02	TAT:33 PAK3:39 RHEB1:60 BUB1:76 WDH01:88 LRP1:91
Abnormality of aortic arch	-0.11474135	11	3.012e-04	7.770e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
CONOTRUNCAL ANOMALY FACE SYNDROME	-0.22508768	21	3.572e-04	8.859e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 DGCRL6:1380 TBX1:1600
Malignant neoplasm of lung	-0.02630665	1805	3.617e-04	8.859e-02	COMT:10 KDM4B:21 BPIFB1:31 TAT:33 ADAM9:47 DNAJB4:52

customGeneSet Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
expressionDirectionalSelection	0.05710956	33	4.544e-01	7.646e-01	KAT8:208 LGALS2:1682 FEN1:1923 TNF646:2085 HSD17B8:2335 KHK:2485
NALFDGWAS	-0.05873016	14	5.097e-01	7.646e-01	GPAM:1197 GID4:1580 MTPP:1967 NSR2:158 TRIB1:4372 TOR1B:5652
HumanLocalAdaptionDietAll	-0.02127660	12	8.212e-01	8.212e-01	GPX1:743 LCT:884 SLC2A4:1656 SEPSCS:4429 TRIP4:6368 GPX3:8345
NA	NA	NA	NA	NA	NA NA NA NA NA NA
NA.1	NA	NA	NA	NA	NA NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA NA
NA.14	NA	NA	NA	NA	NA NA NA NA NA NA
NA.15	NA	NA	NA	NA	NA NA NA NA NA NA
NA.16	NA	NA	NA	NA	NA NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA NA
NA.18	NA	NA	NA	NA	NA NA NA NA NA NA
NA.19	NA	NA	NA	NA	NA NA NA NA NA NA
NA.20	NA	NA	NA	NA	NA NA NA NA NA NA
NA.21	NA	NA	NA	NA	NA NA NA NA NA NA
NA.22	NA	NA	NA	NA	NA NA NA NA NA NA
NA.23	NA	NA	NA	NA	NA NA NA NA NA NA
NA.24	NA	NA	NA	NA	NA NA NA NA NA NA
NA.25	NA	NA	NA	NA	NA NA NA NA NA NA
NA.26	NA	NA	NA	NA	NA NA NA NA NA NA
NA.27	NA	NA	NA	NA	NA NA NA NA NA NA
NA.28	NA	NA	NA	NA	NA NA NA NA NA NA
NA.29	NA	NA	NA	NA	NA NA NA NA NA NA
NA.30	NA	NA	NA	NA	NA NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA NA
NA.35	NA	NA	NA	NA	NA NA NA NA NA NA
NA.36	NA	NA	NA	NA	NA NA NA NA NA NA

GO\_Biological\_Process\_2023 Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cilium Movement (GO:0003341)	0.25969962	47	7.519e-10	4.045e-06	DNAH11:19 DNAI2:36 SPAG17:247 TECT3:365 DNAH9:435 CFAP206:481
Xenome Assembly (GO:0035082)	0.25692897	30	1.125e-06	3.027e-03	LRGUK:141 SPAG17:247 CDC06:526 CENPE:74 SPACA9:748 STK36:928
Regulation Of DNA-templated Transcription	-0.03634291	1447	7.452e-06	9.913e-03	CARM1:18 TCF15:19 GTF2IRD1:54 NUP62:63 NDS1:106 ZNF628:149
Cilium-Dependent Cell Motility (GO:00602)	0.31091204	17	9.111e-06	9.913e-03	DNAH3:232 CDC06:526 TECT3:365 TECT5:791 DNAH17:1027 GAS8:1163
Axonal Dynein Complex Assembly (GO:00072)	0.26722391	23	9.213e-06	9.913e-03	DNAI2:36 CDC06:526 DNAH5:728 DNAH17:1027 TCT1:1033 DNAH11:1716
Neuropeptide Signaling Pathway (GO:00072)	0.15797528	63	1.480e-05	1.327e-02	SC05S1:16 RXP6:35 GPR37:228 LTB4R:329 OPRT1:635 GALR3:697
Regulation Of Heart Rate By Cardiac Conduction	0.20221682	37	2.100e-05	1.614e-02	SCN5A:49 KMD0:37P HCN3:31 KCNKA:554 KCNE2:821 KCNE1:878
Muscle Contraction (GO:0006936)	0.12993070	82	5.460e-05	3.672e-02	CHRNAE:42 ENCB:10 LMOD3:204 CASQ2:245 LTBAR:329 CHRD:514
Regulation Of DNA Metabolic Process (GO:0006971)	-0.11567172	97	8.504e-05	5.084e-02	TERF2:152 USP37:47 RBBP5:56F ESCO1:647 MYC:858 ACTR5:1006
Positive Regulation Of Chemotaxis (GO:0040004)	-0.17416692	41	1.525e-04	5.803e-02	LGMN:174 HSPB1:301 CCL19:329 PRM1:339 IL6:430 VEGFA:446
Fatty Acid Transport (GO:0015908)	-0.18547566	36	1.187e-04	5.803e-02	SLC0A2:146 SLC7A4:141 SLC22A6:60B FAPB6:916 ACSL:1041 PPARG:1166
Regulation Of Gene Expression (GO:0010446)	-0.03928959	829	1.593e-04	7.071e-02	LRN1:48B BTLN:936 TGT21RD1:54 LRP1:91 SNO:106 PRKAG1:107
Cardiac Conduction (GO:0061337)	0.16773310	42	1.709e-04	7.071e-02	SCN5A:49 KMD0:37P HCN3:31 KCNKA:554 KCNE2:821 KCNE1:878
Cilium Movement Involved In Cell Motility	0.33809113	7	2.650e-04	1.002e-01	TECT3:365 TECT5:791 CHAG:1163 TECT3:3764 TECT1:2092 TECT4:2462
Alpha-Amino Acid Biosynthetic Process (GO:0006543)	-0.33043891	10	2.968e-04	1.002e-01	BCAT2:101 SDS:167 SDSL:34A LVLB:561 CPM1:909 MTHFD1:2006
Protein Modification By Small Protein Co	-0.06407081	272	2.979e-04	1.002e-01	ATG3:59 CUL4B:96 KHLH2:97 DTX2:234 UBR1:241 KHLH2:255
Cilium Assembly (GO:0060271)	0.33693779	18	1.434e-04	1.403e-01	CEP19:2 TMEH2:613 DZP1:6 TMEH2:339 DNAI2:36 E2F4:92 AR1:12
Vesicle-Mediated Transport From Endotho	-0.20593736	23	6.300e-04	1.763e-01	SNX16:367 PTPN23:1022 RAB7A:1088 HOOK2:1220 PIK3RA:1354 BECN1:1697
Motile Cilium Assembly (GO:0044458)	0.26330544	14	6.481e-04	1.763e-01	E2F4:92 PTPN27:1427 BBOF1:1688 RSPK:2559 CDC2:3623 MCIDAS:2794
Positive Regulation Of Cellular Compone	-0.10187651	94	6.555e-04	1.763e-01	LRP1:91 ASAP1:100 LGMN:174 TPPP:127 CCL19:329 CRR3:344
Nitrogen Compound Transport (GO:0071705)	-0.08130372	146	7.209e-04	1.847e-01	SLC38A3:38 SLC06A:53 RHAG:71 SLC7A4:87 AP11B:139 RHCG:202
Early Endosome To Late Endosome Transp	-0.20452387	22	9.007e-04	1.959e-01	PTPN22:367 PTPN23:1022 RAB7A:1088 HOOK2:1220 PIK3RA:1354 BECN1:1697
Ventricular Cardiac Muscle Cell Actin P	0.25589950	14	9.174e-04	1.959e-01	SCN5A:49 KCNKA:554 KCNE2:821 KCNE1:878 KP2C:1022 KCNQ1:1830
Negative Regulation Of Apoptotic Process	-0.05015361	375	9.347e-04	1.959e-01	NUP62:63 ALB:80 TBCAM1:110 CUL11A: LGMN:174 GCLC:215
Regulation Of Protein Phosphorylation (G	-0.06464198	221	9.775e-04	1.959e-01	DSD1:106 HSPB1:301 PEBI:3112 TSPYL2:359 AXIN1:360 FKBP8:382
Fatty Acid Catabolic Process (GO:0009062)	-0.12545959	58	9.814e-04	1.959e-01	HADHB:24 H007:286 SLC7A4:141 EHADHD:260 PEK2:407 PLAGL3:1522
Negative Regulation Of Macromolecule Bio	-0.11020580	75	9.831e-04	1.959e-01	RIDA:65 EIF2AK3:138 CAPRIN1:443 AKR1B1:599 PATEL2:603 TSPY2:422
Measurment Of Cell Differentiation (GO:00448)	0.33967506	8	1.201e-03	2.307e-01	ITGA3:369 ITGB4:351 ITGB1:1752 HMGCC:2592 HMGCC:2599 KDR68:320
Diol Biosynthetic Process (GO:0034312)	-0.24836416	14	1.255e-03	2.306e-01	ACER1:184 OPRD:640 SPHK1:752 SPHK2:943 SPTLC2:1933 ACER2:2283
Anterograde Trans-Synaptic Signaling (GO	0.27041974	166	1.332e-03	2.306e-01	CHRNAE:42 DLG4:135 CHRNA4:143 RPS6K4:154 CHRNA2:167 GABRR2:194
Regulation Of Interleukin-2 Production (	-0.14541368	40	1.472e-03	2.405e-01	SCN5A:49 CCL10:172 LITF:214 TNFAIP3:432 CDC6:503 RPS3:307
Striated Muscle Contraction (GO:0006941)	0.13276812	48	1.474e-03	2.405e-01	HOMER3:49 TCAP:145 LMOD3:204 DMD:228 CASQ2:245 TNIN3:582
Positive Regulation Of Receptor-Mediated	-0.15041112	37	1.475e-03	2.405e-01	CUL11:14 CCL6:326 CCL19:329 VEGFA:446 RAB21:389 FMR1:1021
Cellular Response To Acetylcholine (GO:1	0.35142275	9	1.588e-03	2.492e-01	LYGG6D:430 CHRD:514 CHRM3:1203 LYBH:1052 ROCK2:1913 LYPD1:2631
Branched-Chain Amino Acid Metabolic Proc	-0.23496069	15	1.632e-03	2.492e-01	BCAT2:101 BCKDHA:1038 BDT1:399 PCCB:2152 HIBCH:2203 MCCCT1:2244
Positive Regulation Of Endothelial Cell	-0.26213167	12	6.698e-03	2.492e-01	LGMN:174 HSPB1:301 VEGFA:446 MELT:668 TPCA4:2164 RDR:2810
Response To Peptidylarginine (GO:0032494)	-0.04472332	5	1.723e-03	2.506e-01	INAVA:402 IL6:430 IRAK3:721 IRF5:2460 RLEA:2974 NA
Protein Ubiquitination (GO:0016567)	-0.05041259	329	1.795e-03	2.521e-01	ATG3:59 ILK:96 KHLH2:97 PILP2:154 RNF8:228 DTX2:234
Monocarboxylic Acid Transport (GO:001571)	-0.11458398	62	1.827e-03	2.521e-01	SLC10A2:95 SLC7A4:141 SLC10A1:359 UGT1A6:625 SLC10A2:861 FAPB6:916
Negative Regulation Of Leukocyte Profile	-0.044710420	4	1.955e-03	2.522e-01	TNFAIP3:432 IL13:354 ENPP3:966 LYIN:1062 NA:2