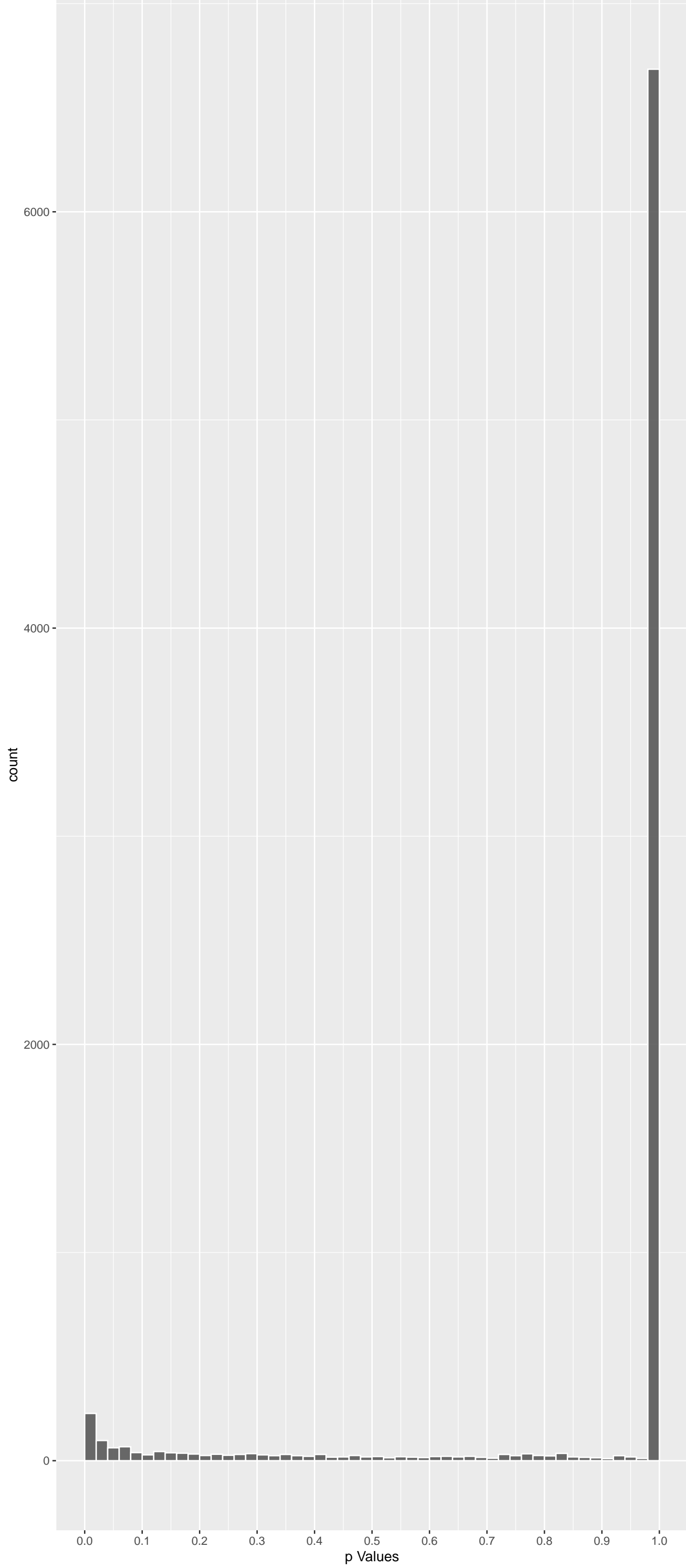


Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
DNAH2	8.237150	1.058164e-15	1.711e-11	2.768e-07
PLEC	7.226544	2.972646e-12	2.404e-08	1.617e-04
NUP88	7.140912	5.562841e-12	2.999e-08	1.617e-04
DNAH14	7.046628	1.099834e-11	4.447e-08	1.798e-04
DNAH9	6.952627	2.151269e-11	6.958e-08	1.916e-04
ANKRD35	6.923874	2.636742e-11	7.107e-08	1.916e-04
SLC47A1	6.719316	1.095480e-10	2.531e-07	5.848e-04
CAPN8	6.583418	2.758519e-10	5.577e-07	1.127e-03
KANK1	6.423459	7.992721e-10	1.436e-06	2.151e-03
ITGB4	6.394726	9.650118e-10	1.463e-06	2.151e-03
KIAA0753	6.390025	9.951546e-10	1.463e-06	2.151e-03
SIK3	6.352709	1.269331e-09	1.711e-06	2.306e-03
SLC17A3	6.187621	1.832363e-09	2.280e-06	2.698e-03
SFSWAP	6.280740	2.021793e-09	2.336e-06	2.698e-03
BDKRB1	6.135253	5.101422e-09	5.157e-06	5.212e-03
ADGRG4	6.141714	4.898159e-09	5.157e-06	5.212e-03
DNAH17	6.060150	8.159671e-09	7.331e-06	6.587e-03
PROM1	-6.060793	8.127129e-09	7.331e-06	6.587e-03
TACR2	5.991025	1.251133e-08	1.065e-05	9.065e-03
SH2D7	5.954386	1.566295e-08	1.267e-05	1.017e-02
CARD14	5.939613	1.714174e-08	1.320e-05	1.017e-02
ESYT3	5.915284	1.987822e-08	1.461e-05	1.074e-02
TMEM131L	-5.897907	2.208852e-08	1.553e-05	1.092e-02
PIEZO1	5.838737	3.155884e-08	2.127e-05	1.330e-02
MTBP	-5.828952	3.346589e-08	2.165e-05	1.330e-02

Positive Rho Non-permuted



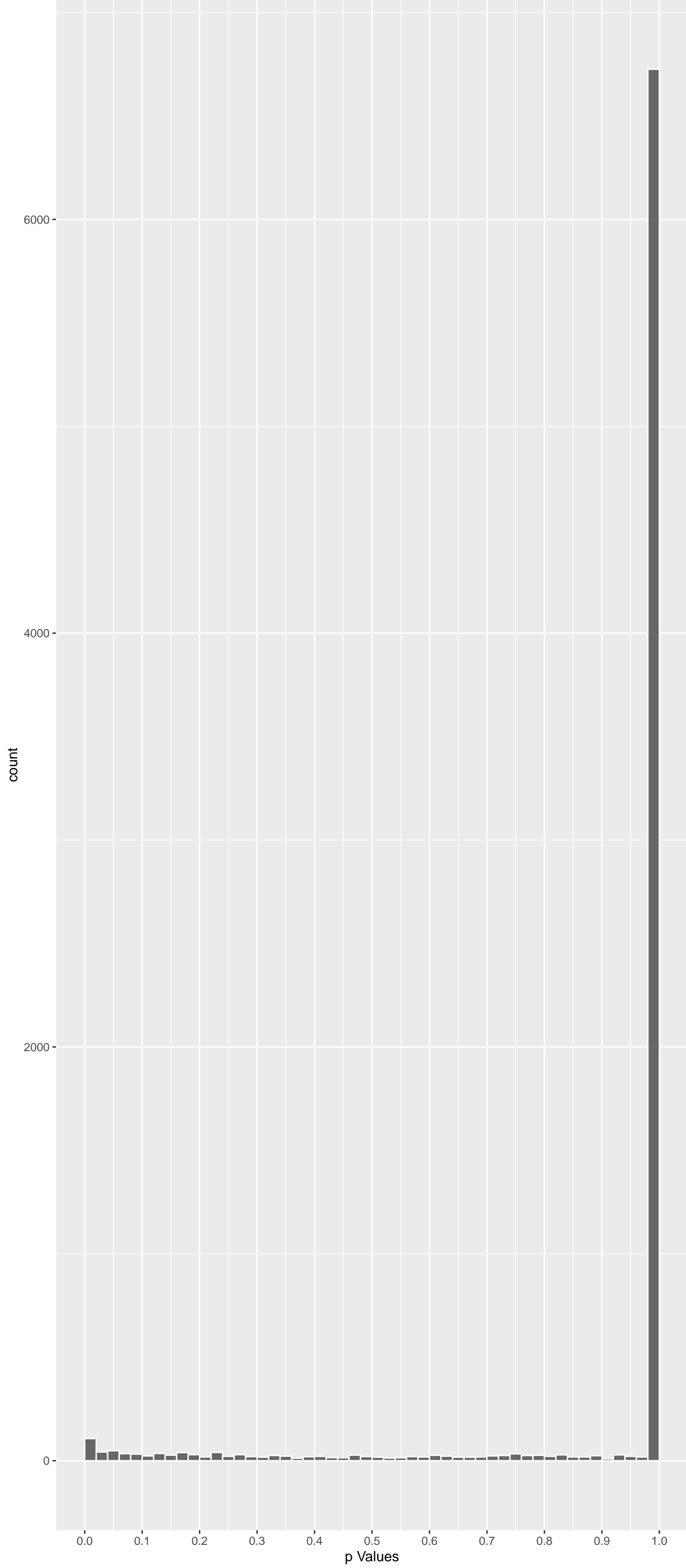
Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
DNAH2	8.237150	1.058164e-15	1.711e-11	2.768e-07
PLEC	7.226544	2.972646e-12	2.404e-08	1.617e-04
NUP88	7.140912	5.562841e-12	2.999e-08	1.617e-04
DNAH14	7.046628	1.099834e-11	4.447e-08	1.798e-04
DNAH9	6.952627	2.151269e-11	6.958e-08	1.916e-04
ANKRD35	6.923874	2.636742e-11	7.107e-08	1.916e-04
SLC47A1	6.719316	1.095480e-10	2.531e-07	5.848e-04
CAPN8	6.583418	2.758519e-10	5.577e-07	1.127e-03
KANK1	6.423459	7.992721e-10	1.436e-06	2.151e-03
ITGB4	6.394726	9.650118e-10	1.463e-06	2.151e-03

Top genes by Q-Value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
DNAH2	8.237150	1.058164e-15	1.711e-11	2.768e-07
PLEC	7.226544	2.972646e-12	2.404e-08	1.617e-04
NUP88	7.140912	5.562841e-12	2.999e-08	1.617e-04
DNAH14	7.046628	1.099834e-11	4.447e-08	1.798e-04
DNAH9	6.952627	2.151269e-11	6.958e-08	1.916e-04
ANKRD35	6.923874	2.636742e-11	7.107e-08	1.916e-04
SLC47A1	6.719316	1.095480e-10	2.531e-07	5.848e-04
CAPN8	6.583418	2.758519e-10	5.577e-07	1.127e-03
ITGB4	6.394726	9.650118e-10	1.463e-06	2.151e-03
KIAA0753	6.390025	9.951546e-10	1.463e-06	2.151e-03
KANK1	6.423459	7.992721e-10	1.436e-06	2.151e-03
SIK3	6.352709	1.269331e-09	1.711e-06	2.306e-03
SLC17A3	6.187621	1.832363e-09	2.280e-06	2.698e-03
SFSWAP	6.280740	2.021793e-09	2.336e-06	2.698e-03
BDKRB1	6.135253	5.101422e-09	5.157e-06	5.212e-03
ADGRG4	6.141714	4.898159e-09	5.157e-06	5.212e-03
DNAH17	6.060150	8.159671e-09	7.331e-06	6.587e-03
PROM1	-6.060793	8.127129e-09	7.331e-06	6.587e-03
TACR2	5.991025	1.251133e-08	1.065e-05	9.065e-03
SH2D7	5.954386	1.566295e-08	1.267e-05	1.017e-02
CARD14	5.939613	1.714174e-08	1.320e-05	1.017e-02
ESYT3	5.915284	1.987822e-08	1.461e-05	1.074e-02
TMEM131L	-5.897907	2.208852e-08	1.553e-05	1.092e-02
PIEZO1	5.838737	3.155884e-08	2.127e-05	1.330e-02
MTBP	-5.828952	3.346589e-08	2.165e-05	1.330e-02

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
PROM1	-6.060793	8.127129e-09	7.331e-06	6.587e-03
TMEM131L	-5.897907	2.208852e-08	1.553e-05	1.092e-02
MTBP	-5.828952	3.346589e-08	2.165e-05	1.330e-02
PPFIA3	-5.613386	1.190435e-07	5.501e-05	2.542e-02
MAN2A1	-5.543938	1.774465e-07	7.756e-05	3.326e-02
CLCNKA	-5.464747	2.781409e-07	1.048e-04	3.935e-02
ABHD11	-5.272046	8.094661e-07	2.525e-04	7.854e-02
FBNBP4	-5.254751	8.893493e-07	2.714e-04	8.281e-02
ELL	-5.226313	1.037542e-06	3.051e-04	8.476e-02
QSER1	-5.216049	1.096680e-06	3.092e-04	8.476e-02

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
CONOTRUNCAL ANOMALY FACE SYNDROME	-0.26967215	21	1.892e-05	1.856e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 COMT:707 GATA6:831
Shprintrin syndrome	-0.20254120	33	5.682e-05	1.862e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 PRODH:607 COMT:707
Tetany	-0.25749709	21	4.424e-05	1.862e-01	HIRA:62 CASR:112 CNVM2:164 TRPM6:177 CLDN16:288 PTH:301
Ciliary Motility Disorders	0.15079213	57	8.324e-05	1.873e-01	DNAH9:5 ARMC4:153 DNAH11:178 SPEF2:448 DNAH5:520 CFAP221:553
DiGeorge Syndrome	-0.14292177	61	1.145e-04	1.873e-01	ALB:20 HIRA:62 SPECCL1:115 DGCR2:211 VEGFA:216 CDC45:279
Junctional split	0.45514706	6	1.129e-04	1.873e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 LAMB3:137 LAMA3:2606
22q11 Deletion Syndrome	-0.25203174	19	1.432e-04	2.006e-01	HIRA:62 HIC2:262 ARVCF:390 DGCR8:430 PRODH:607 COMT:707
Leukemia, Myelocytic, Acute	-0.02932510	1383	3.572e-04	2.181e-01	PROM1:1 ELL:9 ASMTL:27 SDS:30 ABCB1:48 GTGLC3:60
22q11 partial monosomy syndrome	-0.32304931	11	2.074e-04	2.181e-01	HIRA:62 ARVCF:390 PI4KA:591 COMT:707 GNB1L:734 JMJDC1:1018
Adult Medulloblastoma	-0.13249051	58	4.878e-04	2.181e-01	KDM4B:174 MDM2:283 BRD2:287 MYCN:363 BRD4:551 DNMT1:623
Defective enamel matrix	0.15888464	40	5.100e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 GGF2:233 STX16:242
Dysplasia of tooth enamel	0.15888464	40	5.100e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 GGF2:233 STX16:242
Endometrial Carcinoma	-0.03931725	679	5.515e-04	2.181e-01	PROM1:1 ABCB1:48 GTGLC3:60 RXFP1:64 HSD17B6:77 TNF:88
Epidermolysis Bullosa	0.19363594	31	1.914e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 DSC3:180 LAMC2:190 DSP:257
Epidermolysis Bullosa Simplex	0.21766204	21	5.558e-04	2.181e-01	PLEC:2 ITGB4:10 KRT80:59 MMP9:258 KRT14:552 TGM5:1058
Hepatitis C	-0.04185667	598	5.345e-04	2.181e-01	ALB:20 GTGLC3:60 TNF:88 CABIN1:105 EGF:130 AZIN1:140
Hepatocarcinogenesis	-0.04876646	443	4.758e-04	2.181e-01	PROM1:1 ALB:20 TNF:88 MLIP:106 EGF:130 AICDA:152
Herlitz Disease	0.44611872	5	5.507e-04	2.181e-01	ITGB4:10 ITGA6:138 LAMC2:190 LAMB3:137 LAMA3:2606 NA
Medulloblastoma	-0.16219370	41	3.284e-04	2.181e-01	KDM4B:174 BRD2:287 MYCN:363 BRD4:551 DNMT1:623 PTCH2:687
Melanotic medulloblastoma	-0.16219370	41	3.284e-04	2.181e-01	KDM4B:174 BRD2:287 MYCN:363 BRD4:551 DNMT1:623 PTCH2:687
Oral mucosal blisters	0.31935971	10	4.707e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 DSP:257 LAMB3:1337
Polynesain Bronchiectasis	0.17704378	35	2.909e-04	2.181e-01	ARMC4:153 DNAH11:178 DNAH5:520 CDCDC15:598 GAS8:674 RSPH1:875
Posterior embryotoxon	-0.18062890	31	5.023e-04	2.181e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 PEX1:637 COMT:707
Substance Dependence	0.08976103	128	4.647e-04	2.181e-01	NRCAM:41 CTRF:94 ANK6:1106 CSRN93:114 GSOX1:120 TIAM2:124
Thin dental enamel	0.15888464	40	5.100e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 GGF2:233 STX16:242
Malignant neoplasm of lung	-0.02408137	1977	6.411e-04	2.419e-01	PROM1:1 ALB:20 DCAF4:31 R1OX1:13 ADAM9:39 ABCB1:48
Hidradentitis Suppurativa	-0.23744492	17	7.014e-04	2.458e-01	TNF:88 SULT1E1:230 SULT1B1:1464 ELOV1:7579 RBM45:1638 PSEN1:1786
Primary malignant neoplasm of lung	-0.02463774	1842	6.942e-04	2.458e-01	PROM1:1 ALB:20 DCAF4:31 R1OX1:13 ADAM9:39 ABCB1:48
leukemia	-0.02619566	1577	7.342e-04	2.484e-01	PROM1:1 ELL:9 MZF1:16 ALB:20 ABCB1:48 SLC7A4:50
Carcinoma of lung	-0.02337836	2007	8.548e-04	2.572e-01	PROM1:1 ALB:20 DCAF4:31 R1OX1:13 ADAM9:39 ABCB1:48
Embryotoxon	-0.17368952	30	9.963e-04	2.572e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 PEX1:637 COMT:707
Hepatitis	-0.06238154	246	7.885e-04	2.572e-01	PROM1:1 ALB:20 ABCB1:48 TNF:88 VCAM1:125 IL33:156
Liver neoplasms	-0.03006136	1094	9.833e-04	2.572e-01	PROM1:1 MZF1:16 ALB:20 SDS:30 ABCB1:48 SUGP1:57
Parakeratosis	0.24832830	15	8.697e-04	2.572e-01	CARD14:20 NLRP1:85 DSP:257 TNC:348 TRPV3:680 RHBDF2:1836
Seborrheic dermatitis	-0.20986329	21	8.727e-04	2.572e-01	HIRA:62 TNF:88 ARVCF:390 NFE2L2:479 COMT:707 JMJDC1:1018
Substance-Related Disorders	0.08964595	114	9.637e-04	2.572e-01	NRCAM:41 CTRF:94 CSRN93:114 GSOX1:120 TIAM2:124 SYNE1:287
T-lymphocyte immunodeficiency	0.38816434	6	9.920e-04	2.572e-01	RAG1:133 SFTPA1:152 SMARCAL1:524 LBR:555 CD3E:1224 SIPA1:8200
Unilateral primary pulmonary dysgenesis	-0.42895287	5	8.941e-04	2.572e-01	DGCR2:211 DGCR8:430 TBX1:1140 DGCGR6:1444 ESS2:2424 NA
Color Blindness, Red	0.42200294	5	1.083e-03	2.580e-01	ATF6:609 TEX28:722 OPN1LW:1041 GNAT2:1064 PDE6H:2749 NA
Kartagener Syndrome	0.09761045	94	1.090e-03	2.580e-01	DNAH9:5 DNAH17:17 CTRF:94 KRT20:102 ARMC4:153 DNAH11:178

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
DODD_NASOPHARYNGEAL_CARCINOMA_UP	0.04865634	1463	8.213e-10	5.328e-06	DNAH2:1 DNAH9:5 ANKRD35:6 SIK3:12 CARD14:20 CFAP45:25
WP_GPCRS_CLASS_A_THRHODOPSINLIKE	0.11691718	208	6.434e-09	2.087e-05	BDKRB1:16 NPBWRR2:100 MTNR1B:130 SSTR4:173 PTAFR:318 GPR68:347
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON	0.13902808	128	5.748e-08	1.180e-04	HEL22:90 FNDCl:99 NPBWR2:100 COL20A1:155 FAM217B:166 RTGL1:223
JOHNSTONE_PARVB_TARGETS_3_DN	-0.05673816	790	7.278e-08	1.180e-04	MTBP:3 MAN2A1:5 QSER1:10 SLC6A6:51 SMCHD1:52 RBL1:78
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.25526664	34	2.599e-07	3.737e-04	PBXIP1:35 DCST1:63 THBS3:220 ZBTB7B:275 RUSC1:312 PMVK:491
PUJANA_BRCA1_PCC_NETWORK	-0.03974413	1501	3.896e-07	4.213e-04	TMEM131L:2 FNBPA:8 SLC16A5:25 SLC6A6:51 HIRA:62 RBL1:78
ZHANG_BREAST_CANCER_PROGENITORS_UP	-0.07016918	415	1.028e-06	6.950e-04	PROM1:1 SMCHD1:52 CTH:53 CEP192:59 TTC3:65 MAP7D2:72
REACTOME_CLASS_A_1_RHODOPSIN LIKE_RECEPT	0.08276707	295	1.071e-06	6.950e-04	BDKRB1:16 TACR2:18 NPBWR2:100 GPR132:118 MTNR1B:130 SSTR4:173
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.05949181	598	7.689e-07	6.950e-04	ADAM9:39 RBL1:78 SPDL1:86 WDR76:116 HLTf:133 RHOBT3:186
SCHLOSSER_SERUM_RESPONSE_DN	-0.05672426	646	1.004e-06	6.950e-04	UBR2:14 ASMTL:27 PJA2:47 CTH:53 PARG:98 ICAM2:101
DODD_NASOPHARYNGEAL_CARCINOMA_DN	-0.04003223	1244	1.588e-06	9.364e-04	QSER1:10 FGDB:43 CEP192:59 RHL7:178 SPDL1:86 CD80:109
REACTOME_SIGNALING_BY_GPCR	0.05593227	631	1.854e-06	1.003e-03	BDKRB1:16 TACR2:18 ARHGFE11:24 ARHGEF12:32 CAMK2B:37 PIK3R5:95
WP_22Q112_COPY_NUMBER_VARIATION_SYNDROME	-0.12640769	112	3.883e-06	1.938e-03	SLC7A4:50 CLTCL1:55 HIRA:62 CYP26C1:102 DGCR2:211 DEPDC5:224
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	-0.04250066	1026	5.118e-06	2.372e-03	ELL:9 ZNF446:28 GATAD2A:74 MGA:76 RBL1:78 TAF2:87
NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	0.33717555	14	1.253e-05	5.418e-03	COL6A1:61 PCNT:325 DIP2A:374 SPATC1:250 DPP8:282 ARPP19:302
MILL_PSEUDOPODIA_HAPTOTAXIS_UP	-0.05540040	490	2.895e-05	9.574e-03	PJA2:47 SMCHD1:52 CDV3:158 LMP1:250 DPP8:282 ARPP19:302
REACTOME_G_ALPHA_O_SIGNALING_EVENTS	0.08679044	197	2.749e-05	9.574e-03	BDKRB1:16 TACR2:18 GPR132:118 MTNR1:302 PTAFR:318 GPR68:347
REACTOME_KERATINIZATION	0.13115066	85	2.951e-05	9.574e-03	EVLPL:42 KRT80:59 KRT20:102 KRT4:148 DSC3:180 TGM1:199
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	0.13836075	78	2.417e-05	9.574e-03	EVLPL:42 KRT80:59 KRT20:102 KRT4:148 DSC3:180 TGM1:199
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.06493504	357	2.649e-05	9.574e-03	PRODH2:18 SDS:30 CTH:53 DHTKD1:121 AGXT:136 AZIN1:140
STARK_HYPOCAMPUS_22Q11_Q13_DELETION_DN	-0.25464896	22	3.557e-05	1.099e-02	HIRA:62 DGCR2:211 TANGO2:277 ARVCF:390 DGCR8:430 PRODH:607
FISCHER_DREAM_TRAILS	-0.04052402	882	5.104e-05	1.505e-02	MTBP:3 FNBPA:8 ZNF518A:40 SMCHD1:52 CEP192:59 HAUS8:68
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.04828799	595	6.267e-05	1.768e-02	QSER1:10 HAS2:29 ADAM9:39 PJA2:47 SMCHD1:52 CEP192:59
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.05832990	398	8.896e-05	1.864e-02	CFAP45:25 PTPN22:50 CFAP46:83 C7orf57:88 ZHX3:98 DRG3:144
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.03275112	1338	7.184e-05	1.864e-02	MAN2A1:5 PPN24R:12 ASMTL:27 CTH:53 HIRA:62 TAF2:87
MARTENS_TRETINOLIN_RESPONSE_UP	0.04424366	676	9.679e-05	2.415e-02	CARD14:20 SMTNL2:38 GGT6:56 COL6A1:61 PIK3R5:95 ANKK1:106
NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON	0.16237164	46	1.394e-04	3.164e-02	PIEZO1:22 CTU2:52 ANKRD11:602 GAS8:674 BCL2:73 CTRF:943
REACTOME_MUSCLE_CONTRACTION	0.06018808	190	1.414e-04	3.164e-02	CAMK2B:37 DMD:86 CASQ1:108 MYH8:146 SLC8A3:171 ATP1A4:189
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.05406198	427	1.351e-04	3.164e-02	QSER1:10 RBL1:78 WDR76:116 TPX2:161 VEGFA:216 CDC45:279
KEGG_STEROID_HORMONE_BIOSYNTHESIS	-0.20547611	28	1.679e-04	3.631e-02	HSD17B6:77 HSD11B1:167 SULT1E1:230 HSD17B2:466 CYP17A1:499 CYP11A1:608
KINSEY_TARGETS_OF_EWSR1_FULI_FUSION_UP	-0.03232678	1201	1.913e-04	3.956e-02	PROM1:1 GYG2:44 CTH:53 HAUS8:68 MAP7D2:72 SPDL1:86
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	-0.04349600	637	1.951e-04	3.956e-02	QSER1:10 TTX02:16 RLF:81 TPX2:161 ANAPC1:163 ATP13A3:173
REACTOME_GPCR_LIGAND_BINDING	0.05343416	398	2.666e-04	4.941e-02	BDKRB1:16 TACR2:18 NPBWR2:100 GPR132:118 MTNR1B:130 SSTR4:173
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODI	-0.03052690	1298	2.625e-04	4.941e-02	MAN2A1:5 ALB:20 DCAF4:31 ANO8:80 KTN1:128 HLTf:133
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.04753086	509	2.580e-04	4.941e-02	PJA2:47 PARG:98 VCAM1:125 HLTf:133 AZIN1:140 N4BP1:159
BENPORATH_SOX2_TARGETS	-0.04096629	685	2.806e-04	5.057e-02	ABHD11:7 HASE2:29 ANO8:80 PARG:98 CDK12:117
HOUNKPE_HOUSEKEEPER_GENES	-0.03293887	1083	2.903e-04	5.090e-02	ELL:9 MORC2:84 KXD1:99 KDM4B:174 RNF216:178 SLC35E1:214
ALONSO_METASTASIS_UP	-0.04776886	179	3.956e-04	6.021e-02	MDM2:283 MAL:303 MAP4K3:334 KLF10:379 EXOC2:486 FGG:482
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	-0.03821878	751	3.990e-04	6.021e-02	FNBPA:8 ELL:9 UBR2:14 BTN3A3:23 ZNF16:32 FGDB:43
HSIAO_LIVER_SPECIFIC_GENES	-0.07258776	201	3.970e-04	6.021e-02	ALB:20 SDS:30 MGST1:54 AGXT:136 HSD11B1:167 ATP13A3:173

GO\_Biological\_Process\_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Regulation Of Gene Expression (GO:001046	-0.05278078	950	5.983e-08	3.223e-04	MZF1:16 BTN3A3:23 BTNL2:24 ZNF280A:46 KANSL3:49 CUX2:67
Regulation Of DNA-templated Transcription	-0.03771024	1648	7.610e-07	2.050e-03	MZF1:16 ZNF46:28 R1OX1:33 ZNF408:38 ZNF518A:40 ZNF280A:46
Cilium Movement (GO:0003341)	0.20459441	47	1.237e-06	2.222e-03	DNAH9:5 DNAH17:17 DNAH11:178 DNHR1:205 TEK1:299 SPEF2:448
Anterograde Trans-Synaptic Signaling (GO	0.09415976	183	1.186e-05	1.065e-02	MINK1:44 GRIN2A:101 MTNR1B:130 GABRR3:200 PENK:336 TRKB:357
Cilium-Dependent Cell Motility (GO:00602	0.30964719	17	9.893e-06	1.065e-02	DNAH2:1 DNAH17:17 TEK1:299 DNAH3:463 GAS8:674 TEKTA:967
Muscle Contraction (GO:0006936)	0.13526729	88	1.186e-05	1.065e-02	TACR2:18 ARHGFE11:24 MYH13:134 MYH8:146 NOS1:249 CPM12:284
Regulation Of Transcription By RNA Polym	-0.03233138	1714	1.626e-05	1.252e-02	MZF1:16 ZNF446:28 ZNF408:38 ZNF518A:40 KANSL3:49 WIZ:61
Striated Muscle Contraction (GO:0006941)	0.16498924	52	3.909e-05	2.633e-02	ARHGFE11:24 MYH7B:43 DMD:86 MYH8:146 SCN5A:217 NOS1:249
Negative Regulation Of Gene Expression (G	-0.06736602	314	4.439e-05	2.658e-02	RBL1:78 MORC2:84 TNF:88 DAXX:137 TASOR:150 N4BP1:159
Regulation Of DNA Metabolic Process (GO:	-0.10632231	122	5.159e-05	2.780e-02	TAF2:87 PARG:98 SLF1:295 HDAC8:352 EID3:382 USP1:395
Chemical Synaptic Transmission (GO:00072	0.07292523	257	6.116e-05	2.996e-02	MINK1:44 GRIN2A:101 MTNR1B:130 GABRR3:200 PENK:336 TRKB:357
Cellular Component Assembly (GO:0022607)	0.07400571	240	8.371e-05	3.759e-02	CFAP46:83 DMD:86 CD74:111 QSOX1:120 CFAP74:137 SPACA9:147
Cilium Movement Involved In Cell Motilit	0.42633805	7	9.375e-05	3.886e-02	TEK1:299 GAS8:674 TEKTA:967 TEK12:1003 TEKTS:1173 RSPH9:2022
Axoneme Assembly (GO:0035082)	0.19825800	30	7.179e-04	5.706e-02	CFAP46:83 CFAP74:137 SPACA9:147 TLT2:273 GAS8:674 SPAG17:740
Negative Regulation Of DNA-templated Tra	-0.03871945	852	1.564e-04	5.706e-02	MZF1:16 R1OX1:33 CUX2:67 GATAD2A:74 CHD8:79 ZBTB45:82
Regulation Of Heart Rate By Cardiac Cond	0.17341013	39	1.800e-04	5.706e-02	SCN5A:217 DSG2:230 DSP:257 CACNA1G:352 CACNB2:360 KCNQ1:400
Regulation Of Nucleic Acid-Templated Tra	-0.05817142	357	1.746e-04	5.706e-02	MZF1:16 ZNF280A:46 NSD1:83 DAXX:137 LMNB1:151 SRCAP:155
Steroid Metabolic Process (GO:0008020)	-0.13680425	61	2.223e-04	6.654e-02	HSD17B6:77 CYP26C1:102 HSD11B1:167 SULT1E1:230 HSD17B2:466 CYP17A1:499
Action Potential (GO:0001508)	0.18306208	33	2.748e-04	7.428e-02	MYH7B:43 DMD:86 SCN5A:217 KCNQ1:400 ANK3:447 CHRNA4:77
Regulation Of DNA Methylation-Dependent	-0.28077550	14	2.575e-04	7.428e-02	MORC2:84 TASOR:150 TRIM28:739 SAMO1:790 L3MBTL3:966 TET1:1516
Neuropeptide Signaling Pathway (GO:00072	0.13209316	62	3.256e-04	8.354e-02	NPBWR2:100 SSTR4:173 RXFP3:283 PENK:336 GALT:437 CYSLTR2:443
Cellular Response To UV-A (GO:0071492)	0.34370024	9	3.564e-04	8.729e-02	MMP3:226 MME:228 MMP9:258 TIMP1:823 OPN3:394 OPN1SW:1157
Cardiac Conduction (GO:0061337)	0.15320159	44	4.414e-04	1.034e-01	SCN5A:217 DSG2:230 DSP:257 CACNA1G:352 CACNB2:360 KCNQ1:400
Serine Family Amino Acid Biosynthetic Pr	-0.31461599	10	5.712e-04	1.282e-01	CTH:53 SRR:221 MTHFD1:704 SERINC3:608 SEPHS2:1100 PSM1:1159
Regulation Of DNA Repair (GO:0006282)	-0.08858841	125	6.405e-04	1.380e-01	SMCHD1:52 TAF2:87 PARG:98 ERCC5:204 BCL7A:21