

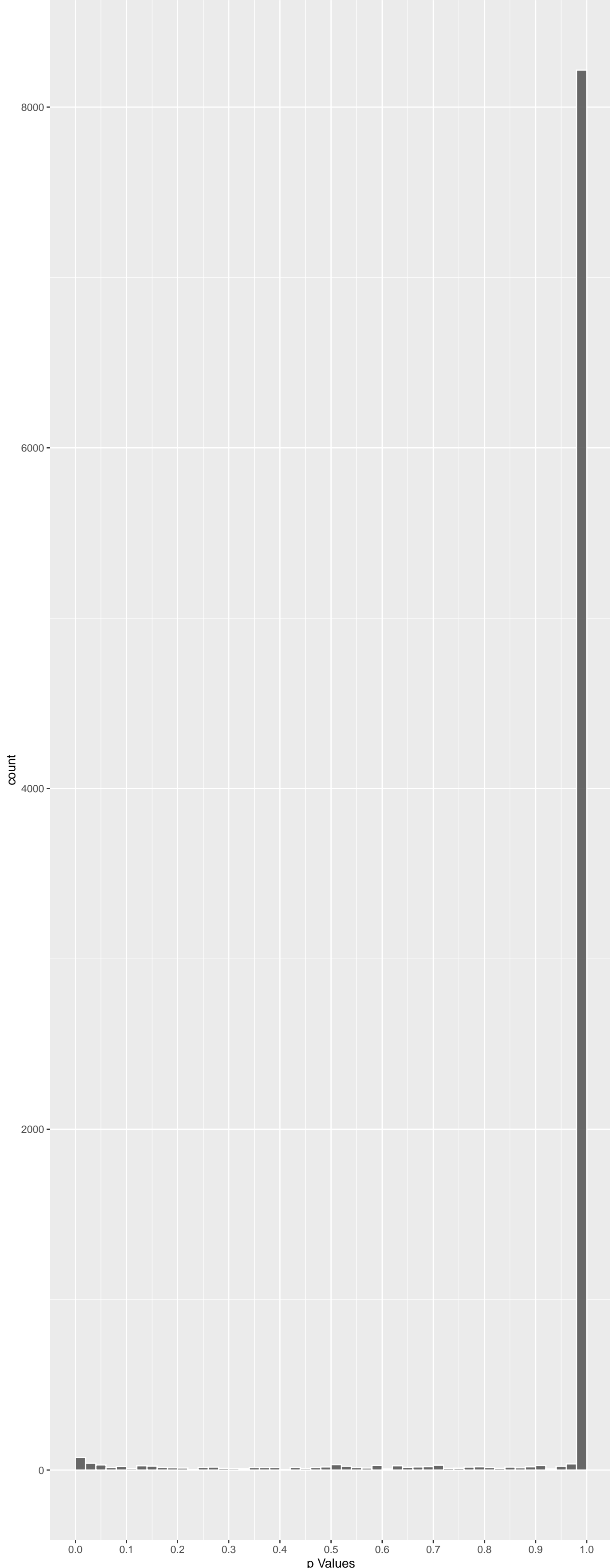
Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
CAPN8	6.921644	2.678586e-11	4.961e-07	9.188e-03
ANKRD35	6.507403	4.587677e-10	4.248e-06	3.934e-02
DNAH2	6.020759	1.041606e-08	5.969e-05	2.764e-01
RXFP4	5.986146	1.289232e-08	5.969e-05	2.764e-01
KIAA0753	5.813330	3.674537e-08	1.361e-04	5.042e-01
POLM	5.670419	8.546905e-08	2.638e-04	5.441e-01
ITGB4	5.624495	1.116306e-07	2.719e-04	5.441e-01
MR1	5.615740	1.174334e-07	2.719e-04	5.441e-01
STYXL2	5.548107	1.732677e-07	3.209e-04	5.441e-01
TACR2	5.552672	1.688013e-07	3.209e-04	5.441e-01
LTk	5.530206	1.919126e-07	3.231e-04	5.441e-01
KIAA0319	5.496047	2.330391e-07	3.597e-04	5.551e-01
SPEM2	5.332192	5.822046e-07	8.295e-04	1.000e+00
TRIM15	5.194936	1.228742e-06	1.626e-03	1.000e+00
HAVCR1	-5.092301	2.122464e-06	1.966e-03	1.000e+00
NLRP8	-5.096558	2.075309e-06	1.966e-03	1.000e+00
POF1B	5.113861	1.893833e-06	1.966e-03	1.000e+00
RABEP1	5.082638	2.118689e-06	1.966e-03	1.000e+00
SPTBN5	5.103607	1.999441e-06	1.966e-03	1.000e+00
ZZEF1	5.123083	1.803478e-06	1.966e-03	1.000e+00
ADGRG4	5.029546	2.949859e-06	2.404e-03	1.000e+00
ARHGAP40	5.019093	3.114961e-06	2.404e-03	1.000e+00
DNAH9	5.024346	3.030909e-06	2.404e-03	1.000e+00
USP43	5.025454	3.013458e-06	2.404e-03	1.000e+00
PLEC	4.996740	3.498459e-06	2.457e-03	1.000e+00

Top genes by Q-Value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
CAPN8	6.92164430	2.678586e-11	4.961e-07	9.188e-03
ANKRD35	6.50740261	4.587677e-10	4.248e-06	3.934e-02
DNAH2	6.02075903	1.041606e-08	5.969e-05	2.764e-01
RXFP4	5.98614558	1.289232e-08	5.969e-05	2.764e-01
KIAA0753	5.81332966	3.674537e-08	1.361e-04	5.042e-01
ITGB4	5.62449543	1.116306e-07	2.719e-04	5.441e-01
MR1	5.61574034	1.174334e-07	2.719e-04	5.441e-01
POLM	5.67041935	8.546905e-08	2.638e-04	5.441e-01
STYXL2	5.54810680	1.732677e-07	3.209e-04	5.441e-01
TACR2	5.55267207	1.688013e-07	3.209e-04	5.441e-01
KIAA0319	5.49604722	2.330391e-07	3.597e-04	5.551e-01
A1BG	-0.49957078	1.000000e+00	1.000e+00	1.000e+00
A1CF	-0.05706727	1.000000e+00	1.000e+00	1.000e+00
A2M	-1.58076657	6.835885e-01	1.000e+00	1.000e+00
A2ML1	2.55975726	6.285079e-02	8.964e-01	1.000e+00
A3GALT2	0.93302016	1.000000e+00	1.000e+00	1.000e+00
A4GALT	0.08197759	1.000000e+00	1.000e+00	1.000e+00
A4GNT	-1.04940329	1.000000e+00	1.000e+00	1.000e+00
AACS	-0.19074670	1.000000e+00	1.000e+00	1.000e+00
AADAC	0.54717125	1.000000e+00	1.000e+00	1.000e+00
AADAC	1.76746823	4.629981e-01	1.000e+00	1.000e+00
AADACL2	2.84186382	2.691039e-02	5.930e-01	1.000e+00
AADACL3	0.84482299	1.000000e+00	1.000e+00	1.000e+00
AADACL4	0.81324866	1.000000e+00	1.000e+00	1.000e+00

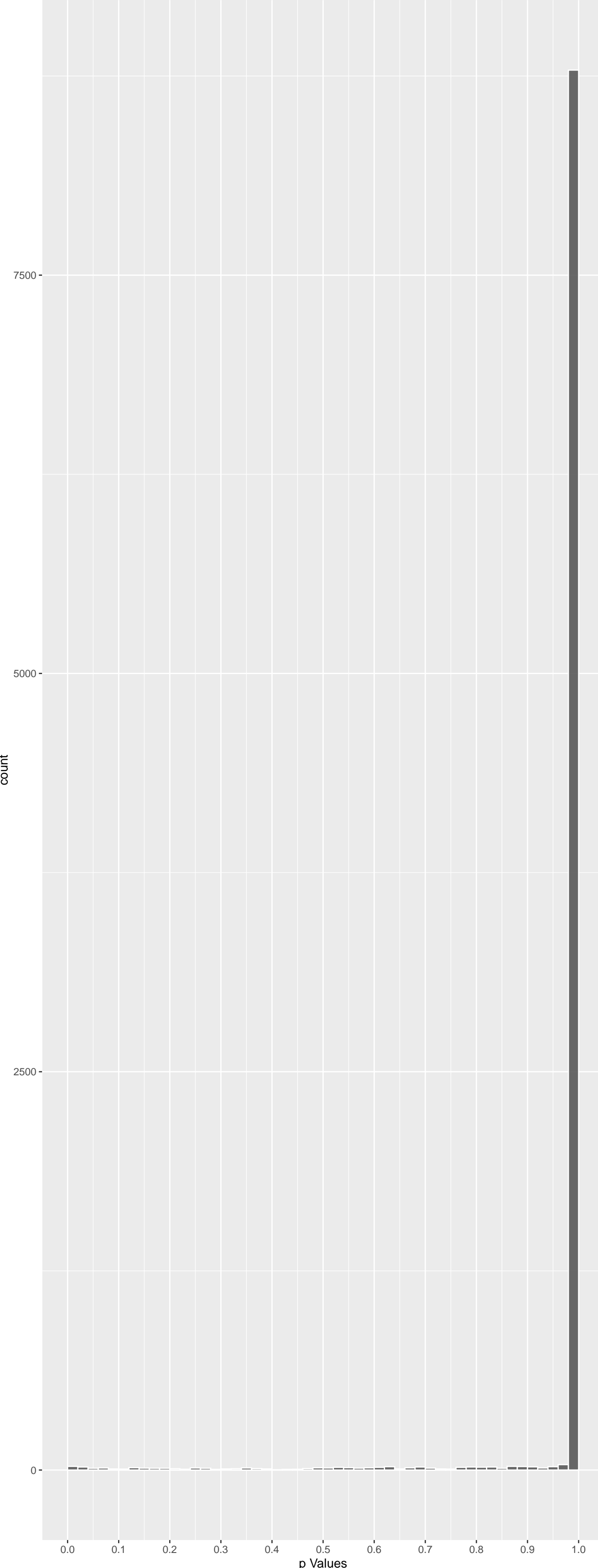
Positive Rho Non-permuted



Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
CAPN8	6.921644	2.678586e-11	4.961e-07	9.188e-03
ANKRD35	6.507403	4.587677e-10	4.248e-06	3.934e-02
DNAH2	6.020759	1.041606e-08	5.969e-05	2.764e-01
RXFP4	5.986146	1.289232e-08	5.969e-05	2.764e-01
KIAA0753	5.813330	3.674537e-08	1.361e-04	5.042e-01
POLM	5.670419	8.546905e-08	2.638e-04	5.441e-01
ITGB4	5.624495	1.116306e-07	2.719e-04	5.441e-01
MR1	5.615740	1.174334e-07	2.719e-04	5.441e-01
STYXL2	5.548107	1.732677e-07	3.209e-04	5.441e-01
TACR2	5.552672	1.688013e-07	3.209e-04	5.441e-01

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
HAVCR1	-5.092301	2.122464e-06	1.966e-03	1.000e+00
NLRP8	-5.096558	2.075309e-06	1.966e-03	1.000e+00
PPP4R1	-4.930509	4.920936e-06	3.038e-03	1.000e+00
DCAF4	-4.848927	7.447876e-06	3.941e-03	1.000e+00
ELL	-4.852274	7.323224e-06	3.941e-03	1.000e+00
SPATA31A5	-4.835944	7.950909e-06	4.091e-03	1.000e+00
ZNF483	-4.821707	8.540089e-06	4.275e-03	1.000e+00
MAP1S	-4.739267	1.286959e-05	5.956e-03	1.000e+00
TTC3	-4.734376	1.318380e-05	5.956e-03	1.000e+00
NSD1	-4.655979	1.934665e-05	7.465e-03	1.000e+00

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num_genes	pval	p.adj	gene.vals
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.09562023	602	1.384e-15	8.987e-12	WDR76:29 KIF18A:32 ZNF644:43 AGGF1:49 ITGB1:89 SLF1:95
REACTOME_KERATINIZATION	0.15220889	202	9.293e-14	3.017e-10	EVPL46 KRT80:67 KRT20:140 KRTAP10:1-179 KRT28:182 DSP:199
ZHANG_BREAST_CANCER_PROGENITORS_UP	-0.10158855	414	1.489e-12	3.222e-09	TTCS3 SMCHD1:12 NCAPD3:26 PROM1:27 SYDE2:44 SLF1:95
REACTOME_FORMATION_OF_THE_CORNFIFIED_ENVE	0.17948676	126	3.550e-12	4.379e-09	EVPL46 KRT80:67 KRT20:140 KRT28:182 DSP:199 KRT84:216
DODD_NASOPHARYNGEAL_CARCINOMA_DN	-0.05833849	1275	3.656e-12	4.379e-09	NCAPD3:26 KIF18A:32 TPX2:39 ZDBF2:45 FGDB62 L3MBTL4:88
JOHNSTONE_PARVB_TARGETS_3_DN	-0.07275562	793	4.046e-12	4.379e-09	SMCHD1:12 ZNF274:16 SLC6A6:18 NDUFS5:28 WDR76:29 KIF18A:32
REACTOME_SENSORY_PERCEPTION	0.07920862	596	4.574e-11	4.244e-08	OR10R2:44 CALHM1:50 OR10S1:62 OR5AU1:79 OTOF:98 ORSQ02:120
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	-0.04703935	673	6.793e-11	5.514e-08	TTCS3 ATP13A3:17 KIF18A:32 TPX2:39 ZNF644:43 DHX36:52
PUJANA_BRCA1_PCC_NETWORK	-0.05008095	1520	1.012e-10	7.300e-08	TMEM131L:15 ATP13A3:17 SLC6A6:18 DAXX:25 TPX2:39 FNBPA:60
FISCHER_DREAM_TARGETS	-0.05746899	921	4.067e-09	2.641e-06	SMCHD1:12 NCAPD3:26 WDR76:29 KIF18A:32 TPX2:39 GATAD2A:55
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.06833373	624	6.348e-09	3.748e-06	SMCHD1:12 TASOR:20 KIF18A:32 ZNF644:43 AGGF1:49 DHX36:52
REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.08441104	384	1.453e-08	7.861e-06	OR10R2:44 OR10S1:62 OR5AU1:79 ORSQ02:120 OR6C65:128 OR10T2:133
KEGG_OLFACTORY_TRANSDUCTION	0.08196571	372	6.023e-08	3.009e-05	OR10R2:44 OR10S1:62 OR5AU1:79 ORSQ02:120 OR6C65:128 OR10T2:133
REACTOME_CELL_CYCLE	-0.06227513	651	6.611e-08	3.067e-05	DAXX:25 NCAPD3:26 KIF18A:32 TPX2:39 HERC2:74 HAUS8:134
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.09790457	249	1.075e-07	4.653e-05	CHRM3:37 PTAFR:70 BDKRB1:82 MTRN1B:94 P2RY4:146 ORH2:175
KINSEY_TARGETS_OF_EWSR1_FLI1_FUSION_UP	-0.05470484	1211	1.576e-07	6.019e-05	PROM1:27 WDR76:29 KIF18A:32 TPX2:39 CYP4F22:46 GEMIN5:84
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.04393348	440	1.568e-07	6.019e-05	NCAPD3:26 WDR76:29 KIF18A:32 TPX2:39 GLMN:92
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04453125	1189	2.800e-07	1.010e-04	TTCS3 MAGEL2:41 PEG3:65 LTN1:70 HERC2:74 SON76
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	-0.05260641	826	3.170e-07	1.083e-04	SMCHD1:12 TMEM131L:15 ATP13A3:17 ZNF292:19 TASOR:20 MYO9B:24
HOUNKPE_HOUSEKEEPING_GENES	-0.04633967	1073	3.478e-07	1.129e-04	ELL4 MORC2:11 RNF216:35 MBD1:37 KDM4B:38 AGGF1:49
SHEN_SMARCA2_TARGETS_UP	-0.07201337	410	5.977e-07	1.848e-04	AGGF1:49 HERC2:74 SON76 TMEM135:80 PTHF3:83 KTN1:117
DODD_NASOPHARYNGEAL_CARCINOMA_UP	0.03748039	1576	8.731e-07	2.577e-04	ANKRD35:2 DNAH2:3 KIAA0319:12 USP43:20 D1A119:21 SPACA9:40
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.03993348	1335	1.180e-06	3.331e-04	PPPAR1:27 RNF26:29 KIF18A:32 KTN1:117 KDSR:125 MLT1:141 CTPS4:142
SCHLOSSER_SERUM_RESPONSE_DN	-0.05520789	655	1.566e-06	4.239e-04	TASOR:20 ARSL:21 PHF3:83 GLMN:92 GRB14:103 CMTR1:113
REACTOME_CELL_CYCLE_MITOTIC	-0.06104403	524	1.861e-06	4.835e-04	NCAPD3:26 KIF18A:32 TPX2:39 HAUS8:134 CYP4F22:46
PUJANA_CHECK1_PCC_NETWORK	-0.05196210	711	2.580e-06	6.444e-04	TMEM131L:15 ATP13A3:17 TPX2:39 GLMN:92 TAF2:144 BIK:166
FEVR_CTNK1B_TARGETS_DN	-0.05898483	530	3.736e-06	8.987e-04	KIF18A:32 DHX36:52 MTBF:64 HAUS8:134 CNOC1:260 NINL:208
MILI_PSEUDOMOD4_HAPTOFALIS_UP	-0.06033634	496	4.586e-06	1.034e-03	SMCHD1:12 AGGF1:49 LTN1:70 ZNF76:28 WDR76:29
MARTORIATI_MDMA_TARGETS_FATAL_LIVER_DN	-0.05970423	502	5.270e-06	1.180e-03	PPPAR1:23 MBD1:37 PLAGL1:53 SON76:169 ER11:197 NIFK1:241
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.05692390	531	7.648e-06	1.655e-03	LTN1:70 CLU:73 LRP2:79 PHF3:83 WSB1:206 FNTA:32
MARTENS_TRETINOLIN_RESPONSE_UP	-0.04682926	782	9.230e-06	1.934e-03	SPEM2:13 PIK3RS:26 ORP42:42 SMTNL2:43 GTG6:45 CARD14:48
MIKKELSEN_MCV8_HCP_WITH_H3K27ME3	0.06256798	426	9.918e-06	2.013e-03	LTK1:11 FAM83F:29 CHAD:68 PDE1B:80 CACNA1G:103 SYT6:180
REACTOME_SIGNALING_BY_GPCR	0.04923620	684	1.225e-05	2.410e-03	RXFPA:4 CHRM3:39 PIK3RS:26 CHRM3:37
WP_NONALCOHOLIC_FATTY_LIVER_DISEASE	-0.03322880	144	1.891e-05	3.613e-03	NDFUS5:28 NDUFS6:155 NDUFB:188 CASP8:227 NDUFA1:258 TNF:462
OSMAN_BLADDER_CANCER_UP	-0.06381166	376	2.231e-05	4.028e-03	NOL2:38 MAN2A1:35 KIF18A:32 KTN1:117 G2E3:215 ATP1B:267
PID_MYC_ACTIV_PATHWAY	-0.13892214	78	2.229e-05	4.028e-03	BCAT1:240 PEG10:338 ACTL6A:409 DDX18:716 BAK7:760 CDC47:806
NIKOLSKY_BREAST_CANCER_IQ21_AMPLICON	0.20918062	34	2.432e-05	4.156e-03	DCST1:61 THBS3:121 PBXIP1:1213 DCST2:227 LINGOA:285 SHC1:367
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	-0.03506427	1306	2.403e-05	4.156e-03	ELL4 ZNF483:7 ZNF274:16 DAXX:25 TPX2:39 PLAGL1:53
REACTOME_CELL_CYCLE_CHECKPOINTS	-0.04747201	270	2.596e-05	4.323e-03	KIF18A:32 HERC2:74 ANAPC1:156 KIF2C:168 RNF8:246 CCNE1:260
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	-0.04401625	791	2.779e-05	4.511e-03	ELL4 MAP1S:8 ZNF274:16 SLC6A6:18 WASHCC2C:33 KDM4B:38

DisGeNET Top pathways by non-permutation

Geneset	stat	num_genes	pval	p.adj	gene.vals
Hepatitis C	-0.05536748	677	1.122e-06	1.102e-02	HAVCR1:2 TSLP:22 CLU:73 DEPDC5:138 PIPISK1:91 DNMT1:203
Leukemia, Myelocytic, Acute	-0.03293358	1494	3.058e-05	1.010e-01	ELL4 NSD1:10 DAXX:25 PROM1:27 SON76 ZNF331:78
Liver carcinoma	-0.02461420	3048	3.086e-05	1.010e-01	HAVCR1:2 MAP1S:8 NSD1:10 PROM1:27 KIF18A:32 KDM4B:38
Liver neoplasms	-0.03518935	1184	5.965e-05	1.464e-01	NSD1:10 PROM1:27 KDM4B:38 CLU:73 SUGF1:77 ITGB1:89
Arthrogryposis	0.06454270	297	1.377e-04	2.705e-01	ITGB4:7 PLEC2:3 EGR2:289 COL6A1:318 FLCN:322 DES:343
Seborrheic dermatitis	-0.22987703	22	1.911e-04	3.127e-01	JMJD1C:233 SLC02A1:416 TIF2:462 HPG0:674 HIRA:1036 ANP328:1223
Acute lymphocytic leukemia	-0.03664729	803	4.772e-04	1.454e-01	TSLP:22 TLF:237 CRLF2:34 PECAM1:75 ITGB1:89 MLLT10:141
Epidermolysis Bullosa Simplex	0.20560821	23	6.427e-04	1.454e-01	ITGB4:7 LATS2:93 KRT80:67 DES:343 GFAP:396 KRT17:500
Extramammary Hematopoiesis (disorder)	-0.20081781	25	5.107e-04	1.454e-01	TSLP:22 TNF:462 TNFSF11:594 VEGFA:733 CA2:797 NPM1:1104
Fanconi Anemia	-0.06161172	268	5.392e-04	1.454e-01	LRP2:79 BIK:166 CASP8:227 RNF8:246 CCNE1:260 TERF2:283
Fatty Liver	-0.04990047	399	6.653e-04	1.454e-01	SUGF1:77 LATS2:93 PPP1R3A:124 DNMT1:203 CASP8:227 MET:247 LGALS3:306
Hepatocarcinogenesis	-0.04886932	464	3.359e-04	1.454e-01	PROM1:27 KDM4B:38 CLU:73 TCL1B:109 DNMT1:203 CASP8:227
Influenza	-0.04534815	508	5.088e-04	1.454e-01	SAFB:106 GYPB:153 CD66:218 CASP8:227 CTLA4:280 CD9:294
leukemia	-0.02563927	1721	5.564e-04	1.454e-01	ELL4 NSD1:10 SMCHD1:12 TSLP:22 DAXX:25 PROM1:27
Steatohepatitis	-0.04425564	510	6.769e-04	1.454e-01	SUGF1:77 LATS2:93 PPP1R3A:124 DNMT1:203 CASP8:227 LGALS3:306
Tetany	-0.22496200	19	6.319e-04	1.454e-01	TRPM6:72 CLDN16:205 JMJD1C:233 PTH:715 HIRA:1036 SLC12A1:1192
Prostate carcinoma	-0.02080305	2731	7.218e-04	1.469e-01	ELL4 MAP1S:8 NSD1:10 DAXX:25 NCAPD3:26 PROM1:27
Junctional split	0.38673271	6	1.035e-03	5.363e-01	ITGB4:7 PLEC2:3 LAMC2:99 ITGA6:1626 LAMB3:1638 LAMA3:9306:5
Seminoma	-0.06727220	201	1.038e-03	5.363e-01	PROM1:27 CLU:73 TCL1B:109 PRAME:193 DNMT1:203 SLC43A1:223
FANCONI ANEMIA, COMPLEMENTATION GROUP A	-0.05970162	232	1.785e-03	5.595e-01	CASP8:227 RNF26:29 TIF2:462 TIF2:462 TIF2:462 TIF2:462
Muscular Dystrophies, Limb-Girdle	0.09649546	85	2.123e-03	5.595e-01	PLEC2:32 RIFOR2:169 SYTN1:239 COL6A1:318 FLCN:322 DES:343
22q11 partial monosomy syndrome	-0.27575628	11	1.541e-03	5.595e-01	PI4KA:225 JMJD1C:233 HIRA:1036 ARVCF:1439 TBLX1:1742 NGN1L1:1826
Adult Medulloblastoma	-0.11917070	57	1.869e-03	5.595e-01	KDM4B:38 EHMT1:143 PRAME:193 DNMT1:203 CCNE1:260 UHRF1:351
Carcinogenesis	-0.01764150	3552	1.635e-03	5.595e-01	MAP1S:8 NSD1:10 SMCHD1:12 DAXX:25 PROM1:27 KIF18A:32
Central neuroblastoma	-0.02444147	1508	1.891e-03	5.595e-01	NSD1:10 PROM1:27 KDM4B:38 TPX2:39 PEG3:65 CLU:73
Congenital myopathy (disorder)	0.08819921	109	1.486e-03	5.595e-01	MYH7B:250 COL6A1:318 FLCN:322 DES:343 MYH8:471 CASQ1:491
DGeorge Syndrome	-0.11504301	60	2.068e-03	5.595e-01	JMJD1C:233 DGCRC6:628 ARSA:693 VEGFA:733 ALB:979 SLC25A1:1007
Granulomatosis	0.29519266	9	2.165e-03	5.595e-01	PTPN22:93 PRTN3:96 NOD2:158 HLA-DPB1:977 CYBB:1126 NCF2:1399
Lone atrial fibrillation	0.24846689	13	1.923e-03	5.595e-01	KCNK3:75 TKS5:425 SCN3B:573 SCN5A:624 KCNE3:835 LMNA:1274
Malignant neoplasm of lung	-0.02111222	2132	1.866e-03	5.595e-01	DCAF:45 NSD1:10 MYO9B:24 PROM1:27 MBD1:37 KDM4B:38
Malignant neoplasm of prostate	-0.01859395	2839	2.165e-03	5.595e-01	ELL4 MAP1S:8 NSD1:10 ZNF292:19 DAXX:25 NCAPD3:26
Malignant tumor of cervix	-0.03348612	747	2.035e-03	5.595e-01	PEG3:65 CLU:73 SUGF1:77 CALCR:100 OGDHL:164 DNMT1:203
Oral mucosal blisters	0.28487604	10	1.812e-03	5.595e-01	ITGB4:7 PLEC2:3 LAMC2:99 DSP:199 ITGA6:1626 LAMB3:1638
Paracoccidioidomycosis	-0.23386157	15	1.714e-03	5.595e-01	CTLA4:280 GPI:349 RBM45:603 IL23R:678 IFNG:690 CD28:717
Plantar hyperkeratosis	0.33929586	7	1.878e-03	5.595e-01	ITGB4:7 PLEC2:3 LAMC2:99 KRT6A:609 LAMB3:1638 COL17A1:9306:5
Primary malignant neoplasm of lung	-0.02247932	1973	1.339e-03	5.595e-01	DCAF:45 NSD1:10 MYO9B:24 PROM1:27 MBD1:37 KDM4B:38
T-lymphocyte immunodeficiency	0.37419809	6	1.502e-03	5.595e-01	CD3E:252 SFTPA1:386 SIPA1:601 RAG1:1005 LBR:2597 SMARCA1:1306:5
Venous malformation	-0.22360262	16	1.958e-03	5.595e-01	AGGF1:49 PECAM1:75 GLMN:92 VEGFA:733 PIK3CA:1412 STAT1:1901
Myeloid Leukemia, Chronic	-0.03273949	751	2.495e-03	5.652e-01	HAVCR1:2 PROM1:27 PECAM1:75 TCL1B:109 IL1RAP:181 PRAME:193
Balkan Nephropathy	-0.22369007	15	2.705e-03	5.652e-01	TNF:462 GTF2IRF1:518 RBM45:603 ALB:979 ABCB1:1052 SLC06A1:2435

customGeneSet Top pathways by non-permutation

Geneset	stat	num_genes	pval	p.adj	gene.vals
HumanLocalAdiponDietAll	-0.07354926	13	4.105e-01	6.157e-01	SLC22A4:2278 LCT:2339 GPX1:2275 AS3MT:9215:5 GPX3:9215:5 CELF1:9215:5
expressionDirectionalSelection	0.06335034	42	3.718e-01	6.157e-01	TRIM40:916 ULR44:2269 KAT8:2339 ZNF646:2746 HLA-DQB1:9306:5 HLA-DRB1:9306:5
NAFLDGWAS	-0.02424242	15	7.747e-01	7.747e-01	ADH1B:1205 GPAM:2597 PNPLA3:9215:5 TM6SF2:9215:5 APOE:9215:5 TRIB1:9215:5
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 non-permutation

Protein-Coupled Receptor Signaling Pat	0.142717120	49	5.514e-04	1.192e-01	CHRM3:37 MTRNR1B:94 OR10J5:303 MCR3:868 CCR1:1204 CHRM2:1370
Negative Regulation Of Gene Expression,	-0.14285420	49	4.466e-04	1.192e-01	MORC2:11 TASOR:20 DNMT1:203 UBR2:212 UHRF2:342 UHRF1:351
Serine Family Amino Acid Biosynthetic Pr	-0.33424500	9	5.160e-04	1.192e-01	CTH1:17 P5PH:220 SERINC5:531 MTHFD1:1159 SERINC3:1472 STR:2431
Long-Chain Fatty Acid Biosynthetic Proc	0.20127531	24	6.433e-04	1.338e-01	ALOX5:153 ALOX12:378 ALOX15B:422 ALOX15:536 ACSBG1:694 GSTM2:806
Sensory Perception Of Taste (GO:0050909)	0.24419124	16	7.126e-04	1.427e-01	CALHM1:50 CALHM3:176 PKG1L2:262 GATAC3:789 ASIC2:1254 PKD2L1:1597
Negative Regulation Of Transcription By	-0.03693959	731	8.943e-04	1.727e-01	NSD1:10 ZNF274:16 MAGEL2:41 GATAD2A:55 IL3:61 PEG3:65
Chromatin Organization (GO:0006325)	-0.05896512	254	1.258e-03	2.345e-01	MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 KDM3:1547 RGDPA:1569 KPNAB4:1629
NLS-bearing Protein Import Into Nucleus	-0.22512730	17	1.312e-03	2.364e-01	MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92
Chromatin Remodeling (GO:0006338)	-0.06209799	220	1.555e-03	2.627e-01	CACNA1G:103 DSP:199 SCN3B:573 SCN5A:624 KCNH6:813 KCNE3:835
Regulation Of Heart Rate By Cardiac Cond	0.14492173	40	1.522e-03	2.627e-01	MYH10:151 MYH7B:250 FLNC:322 UTP:491 KRT19:736 PHACTR1:970
Actinomyosin Structure Organization (GO:00	0.10269002	77	1.854e-03	3.037e-01	POF1B:16 C2NF2:216 VIL1:298 AVIL:351 AIF1:477 ENAH:591
Actin Filament Organization (GO:0007015)	0.05792825	140	1.959e-03	3.116e-01	MBD3L3:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2122 SMARCA5:2300
Facultative Heterochromatin Formation (G	-0.22196569	6	2.114e-03	3.222e-01	MIK1:35 SLTRK4:119 DTNBP1:139 FLRT1:1150 TUNAR:210 IQGAP1:258
Neuron Process Morphogenesis (GO:00408	-0.05713553	139	2.265e-03	3.222e-01	MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:154
Positive Regulation Of Heterochromatin F	-0.24508501	13	2.217e-03	3.222e-01	CYP11A1:347 NSD17B2:604 SRD5A3:646 HD17B6:664 CYP11B1:1285 CYP17A1:1422
Steroid Hormone Biosynthetic Process (GO	-0.20341097	19	1.466e-03	3.222e-01	ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237
Positive Regulation Of Cellular Componen	-0.08367365	111	2.354e-03	3.264e-01	SLC6A6:18 SLC7A9:129 SLC3A1:223 SLC38A2:377 SLC7A6:526 SLC36A2:596
Neutral Amino Acid Transport (GO:0015804	-0.14727018	35	2.576e-03	3.398e-01	

MGI\_Mammalian\_Phentype\_Level\_4 Top pathways by non-perculation

Geneset	stat	num_genes	pval	p.adj	gene.vals
MP00002080 prenatal lethality	-0.04211534	1338	3.328e-06	1.584e-03	NSD1:10 SMCHD1:12 DAXX:25 GATAD2A:55 MTPB:64 LTN1:70
MP0000598 abnormal liver morphology	-0.05640946	482	4.141e-05	8.977e-03	MAN2A1:36 PEGCAM1:75 ITGB1:89 GRB14:103 SAFB:106 CTH1:171
MP00002086 abnormal extraembryonic tissu	-0.05514987	487	5.658e-05	8.977e-03	NSD1:10 SMCHD1:12 DAXX:25 GATAD2A:55 ITGB1:89 PTPRB:94
MP00003313 abnormal cell death	-0.05015547	464	3.402e-04	2.329e-02	DAXX:25 PROM1:27 LRP2:79 ITGB1:89 CTH1:171 DNMT1:203
MP0002085 abnormal embryonic tissue	-0.04337846	655	3.042e-04	2.329e-02	NSD1:10 DAXX:25 GATAD2A:55 TRPM7:62 TRPM7:179 ITGB1:89
MP00004197 abnormal fetal growth/weight/	-0.07777498	177	4.210e-04	3.340e-02	PLAGL1:53 TRPM6:72 ITGB1:89 SAFB:106 ER11:197 MET:247
MP00002088 abnormal embryonic growth/wei	-0.05325451	344	8.670e-04	5.158e-02	DAXX:25 ITGB1:89 LAT2:93 PTPRB:94 EHMT1:143 HSD17B2:252
MP00003121 genomic imprinting	-0.18257629	28	8.440e-04	5.158e-02	SMCHD1:12 MAGEL2:41 PLAGL1:53 PEG3:65 DNMT1:203 PHLD2A:281
MP0003984 embryonic growth retardation	-0.05020428	337	1.345e-03	4.637e-02	DAXX:25 ITGB1:89 LAT2:93 PTPRB:94 EHMT1:143 HSD17B2:252