

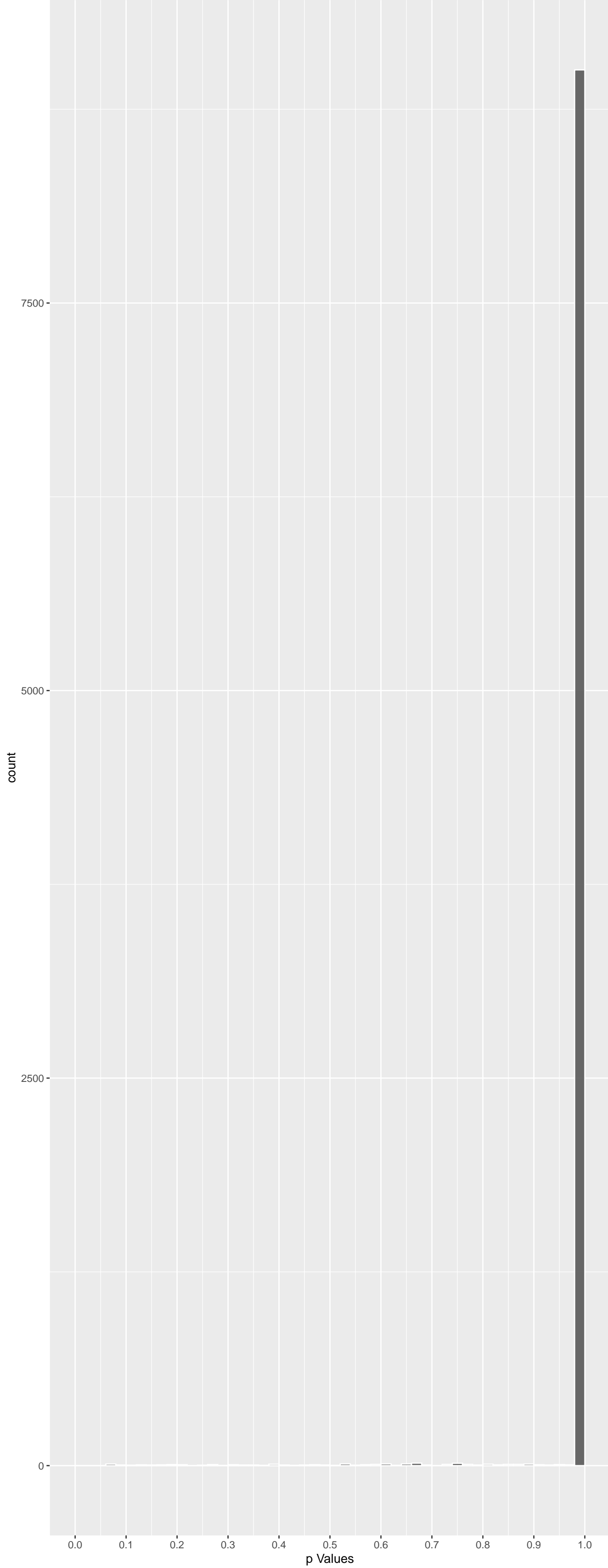
Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
AGGF1	4.767226	1.120680e-05	6.289e-02	1.000e+00
IQCF5	-4.686288	1.669232e-05	6.289e-02	1.000e+00
SCN9A	-4.683399	1.692936e-05	6.289e-02	1.000e+00
TMEM108	-4.710764	1.480740e-05	6.289e-02	1.000e+00
ZSCAN25	4.767820	1.117379e-05	6.289e-02	1.000e+00
ABCB11	4.415066	6.058749e-05	7.312e-02	1.000e+00
ADAMTS6	-4.453890	5.059702e-05	7.312e-02	1.000e+00
ATF6	-4.397161	6.580566e-05	7.312e-02	1.000e+00
C2CD2L	-4.501681	4.045090e-05	7.312e-02	1.000e+00
CADM3	-4.429359	5.670804e-05	7.312e-02	1.000e+00
GRID1	-4.390340	6.790407e-05	7.312e-02	1.000e+00
IQCF3	-4.438592	5.432969e-05	7.312e-02	1.000e+00
NEDD4	4.400831	6.470221e-05	7.312e-02	1.000e+00
PPP4R1	4.414302	6.080186e-05	7.312e-02	1.000e+00
PRTG	4.381047	7.086625e-05	7.312e-02	1.000e+00
TMED3	-4.424097	5.810802e-05	7.312e-02	1.000e+00
TMEM131L	4.429018	5.679796e-05	7.312e-02	1.000e+00
ZNF292	4.504231	3.996817e-05	7.312e-02	1.000e+00
CPB1	4.366130	7.588022e-05	7.417e-02	1.000e+00
CCPG1	4.344249	8.385186e-05	7.787e-02	1.000e+00
LOXHD1	-4.303569	1.008411e-04	8.919e-02	1.000e+00
CNTRL	4.250253	1.281173e-04	9.152e-02	1.000e+00
CYP17A1	4.256039	1.248435e-04	9.152e-02	1.000e+00
MYO9B	4.287161	1.085826e-04	9.152e-02	1.000e+00
TRPM6	4.274327	1.150294e-04	9.152e-02	1.000e+00

Top genes by Q-Value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
A1BG	-1.0418450	1.000000000	1.000e+00	1.000e+00
A1CF	-0.1593210	1.000000000	1.000e+00	1.000e+00
A2M	3.4344400	0.003562677	3.939e-01	1.000e+00
A2ML1	2.3019953	0.128012626	1.000e+00	1.000e+00
A3GALT2	1.0699429	1.000000000	1.000e+00	1.000e+00
A4GALT	1.2481180	1.000000000	1.000e+00	1.000e+00
A4GNT	-0.4807195	1.000000000	1.000e+00	1.000e+00
AAAS	-1.6072936	0.647939803	1.000e+00	1.000e+00
AACS	-0.8338138	0.400099814	1.000e+00	1.000e+00
AADAC	0.5179184	1.000000000	1.000e+00	1.000e+00
AADACL2	-0.4942042	1.000000000	1.000e+00	1.000e+00
AADACL3	-1.9884649	0.280561798	1.000e+00	1.000e+00
AADACL4	-0.5276064	1.000000000	1.000e+00	1.000e+00
AADAT	1.3266170	1.000000000	1.000e+00	1.000e+00
AGAB	2.5683818	0.061304735	1.000e+00	1.000e+00
AAK1	-0.6953668	1.000000000	1.000e+00	1.000e+00
AAMDC	-0.2246477	1.000000000	1.000e+00	1.000e+00
AMP	1.5994834	0.658279364	1.000e+00	1.000e+00
AANP	-1.0254415	1.000000000	1.000e+00	1.000e+00
AAR2	-1.3196261	1.000000000	1.000e+00	1.000e+00
AARD	-1.1574383	1.000000000	1.000e+00	1.000e+00
AARS1	0.17771912	1.000000000	1.000e+00	1.000e+00
AARS2	0.9760784	1.000000000	1.000e+00	1.000e+00
AARSD1	-0.5886980	1.000000000	1.000e+00	1.000e+00
AASDH	3.1021413	0.011527574	6.469e-01	1.000e+00

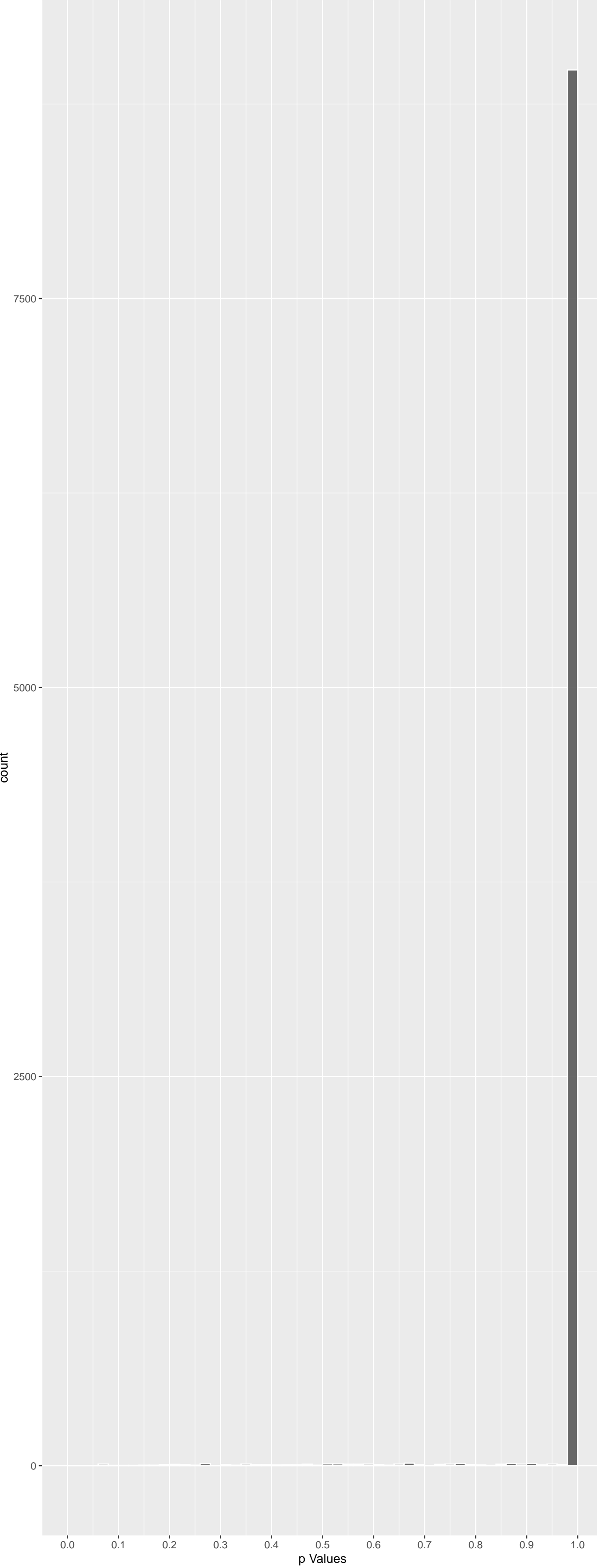
Positive Rho Non-permuted



Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
AGGF1	4.767226	1.120680e-05	6.289e-02	1.000e+00
ZSCAN25	4.767820	1.117379e-05	6.289e-02	1.000e+00
ABCB11	4.415066	6.058749e-05	7.312e-02	1.000e+00
NEDD4	4.400831	6.470221e-05	7.312e-02	1.000e+00
PPP4R1	4.414302	6.080186e-05	7.312e-02	1.000e+00
PRTG	4.381047	7.086625e-05	7.312e-02	1.000e+00
TMEM131L	4.429018	5.679796e-05	7.312e-02	1.000e+00
ZNF292	4.504231	3.996817e-05	7.312e-02	1.000e+00
CPB1	4.366130	7.588022e-05	7.417e-02	1.000e+00
CCPG1	4.344249	8.385186e-05	7.787e-02	1.000e+00

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
IQCF5	-4.686288	1.669232e-05	6.289e-02	1.000e+00
SCN9A	-4.683399	1.692936e-05	6.289e-02	1.000e+00
TMEM108	-4.710764	1.480740e-05	6.289e-02	1.000e+00
ADAMTS6	-4.453890	5.059702e-05	7.312e-02	1.000e+00
ATF6	-4.397161	6.580566e-05	7.312e-02	1.000e+00
C2CD2L	-4.501681	4.045090e-05	7.312e-02	1.000e+00
CADM3	-4.429359	5.670804e-05	7.312e-02	1.000e+00
GRID1	-4.390340	6.790407e-05	7.312e-02	1.000e+00
IQCF3	-4.438592	5.432969e-05	7.312e-02	1.000e+00
TMED3	-4.424097	5.810802e-05	7.312e-02	1.000e+00

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_OLFACTORY_SIGNALING_PATHWAY	-0.08871018	386	2.358e-09	1.531e-05	OR10D3:33 OR6C65:44 OR2L8:69 OR1E2:116 OR9G1:195 OR2M3:245 SCN9A:3 PDE6B:22 OR10D3:33 OR6C65:44 APOA1:51 OR2L8:69
REACTOME_SENSORIAL_PERCEPTION	-0.06741980	598	1.982e-08	5.552e-05	OR6C65:44 OR2L8:69 OR1E2:116 OR9G1:195 OR2M3:245 OR10AD1:265
KEGG_OLFACTORY_TRANSDUCTION	-0.08402253	374	2.565e-08	5.552e-05	KRT5:71 KRTAP4:9-144 KRTAP13:3-204 KRTAP10:8-240 KRTAP24:1-262 KRTAP19-7-323
REACTOME_KERATINIZATION	-0.09769070	206	1.375e-06	2.233e-03	IDO2:48 TM2D:109 RAB11FIP1:10 ANK1:140 ZMAT4:195 PLEKHA2:237
NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON	0.18669163	53	2.589e-06	3.363e-03	MYO9B:11 RAD51AP1:15 KIAA0825:16 CDCA2:20 HJURP:25 NCAPD:37
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.04986785	666	1.225e-05	1.326e-02	GABRA5:13 GABRR3:3 GJA10:65 CDCA2:20 HJURP:25 NCAPD:37
REACTOME_NEURONAL_SYSTEM	-0.06164252	391	2.976e-05	2.761e-02	CADM3:7 GRID1:10 GABRA5:13 GABRR3:3 GJA10:65 CDCA2:20 HJURP:25 NCAPD:37
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.04624334	576	1.560e-04	1.013e-01	ARHGFE4:14 SSTR4:17 MC4R:24 PTH1R:35 VIPR1:54 CHRM2:70
REACTOME_SIGNALING_BY_GPCR	-0.04259649	686	1.513e-04	1.013e-01	HLA-DOB:482 IFNA21:738 IFNA4:740 HLA-G:745 HLA-F:890 IFNA1:926
KEGG_AUTOIMMUNE_THYROID_DISEASE	-0.04549657	50	1.552e-04	1.013e-01	GRID1:10 GABRA5:13 SSTR4:17 MC4R:24 PTH1R:35 MAS1:52
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.06590770	265	2.255e-04	1.332e-01	LAS1L:200 RPL35:259 RPL7:313 PDCD11:363 R1C01:432 RPS19:463
REACTOME_RRNA_PROCESSING	0.07831351	184	2.516e-04	1.362e-01	SSTR4:17 MC4R:24 PTH1R:35 VIPR1:54 CHRM2:70 CHRM3:86
REACTOME_GPCR_LIGAND_BINDING	-0.04956826	450	3.235e-04	1.616e-01	RPL35:259 RPL7:313 SSR3:436 RPS19:463 RPL15:744 RPS27L:910
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_P	0.10730716	93	3.499e-04	1.623e-01	ABCB11:5 CYP27A1:152 ACXO2:223 CYPB81:438 SLC01B1:646 ABCC2:752
WP_DISORDERS_OF_BILE_ACID_SYNTHESIS_AND	0.22795035	20	4.167e-04	1.804e-01	SLC01B1:646 HMOX1:650 ABCC2:752 UGT1A4:1042 ABCG2:1632 DDX3P:2372
REACTOME_HEME_DEGRADATION	-0.03548663	15	6.129e-04	2.057e-01	ABCB11:5 CYP17A1:13 CUBN:17 ACER1A:49 ACOT12:65 LRP2:82
REACTOME_METABOLISM_OF_LIPIDS	0.03784961	722	5.602e-04	2.057e-01	H1-3:19 H1-2:31 CASP7:107 H1-4:137 H1-5:250 DBNL:275
REACTOME_APOPTOTIC_EXECUTION_PHASE	-0.13565227	52	7.157e-04	2.057e-01	RPL35:259 RPL7:313 RPS19:463 ATF3:646 RPL15:744 RPS27L:910
REACTOME_RESPONSE_OF_EIF2AK4_GC2_2O_AMI	0.10623677	83	8.234e-04	2.057e-01	CYP17A1:13 CYP11A1:135 HSD3B2:962 CYP11B1:1073 CYP21A2:1115 HSD3B1:1881
WP_CLASSICAL_PATHWAY_OF_STEROIDOGENESIS	0.24285813	16	7.803e-04	2.057e-01	ABCB11:5 SLC10A1:122 SULT2A1:165 SLC51A:140 AGTPB2:166 ABCG2:752
WP_DRUG_INDUCION_OF_BILE_ACID_PATHWAY	0.24297241	17	7.955e-04	2.057e-01	ZNF292:3 NEDD4:7 ENPP1:30 CENPF:55 ARHGEF7:87 MAN2A1:95
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.04619686	449	8.154e-04	2.057e-01	RREB1:18 PLEKHA5:103 DMN1:116 GGN2:724 AGTPB2:166 SLC16A7:295
JOHNSTONE_PARVB_TARGETS_2_DN	0.06596966	317	6.491e-04	2.057e-01	CCPG1:10 RAD51AP1:15 LAMP2:42 SLC6A6:50 CENPF:55 MLT1:0:67
JOHNSTONE_PARVB_TARGETS_3_DN	0.03638725	793	5.226e-04	2.057e-01	CDCA2:20 EDS1L:35 NCAPD:338 NCAPD:252 CYP11B1:1073 POR:2225 NA
DUTERTRE ESTRADIOL_RESPONSE_24HR_UP	0.05514667	318	7.362e-04	2.057e-01	ATF6:9 GABRA5:13 IGFBP3:18 SCN1A:27 PTPRZ1:57 DOCK4:84
KEGG_RIBOSOME	0.11731992	71	6.321e-04	2.057e-01	CRYGD:124 TDRD7:358 CRYGC:376 CRYBB1:438 SLC01B1:646 ABCC2:752
WP_NUCLEAR_RECEPTORS_IN_LIPID_METABOLISM	0.03119514	32	1.246e-03	2.996e-01	RAD51AP1:15 CDCA2:20 HJURP:25 NCAPD:338 NCAPD:252 CENPF:55
FISCHER_DREAM_TARGETS	0.03119514	922	1.401e-03	3.138e-01	MC4R:24 PRMT6:63 CRH1:114 FOS:131 KMSD:273 GABBR1:341
REACTOME_SIGNALING_TARGETS	0.03560767	699	1.394e-03	3.138e-01	CLCNKA:76 CYP11A1:135 CLCNKB:228 HSD3B2:962 BSNL:1045 AVPR2:9232
ONKEN_UVEAL_MELANOMA_DN	-0.04170037	496	1.516e-03	3.282e-01	COL7A1:59 KRT5:71 CYLD:203 KRT14:522 PLEC:576 ITGB4:769
SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN	-0.06642029	30	1.583e-03	3.316e-01	WDR11:43 PRMT6:63 SYCP3:106 DAZ1:374 DAZ3:387 DAZ2:431
REACTOME_SARS_COV_2_MODULATES_HOST_TRANS	0.15310036	35	1.722e-03	3.494e-01	CSTR14:17 ADRC1:73 CHRNA7:104 CRH1:114 FOS:131 DRD2:507
NIKOLSKY_BREAST_CANCER_17O21_Q25_AMPLICO	-0.05602697	319	1.910e-03	3.544e-01	ADCY1:95 CHRNA7:104 CRH1:114 FOS:131 DRD2:507 CHRNA7:767
REACTOME_SELENOAMINO_ACID_METABOLISM	0.09089364	98	1.882e-03	3.544e-01	APOA1:51 MTHFR:559 KNG1:154 FOS:131 DRD2:507 CHRNA7:767
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.03272455	602	1.863e-03	3.544e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
REACTOME_NEUROTRANSMITTER_RECEPTORS_AND	-0.00504654	189	2.063e-03	3.691e-01	ADCY1:95 DISC1:125 FOS:131 NPS:273 GABBR1:341 CHRP1:506
REACTOME_SARS_COV_1_MODULATES_HOST_TRANS	0.17391546	26	2.143e-03	3.691e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
WP_STEROID_HORMONE_PRECURSOR_BIOSYNTHESI	0.29523468	9	2.160e-03	3.691e-01	CHRM2:70 CRH1:114 FOS:131 TGFB1:145 MET:185 SLC16A4:310
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	0.03135436	826	2.306e-03	3.840e-01	CYP17A1:13 HSD3B2:962 CYP11B1:1073 CYP21A2:1115 HSD3B1:1881 SRD5A1:2279
REACTOME_PYRIMIDINE_SALVAGE	-0.26435020	11	2.396e-03	3.891e-01	ZNF292:3 TMEM131L:4 NEDD4:7 MYO9B:11 MDN1:30 ZFYVE16:46
					TK2:899 UCK2:1027 CDA11:62 UPP1:1615 UCK1:1678 DCK:2204

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Autism Spectrum Disorders	-0.06615692	518	3.069e-07	3.014e-03	GABRA5:13 SSTR4:17 ZNF423:25 SCN1A:27 CARMIL1:30 LRN3:48
Pigmentation Disorders	-0.38567732	10	2.408e-05	1.182e-01	TRPM1:60 KRT5:71 KRT14:522 ASIP:1476 COLEC11:1551 MIFN:1732
Channelopathies	-0.16484933	52	3.953e-05	1.294e-01	SCN9A:3 SCN1A:27 KCNH2:75 CNGB3:120 RYR2:130 KCNA3:521
Male sterility due to Y-chromosome delet	-0.45566107	6	1.109e-04	1.749e-01	DAZ1:374 DAZ3:387 DAZ2:431 DAZ4:534 USP9Y:1029 DDYX3:2372
Partial chromosome Y deletion	-0.45566107	6	1.109e-04	1.749e-01	DAZ1:374 DAZ3:387 DAZ2:431 DAZ4:534 USP9Y:1029 DDYX3:2372
Schizophrenia	-0.02842145	1731	1.247e-04	1.749e-01	CADM3:7 GRID1:10 GABRA5:13 GABRR3:3 SSTR4:17 MC4R:24
Skin Vesicle	-0.46822810	6	7.125e-05	1.749e-01	COL7A1:59 KRT5:71 KRT14:522 PLEC:576 ATP2C1:760 PKP1:1677
Cataract, Puvulent	-0.30716136	11	4.195e-04	4.398e-01	BFSF2:40 HSF4:103 CRYGD:124 CRYGC:376 CRYBB1:486 VIM:531
Adrenocorticotrophic hormone excess	0.44994331	5	4.930e-04	4.398e-01	CYP17A1:13 CYP11A1:135 HSD3B2:962 CYP11B1:1073 POR:2225 NA
Autistic Disorder	-0.04153130	637	3.903e-04	4.398e-01	ATF6:9 GABRA5:13 IGFBP3:18 SCN1A:27 PTPRZ1:57 DOCK4:84
Pseudoepithelia	-0.21921281	21	5.067e-04	4.398e-01	CRYGD:124 TDRD7:358 CRYGC:376 CRYBB1:438 SLC01B1:646 ABCC2:752
Severe myopia	-0.10395926	93	5.375e-04	4.398e-01	ATF6:9 IGFBP3:18 PDE6B:22 CRYBA4:36 TRPM1:60 RBPS:91
CATARACT, AUTOSOMAL DOMINANT	-0.31668006	9	1.002e-03	5.269e-01	BFSF2:40 CRYAA2:112 CRYBB1:486 CRYAA:749 MIP:750 GJA8:922
Spermatogenic Failure, Nonobstructive, Y	-0.33538876	8	1.020e-03	5.269e-01	DAZ1:374 DAZ3:387 DAZ2:431 USP9Y:1029 KMSD:1633 DDX3P:2372
Cocaine Dependence	-0.08364806	132	9.216e-04	5.269e-01	MC4R:24 PRMT6:63 CRH1:114 FOS:131 NPS:273 GABBR1:341
Hypertnriuria	0.39286727	6	8.599e-04	5.269e-01	CLCNKA:76 CYP11A1:135 CLCNKB:228 HSD3B2:962 BSNL:1045 AVPR2:9232
Milium Cyst	-0.22692508	18	8.596e-04	5.269e-01	COL7A1:59 KRT5:71 CYLD:203 KRT14:522 PLEC:576 ITGB4:769
Non-obstructive azoospermia	-0.10990651	76	9.328e-04	5.269e-01	WDR11:43 PRMT6:63 SYCP3:106 DAZ1:374 DAZ3:387 DAZ2:431
Withdrawal Symptoms	-0.11674074	70	7.383e-04	5.269e-01	CSTR14:17 ADRC1:73 CHRNA7:104 CRH1:114 FOS:131 DRD2:507
Substance Withdrawal Syndrome	-0.12550037	56	1.167e-03	5.731e-01	ADCY1:95 CHRNA7:104 CRH1:114 FOS:131 DRD2:507 CHRNA7:767
Drug Eruptions	-0.19861008	22	1.262e-03	5.903e-01	APOA1:51 MTHFR:559 KNG1:154 IFNA1:926 IL18:1505 HLA-B:1530
Color vision defect, severe	-0.14107209	39	2.307e-03	5.963e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
Hyperkinesia, Generalized	-0.12590056	32	2.277e-03	5.963e-01	ADCY1:95 DISC1:125 FOS:131 NPS:273 GABBR1:341 CHRP1:506
Abnormal color vision	-0.14107209	39	2.307e-03	5.963e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
Addictive Behavior	-0.06428634	190	2.298e-03	5.963e-01	CHRM2:70 CRH1:114 FOS:131 TGFB1:145 MET:185 SLC16A4:310
Adrenogonital Syndrome	0.36524106	6	1.946e-03	5.963e-01	CYP17A1:13 HSD3B2:962 CYP11B1:1073 CYP21A2:1115 STP:2225 STAR:9232
Azoospermia	-0.07505563	147	1.714e-03	5.963e-01	SYCP3:106 SOX9:304 DAZ1:374 RBM5:548 DAZ3:387 DAZ2:431
Cocaine-Related Disorders	-0.09554470	90	1.749e-03	5.963e-01	PRMT6:63 CRH1:114 FOS:131 NPS:273 GABBR1:341 CHRR2:396
Drug Withdrawal Symptoms	-0.12802989	52	1.412e-03	5.963e-01	ADCY1:95 CHRNA7:104 CRH1:114 FOS:131 DRD2:507 CHRNA7:767
Fetal polyuria	0.29368286	9	2.281e-03	5.963e-01	CLCNKA:76 CLCNKB:228 GRIFF1:700 BSNL:1045 KNG1:154 ITGA8:2652
Infiltrating Cervical Carcinoma	-0.14178973	42	1.481e-03	5.963e-01	SEC14L2:122 FGFR2:338 MTHFR:559 FZRL1:616 HLA-G:745 EGFR:937
Loss in color vision	-0.14107209	39	2.307e-03	5.963e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
Mood Disorders	-0.05001593	318	2.254e-03	5.963e-01	ADAMT56:5 GABRA5:13 CHRM2:70 CHRM3:86 ADACY1:95 CRH1:114
Nuclear cataract	-0.15810148	32	1.971e-03	5.963e-01	HSF4:103 CRYGD:124 CRYBA2:238 CRYGC:376 CRYBB1:486 BFSF1:680
Recurrent major depressive episodes	-0.17107352	27	2.096e-03	5.963e-01	APOA1:51 CHRM2:70 CRH1:114 DISC1:125 SYNE1:434 CHRR1:506
Renal salt wasting	0.21353567	17	2.304e-03	5.963e-01	CLCNKA:76 CYP11A1:135 CLCNKB:228 SCN1A:622 HSD3B2:962 BSNL:1045
Rheumatic Heart Disease	-0.14113128	39	2.298e-03	5.963e-01	IGFBP3:18 WDR11:43 TGFB1:145 VIM:531 USP:829 IGFB2:1076
Waddling gait	-0.12181361	54	1.969e-03	5.963e-01	PTH1R:35 TGFB1:145 TRAPPC11:268 DNAJB6:671 NEFH:901 SLC6A17:1063
CATARACT, COPPOCK-LIKE	-0.26247696	11	2.575e-03	6.322e-01	BFSF2:40 CRYGD:124 CRYGC:376 CRYBB1:486 VIM:531 GJA8:922
Cholelithiasis	0.07856665	124	2.551e-03	6.322e-01	ABCB11:5 CYP17A1:13 HMCN1:22 SLC10A2:90 ABCG8:99 ANK1:140

customGeneSet Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	0.05937922	13	5.064e-01	7.595e-01	LCT:1484 SLC39A8:1695 AS3MT:9323 GPX1:9232 CELF1:9232 SEPSECS:9232
NAFLDGVAS	-0.05757576	15	4.966e-01	7.595e-01	INSR:723 PNPLA3:1560 FTO:1609 TOR1B:2302 PNPLA2:2703 APOE:9342
expressionDirectionalSelection	0.00297619	42	9.685e-01	9.685e-01	NSL1:601 TLR6:1165 LY6K:1891 TLR10:2376 FADS1:9232 POU5F1:9232
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

Cardiac Conduction (GO:0061337)	-0.12204619	45	4.634e-03	7.277e-01	KCNH2:75 KCND3:500 CAV1:572 HCN1:654 KCNJ1:304 MF2A:1291
Metal Ion Transport (GO:0030001)	-0.06381864	169	2.856e-03	7.277e-01	SCN9A:3 SCN1A:27 CHRNA7:104 RYR2:1171 KCN1:1091 IF2TA:1291
Mitochondrial Gene Expression (GO:0140005)	0.08209163	102	2.128e-03	7.277e-01	MRPS6:107 IARS2:264 POLRMT:300 IARS2:410 FASTKD1:497 MRPS10:590
Regulation Of T Cell Cytokine Production	-0.19902933	17	4.499e-03	7.277e-01	HFE:511 HLA-F-890 TRAF6:1177 TRAF2:1228 FZD5:1399 HLA-A:1574
Cellular Response To Acetylcholine (GO:1	-0.24097440	11	5.651e-03	7.452e-01	CHRNA7:104 LY6G6D:327 SLURP2:1793 CHRNA3:2065 CHRNA2:2443
Cytoplasmic Translation (GO:0021811)	0.08991909	76	7.696e-03	7.452e-01	RPL35:259 RPL7:313 RPS19:463 RPL15:744 FTS1:941 RPS21:1014
Endodermal Cell Differentiation (GO:00335	-0.14008567	31	9.606e-03	7.452e-01	COL7A1:59 SETD2:512 MMP2:681 CTRN:831 MMP14:1330 ITGA4:1597
mRNA Stabilization (GO:0048255)	-0.11230747	50	6.034e-03	7.452e-01	HNRNPU:190 IREB2:363 YIP:367 DAZ1:374 DAZ2:387 DAZ2:431
Mitotic Nuclear Division (GO:0140014)	0.11783912	44	6.864e-03	7.452e-01	SMC4:94 ESPL1:546 NSL1:601 NCAPG2:998 SMC1A:1103 SGO1:1113

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003252 abnormal bile duct	0.25182360	25	1.352e-05	6.436e-03	ABCB11:5 PKHD1:188 CYP8B1:438 AHR:645 MAP3K14:733 ABCG2:752
MP0002398 abnormal eye morphology	0.04399413	813	5.953e-05	1.417e-02	NEDD4:7 ZEB1:92 JAK3:93 MAN2A1:95 ABCG8:91 PRKX:120
MP0005551 abnormal eye electrophysiology	-0.08428508	144	5.449e-04	8.261e-02	PDE6B:22 TRPM1:60 CDHR1:64 GJA10:65 RBC9:39 MATP:111
MP0004249 abnormal blood cell	0.03154060	1241	6.892e-04	8.261e-02	NEDD4:7 MYO9B:11 JAK3:93 MAN2A1:95 PREX1:97
MP0002136 abnormal kidney physiology	0.05218293	286	2.910e-03	0.2031e-01	CUBN1:17 CLDN16:27 TRPV1:64 CLCNKA:76 LRP2:82 MAN2A1:95
MP0004019 abnormal vitamin homeostasis	0.13058466	43	3.131e-03	0.2031e-01	CUBN1:17 CLDN16:27 LRP2:82 CYP27A1:152 RBP7:878 CYP7A1:1173
MP0000716 abnormal immune system	0.02935683	1014	3.414e-03	0.2031e-01	NEDD4:7 ZEB1:92 JAK3:93 MAN2A1:95 PREX1:97
MP0005220 abnormal exocrine pancreas	-0.12655224	46	2.644e-03	0.2031e-01	MAN2B1:74 PKHD1:188 INVS:446 STK11:572 SPTPSN1:638 PTF1A:706
MP0004085 abnormal heartbeat	-0.06515723	160	4.902e-03	0.2031e-01	CHRNA7:104 KCNJ2:188 CDH2:147 RYR2:171 TS2:235 NPL:156 P246
MP0002722 abnormal immune system	0.03475404	623	4.731e-03	0.2031e-01	ZEB1:92 JAK3:93 LRP2:85 TGF1:128 ANK1:140 TRIM21:176
MP0000313 abnormal cell death	0.03751455	464	7.703e-03	3.189e-01	LAMA1:37 LRP2:82 LHX4:242 STX1:308 POLK:332 TERT:370
MP0006546 abnormal pituitary gland	-0.17113579	20	8.140e-03	3.229e-01	GAL-45 DRD2:507 ARNT2:696 PRL1:203 NF1:1471 PDK1:1545
MP0006508 abnormal olfactory	-0.20719075	83	2.942e-03	3.229e-01	ACR1A:5 MAN2A1:95 PREX1:97 CACNA1:634 CACNA1:154 CACNA1:354