

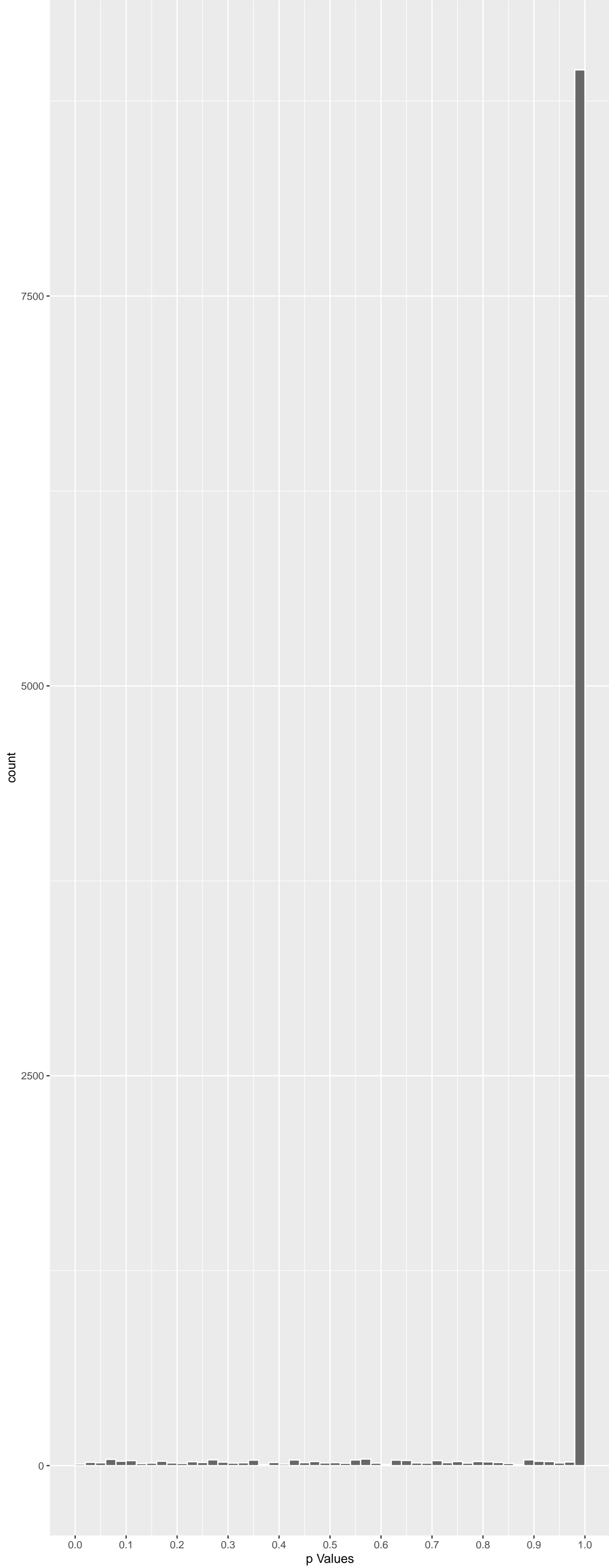
Top genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
KIAA0232	-5.147849	1.580942e-06	8.937e-03	1.000e+00
MDN1	5.110644	1.926377e-06	8.937e-03	1.000e+00
NEDD4	5.277743	7.847063e-07	8.937e-03	1.000e+00
ZMIZ2	-5.173046	1.381850e-06	8.937e-03	1.000e+00
BCLAF3	-5.045065	2.720201e-06	1.010e-02	1.000e+00
ADCY1	-4.950050	4.451672e-06	1.043e-02	1.000e+00
ECSIT	4.925163	5.057399e-06	1.043e-02	1.000e+00
ZNF423	-4.930810	4.913371e-06	1.043e-02	1.000e+00
ZSCAN25	4.977013	3.874387e-06	1.043e-02	1.000e+00
THADA	4.869084	6.727013e-06	1.248e-02	1.000e+00
CCPG1	4.800938	9.475456e-06	1.399e-02	1.000e+00
PRUNE2	4.823842	8.449135e-06	1.399e-02	1.000e+00
ZNF180	4.794123	9.803296e-06	1.399e-02	1.000e+00
TIMMDC1	4.756647	1.181012e-05	1.565e-02	1.000e+00
NSD2	-4.740404	1.279755e-05	1.583e-02	1.000e+00
KIAA0825	4.691994	1.623327e-05	1.883e-02	1.000e+00
SCN9A	-4.670703	1.801025e-05	1.966e-02	1.000e+00
AGGF1	4.625789	2.239051e-05	2.307e-02	1.000e+00
TNNI3K	4.614732	2.361623e-05	2.307e-02	1.000e+00
BNC1	-4.535431	3.449156e-05	2.554e-02	1.000e+00
CLCNKA	4.512398	3.845919e-05	2.554e-02	1.000e+00
DLGAP5	4.543212	3.324209e-05	2.554e-02	1.000e+00
EHMT1	-4.540326	3.370034e-05	2.554e-02	1.000e+00
HMCN1	4.497337	4.128593e-05	2.554e-02	1.000e+00
INTS6L	4.512646	3.841426e-05	2.554e-02	1.000e+00

Top genes by Q-Value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
A1BG	0.10434709	1.000000000	1.000e+00	1.000e+00
A1CF	-0.25982597	1.000000000	1.000e+00	1.000e+00
A2M	3.46530968	0.003177727	1.798e-01	1.000e+00
A2ML1	1.17531866	1.000000000	1.000e+00	1.000e+00
A3GALT2	0.85017984	1.000000000	1.000e+00	1.000e+00
A4GALT	1.56461350	0.706041374	1.000e+00	1.000e+00
A4GNT	-0.79611260	1.000000000	1.000e+00	1.000e+00
AAAS	-0.58382031	1.000000000	1.000e+00	1.000e+00
AACS	-2.49230282	0.076150667	8.465e-01	1.000e+00
ADAC	0.78606005	1.000000000	1.000e+00	1.000e+00
AADACL2	-1.86918684	0.369580949	1.000e+00	1.000e+00
AADACL3	-1.92084405	0.328588228	1.000e+00	1.000e+00
AADACL4	-1.12450012	1.000000000	1.000e+00	1.000e+00
AADAT	-0.55274796	1.000000000	1.000e+00	1.000e+00
AAGAB	2.08469003	0.222584677	1.000e+00	1.000e+00
AAK1	-0.08428419	1.000000000	1.000e+00	1.000e+00
AAMDC	1.25469140	1.000000000	1.000e+00	1.000e+00
AAMP	1.37204284	1.000000000	1.000e+00	1.000e+00
AANAT	-1.02380748	1.000000000	1.000e+00	1.000e+00
AAR2	-0.48293197	1.000000000	1.000e+00	1.000e+00
AARD	-1.28251944	1.000000000	1.000e+00	1.000e+00
AARS1	1.58171810	0.682283633	1.000e+00	1.000e+00
AARS2	2.11391288	0.207136253	1.000e+00	1.000e+00
AARSD1	0.58397265	1.000000000	1.000e+00	1.000e+00
AASDH	3.86590686	0.000664063	8.206e-02	1.000e+00

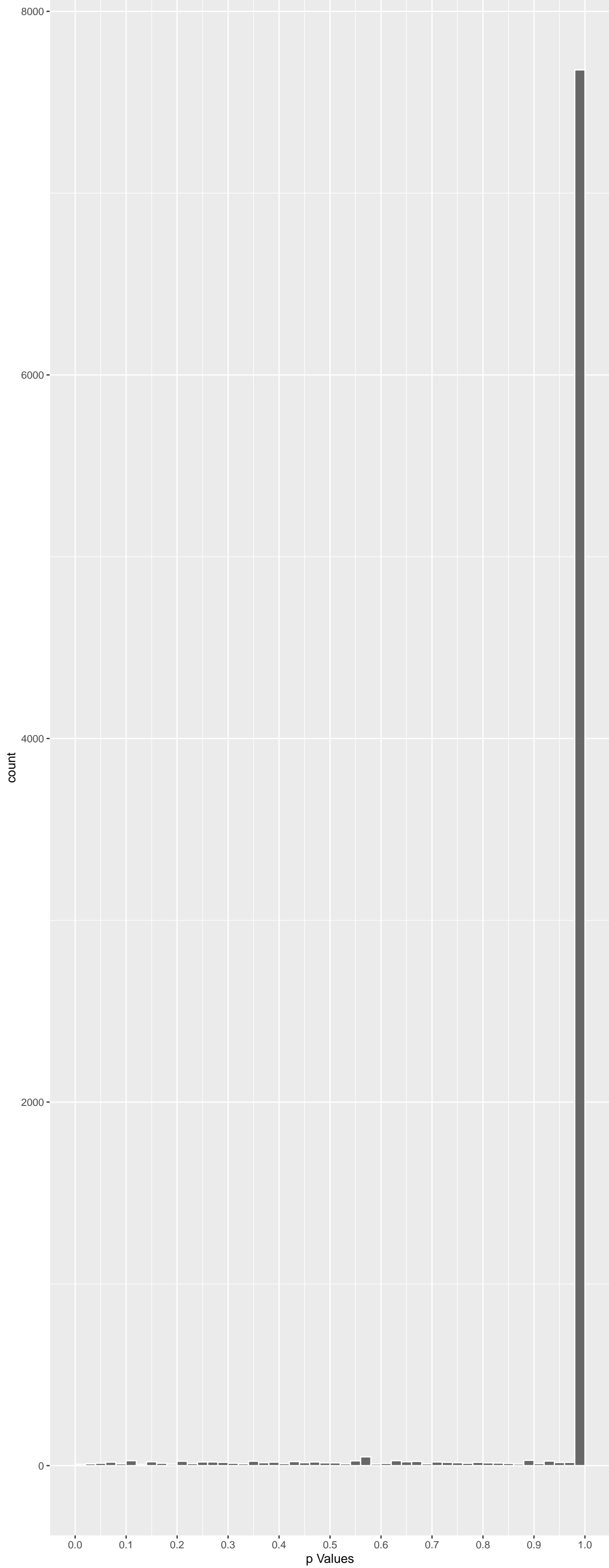
Positive Rho Non-permulated



Top Positive genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
MDN1	5.110644	1.926377e-06	8.937e-03	1.000e+00
NEDD4	5.277743	7.847063e-07	8.937e-03	1.000e+00
ECSIT	4.925163	5.057399e-06	1.043e-02	1.000e+00
ZSCAN25	4.977013	3.874387e-06	1.043e-02	1.000e+00
THADA	4.869084	6.727013e-06	1.248e-02	1.000e+00
CCPG1	4.800938	9.475456e-06	1.399e-02	1.000e+00
PRUNE2	4.823842	8.449135e-06	1.399e-02	1.000e+00
ZNF180	4.794123	9.803296e-06	1.399e-02	1.000e+00
TIMMDC1	4.756647	1.181012e-05	1.565e-02	1.000e+00
KIAA0825	4.691994	1.623327e-05	1.883e-02	1.000e+00

Negative Rho Non-permulated



Top Negative genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
KIAA0232	-5.147849	1.580942e-06	8.937e-03	1.000e+00
ZMIZ2	-5.173046	1.381850e-06	8.937e-03	1.000e+00
BCLAF3	-5.045065	2.720201e-06	1.010e-02	1.000e+00
ADCY1	-4.950050	4.451672e-06	1.043e-02	1.000e+00
ZNF423	-4.930810	4.913371e-06	1.043e-02	1.000e+00
NSD2	-4.740404	1.279755e-05	1.583e-02	1.000e+00
SCN9A	-4.670703	1.801025e-05	1.966e-02	1.000e+00
BNC1	-4.535431	3.449156e-05	2.554e-02	1.000e+00
EHMT1	-4.540326	3.370034e-05	2.554e-02	1.000e+00
IQCF3	-4.544942	3.297030e-05	2.554e-02	1.000e+00

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

	Geneset	stat	num.genes	pval	p.adj	gene.vals
	REACTOME_KERATINIZATION	-0.15192254	206	5.956e-14	3.886e-10	KRTAP4-8:105 LCE2D:142 KRTAP13-1:161 TGM1:176 KRTAP6-1:196 KRT77:206
	MARSON_BOUND_VY_E2F4_UNSTIMULATED	0.07236738	664	2.344e-10	7.612e-07	KIAA0825:10 SPAG5:13 DLGAP5:14 NCAPD2:17 FANGC:19 KNL1:42
	NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.29023139	37	1.003e-09	2.170e-06	GPER1:68 SNX8:154 INTS1:211 CHST12:307 FBXL18:474 ADAP1:644
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.16560682	112	1.433e-09	2.326e-06	ECESIT:4 TIMMDC1:9 LRPPRC:28 TMEM126B:49 TMEM186:192 NDUFAF1:197
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.17816195	90	5.224e-09	6.785e-06	ECESIT:4 TIMMDC1:9 LRPPRC:28 TMEM126B:49 TMEM186:192 NDUFAF1:197
	FISCHER_DREAM_TARGETS	0.05443862	921	2.525e-08	2.697e-05	SPAG5:13 DLGAP5:14 NCAPD2:17 FANGC:19 ARL13B:22 KNL1:42
	WONG_MITOCHONDRIA_GENE_MODULE	0.11013262	214	2.908e-08	2.697e-05	LRPPRC:28 NDUFAF1:197 MRPS15:330 COX7C:360 TOMM7:442 NDUFB1:503
	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.09561569	265	8.741e-08	7.096e-05	SSTR4:14 PTH1R:35 TAAR6:38 GABRA5:43 MC4R:50 CHRNA7:66
	REACTOME_SIGNALING_BY_GPCR	-0.050912227	684	1.510e-07	8.170e-05	ADCY1:4 SSTR4:14 PTH1R:35 ARHGAP4:37 TAAR6:38 MC4R:50
	REACTOME_GPCR_LIGAND_BINDING	-0.07300445	450	1.186e-07	8.170e-05	SSTR4:14 PTH1R:35 TAAR6:38 MC4R:50 GPER1:68 VIPR1:78
	REACTOME_MITOCHONDRIAL_TRANSLATION	0.15796675	93	1.417e-07	8.170e-05	PTCD3:55 MTIF2:61 MRPS23:79 MRPS35:157 MRPS15:330 MRPS31:347
	KEGG_OXIDATIVE_PHOSPHORYLATION	0.14251984	114	1.487e-07	8.170e-05	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593
	REACTOME_TRANSLATION	0.09271378	269	1.722e-07	8.600e-05	PTCD3:55 MTIF2:61 MRPS23:79 MRPS35:157 MRPS15:330 RARS1:333
	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	-0.08371856	324	2.318e-07	1.075e-04	SSTR4:14 TAAR6:38 MC4R:50 GPER1:68 GPR17:99 OPN3:148 MAS1:216
	WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.09400043	251	3.024e-07	1.227e-04	SSTR4:14 MC4R:50 GPER1:68 GPR17:99 OPN3:148 MAS1:216
	WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.21676531	47	2.912e-07	1.227e-04	ECESIT:4 TIMMDC1:9 TMEM126B:49 TMEM186:192 NDUFAF1:197 NDUFS1:384
	REACTOME_NEURONAL_SYSTEM	-0.07517959	391	3.540e-07	1.344e-04	ADCY1:4 GABRR3:25 KCNV1:29 CACNA1B:31 APBA2:32 GABRA5:43
	MOOTHA_VOXPHOS	0.15860306	86	3.725e-07	1.344e-04	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 GATB:549 NDUFA8:570
	WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.15136786	89	5.525e-07	1.888e-04	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 TMEM186:192 NDUFB7:593
	MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.06010626	576	8.889e-07	2.886e-04	KCNV1:29 APBA2:32 CNPX2:40 GABRA5:43 SLC35F3:69 NETO1:70
	REACTOME_COMPLEX_I_BIOGENESIS	-0.02242344	48	1.253e-06	3.698e-04	ECESIT:4 TIMMDC1:9 TMEM126B:49 TMEM186:192 NDUFAF1:197 NDUFS1:384
	JOHNSTONE_PARKIN_TARGETS_3_DN	0.05092821	793	1.204e-06	3.698e-04	CCPG1:7 SPAG5:13 DLGAP5:14 CEP350:88 UBAP2:90 RAD51AP1:116
	KEGG_KARSINOMAS_DISEASE	0.13029560	110	2.371e-06	6.693e-04	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593
	WP_OXIDATIVE_PHOSPHORYLATION	0.18522252	51	4.753e-06	1.286e-03	NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593 NDUFA11:701
	REACTOME_FORMATION_OF_THE_CORNIIFIED_ENVE	-0.11686870	126	5.955e-06	1.487e-03	LCE2D:142 TGM1:176 KRT77:206 PKP1:210 KRT5:260 LCE2A:386
	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.05428397	602	5.779e-06	1.487e-03	NEDD4:1 CCPG1:7 AGGF1:11 DLGAP5:14 LRPPRC:28 KNL1:42
	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.10052860	162	1.025e-05	2.244e-03	ECESIT:4 TIMMDC1:9 LRPPRC:28 TMEM126B:49 TMEM186:192 NDUFAF1:197
	REACTOME_RNA_PROCESSING	0.09472127	183	1.007e-05	2.244e-03	TRMT10C:62 NOL6:152 DTG2:62174 PRORP:201 UTP20:316 ROK1:350
	REACTOME_SENSORY_PERCEPTION	-0.05312373	598	9.710e-06	2.244e-03	SCN9A:7 SCN2A:60 ORGB1:61 OR10D3:137 RLBP1:191 ORG8A:200
	KEGG_HUNTINGTONS_DISEASE	0.10140597	159	1.037e-05	2.244e-03	COX7C:360 NDUFS1:384 CREB3L3:445 NDUFB1:503 ATP5PO:519 TFAM:522
	BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_I	0.09198856	174	2.883e-05	6.040e-03	SPAG5:13 FANGC:19 KNL1:42 ATAD5:59 CDC25C:205 PGPEP1:234
	NIKOLSKY_BREAST_CANCER_22O13_AMPLICON	-0.29098611	17	3.267e-05	6.630e-03	MLC1:208 PLXNB2:268 TTL8:379 PANX2:669 M010L1:753 TRABD:1082
	REACTOME_G_ALPHA_I_SIGNALING_EVENTS	-0.06918268	298	4.098e-05	7.827e-03	ADCY1:4 SSTR4:14 PTH1R:35 ARHGAP4:37 TAAR6:38 MC4R:50
	DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.03474634	1273	4.053e-05	7.827e-03	NEDD4:1 TIMMDC1:9 SPAG5:13 DLGAP5:14 FANGC:19 LRPPRC:28
	FERRERA_EWINGS_SARCOMA_UNSTABLE_VS_STAB	0.09586257	152	4.575e-05	8.253e-03	DLGAP5:14 NCAPD2:17 KNL1:42 ATAD5:59 FANGC:19 PIGS:231
	PEDESSER_METASTASIS_BY_ERBB2_ISOFORM_1	-0.17391181	46	4.493e-05	8.253e-03	RASD1:33 GEM1:65 EPHA2:43 RASGEF1A:507 CARG1:61 ADGRG6:598
	MARTENS_TRETININ_RESPONSE_UP	-0.04245969	784	5.680e-05	9.969e-03	TRIM29:24 PTH1R:35 IGFBP3:49 ACTL7B:56 ORG81:61 GEM1:65
	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	-0.06301062	340	6.728e-05	1.150e-02	BNC1:11 GABRA5:43 VIPR1:78 KCNK1:100 PAX1:200 LAD1:185
	KORKOLA_EMBRYONAL_CARCINOMA_UP	0.10310080	40	7.466e-05	1.243e-02	RAD51AP1:116 NANOG:186 GDF3:292 LRPE:430 TEAD4:628 ENAM:637:730
	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SY	-0.07236192	250	8.315e-05	1.338e-02	ADCY1:4 GABRR3:25 CACNA1B:31 GABRA5:43 CHRNA7:66 KNL1:42:157

DisGeNET Top pathways by non-permutation

	Geneset	stat	num.genes	pval	p.adj	gene.vals
	Autism Spectrum Disorders	-0.07024872	517	5.616e-08	5.514e-04	ZNF423:5 EHMT1:10 SSTR4:14 APBA2:32 HERC2:39 GABRA5:43
	Mitochondrial Diseases	0.07825820	363	3.433e-07	1.686e-03	ECESIT:4 LRPPRC:28 TMEM126B:49 TRMT10C:62 MRPS23:79 MTPAP:153
	Autistic Disorder	-0.05488036	637	2.753e-06	9.012e-03	EHMT1:10 ATF6:13 APBA2:32 DOCK4:42 GABRA5:43 IGFBP3:49
	HIV Infections	-0.05066071	718	4.627e-06	1.136e-02	SSTR4:14 HSPH1:41 GEM1:65 TMEM1320:72 KCNH2:73 VIPR1:78
	Infection	-0.06125344	466	6.667e-06	1.309e-02	PTH1R:35 VIPR1:78 APOC1:96 BCL2L1:272 SLC2A1:272 CALCA:288
	Increased CSF lactate	0.17243484	56	8.150e-06	1.334e-02	TIMMDC1:9 LRPPRC:28 TMEM126B:49 TRMT10C:62 NDUFAF1:197 NDUFS1:384
	Hypertensive disease	-0.03832918	1199	1.094e-05	1.535e-02	ZFAT8: SSTR4:14 TM1L2:30 GOK3:34 IGFBP3:49 MC4R:50
	Primary microcephaly	0.11963364	110	1.495e-05	1.836e-02	FANGC:19 KNL1:42 STIL:82 FANGC:89 TRMT10A:125 CENPJ:241
	Schizophrenia	-0.03138579	1727	2.311e-05	2.522e-02	ADCY1:4 EHMT1:10 SSTR4:14 GABRR3:25 GALT2:30 CACNA1B:31
	Bipolar Disorder	-0.04412458	757	4.296e-05	4.219e-02	ADCY1:4 SSTR4:14 GABRR3:25 CACNA1B:31 TAAR6:38 GABRA5:43
	Lung diseases	-0.06224887	362	5.130e-05	4.580e-02	SSTR4:14 PTH1R:35 COL3A1:82 SEC14L2:248 ADORA1:252 SLC2A1:272
	Obesity	-0.02882536	1786	8.027e-05	6.507e-02	EHMT1:10 ATF6:13 SSTR4:14 CDHR1:19 GALT2:30 GOK3:34
	Withdrawal Symptoms	-0.13680040	69	8.614e-05	6.507e-02	ADCY1:4 SSTR4:14 CHRNA7:66 ADORA1:252 CHRNA4:368 CRP:382
	Eczema	-0.05467004	420	1.319e-04	8.264e-02	TRPM1:45 IL37:59 APOC1:96 EFL1:147 TGM1:176 MAS1:216
	Lactic acidemia	0.09301889	691	1.515e-04	8.264e-02	NSD2:6 IGFBP3:49 IL37:59 GPER1:68 SYNE1:133 SLC22A23:146
	Increased serum lactate	0.11178543	99	1.234e-04	8.264e-02	LRPPRC:28 TRMT10C:62 TWNK:254 TRMT5:482 GFM1:532 POLG2:534
	Lactose intolerance	0.09930189	123	1.457e-04	8.264e-02	TIMMDC1:9 LRPPRC:28 TMEM126B:49 TRMT10C:62 NDUFAF1:197 NDUFS1:384
	Myocardial Infarction	-0.03787722	891	1.502e-04	8.264e-02	GPER1:68 COL3A1:82 APOC1:96 GPR17:99 CDCP1:104 ARC:110
	Color vision defect, severe	-0.17121482	39	2.167e-04	8.867e-02	ATF6:13 CDHR1:19 RLBP1:191 CNGB3:199 PDE6C:328 ELOVL4:577
	Abnormal color vision	-0.17121482	39	2.167e-04	8.867e-02	ATF6:13 CDHR1:19 RLBP1:191 CNGB3:199 PDE6C:328 ELOVL4:577
	Heart failure	-0.04065824	732	2.070e-04	8.867e-02	KCNH2:73 APOC1:96 GPR17:99 ARC:110 TRMT10C:62 MAS1:216
	Loss in color vision	-0.17121482	39	2.167e-04	8.867e-02	ATF6:13 CDHR1:19 RLBP1:191 CNGB3:199 PDE6C:328 ELOVL4:577
	Mood Disorders	-0.06093403	318	1.982e-04	8.867e-02	ADCY1:4 TAAR6:38 GABRA5:43 HTT:128 PPP1R3B:156 VSN1:253
	Pain	-0.05122460	452	2.060e-04	8.867e-02	SCN9A:7 SSTR4:14 SCN2A:60 ASAP1:136 GRM8:178 ERBB4:246
	Epidemiology Bullous Simplex	-0.21871893	23	2.828e-04	1.111e-01	KRT5:260 VIM:352 PLEC:50 BHLHE23:626 TGM5:830 KRT17:1301
	Depressive Symptoms	-0.08905646	139	3.957e-04	1.117e-01	NKPD1:126 HT1:128 TGFBI:290 EGFR:335 CCR3:382 IFNA13:562
	Addictive Behavior	-0.07495692	189	2.917e-04	1.329e-01	MET:167 BCL2L1:1226 ERBB4:246 TGFBI:290 EGFR:335 CHRNA3:368
	Arteriosclerosis	-0.03329713	984	4.872e-04	1.329e-01	EHMT1:10 OSBP:22 GOK3:34 MC4R:50 SLC17A4:55 IL37:59
	Atherosclerosis	-0.03272716	1027	4.683e-04	1.329e-01	EHMT1:10 OSBP:22 GOK3:34 IGFBP3:49 MC4R:50 SLC17A4:55
	Borderline Personality Disorder	-0.09976691	104	4.459e-04	1.329e-01	SCN9A:7 APBA2:32 ERBB4:246 ANGPT1:278 EGFR:335 HTR1B:137
	Chronic Obstructive Airway Disease	-0.04216855	609	4.218e-04	1.329e-01	EHMT1:10 CHRNA7:66 VIPR1:78 CRYGC:90 KCNK1:100 ENTDP1:127
	Congestive heart failure	-0.03739489	793	3.945e-04	1.329e-01	KCNH2:73 COL3A1:82 APOC1:96 GPR17:99 ARC:110 HT1:128
	Coronary Arteriosclerosis	-0.03949428	704	4.029e-04	1.329e-01	EHMT1:10 GALT2:30 GOK3:34 GPER1:68 INDO1:80 COL3A1:82
	Dermatologic disorders	-0.05314122	370	4.757e-04	1.329e-01	APBA2:32 GEM1:65 TGM1:176 ZNF627:229 ALOX12B:234 TRPV6:259
	Hypersinulism	-0.05377551	360	4.849e-04	1.329e-01	EHMT1:10 CDHR1:19 GOK3:34 HERC2:39 IGFBP3:49 MC4R:50
	Inflammatory Bowel Diseases	-0.03688113	810	4.155e-04	1.329e-01	ATF6:13 IGFBP3:49 IL37:59 GPER1:68 VIPR1:78 REG1B:113
	Cardiovascular Diseases	-0.03815857	721	5.455e-04	1.422e-01	EHMT1:10 ATF6:13 IGFBP3:49 SCN2A:60 DCLK1:63 GPER1:68
	Drug Withdrawal Symptoms	-0.13857430	52	5.501e-04	1.422e-01	ADCY1:4 CHRNA7:66 ADORA1:252 CRP:382 CRH:743 CHRNA5:774
	Acute Coronary Syndrome	-0.06392929	239	6.878e-04	1.535e-01	GEM1:65 COL3A1:82 F5:205 CLU:289 TGFBI:290 EGFR:335
	Age related macular degeneration	-0.05322420	351	6.475e-04	1.535e-01	CDHR1:19 TRPM1:45 ZBTB41:52 GEM1:65 CNGB3:199 FLT1:245

customGeneSet Top pathways by non-permutation

	Geneset	stat	num.genes	pval	p.adj	gene.vals
	HumanLocalAdaptionDietAll	0.06950067	13	4.367e-01	6.550e-01	SLC39A8:1779 LCT:2540 AS3MT:9689 GPX1:9689 GPX3:9689 CELF1:9689
	NALFDGVIAS	-0.09636364	15	2.552e-01	6.550e-01	PNPLA3:494 FTO:936 APOE1:541 PNPLA2:1556 GID4:1673 GPAM:1865
	expressionDirectionalSelection	0.02380952	42	7.371e-01	7.371e-01	TLR10:882 TLR6:1223 HSD17B8:271 ZBTB12:2936 HLA-DQB1:9689 HLA-DRB1:9689
	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

Lymphocyte Activation involved in Immune	-0.21637593	23	3.266e-04	5.385e-02	IFNA3:359 FZRL1:334 IFNA1:6267 IFNAR2:962 IFNA21:363 IFNA8:1396
DNA Repair (GO:0006281)	0.06177301	281	3.844e-04	5.927e-02	FANGC1:9 STON1:48 MLH3:85 FANCA:89 MBD4:106 RAD51AP1:116
Calcium Ion Import Across Plasma Membran	-0.17565077	34	3.948e-04	5.927e-02	SCN9A:7 CACNA1B:31 TRPM1:45 SCN1A:57 SCN2A:60 TRPV6:259
Chemical Synaptic Transmission (GO:00072	-0.06355560	263	4.056e-04	5.927e-02	GABRR3:25 CACNA1B:31 APBA2:32 CABRA5:43 CHRNA7:66 ECXO2:42
Protein Localization To Microtubule Orga	0.26489487	15	3.825e-04	5.927e-02	SPAG5:13 CZCD3:26 STIL:82 CEP192:110 CEP250:479 PIBF1:613
Calcium Ion Transport (GO:0006816)	-0.09691286	110	4.533e-04	6.023e-02	TRPM1:45 CHRNA7:66 TRPV6:259 SLC8A3:282 CLU:289 ATP2A2:321
Double-Strand Break Repair (GO:0006302)	0.08012838	161	4.627e-04	6.023e-02	STON1:48 RAD51AP1:116 UIMC1:127 RNF168:160 EVY3:259 RRM1:288
Inorganic Cation Transmembrane Transport	-0.06107921	280	4.574e-04	6.023e-02	SCN9A:7 KCNV1:29 TRPM1:45 SCN2A:60 KCNH2:73 KCNK1:100

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003252 abnormal bile duct	0.12167463	25	2.379e-04	1.132e-01	PKHD1:63 CYP8B1:277 ABCB11:478 ABCG5:76 MAP3K14:1341 ATXN2:1537
MP00011970 abnormal pain threshold	-0.08162940	152	5.863e-04	1.395e-01	ADCY1:4 SSTR4:14 CACNA1B:31 PTPRZ1:108 TSHZ3:144 GABRR1:186
MP0004085 abnormal heartbeat	-0.07575663	160	1.100e-03	1.451e-01	CACNA1B:31 KCNH2:73 SYNE1:133 ERBB4:246 CALCA:288 ATP2A2:321
MP0005551 abnormal eye electrophysiolog	-0.07775899	144	1.524e-03	1.451e-01	CDHR1:19 TRPM1:45 GABRR1:186 CNGB3:199 GJA10:202 RBP2:217
MP0002085 abnormal embryonic tissue	0.03814621	654	1.505e-03	1.451e-01	ECST1:4 ARL13B:22 CUBN:23 CZCD3:26 STIL:82 TRPM6:103
MP0002398 abnormal bone marrow	0.03398462	813	1.928e-03	1.530e-01	NEDD4:1 JAK3:33 TPO:65 HPS3:70 AIRE:75 NFATC3:83
MP0005253 abnormal eye physiology	-0.08935214	95	2.784e-03	1.656e-01	BFSF2:28 TRPM1:45 CRYGC:30 RLBP1:191 CNGB3:199 CSTB:555
MP0003635 abnormal synaptic transmissio	-0.04368387	425	2.721e-03	1.656e-01	ADCY1:4 SCN9A:7 CACNA1B:31 GABRA5:43 SCN1A:57 CHRNA7:66
MP0005388 respiratory system phenotype	-0.07320463	130	4.276e-03	2.035e-01	SSTR4:14 TOM1L2:92 SYNE1:133 TSHZ3:144 DBNL2:12 CYLD:302
MP0002133 abnormal respiratory system	-0.07320463	130	4.276e-03	2.035e-01	SSTR4:14 TOM1L2:92 SYNE1:133 TSHZ3:144 DBNL2:12 CYLD:302
MP0009745 abnormal behavioral response	-0.05654969	205	5.919e-03	2.561e-01	EHHMT1:10 CACNA1B:31 GABRA5:43 SCN1A:57 CHRNA7:66 CALCA:288
MP0002084 abnormal developmental patter	0.04144554	364	8.107e-03	2.968e-01	ECST1:4 ARL13B:22 CUBN:23 CZCD3:26 STIL:82 INTU:161