

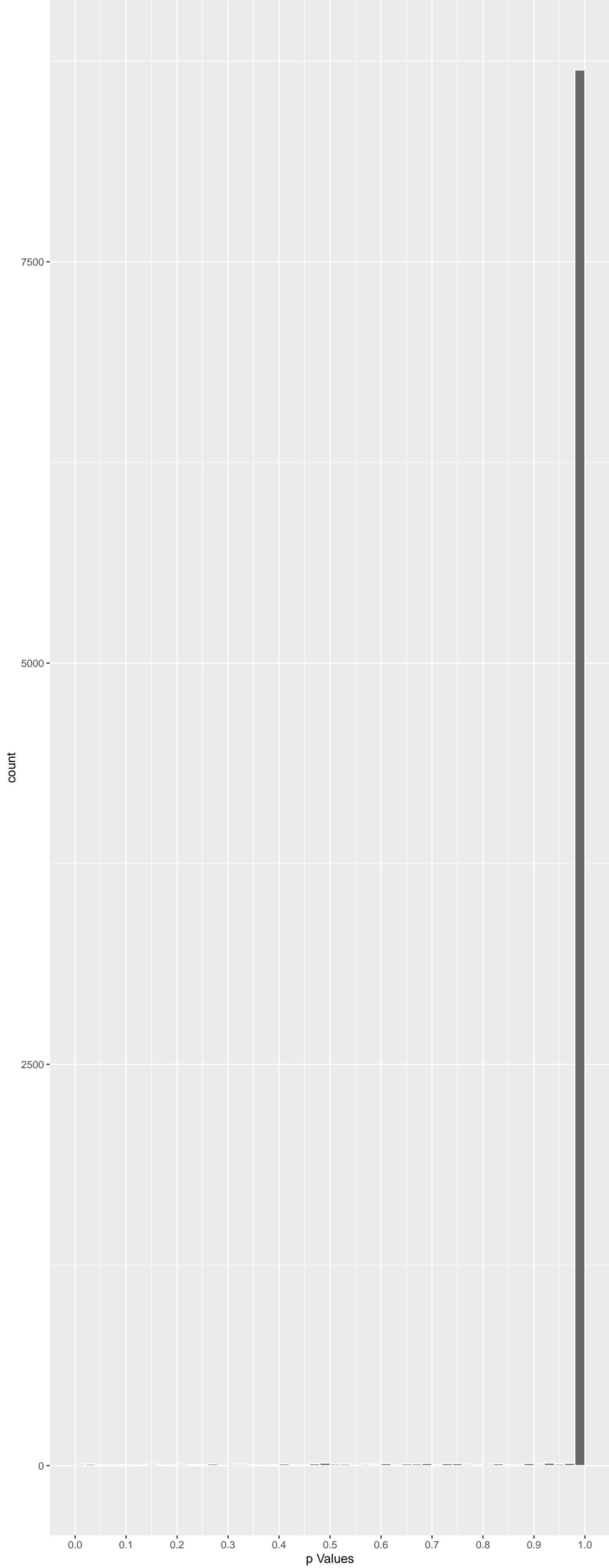
Top genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
ADGRG4	5.725569	6.185247e-08	1.145e-03	1.000e+00
HERC2	-5.570352	1.525347e-07	1.411e-03	1.000e+00
PRUNE2	5.380542	4.455709e-07	2.748e-03	1.000e+00
JCAD	5.087061	2.181930e-06	8.183e-03	1.000e+00
ZZEF1	5.084550	2.210996e-06	8.183e-03	1.000e+00
ZFP3	5.020676	3.089404e-06	9.528e-03	1.000e+00
ARHGEF6	4.947157	4.518309e-06	1.099e-02	1.000e+00
GABRA5	-4.937429	4.749554e-06	1.099e-02	1.000e+00
DCUN1D2	4.802543	9.399798e-06	1.485e-02	1.000e+00
MET	-4.797737	9.628084e-06	1.485e-02	1.000e+00
RBM6	-4.818171	8.692799e-06	1.485e-02	1.000e+00
TMEM108	-4.809224	9.091034e-06	1.485e-02	1.000e+00
SLC2A7	4.760449	1.158975e-05	1.532e-02	1.000e+00
ZNF134	-4.768790	1.112014e-05	1.532e-02	1.000e+00
NUP133	-4.729633	1.349555e-05	1.665e-02	1.000e+00
ADAMTS6	-4.688741	1.649350e-05	1.696e-02	1.000e+00
CEP250	4.690691	1.633701e-05	1.696e-02	1.000e+00
CNGB3	-4.689442	1.643710e-05	1.696e-02	1.000e+00
CRISP1	-4.636898	2.122059e-05	2.067e-02	1.000e+00
ACAD10	4.607981	2.439582e-05	2.150e-02	1.000e+00
GLMP	4.614080	2.369039e-05	2.150e-02	1.000e+00
SCN9A	-4.593226	2.618678e-05	2.203e-02	1.000e+00
ZBTB41	-4.576972	2.830523e-05	2.277e-02	1.000e+00
TMEM187	4.553255	3.169330e-05	2.444e-02	1.000e+00
APOA1	-4.534140	3.470311e-05	2.569e-02	1.000e+00

Top genes by Q-Value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
A1BG	-1.25989679	1.0000000000	1.000e+00	1.000e+00
A1CF	-0.17637267	1.0000000000	1.000e+00	1.000e+00
A2M	1.84464334	0.3905366274	1.000e+00	1.000e+00
A2ML1	3.90733414	0.0005599204	1.400e-01	1.000e+00
A3GALT2	1.56995511	0.6985533355	1.000e+00	1.000e+00
A4GALT	1.11423287	1.0000000000	1.000e+00	1.000e+00
A4GNT	-1.14445746	1.0000000000	1.000e+00	1.000e+00
AAAS	-1.42511585	0.9247422925	1.000e+00	1.000e+00
AACS	-1.19937757	1.0000000000	1.000e+00	1.000e+00
AADAC	1.74237296	0.4886592240	1.000e+00	1.000e+00
AADACL2	1.77930347	0.45111401324	1.000e+00	1.000e+00
AADACL3	-1.07358971	1.0000000000	1.000e+00	1.000e+00
AADACL4	0.07503859	1.0000000000	1.000e+00	1.000e+00
AADAT	-0.64342500	1.0000000000	1.000e+00	1.000e+00
AAGAB	2.82174502	0.0524885121	1.000e+00	1.000e+00
AAK1	1.55603891	0.7181930373	1.000e+00	1.000e+00
AAMDC	0.57169407	1.0000000000	1.000e+00	1.000e+00
AAMP	2.26404168	0.1414293098	1.000e+00	1.000e+00
AANAT	1.22882986	1.0000000000	1.000e+00	1.000e+00
AAR2	-1.06288872	1.0000000000	1.000e+00	1.000e+00
AARD	0.02687814	1.0000000000	1.000e+00	1.000e+00
AARS1	0.55476085	1.0000000000	1.000e+00	1.000e+00
AARS2	2.43412407	0.0895672639	1.000e+00	1.000e+00
AARSD1	-0.77528826	1.0000000000	1.000e+00	1.000e+00
AASDH	1.87539470	0.3644306663	1.000e+00	1.000e+00

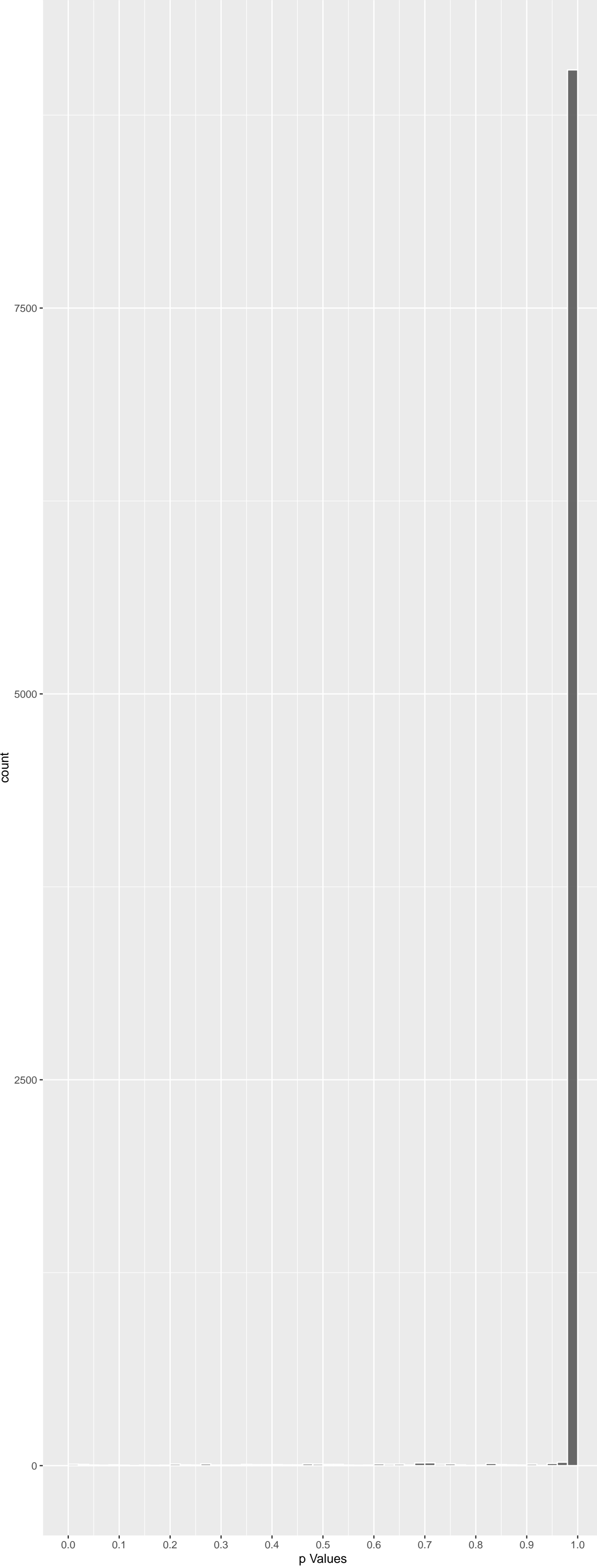
Positive Rho Non-permulated



Top Positive genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
ADGRG4	5.725569	6.185247e-08	1.145e-03	1.000e+00
PRUNE2	5.380542	4.455709e-07	2.748e-03	1.000e+00
JCAD	5.087061	2.181930e-06	8.183e-03	1.000e+00
ZZEF1	5.084550	2.210996e-06	8.183e-03	1.000e+00
ZFP3	5.020676	3.089404e-06	9.528e-03	1.000e+00
ARHGEF6	4.947157	4.518309e-06	1.099e-02	1.000e+00
DCUN1D2	4.802543	9.399798e-06	1.485e-02	1.000e+00
SLC2A7	4.760449	1.158975e-05	1.532e-02	1.000e+00
CEP250	4.690691	1.633701e-05	1.696e-02	1.000e+00
ACAD10	4.607981	2.439582e-05	2.150e-02	1.000e+00

Negative Rho Non-permulated



Top Negative genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
HERC2	-5.570352	1.525347e-07	1.411e-03	1.000e+00
GABRA5	-4.937429	4.749554e-06	1.099e-02	1.000e+00
MET	-4.797737	9.628084e-06	1.485e-02	1.000e+00
RBM6	-4.818171	8.692799e-06	1.485e-02	1.000e+00
TMEM108	-4.809224	9.091034e-06	1.485e-02	1.000e+00
ZNF134	-4.768790	1.112014e-05	1.532e-02	1.000e+00
NUP133	-4.729633	1.349555e-05	1.665e-02	1.000e+00
ADAMTS6	-4.688741	1.649350e-05	1.696e-02	1.000e+00
CNGB3	-4.689442	1.643710e-05	1.696e-02	1.000e+00
CRISP1	-4.636898	2.122059e-05	2.067e-02	1.000e+00

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON	-0.32785611	21	1.979e-07	1.285e-03	PCSK6:244 TARSK:497 LYSMD4:547 ARDCD4:710 LRRK1:766 SNRPA1:828
DODD_NASOPHARYNGEAL_CARCCINOMA_DN	-0.03993861	1274	1.974e-06	6.410e-03	NUP133:7 APOC1:19 NUP205:22 GALNT2:30 NUP155:34 NSD2:82
ZHANG_BREAST_CANCER_PROGNETITORS_LP	-0.06207104	414	1.538e-05	2.497e-02	MET:5 PRPS2:26 TRPS1:28 NUP155:34 BCLAF3:48 PAXBP1:109
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	-0.03602415	1306	1.430e-05	2.497e-02	MET:5 EHMT1:14 ZNF274:29 ZIM2:49 ZNF214:51 MTFH9:662
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACT	-0.07605665	258	2.661e-05	3.456e-02	MET:5 PRL:92 TGFBI:97 TSLP:117 TNF:254 FLT1:1312
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.03604673	1189	3.215e-05	3.479e-02	HERC2:1 MET:5 LTN1:15 SCN2A:16 ARHGEF4:32 ATP2B1:56
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.20294201	34	4.219e-05	3.914e-02	THBS3:14 ADAM15:60 DCST1:98 ZBTB78:226 PYGO2:259 RUCP1:318
BRIDEAU_IMPRINTED_GENES	-0.15143650	58	6.650e-05	5.398e-02	ATP10A:20 IGFB1:105 UBE3A:201 CNTN3:224 MAGEL2:234 CALCR:314
REACTOME_PROLACTIN_RECEPTOR_SIGNALING	-0.28533212	15	1.300e-04	9.383e-02	PRL:92 PRLR:805 JAK2:812 GH1:821 CSH1:835 GH1:982
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME	-0.13786708	63	1.544e-04	1.003e-01	HERC2:1 GABRA5:2 ATP10A:20 MDM4:85 GABRG3:148 OCA2:170
WP_PHOTODYNAMIC_THERAPYINDUCED_AP1_SURVI	-0.15598790	48	1.849e-04	1.092e-01	FOS:169 TNF:254 BAX:283 BCL2L1:1139 CNNE1:466 MAPK8:494
REACTOME_FORMATION_OF_SENESCENCE_ASSOCIA	-0.25942608	17	1.227e-04	1.151e-01	H1-4:172 H1-1374 UBN1:478 H1-3:720 CABIN1:741 EP400:919
WP_OVERVIEW_OF_PROINFLAMMATORY_AND_PROFI	-0.09259063	126	3.341e-04	1.696e-01	AREG:95 TGFBI:97 TSLP:117 IL33:146 TNF:254 IL18:321
REACTOME_PROCESSING_OF_CAPPED_INTRON_CON	-0.06463052	253	4.072e-04	1.889e-01	NUP133:7 NUP205:22 NUP155:34 SYMPK:68 U2AF1L4:300 THOC5:364
RODRIGUES_THYROID_CARCCINOMA_POORLY_DIFFE	-0.04199629	602	4.518e-04	1.956e-01	NUP155:34 MPHOSPH10:43 E2F5:57 GPM52:174 ORC6:193 NETO2:221
BIOCARTA_PEP1_PATHWAY	0.34902846	8	6.058e-04	2.149e-01	CELA1:27 CELA2B:468 SLPI:511 CELA3B:611 CELA2A:778 ELANE:1483
HOLLERN_EMT_BREAST_TUMOR_DN	0.09143831	118	6.255e-04	2.149e-01	CLIC3:156 SDR42E1:230 EVPL:297 ENDOU:328 POF1B:391 PTPRF:425
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVIE	0.08905522	126	5.599e-04	2.149e-01	KRT39:139 KRT84:170 SPRR2A:204 EVPL:297 KRT20:322 KRT72:454
RODRIGUES_THYROID_CARCCINOMA_ANAPLASTIC_U	-0.03896305	673	5.952e-04	2.149e-01	COL7A1:25 MPHOSPH10:43 CNOT1:55 ATP2B1:56 CDH2:87 AREG:95
NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-0.08674479	127	7.404e-04	2.193e-01	RBM12B:35 ZBTB10:118 SNX16:134 RALYL:200 PIRAP2:213 MMP16:242
REACTOME_CELL_SURFACE_INTERACTIONS_AND_TH	-0.08374567	137	7.190e-04	2.193e-01	TGFB1:97 GRB14:223 PIK3CA:308 GYPC:378 SIRPA:485 JAML:489
KEGG_P53_SIGNALING_PATHWAY	-0.11919283	67	7.431e-04	2.193e-01	MDM4:85 IGFBP3:111 SHIS45:132 BAX:283 CHEK1:369 CNE1:1466
MILI_PEGUODODIA_HAPTOXIS_UP	-0.04392626	496	1.043e-04	2.635e-01	LTN1:15 CAMSAP2:47 BCLAF3:48 WPM1:52 SHEN1:108 RNF131:149
DANG_BOUND_BY_MYC	-0.03081833	1010	9.878e-04	2.635e-01	MET:5 ZNF134:6 PRPS2:26 ZNF274:29 NUP155:34 SYMPK:68
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.04291957	517	9.485e-04	2.635e-01	GABRA5:2 CAMSAP2:47 ATP2B1:56 CHL1:62 SARSL:121 DCTN1:147
PID_E2F_PATHWAY	-0.11405483	69	1.055e-03	2.635e-01	E2F5:57 RBL2:80 CASP7:131 CDC25A:150 MYBL2:391 CCNE1:466
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF	-0.13697975	47	1.160e-03	2.660e-01	CNOT1:55 RBL2:80 BAX:283 CNE1:466 CDK1:852 CNOT1:1946
JOHNSTONE_PARVB_TARGETS_3_DN	-0.03414968	793	1.133e-03	2.660e-01	PRPS2:26 SETD2:27 ZNF274:29 UAP1:71 MDM4:85 ZNF22:119
BLUM_RESPONSE_TO_SALIRASIB_DN	-0.05231811	326	1.188e-03	2.660e-01	GALNT2:30 CDC25A:150 FOS:169 GPM52:174 ORC6:193 PTKB:361
SHEN_SMARCA2_TARGETS_UP	-0.04638322	410	1.300e-03	2.814e-01	PRL92:11 NUP133:7 PSMF1:206 CAPN7:287 NPTN:376 WDR11:503
KEGG_GRAFT_VERSUS_HOST_DISEASE	-0.14999908	37	1.593e-03	3.336e-01	TNF:254 HLA-DQB3:384 HLA-DQA1:502 ATG5:265 CDK1:852
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SY	-0.03504975	698	1.670e-03	3.389e-01	TGFB1:97 TSLP:117 CRK1:37 TNF:254 CALCR:314 HLA-DQA1:502
REACTOME_SPERM_MOTILITY_AND_TAXES	-0.130130682	9	1.746e-03	3.456e-01	BFSPP2:93 CRYBB1:214 CRYAA2:956 STS:1054 GJA8:1826 MIP:2175
ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_D	-0.08462091	23	1.998e-03	3.555e-01	TGFB1:97 CRK1:37 PHB2:199 PDE6B:247 TNF:254 TLR8:267
MIKKELSEN_ES_LCP_WITH_H3K4ME3	0.03648595	684	2.060e-03	3.565e-01	CYLD:42 TDRD7:46 ARSF:79 AREG:95 TGFBI:97 HERC5:108
REACTOME_TLR1_SIGNALING	-0.31340549	8	2.141e-03	3.565e-01	ATP2B1:56 TGFBI:97 IGFB1:105 PHB2:199 CRH:215 INSR:231
REACTOME_UPTAKE_OF_DIETARY_COBALAMINS_IN	-0.03532171	655	2.122e-03	3.565e-01	MET:5 SETD2:27 CYLD:42 CHL1:62 NSD2:82 TGFBI:97
SCHLOSSER_SERUM_RESPONSE_DN	0.23697885	14	2.139e-03	3.565e-01	MDM4:85 TGFBI:97 IGFB1:105 PHB2:199 CRH:215 INSR:231
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.07738365	131	2.238e-03	3.624e-01	MET:5 SETD2:27 CYLD:42 CHL1:62 NSD2:82 TGFBI:97
MIKKELSEN_ES_LCP_WITH_H3K4ME3	0.07738365	131	2.238e-03	3.624e-01	MDM4:85 TGFBI:97 IGFB1:105 PHB2:199 CRH:215 INSR:231

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Adenocarcinoma in Situ	-0.22462139	29	2.842e-05	2.791e-01	CDH2:87 ASAP1:488 DPYD:507 SEC14L2:664 PAPOLA:918 STS:1054
Carcinosarcoma	-0.17316279	43	8.589e-05	4.217e-01	MET:5 TGFBI:97 IGFB1:105 PHB2:199 PIK3CA:308 SOX9:515
Allergic Reaction	-0.12627535	61	6.522e-04	6.250e-01	KNG1:45 TGFBI:97 TNF:254 IL18:321 HLA-DQA1:502 CX3CL1:625
Anal squamous cell carcinoma	-0.28741944	12	5.659e-04	6.250e-01	PIK3CA:308 MDM2:757 DCC:1247 NLFIE:1264 TP53:139 CDKN2A:1536
Cataract	-0.04542582	484	6.695e-04	6.250e-01	CNGB3:8 COL7A1:25 TDRD7:46 ATP2B1:56 SUMF1:76 RBP3:83
Cervical Squamous Intraepithelial Neopla	-0.14195945	47	7.638e-04	6.250e-01	MET:5 TGFBI:97 TNF:254 LAMB2:286 HMGB1:551 MTHFR:662
Hepatitis C	-0.03838935	677	7.359e-04	6.250e-01	MET:5 APOA1:13 APOC1:19 TGFBI:97 CLU:101 IGFB1:105
insulinoma	-0.08206995	164	2.953e-04	6.250e-01	MET:5 EHMT1:14 PRL:92 TGFBI:97 IGFB1:105 SDS:173
Liver carcinoma	-0.02026726	3047	6.026e-04	6.250e-01	MET:5 APOA1:13 SETD2:27 GALNT2:30 CYLD:42 KNG1:45
Prader-Willi Syndrome	-0.10739578	88	5.035e-04	6.250e-01	HERC2:1 GABRA5:2 ATP10A:20 ZNF274:29 GABRG3:148 OCA2:170
Stable angina	-0.12132354	70	4.525e-04	6.250e-01	APOA1:13 TGFBI:97 IGFB1:105 IL33:146 TNF:254 CX3CL1:625
Tumor Immunity	-0.09083163	122	5.398e-04	6.250e-01	AREG:95 IL33:146 FOS:169 HAVCR1:198 TNF:254 TLR8:267
Leukemia, Myelocytic, Acute	-0.02567732	1494	1.152e-03	6.286e-01	MET:5 SETD2:27 TRPS1:28 CHL1:62 ZNF331:74 MDM4:85
Bilateral cataracts (disorder)	-0.09453982	104	8.768e-04	6.286e-01	TDRD7:46 BFSPP2:93 TGFBI:97 MGST1:207 AKR1B1:212 EPHA2:356
Cervical Intraepithelial Neoplasia	-0.06942076	187	1.089e-04	6.286e-01	MET:5 TGFBI:97 SYCP3:196 TNF:254 BAX:283 LAMB2:286
Cholestasis in newborn	0.10161197	87	1.064e-03	6.286e-01	GPBAR1:31 PEX1:173 HAMP:271 SLC10A2:273 LIPA:287 MPI:288
Influenza	-0.04241087	508	1.150e-03	6.286e-01	CYLD:42 TDRD7:46 ARSF:79 AREG:95 TGFBI:97 HERC5:108
Myasthenia Gravis	-0.07077270	156	9.131e-04	6.286e-01	TGFBI:97 TSLP:117 CRK1:37 TNF:254 CALCR:314 HLA-DQA1:502
CATARACT, AUTOSOMAL DOMINANT	-0.29751104	9	1.997e-03	6.674e-01	BFSPP2:93 CRYBB1:214 CRYAA2:956 STS:1054 GJA8:1826 MIP:2175
Tuberculosis, Pulmonary	-0.07405264	150	1.779e-03	6.674e-01	TGFB1:97 CRK1:37 PHB2:199 PDE6B:247 TNF:254 TLR8:267
Acute inflammatory demyelinating polyneu	-0.32422268	7	2.971e-03	6.674e-01	TNF:254 PTGDS:302 TNFRSF1A:858 ALB:1419 PMP22:1499 HLA-DRB1:9284.5
Adenovirus Infections	-0.09567072	85	2.318e-03	6.674e-01	TRPS1:28 MDM4:85 CDC25A:150 TNF:254 BAX:283 CHEK1:369
Anasarca	-0.16972994	26	2.743e-03	6.674e-01	APOA1:13 KNG1:45 TGFBI:97 TNF:254 VIP:917 PTGS2:964 CASP8:1005
Anti-Basement Membrane Glomerulonephriti	-0.15029550	36	1.810e-03	6.674e-01	CLU:101 TNF:254 MAPK8:494 CX3CL1:625 ITGA4:1477 PTK2B:1508
Carcinoma of bladder	-0.02953013	1013	1.710e-03	6.674e-01	MET:5 SETD2:27 KNG1:45 MDM4:85 CDH2:87 TGFBI:97
Central neuroblastoma	-0.02391509	1507	2.374e-03	6.674e-01	HERC2:1 SETD2:27 CYLD:42 KNG1:45 CNOT1:55 CHL1:62
Cervix carcinoma	-0.02932364	943	2.668e-03	6.674e-01	MET:5 SETD2:27 CYLD:42 CHL1:62 NSD2:82 TGFBI:97
Choriocarcinoma	-0.05287199	279	2.456e-03	6.674e-01	MDM4:85 TGFBI:97 IGFB1:105 PHB2:199 CRH:215 INSR:231
Epithelial ovarian cancer	-0.02650156	1150	2.852e-03	6.674e-01	MET:5 SETD2:27 KNG1:45 RBL2:80 MDM4:85 PRL:92
Extramedullary Plasmacytoma	-0.24780234	12	2.956e-03	6.674e-01	PECAM1:679 ANGP1:1132 ENG:1334 TP53:1339 CDKN2A:1536 PRM3:1703
Generalized hypopigmentation	-0.23851841	14	2.002e-03	6.674e-01	HERC2:1 MAGEL2:234 NDN:1164 OCLR1:1727 MKRN3:2059 LEMO3:2181
Glioblastoma	-0.02250462	1686	2.672e-03	6.674e-01	MET:5 APOA1:13 SETD2:27 CD109:31 CNOT1:55 RBL2:80
HIV Infections	-0.03300997	717	2.856e-03	6.674e-01	ZNF134:6 APOA1:13 CYLD:42 CNOT1:55 CDH2:87 TGFBI:97
Human metapneumovirus infection	-0.32969415	7	2.521e-03	6.674e-01	TSLP:117 TNF:254 NCR1:424 PIPK1:903 ISYNA1:1940 SGT:9284.5
Hyperinulnism	-0.04804065	359	1.854e-03	6.674e-01	HERC2:1 EHMT1:14 APOC1:19 MCR4:61 RBP3:83 PRL:92
Infection	-0.043232542	463	1.494e-03	6.674e-01	APOA1:13 APOC1:19 CYLD:42 TGFBI:97 IGFB1:105 IL33:146
Male sterility due to Y-chromosome delet	-0.37276775	6	1.566e-03	6.674e-01	DAZ1:567 DAZ4:714 DAZ3:851 DAZ2:997 USP9Y:1817 DDXX3Y:9284.5
Neuroblastoma	-0.02309536	1547	2.990e-03	6.674e-01	HERC2:1 MET:5 SETD2:27 CYLD:42 KNG1:45 CNOT1:55
Oncocytic Neoplasm	-0.12687192	47	2.631e-03	6.674e-01	PRL:92 ZFP42:123 MST1:329 CLDN8:651 PTGS2:964 CD8:1033
Partial chromosome Y deletion	-0.37276775	6	1.566e-03	6.674e-01	DAZ1:567 DAZ4:714 DAZ3:851 DAZ2:997 USP9Y:1817 DDXX3Y:9284.5

customGeneSet Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	0.05735493	13	5.210e-01	7.814e-01	SLC39A8:2409 LCT:9221.5 AS3MT:9221.5 GPX3:9221.5 CELF1:9221.5 SEPSECS:9221.5
NAFLDGOVAV	-0.06787879	15	4.228e-01	7.814e-01	INSR:231 TOR1B:959 GID4:1220 FTO:1677 GPM1:1954 PNPLA3:9284.5
expressionDirectionalSelection	0.01147959	42	8.714e-01	8.714e-01	DEFB8:2262 HLA-DRB1:9221.5 FADS1:9221.5 POU5F1:9221.5 HLA-DRB5:9221.5 KAT8:9221.5
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

B Cell Mediated Immunity (GO:0019724)	0.0606075078	14	4.365e-01	9.999e-01	SLA2:529 CD24:1137 IL12R:1639 CD70:9222.5 FCGR2B:9221.5 CD19:9221.5
B Cell Proliferation (GO:0042100)	-0.0135116271	31	7.946e-01	9.999e-01	CR2:655 IFNK:1068 IFNA4:1801 IFNA7:2248 IL10:9284.5 CD28:9284.5
B Cell Receptor Signaling Pathway (GO:00	0.0373077305	32	6.653e-01	9.999e-01	TRC:447 PLCG2:960 NFAM1:1463 BCAR1:1497 LCK:1704 BCL2:2418
BMP Signaling Pathway (GO:0030509)	0.0172347396	61	6.418e-01	9.999e-01	GD3F:105 AMHR2:378 INHBA:618 RGMB:790 SLC39A5:888 HIVEP1:1190
C-terminal Protein Amino Acid Modificati	-0.0060169575	11	9.449e-01	9.999e-01	ATG5:992 AGLB5:9284.5 GPLD1:9284.5 IGMT:9284.5 AGTPBP1:9284.5 ATG16L1:9284.5
C-terminal Protein Deglutamylation (GO:0	0.0943438670	4	5.134e-01	9.999e-01	FOLH1:2278 AGLB5:9221.5 AGTPBP1:9221.5 AGLB4:9221.5 NA NA
C-terminal Protein Lipidation (GO:000650	-0.1113140656	4	4.407e-01	9.999e-01	ATG5:992 GPLD1:9284.5 ATG16L1:9284.5 AGT:9284.5 NA NA
C4-dicarboxylate Transport (GO:0015740)	-0.1179322231	12	1.591e-01	9.999e-01	LRR8C:158 SLC25A13:987 SLC25A18:644 SLC1A6:1113 SLC13A2:9221.5 SLC13A5:9221.5
CD4-positive, Alpha-Beta T Cell Activati	-0.2278829542	4	1.144e-01	9.999e-01	HMOB1:551 TNFSF4:1083 STOM1:9284.5 NKKG7:9284.5 NA NA
CD40 Signaling Pathway (GO:0023035)	-0.1207738910	7	2.685e-01	9.999e-01	PHB2:199 CD86:1566 NR3C1:2310 ITGB1:9284.5 TNIP2:9284.5 ITGA5:9284.5
CENP-A Containing Chromatin Assembly (GO	0.0918226542	6	3.460e-01	9.999e-01	HJURP:95 NASP:1138 CENPW:9221.5 CENP1:9221.5 OIP5:9221.5 M181A:16349
COPI Coating Of Golgi Vesicle (GO:004820	-0.1523288460	5	2.381e-01	9.999e-01	ARFGAP3:1984 TMED2:9426 TMED10:9284.5 GBF1:9284.5 TMED2:9284.5 NA

MGI\_Mammalian\_Phenotype\_Level\_4 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0008875 abnormal xenobiotic pharmacok	0.176566733	20	6.330e-03	9.112e-01	ADH7:223 ABCC3:298 AHR:321 POR:705 ABCC2:841 SLC47A1:991
MP0002086 abnormal extraembryonic tissu	-0.035487163	487	9.569e-03	9.112e-01	MET5: SETD2:27 CDH2:87 TGFBI:97 IGFB2:105 FGG:135
MP0002080 prenatal lethality	-0.024703358	1338	6.387e-03	9.112e-01	HERAC2:1 MET5: NUP133:7 HEMT1:14 LTN1:15 SETD2:27
MP0003252 abnormal bile duct	0.149933859	25	9.572e-03	9.112e-01	MAPK3I4:281 AHR:321 PKHD1:341 CYPB81:371 ABCG5:428 ABCB4:653
MP0001666 abnormal nutrient absorption	0.16261072	46	3.162e-03	9.112e-01	TREH:166 SLC24A:10 SLC10A2:273 CYPB81:371 ABCG5:428 NPC1L1:553
MP0000843 abnormal cutaneous collagen	-0.064579574	15	3.869e-01	9.188e-01	LBN1:658 CDN:782 TNXB:2241 PLD3:9284.5 THBS2:9284.5 COL3A1:9284.5
MP0002909 abnormal adrenal gland	-0.059922063	23	3.205e-01	9.188e-01	FRK6:64 CKNK3:1348 DRD5:1952 CHGA:9284.5 FOXA1:9284.5 CHGA:9284.5
MP0001730 embryonic growth arrest	-0.019075390	182	3.807e-01	9.188e-01	NUP133:7 RBL2:80 DCTN1:147 PKIC3A:308 FLT1:312 CHD8:530
MP0001731 abnormal postnatal growth	-0.007862130	592	5.311e-01	9.188e-01	MET5: LTN1:15 COLA7:25 SUMF1:76 AREG:95 IRR2:61
MP0002210 abnormal sex determination	-0.034019461	349	3.308e-02	9.188e-01	SPAG16:103 OCA2:170 TAF4B:175 SYCP3:196 UBE3A:201 SLC14A1:228
MP0000598 abnormal liver morphology	-0.016970750	482	2.175e-01	9.188e-01	MET5: APOA1:13 TGFBI:97 F11:106 OCA2:170 ASAH1:211
MP0005334 abnormal fat pad	-0.035393303	152	1.361e-01	9.188e-01	IGFBP3:111 OCA2:170 INSR:231 IL18:321 GPR142:43 HDC:471
MP0005303 cardiomyopathy	-0.049576922	70	1.534e-01	9.188e-01	MYOZ2:209 HEXIM1:834 IGF1R:878 MCOLN1:1079 CAV1:1483 ERBB4:1484
MP0001765 abnormal ion homeostasis	-0.034197306	110	2.187e-01	9.188e-01	PTH1R:307 CALCR:314 SLC24A2:505 PTERG5:337 FGF23:693 PRLR:805
MP0004043 abnormal pH regulation	-0.070367133	13	3.801e-01	9.188e-01	SLC26A7:819 SLC4A4:1153 SLC4A10:1179 HIF1AN:9284.5 SOD2:9284.5 ERCC1:9284.5