

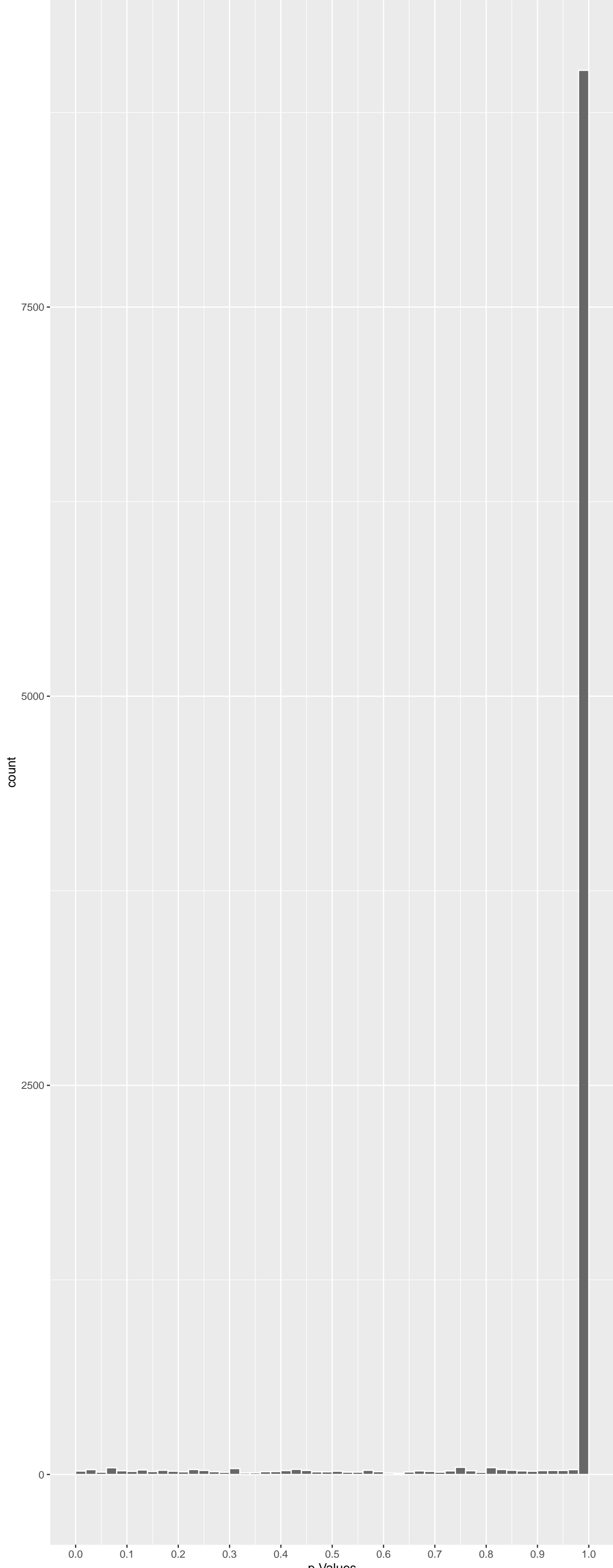
Top genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
CAPN8	-6.768738	7.794623e-11	1.442e-06	2.669e-02
PSAPL1	-5.725153	6.200425e-08	5.737e-04	1.000e+00
DAXX	5.586745	1.388187e-07	6.381e-04	1.000e+00
PER2	-5.548984	1.724010e-07	6.381e-04	1.000e+00
RXFP4	-5.602400	1.268427e-07	6.381e-04	1.000e+00
EVPL	-5.461393	2.834485e-07	8.742e-04	1.000e+00
ACAD10	-5.306935	6.689036e-07	1.768e-03	1.000e+00
KIF18A	5.261459	8.575005e-07	1.984e-03	1.000e+00
NDUFB5	5.148969	1.571534e-06	2.180e-03	1.000e+00
NRDE2	-5.139918	1.649153e-06	2.180e-03	1.000e+00
NRK	5.178792	1.339967e-06	2.180e-03	1.000e+00
NSD1	5.158426	1.494206e-06	2.180e-03	1.000e+00
PNMA8B	-5.214138	1.108041e-06	2.180e-03	1.000e+00
SYDE2	5.182213	1.315611e-06	2.180e-03	1.000e+00
PLEC	-5.058833	2.530986e-06	3.122e-03	1.000e+00
BNC1	-5.005485	3.343286e-06	3.867e-03	1.000e+00
P2RY4	-4.949166	4.471931e-06	4.868e-03	1.000e+00
USP43	-4.908166	5.515910e-06	5.671e-03	1.000e+00
ITGB4	-4.891843	5.993779e-06	5.770e-03	1.000e+00
SLC17A4	-4.884041	6.236001e-06	5.770e-03	1.000e+00
SENP7	4.869038	6.728586e-06	5.929e-03	1.000e+00
MR1	-4.842857	7.679122e-06	6.459e-03	1.000e+00
GOLGA2	-4.807279	9.179947e-06	7.155e-03	1.000e+00
TRANK1	-4.805117	9.279675e-06	7.155e-03	1.000e+00
CATSPERB	4.765008	1.133078e-05	7.488e-03	1.000e+00

Top genes by Q-Value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
CAPN8	-6.76873819	7.794623e-11	1.442e-06	2.669e-02
A1BG	1.75891892	4.715477e-01	1.000e+00	1.000e+00
A1CF	-0.07117502	1.000000e+00	1.000e+00	1.000e+00
A2M	1.73948569	4.916962e-01	1.000e+00	1.000e+00
A2ML1	-3.35894792	4.694389e-03	1.833e-01	1.000e+00
A3GALT2	-0.98844051	1.000000e+00	1.000e+00	1.000e+00
A4GALT	0.40572801	1.000000e+00	1.000e+00	1.000e+00
A4GNT	0.50982277	1.000000e+00	1.000e+00	1.000e+00
AAAS	1.06849216	1.000000e+00	1.000e+00	1.000e+00
AACS	-1.44688272	8.875786e-01	1.000e+00	1.000e+00
AADAC	-1.22460796	1.000000e+00	1.000e+00	1.000e+00
AADACL2	-4.00039945	3.794299e-04	4.829e-02	1.000e+00
AADACL3	-0.85736138	1.000000e+00	1.000e+00	1.000e+00
AADACL4	-1.54674698	7.286553e-01	1.000e+00	1.000e+00
AADAT	0.15659592	1.000000e+00	1.000e+00	1.000e+00
AAGAB	-0.87447872	1.000000e+00	1.000e+00	1.000e+00
AAK1	-1.94158524	3.131240e-01	1.000e+00	1.000e+00
AAMDC	0.51067043	1.000000e+00	1.000e+00	1.000e+00
AAMP	-1.11647474	1.000000e+00	1.000e+00	1.000e+00
AAAT	-2.83072171	2.786587e-02	4.816e-01	1.000e+00
AAR2	0.75828167	1.000000e+00	1.000e+00	1.000e+00
AARD	-2.00680413	2.686231e-01	1.000e+00	1.000e+00
AARS1	1.13559389	1.000000e+00	1.000e+00	1.000e+00
AARS2	-0.61191290	1.000000e+00	1.000e+00	1.000e+00
AARSD1	1.57534385	6.910620e-01	1.000e+00	1.000e+00

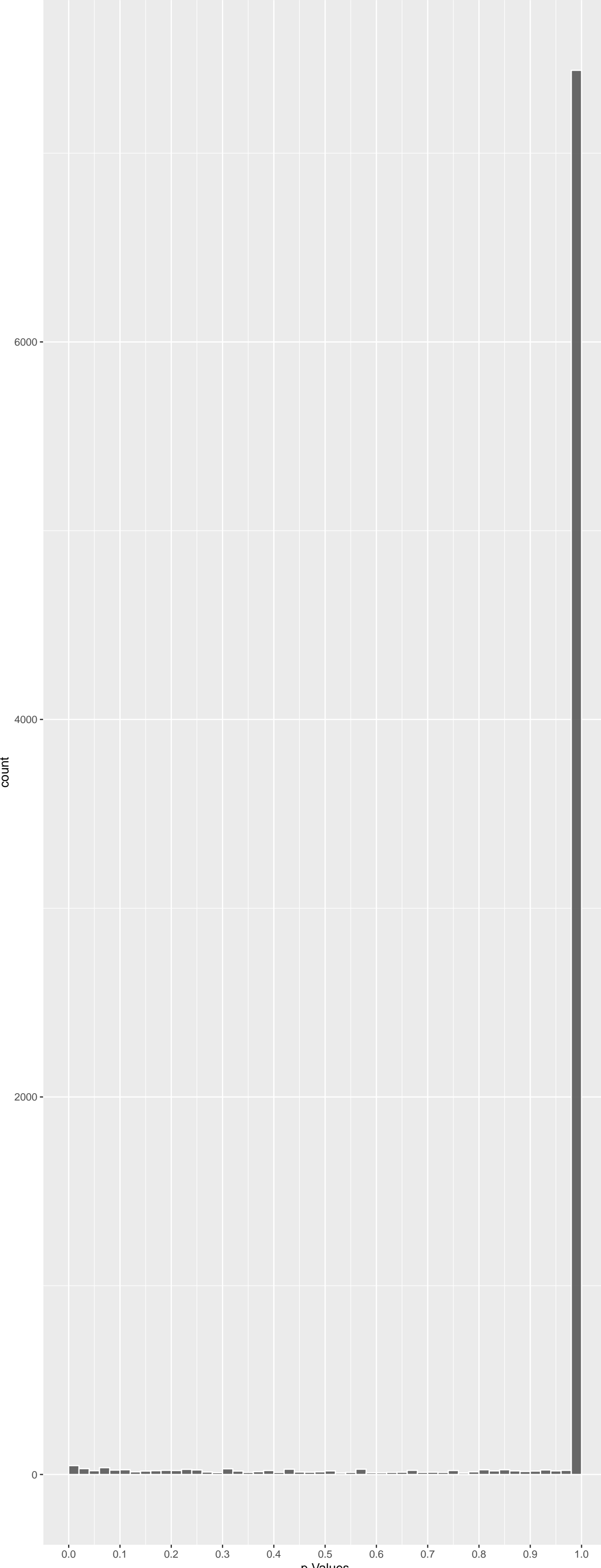
Positive Rho Non-permulated



Top Positive genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
DAXX	5.586745	1.388187e-07	6.381e-04	1.000e+00
KIF18A	5.261459	8.575005e-07	1.984e-03	1.000e+00
NDUFB5	5.148969	1.571534e-06	2.180e-03	1.000e+00
NRK	5.178792	1.339967e-06	2.180e-03	1.000e+00
NSD1	5.158426	1.494206e-06	2.180e-03	1.000e+00
SYDE2	5.182213	1.315611e-06	2.180e-03	1.000e+00
SENPT	4.869038	6.728586e-06	5.929e-03	1.000e+00
CATSPERB	4.765008	1.133078e-05	7.488e-03	1.000e+00
CENPT	4.782414	1.039217e-05	7.488e-03	1.000e+00
UIMC1	4.753101	1.201922e-05	7.624e-03	1.000e+00

Negative Rho Non-permulated



Top Negative genes by P-value non-permulated

Gene	Rho	P	p.adj	qValueNoperm
CAPN8	-6.768738	7.794623e-11	1.442e-06	2.669e-02
PSAPL1	-5.725153	6.200425e-08	5.737e-04	1.000e+00
PER2	-5.548984	1.724010e-07	6.381e-04	1.000e+00
RXFP4	-5.602400	1.268427e-07	6.381e-04	1.000e+00
EVPL	-5.461393	2.834485e-07	8.742e-04	1.000e+00
ACAD10	-5.306935	6.689036e-07	1.768e-03	1.000e+00
NRDE2	-5.139918	1.649153e-06	2.180e-03	1.000e+00
PNMA8B	-5.214138	1.108041e-06	2.180e-03	1.000e+00
PLEC	-5.058833	2.530986e-06	3.122e-03	1.000e+00
BNC1	-5.005485	3.343286e-06	3.867e-03	1.000e+00

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_KERATINIZATION	-0.20873189	202	1.659e-24	1.077e-20	EVPL5: KRT20:47 DSP:49 KRT80:78 KRT17:80 KRT13:86
REACTOME_FORMATION_OF_THE_CORNIFIED_ENV	-0.25072635	126	2.625e-22	8.523e-19	EVPL5: KRT20:47 DSP:49 KRT80:78 KRT17:80 KRT13:86
DODD_NASOPHARYNGEAL_CARINOMA_DN	-0.22031450	1273	4.423e-18	9.574e-15	KIF18A:2 FGD6:14 TFAM:29 LRPPRC:41 ZNF557:45 TPX2:52
FISCHER_DREAM_TARGETS	0.08327049	920	1.632e-17	2.649e-14	KIF18A:2 OBI1:11 TRIM59:33 CENPC:51 WDR76:54
RODRIGUES_THYROID_CARINOMA_POORLY_DIFFE	0.10155905	602	2.198e-17	2.855e-14	KIF18A:2 ZNF644:25 TFAM:29 LRPPRC:41 WDR76:54 NIFK:58
JOHNSTONE_PARVB_TARGETS_3_DN	0.08421993	793	9.888e-16	1.070e-12	KIF18A:2 SENP7:7 OBI1:11 CEP350:20 TFAM:29 UBAP2:47
REACTOME_CELL_CYCLE	0.08768495	647	3.384e-14	3.140e-11	DAXX:1 KIF18A:2 CENP7:8 UIMC1:10 CENPC:51 KIF2C:64 PHF20:65
ZHANG_BREAST_CANCER_PROGENITORS_UP	0.09460831	414	4.419e-11	1.888e-08	SYDE2:3 TRIM59:33 SLF1:60 CTH:62 KIF2C:64 SMCHD1:74
REACTOME_CELL_CYCLE_CHECKPOINTS	0.11733024	268	4.036e-11	1.888e-08	KIF18A:2 CENP7:8 UIMC1:10 CENPC:51 KIF2C:64 PHF20:65
WP_GPCRS_CLASS_A_RHOODPSINLIKE	-0.11865440	249	1.197e-10	6.793e-08	P2RY4:11 SSTR4:67 PTAFR:70 BDKR1:238 SSTR3:294 ACKR3:299
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.07569126	624	1.255e-10	6.793e-08	KIF18A:2 OBI1:11 CEP350:20 TASOR:23 ZNF644:25 CENPC:51
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	0.08967520	440	1.243e-10	6.793e-08	KIF18A:2 LRPPRC:41 GLMN:48 TPX2:52 WDR76:54 KIF2C:64
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	0.05499208	1210	1.611e-10	8.046e-08	KIF18A:2 OBI1:11 TPX2:52 WDR76:54 NIFK:58 SLF1:60
MARTENS_TRETINOLIN_RESPONSE_UP	-0.06711415	782	2.082e-10	9.656e-08	PIK3R5:23 CEP170B:26 MUC2:32 RNF186:36 CARD14:38 TRIM29:53
RODRIGUES_THYROID_CARINOMA_ANAPLASTIC_U	0.07194496	673	2.291e-10	9.917e-08	KIF18A:2 ZNF644:25 ATP13A3:35 TPX2:52 NIFK:58 RESF1:76
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.07182736	664	3.189e-10	1.294e-07	UBAP2:47 TPX2:52 WDR76:54 KIF2C:64 TTK:84 KIF2P3:85
REACTOME_CELL_CYCLE_MITOTIC	0.08034050	520	4.058e-10	1.550e-07	KIF18A:2 CENP7:8 ESCO1:32 CENPC:51 TPX2:52 KIF2C:64
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.25677589	47	1.131e-09	4.079e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUF5:59 NDUF70:101
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.16613187	112	1.272e-09	4.284e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUF5:59
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.18503144	90	1.319e-09	4.284e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUF5:59
PUJANA_BRCA1_PCC_NETWORK	0.04611602	1515	2.778e-09	8.590e-07	DAXX:1 TFAM:29 ATP13A3:35 GLMN:48 CENPC:51 TPX2:52 LRPPRC:41
WONG_MITOCHONDRIA_GENE_MODULE	0.11585824	214	6.580e-09	1.942e-06	NDUFB5:6 NDUFB10:12 ZNF644:25 NDUFB8:31 TPX2:52 LRPPRC:41
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN	0.04251398	1698	8.005e-09	2.260e-06	MGA1:7 CRLF2:11 ZNF644:25 PLA2R1:44 PHF20:65 PHF3:72
KEGG_OXIDATIVE_PHOSPHORYLATION	0.15484821	114	1.139e-08	3.083e-06	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUF5:59 NDUF1A1:108 ATP5PB:155
REACTOME_MITOTIC_PROMETAPHASE	0.11708675	195	1.778e-08	4.620e-06	KIF18A:2 CENP7:8 CENPC:51 KIF2C:64 NDC80:142 AKAP9:149
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.17225577	89	1.966e-08	4.911e-06	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUF5:59 ATP5PB:155 NDUF53:224
KIM_WT1_TARGETS_DN	0.07765376	445	2.116e-08	4.989e-06	KIF18A:2 FGD6:14 CEP350:20 CENPC:51 KIF2C:64 PHF3:72
MOOTHA_VOXPHOS	0.17473315	86	2.151e-08	4.989e-06	NDUFB5:6 NDUFB10:12 NDUF5:59 ATP5PB:155 NDUF53:224 ATP5PD:229
REACTOME_CELL_CYCLE_BIOGENESIS	0.23307878	48	2.322e-08	5.201e-06	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUF5:59 NDUF1A1:108
REACTOME_CLASS_A_1_RHOODPSIN_LIKE_RECEPT	-0.08958244	324	3.310e-08	6.775e-06	RXFPA:3 P2RY4:11 SSTR4:67 PTAFR:70 TACR2:184 GPR132:188
REACTOME_SENSORY_PERCEPTION	-0.06642596	596	3.361e-08	7.040e-06	CALHM1:46 PCDH15:57 OTOF:159 OR10S1:127 OR10R2:225 OR5M10:260
REACTOME_M_PHASE	0.08204169	384	3.631e-08	7.686e-06	KIF18A:2 CENP7:8 CENPC:51 KIF2C:64 UMP205:87 TPR:97
SHEM_SMARCA2_TARGETS_UP	0.07965747	409	4.391e-08	8.641e-06	CEP350:20 TMEM126B:43 CENPC:51 PHF3:72 KIF2C:64 TRMT1L:106
REACTOME_SIGNALING_BY_GPCR	-0.06072576	682	7.135e-08	1.363e-05	RXFPA:3 P2RY4:11 ARHGEF1:21 PTPN22:33 SSTR4:67 PTAFR:70
WONG_EMBRYONIC_STEM_CELL_CORE	0.08774903	318	7.872e-08	1.461e-05	NDUFB10:12 NDUFB8:31 NIFK:58 TTK:84 NDUF1A1:108 NDC80:142
WP_OXIDATIVE_PHOSPHORYLATION	0.21587730	51	9.681e-08	1.746e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUF5:59 NDUF1A1:108 ATP5PB:155
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUS	0.13120776	138	1.048e-07	1.839e-05	TPX2:52 KIF2C:64 TTK:84 NDC80:142 KIF4A:220 DLGAP:574
NYUTTEN_EZH2_TARGETS_DN	0.05082026	959	1.152e-07	1.917e-05	NDUFB10:12 ZNF644:25 TFAM:29 TPX2:52 WDR76:54 SLF1:60
FEVR_CTNNB1_TARGETS_DN	0.06758516	529	1.138e-07	1.917e-05	KIF18A:2 TFAM:29 TTK:84 LRPA1:118 CD2AP:119 GRSF1:123
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.12005591	162	1.373e-07	2.229e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUF5:59

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Mitochondrial Diseases	0.07876704	363	2.883e-07	2.831e-03	NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUF5:59
Increased CSF lactate	0.16384078	56	2.249e-05	4.417e-02	LRPPRC:41 TMEM126B:43 NDUF1A1:108 FASTKD2:143 TIMMD01:211 NDUF53:224
Left ventricular non-compaction cardiomyo	-0.22031450	31	2.191e-05	4.417e-02	PLEC:9 DSP:49 MUL1:331 TTN:480 PKRIN:605 MYH7B:1066
Palmoplanlar Keratosis	-0.12860891	95	1.508e-05	4.417e-02	PLEC:9 CARD14:38 DSP:49 KRT17:80 PKP1:120 ALOX12B:122
Primary myocardiophaly	0.12050223	110	1.296e-05	4.417e-02	NIPBL:124 TRMT10A:194 THADA:297 MRCN1:163 SASS6:355 KNLK1:439
Erythrokeratoderma	-0.18748458	41	3.290e-05	5.385e-02	CARD14:38 DSP:49 KRT17:80 ALOX12B:122 FAM83G:285 RHBDP2:302
Increased serum lactate	0.11595816	99	6.818e-05	8.369e-02	LRPPRC:41 TMEM70:101 FASTKD2:143 TWNK:178 NDUF53:224 RHBDF2:243
Parakeratosis	-0.28835621	16	6.520e-05	8.369e-02	CARD14:38 DSP:49 TNC:60 NLRP1:300 RHBDF2:302 TRPV3:1493
Epidermolytic Bullosa Simplex	-0.23341254	23	1.069e-04	1.166e-01	PLEC:9 ITGB4:13 KRT80:78 KRT17:80 TGM5:249 KRT9:33
Hypotrichosis	-0.14484698	57	1.566e-04	1.398e-01	PKP1:120 ALOX12B:122 TGM1:190 ABCA12:368 KRT17:502 DSG4:671
Seckel syndrome	0.18787626	34	1.505e-04	1.398e-01	CEP152:206 DNA2:473 CENPJ:475 DNMT1:654 CENPE:781 ATR:783
Pachonychia Congenita	-0.30902012	12	2.101e-04	1.719e-01	KRT80:78 KRT17:80 KRT6B:372 KRT9:413 SLURP1:1017 KRT6A:1244
Anemia, Macrocytic	0.18542640	33	2.283e-04	1.724e-01	SFXN4:263 TET2:348 SF3B1:702 ADH1B:776 RPL26:920 RPS26:1416
Psychomotor retardation, mild	0.23860386	19	3.179e-04	1.856e-01	RNF168:66 CEP152:206 CENPJ:475 CDC6:833 CENPE:781 ATR:783
Acanthosis	-0.18134126	33	3.130e-04	1.856e-01	CARD14:38 KRT13:86 ALOX12B:122 TGM1:190 NLRP1:300 GJB4:433
Amphetamine-Related Disorders	-0.12343500	70	3.591e-04	1.856e-01	MYO5B:353 ZNF423:402 HTR6:440 SLCO6A3:558 PRDM2:610 HTR1B:806
Amphetamine Abuse	-0.12343500	70	3.591e-04	1.856e-01	MYO5B:353 ZNF423:402 HTR6:440 SLCO6A3:558 PRDM2:610 HTR1B:806
Amphetamine Addiction	-0.12343500	70	3.591e-04	1.856e-01	MYO5B:353 ZNF423:402 HTR6:440 SLCO6A3:558 PRDM2:610 HTR1B:806
Mild global developmental delay	0.23860386	19	3.179e-04	1.856e-01	RNF168:66 CEP152:206 CENPJ:475 CDC6:833 CENPE:781 ATR:783
Glycogen Storage Disease Type V	-0.27163278	14	4.334e-04	2.128e-01	SLC2A4:178 PYGM:309 ATP2A1:774 MADD:867 AMPD1:878 PYGL:944
Absent earlobe	-0.28887269	12	5.305e-04	2.429e-01	CEP152:206 CENPJ:475 CENPE:781 ATR:783 RBP8:899 PLK4:1051
Cornelia De Lange Syndrome	0.18884307	28	5.442e-04	2.429e-01	NIPBL:124 AFFA:360 CENPJ:475 ATR:783 ESCO2:1248 NAALADL2:1294
Arthrogryposis	-0.05783313	297	6.358e-04	2.715e-01	PLEC:9 ITGB4:13 ODF1:59 TSC1:79 CHRNA4:138 COL6A1:192
NADH:(1) Oxidoreductase deficiency	0.19555160	25	7.146e-04	2.825e-01	NDUFB10:12 TMEM126B:43 NDUF1A1:108 TIMMD01:211 NDUF53:224 NDUF1A1:321
Poor school performance	0.03266879	946	7.191e-04	2.825e-01	NSD1:5 MAGEL2:36 CLCNKA:75 CLCNKB:90 SRCAP:93 TPR:97
Coughing	-0.10457802	86	8.106e-04	3.062e-01	PER2:4 DSP:49 TSC1:79 RTEL1:170 TACR2:184 PRTN3:229
Hyperkeratosis, Epidermolytic	-0.24087328	16	8.511e-04	3.095e-01	DSP:49 KRT80:78 ALOX12B:122 TGM1:190 KRT9:413 GJB4:433
Monilethrix	-0.42754797	5	9.294e-04	3.260e-01	KRT80:78 DSG4:671 KRT81:921 KRT86:2405 KRT83:2689 NA
Periodic syndrome	0.11830447	5	1.191e-03	4.033e-01	TNF:515 XBP1:1018 NLRP3:1456 MEV1:900 TNFRSF1A:2981 NA
Hypertrichosis	0.13335347	49	1.249e-03	4.088e-01	NDUF53:224 NDUF1A2:310 BMS1:929 NDUF1A0:1004 SRD5A3:1049 INSR:1200
Junctional split	-0.37872272	6	1.315e-03	4.164e-01	PLEC:9 ITGB4:13 LAMC2:745 ITGA6:1729 LAMB3:2165 LAMA3:8811.5
Bulbous nasal tip	0.10253736	80	1.536e-03	4.308e-01	AP4E1:15 SRCAP:93 JMD1C:126 SEC24C:413 DOCK6:448 DYRK1A:565
Bulbous nose	0.10253736	80	1.536e-03	4.308e-01	AP4E1:15 SRCAP:93 JMD1C:126 SEC24C:413 DOCK6:448 DYRK1A:565
Potato nose	0.10253736	80	1.536e-03	4.308e-01	AP4E1:15 SRCAP:93 JMD1C:126 SEC24C:413 DOCK6:448 DYRK1A:565
T-lymphocyte immunodeficiency	-0.37444618	6	1.491e-03	4.308e-01	CD3E:214 SIPA1:545 LBR:911 RAG1:1117 SFTPA1:2368 SMARCA1:8811.5
Dull intelligence	0.03111849	911	1.653e-03	4.386e-01	NSD1:5 MAGEL2:36 CLCNKA:75 CLCNKB:90 SRCAP:93 NIPBL:124
Low intelligence	0.03111849	911	1.653e-03	4.386e-01	NSD1:5 MAGEL2:36 CLCNKA:75 CLCNKB:90 SRCAP:93 NIPBL:124
Acidosis, Lactic	0.07253296	153	1.996e-03	5.100e-01	TFAM:29 LRPPRC:41 TMEM126B:43 TMEM70:101 NDUF1A1:108 FASTKD2:143
Conduction disorder of the heart	-0.10081556	78	2.100e-03	5.100e-01	DSP:49 DSG2:364 MPO:431 FLNC:441 DES:451 TTN:480
Granulomatosis	-0.29561828	9	2.133e-03	5.100e-01	PRTN3:229 NOD2:289 CYBB:811 NCF2:945 NCF1:1055 PTPN22:1299

customGeneSet Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	-0.06950067	13	4.367e-01	8.580e-01	SLC22A5:2454 AS3MT:8811.5 GPX1:8811.5 GPX3:8811.5 CELF1:8811.5 SEPSECS:8811.5
NAFLDQWAS	0.01515152	15	8.580e-01	8.580e-01	ADH1B:776 MTARC1:1149 INSR:1200 TOR1B:2862 TM6SF2:9694.5 APOE:9694.5
expressionDirectionalSelection	0.03316327	42	6.401e-01	8.580e-01	HLA-DOA1:379 TLR10:521 SCAPER:605 UBE2U:1672 HLA-DQA2:2216 ZBTB12:2383
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

Geneset	stat	num.genes	pval	p.adj	gene.vals
Intermediate Filament Organization (GO:0	-0.30511671	65	1.877e-17	1.015e-13	KRT20:47 DSP:49 KRT80:78 KRT17:80 KRT13:86 PKP1:120
NADH Dehydrogenase Complex Assembly (GO:	0.26962338	49	6.744e-11	1.215e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUF5:59 NDUF1A1:108
Mitochondrial Respiratory Chain Complex	0.26962338	49	6.744e-11	1.215e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUF5:59 NDUF1A1:108
Mitochondrial Respiratory Chain Complex	0.20256838	82	2.370e-10	3.203e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUF5:59 NDUF1A1:108
Aerobic Electron Transport Chain (GO:0010	0.19732127	64	4.893e-08	4.077e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUF5:59 NDUF53:224 NDUF1A1:321
Mitochondrial ATP Synthase Coupled Elec	0.19621478	65	4.578e-08	4.077e-05	NDUFB5:6 NDUFB10:12 NDUFB