

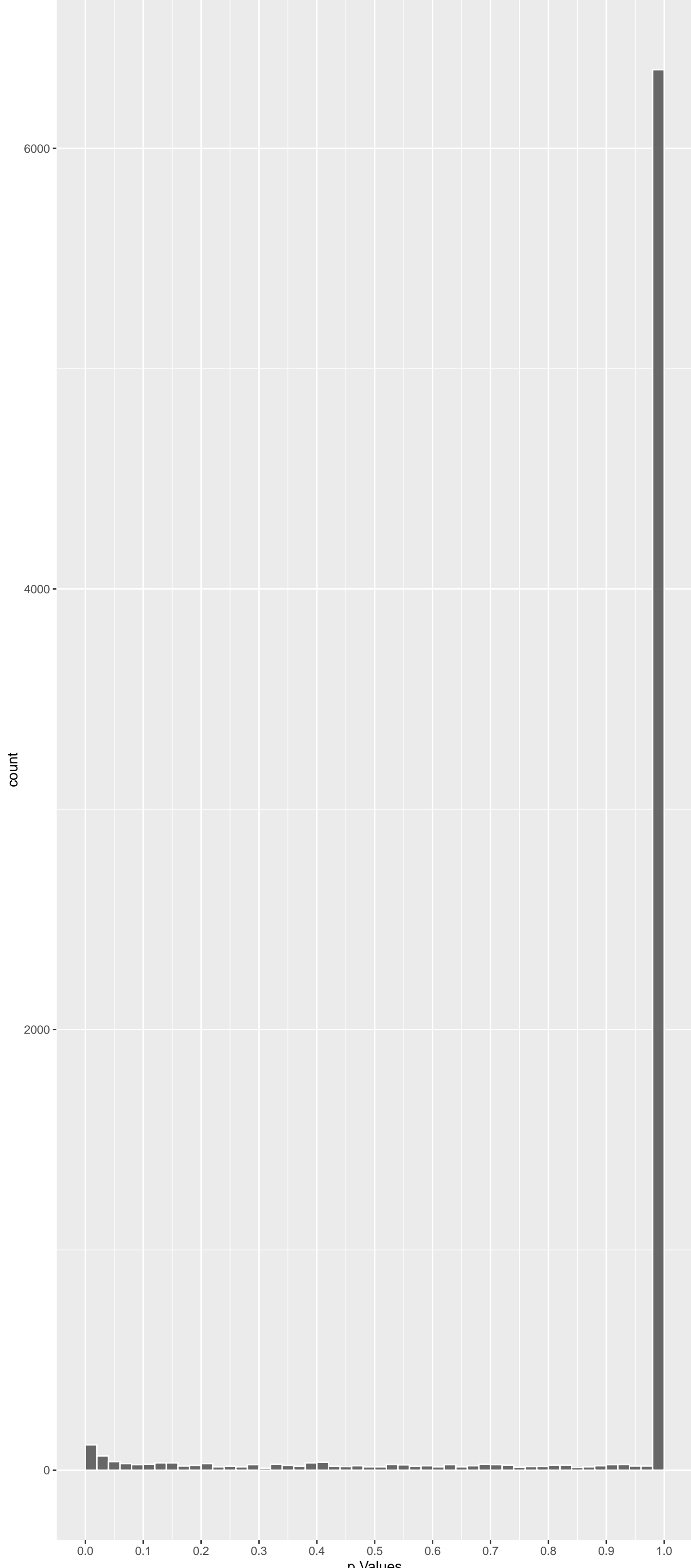
Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
PLEC	-7.520817	3.266093e-13	5.282e-09	8.543e-05
CAPN8	-7.183466	4.077956e-12	3.298e-08	2.667e-04
PKD1L1	-7.001313	1.521446e-11	8.202e-08	4.422e-04
TRANK1	-6.810289	5.844172e-11	2.363e-07	9.033e-04
ZFYVE9	6.753935	8.633311e-11	2.793e-07	9.033e-04
PER2	-6.500839	4.792392e-10	1.292e-06	3.482e-03
CAMSAP1	-6.345555	1.329749e-09	3.072e-06	7.098e-03
DNAH9	-6.224521	2.898170e-09	5.859e-06	1.184e-02
C7orf57	-6.173059	4.018862e-09	7.222e-06	1.298e-02
OFD1	-6.092896	6.653163e-09	1.076e-05	1.740e-02
SLC17A4	-5.968967	1.432562e-08	2.106e-05	2.939e-02
EVPL	-5.949085	1.617875e-08	2.180e-05	2.939e-02
TGM1	-5.856601	2.834613e-08	3.526e-05	4.387e-02
PYGM	-5.755945	5.169514e-08	4.918e-05	4.679e-02
SRCAP	5.771540	4.713030e-08	4.918e-05	4.679e-02
DSP	-5.780234	4.475795e-08	4.918e-05	4.679e-02
POLD2	-5.761885	4.990793e-08	4.918e-05	4.679e-02
TMEM63A	-5.684435	7.874744e-08	7.075e-05	6.357e-02
TACR2	-5.603676	1.259116e-07	1.072e-04	9.123e-02
KIAA0753	-5.556383	1.652536e-07	1.336e-04	1.081e-01
ZBTB21	-5.531050	1.909919e-07	1.471e-04	1.133e-01
CEP170B	-5.495739	2.334462e-07	1.716e-04	1.262e-01
TRPM5	-5.445470	3.100132e-07	2.089e-04	1.408e-01
DYNC2H1	-5.446170	3.087957e-07	2.089e-04	1.408e-01
IQANK1	-5.418449	3.607104e-07	2.334e-04	1.487e-01

Top genes by Q-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
PLEC	-7.520817	3.266093e-13	5.282e-09	8.543e-05
CAPN8	-7.183466	4.077956e-12	3.298e-08	2.667e-04
PKD1L1	-7.001313	1.521446e-11	8.202e-08	4.422e-04
ZFYVE9	6.753935	8.633311e-11	2.793e-07	9.033e-04
TRANK1	-6.810289	5.844172e-11	2.363e-07	9.033e-04
PER2	-6.500839	4.792392e-10	1.292e-06	3.482e-03
CAMSAP1	-6.345555	1.329749e-09	3.072e-06	7.098e-03
DNAH9	-6.224521	2.898170e-09	5.859e-06	1.184e-02
C7orf57	-6.173059	4.018862e-09	7.222e-06	1.298e-02
OFD1	-6.092896	6.653163e-09	1.076e-05	1.740e-02
SLC17A4	-5.968967	1.432562e-08	2.106e-05	2.939e-02
EVPL	-5.949085	1.617875e-08	2.180e-05	2.939e-02
TGM1	-5.856601	2.834613e-08	3.526e-05	4.387e-02
PYGM	-5.755945	5.169514e-08	4.918e-05	4.679e-02
SRCAP	5.771540	4.713030e-08	4.918e-05	4.679e-02
DSP	-5.780234	4.475795e-08	4.918e-05	4.679e-02
POLD2	-5.761885	4.990793e-08	4.918e-05	4.679e-02
TMEM63A	-5.684435	7.874744e-08	7.075e-05	6.357e-02
TACR2	-5.603676	1.259116e-07	1.072e-04	9.123e-02
KIAA0753	-5.556383	1.652536e-07	1.336e-04	1.081e-01
ZBTB21	-5.531050	1.909919e-07	1.471e-04	1.133e-01
CEP170B	-5.495739	2.334462e-07	1.716e-04	1.262e-01
TRPM5	-5.445470	3.100132e-07	2.089e-04	1.408e-01
DYNC2H1	-5.446170	3.087957e-07	2.089e-04	1.408e-01
ITGB4	-5.238053	9.736773e-07	3.841e-04	1.487e-01

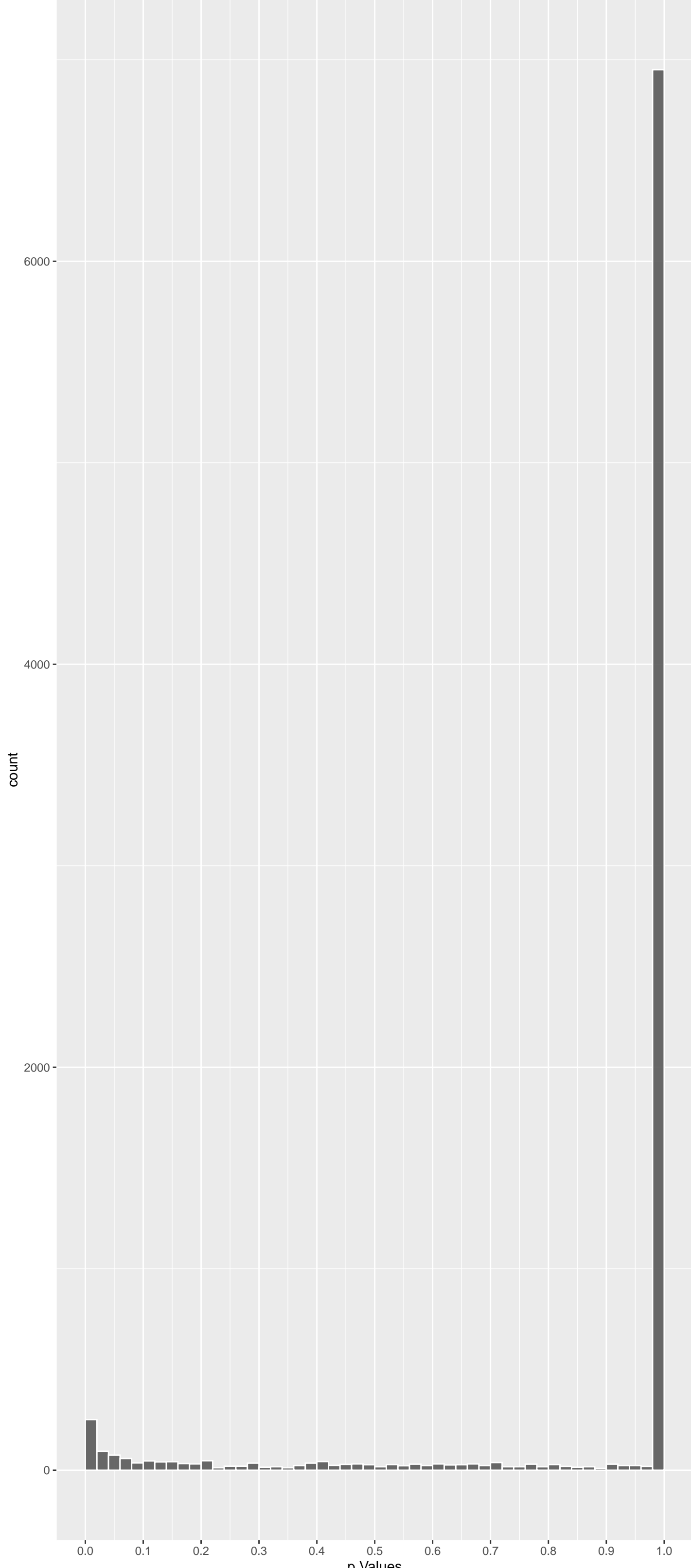
Positive Rho Non-permuted



Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
ZFYVE9	6.753935	8.633311e-11	2.793e-07	9.033e-04
SRCAP	5.771540	4.713030e-08	4.918e-05	4.679e-02
SCARF1	5.282567	7.643190e-07	3.627e-04	1.487e-01
DAXX	5.269947	8.187774e-07	3.627e-04	1.487e-01
PLA2R1	5.206789	1.152816e-06	4.237e-04	1.511e-01
PTPRB	5.198360	1.206327e-06	4.298e-04	1.511e-01
CATSPERB	5.170543	1.400488e-06	4.622e-04	1.526e-01
ACIN1	5.104601	1.988958e-06	6.069e-04	1.681e-01
LRPPRC	5.089314	2.156170e-06	6.132e-04	1.681e-01
CATSPERE	5.082316	2.237161e-06	6.132e-04	1.681e-01

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
PLEC	-7.520817	3.266093e-13	5.282e-09	8.543e-05
CAPN8	-7.183466	4.077956e-12	3.298e-08	2.667e-04
PKD1L1	-7.001313	1.521446e-11	8.202e-08	4.422e-04
TRANK1	-6.810289	5.844172e-11	2.363e-07	9.033e-04
PER2	-6.500839	4.792392e-10	1.292e-06	3.482e-03
CAMSAP1	-6.345555	1.329749e-09	3.072e-06	7.098e-03
DNAH9	-6.224521	2.898170e-09	5.859e-06	1.184e-02
C7orf57	-6.173059	4.018862e-09	7.222e-06	1.298e-02
OFD1	-6.092896	6.653163e-09	1.076e-05	1.740e-02
SLC17A4	-5.968967	1.432562e-08	2.106e-05	2.939e-02

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Left ventricular noncompaction cardiomyo	-0.26601716	28	1.112e-06	6.826e-03	PLEC:1 DSP:13 MYH7B:153 MUL1:247 TNNT2:543 PLEKHM2:1049
Mitochondrial Diseases	0.07592552	346	1.391e-06	6.826e-03	LRPPRC:10 GTGLC3:11 TMEM126B:18 TMEM70:30 NDUFS5:33 NDUFB4:74
Adult Medulloblastoma	0.14795950	58	9.843e-05	1.032e-01	DNMT1:184 BRD4:368 L3MBTL3:386 KDM4B:437 ERBB2:795 KDM4B:437 NDLK5:42
Fibrosarcoma	0.07386566	259	4.575e-05	1.032e-01	ANGPT4:25 CASP8:126 EGF:143 LRIF1:145 SLC6A1:161 UCN:220
Increased CSF lactate	0.15442003	53	1.018e-04	1.032e-01	LRPPRC:10 TMEM126B:18 NDUFA12:202 AIFM1:282 TIMMDC1:328 NDUFAF1:410
Junctional split	-0.46371259	6	8.366e-05	1.032e-01	PLEC:1 ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995
Medulloblastoma	0.17622685	41	9.519e-05	1.032e-01	DNMT1:184 BRD4:368 L3MBTL3:386 KDM4B:437 ERBB2:795 PTCB2:956
Melanotic neuroblastoma	0.17622685	41	9.519e-05	1.032e-01	DNMT1:184 BRD4:368 L3MBTL3:386 KDM4B:437 ERBB2:795 PTCB2:956
Primary microcephaly	0.10932727	105	1.105e-04	1.032e-01	FANCM:116 ORC1:170 CKAP2L:179 CENPE:206 CEP135:223 TRMT10A:301
Substance-Related Disorders	-0.10816477	114	6.811e-05	1.032e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNPs:243 CFTR:374 SLC18A2:411
Substance Dependence	-0.09860697	128	1.157e-04	1.032e-01	NRCAM:48 CADPS2:99 PCDH15:110 HTR1B:174 ADH7:238 CSRNPs:243
Organic Mental Disorders, Substance-Indu	-0.10346026	107	2.227e-04	1.159e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNPs:243 CFTR:374 SLC45A2:422
Desmoplastic Medulloblastoma	0.15413075	48	2.224e-04	1.159e-01	DNMT1:184 BRD4:368 L3MBTL3:386 KDM4B:437 ERBB2:795 PTCB2:956
Epidermolysis bullosa inversa dystrophic	-0.43534572	6	2.216e-04	1.159e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMC1:903 LAMA3:1413 COL17A1:2995
NADH:Q(1) Oxidoreductase deficiency	0.21594760	25	1.866e-04	1.159e-01	TMEM126B:18 AIFM1:282 TIMMDC1:328 NDUFB10:401 NDUFAF1:410 NDUFB11:813
Parakeratosis	-0.27518653	15	2.245e-04	1.159e-01	DSP:13 CARD14:84 NLRP1:197 TNC:210 IL23A:663 RHBDT:1112
Plantar hyperkeratosis	-0.44505934	6	1.597e-04	1.159e-01	PLEC:1 ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995
Prescription Drug Abuse	-0.10346026	107	2.227e-04	1.159e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNPs:243 CFTR:374 SLC45A2:422
Substance abuse problem	-0.09291603	138	1.694e-04	1.159e-01	NRCAM:48 CADPS2:99 PCDH15:110 IL16:122 HTR1B:174 CSRNPs:243
Epidermolysis Bullosa Simplex	-0.22500876	21	3.585e-04	1.675e-01	PLEC:1 ITGB4:37 KRT80:50 KRT17:344 MMP9:451 DES:464
Joint hyperflexibility	0.10052284	106	3.566e-04	1.675e-01	SRCAP:2 ORC1:170 CENPE:206 SOS1:276 LMX1B:303 RAF1:619
Drug Dependence	-0.08061129	161	4.300e-04	1.758e-01	PER2:5 NRCAM:48 CADPS2:99 PCDH15:110 GRM3:113 HTR1B:174
Herlitz Disease	-0.45638109	5	4.089e-04	1.758e-01	ITGB4:37 LAMC2:340 LAMB3:424 ITGA6:1212 LAMA3:1413 NA
Specific learning disability	0.10876446	88	4.279e-04	1.758e-01	NSD1:15 CKAP2L:179 LTBP4:292 TWNK:294 JMJDC1:348 DGCGR:603
Anemia, Macrocytic	0.17408436	33	5.408e-04	2.036e-01	TET2:81 RPL26:478 SFXN:1068 RPL27:1139 GATA1:1161 TP53:1528
CONOTRUNCAL ANOMALY FACE SYNDROME	0.103690375	21	5.811e-04	2.036e-01	JMJDC1:348 GDF1:371 DGCGR:603 NKX2-6:714 SEC24C:1103 TBX1:1105
Drug habituation	-0.08856437	127	5.812e-04	2.036e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNPs:243 CFTR:374 SLC45A2:422
Persistent truncus arteriosus	0.21699669	21	5.778e-04	2.036e-01	JMJDC1:348 GDF1:371 NKX2-6:714 GJA5:818 SEC24C:1103 TBX1:1105
Congenital pyloric atresia	-0.44201687	5	6.192e-04	2.095e-01	PLEC:1 ITGB4:37 LAMC2:340 ITGA6:1212 COL17A1:2995 NA
EPIDERMOLYSIS BULLOSA, JUNCTIONAL, LOCAL	-0.43399892	5	7.676e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Adult junctional epidermolysis bullosa (-0.43399892	5	7.676e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Epidermolysis Bullosa Progressiva	-0.43399892	5	7.676e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Increased serum lactate	0.10080561	95	6.966e-04	2.117e-01	LRPPRC:10 TMEM70:30 NDUFA12:202 AIFM1:282 TWNK:294 POLG2:443
JEB-I	-0.43399892	5	7.676e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Oral mucosal blisters	-0.31105218	10	6.593e-04	2.117e-01	PLEC:1 DSP:13 ITGB4:37 LAMC2:340 LAMB3:424 ITGA6:1212
Palmar hyperhidrosis	-0.43399892	5	7.676e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Drug Use Disorders	-0.09243524	110	8.261e-04	2.191e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNPs:243 CFTR:374 SLC45A2:422
MITOCHONDRIAL COMPLEX I DEFICIENCY	0.18452191	27	9.073e-04	2.343e-01	TMEM126B:18 TMEMDC1:328 NDUFAF1:410 NDUFB11:813 NDUFS8:852 GDAP1:905
Shprintzen syndrome	0.16602109	33	9.694e-04	2.439e-01	JMJDC1:348 PRODH:435 DGCGR:603 CLDN5:612 CHRD:814 DGCRL:973
Abnormality of brain morphology	-0.11872182	64	1.031e-03	2.530e-01	MCPH1:215 ULK2:305 SACS:328 SLC18A2:411 GRIP1:423 SYNE1:456

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
FISCHER_DREAM_TARGETS	0.07526136	882	5.347e-14	3.237e-10	CEP192:17 KIF18A:27 RBL1:42 SMCHD1:43 ZNF518A:46 EHB1P1:80
JOHNSTONE_PARVB_TARGETS_3_DN	0.07841489	790	9.979e-14	3.237e-10	TFAM:13 QSER1:20 KIF18A:27 NDUFS5:33 RBL1:42 SMCHD1:43
DODD_NASOPHARYNGEAL_CARCINOMA_UP	-0.05739325	1463	4.375e-13	9.462e-10	PER2:5 CAMSAP1:6 DNAH9:7 C7orf57:8 EVPL:11 TGM1:12
DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.06125876	1244	6.797e-13	1.102e-09	LRPPRC:10 TFAM:13 CEP192:17 QSER1:20 KIF18A:27 TMEM70:30
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.08228366	598	8.095e-12	1.050e-08	LRPPRC:10 TFAM:13 KIF18A:27 ZNF644:37 RBL1:42 ADAM9:51
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.07863949	595	7.111e-11	7.689e-08	CEP192:17 QSER1:20 ZNF302:22 BPTF:26 KIF18A:27 RLF:29
WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.12548679	208	4.734e-10	4.388e-07	BDKRB1:58 SSTR4:76 FFAR2:85 GPR37L:189 HTR1B:174 P2RY4:194
PUJANA_BRCA1_PCC_NETWORK	0.04749485	1501	1.332e-09	1.080e-06	DAXX:4 TMEM131L:9 TFAM:13 RBL1:42 NR2C1:57 TCL1A:71
REACTOME_FORMATION_OF_THE_CORNIFIED_ENV	-0.19249212	78	4.244e-09	3.060e-06	EVPL:11 TGM1:12 DSP:13 KRT80:50 KRT20:51 KRT15:83
REACTOME KERATINIZATION	-0.18314672	85	5.435e-09	3.526e-06	EVPL:11 TGM1:12 DSP:13 KRT80:50 KRT20:51 KRT15:83
KINSEY_TARGETS_OF_EWSR1_FLI1_FUSION_UP	0.04928145	1201	1.296e-08	7.645e-06	KIF18A:27 TMEM70:30 LARPA:89 TPX2:98 TEAD2:106 TMPO:129
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.06972889	555	2.279e-08	1.232e-05	SLC7A14:141 JAG2:47 CAMK2B:64 PCNX2:158 DSG2:177 THBS4:214
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.15995050	101	2.849e-08	1.422e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	0.05120458	1026	3.935e-08	1.824e-05	DAXX:4 LRPPRC:10 MGA:14 ZNF302:22 RBL1:42 NR2C1:57
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO	-0.13865741	128	6.233e-08	2.594e-05	HELZ2:96 FAM217B:170 ARFGAP1:260 COL20A1:270 TOMM34:324 NPBWRR2:407
REACTOME_SIGNALING_BY_GPCR	-0.06342328	631	6.397e-08	2.594e-05	TACR2:17 GPR132:32 ARHGGEF11:42 BDKRB1:58 CAMK2B:64 SSTR4:76
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.07418927	452	7.247e-08	2.766e-05	ZFYVE9:1 LRPPRC:10 BPTF:26 UBR2:36 SMCHD1:43 EIF4G3:52
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.06147432	661	8.368e-08	3.016e-05	ETAA1:39 RBL1:42 TPX2:98 HASPIN:105 FANCM:116 WDR76:130
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.17077547	81	1.094e-07	3.735e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
REACTOME_NEURONAL_SYSTEM	-0.07854928	386	1.292e-07	4.190e-05	KCNV2:62 CAMK2B:64 KCNN3:183 KCNF1:195 PANX1:216 CACNA1E:235
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	0.06100706	637	1.742e-07	5.381e-05	QSER1:20 KIF18A:27 RLF:29 TPTE:31 ZNF644:37 MFN1:73
REACTOME_CLASS_A_1_RHODOPSIN LIKE_RECEPT	-0.08789174	295	2.217e-07	6.539e-05	TACR2:17 GPR132:32 BDKRB1:58 SSTR4:76 FFAR2:85 GPR37L:189
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.12282450	149	2.355e-07	6.545e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
BENPORATH_CYCLING_GENES	0.06175136	606	2.421e-07	6.545e-05	ZNF414:72 CSH2:68 TPX2:98 TMPO:129 CCNB1:141 LRIF1:145
REACTOME_CELL_CYCLES	0.06057985	622	2.906e-07	7.251e-05	DAXX:4 CEP192:17 KIF18A:27 CENPT:41 KRT15:83
REACTOME_COMPLEX_I_BIOGENESIS	0.21432722	48	2.808e-07	7.251e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 TIMMDC1:328
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	0.07191598	427	3.821e-07	9.183e-05	LRPPRC:10 QSER1:20 KIF18A:27 RBL1:42 AFP:79 TPX2:98
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.21264431	47	4.589e-07	1.066e-04	TMEM126B:18 TMEM70:30 NDUFS5:33 NDUFB4:74 DMAPC1:112 NDUFA12:202
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.09087926	260	4.801e-07	1.074e-04	TACR2:17 BDKRB1:58 SSTR4:76 GRM3:113 TAAR6:129 HTR1B:174
ZHANG_BREAST_CANCER_PROGENITORS_UP	0.07155700	415	6.269e-07	1.356e-04	CEP192:17 RBL1:42 SMCHD1:43 SYDE2:53 ADAMTS20:78 TMPO:129
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	0.05036052	827	1.042e-06	2.181e-04	ZFYVE9:1 TMEM131L:9 LRPPRC:10 ATP2B4:21 BPTF:26 RLF:29
SHEN_SMARCA2_TARGETS_UP	0.07021190	408	1.242e-06	2.519e-04	TMEM126B:18 ZNF302:22 UBR2:36 MAP4K3:91 ANKHD1:99 AGGF1:123
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.16113155	75	1.419e-06	2.743e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
WONG_MITOCHONDRIA_GENE_MODULE	0.09950710	198	1.438e-06	2.743e-04	LRPPRC:10 TFAM:13 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	0.03302400	1338	1.875e-06	3.476e-04	ZNF302:22 NIPSNAP1:69 CASP8:126 BPTF:134 PPP4R1:156 CTH:160
KIM_WT1_TARGETS_DN	0.06605548	432	2.728e-06	4.916e-04	ZNF302:22 KIF18A:27 TPTE:31 LARPA:89 MAP4K3:91 CENPC:127
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.21642022	38	3.917e-06	6.572e-04	IQCE:375 TMEM184A:376 BRAT1:512 MRNB2:552 MAD1L1:601 FBXL18:658
REACTOME_RESOLUTION_OF_SISTER_CHROMATID	0.12256632	119	3.950e-06	6.572e-04	KIF18A:27 CENPT:41 CENPC:127 CCNB1:141 SPDL1:149 CENPE:206
REACTOME_MUSCLE_CONTRACTION	-0.09712311	190	4.038e-06	6.572e-04	NEB:26 CACNA1G:54 CAMK2B:64 MYBP2C:71 RYR3:205 TNNT2:207
JAEGER_METASTASIS_DN	-0.09115185	216	4.052e-06	6.572e-04	PER2:5 EVPL:11 DSP:13 ITGB4:37 NRCAM:48 CLIC3:57

GO Biological_Process_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NADH Dehydrogenase Complex Assembly (GO:0000000)	0.22989712	48	3.654e-08	6.956e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 DMAPC1:112 NDUFC2:270 NDUFB5:358
Mitochondrial Respiratory Chain Complex	0.22989712	48	3.654e-08	6.956e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 DMAPC1:112 NDUFC2:270 NDUFB5:358
Mitochondrial Respiratory Chain Complex	0.18138349	77	3.873e-08	6.956e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 DMAPC1:112 NDUFC2:270 AIFM1:282
Intermediate Filament Organization (GO:0000000)	-0.21587292	50	1.312e-07	1.769e-04	DSP:13 KRT80:50 KRT20:51 KRT15:83 KRT78:135 KRT11:30
Muscle Contraction (GO:0006936)	-0.16039684	88	2.059e-07	2.219e-04	TACR2:17 MYH13:27 ARHGEF11:42 MYOM2:91 MYOF:196 RYR3:205
Oxidative Phosphorylation (GO:0006119)	0.19867736	55	3.528e-07	3.168e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Proton Motive Force-Driven Mitochondrial	0.21079171	47	5.838e-07	3.945e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Regulation Of DNA-templated Transcription	0.08097300	1648	5.857e-07	3.945e-04	SRCAP:2 DAXX:4 TFAM:13 NSD1:15 ATP2B4:21 BPTF:26
Chemical Synaptic Transmission (GO:00072)	-0.03940294	257	9.872e-07	5.910e-04	RIMBP2:53 GRM3:113 HTR1B:174 CACNA1E:235 GABRR1:255 GABRR3:322
Monocatalytic Cation Transmembrane Transport	-0.08537799	273	1.338e-06	7.209e-04	TRPM5:22 CACNA1G:54 KCNV2:62 TRPV6:134 KCNN3:183 KCNF1:195
Aerobic Respiration (GO:0009060)	0.18814482	54	1.762e-06	8.631e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Aerobic Electron Transport Chain (GO:001)	0.18656468	54	2.150e-06	9.652e-04	NDUFS5:33 NDUFB4:74 NDUFC2:270 NDUFB5:358 NDUFB10:401 NDUFAF1:410
Mitochondrial ATP Synthesis Coupled Elec	0.18391519	55	2.424e-06	1.005e-03	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Atrial Cardiac Muscle Cell Action Potent	-0.40435434	11	3.426e-06	1.319e-03	CACNB2:371 KCNQ1:549 KCNN2:643 SCN5A:1268 GJC1:1501 KCNE5:1549
Striated Muscle Contraction (GO:0006941)	-0.18412530	52	4.437e-06	1.594e-03	ARHGEF11:42 MYH7B:153 RYR3:205 TNNT2:207 MYH6:306 TNNT3:243
Proton Motive Force-Driven ATP Synthesis	0.18169535	51	7.270e-06	2.351e-03	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
tRNA Methylation (GO:0030488)	0.21592462	36	7.418e-06	2.351e-03	THADA:65 BCND13D:164 TRMT10A:301 KRT18B:349 TRMT61B:373 TRMT1L:477
Anterograde Trans-Synaptic Signaling (GO:0000000)	-0.09305266	183	1.500e-05	4.489e-03	GRM3:113 HTR1B:174 CACNA1E:235 GABRR1:255 GABRR3:322 GPR176:370
Regulation Of Transcription By RNA Polym	0.03230745	1714	1.650e-05	4.679e-03	SRCAP:2 NSD1:15 ATP2B4:21 BPTF:26 RBL1:42
Neuron Projection Morphogenesis (GO:00048)	-0.10705733	135	1.821e-05	4.907e-03	NRCAM:48 DIP2A:250 DTNBP1:264 DBNL330 TRIO:389 SLITRK1:488
Regulation Of Gene Expression (GO:001046)	0.04120891	950	2.325e-05	9.956e-03	SRCAP:2 DAXX:4 NSD1:15 ATP2B4:21 BPTF:26 RBL1:42
Regulation Of DNA Methylation-Dependent	0.32512842	14	2.535e-05	6.209e-03	TET1:159 SETDB2:252 TASOR:370 L3MBTL3:386 AT7IP7:2749 SAMD01:812
Mitochondrial Electron Transport, NADH T	0.21778975	31	2.844e-05	6.662e-03	NDUFS5:33 NDUFB4:74 NDUFC2:270 NDUFB5:358 NDUFB10:401 NDUFAF1:410