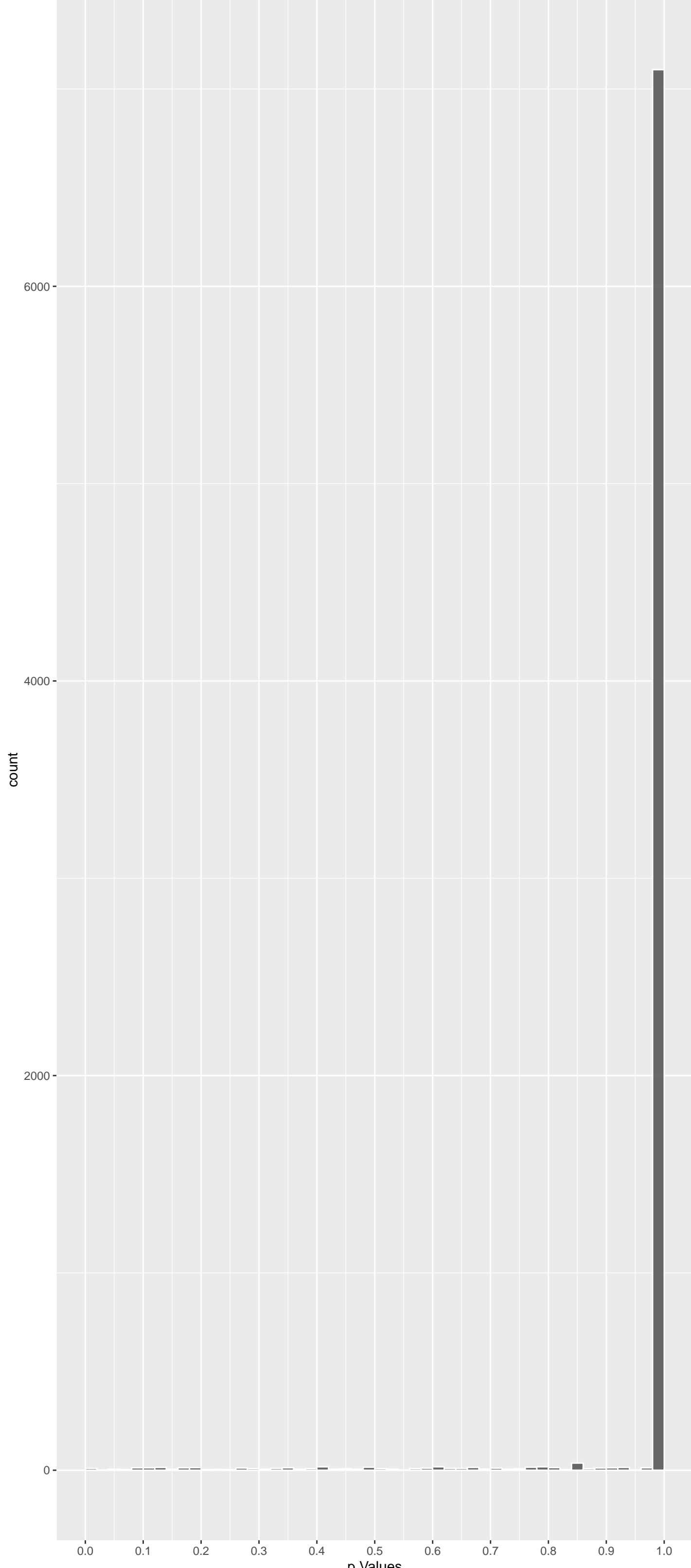


Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
CATSPERB	6.101508	6.304335e-09	8.668e-05	7.011e-01
CTNND1	-6.016147	1.071704e-08	8.668e-05	7.011e-01
PER2	-5.238162	9.731000e-07	3.863e-03	1.000e+00
ABCB4	-5.283561	7.601792e-07	3.863e-03	1.000e+00
OFD1	-5.166260	1.432950e-06	3.863e-03	1.000e+00
RIMS1	-5.166852	1.428419e-06	3.863e-03	1.000e+00
PTCD3	5.077052	2.300014e-06	3.973e-03	1.000e+00
MAP3K15	-5.093083	2.113730e-06	3.973e-03	1.000e+00
LGR6	-5.107603	1.957630e-06	3.973e-03	1.000e+00
S100A6	-5.064535	2.456390e-06	3.973e-03	1.000e+00
BDNF	-5.017294	3.144256e-06	4.624e-03	1.000e+00
TRPV6	-4.963328	4.157719e-06	5.605e-03	1.000e+00
MTBP	-4.896094	5.865609e-06	7.299e-03	1.000e+00
RASGEF1C	-4.831824	8.117282e-06	9.379e-03	1.000e+00
BTBD18	-4.813109	8.916018e-06	9.615e-03	1.000e+00
EXOC2	-4.783959	1.031252e-05	9.806e-03	1.000e+00
KLHDC2	-4.737793	1.296347e-05	9.806e-03	1.000e+00
MTCL1	-4.746136	1.244038e-05	9.806e-03	1.000e+00
TMEM63A	-4.748397	1.230214e-05	9.806e-03	1.000e+00
COBL	-4.732047	1.333602e-05	9.806e-03	1.000e+00
THADA	4.746728	1.240405e-05	9.806e-03	1.000e+00
TMEM116	4.758887	1.167982e-05	9.806e-03	1.000e+00
RGS9	-4.645805	2.032520e-05	1.370e-02	1.000e+00
ASIC3	-4.646878	2.021977e-05	1.370e-02	1.000e+00
PIP	4.606413	2.458050e-05	1.450e-02	1.000e+00

Positive Rho Non-permuted



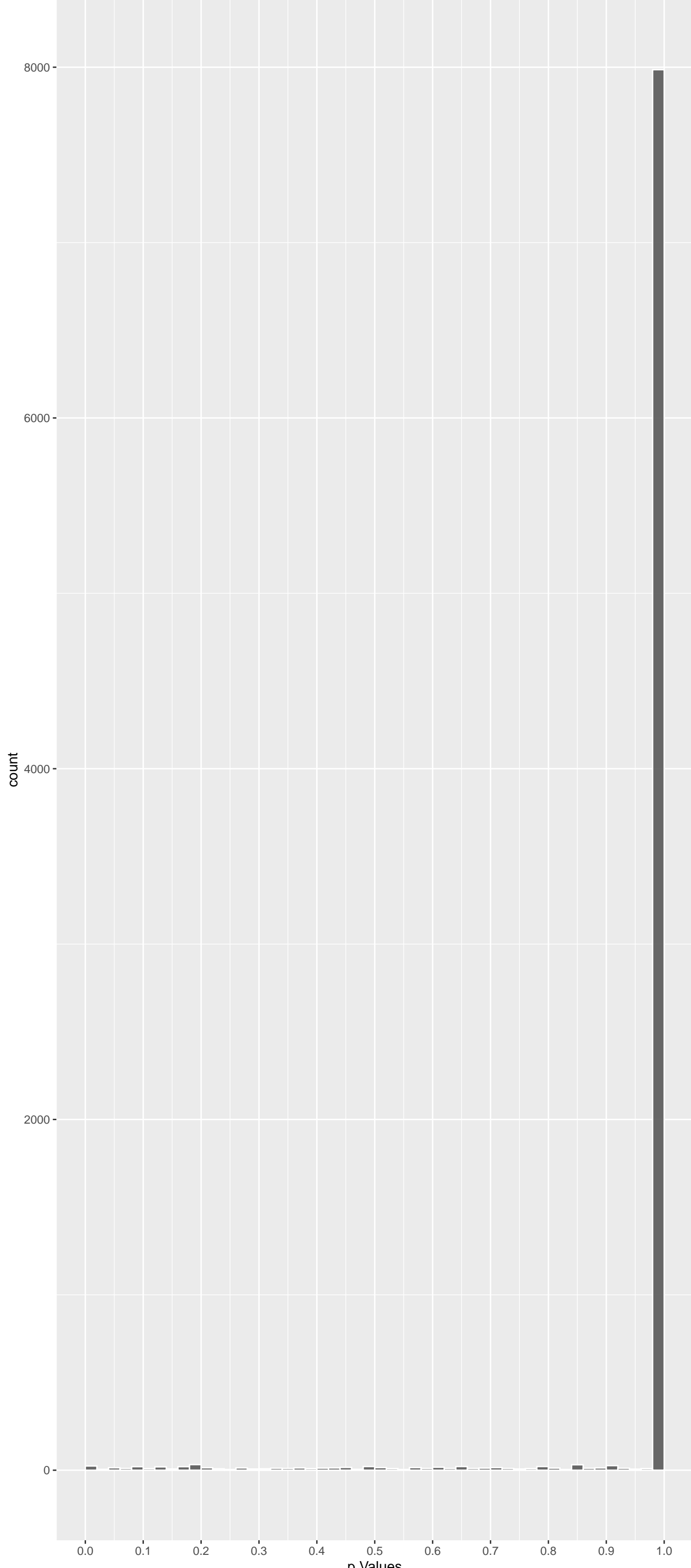
Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
CATSPERB	6.101508	6.304335e-09	8.668e-05	7.011e-01
PTCD3	5.077052	2.300014e-06	3.973e-03	1.000e+00
THADA	4.746728	1.240405e-05	9.806e-03	1.000e+00
TMEM116	4.758887	1.167982e-05	9.806e-03	1.000e+00
PIP	4.606413	2.458050e-05	1.450e-02	1.000e+00
HASPIN	4.614143	2.368329e-05	1.450e-02	1.000e+00
N4BP2L2	4.594788	2.599133e-05	1.450e-02	1.000e+00
BRWD1	4.583641	2.741691e-05	1.466e-02	1.000e+00
LRPPRC	4.548109	3.247799e-05	1.592e-02	1.000e+00
CATSPERE	4.448589	5.186185e-05	2.397e-02	1.000e+00

Top genes by Q-Value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
CATSPERB	6.10150821	6.304335e-09	8.668e-05	7.011e-01
CTNND1	-6.01614709	1.071704e-08	8.668e-05	7.011e-01
ARF5	0.91452919	1.000000e+00	1.000e+00	1.000e+00
M6PR	1.18759611	1.000000e+00	1.000e+00	1.000e+00
FKBP4	-2.60850614	5.456303e-02	8.921e-01	1.000e+00
CYP26B1	-1.28073712	1.000000e+00	1.000e+00	1.000e+00
NDUFAF7	1.85129277	3.847647e-01	1.000e+00	1.000e+00
FUCA2	-0.17088577	1.000000e+00	1.000e+00	1.000e+00
DBNDD1	0.43426539	1.000000e+00	1.000e+00	1.000e+00
HS3ST1	-1.05931264	1.000000e+00	1.000e+00	1.000e+00
SEMA3F	-0.10778990	1.000000e+00	1.000e+00	1.000e+00
CFTR	0.96695510	1.000000e+00	1.000e+00	1.000e+00
CYP51A1	-0.91834074	1.000000e+00	1.000e+00	1.000e+00
USP28	-1.86858734	3.700815e-01	1.000e+00	1.000e+00
SLC7A2	1.50026911	8.012682e-01	1.000e+00	1.000e+00
HSPB6	-0.98937526	1.000000e+00	1.000e+00	1.000e+00
PDK4	-1.47676252	8.384358e-01	1.000e+00	1.000e+00
USH1C	0.13256474	1.000000e+00	1.000e+00	1.000e+00
RALA	-0.31483366	1.000000e+00	1.000e+00	1.000e+00
BAIAP2L1	-3.46544410	3.176139e-03	2.057e-01	1.000e+00
CACNG3	0.02038346	1.000000e+00	1.000e+00	1.000e+00
TMEM132A	-3.92968797	5.103370e-04	9.354e-02	1.000e+00
DVL2	3.02156905	1.508810e-02	4.852e-01	1.000e+00
RPAP3	2.10402227	2.122590e-01	1.000e+00	1.000e+00
HOXA11	-0.93926661	1.000000e+00	1.000e+00	1.000e+00

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
CTNND1	-6.016147	1.071704e-08	8.668e-05	7.011e-01
PER2	-5.238162	9.731000e-07	3.863e-03	1.000e+00
ABCB4	-5.283561	7.601792e-07	3.863e-03	1.000e+00
OFD1	-5.166260	1.432950e-06	3.863e-03	1.000e+00
RIMS1	-5.166852	1.428419e-06	3.863e-03	1.000e+00
MAP3K15	-5.093083	2.113730e-06	3.973e-03	1.000e+00
LGR6	-5.107603	1.957630e-06	3.973e-03	1.000e+00
S100A6	-5.064535	2.456390e-06	3.973e-03	1.000e+00
BDNF	-5.017294	3.144256e-06	4.624e-03	1.000e+00
TRPV6	-4.963328	4.157719e-06	5.605e-03	1.000e+00

## DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Increased CSF lactate	0.158782803	53	6.443e-05	6.321e-01	LRPPRC:9 TMEM126B:49 COX20:117 TIMMDC1:134 SC01:146 TRMT10C:379
46, XX Testicular Disorders of Sex Devel	-0.119156347	7	2.749e-01	9.862e-01	SOX9:346 SOX3:574 NR5A1:8402 RSP01:8402 FOXL2:8402 NR0B1:8402
46, XY Disorders of Sex Development	-0.083647749	15	2.603e-01	9.862e-01	SOX9:346 WTI:520 CYB5A:866 TLX1:879 ZFP362:1744 CYP11A1:1792
46, XY female	-0.019573910	16	7.864e-01	9.862e-01	SOX9:346 DMRT1:571 STAR:1399 UBLA4:2748 NR0B1:8402 HSD17B3:8402
46, XY partial gonadal dysgenesis	-0.118475652	10	1.945e-01	9.862e-01	SOX9:346 WTI:520 ZFP362:1744 NR5A1:8402 NR0B1:8402 MAP3K1:8402
5,10-Methylerythroidtetrahydrofolate reductase	0.034439797	18	6.130e-01	9.862e-01	AKAP9:96 XRCC4:1520 MTHFR:2057 CASP9:2072 GPX3:7775 SERPINE1:7775
Abortion, Habitual	-0.016607939	4	9.068e-01	9.862e-01	VEGFA:196 F2:8402 F5:8402 MTHFR:14120 NA NA
Abortion, Tubal	0.044630694	93	1.374e-01	9.862e-01	SPAG5:67 ECM2:147 ARNT:244 LR2:252 FN1:860 CD84:879
Achondrogenesis, type I (disorder)	0.186325646	5	1.490e-01	9.862e-01	DCN:823 SLC26A2:1436 SLC26A3:7775 SLC26A5:7775 SLC26A4:7775 NA
Acidosis, lactic	0.047703268	151	4.352e-02	9.862e-01	LRPPRC:9 TMEM126B:49 POLG:66 COX20:117 TIMMDC1:134 SC01:146
ACROMESOMELIC DYSPLASIA, MAROTEAUX TYPE	0.021937631	4	8.792e-01	9.862e-01	IGF1:7775 NPFC:7775 NRP2:7775 GDF5:7775 NA
ACTH Syndrome, Ectopic	-0.132587835	5	3.045e-01	9.862e-01	GHSR:1879 AVPR1B:2437 CRH:8402 NR3C1:8402 PAK3:8402 NA
Acute Myeloid Leukemia, M1	0.012438814	105	6.601e-01	9.862e-01	CSF1R:114 ASXL2:200 NF1:255 KMT2A:307 KIT:614 MN1:694
Acute myeloid leukemia, minimal differen	0.058537749	19	3.771e-01	9.862e-01	KMT2A:307 FLT3:744 NCR1:869 DNMT3A:918 ZMYND11:1909 RUNX1:7775
Adenocarcinoma of lung, stage I	0.015389780	18	8.212e-01	9.862e-01	ADAM12:831 ACTN4:996 MET:7775 H0XA9:7775 MYC:7775 EIF4EBP1:7775
Adenocarcinoma of lung, stage IV	0.026144550	18	7.010e-01	9.862e-01	ERBB2:604 BRAF:858 MET:7775 TP53:7775 KRAS:7775 RET:7775
Adenocarcinoma, Basal Cell	-0.012082927	103	6.722e-01	9.862e-01	NR112:142 VEGFA:196 HRH4:199 CA2:220 DAPK1:363 CDKN1C:707
Adenocarcinoma, Clear Cell	0.003775512	95	8.989e-01	9.862e-01	ATF1:239 HAGH:266 BRCA2:365 ERBB2:604 NEU3:676 TTFAM:748
Adenocarcinoma, Endometrioid	0.014647367	54	7.098e-01	9.862e-01	ABCC1:410 NDC80:483 CCL22:581 ERBB2:604 BRAF:858 SHBG:882
Adenocarcinoma, intestinal type	0.013162989	12	8.746e-01	9.862e-01	BRAF:858 CDX2:1499 TP53:7775 KRAS:7775 EGFR:7775 CDKN2A:7775
Adenocarcinoma, metastatic	0.048615950	12	5.598e-01	9.862e-01	ERBB2:604 HSPA5:1913 MYC:7775 KRAS:7775 EGF:7775 ESR2:7775
Adenocarcinoma, Oxyphilic	-0.010736755	105	7.043e-01	9.862e-01	NR112:142 VEGFA:196 HRH4:199 CA2:220 DAPK1:363 CDKN1C:707
Adenocarcinoma, Scirrhous	0.082933467	6	4.817e-01	9.862e-01	FGFR2:1475 MMP15:1586 MET:7775 MMP14:7775 FUT1:7775 TIMP3:14366
Adenocarcinoma, Tubular	-0.009513873	108	7.331e-01	9.862e-01	NR112:142 VEGFA:196 HRH4:199 CA2:220 DAPK1:363 CDKN1C:707
Adenoma, Basal Cell	-0.035625897	27	5.218e-01	9.862e-01	TXNRD1:1037 KCNJL5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Microcystic	-0.023779433	34	6.315e-01	9.862e-01	TXNRD1:1037 KCNJL5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Monomorphic	-0.035625897	27	5.218e-01	9.862e-01	TXNRD1:1037 KCNJL5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Tubercular	-0.033571262	28	5.388e-01	9.862e-01	TXNRD1:1037 KCNJL5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Villous	0.07958614	14	3.009e-01	9.862e-01	BRAF:858 MLH1:1591 TP53:7775 KRAS:7775 APC:7775 TP63:7775
Adrenal hyperplasia, bilateral	-0.119390282	3	4.738e-01	9.862e-01	KCNJ5:1560 PRKAR1A:8402 REN1:8402 NA NA NA
Adrenoleukodystrophy, neonatal	-0.089567844	15	2.298e-01	9.862e-01	PEX11B:1447 PEX3:1472 PEX10:1728 HDN17B4:1990 PEX19:8402 PEX1:8402
Affective Disorders, Psychotic	0.073070835	12	3.750e-01	9.862e-01	FKBP5:226 DISC1:1616 BCL2L1:0:1661 MTHFR:2057 IL1RN:7775 HP:7775
Agammaglobulinemia, non-Bruton type	0.018260725	7	8.671e-01	9.862e-01	LRRCA8A:1863 CD79B:7775 CD79A:7775 PIK3R1:7775 BLNK:7775 TCF3:7775
Aganglionosis, Colonic	-0.047277902	19	4.756e-01	9.862e-01	RASGEF1A:762 F2R:1498 FH:1804 EDN3:2622 TP53:8402 RET:8402
Aganglionosis, Rectosigmoid Colon	0.021625126	8	8.323e-01	9.862e-01	NRG1:2045 RET:7775 CAVIN2:7775 UTP25:7775 ECE1:7775 EDNRB:7775
Albinism, Ocular	-0.014701349	27	7.998e-01	9.862e-01	GPR143:108 PMPCA:47 XG:785 SLC45A2:1469 BLOC156:1986 TYRP1:8402
Albinism, Oculocutaneous	0.035190354	30	5.048e-01	9.862e-01	BRCA2:365 KIT:614 BRAF:858 CSF3:7775 NRAS:7775 PIK3CA:7775
ALBINOIDISM, OCULOCUTANEOUS, AUTOSOMAL D	0.025659588	25	6.570e-01	9.862e-01	HPS3:32 DBH:140 MLANA:886 SOX10:7775 TYRP1:7775 ZEB2:7775
Alcoholic Intoxication, Chronic	-0.019586364	376	1.949e-01	9.862e-01	BDNF:9 ADH7:49 SLC6A6:68 IGSF2:101 DUSP8:186 NPY2R:266
Alopecia, Male Pattern	-0.009540626	27	8.638e-01	9.862e-01	CD34:307 VDR:378 ZDHHC13:536 PARP1:905 ZFP362:1744 GGCT:2593

## EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.14280990	101	7.208e-07	3.506e-03	LRPPRC:9 TMEM126B:49 ATP5PD:69 UQCRRH:87 NDUFB7:97 COX20:117
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.15412451	81	1.646e-06	3.506e-03	LRPPRC:9 TMEM126B:49 UQCRRH:87 NDUFB7:97 COX20:117 TIMMDC1:134
REACTOME_COMPLEX_I_BIOGENESIS	0.19771154	48	2.161e-06	3.506e-03	TMEM126B:49 NDUFB7:97 TIMMDC1:134 NDUFB10:196 NDUFB4:411 NDUFA9:541
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.20402989	47	1.311e-06	3.506e-03	TMEM126B:49 DMAC1:64 NDUFB7:97 TIMMDC1:134 TMEM70:190 NDUFB10:196
REACTOME_TRANSPORT_OF_SMALL_MOLECULES	-0.05023780	669	1.059e-05	1.374e-02	ABCB4:2 TRPV6:10 ASIC3:19 ANO6:37 SLC43A1:51 ATP6VD02:52
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.10323753	149	1.395e-05	1.509e-02	LRPPRC:9 TMEM126B:49 ATP5PD:69 UQCRRH:87 NDUFB7:97 COX20:117
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRAN	-0.08072167	237	1.935e-05	1.794e-02	SLC43A1:51 SLC02A1:56 SLC6A20:59 SLC6A6:68 SLC27A4:72 SLC25A18:124
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.19603025	38	2.904e-05	2.204e-02	FBXL18:31 TNRC18:107 BRAT1:116 SNX8:122 SUN1:176 TMEM184A:224
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.13930894	75	3.057e-05	2.204e-02	ATP5PD:69 UQCRRH:87 NDUFB7:97 SC01:146 NDUFB10:196 ATP5PO:316
FISCHER_DREAM_TARGETS	0.04118708	882	3.837e-05	2.489e-02	HASPIN:5 AHCTF1:15 NEIL3:42 SPAG5:67 CEP295:76 LCORL1:113
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.08684125	179	6.287e-05	3.399e-02	SPAG5:67 CKAP2L:127 MELK:175 BLM:213 SUN7:224 C21orf62:241
WP_OXIDATIVE_PHOSPHORYLATION	0.17061710	46	6.264e-05	3.399e-02	ATP5PD:69 NDUFB7:97 NDUFB10:196 ATP5PB:335 NDUFB4:411
REACTOME_NEURONAL_SYSTEM	-0.05872053	386	7.908e-05	3.745e-02	RIMS1:4 PPIFA4:62 KCNC2:91 EPB41L3:127 PRKAR1B:137 KCNH4:146
RODRIGUES_THYROID_CARCIINOMA_POORLY_DIFFE	0.04744423	598	8.080e-05	3.745e-02	BRWD1:8 LRPPRC:9 HPS3:32 GTBPB10:74 ENO1:115 CIT:129
REACTOME_SPERM_MOTILITY_AND_TAXES	0.39177148	8	1.243e-04	5.377e-02	CATSPERG:1 CATSPERG:7 CATSPER3:704 CATSPER4:1113 CATSPER2:1296 HVCN1:1539
DODD_NASOPHARYNGEAL_CARCIINOMA_DN	0.03253679	1244	1.360e-04	5.513e-02	PTCD3:2 LRPPRC:9 AHCTF1:15 NEIL3:42 SPAG5:67 GTBPB10:74
BENPORATH_ES_WITH_H3K27ME3	-0.03487528	983	2.446e-04	9.052e-02	RASGEF1C:12 RGS9:20 SLC27A2:55 SLC02A1:56 SLC6A20:59 LYSMD2:73
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.06609280	260	2.511e-04	9.052e-02	HRH2:118 P2RY4:121 PTH2R:166 HRH4:199 HRH1:207 NPY2R:266
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	0.10405672	100	3.268e-04	1.116e-01	MMP25:58 HS3ST6:181 NDUFB10:196 PRSS27:240 HAGH:266 NWP:391
MEBARKI_HCC_PROGENITOR_FDZBCRD_UP	0.04518910	501	5.654e-04	1.834e-01	HASPIN:5 PLEKHG4:31 SHG3L3:119 CDC7:124 CKAP2L:127 CIT:129
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.04248905	555	6.595e-04	1.945e-01	RASGEF1C:12 SLC27A2:55 SLC6A20:59 HRH2:118 SPRN:132 PSD:197
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS	-0.09795797	102	6.356e-04	1.945e-01	SLC43A1:51 SLC6A20:59 SLC6A6:68 SLC25A18:124 SLC6A14:129 SLC4A1:381
NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	-0.20822667	22	7.227e-04	1.993e-01	LPCAT1:117 LRRCA14B:482 TPPP:1208 R5A:1226 SLC9A3:1293 SLC12A7:1671
SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN	-0.05086104	376	7.371e-04	1.993e-01	PER2:3 ENPP3:71 LYSMD2:73 GPRASP1:99 MMP16:144 AHR:169
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.04629055	452	7.796e-04	2.023e-01	LRPPRC:9 FAT11:17 GOLGA4:26 USP13:27 ZFYVE9:52 FILP1L:65
MOOTHA_VOXPHOS	0.11282403	72	9.374e-04	2.339e-01	ATP5PD:69 UQCRRH:87 NDUFB7:97 ATP5PO:316 ATP5PB:335 NDUFB4:411
REACTOME_CELL_CYCLE	0.03865575	622	1.064e-03	2.556e-01	AHCTF1:15 MLH3:61 CENTP:70 AKAP9:96 CDC7:124 PSMB1:1128
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.03723610	661	1.170e-03	2.711e-01	HASPIN:5 AHCTF1:15 ANKFY1:25 NEIL3:42 SPAG5:67 ATP5PD:69
GRESHOCK_CANCER_COPY_NUMBER_UP	0.05308983	312	1.299e-03	2.907e-01	BIRC3:18 BLM:213 ATF1:239 ARNT:244 NF1:255 DDX6:267
KEGG_HUNTINGTONS_DISEASE	0.07582335	149	1.418e-03	3.067e-01	DNAH2:38 ATP5PD:69 UQCRRH:87 NDUFB7:97 NDUFB10:196 ATP5PO:316
VILLANUEVA_LIVER_CANCER_KRT19_UP	0.07308321	158	1.544e-03	3.106e-01	CDC7:124 CKAP2L:127 CEP135:142 MELK:175 BLM:213 ARID3A:290
RODRIGUES_THYROID_CARCIINOMA_ANAPLASTIC_U	0.03703657	637	1.514e-03	3.106e-01	BRWD1:8 BIRC3:18 SYTL2:30 HPS3:32 GTBPB10:74 LCOLR1:113
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.03811858	595	1.580e-03	3.106e-01	N4BP2L2:7 ARMT1:14 AHCTF1:15 GOLGA4:26 CSPP1:44 NARS1:90
WP_PROXIMAL_TUBULE_TRANSPORT	-0.12831693	49	1.893e-03	3.611e-01	ATP6VD02:52 SLC6A20:59 CA2:220 SLC22A6:247 ATP6V1B1:382 SLC1A1:495
REACTOME_SLC_TRANSPORTER_DISORDERS	-0.09428769	90	2.004e-03	3.714e-01	SLC02A1:56 SLC6A20:59 SLC27A4:72 SLC6A14:129 NUP160:177 NUP210:273
REACTOME_TRANSPORT_OF_BILE_SALTS_AND_ORG	-0.08731370	82	2.330e-03	4.199e-01	SLC6A20:59 SLC6A6:68 SLC6A14:129 SLC30A10:133 SLC22A6:247 RHCG:260
REACTOME_PI3K_AKT_SIGNALING_IN_CANCER	0.08632113	102	2.611e-03	4.458e-01	CHUK:104 GAPB1:183 KL:263 RPS6BK2:332 FGFR1:373 MLST8:375
REACTOME_TRIGLYCERIDE_METABOLISM	-0.14519593	36	2.576e-03	4.458e-01	MOGAT3:259 LPIN2:373 MOGAT2:719 FABP5:934 ABHD5:195 DGAT2:1270
REACTOME_MITOCHONDRIAL_TRANSLATION	0.09058098	92	2.693e-03	4.479e-01	PTCD3:2 OXAL1:62 MRPS17:162 MRPL37:297 MRPS31:320 MTF12:460
MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27	-0.06149309	199	2.827e-03	4.586e-01	SLC30A10:133 PTGFRN:147 BAIAP2L1:162 PCDH8:366 GPR88:400 MAPK8IP2:402

## GO\_Biological\_Process\_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NADH Dehydrogenase Complex Assembly (GO:0000000)	0.21641653	48	2.173e-07	3.902e-04	TMEM126B:49 OXA1L:62 DMAC1:64 NDUFB7:97 TIMM21:153 NDUFB10:196
Mitochondrial Respiratory Chain Complex	0.21641653	48	2.173e-07	3.902e-04	TMEM126B:49 OXA1L:62 DMAC1:64 NDUFB7:97 TIMM21:153 NDUFB10:196
Mitochondrial Respiratory Chain Complex	0.17669887	77	8.578e-08	3.902e-04	TMEM126B:49 OXA1L:62 DMAC1:64 NDUFB7:97 COX20:117 SC01:146
Inorganic Cation Transmembrane Transport	-0.08580694	277	9.960e-07	1.342e-03	TRPV6:10 ASIC3:19 ANO6:37 SLC6A20:59 SLC6A6:68 KCNC2:91
Monoatomic Cation Transmembrane Transport	-0.08226283	273	3.207e-06	3.455e-03	TRPV6:10 ASIC3:19 ANO6:37 SLC6A20:59 SLC6A6:68 KCNC2:91
Intermediate Filament Organization (GO:0000000)	-0.18666349	50	5.041e-06	4.527e-03	KRT32:24 KRT31:65 KRT82:85 KRT21:198 KRT26:210 KRT40:261
Oxidative Phosphorylation (GO:0006119)	0.15607240	55	6.316e-05	4.254e-02	ATP5PD:69 UQCRRH:87 NDUFB7:97 NDUFB10:196 ATP5PO:316 ATP5PB:335
Proton Motive Force-Driven Mitochondrial	0.16801750	47	6.167e-05	4.254e-02	ATP5PD:69 NDUFB7:97 NDUFB10:196 ATP5PO:316 ATP5PB:335 NDUFB4:411
Proton Motive Force-Driven ATP Synthesis	0.14977963	51	2.175e-04	1.302e-01	ATP5PD:69 NDUFB7:97 NDUFB10:196 ATP5PO:316 ATP5PB:335 NDUFB4:411
Very Long-Chain Fatty Acid Catabolic Pro	-0.42998285	6	2.648e-04	1.427e-01	SLC27A2:55 SLC27A4:72 ACOX1:971 ABCD4:1866 ABCD3:1912 ABCD2:2030
Mitochondrial Electron Transport, NADH T	0.18649945	31	3.275e-04	1.604e-01	NDUFB7:97 NDUFB10:196 NDUFB4:411 NDUFA9:541 NDUFC2:586 NDUFB6:722
Mitochondrial RNA Metabolic Process (GO:0000000)	0.23356879	19	4.251e-04	1.908e-01	FASTKD5:80 POLRMT:169 FASTKD1:186 TWNK:199 PNPT1:343 MTERF1:417
Aerobic Electron Transport Chain (GO:0000000)	0.13255593	54	7.600e-04	2.711e-01	UQCRRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 UQCRRF1:476 NDUFA9:541
Aerobic Respiration (GO:0009060)	0.13329596	54	7.098e-04	2.711e-01	OXA1L:62 UQCRRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 NDUFA9:541
Interstrand Cross-Link Repair (GO:003629)	0.16490447	35	7.389e-04	2.711e-01	NEIL3:42 RNF168:148 DCLRE1C:305 XPA:352 FANCI:356 FANCE:492
Mitochondrial ATP Synthesis Coupled Elec	0.13072895	55	8.051e-04	2.711e-01	UQCRRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 UQCRRF1:476 NDUFA9:541
Mitochondrial Gene Expression (GO:014005)	0.09509888	100	1.034e-03	3.277e-01	PTCD3:2 FASTKD5:80 MRPS17:162 POLRMT:169 FASTKD1:186 TWNK:199
Cellular Respiration (GO:0045333)	-0.11161116	71	1.215e-03	3.636e-01	OXA1L:62 UQCRRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 UQCRRF1:476
Potassium Ion Transmembrane Transport (G	-0.08904021	132	1.353e-03	3.838e-01	KCNC2:91 KCNH4:146 KCNT2:184 KCNE5:203 KCNQ5:231 NALCN:552
Potassium Ion Transport (GO:0006813)	-0.08340288	120	1.634e-03	4.403e-01	KCNC2:91 KCNH4:146 KCNQ5:231 NALCN:552 KCNV1:560 KCNA4:573
Learning (GO:0007612)	-0.14142664	41	1.738e-03	4.458e-01	SHANK1:368 LGMN:372 TH:375 GPR84:40 MAPKBP2:402 SHANK3:485
Chloride Transport (GO:0006821)	-0.10372887	73	2.026e-05	5.401e-01	ANO6:37 ANO3:300 GABRB3:333 SLC4A1:381 ANO4:450 SLC1A1:495
Cilium-Dependent Cell Motility (GO:00602)	-0.20721269	17	1.102e-03	6.287e-01	DNAH2:38 DNAH1:743 DNAH3:1462 TEK1:1719 RSPH9:1544 RFXB3:1943
Fatty Acid Transport (GO:0015908)	-0.14033726	37	3.151e-03	6.287e-01	SDO2A1:56 SLC27A4:72 SLC22A6:247 SLC22A8:59 CD36:596 FAFS:934
Monoatomic Ion Transport (GO:0006811)	-0.04826366	104	0.303e-03	6.287e-01	ANO6:37 SLC25A18:124 PIEZO2:304 SLC1A1:381 SLC1A1:495 SLC1A7:1566
Positive Regulation Of Long-Term Synapti	-0.24880986	12	2.843e-03	6.287e-01	LGMN:372 SHANK3:485 INS:501 SLC18A3:598 ZDHHC42:652 SHISA7:567
Positive Regulation Of Metabolic Process	-0.08640351	101	2.737e-03	6.287e-01	PER2:3 PTH2R:166 EHMT1:168 VEGFA:196 GRB10:297 CNOT3:478
Acylglycerol Biosynthetic Process (GO:0000000)	-0.17942042	21	4.431e-03	7.618e-01	MOGAT3:259 PLAT2G4:306 LIPIN2:373 PNPLA3:379 MOGAT2:719 DGAT2:1270
Amino-Acid Betaine Transport (GO:0015838)	-0.13146114	7	4.322e-03	7.618e-01	SLC6A20:59 SLC7A6:62 SLC22A4:131 SLC25A29:1241 SLC22A5:1573 SLC22A16:8402
Axone Assembly (GO:0035082)	0.13255586	30	3.135e-03	7.618e-01	CDC40:249 SPAG1:272 SPAG17:665 GAPP1:909 RSPH9:1544 RSP1:1568
Long-Chain Fatty Acid Transport (GO:00015)	-0.17105481	23	4.524e-03	7.618e-01	SLC27A2:55 SLC27A4:72 SLC65:596 FAFS:934 SLC27A1:1123 ABCD4:1866
Positive Regulation Of Cold-Induced Ther	-0.08574343	93	4.321e-03	7.618e-01	PER2:3 PTH2R:166 EHMT1:168 VEGFA:196 GRB10:297 CNOT3:478
Cell Surface Pattern Recognition Recepto	-0.40224916	4	3.086e-03	7.748e-01	COLEC10:1193 FFAR2:1247 COLEC11:1813 EHHADH:2145 NA:34
Epithelial Cell Differentiation (GO:0030)	-0.07589654	113	5.400e-03	7.748e-01	KRT32:24 KRT31:65 VEGFA:196 KRT21:198 KRT26:210 RHCV:260
Mitochondrial RNA Processing (GO:0000963)	0.26931602	9	1.147e-03	7.748e-01	FASTKD5:80 FASTKD1:186 PNPT1:343 TRMT10C:379 FASTKD3:1587 SVP3L1:7775
Protein Localization To Centrosome (GO:0000000)	0.19465724	7	2.456e-03	7.748e-01	SPAG6:67 GOLGB1:453 CEP250:708 MMB1:851 CEP131:1087 CC2CD3:1448
Skeletal System Morphogenesis (GO:004870)	0.13101726	18	5.161e-03	7.748e-01	FGFR1:373 HOXD4:588 SFP22:65 LAMA5:889 DMSAL1:984 LRPL:1861
Triglyceride Biosynthetic Process (GO:0000000)	-0.19664924	17	5.005e-03	7.748e-01	MOGAT3:259 PLK1:373 PNPLA3:379 MOGAT1:729 DGAT2:1270 GPM:1398
Memory (GO:0007613)	-0.10794347	53	6.599e-03	9.117e-01	BDNF:9 KRN2:349 SHANK1:368 LGMN:372 TH:375 SHANK3:485
Regulation Of Nuclear Division (GO:000517)	0.18874879	17	7.061e-03	9.492e-01	FBXO43:143 KIF20B:615 CDC25C:276 PDXP:1200 PRMT5:1224 FBXO5:2024