

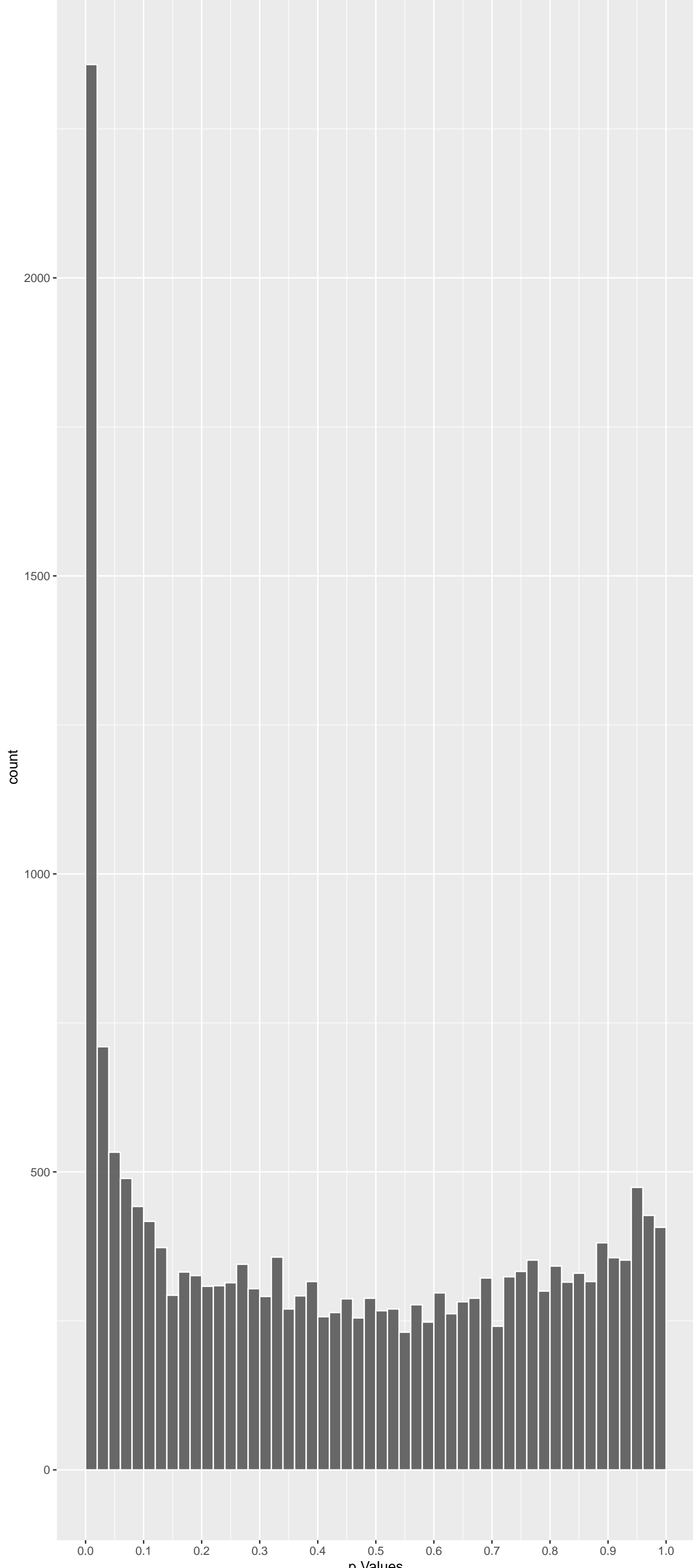
Top genes by P-value non-permulated

Gene	Rho	N	P	p.adj	qValueNoperm
CCPG1	0.3169889	206	7.556e-16	1.417e-11	2.658e-07
MRGPRE	0.4673325	125	2.690e-14	2.266e-10	1.345e-06
PER2	0.2583903	223	3.624e-14	2.266e-10	1.345e-06
SHANK2	0.2669847	212	6.116e-14	2.868e-10	1.345e-06
AFDN	0.2488617	212	4.281e-13	1.439e-09	4.498e-06
SORL1	0.2435694	216	4.603e-13	1.439e-09	4.498e-06
USP43	0.2397915	216	6.961e-13	1.865e-09	4.998e-06
TET1	0.2295643	221	1.189e-12	2.712e-09	5.510e-06
TMEM126B	0.2580885	196	1.301e-12	2.712e-09	5.510e-06
TET2	0.2230513	225	1.566e-12	2.938e-09	5.510e-06
TRANK1	0.2332838	205	5.254e-12	8.958e-09	1.527e-05
PKP1	0.2561538	181	1.119e-11	1.645e-08	2.373e-05
SLC17A4	0.2280774	203	1.140e-11	1.645e-08	2.373e-05
MKI67	0.2362785	191	2.081e-11	2.724e-08	3.285e-05
UBAP2	0.2133489	211	2.179e-11	2.724e-08	3.285e-05
MYH2	0.2219977	202	2.390e-11	2.802e-08	3.285e-05
FAM13B	0.2329429	189	3.650e-11	4.027e-08	4.220e-05
GPR37L1	0.2584033	170	3.887e-11	4.050e-08	4.220e-05
TRPM5	0.2199967	198	4.602e-11	4.543e-08	4.308e-05
FAAP100	0.2182168	199	4.925e-11	4.618e-08	4.308e-05
PLEC	0.2020010	214	5.401e-11	4.824e-08	4.308e-05
SPATA2L	0.2356991	180	8.282e-11	7.060e-08	5.835e-05
SMIM26	0.2680063	158	8.775e-11	7.156e-08	5.835e-05
ADAMTS20	0.1877531	222	1.183e-10	8.873e-08	6.605e-05
SRFBP1	0.2036752	205	1.149e-10	8.873e-08	6.605e-05

Top genes by Q-Value non-permulated

Gene	Rho	N	P	p.adj	qValueNoperm
CCPG1	0.3169889	206	7.556e-16	1.417e-11	2.658e-07
MRGPRE	0.4673325	125	2.690e-14	2.266e-10	1.345e-06
PER2	0.2583903	223	3.624e-14	2.266e-10	1.345e-06
SHANK2	0.2669847	212	6.116e-14	2.868e-10	1.345e-06
AFDN	0.2488617	212	4.281e-13	1.439e-09	4.498e-06
SORL1	0.2435694	216	4.603e-13	1.439e-09	4.498e-06
USP43	0.2397915	216	6.961e-13	1.865e-09	4.998e-06
TET1	0.2295643	221	1.189e-12	2.712e-09	5.510e-06
TET2	0.2230513	225	1.566e-12	2.938e-09	5.510e-06
TMEM126B	0.2580885	196	1.301e-12	2.712e-09	5.510e-06
TRANK1	0.2332838	205	5.254e-12	8.958e-09	1.527e-05
PKP1	0.2561538	181	1.119e-11	1.645e-08	2.373e-05
SLC17A4	0.2280774	203	1.140e-11	1.645e-08	2.373e-05
MKI67	0.2362785	191	2.081e-11	2.724e-08	3.285e-05
MYH2	0.2219977	202	2.390e-11	2.802e-08	3.285e-05
UBAP2	0.2133489	211	2.179e-11	2.724e-08	3.285e-05
FAM13B	0.2329429	189	3.650e-11	4.027e-08	4.220e-05
GPR37L1	0.2584033	170	3.887e-11	4.050e-08	4.220e-05
FAAP100	0.2182168	199	4.925e-11	4.618e-08	4.308e-05
PLEC	0.2020010	214	5.401e-11	4.824e-08	4.308e-05
SMIM26	0.2680063	158	8.775e-11	7.156e-08	5.835e-05
SPATA2L	0.2356991	180	8.282e-11	7.060e-08	5.835e-05
ADAMTS20	0.1877531	222	1.183e-10	8.873e-08	6.605e-05
CEP170B	0.1970222	206	2.081e-10	1.207e-07	6.605e-05

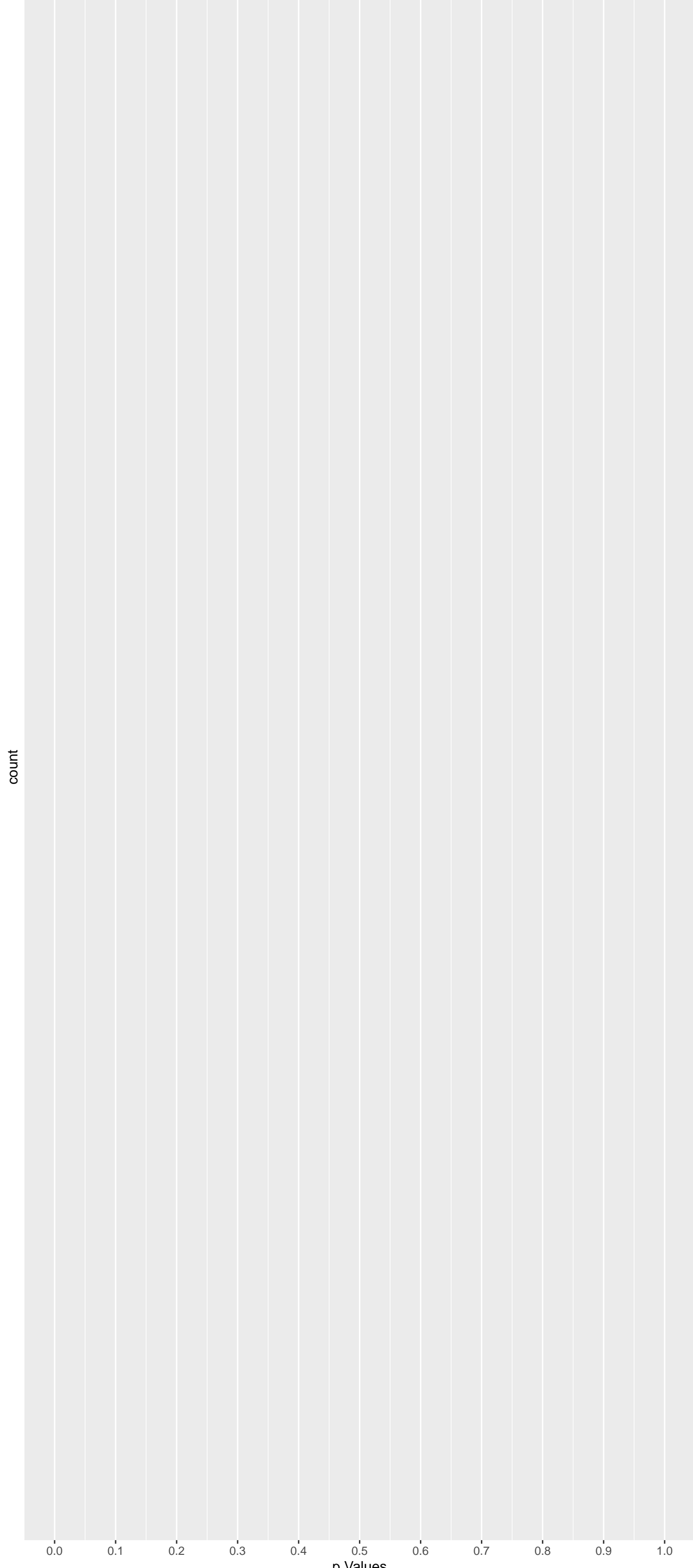
Positive Rho Non-permulated



Top Positive genes by P-value non-permulated

Gene	Rho	N	P	p.adj	qValueNoperm
CCPG1	0.3169889	206	7.556e-16	1.417e-11	2.658e-07
MRGPRE	0.4673325	125	2.690e-14	2.266e-10	1.345e-06
PER2	0.2583903	223	3.624e-14	2.266e-10	1.345e-06
SHANK2	0.2669847	212	6.116e-14	2.868e-10	1.345e-06
AFDN	0.2488617	212	4.281e-13	1.439e-09	4.498e-06
SORL1	0.2435694	216	4.603e-13	1.439e-09	4.498e-06
USP43	0.2397915	216	6.961e-13	1.865e-09	4.998e-06
TET1	0.2295643	221	1.189e-12	2.712e-09	5.510e-06
TMEM126B	0.2580885	196	1.301e-12	2.712e-09	5.510e-06
TET2	0.2230513	225	1.566e-12	2.938e-09	5.510e-06

Negative Rho Non-permulated



Top Negative genes by P-value non-permulated

Gene	Rho	N	P	p.adj	qValueNoperm
NA	NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA	NA
NA.2	NA	NA	NA	NA	NA
NA.3	NA	NA	NA	NA	NA
NA.4	NA	NA	NA	NA	NA
NA.5	NA	NA	NA	NA	NA
NA.6	NA	NA	NA	NA	NA
NA.7	NA	NA	NA	NA	NA
NA.8	NA	NA	NA	NA	NA
NA.9	NA	NA	NA	NA	NA

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

Geneset	stat	num.genes	pval	p.adj	gene.vals
Skin Development (GO:0043588)	0.17289050	66	1.210e-06	6.545e-03	DSP:51 OPN3:367 ITGB4:406 MED1:466 COL3A1:815 EVPL:861
NADH Dehydrogenase Complex Assembly (GO:018430286)	0.18430286	49	8.153e-06	1.469e-02	TMEM126B:9 NDUF4A11:112 ECOS1T:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Mitochondrial Respiratory Chain Complex	0.18430286	49	8.153e-06	1.469e-02	TMEM126B:9 NDUF4A11:112 ECOS1T:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Calcium Ion Transmembrane Import Into Cy	0.13956176	79	1.829e-05	2.073e-02	TRPV6:52 CACNA11:278 CACNA1S:283 CACNA1E:310 SLC24A4:313 CACNA1G:528
Calcium Ion Transmembrane Transport (GO:014010667)	0.14010667	78	1.917e-05	2.073e-02	TRPM5:19 TRPV6:52 SLC24A3:237 CACNA1S:283 SLC24A4:313 ATP2C2:397
Keratinoocyte Differentiation (GO:0030216)	0.18654782	40	4.483e-05	4.040e-02	DSP:51 OPN3:367 MED1:466 EVPL:861 KRT16:1278 TGM1:1291
Natural Killer Cell Activation Involved	0.24586600	22	6.564e-05	4.436e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 FCGR3A:1832 IFNA7:2164
Regulation Of Peptidyl-Serine Phosphoryl	0.27234135	18	6.338e-05	4.436e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNG:1395 IFNA7:2164
Positive Regulation Of Intracellular Tra	0.18140351	39	8.901e-05	5.347e-02	SORL1:6 SPAG5:369 MBD1:686 NEDD4:1044 PRR5L:1322 KIF20B:1349
Epidermis Development (GO:0008544)	0.11824992	84	1.819e-04	7.632e-02	DSP:51 HOXB13:169 FLOT2:610 EVPL:861 LCE2B:935 MANSCA:968
Intermediate Filament Organization (GO:013516074)	0.13516074	65	1.659e-04	7.632e-02	PKP1:12 DSP:51 KRT17:196 KRT80:222 KRT20:247 DES:402
mRNA Methylation (GO:0080009)	0.15675803	15	1.976e-04	7.632e-02	TRMT61B:632 TRMT10C:646 METTL8:787 NSUN2:1916 CMTR1:1970 TRMT61A:2821
Mitochondrial Respiratory Chain Complex	0.11951587	82	1.855e-04	7.632e-02	TMEM126B:9 NDUF4A11:112 ECOS1T:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Positive Regulation Of Peptidyl-Serine P	0.26217905	17	1.824e-04	7.632e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNG:1395 IFNA7:2164 IFNA14:2417
Epidermal Cell Differentiation (GO:000099)	0.14786169	52	2.273e-04	7.951e-02	DSP:51 OPN3:367 MED1:466 EVPL:861 OVOL3:1046 KRT16:1278
Homophilic Cell Adhesion Via Plasma Memb	0.13678365	60	2.500e-04	7.951e-02	SDK1:32 TRO:59 DSG2:195 ITGB1:346 NEXN:371 LICAM:594
Positive Regulation Of Neuron Apoptotic	-0.22115776	23	2.416e-04	7.951e-02	ITGAM:427 FBXW7:508 BAX:877 TFA2P1A:104 TNF:1615 CDK5R1:2334
Regulation Of Protein Localization To Nu	-0.14268264	51	4.263e-04	1.281e-01	PARP9:167 KAT7:263 DTX3L:369 YVHAZ:437 OTUD7B:839 TYK2:887
Internal Protein Amino Acid Acetylation	-0.35641964	8	4.811e-04	1.369e-01	KAT7:263 MAPT:350 NAA10:955 KAT5:1702 KAT2A:2218 KAT2B:2985
Calcium Ion Transport (GO:0006816)	0.09393300	110	6.753e-04	1.826e-01	TRPM5:19 TRPV6:52 SLC24A3:237 CACNA1S:283 SLC24A4:313 ATP2C2:397
Actin-Miosin Filament Sliding (GO:003327)	0.30312187	10	9.027e-04	2.236e-01	MYH2:16 MYL6B:461 TNNT2:704 MYH3:783 MYH4:944 MYH8:3483
Calcium Ion Import Across Plasma Membran	0.16092912	34	1.168e-03	2.236e-01	TRPV6:52 CACNA11:278 CACNA1S:283 CACNA1E:310 SLC24A4:313 CACNA1G:528
Gene Expression (GO:0010487)	-0.05890262	266	9.807e-04	2.236e-01	RBM39:16.5 RPS4Y2:16.5 GSPT2:98 CHTOP:128 MRPS21:169 EXOSC9:198
Lymphocyte Activation Involved In Immune	0.19584182	23	1.151e-03	2.236e-01	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNA7:2164 IFNA14:2417
mRNA Modification (GO:0016556)	0.18349639	27	9.681e-04	2.236e-01	TRMT61B:632 TRMT10C:646 METTL8:787 PUS7L:1000 DKC1:1209 NSUN2:1916
Natural Killer Cell Activation (GO:00301)	0.14090453	44	1.227e-03	2.236e-01	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 CD2:1483 NCR3:13615
Protein Insertion Into ER Membrane (GO:0137729637)	-0.17779637	28	1.226e-03	2.236e-01	MMGT1:252 TRAM1:1127 CDC47:1414 RAB5F:1611 GET3:1771 EMC4:2305.5
Regulation Of Vesicle Size (GO:0097494)	-0.24282030	14	1.241e-03	2.236e-01	BLOC1S1:1154 KXD1:1893 BORCS28:210 BORCS7:2355 RAB5A:2966 AP2M1:3456
Semaphorin-Plexin Signaling Pathway Invo	-0.06325284	12	1.083e-03	2.236e-01	PLXNC1:766 PLXNA4:842 PLXNB2:1102 PLXNB3:2191 SEMA3A:2999 PLXNA1:3281
Transcription Initiation At RNA Polymera	-0.10953066	73	1.224e-03	2.236e-01	MED20:142 TAF11L:538 GTF2H2:722 GTF2B:735 TAF11L:572 MED30:927
Mitotic Sister Chromatid Segregation (GO:00903716)	0.08903716	109	1.339e-03	2.263e-01	DLGAP5:27 KIF18A:78 CFP192:96 KIF22:192 OFD1:224 KIF2C:231
Regulation Of Neuron Migration (GO:00012)	0.17516094	28	1.339e-03	2.263e-01	KIF26A:120 TNN:456 COL3A1:815 ULK4:962 IGSF10:1014 PLXNB2:1102
ERBB Signaling Pathway (GO:0038127)	0.12674094	53	1.422e-03	2.330e-01	PTK2:705 AKT1:1040 PLCG1:1068 PLC1:8177 EGFR:1249 PIK3C2A:1328
mRNA Processing (GO:0006397)	-0.06716858	187	1.575e-03	2.505e-01	RBM22:16.5 MTRER:135 SFPO:265 VDRB8:321 CPSF7:699 SART3:847
Positive Regulation Of Calcium Ion Trans	0.14187187	41	1.677e-03	2.591e-01	CASQ1:277 GPER1:336 CAPN3:834 CEMIP:909 P2RX7:1001 PLOG1:1068
Muscle Contraction (GO:0006936)	0.09468339	91	1.817e-03	2.730e-01	MYH2:16 MYH13:89 MYOF:243 CACNA1S:283 DES:402 MYH1:438
Establishment Or Maintenance Of Apical/B	0.18325259	24	1.889e-03	2.734e-01	PATJ:228 SCRIB:258 PARDB3:633 DLG3:1710 LGLL1:1783 OOEPE:1819
Negative Regulation Of Inflammatory Resp	-0.08650726	107	2.016e-03	2.734e-01	TRIM65:45 FNDCA1:133 TNFAIP6:278 AP0A1:286 IL2D2:322 PRKCD:357
Presynaptic Active Zone Organization (GO:0139910733)	-0.39910733	5	1.996e-03	2.734e-01	ERC2:277 ERC1:545 CAST:2550 PCLO:2855 RAB3A:3194 NA
Regulation Of Smooth Muscle Contraction	0.19941021	20	2.022e-03	2.734e-01	CTTN:279 TACR2:615 PLCE1:1177 KCNB2:1411 SETD3:1793 CHRM2:1938

## EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HOUNKPE_HOUSEKEEPING_GENES	-0.06632010	1063	3.793e-13	2.463e-09	ARL8B:16.5 CAB39:16.5 CUL3:16.5 TMEM203:16.5 PDCD7:54 PSMD10:76
REACTOME_METABOLISM_OF_RNA	-0.07958533	645	6.273e-12	2.037e-08	RBM39:16.5 RBM22:16.5 SNRPC:16.5 RPS4Y2:16.5 PDCD7:54 PSMD10:76
REACTOME_KERATINIZATION	0.12923156	214	7.558e-11	1.636e-07	PKP1:12 DSP:51 KRTAP6:1.55 KRTAP10:1.163 KRTAP10:3.164 DSG2:195
REACTOME_FORMATION_OF_THE_CORNFIFIED_ENVE	0.15619422	128	1.065e-09	1.730e-06	PKP1:12 DSP:51 DSG2:195 KRT17:196 KRT80:222 KRT20:247
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.05241809	1180	1.672e-09	2.172e-06	CAB39:16.5 STAM:16.5 NQO1:16.5 TBPL1:16.5 MEMO1:16.5 SEC61A2:16.5
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	-0.06327535	749	4.334e-09	4.020e-06	CUL3:16.5 NQO1:16.5 H2AC18:16.5 H2BC3:16.5 RPS4Y2:16.5 AKT3:34.5
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.04846457	1329	3.933e-09	4.020e-06	CAB39:16.5 STAM:16.5 RBM39:16.5 TBPL1:16.5 PSMD10:76 SAV1:103
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	0.27003870	37	3.116e-08	1.003e-05	INTS1:203 GPER1:336 ZFAND2A:357 SNX8:722 MAD1L1:854 AP521:942
MARTENS_TRETINOIN_RESPONSE_DN	-0.06179440	733	3.190e-08	1.003e-05	TRIM65:45 OR7G2:55 HDGF:77 IRAK3:105 ATGAD:107 CHMP2A:119
REACTOME_INFECTIOUS_DISEASE	-0.05651316	876	1.610e-08	1.045e-05	CUL3:16.5 STAM:16.5 H2AC18:16.5 H2BC3:16.5 RPS4Y2:16.5 AKT3:34.5
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODI	-0.04114297	1379	3.715e-07	2.027e-04	CUL3:16.5 STAM:16.5 H2AC18:16.5 TRAPP2C:16.5 WDR48:16.5 COP22:46.2
REACTOME_REGULATION_OF_EXPRESSION_OF_SLI	-0.12190487	146	3.748e-07	2.027e-04	RPS4Y2:16.5 PSMD10:76 GSPT2:98 RPLP0:232 PSMB6:282 NUP35:541
PUJANA_BRCA1_PCC_NETWORK	-0.03907607	1514	4.714e-07	2.355e-04	RAP1B:16.5 TBPL1:16.5 SNRPC:16.5 FAM120A:41.5 MMP20:48 BRAF:67
HSIAO_HOUSEKEEPING_GENES	-0.07799012	349	5.994e-07	2.780e-04	H2AC18:16.5 PSD:64 CD164:65 STOM:176 AARS1:184 RPLP0:232
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_D	-0.05830100	573	1.977e-06	8.560e-04	CD164:65 YME1L1:106 CNOT2:181 ARPC5L:196 CCNC:216 RPL7A:218
DANG_BOUND_BY_MYC	-0.04443417	1001	2.237e-06	9.080e-04	RBM39:16.5 H2AC18:16.5 CD164:65 PSMD10:76 HMOX1:122 CNPY2:163
BENPORATH_MYC_MAX_TARGETS	-0.05146216	727	2.511e-06	9.592e-04	RBM39:16.5 H2AC18:16.5 CD164:65 PSMD10:76 SAV1:103 MED20:142
REACTOME_UB_SPECIFIC_PROCESSING_PROTEASE	-0.09202678	214	3.566e-06	1.286e-03	H2AC18:16.5 WDR48:16.5 H2BC3:16.5 PSMD10:76 USP17L24:209 H2AC12:233
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	-0.08916174	221	5.046e-06	1.725e-03	H2AC18:16.5 H2BC3:16.5 PSMD10:76 KMT2D:172 GPAM:178 PSMB6:282
REACTOME_PROCESSING_OF_CAPPED_INTRON_CON	-0.08315536	250	6.116e-06	1.986e-03	RBM39:16.5 RBM22:16.5 SNRPC:16.5 PDCD7:54 CHTOP:128 MTRX1:135
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.07042644	347	6.804e-06	2.008e-03	NQO1:16.5 RPS4Y2:16.5 PSMD10:76 BCKDK9:1 RPLP0:232 OAZ3:235
REACTOME_SARS_COV_1_INFECTION	-0.11858563	121	6.694e-06	2.008e-03	RPS4Y2:16.5 CHMP2A:119 PARP9:167 NMI:201 ST3GAL4:289 YVHAZ:437
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_O	-0.12133523	114	7.708e-06	2.176e-03	H2AC18:16.5 H2BC3:16.5 PSMD10:76 PSMB6:282 H2BC10:447 UTP14A:538
REACTOME_RRNA_PROCESSING	-0.09369094	182	1.334e-05	3.609e-03	RPS4Y2:16.5 MTRX1:135 EXOSC9:198 RPLP0:232 WDR3:497 NUP35:541
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.09138653	186	1.749e-05	4.542e-03	MKI67:14 DLGAP5:27 PARPBP:76 KIF18A:78 SG02:135 KIF22:192
DAZARD_RESPONSE_TO_UVC_SSC_UP	-0.12310743	100	2.115e-05	5.528e-03	CCNC:216 TACSTD2:225 KYAT3:379 YVHAZ:437 PMAIP1:548 MAP2K1:558
REACTOME_CYCLIN_A_CDK4_ASSOCIATED_EVENTS	-0.13648570	80	2.452e-05	5.897e-03	AKT3:34.5 PSMD10:76 PSMB6:282 PSMA4:492 MNAT1:728 RBL2:790
BRUINS_UVC_RESPONSE_LATE	-0.03767346	1077	3.311e-05	7.194e-03	ARL8B:16.5 CAB39:16.5 MEMO1:16.5 TRAPP2C:16.5 COP22:16.5 TCF19:50
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_P	-0.12561462	92	3.144e-05	7.194e-03	SEC61A2:16.5 RPS4Y2:16.5 RPLP0:232 RPL36:769 SSR3:891 RPL3L:897
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	-0.11112684	117	3.324e-05	7.194e-03	AKT3:34.5 PSMD10:76 PSMB6:282 RUNC2:429.5 PSMA4:492 FBXW7:508
REACTOME_INFLUENZA_INFECTION	-0.10309685	132	4.354e-05	9.122e-03	RPS4Y2:16.5 RPLP0:232 KPNA4:296 SLC25A6:299 NUP35:541 SEC13:623
REACTOME_TCF_DEPENDENT_SIGNALING_IN_RESP	-0.08093447	214	4.573e-05	9.279e-03	CUL3:16.5 H2AC18:16.5 H2BC3:16.5 PSMD10:76 KMT2D:172 CENK1G:257
REACTOME_HIV_INFECTION	-0.08053257	215	4.788e-05	9.422e-03	PSMD10:76 CHMP2A:119 TAF1:519 PSMB6:282 SLC25A6:299 LCK:360
REACTOME_HCMV_LATE_EVENTS	-0.11552157	103	5.133e-05	9.805e-03	H2AC18:16.5 H2BC3:16.5 CHMP2A:119 H2AC12:233 H2BC10:447 NUP35:541
THUM_SYSTOLIC_HEART_FAILURE_UP	-0.05969294	389	5.497e-05	1.020e-02	ARL8B:16.5 CP:102 IRF8:109 ZNF672:200 KPNA4:296 FAS:361
REACTOME_SPERM_MOTILITY_AND_TAXES	0.06868360	9	6.567e-05	1.057e-02	CATSPER2:99 CATSPERB:536 CATSPER3:587 CATSPERD:760 CATSPERG:1188 HVCN1:2106
REACTOME_SIGNALING_BY_ROBO_RECEPTORS	-0.08404975	188	7.161e-05	1.057e-02	RPS4Y2:16.5 PSMD10:76 GSPT2:98 RPLP0:232 PSMB6:282 PSMA4:492
REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	0.27149927	18	6.661e-05	1.057e-02	SEMA7A:97 ITGB1:346 PLXNC1:766 PLXNA4:842 PTPRC:1714 SEMA4D:2068
REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESS	-0.10093025	131	6.696e-05	1.057e-02	H2AC18:16.5 H2BC3:16.5 GPAM:178 STAG2:347 H2BC10:447 SP1:593
REACTOME_NONSENSE_MEDIATED_DECAY_NMD	-0.11948685	93	6.860e-05	1.057e-02	RPS4Y2:16.5 GSPT2:98 RPLP0:232 RPL36:769 RPL3L:897 RPS3:948.5

## DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cerebral Ischemia	-0.07316557	240	9.904e-05	4.867e-01	ASIC1:16.5 KCNK3:56 REN:132 KCN1J3:171 BDNF:193 CREB1:221
Esophagitis	-0.14786041	58	9.914e-05	4.867e-01	NQO1:16.5 PDLIM3:188 PLCL1:242 YVHAZ:437 IL10:581 GPHN:900.5
Bell Palsy	0.11296138	87	2.742e-04	4.921e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
Erythrokeratoderma	0.16605376	41	2.353e-04	4.921e-01	DSP:51 DSG2:195 KRT17:196 DES:402 SLURP1:458 GJBA:521
Leukokeratosis	0.21915410	23	2.750e-04	4.921e-01	KRT17:196 CTTN:279 CTC1:756 DKC1:1209 KRT16:1278 AKT:1302
Thyroid Agenesis	-0.20101517	27	3.007e-04	4.921e-01	FOXE1:70 THRA:346 PRKARIA:637 TSHB:870 LHXA:1055 DUXO2:1201
Stiff-Person Syndrome	-0.27551525	14	3.581e-04	5.023e-01	GAD1:63 GP6:514.5 GPHN:900.5 NUDT10:2115 SLC6A5:2189 HLA-DQB1:2574
Anaphylaxis (non medication)	-0.16535181	38	4.218e-04	5.176e-01	CD63:306 F9:423 IL10:581 HACD1:668 STAT6:823 TM7SF2:1153
Abnormality of the skull	0.11904777	68	6.928e-04	5.233e-01	CENPJ:337 ESCO2:567 CEP152:831 CENPE:846 IFT122:880 RBBP8:1122
Facial Paresis	0.10632062	88	5.729e-04	5.233e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
Hyperdiploid B Acute Lymphoblastic Leuke	-0.18773742	28	5.865e-04	5.233e-01	CEBPE:154 KRAS:970 CD19:991 ASPG:1413 PIP4K2A:1568 TTNF:1615
Long QT Syndrome 2	0.29593776	11	6.773e-04	5.233e-01	GOLGA2:250 KCNH2:663 ALG10:923 KCNQ1:2351 SCN5A:3466 KCNE1:3620
Sarcoma	-0.04123981	605	5.862e-04	5.233e-01	NQO1:16.5 BRAF:67 HDGF:77 LIN28A:78 IRF10:109 M1TF:111
Facial muscle weakness of muscles innerv	0.10447054	84	9.434e-04	6.617e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
46, XX Testicular Disorders of Sex Devel	-0.24074597	9	1.238e-02	6.715e-01	SOX10:694 FOLX2:1561 NR5A1:2066 SOX9:3151 AR:3201 RSP01:4096
Bulbo cavernosus Reflex, Decreased	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Child Development Disorders, Specific	0.15439931	23	1.038e-02	6.715e-01	CHRNA4:732 DRD2:964 KNTN1:1030 KCNQ2:1366 SLC6A8:1549 SHANK3:1682
Conjunctivitis, recurrent	-0.11712136	39	1.140e-02	6.715e-01	BLNK:551 ERCC6:765 CD19:991 TP63:1069 XPC:1332 SAT1:1846
Creatinine measurement, serum (procedure	0.09668360	63	7.993e-03	6.715e-01	WDR72:93 ALMS1:194 PTFN1:2280 CACNA1S:283 CDK12:382 SPATA5L1:520
Epilepsy, Rolandic	0.13180789	30	1.248e-02	6.715e-01	KCNQ3:240 SNIP1:1205 RFXO3:1299 KCNQ2:1366 ADAMTS4:1402 SHANK3:1682
Keratoderma, Palmaplantar, Diffuse	0.23389964	12	5.024e-03	6.715e-01	SLURP1:458 RHBDF2:1174 KRT16:1278 TPO2:1509 SOX2:1397 S5 DNMT3A:2024
Mental Retardation, Psychosocial	0.08871815	130	6.901e-03	6.715e-01	SHANK2:4 NSD1:62 CALCA:109 AP4E1:230 NDS1:1365 CACNA1G:528
Neoplasia Recurrence, Local	-0.12910220	36	3.666e-03	6.715e-01	LIMD2:72 YVHAZ:437 CXCL9:1338 TP52:1509 SOX2:1397 S5 DNMT3A:2024
Nephritis, Interstitial	-0.16242781	31	1.753e-03	6.715e-01	APOA1:286 BAH:877 CCL7:988 CYP2C9:990 TM7SF2:1153 CCL1:1704
PALMOPANTAR KERATODERMA, NONEPIDERMOLYT	0.31773886	7	3.599e-03	6.715e-01	KRT80:228 RHBDF2:1174 KRT16:1278 TTX2:1208 AQP5:4075 CCL7:15086
Periodontitis, Juvenile	0.08736900	85	5.405e-03	6.715e-01	MUC2:342 NOD2:571 CAMP:920 HTRA1:995 IL12RB2:1019 AKT1:1040
PERIODONTITIS, LOCALIZED AGGRESSIVE	0.39580980	4	6.111e-03	6.715e-01	MYOM2:1389 CLU:1989 DGKA:2155 IL1B:2255 NA NA
Psychomotor retardation, mild	0.17667902	19	7.887e-03	6.715e-01	RNF168:117 CENPJ:337 CEP152:831 CENPE:846 RBBP8:1122 ATXN:1306
Reflex, Abnormal	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Acoustic, Abnormal	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Anal, Absent	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Anal, Decreased	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Ankle, Abnormal	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Ankle, Decreased	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Biceps, Abnormal	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Biceps, Absent	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Biceps, Decreased	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Corneal, Absent	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Gag, Absent	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Gag, Decreased	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA