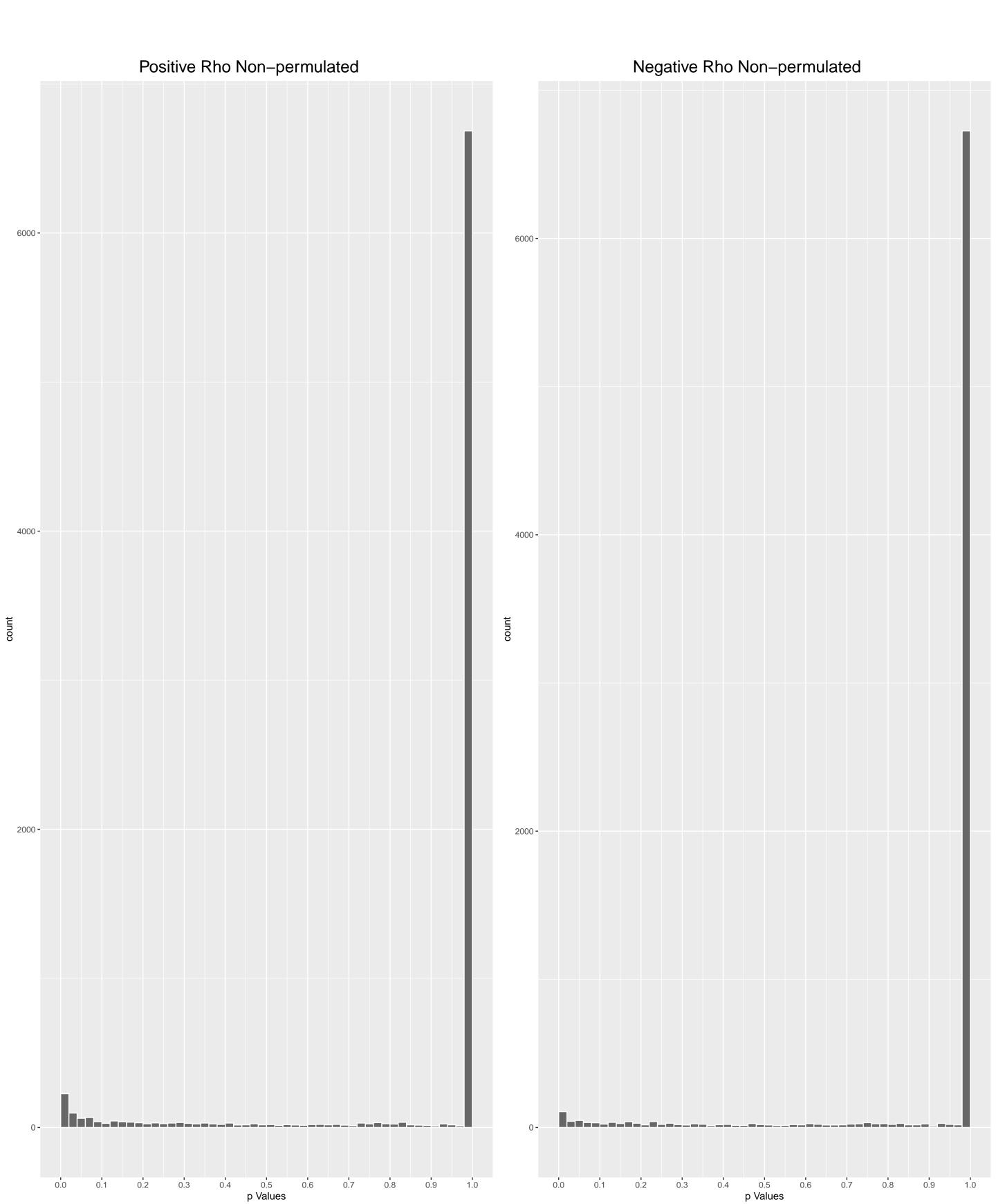




Gene

qValueNoperm



Top Positive genes by P-value non-permulated

Top Negative genes by P-value non-permulated

PLEC	7.226544	2.972646e-12	2.404e-08	1.617e-04
NUP88	7.140912	5.562841e-12	2.999e-08	1.617e-04
DNAH14	7.046628	1.099834e-11	4.447e-08	1.798e-04
DNAH9	6.952627	2.151269e-11	6.958e-08	1.916e-04
ANKRD35	6.923874	2.636742e-11	7.107e-08	1.916e-04
SLC47A1	6.719316	1.095480e-10	2.531e-07	5.848e-04
CAPN8	6.583418	2.758519e-10	5.577e-07	1.127e-03
KANK1	6.423459	7.992721e-10	1.436e-06	2.151e-03
ITGB4	6.394726	9.650118e-10	1.463e-06	2.151e-03

 Gene
 Rho
 P
 p.adj
 qValueNoperm

 DNAH2
 8.237150
 1.058164e-15
 1.711e-11
 2.768e-07

PROM1	-6.060793	8.127129e-09	7.331e-06	6.587e-03
TMEM131L	-5.897907	2.208852e-08	1.553e-05	1.092e-02
MTBP	-5.828952	3.346589e-08	2.165e-05	1.330e-02
PPFIA3	-5.613386	1.190435e-07	5.501e-05	2.542e-02
MAN2A1	-5.543938	1.774465e-07	7.756e-05	3.326e-02
CLCNKA	-5.464747	2.781409e-07	1.046e-04	3.935e-02
ABHD11	-5.272046	8.094661e-07	2.525e-04	7.854e-02
FNBP4	-5.254751	8.893493e-07	2.714e-04	8.281e-02
ELL	-5.226313	1.037542e-06	3.051e-04	8.476e-02
QSER1	-5.216049	1.096680e-06	3.092e-04	8.476e-02

Gene Rho P p.adj qValueNoperm

Geneset	stat	num.genes	pval	p.adj	gene.vals
CONOTRUNCAL ANOMALY FACE SYNDROME	-0.26967215	21	1.892e-05	1.856e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 COMT:707 GATA6:831
Shprintzen syndrome	-0.20254120	33	5.692e-05	1.862e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 PRODH:607 COMT:707
Tetany	-0.25749709	21	4.424e-05	1.862e-01	HIRA:62 CASR:112 CNNM2:164 TRPM6:177 CLDN16:288 PTH:301
Ciliary Motility Disorders	0.15079213	57	8.324e-05	1.873e-01	DNAH9:5 ARMC4:153 DNAH11:178 SPEF2:448 DNAH5:520 CFAP221:553
DiGeorge Syndrome	-0.14292177	61	1.145e-04	1.873e-01	ALB:20 HIRA:62 SPECC1L:115 DGCR2:211 VEGFA:216 CDC45:279
Junctional split	0.45514706	6	1.129e-04	1.873e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 LAMB3:1337 LAMA3:2606
22q11 Deletion Syndrome	-0.25203174	19	1.432e-04	2.006e-01	HIRA:62 HIC2:262 ARVCF:390 DGCR8:430 PRODH:607 COMT:707
Leukemia, Myelocytic, Acute	-0.02932510	1383	3.572e-04	2.181e-01	PROM1:1 ELL:9 ASMTL:27 SDS:30 ABCB1:48 GGTLC3:60
22q11 partial monosomy syndrome	-0.32304931	11	2.074e-04	2.181e-01	HIRA:62 ARVCF:390 PI4KA:591 COMT:707 GNB1L:734 JMJD1C:1018
Adult Medulloblastoma	-0.13249051	58	4.878e-04	2.181e-01	KDM4B:174 MDM2:283 BRD2:287 MYCN:363 BRD4:551 DNMT1:623
Defective enamel matrix	0.15888464	40	5.100e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 FGFR2:233 STX16:242
Dysplasia of tooth enamel	0.15888464	40	5.100e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 FGFR2:233 STX16:242
Endometrial Carcinoma	-0.03931725	679	5.515e-04	2.181e-01	PROM1:1 ABCB1:48 GGTLC3:60 RXFP1:64 HSD17B6:77 TNF:88
Epidermolysis Bullosa	0.19363594	31	1.914e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 DSC3:180 LAMC2:190 DSP:257
Epidermolysis Bullosa Simplex	0.21766204	21	5.558e-04	2.181e-01	PLEC:2 ITGB4:10 KRT80:59 MMP9:258 KRT14:552 TGM5:1058
Hepatitis C	-0.04185967	598	5.345e-04	2.181e-01	ALB:20 GGTLC3:60 TNF:88 CABIN1:105 EGF:130 AZIN1:140
Hepatocarcinogenesis	-0.04876646	443	4.758e-04	2.181e-01	PROM1:1 ALB:20 TNF:88 MLIP:106 EGF:130 AICDA:152
Herlitz Disease	0.44611872	5	5.507e-04	2.181e-01	ITGB4:10 ITGA6:138 LAMC2:190 LAMB3:1337 LAMA3:2606 NA
Medullomyoblastoma	-0.16219370	41	3.284e-04	2.181e-01	KDM4B:174 BRD2:287 MYCN:363 BRD4:551 DNMT1:623 PTCH2:687
Melanotic medulloblastoma	-0.16219370	41	3.284e-04	2.181e-01	KDM4B:174 BRD2:287 MYCN:363 BRD4:551 DNMT1:623 PTCH2:687
Oral mucosal blisters	0.31935971	10	4.707e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 DSP:257 LAMB3:1337
Polynesian Bronchiectasis	0.17704378	35	2.909e-04	2.181e-01	ARMC4:153 DNAH11:178 DNAH5:520 CCDC151:598 GAS8:674 RSPH1:875
Posterior embryotoxon	-0.18062890	31	5.023e-04	2.181e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 PEX13:657 COMT:707
Substance Dependence	0.08976103	128	4.647e-04	2.181e-01	NRCAM:41 CFTR:94 ANKK1:106 CSRNP3:114 QSOX1:120 TIAM2:124
Thin dental enamel	0.15888464	40	5.100e-04	2.181e-01	PLEC:2 ITGB4:10 ITGA6:138 LAMC2:190 FGFR2:233 STX16:242
Malignant neoplasm of lung	-0.02408137	1977	6.411e-04	2.419e-01	PROM1:1 ALB:20 DCAF4:31 RIOX1:33 ADAM9:39 ABCB1:48
Hidradenitis Suppurativa	-0.23744492	17	7.014e-04	2.458e-01	TNF:88 SULT1E1:230 SULT1B1:1464 ELOVL7:1579 RBM45:1638 PSEN1:1786
Primary malignant neoplasm of lung	-0.02463774	1842	6.942e-04	2.458e-01	PROM1:1 ALB:20 DCAF4:31 RIOX1:33 ADAM9:39 ABCB1:48
leukemia	-0.02619566	1577	7.342e-04	2.484e-01	PROM1:1 ELL:9 MZF1:16 ALB:20 ABCB1:48 SLC7A4:50
Carcinoma of lung	-0.02337836	2007	8.548e-04	2.572e-01	PROM1:1 ALB:20 DCAF4:31 RIOX1:33 ADAM9:39 ABCB1:48
Embryotoxon	-0.17368952	30	9.963e-04	2.572e-01	HIRA:62 DGCR2:211 ARVCF:390 DGCR8:430 PEX13:657 COMT:707
Hepatitis	-0.06238154	246	7.885e-04	2.572e-01	PROM1:1 ALB:20 ABCB1:48 TNF:88 VCAM1:125 IL33:156
Liver neoplasms	-0.03006136	1094	9.833e-04	2.572e-01	PROM1:1 MZF1:16 ALB:20 SDS:30 ABCB1:48 SUGP1:57
Parakeratosis	0.24832830	15	8.697e-04	2.572e-01	CARD14:20 NLRP1:85 DSP:257 TNC:348 TRPV3:680 RHBDF2:1836
Seborrheic dermatitis	-0.20986329	21	8.727e-04	2.572e-01	HIRA:62 TNF:88 ARVCF:390 NFE2L2:479 COMT:707 JMJD1C:1018
Substance–Related Disorders	0.08964595	114	9.637e-04	2.572e-01	NRCAM:41 CFTR:94 CSRNP3:114 QSOX1:120 TIAM2:124 SYNE1:287
T-lymphocyte immunodeficiency	0.38816434	6	9.920e-04	2.572e-01	RAG1:133 SFTPA1:152 SMARCAL1:524 LBR:555 CD3E:1224 SIPA1:8200
Unilateral primary pulmonary dysgenesis	-0.42895287	5	8.941e-04	2.572e-01	DGCR2:211 DGCR8:430 TBX1:1140 DGCR6:1444 ESS2:2424 NA
Color Blindness, Red	0.42200294	5	1.083e-03	2.580e-01	ATF6:609 TEX28:722 OPN1LW:1041 GNAT2:1064 PDE6H:2749 NA
Kartagener Syndrome	0.09761045	94	1.090e-03	2.580e-01	DNAH9:5 DNAH17:17 CFTR:94 KRT20:102 ARMC4:153 DNAH11:178

## EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
DODD_NASOPHARYNGEAL_CARCINOMA_UP	0.04865634	1463	8.213e-10	5.328e-06	DNAH2:1 DNAH9:5 ANKRD35:6 SIK3:12 CARD14:20 CFAP45:25
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.11697118	208	6.434e-09	2.087e-05	BDKRB1:16 NPBWR2:100 MTNR1B:130 SSTR4:173 PTAFR:318 GPR68:347
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO	0.13902808	128	5.748e-08	1.180e-04	HELZ2:90 FNDC11:99 NPBWR2:100 COL20A1:155 FAM217B:166 RTEL1:223
JOHNSTONE_PARVB_TARGETS_3_DN	-0.05673816	790	7.278e-08	1.180e-04	MTBP:3 MAN2A1:5 QSER1:10 SLC6A6:51 SMCHD1:52 RBL1:78
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.25526664	34	2.599e-07	3.373e-04	PBXIP1:35 DCST1:63 THBS3:220 ZBTB7B:275 RUSC1:312 PMVK:491
PUJANA_BRCA1_PCC_NETWORK	-0.03974413	1501	3.896e-07	4.213e-04	TMEM131L:2 FNBP4:8 SLC16A5:25 SLC6A6:51 HIRA:62 RBL1:78
ZHANG_BREAST_CANCER_PROGENITORS_UP	-0.07016918	415	1.028e-06	6.950e-04	PROM1:1 SMCHD1:52 CTH:53 CEP192:59 TTC3:65 MAP7D2:72
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	0.08276707	295	1.071e-06	6.950e-04	BDKRB1:16 TACR2:18 NPBWR2:100 GPR132:118 MTNR1B:130 SSTR4:173
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.05949181	598	7.689e-07	6.950e-04	ADAM9:39 RBL1:78 SPDL1:86 WDR76:116 HLTF:133 RHOBTB3:186
SCHLOSSER_SERUM_RESPONSE_DN	-0.05672426	646	1.004e-06	6.950e-04	UBR2:14 ASMTL:27 PJA2:47 CTH:53 PARG:98 ICAM2:101
DODD_NASOPHARYNGEAL_CARCINOMA_DN	-0.04093223	1244	1.588e-06	9.364e-04	QSER1:10 FGD6:43 CEP192:59 RBL1:78 SPDL1:86 CD80:109
REACTOME_SIGNALING_BY_GPCR	0.05593227	631	1.854e-06	1.003e-03	BDKRB1:16 TACR2:18 ARHGEF11:24 ARHGEF12:32 CAMK2B:37 PIK3R5:95
WP_22Q112_COPY_NUMBER_VARIATION_SYNDROME	-0.12640769	112	3.883e-06	1.938e-03	SLC7A4:50 CLTCL1:55 HIRA:62 CYP26C1:102 DGCR2:211 DEPDC5:224
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	-0.04250066	1026	5.118e-06	2.372e-03	ELL:9 ZNF446:28 GATAD2A:74 MGA:76 RBL1:78 TAF2:87
NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	0.33717555	14	1.253e-05	5.418e-03	COL6A1:61 PCNT:325 DIP2A:374 SPATC1L:544 COL6A2:937 MCM3AP:978
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-0.05540040	490	2.895e-05	9.574e-03	PJA2:47 SMCHD1:52 CDV3:158 LTN1:250 DPP8:282 ARPP19:302
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	0.08679044	197	2.749e-05	9.574e-03	BDKRB1:16 TACR2:18 GPR132:118 MMP3:226 PTAFR:318 GPR68:347
REACTOME_KERATINIZATION	0.13115066	85	2.951e-05	9.574e-03	EVPL:42 KRT80:59 KRT20:102 KRT4:148 DSC3:180 TGM1:199
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	0.13836075	78	2.417e-05	9.574e-03	EVPL:42 KRT80:59 KRT20:102 KRT4:148 DSC3:180 TGM1:199
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.06493504	357	2.649e-05	9.574e-03	PRODH2:18 SDS:30 CTH:53 DHTKD1:121 AGXT:136 AZIN1:140
STARK_HYPPOCAMPUS_22Q11_DELETION_DN	-0.25464896	22	3.557e-05	1.099e-02	HIRA:62 DGCR2:211 TANGO2:277 ARVCF:390 DGCR8:430 PRODH:607
FISCHER_DREAM_TARGETS	-0.04052402	882	5.104e-05	1.505e-02	MTBP:3 FNBP4:8 ZNF518A:40 SMCHD1:52 CEP192:59 HAUS8:68
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.04828799	595	6.267e-05	1.768e-02	QSER1:10 HAS2:29 ADAM9:39 PJA2:47 SMCHD1:52 CEP192:59
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.05832990	398	6.896e-05	1.864e-02	CFAP45:25 PTPN22:50 CFAP46:83 C7orf57:88 ZHX3:98 DRC3:144
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.03275112	1338	7.184e-05	1.864e-02	MAN2A1:5 PPP4R1:12 ASMTL:27 CTH:53 HIRA:62 TAF2:87
MARTENS_TRETINOIN_RESPONSE_UP	0.04424366	676	9.679e-05	2.415e-02	CARD14:20 SMTNL2:38 GGT6:56 COL6A1:61 PIK3R5:95 ANKK1:106
NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON	0.16237164	46	1.394e-04	3.164e-02	PIEZO1:22 CTU2:572 ANKRD11:602 GAS8:674 CBFA2T3:838 CPNE7:943
REACTOME_MUSCLE_CONTRACTION	0.08018808	190	1.414e-04	3.164e-02	CAMK2B:37 DMD:86 CASQ1:108 MYH8:146 SLC8A3:171 ATP1A4:189
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.05406198	427	1.351e-04	3.164e-02	QSER1:10 RBL1:78 WDR76:116 TPX2:161 VEGFA:216 CDC45:279
KEGG_STEROID_HORMONE_BIOSYNTHESIS	-0.20547611	28	1.679e-04	3.631e-02	HSD17B6:77 HSD11B1:167 SULT1E1:230 HSD17B2:466 CYP17A1:499 CYP11A1:608
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	-0.03232678	1201	1.913e-04	3.956e-02	PROM1:1 GYG2:44 CTH:53 HAUS8:68 MAP7D2:72 SPDL1:86
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	-0.04349600	637	1.951e-04	3.956e-02	QSER1:10 TTC3:65 RLF:81 TPX2:161 ANAPC1:163 ATP13A3:173
REACTOME_GPCR_LIGAND_BINDING	0.05343416	398	2.666e-04	4.941e-02	BDKRB1:16 TACR2:18 NPBWR2:100 GPR132:118 MTNR1B:130 SSTR4:173
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODI	-0.03052690	1298	2.625e-04	4.941e-02	MAN2A1:5 ALB:20 DCAF4:31 ANO8:80 KTN1:128 HLTF:133
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.04753086	509	2.580e-04	4.941e-02	PJA2:47 PARG:98 VCAM1:125 HLTF:133 AZIN1:140 N4BP1:159
BENPORATH_SOX2_TARGETS	-0.04096629	685	2.806e-04	5.057e-02	ABHD11:7 HAS2:29 CTH:53 ANO8:80 PARG:98 CDK12:117
HOUNKPE_HOUSEKEEPING_GENES	-0.03293887	1083	2.903e-04	5.090e-02	ELL:9 MORC2:84 KXD1:99 KDM4B:174 RNF216:178 SLC35E1:214
ALONSO_METASTASIS_UP	-0.07688606	179	3.956e-04	6.021e-02	MDM2:283 MAL:303 MAP4K3:334 KLF10:379 EXOC2:486 FGG:488
DUNTA EDT. DUOTODYNIANIO THEDADY OTDEGO HD	0.00004070	754	0.000- 0.4	0.004 00	ENDRAGO ELLO LIBROJA A DENOAGOO ZNEAGOO EORGAO

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

3.990e-04 6.021e-02

3.970e-04 6.021e-02

FNBP4:8 ELL:9 UBR2:14 BTN3A3:23 ZNF16:32 FGD6:43

ALB:20 SDS:30 MGST1:54 AGXT:136 HSD11B1:167 ATP13A3:173

BUYTAERT\_PHOTODYNAMIC\_THERAPY\_STRESS\_UP -0.03821878

-0.07258776

HSIAO\_LIVER\_SPECIFIC\_GENES

Geneset	stat	num.genes	pval	p.adj	gene.vals
Regulation Of Gene Expression (GO:001046	-0.05278078	950	5.983e-08		MZF1:16 BTN3A3:23 BTNL2:24 ZNF280A:46 KANSL3:49 CUX2:67
Regulation Of DNA-templated Transcriptio	-0.03771024	1648	7.610e-07	2.050e-03	MZF1:16 ZNF446:28 RIOX1:33 ZNF408:38 ZNF518A:40 ZNF280A:46
Cilium Movement (GO:0003341)	0.20459441	47	1.237e-06	2.222e-03	DNAH9:5 DNAH17:17 DNAH11:178 DNHD1:205 TEKT1:299 SPEF2:448
Anterograde Trans-Synaptic Signaling (GO	0.09415976	183	1.186e-05	1.065e-02	MINK1:44 GRIN2A:101 MTNR1B:130 GABRR3:200 PENK:336 HTR3B:357
Cilium–Dependent Cell Motility (GO:00602	0.30964719	17	9.893e-06	1.065e-02	DNAH2:1 DNAH17:17 TEKT1:299 DNAH3:463 GAS8:674 TEKT4:967
Muscle Contraction (GO:0006936)	0.13526729	88	1.186e-05	1.065e-02	TACR2:18 ARHGEF11:24 MYH13:134 MYH8:146 NOS1:249 CKMT2:284
Regulation Of Transcription By RNA Polym	-0.03233138	1714	1.626e-05	1.252e-02	MZF1:16 ZNF446:28 ZNF408:38 ZNF518A:40 KANSL3:49 WIZ:61
Striated Muscle Contraction (GO:0006941)	0.16498924	52	3.909e-05	2.633e-02	ARHGEF11:24 MYH7B:43 DMD:86 MYH8:146 SCN5A:217 NOS1:249
Negative Regulation Of Gene Expression (	-0.06736602	314	4.439e-05	2.658e-02	RBL1:78 MORC2:84 TNF:88 DAXX:137 TASOR:150 N4BP1:159
Regulation Of DNA Metabolic Process (GO:	-0.10632231	122	5.159e-05	2.780e-02	TAF2:87 PARG:98 SLF1:295 HDAC8:352 EID3:382 USP1:395
Chemical Synaptic Transmission (GO:00072	0.07292523	257	6.116e-05	2.996e-02	MINK1:44 GRIN2A:101 MTNR1B:130 GABRR3:200 PENK:336 HTR3B:357
Cellular Component Assembly (GO:0022607)	0.07400571	240	8.371e-05	3.759e-02	CFAP46:83 DMD:86 CD74:111 QSOX1:120 CFAP74:137 SPACA9:147
Cilium Movement Involved In Cell Motilit	0.42633805	7	9.375e-05	3.886e-02	TEKT1:299 GAS8:674 TEKT4:967 TEKT2:1003 TEKT5:1173 RSPH9:2022
Axoneme Assembly (GO:0035082)	0.19825800	30	1.719e-04	5.706e-02	CFAP46:83 CFAP74:137 SPACA9:147 TTC12:273 GAS8:674 SPAG17:740
Negative Regulation Of DNA-templated Tra	-0.03871945	852	1.564e-04	5.706e-02	MZF1:16 RIOX1:33 CUX2:67 GATAD2A:74 CHD8:79 ZBTB45:82
Regulation Of Heart Rate By Cardiac Cond	0.17341013	39	1.800e-04	5.706e-02	SCN5A:217 DSG2:230 DSP:257 CACNA1G:352 CACNB2:360 KCNQ1:400
Regulation Of Nucleic Acid-Templated Tra	-0.05817142	357	1.746e-04	5.706e-02	MZF1:16 ZNF280A:46 NSD1:83 DAXX:137 LMX1B:151 SRCAP:155
Steroid Metabolic Process (GO:0008202)	-0.13680425	61	2.223e-04	6.654e-02	HSD17B6:77 CYP26C1:102 HSD11B1:167 SULT1E1:230 HSD17B2:466 CYP17A1:499
Action Potential (GO:0001508)	0.18306208	33	2.748e-04	7.428e-02	MYH7B:43 DMD:86 SCN5A:217 KCNQ1:400 ANK3:447 CHRNA4:477
Regulation Of DNA Methylation–Dependent	-0.28077550	14	2.757e-04	7.428e-02	MORC2:84 TASOR:150 TRIM28:739 SAMD1:790 L3MBTL3:966 TET1:1516
Neuropeptide Signaling Pathway (GO:00072	0.13209316	62	3.256e-04	8.354e-02	NPBWR2:100 SSTR4:173 RXFP3:283 PENK:336 GALR1:437 CYSLTR2:443
Cellular Response To UV-A (GO:0071492)	0.34370024	9	3.564e-04	8.729e-02	MMP3:226 MME:228 MMP9:258 TIMP1:823 OPN3:994 OPN1SW:1157
Cardiac Conduction (GO:0061337)	0.15320159	44	4.414e-04	1.034e-01	SCN5A:217 DSG2:230 DSP:257 CACNA1G:352 CACNB2:360 KCNQ1:400
Serine Family Amino Acid Biosynthetic Pr	-0.31461599	10	5.712e-04	1.282e-01	CTH:53 SRR:221 MTHFD1:704 SERINC3:708 SEPHS2:1100 PSPH:1159
Regulation Of DNA Repair (GO:0006282)	-0.08858841	125	6.405e-04	1.380e-01	SMCHD1:52 TAF2:87 PARG:98 ERCC6:204 BCL7A:219 DPF2:229
Axonemal Dynein Complex Assembly (GO:007	0.19600111	24	8.907e-04	1.846e-01	DNAH2:1 DNAH17:17 TTC12:273 DNAH5:520 DNAH8:1094 DNAI1:1411
Chromatin Organization (GO:0006325)	-0.06284819	233	9.936e-04	1.912e-01	HIRA:62 GATAD2A:74 CHD8:79 MORC2:84 CABIN1:105 DAXX:137
Regulation Of Catecholamine Secretion (G	0.18351877	27	9.680e-04	1.912e-01	DTNBP1:93 SYT8:203 CHRNA4:477 SYT6:690 SYT2:767 SYT11:986
G Protein-Coupled Receptor Signaling Pat	0.13718614	47	1.147e-03	2.131e-01	MTNR1B:130 OR10J5:293 MC3R:458 HTR2B:654 MTNR1A:862 VIPR1:982
Positive Regulation Of Transcription By	-0.25907549	13	1.220e-03	2.192e-01	ELL:9 CHD8:79 ICE2:113 ERCC6:204 DDX21:850 SMARCA5:2291
Regulation Of Tyrosine Phosphorylation O	-0.12041766	59	1.391e-03	2.418e-01	TNF:88 IL23R:170 VEGFA:216 LYN:309 IL4:316 TSLP:333
Negative Regulation Of Gene Expression,	-0.13430714	47	1.455e-03	2.449e-01	UBR2:14 MORC2:84 TASOR:150 CBX3:278 DNMT1:623 SIRT6:669
Peptidyl-Lysine Modification (GO:0018205	-0.09869656	85	1.682e-03	2.746e-01	CTH:53 LOX:276 MDM2:283 SLF1:295 SENP7:332 EID3:382
3'-Phosphoadenosine 5'-Phosphosulfate Me	-0.23973207	14	1.900e-03	2.887e-01	SULT1E1:230 SULT1A3:882 SULT2B1:999 SULT1B1:1464 BPNT1:1697 SULT1A2:1751
Myofibril Assembly (GO:0030239)	0.13243262	45	2.127e-03	2.887e-01	CASQ1:108 MYH3:362 MYOM2:411 FLNC:422 KRT19:475 CSRP3:657
Negative Regulation Of Macromolecule Bio	-0.09417884	90	2.043e-03	2.887e-01	IGF2BP2:386 ZAR1:511 INPP5K:580 PATL2:601 MRPL13:632 CPEB3:667
Negative Regulation Of Transcription By	-0.03657880	617	2.144e-03		MZF1:16 CUX2:67 GATAD2A:74 CHD8:79 ZBTB45:82 NSD1:83
Positive Regulation Of DNA Metabolic Pro	-0.08876676	103	1.884e-03		SMCHD1:52 EGF:130 ERCC6:204 BRPF3:450 SIRT6:669 DHX36:723
Positive Regulation Of Heterochromatin F	-0.26768477	11	2.112e-03		MORC2:84 TASOR:150 TRIM28:739 SETDB2:1735 PPHLN1:1956 TPR:2162
Ventricular Cardiac Muscle Cell Action P	0.22273546	16	2.041e-03		SCN5A:217 KCNQ1:400 SCN3B:549 KCNE1:1858 KCNE2:1905 KCNE4:2006

## MGI\_Mammalian\_Phenotype\_Level\_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0000598 abnormal liver morphology	-0.05754598	472	3.536e-05	1.076e-02	MAN2A1:5 CTH:53 TNF:88 HEXB:107 AZIN1:140 GRB14:188
MP0002086 abnormal extraembryonic tissu	-0.05653950	476	4.521e-05	1.076e-02	HAS2:29 SMCHD1:52 HIRA:62 GATAD2A:74 NSD1:83 VCAM1:125
MP0002136 abnormal kidney physiology	-0.06893485	279	1.030e-04	1.634e-02	MAN2A1:5 CLCNKA:6 ALB:20 SLC7A9:34 TRPV1:95 IL12RB2:100
MP0002085 abnormal embryonic tissue	-0.04457540	653	2.173e-04	2.586e-02	HAS2:29 HIRA:62 CUX2:67 GATAD2A:74 CHD8:79 NSD1:83
MP0002135 abnormal kidney morphology	-0.04583655	450	1.265e-03	1.204e-01	MAN2A1:5 SLC7A9:34 TET2:94 TRPV1:95 IL12RB2:100 HEXB:107
MP0009643 abnormal urine homeostasis	-0.05718825	227	3.492e-03	2.025e-01	MAN2A1:5 CLCNKA:6 ALB:20 SLC7A9:34 CTH:53 CASR:112
MP0005253 abnormal eye physiology	0.08705532	92	4.139e-03	2.025e-01	DMD:86 MMP9:258 EGFLAM:291 CACNB2:360 CHD7:432 LBR:555
MP0003121 genomic imprinting	-0.17580658	23	3.566e-03	2.025e-01	SMCHD1:52 HDAC8:352 ARID4A:388 DNMT1:623 NDN:834 HELLS:1258
MP0002148 abnormal hypersensitivity rea	0.08250472	102	4.254e-03	2.025e-01	CD74:111 SSTR4:173 MMP3:226 MME:228 MMP9:258 PTAFR:318
MP0001697 abnormal embryo size	-0.04246100	413	4.082e-03	2.025e-01	HIRA:62 GATAD2A:74 VCAM1:125 DAXX:137 PTPRB:193 MDM2:283
MP0002084 abnormal developmental patter	-0.04207505	360	7.564e-03	3.273e-01	HAS2:29 HIRA:62 GATAD2A:74 CHD8:79 NSD1:83 DAXX:137
MP0005636 abnormal mineral homeostasis	-0.06403467	134	1.123e-02	3.342e-01	ALB:20 CASR:112 SLC26A3:169 TRPM6:177 CLDN16:288 NFE2L2:479
MP0003077 abnormal cell cycle	-0.06028326	155	1.041e-02	3.342e-01	CUX2:67 FANCM:126 MDM2:283 BRD2:287 MYBL2:477 TMPO:483
MP0005551 abnormal eye electrophysiolog	0.06491521	139	8.885e-03	3.342e-01	DMD:86 EGFLAM:291 RBP4:337 CACNB2:360 GJA10:410 EPAS1:419
MP0000313 abnormal cell death	-0.03604516	457	1.068e-02	3.342e-01	PROM1:1 CTH:53 PARG:98 HEXB:107 DAXX:137 TFAM:197
MP0002080 prenatal lethality	-0.02321103	1339	1.080e-02	3.342e-01	MTBP:3 UBR2:14 HAS2:29 SMCHD1:52 HIRA:62 CUX2:67
MP0001664 abnormal digestion	0.08168217	80	1.202e-02	3.364e-01	CFTR:94 NOS1:249 KCNQ1:400 SALL1:797 DLX2:839 SLC15A1:845
MP0002088 abnormal embryonic growth/wei	-0.03949346	336	1.519e-02	4.016e-01	HAS2:29 HIRA:62 DAXX:137 PTPRB:193 ENPP2:220 MDM2:283
MP0000609 abnormal liver physiology	-0.03646665	374	1.846e-02	4.076e-01	MAN2A1:5 ALB:20 RBL1:78 TNF:88 TRPV1:95 IL12RB2:100
MP0005332 abnormal amino acid	-0.06282592	116	2.043e-02	4.076e-01	SLC7A9:34 SLC6A6:51 CTH:53 SRR:221 LEPR:312 ARG1:507
MP0003984 embryonic growth retardation	-0.03792937	328	2.113e-02	4.076e-01	HAS2:29 HIRA:62 DAXX:137 PTPRB:193 ENPP2:220 MDM2:283
MP0000343 altered response to	0.09255960	52	2.141e-02	4.076e-01	TGM2:127 SLC2A4:151 MMP9:258 CYSLTR2:443 MMP7:514 TIMP1:823
MP0002113 abnormal skeleton development	-0.03539480	384	2.061e-02	4.076e-01	MZF1:16 HAS2:29 RBL1:78 CASR:112 LMX1B:151 TRPM6:177
MP0003635 abnormal synaptic transmissio	0.03398759	425	1.986e-02	4.076e-01	CAMK2B:37 NRCAM:41 GRIN2A:101 SLC8A3:171 MMP3:226 NOS1:249
MP0008469 abnormal protein level	-0.03538102	385	2.051e-02	4.076e-01	CTH:53 TNF:88 IL12RB2:100 HEXB:107 SCARB1:141 FCGRT:189
MP0003122 maternal imprinting	-0.17632554	14	2.247e-02	4.115e-01	ARID4A:388 NDN:834 SGCE:1341 DLK1:1817 IGF2:2182 MEST:2371
MP0003656 abnormal erythrocyte physiolo	-0.13774401	22	2.553e-02	4.191e-01	MAN2A1:5 NFE2L2:479 KLF1:674 ANK1:1416 PRKAA1:1946 AQP9:2154
MP0003137 abnormal impulse conducting	0.08195841	64	2.398e-02	4.191e-01	DMD:86 SCN5A:217 MMP9:258 SYNE1:287 CACNA1G:352 KCNQ1:400
MP0001756 abnormal urination	-0.07242938	81	2.504e-02	4.191e-01	CLCNKA:6 ALB:20 TRPV1:95 LEPR:312 SLC14A2:636 SLC26A7:666
MP0002169 no abnormal phenotype	-0.02105910	1166	2.752e-02	4.316e-01	PROM1:1 ALB:20 HAS2:29 ADAM9:39 RBL1:78 CYP26C1:102
MP0000003 abnormal adipose tissue	-0.10906151	34	2.811e-02	4.316e-01	ERCC6:204 BRD2:287 PGF:389 FLT4:762 LPL:821 PRKAR1A:1544
MP0004085 abnormal heartbeat	0.04993082	158	3.221e-02	4.358e-01	BDKRB1:16 TGM2:127 SCN5A:217 NOS1:249 SYNE1:287 CACNA1G:352
MP0000751 myopathy	0.13603281	21	3.116e-02	4.358e-01	PLEC:2 COL6A1:61 DMD:86 COL15A1:366 TCAP:2111 COX10:2170
MP0010329 abnormal lipoprotein level	-0.06851487	82	3.296e-02	4.358e-01	SCARB1:141 HSD11B1:167 PCSK9:198 LEPR:312 PPARA:460 PON2:49
MP0000383 abnormal hair follicle	0.13328435	22	3.070e-02	4.358e-01	DICER1:177 PKP3:213 FGFR2:233 KRT14:552 TRPV3:680 PTK2:1034
MP0002873 normal phenotype	-0.02060332	1171	3.080e-02		PROM1:1 ALB:20 HAS2:29 ADAM9:39 RBL1:78 CYP26C1:102
MP0001970 abnormal pain threshold	0.05015253	150	3.593e-02	4.386e-01	BDKRB1:16 ABCC3:77 SSTR4:173 MMP9:258 AFF2:319 PENK:336
MP0004947 skin inflammation	0.07325368	70	3.494e-02		RAG1:133 PKP3:213 MME:228 FGFR2:233 CBL:376 ITGA3:597
MP0001944 abnormal pancreas morphology	-0.04688084	173	3.563e-02		TFAM:197 LTA:208 BRD2:287 LEPR:312 ATXN2:321 AQP7:381
	-0.02730565	534		4.391e-01	MAN2A1:5 RBL1:78 TNF:88 RAPGEF6:91 CD80:109 GRB14:188

tissue\_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
leg.skin	0.08368782	217	2.613e-05		ANKRD35:6 CARD14:20 RNF222:34 EVPL:42 GGT6:56 KRT80:59
skeletal.muscle	0.08053771	239		7.056e-04	SMTNL2:38 CASQ1:108 FSD2:125 TACC2:136 MYH8:146 SLC2A4:151
EBV.lymphocyte	-0.04702141	671		1.067e-03	TMEM131L:2 MTBP:3 HAUS8:68 RBL1:78 SPDL1:86 TNF:88
suprapubic.skin	0.07776598	194		2.905e-03	CARD14:20 RNF222:34 EVPL:42 GGT6:56 KRT80:59 BNC1:80
liver	-0.05760341	328	4.162e-04	4.495e-03	PRODH2:18 ALB:20 SDS:30 CTH:53 MOGAT1:73 HSD17B6:77
esophagus.mucosa	0.06801220	220		5.236e-03	BDKRB1:16 IQANK1:29 RNF222:34 EVPL:42 FAM83H:75 BNC1:80
thyroid	-0.08040482	151	7.092e-04	5.471e-03	CLCNKA:6 HIRA:62 ISM1:135 GGTLC1:180 VEGFA:216 IDO2:255
left.ventricle	0.10426275	68	3.038e-03	2.050e-02	MYH7B:43 FSD2:125 NRAP:185 SCN5A:217 CKMT2:284 MYOM2:411
pancreas	-0.08522425	94	4.466e-03	2.525e-02	PRODH2:18 CASR:112 EGF:130 ARSL:182 SLC43A1:200 FBXW12:323
vagina	0.08615132	91	4.677e-03	2.525e-02	RNF222:34 EVPL:42 BNC1:80 MAB21L4:154 DSC3:180 ENDOU:232
atrium.auricle	0.07502208	90	1.430e-02	7.019e-02	FSD2:125 NRAP:185 SCN5A:217 CKMT2:284 MYOM2:411 MYOM3:516
cortex.kidney	-0.05982906	114	2.817e-02	1.267e-01	CLCNKB:13 PRODH2:18 CASR:112 OGDHL:190 ATP6V0D2:235 CLDN16:288
cerebral.cortex	0.06060004	107	3.116e-02	1.294e-01	CALHM1:81 ADGRA1:167 HTR3B:357 KCNH3:368 SNPH:453 CIT:483
adrenal.gland	-0.04889247	108	8.070e-02	2.971e-01	ADGRV1:36 ABCB1:48 MGST1:54 SCARB1:141 KLF14:451 CYP17A1:499
testis	0.01503679	1377	8.252e-02	2.971e-01	DNAH2:1 DNAH14:4 DNAH9:5 DNAH17:17 SH2D7:19 CFAP45:25
peyers.patch	0.03622853	167	1.090e-01	3.680e-01	EPS8L3:27 SLC17A4:46 SLC28A1:82 TRPM5:92 KRT20:102 ANPEP:129
esophagus.muscularis.mucosa	0.08110039	26	1.528e-01	4.583e-01	PRUNE2:187 SYNM:240 FAM83D:906 CHRM3:1269 NTN1:1764 KCNMB1:1998
sigmoid.colon	0.05860741	52	1.447e-01	4.583e-01	TACR2:18 PLEKHO1:300 PLA2G2C:375 NTSR1:872 PDE9A:1037 ROR2:1459
eye.development	-0.04164933	67	2.399e-01	6.817e-01	BMP4:1161 FOXC1:1321 PAX6:1787 MSX1:1901 PITX3:2229 ONECUT1:2233
cerebellar.hemisphere	-0.01447233	510	2.753e-01	7.433e-01	MTBP:3 PPFIA3:4 CRB1:45 FAM169A:56 MAP7D2:72 ERAS:139
transverse.colon	0.02533953	149	2.891e-01	7.433e-01	EPS8L3:27 SLC17A4:46 TRIM15:89 KRT20:102 B3GNT6:210 PLEKHG6:215
aorta	0.02354315	154	3.168e-01	7.438e-01	ECM2:112 PCDH11X:126 ACTN1:128 C1QTNF8:142 ADAMTSL3:195 AEBP1:227
C1.spinal.cord	-0.02190278	181	3.136e-01	7.438e-01	ENPP2:220 SEC14L5:223 SLC44A1:306 SLCO1A2:454 SCD:519 KLK6:523
Brodmann.area.24	-0.05001748	31	3.358e-01	7.555e-01	DDN:506 NTRK2:932 SLC6A1:1034 SLC25A18:1232 NCS1:1629 UPP2:1764
lung	-0.02190311	139	3.758e-01	7.647e-01	GGTLC1:180 PTPRB:193 LRRK2:475 IL18R1:493 COL6A6:745 LRRN4:868
pituitary.gland	-0.01751321	212	3.843e-01	7.647e-01	ARHGAP36:218 IL4:316 CLUL1:472 PRRG2:542 RADX:633 DGKK:685
putamen	-0.06260711	15	4.015e-01	7.647e-01	KCNH4:533 ANO3:547 FAM237A:7974 GPR88:7974 LRRC10B:7974 SYNDIG1L:7974
substantia.nigra	-0.06862539	12	4.106e-01	7.647e-01	DBX2:1143 CHRM5:7974 FOXB1:7974 C10orf105:7974 KCNE5:7974 KLHL1:7974
tibial.artery	0.02444088	110	3.783e-01	7.647e-01	TNC:348 TAGLN:504 INHBA:536 CDH6:682 SUSD5:775 MCAM:870
amygdala	0.07214815	9	4.537e-01	7.960e-01	PTPRZ1:577 PCDH15:668 BCAN:8200 LHFPL3:8200 NEUROD2:8200 NEUROD6:820
caudate.nucleus	-0.04219514	26	4.569e-01	7.960e-01	ANO3:547 ETNPPL:710 RGS14:2188 PSD2:2670 HS3ST5:7974 AQP4:7974
tibial.nerve	-0.01515533	192	4.730e-01	7.982e-01	MLIP:106 ABCA9:127 SECISBP2L:213 LEPR:312 EHBP1:347 MYCN:363

6.078e-01 8.675e-01 6.167e-01 8.675e-01

6.747e-01 8.675e-01

182 4.936e-01 8.078e-01 NRCAM:41 CALHM1:81 GRIN2A:101 CSRNP3:114 DACH2:253 HTR3B:357

8 5.114e-01 8.122e-01 F2RL2:1583 ADCY5:2615 BARX1:7974 COL4A5:7974 GADL1:7974 HOXA4:7974

6.430e-01 8.675e-01 UPK1A:1728 CLEC3A:2842 ACER2:7974 ARL14:7974 CYP4B1:7974 DHRS2:7974 6.025e-01 8.675e-01 LRFN5:1753 PAPPA2:2113 RIPOR3:2547 GDF7:7974 TRHDE:7974 ADRA1D:7974

6.228e-01 8.675e-01 CNIH2:931 NEUROD2:7974 NEUROD6:7974 SLC17A7:7974 HRK:7974 OLIG2:7974

BDKRB1:16 PWP2:57 TGM2:127 NXNL2:208 GUCY1A2:224 SPEF2:448

BTNL9:245 LPL:821 IL6:836 GFPT2:1206 LEP:1641 CIDEC:1997

PCDH11X:126 OTOF:140 SV2C:229 DACH2:253 PENK:336 CACNA1E:389

Brodmann.area.9

bladder

endocervix

greater.omentum

hippocampus.proper

nucleus.accumbens

esophagogastric.junction -0.06706076

0.01483959

-0.03012238

11

-0.02736170

0.01754893

-0.02521412

-0.04285094

0.01232437