





RXFP4	5.986146	1.289232e-08	5.969e-05	2.764e-01
KIAA0753	5.813330	3.674537e-08	1.361e-04	5.042e-01
POLM	5.670419	8.546905e-08	2.638e-04	5.441e-01
ITGB4	5.624495	1.116306e-07	2.719e-04	5.441e-01
MR1	5.615740	1.174334e-07	2.719e-04	5.441e-01
STYXL2	5.548107	1.732677e-07	3.209e-04	5.441e-01
TACR2	5.552672	1.688013e-07	3.209e-04	5.441e-01

6.921644 2.678586e-11 4.961e-07

3.934e-02

2.764e-01

ANKRD35 6.507403 4.587677e-10 4.248e-06

DNAH2 6.020759 1.041606e-08 5.969e-05

PPP4R1	-4.930509	4.920936e-06	3.038e-03	1.000e+00
DCAF4	-4.848927	7.447876e-06	3.941e-03	1.000e+00
ELL	-4.852274	7.323224e-06	3.941e-03	1.000e+00
SPATA31A5	-4.835944	7.950909e-06	4.091e-03	1.000e+00
ZNF483	-4.821707	8.540089e-06	4.275e-03	1.000e+00
MAP1S	-4.739267	1.286959e-05	5.956e-03	1.000e+00
TTC3	-4.734376	1.318380e-05	5.956e-03	1.000e+00
NSD1	-4.655979	1.934665e-05	7.465e-03	1.000e+00

-5.092301 2.122464e-06 1.966e-03

-5.096558 2.075309e-06 1.966e-03

1.000e+00

HAVCR1

Geneset	stat	num.genes	pval	p.adj	gene.vals
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.09562023	602		8.987e-12	WDR76:29 KIF18A:32 ZNF644:43 AGGF1:49 ITGB1:89 SLF1:95
REACTOME_KERATINIZATION	0.15220889	202	9.293e-14	3.017e-10	EVPL:46 KRT80:67 KRT20:140 KRTAP10-1:179 KRT28:182 DSP:199
ZHANG_BREAST_CANCER_PROGENITORS_UP	-0.10158855	414	1.489e-12	3.222e-09	TTC3:9 SMCHD1:12 NCAPD3:26 PROM1:27 SYDE2:44 SLF1:95
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	0.17948676	126	3.550e-12	4.379e-09	EVPL:46 KRT80:67 KRT20:140 KRT28:182 DSP:199 KRT84:216
DODD_NASOPHARYNGEAL_CARCINOMA_DN	-0.05833849	1275	3.656e-12	4.379e-09	NCAPD3:26 KIF18A:32 TPX2:39 ZDBF2:45 FGD6:82 L3MBTL4:88
JOHNSTONE_PARVB_TARGETS_3_DN	-0.07275562	793	4.046e-12	4.379e-09	SMCHD1:12 ZNF274:16 SLC6A6:18 NDUFS5:28 WDR76:29 KIF18A:32
REACTOME_SENSORY_PERCEPTION	0.07920862	596	4.574e-11	4.244e-08	OR10R2:44 CALHM1:50 OR10S1:62 OR5AU1:79 OTOF:98 OR9Q2:120
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	-0.07403935	673	6.793e-11	5.514e-08	TTC3:9 ATP13A3:17 KIF18A:32 TPX2:39 ZNF644:43 DHX36:52
PUJANA_BRCA1_PCC_NETWORK	-0.05008095	1520	1.012e-10	7.300e-08	TMEM131L:15 ATP13A3:17 SLC6A6:18 DAXX:25 TPX2:39 FNBP4:60
FISCHER_DREAM_TARGETS	-0.05746899	921	4.067e-09	2.641e-06	SMCHD1:12 NCAPD3:26 WDR76:29 KIF18A:32 TPX2:39 GATAD2A:55
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.06833373	624	6.348e-09	3.748e-06	SMCHD1:12 TASOR:20 KIF18A:32 ZNF644:43 AGGF1:49 DHX36:52
REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.08441104	384	1.453e-08	7.861e-06	OR10R2:44 OR10S1:62 OR5AU1:79 OR9Q2:120 OR6C65:128 OR10T2:133
KEGG_OLFACTORY_TRANSDUCTION	0.08196571	372	6.023e-08	3.009e-05	OR10R2:44 OR10S1:62 OR5AU1:79 OR9Q2:120 OR6C65:128 OR10T2:133
REACTOME_CELL_CYCLE	-0.06227513	651	6.611e-08	3.067e-05	DAXX:25 NCAPD3:26 KIF18A:32 TPX2:39 HERC2:74 HAUS8:134
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.09790457	249	1.075e-07	4.653e-05	CHRM3:37 PTAFR:70 BDKRB1:82 MTNR1B:94 P2RY4:146 OR2H2:175
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	-0.04507484	1211	1.576e-07	6.019e-05	PROM1:27 WDR76:29 KIF18A:32 TPX2:39 CYP4F22:46 GEMIN5:84
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.07309393	440	1.568e-07	6.019e-05	NCAPD3:26 WDR76:29 KIF18A:32 TPX2:39 GLMN:92 QSER1:123
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04453125	1189	2.800e-07	1.010e-04	TTC3:9 MAGEL2:41 PEG3:65 LTN1:70 HERC2:74 SON:76
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	-0.05260641	826	3.170e-07	1.083e-04	SMCHD1:12 TMEM131L:15 ATP13A3:17 ZNF292:19 TASOR:20 MYO9B:24
HOUNKPE_HOUSEKEEPING_GENES	-0.04633967	1073	3.478e-07	1.129e-04	ELL:4 MORC2:11 RNF216:35 MBD1:37 KDM4B:38 AGGF1:49
SHEN_SMARCA2_TARGETS_UP	-0.07201337	410	5.977e-07	1.848e-04	AGGF1:49 HERC2:74 SON:76 TMEM135:80 PHF3:83 KTN1:117
DODD_NASOPHARYNGEAL_CARCINOMA_UP	0.03748039	1576	8.731e-07	2.577e-04	ANKRD35:2 DNAH2:3 KIAA0319:12 USP43:20 DNAH9:21 SPACA9:40
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.03993348	1335	1.180e-06	3.331e-04	PPP4R1:3 MAN2A1:36 KTN1:117 KDSR:125 MLLT10:141 CTPS2:142
SCHLOSSER_SERUM_RESPONSE_DN	-0.05520789	655	1.566e-06	4.239e-04	TASOR:20 ARSL:21 PHF3:83 GLMN:92 GRB14:103 CMTR1:113
REACTOME_CELL_CYCLE_MITOTIC	-0.06104403	524	1.861e-06	4.835e-04	NCAPD3:26 KIF18A:32 TPX2:39 HAUS8:134 ANAPC1:156 KIF2C:168
PUJANA_CHEK2_PCC_NETWORK	-0.05196210	711	2.580e-06	6.444e-04	TMEM131L:15 ATP13A3:17 TPX2:39 GLMN:92 TAF2:144 BIK:166
FEVR_CTNNB1_TARGETS_DN	-0.05889483	530	3.736e-06	8.987e-04	KIF18A:32 DHX36:52 MTBP:64 HAUS8:134 DNMT1:203 NINL:208
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-0.06033634	496	4.458e-06	1.034e-03	SMCHD1:12 AGGF1:49 LTN1:70 ZNF326:169 ERI1:197 NIFK:245
MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN	-0.05952733	502	5.270e-06	1.180e-03	PPP4R1:3 MBD1:37 PLAGL1:53 SON:76 SAFB2:126 MLLT10:141
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.05692390	531	7.648e-06	1.655e-03	LTN1:70 CLU:73 LRP2:79 PHF3:83 WSB1:206 FNTA:232
MARTENS_TRETINOIN_RESPONSE_UP	0.04682926	782	9.230e-06	1.934e-03	SPEM2:13 PIK3R5:26 OPLAH:42 SMTNL2:43 GGT6:45 CARD14:48
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	0.06256798	426	9.918e-06	2.013e-03	LTK:11 FAM83F:29 CHAD:68 PDE1B:80 CACNA1G:103 SYT6:180
REACTOME_SIGNALING_BY_GPCR	0.04923620	684	1.225e-05	2.410e-03	RXFP4:4 TACR2:9 PIK3R5:26 CHRM3:37 ARHGEF11:38 PTAFR:70
WP_NONALCOHOLIC_FATTY_LIVER_DISEASE	-0.10332280	144	1.891e-05	3.613e-03	NDUFS5:28 NDUFB5:155 NDUFB8:188 CASP8:227 NDUFA11:258 TNF:462
OSMAN_BLADDER_CANCER_UP	-0.06381166	376	2.233e-05	4.028e-03	NOL9:23 MAN2A1:36 DHX36:52 KTN1:117 G2E3:215 ATP11B:267
PID_MYC_ACTIV_PATHWAY	-0.13892214	78	2.229e-05		BCAT1:240 PEG10:338 ACTL6A:409 DDX18:716 BAX:760 CDCA7:806
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.20918062	34	2.432e-05	4.156e-03	DCST1:61 THBS3:121 PBXIP1:213 DCST2:227 LINGO4:285 SHC1:367
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	-0.03506427	1306		4.156e-03	ELL:4 ZNF483:7 ZNF274:16 DAXX:25 TPX2:39 PLAGL1:53
REACTOME CELL CYCLE CHECKPOINTS	-0.07447201	270		4.323e-03	KIF18A:32 HERC2:74 ANAPC1:156 KIF2C:168 RNF8:246 CCNE1:260
DUNTAEDT DUOTODYNAMIO THERADY OTDESS HE	0.04404635	704		1.514 00	FULL MARKS STATESTA AS OLDONO AS MACULOSO OS ACRAMAS OS

DisGeNET Top pathways by non-permulation

ELL:4 MAP1S:8 ZNF274:16 SLC6A6:18 WASHC2C:33 KDM4B:38

AGGF1:49 PECAM1:75 GLMN:92 VEGFA:733 PIK3CA:1412 STAT1:1901

2.495e-03 5.652e-01 HAVCR1:2 PROM1:27 PECAM1:75 TCL1B:109 IL1RAP:181 PRAME:193

2.705e-03 5.652e-01 TNF:462 GTF2IRD1:518 RBM45:603 ALB:979 ABCB1:1052 SLCO6A1:2435

BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP -0.04401625

Venous malformation

Myeloid Leukemia, Chronic

Balkan Nephropathy

NA.36

-0.22360262

-0.03273949

-0.22369007

Geneset	stat	num.genes	pval	p.adj	gene.vals
Hepatitis C	-0.05536748	677	1.122e-06	1.102e-02	HAVCR1:2 TSLP:22 CLU:73 DEPDC5:138 PPIP5K1:191 DNMT1:203
Leukemia, Myelocytic, Acute	-0.03293358	1494	3.058e-05	1.010e-01	ELL:4 NSD1:10 DAXX:25 PROM1:27 SON:76 ZNF331:78
Liver carcinoma	-0.02461420	3048	3.086e-05	1.010e-01	HAVCR1:2 MAP1S:8 NSD1:10 PROM1:27 KIF18A:32 KDM4B:38
Liver neoplasms	-0.03518935	1184	5.965e-05	1.464e-01	NSD1:10 PROM1:27 KDM4B:38 CLU:73 SUGP1:77 ITGB1:89
Arthrogryposis	0.06454270	297	1.377e-04	2.705e-01	ITGB4:7 PLEC:23 EGR2:289 COL6A1:318 FLNC:322 DES:343
Seborrheic dermatitis	-0.22978703	22	1.911e-04	3.127e-01	JMJD1C:233 SLCO2A1:416 TNF:462 HPGD:674 HIRA:1036 ANP32B:1223
Acute lymphocytic leukemia	-0.03664729	803	4.772e-04	4.154e-01	TSLP:22 PROM1:27 CRLF2:34 PECAM1:75 ITGB1:89 MLLT10:141
Epidermolysis Bullosa Simplex	0.20560821	23	6.427e-04	4.154e-01	ITGB4:7 PLEC:23 KRT80:67 DES:343 GFAP:396 KRT17:500
Extramedullary Hematopoiesis (disorder)	-0.20081781	25	5.107e-04	4.154e-01	TSLP:22 TNF:462 TNFSF11:594 VEGFA:733 CA2:797 NPM1:1104
Fanconi Anemia	-0.06161172	268	5.392e-04	4.154e-01	LRP2:79 BIK:166 CASP8:227 RNF8:246 CCNE1:260 TERF2:283
Fatty Liver	-0.04990047	399	6.653e-04	4.154e-01	SUGP1:77 LATS2:93 DNMT1:203 CASP8:227 MET:247 LGALS3:306
Hepatocarcinogenesis	-0.04886932	464	3.359e-04	4.154e-01	PROM1:27 KDM4B:38 CLU:73 TCL1B:109 DNMT1:203 CASP8:227
Influenza	-0.04534815	508	5.088e-04	4.154e-01	SAFB:106 GYPB:153 CD86:218 CASP8:227 CTLA4:280 CD9:294
leukemia	-0.02563927	1721	5.564e-04	4.154e-01	ELL:4 NSD1:10 SMCHD1:12 TSLP:22 DAXX:25 PROM1:27
Steatohepatitis	-0.04425564	510	6.769e-04	4.154e-01	SUGP1:77 LATS2:93 PPP1R3A:124 DNMT1:203 CASP8:227 LGALS3:306
Tetany	-0.22649200	19	6.319e-04	4.154e-01	TRPM6:72 CLDN16:205 JMJD1C:233 PTH:715 HIRA:1036 SLC12A1:1192
Prostate carcinoma	-0.02080305	2731	7.218e-04	4.169e-01	ELL:4 MAP1S:8 NSD1:10 DAXX:25 NCAPD3:26 PROM1:27
Junctional split	0.38673271	6	1.035e-03	5.363e-01	ITGB4:7 PLEC:23 LAMC2:99 ITGA6:1626 LAMB3:1638 LAMA3:9306.5
Seminoma	-0.06727220	201	1.038e-03	5.363e-01	PROM1:27 CLU:73 TCL1B:109 PRAME:193 DNMT1:203 SLC43A1:223
FANCONI ANEMIA, COMPLEMENTATION GROUP A	-0.05970162	232	1.785e-03	5.595e-01	CASP8:227 RNF8:246 TERF2:283 TTK:288 BACH1:309 AFP:318
Muscular Dystrophies, Limb-Girdle	0.09649546	85	2.123e-03	5.595e-01	PLEC:23 RIPOR2:169 SYVN1:239 COL6A1:318 FLNC:322 DES:343
22q11 partial monosomy syndrome	-0.27575628	11	1.541e-03	5.595e-01	PI4KA:225 JMJD1C:233 HIRA:1036 ARVCF:1439 TBX1:1742 GNB1L:1826
Adult Medulloblastoma	-0.11917070	57	1.869e-03	5.595e-01	KDM4B:38 EHMT1:143 PRAME:193 DNMT1:203 CCNE1:260 UHRF1:351
Carcinogenesis	-0.01764150	3552	1.635e-03	5.595e-01	MAP1S:8 NSD1:10 SMCHD1:12 DAXX:25 PROM1:27 KIF18A:32
Central neuroblastoma	-0.02444147	1508	1.891e-03	5.595e-01	NSD1:10 PROM1:27 KDM4B:38 TPX2:39 PEG3:65 CLU:73
Congenital myopathy (disorder)	0.08819921	109	1.486e-03	5.595e-01	MYH7B:250 COL6A1:318 FLNC:322 DES:343 MYH8:471 CASQ1:491
DiGeorge Syndrome	-0.11504301	60	2.068e-03	5.595e-01	JMJD1C:233 DGCR6:628 ARSA:693 VEGFA:733 ALB:979 SLC25A1:1007
Granulomatosis	0.29519266	9	2.165e-03	5.595e-01	PTPN22:93 PRTN3:96 NOD2:158 HLA-DPB1:977 CYBB:1126 NCF2:1399
Lone atrial fibrillation	0.24846689	13	1.923e-03	5.595e-01	KCNN3:75 TBX5:425 SCN3B:573 SCN5A:624 KCNE3:835 LMNA:1274
Malignant neoplasm of lung	-0.02111222	2132	1.866e-03	5.595e-01	DCAF4:5 NSD1:10 MYO9B:24 PROM1:27 MBD1:37 KDM4B:38
Malignant neoplasm of prostate	-0.01859395	2839	2.165e-03	5.595e-01	ELL:4 MAP1S:8 NSD1:10 ZNF292:19 DAXX:25 NCAPD3:26
Malignant tumor of cervix	-0.03348612	747	2.035e-03	5.595e-01	PEG3:65 CLU:73 SUGP1:77 CALCR:100 OGDHL:164 DNMT1:203
Oral mucosal blisters	0.28487604	10	1.812e-03	5.595e-01	ITGB4:7 PLEC:23 LAMC2:99 DSP:199 ITGA6:1626 LAMB3:1638
Paracoccidioidomycosis	-0.23386157	15	1.714e-03	5.595e-01	CTLA4:280 GPI:349 RBM45:603 IL23R:678 IFNG:690 CD28:717
Plantar hyperkeratosis	0.33929586	7	1.878e-03	5.595e-01	ITGB4:7 PLEC:23 LAMC2:99 KRT6A:609 LAMB3:1638 COL17A1:9306.5
Primary malignant neoplasm of lung	-0.02247932	1973	1.339e-03	5.595e-01	DCAF4:5 NSD1:10 MYO9B:24 PROM1:27 MBD1:37 KDM4B:38
T-lymphocyte immunodeficiency	0.37419809	6	1.502e-03	5.595e-01	CD3E:252 SFTPA1:386 SIPA1:601 RAG1:1005 LBR:2597 SMARCAL1:9306.5
V 16 C	0.0000000	40	4.050 00	F FOF 04	ACCEA 40 DECAMA 75 OLANI 00 VECEA 700 DIVOCA 4440 OTATA 4004

customGeneSet Top pathways by non-permulation

1.958e-03 5.595e-01

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	-0.07354926	13	4.105e-01	6.157e-01	SLC22A4:2278 LCT:2339 GPX1:2775 AS3MT:9215.5 GPX3:9215.5 CELF1:9215.5
expressionDirectionalSelection	0.06335034	42	3.718e-01	6.157e-01	TRIM40:916 LILRA4:2269 KAT8:2339 ZNF646:2746 HLA-DQB1:9306.5 HLA-DRB1:9306.5
NAFLDGWAS	-0.02424242	15	7.747e-01	7.747e-01	ADH1B:1205 GPAM:2597 PNPLA3:9215.5 TM6SF2:9215.5 APOE:9215.5 TRIB1:9215.5
NA	NA	NA	NA	NA	NA NA NA NA NA
NA.1	NA	NA	NA	NA	NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA
NA.14	NA	NA	NA	NA	NA NA NA NA NA
NA.15	NA	NA	NA	NA	NA NA NA NA NA
NA.16	NA	NA	NA	NA	NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA
NA.18	NA	NA	NA	NA	NA NA NA NA NA
NA.19	NA	NA	NA	NA	NA NA NA NA NA
NA.20	NA	NA	NA	NA	NA NA NA NA NA
NA.21	NA	NA	NA	NA	NA NA NA NA NA
NA.22	NA	NA	NA	NA	NA NA NA NA NA
NA.23	NA	NA	NA	NA	NA NA NA NA NA
NA.24	NA	NA	NA	NA	NA NA NA NA NA
NA.25	NA	NA	NA	NA	NA NA NA NA NA
NA.26	NA	NA	NA	NA	NA NA NA NA NA
NA.27	NA	NA	NA	NA	NA NA NA NA NA
NA.28	NA	NA	NA	NA	NA NA NA NA NA
NA.29	NA	NA	NA	NA	NA NA NA NA NA
NA.30	NA	NA	NA	NA	NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA
NA.35	NA	NA	NA	NA	NA NA NA NA NA

GO_Biological_Process_2023 Top pathways by non-permulation

Detection Of Chemical Stimulus Involved 124 1,713=-09 3,08806 OR1092340 OR1092330 OR1092303 OR10923030 Intermediate Filament Organization (CO	Detection Of Chemical Stimulus Involved	0.15771282	126	1.031e-09	3.088e-06	OR10R2:44 OR10S1:62 OR10T2:133 OR2H2:175 OR2K2:293 OR10J5:303
Regulation Of Transcription By RNA Polym -0.03359959 1925 2.139e-08 2.313e-03 NSD110 ZNE72416 ZNE92:19 MAGEL241 ZNF644.43 DHX96.52 Muscie Centraction (GO:0006936) 0.12789129 92 2.237e-05 1.643e-02 TACR2.9 ARHGEF11:38 RYR3:160 CHRN82:256 MYH13:275 DES:343 Regulation Of DNA Metabolic Process (GO: -0.11081365 122 2.337e-05 1.643e-02 SLF1:95 TAF2:148 SUPT20H:231 SLF2:223 OBIL:279 TERF2:283 Supramolecular Fiber Organization (GO:000 0.0798479 305 2.189e-05 1.643e-02 SLF1:95 TAF2:148 SUPT20H:231 SLF2:223 OBIL:279 TERF2:283 Supramolecular Fiber Organization (GO:000 0.0798479 305 2.189e-05 1.643e-02 SLF1:95 TAF2:148 SUPT20H:231 SLF2:223 OBIL:279 TERF2:283 Supramolecular Fiber Organization (GO:000704 0.03931521 980 3.951e-05 2.374e-02 NSD1:10 ZNF274:16 DAXX:25 MAGEL2:41 CARTAD:2A.55 IL33:61 Regulation Of DNA-templated Transcription -0.02879991 1834 6.675e-05 3.020e-02 SLF1:34 ND1:10 ZNF274:16 ZNF292:19 DAXX:25 MAGEL2:41 ZNF644:34 Nogative Regulation Of Catecholamine Secretion (GO:00072 0.06882225 264 1.486e-04 4.819e-02 SNF1:10 ZNF274:16 ZNF292:19 DAXX:25 MAGEL2:41 ZNF644:34 Regulation Of Catecholamine Secretion (GO:00072 0.06882225 264 1.486e-04 4.819e-02 SNF1:12 DTN8:139 SYT6:180 CHRN8:2:255 FAR8:324 CKNM81:212 Regulation Of Tyrosine Phosphory (GO:0000787975 191 1.486e-04 4.819e-02 MINK1:35 CHRN3:37 MTNR:1994 GPR176:185 GABRRS:204 KCNM81:212 Regulation Of Tyrosine Phosphory (GO:000000000000000000000000000000000000	Detection Of Chemical Stimulus Involved	0.15684281	124	1.713e-09	3.088e-06	OR10R2:44 OR10S1:62 OR10T2:133 OR2H2:175 OR2K2:293 OR10J5:303
Rogulation Of Transcription by RNA Polym -0.0335989 1925 2.139e-08 2.139e-08 2.139e-09 1.643e-02 TACR2:9 ARHGEF11:38 RYR3:160 CHRNB:2:55 MYH13:275 DES:343 Regulation Of DNA Metabolic Process (GO0.11081985 122 2.439e-05 1.643e-02 SLF1:395 TAF2:144 SUPT20H:231 SLF2:234 OBIt:279 TERF2:283 Supramolecular Fiber Organization (GO:00 0.07094799 305 2.189e-05 1.643e-02 POFIB:16 (RYR8):679 CEPT26:131 KRT20:140 KRT28:182 DSP:199 Negative Regulation Of DNA-templated Transcriptio -0.03319521 90 3.951e-05 2.374e-02 NSD:10:2797274:16 DAXX:25 MAGEL2:41 GATD:2A:55 IL33:61 Positive Regulation Of DNA-templated Transcriptio -0.03509275 1203 5.585e-05 3.02e-02 ELL:4 NSD:11:0 DHX36:52 PLAGIL:38 GATD:2A:55 IL33:61 Regulation Of DNA-templated Transcriptio -0.02879991 1834 6.875e-05 3.879e-02 NSD:10:27147-16 DAXX:25 DHX36:52 ITGB8:146 DNMT:203 Negative Regulation Of Gene Expression (-0.06314614 328 9.050e-05 3.862e-02 SYT8:126 DTNBP1:139 SYT6:180 CHRNB:225 FRAB:342 CHRNA-4811 Chemical Synaptic Transmission (GO:00077 2.0683225 2.489e-04 4.819e-02 SYT8:126 DTNBP1:139 SYT6:180 CHRNB:225 FRAB:342 CHRNA-4811 Chemical Synaptic Transmission (GO:00077 2.07097875 191 1.486e-04 5.357e-02 MINN:135 CHRNB:37 MTNRIB:94 GPRT:6:165 GABRR:320 KCNMB1:212 Regulation Of Transcription By -0.26893488 15 3.464e-04 9.57e-02 SYT8:126 DTNBP1:139 SYT6:180 CHRNB:225 SYT13:1094 SYT2:1302 Positive Regulation Of Transcription By -0.26893488 15 3.464e-04 9.857e-02 SYT8:125 DTNBP1:139 SYT6:180 CHRNB:225 SYT13:1094 SYT2:1302 Positive Regulation Of Transcription By -0.26893488 15 3.464e-04 9.857e-02 SYT8:125 DTNBP1:139 SYT6:180 CHRNB:225 SYT13:1094 SYT2:1302 Positive Regulation Of Transcription By -0.3384507 7 4.087e-04 1.052e-01 ALOXE:3153 ALOXI55:32 GATD:2605 GSTM:11675 CHRNB:1370 Negative Regulation Of Transcription By -0.33445500 9 5.160e-04 1.192e-01 ALOXE:3153 ALOXI55:32 GATD:2605 GSTM:11675 CHRNB	Intermediate Filament Organization (GO:0	0.21809065	65	1.229e-09	3.088e-06	KRT80:67 KRT20:140 KRT28:182 DSP:199 KRT84:216 KRT39:244
Muscle Contraction (GO.0006336) 0,12788129 92 2,287e-05 1,643e-02 SLF1:95 TAZP:144 SUPT20H:231 SLF2:34 OBI-279 TERF2:283	Sensory Perception Of Smell (GO:0007608)	0.10666859	205	1.511e-07	2.042e-04	OR10R2:44 OR10S1:62 OR9Q2:120 OR10T2:133 OR2H2:175 OR8H3:201
Regulation Of DNA Metabolic Process (GO - 0.11081365 122	Regulation Of Transcription By RNA Polym	-0.03359959	1925	2.139e-06	2.313e-03	NSD1:10 ZNF274:16 ZNF292:19 MAGEL2:41 ZNF644:43 DHX36:52
Supramolecular Fiber Organization (GO:000 0.07/09/199 305 2.1896-05 1.6438-02 POF18-16 KRT80-67 CEP128-131 KRT20-140 KRT28-182 DSP-199 Nogative Regulation Of DNAtemplated Tra	Muscle Contraction (GO:0006936)	0.12788129	92	2.287e-05	1.643e-02	TACR2:9 ARHGEF11:38 RYR3:160 CHRNB2:255 MYH13:275 DES:343
Negative Regulation Of DNA-templated Tra	Regulation Of DNA Metabolic Process (GO:	-0.11081365	122	2.430e-05	1.643e-02	SLF1:95 TAF2:144 SUPT20H:231 SLF2:234 OBI1:279 TERF2:283
Positive Regulation Of DNA-templated Transcription -0.03509275 1203 6.875e-05 3.020e-02 NSD:110 DHX3652 PLAGL1:53 GATAD2A:55 IL33:61 Regulation Of DNA-templated Transcription -0.06314614 328 9.096e-05 3.675e-05 3.799e-02 NSD:110 ZNF274:16 ZNF292:19 DAXX:25 MAGEL2:41 ZNF64:43 Negative Regulation Of Gene Expression (-0.06314614 328 9.096e-05 3.862e-02 NSD:110 ZNF274:16 ZNF292:19 DAXX:25 MAGEL2:41 ZNF64:43 Noncoloration of Catecholamine Secretion (G0.00735994 7 9.286e-05 3.862e-02 SYT8:126 DTN8P1:139 SYT6:180 CHRNB:2:255 FFAR3:424 CHRNAr.811 Chemical Synaptic Transmission (G. 0.0072 0.06882225 264 1.248e-04 4.819e-02 MINK135 CHRM3:37 MTNR18:94 GPR176:185 GABRR3:204 KCNMB1:212 Anterogrado Trans-Synaptic Signaling (GO	Supramolecular Fiber Organization (GO:00	0.07094799	305	2.189e-05	1.643e-02	POF1B:16 KRT80:67 CEP126:131 KRT20:140 KRT28:182 DSP:199
Regulation Of DNA-templated Transcriptio -0.08374914 -0.09374914 -0.08374914 -0.08374914 -0.09374914 -	Negative Regulation Of DNA-templated Tra	-0.03931521	980	3.951e-05	2.374e-02	NSD1:10 ZNF274:16 DAXX:25 MAGEL2:41 GATAD2A:55 IL33:61
Negalive Regulation Of Gene Expression (Positive Regulation Of DNA-templated Tra	-0.03509275	1203	5.585e-05	3.020e-02	ELL:4 NSD1:10 DHX36:52 PLAGL1:53 GATAD2A:55 IL33:61
Regulation Of Catecholamine Secretion (G 0.21735904 27 9.286e-05 3.862e-02 SYT8:126 DTNBP1:139 SYT6:180 CHRNB2:255 FFAR3:424 CHRNA4:811 Chemical Synaptic Transmission (GO:00072 0.00882225 264 1.248e-04 4.819e-02 MINK1:35 CHRM3:37 MTNR18:94 GPR176:165 GABRR3:204 KCNMB1:212 Regulation Of Tyrosine Phosphorylation O -0.12225566 65 2.288e-04 7.731e-02 TSLP:22 SH2B3:428 0SM:446 TNF-462 IL3:514 IL23R:678 Regulation Of Dopamine Secretion (GO:001 0.22273742 22 2.991e-04 9.514e-02 SYT8:126 DTNBP1:139 SYT6:180 CHRNB2:255 SYT3:13094 SYT2:1302 Positive Regulation Of Tyrosine Phosphory Interference of Color of Co	Regulation Of DNA-templated Transcriptio	-0.02879991	1834	6.875e-05	3.379e-02	NSD1:10 ZNF274:16 ZNF292:19 DAXX:25 MAGEL2:41 ZNF644:43
Chemical Synaptic Transmission (G0:00072 0.06882225 264 1.248e-04 4.819e-02 MINK1:35 CHRM3:37 MTNR1B:94 GPR176:165 GABRR3:204 KCNMB1:212 Anterograde Transmission (G0:000 0.07978795 191 1.486e-04 5.357e-02 MINK1:35 CHRM3:37 MTNR1B:94 GPR176:165 GABRR3:204 KCNMB1:212 Regulation Of Tyrosine Phosphorylation 0.07978795 191 1.486e-04 5.357e-02 MINK1:35 CHRM3:37 MTNR1B:94 GPR176:165 GABRR3:204 KCNMB1:212 2.281e04 7.731e-02 TSLP:22 SH2B:4249 OSM:445 ETNE42 IL35:141 IL238:678 191 192	Negative Regulation Of Gene Expression (-0.06314614	328	9.060e-05	3.862e-02	MORC2:11 TASOR:20 DAXX:25 DHX36:52 ITGB8:146 DNMT1:203
Anterograde Trans-Synaptic Signaling (GO 0.07978795 191 1.486e-04 5.357e-02 MINK1:35 CHRM3:37 MTNR1B:94 GPR176:165 GABRR3:204 KCNMB1:212 Regulation Of Dropamine Secretion (GO:001 0.2225566 65 2.288e-04 7.73fe-02 TSLP:22 SH2B3:428 OSM:446 TNF:462 IL3:514 IL23R:678 Regulation Of Dropamine Secretion (GO:001 0.22273742 22 2.991e-04 9.514e-02 SYT8:126 DTNBP1:139 SYT6:180 CHRMB2:255 SYT13:094 SYT2:1302 Positive Regulation Of Transcription By -0.26683468 15 3.464e-04 9.857e-02 ELL4 CHD8:116 ERCC6:302 ICE2:331 DER:337 ZNF143:1068 Positive Regulation Of Tyrosine Phosphor -0.13964603 55 3.431e-04 9.857e-02 TSLP:22 OSM:446 TNF:462 IL3:514 IL23R:678 IPRG:690 Hepoxilin Biosynthetic Process (GO:00511 0.38574307 7 4.087e-04 1.052e-01 ALOXE3:153 ALOX15B:422 ALOX15:535 GSTM2:806 GSTM1:1875 ALOX12B:1994 Positive Regulation Of Transcription By -0.03488770 906 4.364e-04 1.072e-01 ELL4 DHX36:52 PLAGI:153 IL33:61 PEG3:65 CHD8:116 GProtein-Coupled Receptor Signaling Pat 0.14271720 49 5.514e-04 1.192e-01 CHRM3:37 MTNR1B:94 OR103:5303 MC3R:868 CCR1:1204 CHRM2:1370 Negative Regulation Of Gene Expression, -0.14285420 49 5.446e-04 1.192e-01 CHM3:37 MTNR1B:94 OR103:5303 MC3R:868 CCR1:1204 CHRM2:1370 Negative Regulation Of Tanscription By -0.03445709 5 5.160e-04 1.192e-01 CTH:171 PSPH:220 SERINC5:531 MTHFD1:1196 SERINC3:1472 SRR:2431 Long-Chain Fatty Acid Biosynthetic Proces (GO:0055090) 0.244411924 16 7.126e-04 1.427e-01 CALHM1:50 CALHM3:176 PKD1L3:262 GNAT3:789 ASIC2:1254 PKD2L1:1597 Negative Regulation Of Transcription By -0.03643959 731 8.943e-04 1.727e-01 NSD1:10 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.22512730 17 1.312e-03 2.336e-01 MCRC:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.22512730 17 1.312e-03 2.336e-01 MCRC:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.22516730 17 1.312e-03 2.336e-01 MCRC:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.2	Regulation Of Catecholamine Secretion (G	0.21735904	27	9.286e-05	3.862e-02	SYT8:126 DTNBP1:139 SYT6:180 CHRNB2:255 FFAR3:424 CHRNA4:811
Regulation Of Tyrosine Phosphorylation O Regulation Of Dopamine Secretion (GO:001 Regulation Of Dopamine Secretion (GO:001 Regulation Of Transcription By Positive Regulation Of Tyrosine Phosphor -0.13964603 -0.26683468 -0.3464e-04 -0.45867e-02 -0.26683468 -0.45867e-02 -0.38574307 -0.45868468 -0.45864603 -0.48876-04 -0.45864603 -	Chemical Synaptic Transmission (GO:00072	0.06882225	264	1.248e-04	4.819e-02	MINK1:35 CHRM3:37 MTNR1B:94 GPR176:165 GABRR3:204 KCNMB1:212
Regulation Of Dopamine Secretion (GO:001 0.22273742 22 2.991e-04 9.514e-02 SYT8:126 DTNBP1:139 SYT6:180 CHRNB2:255 SYT13:1094 SYT2:1302 Positive Regulation Of Transcription By -0.26683468 15 3.464e-04 9.857e-02 ELL:4 CHDB:116 ERCC6:302 ICE2:331 DEK:337 ZNF143:1068 Positive Regulation Of Tyrosine Phosphor -0.13964603 55 3.431e-04 9.857e-02 TSLP:22 OSM:446 TNF:462 IL3:514 IL23R:678 IFNG:690 Hepoxilin Biosynthetic Process (GO:00511 0.38574307 7 4.087e-04 1.052e-01 ALOXE3:153 ALOX15B:422 ALOX15:355 GSTM2:806 GSTM1:1875 ALOX12B:1994 Hepoxilin Metabolic Process (GO:0051121) 0.38574307 7 4.087e-04 1.052e-01 ALOXE3:153 ALOX15B:422 ALOX15:355 GSTM2:806 GSTM1:1875 ALOX12B:1994 Positive Regulation Of Transcription By -0.03488770 906 4.364e-04 1.072e-01 ELL:4 DHX36:52 PLAGL:53 IL33:61 PEG3:65 CHD8:116 GProtein-Coupled Receptor Signaling Pat 0.14271720 49 5.514e-04 1.192e-01 CHRM3:37 MTNRIB:194 OPRIOJ.533 MG3R:868 CGR1:1204 CHRM2:1370 Negative Regulation Of Gene Expression, -0.14285420 49 5.446e-04 1.192e-01 CHRM3:37 MTNRIB:194 OPRIOJ.5331 MG3R:868 CGR1:1204 CHRM2:1370 Serine Family Amino Acid Biosynthetic Proce 0.20127531 24 6.433e-04 1.192e-01 CHRM2:338 ALOX15B:422 ALOX15:535 ACSBG1:694 GSTM2:806 SSTM2:806 S	Anterograde Trans-Synaptic Signaling (GO	0.07978795	191	1.486e-04	5.357e-02	MINK1:35 CHRM3:37 MTNR1B:94 GPR176:165 GABRR3:204 KCNMB1:212
Positive Regulation Of Transcription By	Regulation Of Tyrosine Phosphorylation O	-0.13225566	65	2.288e-04	7.731e-02	TSLP:22 SH2B3:428 OSM:446 TNF:462 IL3:514 IL23R:678
Positive Regulation Of Tyrosine Phosphor	Regulation Of Dopamine Secretion (GO:001	0.22273742	22	2.991e-04	9.514e-02	SYT8:126 DTNBP1:139 SYT6:180 CHRNB2:255 SYT13:1094 SYT2:1302
Hepoxilin Biosynthetic Process (GO:00511 0.38574307 7 4.087e-04 1.052e-01 ALOXE3:153 ALOX15B:422 ALOX15:535 GSTM2:806 GSTM1:1875 ALOX12B:1994	Positive Regulation Of Transcription By	-0.26683468	15	3.464e-04	9.857e-02	ELL:4 CHD8:116 ERCC6:302 ICE2:331 DEK:337 ZNF143:1068
Hepoxilin Metabolic Process (GC:0051121) 0.38574307 7 4.087e-04 1.052e-01 ALOXE3:153 ALOX15:335 GSTM2:806 GSTM1:1875 ALOX12B:1994 Positive Regulation Of Transcription By -0.03488770 906 4.364e-04 1.072e-01 ELL:4 DHX36:52 PLAGL1:53 IL33:61 PEG3:65 CHD8:116 Positive Regulation Of Gene Expression, -0.14285420 49 5.514e-04 1.192e-01 CHRM3:37 MTNR1B:94 ORIDJS:303 MC3R:868 CCR1:1204 CHRM2:1370 North Control of Gene Expression, -0.14285420 49 5.466e-04 1.192e-01 CHRM3:37 MTNR1B:94 ORIDJS:303 MC3R:868 CCR1:1204 CHRM2:1370 North Control of Gene Expression, -0.14285420 49 5.466e-04 1.192e-01 CTH:171 PSPH:220 SERINC5:531 MTHFD1:1196 SERINC3:1472 SRR:2431 Long-Chain Fatty Acid Biosynthetic Proce 0.20127531 24 6.433e-04 1.338e-01 ALOXE3:153 ALOX12:378 ALOX15B:422 ALOX15:535 ACSBG1:694 GSTM2:806 Sensory Perception Of Taste (GO:00050909) 0.24441924 16 7.126e-04 1.427e-01 CALHM1:50 CALHM3:176 PKD1L3:262 GNAT3:789 ASIC:1254 PKD2L1:1597 NSD1:10 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 IL33:61 PEG3:65 NLS-bearing Protein Import Into Nucleus -0.05896512 254 1.258e-03 2.345e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NSD1:10 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NGRC2:11	Positive Regulation Of Tyrosine Phosphor	-0.13964603	55	3.431e-04	9.857e-02	TSLP:22 OSM:446 TNF:462 IL3:514 IL23R:678 IFNG:690
Positive Regulation Of Transcription By Grotein—Coupled Receptor Signaling Pat	Hepoxilin Biosynthetic Process (GO:00511	0.38574307	7	4.087e-04	1.052e-01	ALOXE3:153 ALOX15B:422 ALOX15:535 GSTM2:806 GSTM1:1875 ALOX12B:1994
G Protein–Coupled Receptor Signaling Pat 0.14271720 49 5.514e-04 1.192e-01 CHRM3:37 MTNR1B:94 OR10J5:303 MC3R:868 CCR1:1204 CHRM2:1370 Negative Regulation Of Gene Expression, Serine Family Amino Acid Biosynthetic Processing Protein Informatin Remodeling (GO:00050909) 49 5.514e-04 1.192e-01 CHRM3:37 MTNR1B:94 OR10J5:303 MC3R:868 CCR1:1204 CHRM2:1370 Serine Family Amino Acid Biosynthetic Proce 0.20127531 24 6.433e-04 1.338e-01 ALOXE3:153 ALOX12:378 ALOX15:535 ACSBG1:694 GSTM2:806 Sensory Perception Of Taste (GO:0050909) 0.24441924 16 7.126e-04 1.427e-01 CALHM1:50 CALHM3:176 PKD1L3:262 GNAT3:789 ASIC2:1254 PKD2L1:1597 Negative Regulation Of Transcription By Chromatin Organization (GO:0006325) -0.03643959 731 8.943e-04 1.727e-01 NSD1:10 ZNF274:16 MAGEL2:41 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.2512730 17 1.312e-03 2.364e-01 RGPD8:214 KPNA7:412 RGPD3:631 KPNA3:1547 RGPD4:1569 KPNA4:1629 Chromatin Remodeling (GO:0006338) -0.06207969 220 1.555e-03 2.627e-01 MCRC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92 Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01	Hepoxilin Metabolic Process (GO:0051121)	0.38574307	7	4.087e-04	1.052e-01	ALOXE3:153 ALOX15B:422 ALOX15:535 GSTM2:806 GSTM1:1875 ALOX12B:1994
Negative Regulation Of Gene Expression, -0.14285420 49	Positive Regulation Of Transcription By	-0.03488770	906	4.364e-04	1.072e-01	ELL:4 DHX36:52 PLAGL1:53 IL33:61 PEG3:65 CHD8:116
Serine Family Amino Acid Biosynthetic Pr -0.33424500 9 5.160e-04 1.192e-01 CTH:171 PSPH:220 SERINC5:531 MTHFD1:1196 SERINC3:1472 SRR:2431 Long-Chain Fatty Acid Biosynthetic Proce 0.20127531 24 6.433e-04 1.338e-01 ALOXE3:153 ALOX12:378 ALOX15B:422 ALOX15:535 ACSBG1:694 GSTM2:806 Sensory Perception Of Taste (G0:0050909) 0.24441924 16 7.126e-04 1.427e-01 CALHM1:50 CALHM3:176 PKD1L3:262 GNAT3:789 ASIC2:1254 PKD2L1:1597 Negative Regulation Of Transcription By -0.03643959 731 8.943e-04 1.727e-01 NSD1:10 ZNF274:16 MAGEL2:41 GATAD2A:55 IL33:61 PEG3:65 Chromatin Organization (GO:0006325) -0.05896512 254 1.258e-03 2.345e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.22512730 17 1.312e-03 2.364e-01 RGPD8:214 KPNA7:412 RGPD3:631 KPNA3:1547 RGPD4:1569 KPNA4:1629 Chromatin Remodeling (GO:0006338) -0.06207969 220 1.555e-03 2.627e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92 Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01 CACNA1G:103 DSP:199 SCN3B:573 SCN5A:624 KCNH6:813 KCNE3:835	G Protein-Coupled Receptor Signaling Pat	0.14271720	49	5.514e-04	1.192e-01	CHRM3:37 MTNR1B:94 OR10J5:303 MC3R:868 CCR1:1204 CHRM2:1370
Long-Chain Fatty Acid Biosynthetic Proce Sensory Perception Of Taste (GO:0050909) 0.24441924 16 7.126e-04 1.427e-01 CALHM1:50 CALHM3:176 PKD1L3:262 GNAT3:789 ASIC2:1254 PKD2L1:1597 Negative Regulation Of Transcription By -0.03643959 731 8.943e-04 1.727e-01 NSD1:10 ZNF274:16 MAGEL2:41 GATAD2A:55 IL33:61 PEG3:65 Chromatin Organization (GO:0006325) -0.05896512 254 1.258e-03 2.345e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.22512730 17 1.312e-03 2.364e-01 RGPD8:214 KPNA7:412 RGPD3:631 KPNA3:1547 RGPD4:1569 KPNA4:1629 Chromatin Remodeling (GO:0006338) -0.06207969 220 1.555e-03 2.627e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92 Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01 CACNA1G:103 DSP:199 SCN38:573 SCN5A:624 KCNH6:813 KCNE3:835 Actomyosin Structure Organization (GO:00 0.10269002 77 1.854e-03 3.037e-01 MYH10:151 MYH7B:250 FLNC:322 CASQ1:491 KRT19:736 PHACTR1:970 Actin Filament Organization (GO:0007015) Facultative Heterochromatin Formation (G -0.22196569 16 2.114e-03 3.222e-01 MBD3L5:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2212 SMARCA5:2300 Neuron Projection Morphogenesis (GO:0048 0.07513553 139 2.265e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514 Steroid Hormone Biosynthetic Process (GO -0.20341097 19 2.146e-03 3.222e-01 CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422 Positive Regulation Of Cellular Componen -0.08367365 111 2.354e-03 3.264e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Negative Regulation Of Gene Expression,	-0.14285420	49	5.446e-04	1.192e-01	MORC2:11 TASOR:20 DNMT1:203 UBR2:212 UHRF2:342 UHRF1:351
Sensory Perception Of Taste (GO:0050909) 0.24441924 16 7.126e-04 1.427e-01 CALHM1:50 CALHM3:176 PKD1L3:262 GNAT3:789 ASIC2:1254 PKD2L1:1597 Negative Regulation Of Transcription By -0.03643959 731 8.943e-04 1.727e-01 NSD1:10 ZNF274:16 MAGEL2:41 GATAD2A:55 IL33:61 PEG3:65 Chromatin Organization (GO:0006325) -0.05896512 254 1.258e-03 2.345e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.22512730 17 1.312e-03 2.364e-01 RGPD8:214 KPNA7:412 RGPD3:631 KPNA3:1547 RGPD4:1569 KPNA4:1629 Chromatin Remodeling (GO:0006338) -0.06207969 220 1.555e-03 2.627e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92 Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01 CACNA1G:103 DSP:199 SCN3B:573 SCN5A:624 KCNH6:813 KCNE3:835 Actomyosin Structure Organization (GO:000 0.10269002 77 1.854e-03 3.037e-01 MYH10:151 MYH7B:250 FLNC:322 CASQ1:491 KRT19:736 PHACTR1:970 Actin Filament Organization (GO:00007015) 0.07592925 140 1.959e-03 3.116e-01 POF1B:16 CNN2:283 VIL1:298 AVIL:351 AIF1:477 ENAH:591	Serine Family Amino Acid Biosynthetic Pr	-0.33424500	9	5.160e-04	1.192e-01	CTH:171 PSPH:220 SERINC5:531 MTHFD1:1196 SERINC3:1472 SRR:2431
Negative Regulation Of Transcription By Chromatin Organization (GO:0006325) -0.05896512 254 1.258e-03 2.345e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106 NLS-bearing Protein Import Into Nucleus -0.22512730 17 1.312e-03 2.364e-01 RGPD8:214 KPNA7:412 RGPD3:631 KPNA3:1547 RGPD4:1569 KPNA4:1629 Chromatin Remodeling (GO:0006338) -0.06207969 220 1.555e-03 2.627e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92 Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92 Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01 CACNA1G:103 DSP:199 SCN3B:573 SCN5A:624 KCNH6:813 KCNE3:835 Actomyosin Structure Organization (GO:00 0.10269002 77 1.854e-03 3.037e-01 MYH10:151 MYH7B:250 FLNC:322 CASQ1:491 KRT19:736 PHACTR1:970 Actin Filament Organization (GO:0007015) 0.07592925 140 1.959e-03 3.116e-01 POF1B:16 CNN2:283 VIL1:298 AVIL:351 AIF1:477 ENAH:591 Facultative Heterochromatin Formation (G -0.22196569 16 2.114e-03 3.222e-01 MBD3L5:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2212 SMARCA5:2300 Neuron Projection Morphogenesis (GO:0048 0.07513553 139 2.265e-03 3.222e-01 MINK1:35 SLITRK4:119 DTNBP1:139 FLRT1:150 TUNAR:210 IQGAP1:258 Positive Regulation Of Heterochromatin F -0.24508501 13 2.217e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514 Steroid Hormone Biosynthetic Process (GO -0.20341097 19 2.146e-03 3.222e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Long-Chain Fatty Acid Biosynthetic Proce	0.20127531	24	6.433e-04	1.338e-01	ALOXE3:153 ALOX12:378 ALOX15B:422 ALOX15:535 ACSBG1:694 GSTM2:806
Chromatin Organization (GO:0006325)	Sensory Perception Of Taste (GO:0050909)	0.24441924	16	7.126e-04	1.427e-01	CALHM1:50 CALHM3:176 PKD1L3:262 GNAT3:789 ASIC2:1254 PKD2L1:1597
NLS-bearing Protein Import Into Nucleus -0.22512730 17 1.312e-03 2.364e-01 RGPD8:214 KPNA7:412 RGPD3:631 KPNA3:1547 RGPD4:1569 KPNA4:1629 Chromatin Remodeling (GO:0006338) -0.06207969 220 1.555e-03 2.627e-01 MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92 Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01 CACNA1G:103 DSP:199 SCN3B:573 SCN5A:624 KCNH6:813 KCNE3:835 Actomyosin Structure Organization (GO:00 0.10269002 77 1.854e-03 3.037e-01 MYH10:151 MYH7B:250 FLNC:322 CASQ1:491 KRT19:736 PHACTR1:970 Actin Filament Organization (GO:0007015) 0.07592925 140 1.959e-03 3.116e-01 POF1B:16 CNN2:283 VIL1:298 AVIL:351 AIF1:477 ENAH:591 Facultative Heterochromatin Formation (G -0.22196569 16 2.114e-03 3.222e-01 MBD3L5:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2212 SMARCA5:2300 Neuron Projection Morphogenesis (GO:0048 0.07513553 139 2.265e-03 3.222e-01 MINK1:35 SLITRK4:119 DTNBP1:139 FLRT1:150 TUNAR:210 IQGAP1:258 Positive Regulation Of Heterochromatin F -0.24508501 13 2.217e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514	Negative Regulation Of Transcription By	-0.03643959	731	8.943e-04	1.727e-01	NSD1:10 ZNF274:16 MAGEL2:41 GATAD2A:55 IL33:61 PEG3:65
Chromatin Remodeling (GO:0006338)	Chromatin Organization (GO:0006325)	-0.05896512	254	1.258e-03	2.345e-01	MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 SAFB:106
Regulation Of Heart Rate By Cardiac Cond 0.14492173 40 1.522e-03 2.627e-01 CACNA1G:103 DSP:199 SCN3B:573 SCN5A:624 KCNH6:813 KCNE3:835 Actomyosin Structure Organization (GO:00 0.10269002 77 1.854e-03 3.037e-01 MYH10:151 MYH7B:250 FLNC:322 CASQ1:491 KRT19:736 PHACTR1:970 Actin Filament Organization (GO:0007015) 0.07592925 140 1.959e-03 3.116e-01 POF1B:16 CNN2:283 VIL1:298 AVIL:351 AIF1:477 ENAH:591 Facultative Heterochromatin Formation (G -0.22196569 16 2.114e-03 3.222e-01 MBD3L5:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2212 SMARCA5:2300 Neuron Projection Morphogenesis (GO:0048 0.07513553 139 2.265e-03 3.222e-01 MINK1:35 SLITRK4:119 DTNBP1:139 FLRT1:150 TUNAR:210 IQGAP1:258 Positive Regulation Of Heterochromatin F -0.24508501 13 2.217e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514 Steroid Hormone Biosynthetic Process (GO -0.20341097 19 2.146e-03 3.222e-01 CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422 Positive Regulation Of Cellular Componen -0.08367365 111 2.354e-03 3.264e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234	NLS-bearing Protein Import Into Nucleus	-0.22512730	17	1.312e-03	2.364e-01	RGPD8:214 KPNA7:412 RGPD3:631 KPNA3:1547 RGPD4:1569 KPNA4:1629
Actomyosin Structure Organization (GO:00 0.10269002 77 1.854e-03 3.037e-01 MYH10:151 MYH7B:250 FLNC:322 CASQ1:491 KRT19:736 PHACTR1:970 Actin Filament Organization (GO:0007015) 0.07592925 140 1.959e-03 3.116e-01 POF1B:16 CNN2:283 VIL1:298 AVIL:351 AIF1:477 ENAH:591 Facultative Heterochromatin Formation (G -0.22196569 16 2.114e-03 3.222e-01 MBD3L5:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2212 SMARCA5:2300 Neuron Projection Morphogenesis (GO:0048 0.07513553 139 2.265e-03 3.222e-01 MINK1:35 SLITRK4:119 DTNBP1:139 FLRT1:150 TUNAR:210 IQGAP1:258 Positive Regulation Of Heterochromatin F -0.24508501 13 2.217e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514 Steroid Hormone Biosynthetic Process (GO -0.20341097 19 2.146e-03 3.222e-01 CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422 Positive Regulation Of Cellular Componen -0.08367365 111 2.354e-03 3.264e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Chromatin Remodeling (GO:0006338)	-0.06207969	220	1.555e-03	2.627e-01	MORC2:11 ZNF274:16 DAXX:25 KDM4B:38 GATAD2A:55 GLMN:92
Actin Filament Organization (GO:0007015) 0.07592925 140 1.959e-03 3.116e-01 POF1B:16 CNN2:283 VIL1:298 AVIL:351 AIF1:477 ENAH:591 Facultative Heterochromatin Formation (G -0.22196569 16 2.114e-03 3.222e-01 MBD3L5:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2212 SMARCA5:2300 Neuron Projection Morphogenesis (GO:0048 0.07513553 139 2.265e-03 3.222e-01 MINK1:35 SLITRK4:119 DTNBP1:139 FLRT1:150 TUNAR:210 IQGAP1:258 Positive Regulation Of Heterochromatin F -0.24508501 13 2.217e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514 Steroid Hormone Biosynthetic Process (GO -0.20341097 19 2.146e-03 3.222e-01 CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422 Positive Regulation Of Cellular Componen -0.08367365 111 2.354e-03 3.264e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Regulation Of Heart Rate By Cardiac Cond	0.14492173	40	1.522e-03	2.627e-01	CACNA1G:103 DSP:199 SCN3B:573 SCN5A:624 KCNH6:813 KCNE3:835
Facultative Heterochromatin Formation (G	Actomyosin Structure Organization (GO:00	0.10269002	77	1.854e-03	3.037e-01	MYH10:151 MYH7B:250 FLNC:322 CASQ1:491 KRT19:736 PHACTR1:970
Neuron Projection Morphogenesis (GO:0048 0.07513553 139 2.265e-03 3.222e-01 MINK1:35 SLITRK4:119 DTNBP1:139 FLRT1:150 TUNAR:210 IQGAP1:258 Positive Regulation Of Heterochromatin F -0.24508501 13 2.217e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514 Steroid Hormone Biosynthetic Process (GO -0.20341097 19 2.146e-03 3.222e-01 CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422 Positive Regulation Of Cellular Componen -0.08367365 111 2.354e-03 3.264e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Actin Filament Organization (GO:0007015)	0.07592925	140	1.959e-03	3.116e-01	POF1B:16 CNN2:283 VIL1:298 AVIL:351 AIF1:477 ENAH:591
Positive Regulation Of Heterochromatin F -0.24508501 13 2.217e-03 3.222e-01 MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514 Steroid Hormone Biosynthetic Process (GO Positive Regulation Of Cellular Componen 19 2.146e-03 3.222e-01 CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Facultative Heterochromatin Formation (G	-0.22196569	16	2.114e-03	3.222e-01	MBD3L5:345 MBD3L3:892 HDAC1:1568 HELLS:1967 MBD3L2B:2212 SMARCA5:2300
Steroid Hormone Biosynthetic Process (GO -0.20341097 19 2.146e-03 3.222e-01 CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422 Positive Regulation Of Cellular Componen -0.08367365 111 2.354e-03 3.264e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Neuron Projection Morphogenesis (GO:0048	0.07513553	139	2.265e-03	3.222e-01	MINK1:35 SLITRK4:119 DTNBP1:139 FLRT1:150 TUNAR:210 IQGAP1:258
Positive Regulation Of Cellular Componen -0.08367365 111 2.354e-03 3.264e-01 ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237	Positive Regulation Of Heterochromatin F	-0.24508501	13	2.217e-03	3.222e-01	MORC2:11 TASOR:20 RESF1:107 TPR:804 SETDB2:1222 MPHOSPH8:1514
·	Steroid Hormone Biosynthetic Process (GO	-0.20341097	19	2.146e-03	3.222e-01	CYP11A1:347 HSD17B2:604 SRD5A3:646 HSD17B6:664 CYP11B1:1285 CYP17A1:1422
Neutral Amino Acid Transport (GO:0015804 -0.14727018 35 2.576e-03 3.398e-01 SLC6A6:18 SLC7A9:129 SLC43A1:223 SLC38A2:377 SLC7A6:526 SLC36A2:596	Positive Regulation Of Cellular Componen	-0.08367365	111	2.354e-03	3.264e-01	ATP10A:31 CLU:73 SLF1:95 BIK:166 SLF2:234 CALY:237
	Neutral Amino Acid Transport (GO:0015804	-0.14727018	35	2.576e-03	3.398e-01	SLC6A6:18 SLC7A9:129 SLC43A1:223 SLC38A2:377 SLC7A6:526 SLC36A2:596

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Concact	Stat	mann.genes	Pvai	p.aaj	generals
MP0002080 prenatal lethality	-0.04211534	1338	3.328e-06	1.584e-03	NSD1:10 SMCHD1:12 DAXX:25 GATAD2A:55 MTBP:64 LTN1:70
MP0000598 abnormal liver morphology	-0.05640946	482	4.141e-05	8.977e-03	MAN2A1:36 PECAM1:75 ITGB1:89 GRB14:103 SAFB:106 CTH:171
MP0002086 abnormal extraembryonic tissu	-0.05514987	487	5.658e-05	8.977e-03	NSD1:10 SMCHD1:12 DAXX:25 GATAD2A:55 ITGB1:89 PTPRB:94
MP0000313 abnormal cell death	-0.05015547	464	3.402e-04	3.239e-02	DAXX:25 PROM1:27 LRP2:79 ITGB1:89 CTH:171 DNMT1:203
MP0002085 abnormal embryonic tissue	-0.04337846	655	3.042e-04	3.239e-02	NSD1:10 DAXX:25 GATAD2A:55 TRPM6:72 LRP2:79 ITGB1:89
MP0004197 abnormal fetal growth/weight/	-0.07777498	177	4.210e-04	3.340e-02	PLAGL1:53 TRPM6:72 ITGB1:89 SAFB:106 ERI1:197 MET:247
//P0002088 abnormal embryonic growth/wei	-0.05352451	344	8.670e-04	5.158e-02	DAXX:25 ITGB1:89 LATS2:93 PTPRB:94 EHMT1:143 HSD17B12:252
MP0003121 genomic imprinting	-0.18257629	28		5.158e-02	SMCHD1:12 MAGEL2:41 PLAGL1:53 PEG3:65 DNMT1:203 PHLDA2:281
MP0003984 embryonic growth retardation	-0.05202428	337		6.437e-02	DAXX:25 ITGB1:89 LATS2:93 PTPRB:94 EHMT1:143 HSD17B12:252
MP0003635 abnormal synaptic transmissio	0.04664870	426	1.352e-03	6.437e-02	CHRM3:37 PTPRZ1:112 RYR3:160 TNC:161 KCNH3:223 CHRNB2:255
MP0003077 abnormal cell cycle	-0.07315811	153		7.913e-02	ITGB1:89 LATS2:93 BIRC6:350 MYBL2:384 MDM4:400 MDM2:453
MP0001697 abnormal embryo size	-0.04605806	407		7.913e-02	DAXX:25 GATAD2A:55 LRP2:79 ITGB1:89 LATS2:93 PTPRB:94
MP0005380 embryogenesis phenotype	-0.04201709	418		1.338e-01	DAXX:25 ITGB1:89 LATS2:93 PTPRB:94 EHMT1:143 OOEP:147
MP0005389 reproductive system phenotype	-0.09963290	70		1.338e-01	TRPM6:72 FGF23:204 CCNE1:260 INSL3:353 PTGS2:598 BAX:760
1P0001672 abnormal embryogenesis/ devel	-0.04201709	418		1.338e-01	DAXX:25 ITGB1:89 LATS2:93 PTPRB:94 EHMT1:143 OOEP:147
MP0000266 abnormal heart morphology	-0.03265123	712		1.438e-01	SLC6A6:18 PLAGL1:53 CLU:73 ITGB1:89 LATS2:93 PTPRB:94
MP0003122 maternal imprinting	-0.20174607	16		1.470e-01	MAGEL2:41 PLAGL1:53 PEG3:65 PEG10:338 IGF2:874 NDN:1226
MP0000749 muscle degeneration	0.12207697	37		2.740e-01	PLEC:23 DES:343 DMD:576 MYOF:652 LMNA:1274 DYSF:1313
MP000609 abnormal liver physiology	-0.03833195	379		2.984e-01	MAN2A1:36 PECAM1:75 HK1:160 MET:247 ERCC6:302 SIRPA:317
MP0000689 abnormal spleen morphology	-0.03212769	551		2.984e-01	MAN2A1:36 PECAM1:75 GRB14:103 HK1:160 DNMT1:203 FGF23:204
MP0002272 abnormal nervous system	0.05253807	197		2.984e-01	PLEC:23 CHRM3:37 CACNA1G:103 PER3:141 CDH23:219 KCNH3:223
MP0005551 abnormal eye electrophysiolog	0.05984820	144		3.047e-01	EGFLAM:124 GJA10:173 CDH23:219 C3:482 DMD:576 CPLX4:583
MP0000751 myopathy	0.14552725	23		3.279e-01	PLEC:23 COL6A1:318 LAMA2:534 DMD:576 GAA:1454 SCN8A:1470
MP0003935 abnormal craniofacial develop	-0.04500860	246		3.337e-01	TRPM6:72 ITGB1:89 LATS2:93 ITGB8:146 UHRF1:351 ENAM:401
MP0000579 abnormal nail morphology	0.14907618	21		3.386e-01	ITGB4:7 GLI3:401 KRT17:500 KRT6A:609 KRT6B:1034 FGFR2:1056
MP0003879 abnormal hair cell	0.13631960	25		3.386e-01	
MP0005636 abnormal mineral homeostasis	-0.05621379	141		3.458e-01	TRPM6:72 LRP2:79 CALCR:100 HK1:160 CLDN16:205 CYP11A1:347
MP0001486 abnormal startle reflex	0.06934208	96		3.458e-01	OTOF:98 CDH23:219 PCDH15:627 DRD2:828 NTSR1:1044 DNAJC5:108
MP0004145 abnormal muscle electrophysio	0.17029953	15		3.458e-01	CASQ1:491 DMD:576 MUSK:737 KCNH2:1189 CACNG1:1271 CLCN1:168
MP0002925 abnormal cardiovascular devel	-0.03069466	519		3.458e-01	GATAD2A:55 PTPRB:94 ITGB8:146 CASP8:227 HSD17B12:252 CCNE1:20
1P0003221 abnormal cardiomyocyte apopto	-0.03009400	40		3.458e-01	CASP8:227 BACH1:309 MDM2:453 TFAM:504 PLRG1:799 MAPK8:971
	-0.10019449	453		3.436e=01 3.611e=01	MAN2A1:36 PECAM1:75 LRP2:79 SLC7A9:129 HK1:160 FABP2:196
MP0002135 abnormal kidney morphology		37		3.611e=01	ETNK2:104 OOEP:147 ZAR1:255 GPR3:545 DPPA4:707 ATOX1:813
MP0003718 maternal effect	-0.10616432 -0.03983631	277		3.611e=01	ITGB1:89 LATS2:93 ERI1:197 DNMT1:203 RNF8:246 CCNE1:260
MP0000350 abnormal cell proliferation MP0002128 abnormal blood circulation	-0.03963631	409		3.759e-01	ITGB1:89 LATS2:93 ITGB8:146 CASP8:227 MET:247 BIRC6:350
MP0001765 abnormal ion homeostasis	-0.03266490	110		3.759e=01 3.933e=01	TRPM6:72 LRP2:79 ITGB1:89 CALCR:100 FGF23:204 CLDN16:205
MP0000383 abnormal hair follicle				3.933e-01 3.933e-01	PKP3:326 TRPV3:667 FGFR2:1056 KRT14:1290 KSR1:1327 ZDHHC21:13
	0.13337439 0.06835664	22 81		4.198e-01	CHRM3:37 P2RY4:146 CHRNB2:255 FFAR3:424 SLC15A1:489 NOS1:70
MP0001664 abnormal digestion				4.198e-01	FGF23:204 CCNE1:260 INSL3:353 BCL2L2:883 EFEMP1:1509 FOXC1:17
MP0002160 abnormal reproductive system MP0002837 dystrophic cardiac calcinosis	-0.09691408	40			
	0.20117360	9	3.6736-02	4.344e-01	SLC2A4:271 DES:343 MMP9:731 SCG5:1632 GSTZ1:9306.5 DNM1L:9306

Geneset	stat	num.genes	pval	p.adj	gene.vals
leg.skin	0.104069485	286	2.136e-09	1.153e-07	ANKRD35:2 POF1B:16 ARHGAP40:22 FAM83F:29 PSAPL1:36 GGT6:45
EBV.lymphocyte	-0.052615685	751	1.975e-06	5.332e-05	TMEM131L:15 NCAPD3:26 WDR76:29 KIF18A:32 TPX2:39 MTBP:64
suprapubic.skin	0.078928035	257	1.615e-05	2.907e-04	FAM83F:29 PSAPL1:36 GGT6:45 EVPL:46 CARD14:48 RNF222:54
vagina	0.078839725	118	3.232e-03	4.364e-02	EVPL:46 RNF222:54 BNC1:87 CRYBG2:111 NOD2:158 ENDOU:346
esophagus.mucosa	0.046929457	261	9.786e-03	1.057e-01	EVPL:46 PTK6:52 IQANK1:53 RNF222:54 FAM83H:72 BDKRB1:82
skeletal.muscle	0.042051902	258	2.134e-02	1.921e-01	STYXL2:10 SMTNL2:43 TACC2:115 ANKRD23:149 FSD2:218 SLC2A4:271
liver	-0.032980979	396	2.664e-02	2.055e-01	GRB14:103 HGD:122 CTH:171 NAT2:273 AKR1D1:293 AFP:318
adrenal.gland	-0.052176104	115	5.432e-02	3.218e-01	PLBD2:323 CYP11A1:347 MGST1:352 APOC1:418 ADGRV1:429 ALAS1:864
fallopian.tube	0.070659744	60	5.892e-02	3.218e-01	ADGRG4:19 CROCC2:236 MRGPRD:253 SCGB2A1:295 VNN3:430 MSLNL:513
peyers.patch	0.038442257	196	6.556e-02	3.218e-01	EPS8L3:32 TREH:58 KRT20:140 ACY3:145 RNF186:230 MUC2:260
sigmoid.colon	0.075089071	51	6.408e-02	3.218e-01	TACR2:9 PLA2G2C:185 MRGPRD:253 DES:343 PLEKHO1:442 NTSR1:1044
pancreas	-0.047349953	117	7.821e-02	3.520e-01	ARSL:21 FBXW12:81 PNLIPRP1:182 SLC43A1:223 CPB1:509 REG1A:519
left.ventricle	0.060025849	69	8.548e-02	3.551e-01	FSD2:218 MYH7B:250 MYZAP:507 SCN5A:624 SMPX:788 NRAP:881
thyroid	-0.035518079	175	1.075e-01	4.145e-01	LRP2:79 RASSF4:112 ISM1:137 PLA2R1:172 TMEM171:192 WDR86:222
transverse.colon	0.035363258	168	1.162e-01	4.182e-01	RXFP4:4 TRIM15:14 EPS8L3:32 AGR3:135 KRT20:140 LEFTY1:172
uterus	-0.052472338	62	1.540e-01	5.197e-01	ATP2B4:274 MEIS1:1004.5 ADAMTS19:1074 SSC5D:1283 MOXD1:1819 RSPO3:1878
blood	0.020508410	342	1.986e-01	5.958e-01	PIK3R5:26 PTAFR:70 ACAP1:78 PRTN3:96 RIPOR2:169 VNN2:196
endocervix	0.043198208	76	1.942e-01	5.958e-01	BDKRB1:82 TGM2:155 PWP2:198 GUCY1A2:403 BDKRB2:747 ELFN1:950
testis	-0.009439596	1637	2.377e-01	6.755e-01	POTEE:51 DPPA2:56 PDILT:57 CRISP1:58 ARL9:85 FAM169A:90
C1.spinal.cord	-0.023713046	194	2.584e-01	6.977e-01	MKRN3:69 SLCO1A2:224 FGF1:423 SRARP:470 ENPP2:515 CERS1:605
breast	0.063849122	20	3.232e-01	7.126e-01	TNN:533 THRSP:542 MUCL1:679 SCGB2A2:1503 NPY2R:2489 ABCB5:9306.5
cerebral.cortex	0.028490719	109	3.061e-01	7.126e-01	CALHM1:50 PNMA8B:118 KCNH3:223 CHRNB2:255 ARNT2:360 KIF5A:613
esophagogastric.junction	-0.094286977	9	3.275e-01	7.126e-01	RTL3:1647 GADL1:1956 F2RL2:2453 ADCY5:9215.5 BARX1:9215.5 COL4A5:9215.5
minor.salivary.gland	0.031406047	91	3.021e-01	7.126e-01	SLPI:248 CRACR2A:368 MUC16:541 EHF:562 TCN1:602 KRT7:617
subcutaneous.adipose	0.031410864	81	3.299e-01	7.126e-01	SYNE3:320 GPBAR1:384 THRSP:542 GPD1:556 PRG4:924 RDH5:985
amygdala	0.082670313	9	3.906e-01	8.112e-01	PTPRZ1:112 PCDH15:627 BCAN:1308 NEUROD2:9306.5 NEUROD6:9306.5 SLC17A7:9306.5
aorta	0.019263239	156	4.092e-01	8.137e-01	MYH10:151 ECM2:193 ADAMTSL3:264 MEGF6:342 GLIPR1:654 C1QTNF8:741
atrium.auricle	0.023035410	95	4.395e-01	8.137e-01	FSD2:218 ALPK2:297 TBX5:425 SCN5A:624 MYBPHL:734 SMPX:788
bladder	-0.020352735	29	7.047e-01	8.137e-01	SLC14A1:1353 WFDC13:2075 CLEC3A:2276 ACER2:2577 ABCC4:9215.5 AKR1B10:9215.5
Brodmann.area.9	-0.009762442	184	6.502e-01	8.137e-01	NPM2:475 ENC1:919 PCDH8:1110 SERPINI1:1156 SCG3:1560 YWHAH:1562
caudate.nucleus	-0.019704479	27	7.233e-01	8.137e-01	SLC1A2:2044 ANO3:2846 HS3ST5:9215.5 ACBD7:9215.5 AQP4:9215.5 CHAT:9215.5
cerebellar.hemisphere	0.005282702	532	6.834e-01	8.137e-01	KIAA0319:12 ANKRD34C:28 CHAD:68 MINAR1:100 SLITRK4:119 PER3:141
cerebellum	0.006073079	403	6.806e-01	8.137e-01	CACNA1G:103 ESYT3:156 SLC22A31:166 SSTR4:183 GLRA4:229 MRGPRD:253
coronary.artery	-0.034967239	15	6.393e-01	8.137e-01	COL4A1:2508 CCDC3:2601 PCOLCE2:2661 SPINK13:2939 CCN3:9215.5 MYO18B:9215.5
cortex.kidney	-0.011900380	131	6.398e-01	8.137e-01	HAVCR1:2 MCCD1:99 OGDHL:164 PLCXD2:173 CLDN16:205 ENAM:401
ectocervix	-0.039405468	26	4.871e-01	8.137e-01	LRFN5:370 FGF7:2324 GDF7:2791 MMRN1:2841 TRHDE:9215.5 ADRA1D:9215.5
esophagus.muscularis.mucosa	0.034116600	28	5.325e-01	8.137e-01	CHRM3:37 SYNM:143 KCNMB1:212 PRUNE2:314 CYSLTR1:1360 FAM83D:2905

BNC1:87 FFAR3:424 ALOX15:535 MUC16:541 THRSP:542 ITLN1:1256

MAGEL2:41 CALCR:100 CALY:237 PABPC1L2B:573 SST:635 RTP5:1191

7.188e-01 8.137e-01 CNIH2:2221 NEUROD2:9215.5 NEUROD6:9215.5 SLC17A7:9215.5 HRK:9215.5 OLIG2:9215.5

5.496e-01 8.137e-01

5.047e-01 8.137e-01

greater.omentum

hippocampus.proper

hypothalamus

0.028088781 -0.028855721

-0.021913029

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