



qValueNoperm



	ADAMTS6	-4.453890	5.059702e-05	7.312e-02	1.000e+00
ADAMTS6 ATF6 C2CD2L CADM3 GRID1 IQCF3 TMED3	-4.397161	6.580566e-05	7.312e-02	1.000e+00	
	C2CD2L	-4.501681	4.045090e-05	7.312e-02	1.000e+00
	CADM3	-4.429359	5.670804e-05	7.312e-02	1.000e+00
	GRID1	-4.390340	6.790407e-05	7.312e-02	1.000e+00
	IQCF3	-4.438592	5.432969e-05	7.312e-02	1.000e+00
	TMED3	-4.424097	5.810802e-05	7.312e-02	1.000e+00

-4.686288 1.669232e-05 6.289e-02

-4.683399 1.692936e-05 6.289e-02

TMEM108 -4.710764 1.480740e-05 6.289e-02

1.000e+00

1.000e+00

1.000e+00

PPP4R1	4.414302	6.080186e-05	7.312e-02	1.000e+00
PRTG	4.381047	7.086625e-05	7.312e-02	1.000e+00
TMEM131L	4.429018	5.679796e-05	7.312e-02	1.000e+00
ZNF292	4.504231	3.996817e-05	7.312e-02	1.000e+00
CPB1	4.366130	7.588022e-05	7.417e-02	1.000e+00
CCPG1	4.344249	8.385186e-05	7.787e-02	1.000e+00

4.767226 1.120680e-05 6.289e-02

4.767820 1.117379e-05 6.289e-02

4.415066 6.058749e-05 7.312e-02

4.400831 6.470221e-05 7.312e-02

AGGF1

ZSCAN25

ABCB11

NEDD4

qValueNoperm

1.000e+00

1.000e+00

1.000e+00

1.000e+00

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_OLFACTORY_SIGNALING_PATHWAY	-0.08871018	386	2.358e-09	1.531e-05	OR10D3:33 OR6C65:44 OR2L8:69 OR1E2:116 OR9G1:195 OR2M3:245
REACTOME_SENSORY_PERCEPTION	-0.06741980	598	1.982e-08	5.552e-05	SCN9A:3 PDE6B:22 OR10D3:33 OR6C65:44 APOA1:51 OR2L8:69
KEGG_OLFACTORY_TRANSDUCTION	-0.08402253	374	2.565e-08	5.552e-05	OR6C65:44 OR2L8:69 OR1E2:116 OR9G1:195 OR2M3:245 OR10AD1:265
REACTOME_KERATINIZATION	-0.09769070	206	1.375e-06	2.233e-03	KRT5:71 KRTAP4-9:144 KRTAP13-3:204 KRTAP10-8:240 KRTAP24-1:262 KRTAP19-7:323
NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON	0.18669163	53	2.589e-06	3.363e-03	IDO2:48 TM2D2:109 RAB11FIP1:110 ANK1:140 ZMAT4:195 PLEKHA2:237
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.04986785	666	1.225e-05	1.326e-02	MYO9B:11 RAD51AP1:15 KIAA0825:16 CDCA2:20 HJURP:25 NCAPD3:38
REACTOME_NEURONAL_SYSTEM	-0.06164252	391	2.976e-05	2.761e-02	GABRA5:13 GABRR3:16 GJA10:65 KCNH2:75 ADCY1:95 CHRNA7:104
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.04624334	576	1.560e-04	1.013e-01	CADM3:7 GRID1:10 GABRA5:13 POU2F3:23 SLC35F3:50 PAX1:72
REACTOME_SIGNALING_BY_GPCR	-0.04259649	686	1.513e-04	1.013e-01	ARHGEF4:14 SSTR4:17 MC4R:24 PTH1R:35 VIPR1:54 CHRM2:70
KEGG_AUTOIMMUNE_THYROID_DISEASE	-0.15464967	50	1.552e-04	1.013e-01	HLA-DOB:482 IFNA21:738 IFNA4:740 HLA-G:745 HLA-F:890 IFNA1:926
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.06590770	265	2.255e-04	1.332e-01	GRID1:10 GABRA5:13 SSTR4:17 MC4R:24 PTH1R:35 MAS1:52
REACTOME_RRNA_PROCESSING	0.07831351	184	2.516e-04	1.362e-01	LAS1L:200 RPL35:259 RPL7:313 PDCD11:363 RIOK1:432 RPS19:463
REACTOME_GPCR_LIGAND_BINDING	-0.04956826	450	3.235e-04	1.616e-01	SSTR4:17 MC4R:24 PTH1R:35 VIPR1:54 CHRM2:70 CHRM3:86
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_P	0.10730716	93	3.499e-04	1.623e-01	RPL35:259 RPL7:313 SSR3:436 RPS19:463 RPL15:744 RPS27L:910
WP_DISORDERS_OF_BILE_ACID_SYNTHESIS_AND_	0.22795035	20	4.167e-04	1.804e-01	ABCB11:5 CYP27A1:152 ACOX2:223 CYP8B1:438 SLCO1B1:646 ABCC2:752
REACTOME_HEME_DEGRADATION	0.25546363	15	6.129e-04	2.057e-01	SLCO1B1:646 HMOX1:650 ABCC2:752 UGT1A4:1042 ABCG2:1428 FABP1:1893
REACTOME_METABOLISM_OF_LIPIDS	0.03784961	722	5.602e-04	2.057e-01	ABCB11:5 CYP17A1:13 CUBN:17 ACER1:49 ACOT12:65 LRP2:82
REACTOME_APOPTOTIC_EXECUTION_PHASE	-0.13565227	52	7.157e-04	2.057e-01	H1-3:19 H1-2:31 CASP7:107 H1-4:137 H1-5:250 DBNL:275
REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMI	0.10623677	83	8.234e-04	2.057e-01	RPL35:259 RPL7:313 RPS19:463 ATF3:496 RPL15:744 RPS27L:910
WP_CLASSICAL_PATHWAY_OF_STEROIDOGENESIS_	0.24258153	16	7.803e-04	2.057e-01	CYP17A1:13 CYP11A1:135 HSD3B2:962 CYP11B1:1073 CYP21A2:1115 HSD3B1:1881
WP_DRUG_INDUCTION_OF_BILE_ACID_PATHWAY	0.23497241	17	7.955e-04	2.057e-01	ABCB11:5 SLC10A1:122 SULT2A1:165 SLC51A:443 SLCO1B1:646 ABCC2:752
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.04619696	449	8.154e-04	2.057e-01	ZNF292:3 NEDD4:7 MDN1:30 CENPF:55 ARHGEF7:87 MAN2A1:95
JOHNSTONE_PARVB_TARGETS_2_DN	0.05579686	317	6.491e-04	2.057e-01	RREB1:18 PLEKHA5:103 ENPP1:116 GCNT2:144 AGTPBP1:185 SLC16A7:295
JOHNSTONE_PARVB_TARGETS_3_DN	0.03638725	793	5.226e-04	2.057e-01	CCPG1:10 RAD51AP1:15 LAMP2:42 SLC6A6:50 CENPF:55 MLLT10:67
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP	0.05514667	318	7.362e-04	2.057e-01	CDCA2:20 EPS15L1:35 NCAPD3:38 NCAPD2:54 DLGAP5:72 FANCG:104
KEGG_RIBOSOME	0.11731992	71	6.321e-04	2.057e-01	RPL35:259 RPL7:313 RPS19:463 RPL15:744 RPS27L:910 RPS21:1014
WP_NUCLEAR_RECEPTORS_IN_LIPID_METABOLISM	0.16489117	32	1.246e-03	2.996e-01	ABCB11:5 PPARD:254 CYP8B1:438 ABCC2:752 ABCG5:901 CYP2B6:989
FISCHER_DREAM_TARGETS	0.03119514	922	1.401e-03	3.138e-01	RAD51AP1:15 CDCA2:20 HJURP:25 NCAPD3:38 NCAPD2:54 CENPF:55
BENPORATH_SOX2_TARGETS	0.03560767	699	1.394e-03	3.138e-01	SUGP2:51 MLLT10:67 LRP2:82 NANOG:124 NBR1:127 AASDH:147
ONKEN_UVEAL_MELANOMA_DN	0.04170037	496	1.516e-03	3.282e-01	ECSIT:44 SLC41A3:101 RAB11FIP1:110 SLC25A36:123 CIRBP:142 ST3GAL6:225
SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN	-0.16664209	30	1.583e-03	3.316e-01	EREG:200 CALD1:294 PLEC:576 EGFR:937 ITGA2:1278 IGF1R:1396
REACTOME_SARS_COV_2_MODULATES_HOST_TRANS	0.15310036	35	1.722e-03	3.494e-01	RPS19:463 SMN1:533 SMN2:586 RPS27L:910 RPS21:1014 RPS3:1360
NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICO	-0.05062697	319	1.910e-03	3.544e-01	HOXB13:68 RPTOR:127 NT5C:158 TTYH2:270 SOX9:304 OTOP2:362
REACTOME_SELENOAMINO_ACID_METABOLISM	0.09089354	98	1.882e-03	3.544e-01	RPL35:259 RPL7:313 CBS:371 RPS19:463 GNMT:585 NNMT:723
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.03724645	602	1.863e-03	3.544e-01	AGGF1:2 NEDD4:7 CCPG1:10 RAD51AP1:15 CENPF:55 MICAL2:61
REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_	-0.06504654	189	2.063e-03	3.691e-01	GABRA5:13 GABRR3:16 ADCY1:95 CHRNA7:104 GABRR1:162 KIF17:211
REACTOME_SARS_COV_1_MODULATES_HOST_TRANS	0.17391546	26	2.143e-03	3.691e-01	RPS19:463 RPS27L:910 RPS21:1014 RPS3:1360 RPS10:1605 RPS25:1669
WP_STEROID_HORMONE_PRECURSOR_BIOSYNTHESI	0.29523468	9	2.160e-03	3.691e-01	CYP17A1:13 CYP11A1:135 HSD3B2:962 CYP21A2:1115 HSD3B1:1881 SRD5A1:2279
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	0.03135436	826	2.306e-03	3.840e-01	ZNF292:3 TMEM131L:4 NEDD4:7 MYO9B:11 MDN1:30 ZFYVE16:46

DisGeNET Top pathways by non-permulation

2.396e-03 3.891e-01

TK2:899 UCK2:1027 CDA:1162 UPP1:1615 UCK1:1678 DCK:2204

BFSP2:40 CRYGD:124 CRYGC:376 CRYBB1:486 VIM:531 GJA8:922

NA NA NA NA NA NA

NA NA NA NA NA

2.551e-03 6.322e-01 ABCB11:5 CYP17A1:13 HMCN1:22 SLC10A2:90 ABCG8:99 ANK1:140

REACTOME_PYRIMIDINE_SALVAGE

-0.26435020

-0.26247696

0.07856665

11

124

CATARACT, COPPOCK-LIKE

Cholelithiasis

NA.35

NA.36

Geneset	stat	num.genes	pval	p.adj	gene.vals
Autism Spectrum Disorders	-0.06615692	518	3.069e-07	3.014e-03	GABRA5:13 SSTR4:17 ZNF423:25 SCN1A:27 CARMIL1:30 LRRN3:48
Pigmentation Disorders	-0.38567732	10	2.408e-05	1.182e-01	TRPM1:60 KRT5:71 KRT14:522 ASIP:1476 COLEC11:1551 MITF:1732
Channelopathies	-0.16484933	52	3.953e-05	1.294e-01	SCN9A:3 SCN1A:27 KCNH2:75 CNGB3:120 RYR2:171 KCNA3:521
Male sterility due to Y-chromosome delet	-0.45566107	6	1.109e-04	1.749e-01	DAZ1:374 DAZ3:387 DAZ2:431 DAZ4:534 USP9Y:1029 DDX3Y:2372
Partial chromosome Y deletion	-0.45566107	6	1.109e-04	1.749e-01	DAZ1:374 DAZ3:387 DAZ2:431 DAZ4:534 USP9Y:1029 DDX3Y:2372
Schizophrenia	-0.02842145	1731	1.247e-04	1.749e-01	CADM3:7 GRID1:10 GABRA5:13 GABRR3:16 SSTR4:17 MC4R:24
Skin Vesicle	-0.46822810	6	7.125e-05	1.749e-01	COL7A1:59 KRT5:71 KRT14:522 PLEC:576 ATP2C1:780 PKP1:1677
Cataract, Pulverulent	-0.30716136	11	4.195e-04	4.398e-01	BFSP2:40 HSF4:103 CRYGD:124 CRYGC:376 CRYBB1:486 VIM:531
Adrenocorticotropic hormone excess	0.44994331	5	4.930e-04	4.398e-01	CYP17A1:13 CYP11A1:135 HSD3B2:962 CYP11B1:1073 POR:2225 NA
Autistic Disorder	-0.04151310	637	3.903e-04	4.398e-01	ATF6:9 GABRA5:13 IGFBP3:18 SCN1A:27 PTPRZ1:57 DOCK4:84
Pseudoaphakia	-0.21921281	21	5.067e-04	4.398e-01	CRYGD:124 TDRD7:358 CRYGC:376 CRYBB1:486 VIM:531 ATP2B1:636
Severe myopia	-0.10395926	93	5.375e-04	4.398e-01	ATF6:9 IGFBP3:18 PDE6B:22 CRYBA4:36 TRPM1:60 RBP3:91
CATARACT, AUTOSOMAL DOMINANT	-0.31668006	9	1.002e-03	5.269e-01	BFSP2:40 CRYAA2:112 CRYBB1:486 CRYAA:749 MIP:750 GJA8:922
Spermatogenic Failure, Nonobstructive, Y	-0.33538876	8	1.020e-03	5.269e-01	DAZ1:374 DAZ3:387 DAZ2:431 USP9Y:1029 KDM5D:1633 DDX3Y:2372
Cocaine Dependence	-0.08364806	132	9.216e-04	5.269e-01	MC4R:24 PRMT6:63 CRH:114 FOS:131 NPS:273 GABBR1:341
Hypernatriuria	0.39286727	6	8.599e-04	5.269e-01	CLCNKA:76 CYP11A1:135 CLCNKB:228 HSD3B2:962 BSND:1045 AVPR2:9232
Milium Cyst	-0.22692508	18	8.596e-04	5.269e-01	COL7A1:59 KRT5:71 CYLD:203 KRT14:522 PLEC:576 ITGB4:769
Non-obstructive azoospermia	-0.10990651	76	9.328e-04	5.269e-01	WDR11:43 PRMT6:63 SYCP3:106 DAZ1:374 DAZ3:387 DAZ2:431
Withdrawal Symptoms	-0.11674074	70	7.383e-04	5.269e-01	SSTR4:17 ADCY1:95 CHRNA7:104 CRH:114 FOS:131 DRD2:507
Substance Withdrawal Syndrome	-0.12550037	56	1.167e-03	5.731e-01	ADCY1:95 CHRNA7:104 CRH:114 FOS:131 DRD2:507 CHRNB4:767
Drug Eruptions	-0.19861008	22	1.262e-03	5.903e-01	APOA1:51 MTHFR:559 KNG1:564 IFNA1:926 IL18:1505 HLA-B:1530
Color vision defect, severe	-0.14107209	39	2.307e-03	5.963e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
Hyperkinesia, Generalized	-0.15590056	32	2.277e-03	5.963e-01	ADCY1:95 DISC1:125 FOS:131 NPS:273 GABBR1:341 CRHR1:506
Abnormal color vision	-0.14107209	39	2.307e-03	5.963e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
Addictive Behavior	-0.06428634	190	2.298e-03	5.963e-01	CHRM2:70 CRH:114 FOS:131 TGFB1:145 MET:185 SLC16A4:310
Adrenogenital Syndrome	0.36524106	6	1.946e-03	5.963e-01	CYP17A1:13 HSD3B2:962 CYP11B1:1073 CYP21A2:1115 POR:2225 STAR:9232
Azoospermia	-0.07505563	147	1.714e-03	5.963e-01	SYCP3:106 SOX9:304 DAZ1:374 RBM5:384 DAZ3:387 DAZ2:431
Cocaine-Related Disorders	-0.09554470	90	1.749e-03	5.963e-01	PRMT6:63 CRH:114 FOS:131 NPS:273 GABBR1:341 CRHR2:396
Drug Withdrawal Symptoms	-0.12802989	52	1.412e-03	5.963e-01	ADCY1:95 CHRNA7:104 CRH:114 FOS:131 DRD2:507 CHRNB4:767
Fetal polyuria	0.29368286	9	2.281e-03	5.963e-01	CLCNKA:76 CLCNKB:228 GREB1L:700 BSND:1045 KCNJ1:1454 ITGA8:2652
Infiltrating Cervical Carcinoma	-0.14178973	42	1.481e-03	5.963e-01	SEC14L2:122 FGFR2:338 MTHFR:559 F2RL1:616 HLA-G:745 EGFR:937
Loss in color vision	-0.14107209	39	2.307e-03	5.963e-01	ATF6:9 CDHR1:64 PRPH2:111 CNGB3:120 GNAT2:704 CACNA1F:828
Mood Disorders	-0.05001593	318	2.254e-03	5.963e-01	ADAMTS6:5 GABRA5:13 CHRM2:70 CHRM3:86 ADCY1:95 CRH:114
Nuclear cataract	-0.15810148	32	1.971e-03	5.963e-01	HSF4:103 CRYGD:124 CRYBA2:238 CRYGC:376 CRYBB1:486 BFSP1:680
Recurrent major depressive episodes	-0.17107352	27	2.096e-03	5.963e-01	APOA1:51 CHRM2:70 CRH:114 DISC1:125 SYNE1:434 CRHR1:506
Renal salt wasting	0.21353567	17	2.304e-03	5.963e-01	CLCNKA:76 CYP11A1:135 CLCNKB:228 SCNN1A:622 HSD3B2:962 BSND:1045
Rheumatic Heart Disease	-0.14113128	39	2.298e-03	5.963e-01	IGFBP3:18 WDR11:43 TGFB1:145 VIM:531 USP4:829 IGF2:1076
Waddling gait	-0.12181361	54	1.969e-03	5.963e-01	PTH1R:35 TGFB1:145 TRAPPC11:268 DNAJB6:671 NEFH:901 SLC6A17:1063
CATABACT CORROCK LIKE	0.00047000	4.4	0.575 - 00	0.000- 04	DECDO: 40 ODVOD: 404 ODVOD: 070 ODVDD4: 400 V/M-F04 O MO: 000

customGeneSet Top pathways by non-permulation

2.575e-03 6.322e-01

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	0.05937922	13	-	7.595e-01	
NAFLDGWAS	-0.05757576	15		7.595e=01 7.595e=01	INSR:723 PNPLA3:1560 FTO:1609 TOR1B:2302 PNPLA2:2703 APOE:9342
expressionDirectionalSelection	0.00297619	42		9.665e-01	NSL1:601 TLR6:1165 LY6K:1891 TLR10:2376 FADS1:9232 POU5F1:9232
NA	0.00297019 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 NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA
NA.6	NA NA	NA NA	NA NA	NA NA	NA NA NA NA NA NA
NA.7	NA	NA	NA NA	NA	NA NA NA NA NA
NA.7 NA.8	NA NA	NA NA	NA NA	NA NA	NA NA NA NA NA
NA.9	NA NA	NA NA	NA NA	NA NA	NA NA NA NA NA NA
NA.9 NA.10				NA NA	
NA.10 NA.11	NA NA	NA NA	NA NA	NA NA	NA NA NA NA NA NA NA NA NA NA NA
	NA				
NA.12	NA	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

GO_Biological_Process_2023 Top pathways by non-permulation

NA

Geneset	stat	num.genes	pval	p.adj	gene.vals
Sensory Perception Of Smell (GO:0007608)	-0.11506730	207	1.256e-08	6.791e-05	OR10D3:33 OR2L8:69 NXNL2:147 OR2M3:245 OR10AD1:265 OR2AJ1:302
Detection Of Chemical Stimulus Involved	-0.13785500	128	7.544e-08	1.360e-04	OR10D3:33 OR2L8:69 OR2M3:245 OR10AD1:265 OR2AJ1:302 OR2L3:403
Detection Of Chemical Stimulus Involved	-0.13999989	126	5.995e-08	1.360e-04	OR10D3:33 OR2L8:69 OR2M3:245 OR10AD1:265 OR2AJ1:302 OR2L3:403
Regulation Of Synaptic Transmission, Glu	-0.15146275	53	1.377e-04	1.861e-01	CDH2:167 NPS:273 TSHZ3:319 DRD2:507 DGKI:596 HCN1:654
Sister Chromatid Segregation (GO:0000819	0.17722826	34	3.498e-04	3.783e-01	SMC4:94 ESPL1:546 CHAMP1:577 NSL1:601 NCAPG2:998 SMC1A:1103
G Protein-Coupled Receptor Signaling Pat	-0.13438339	49	1.143e-03	4.601e-01	PTH1R:35 VIPR1:54 CHRM2:70 CHRM3:86 HRH3:584 CCR1:710
Calcium Ion Import Across Plasma Membran	-0.16021020	34	1.229e-03	4.601e-01	SCN9A:3 SCN1A:27 SLC8A3:53 TRPM1:60 SCN2A:280 SLC24A2:578
Heme Catabolic Process (GO:0042167)	0.29890094	10	1.064e-03	4.601e-01	SLCO1B1:646 HMOX1:650 ABCC2:752 UGT1A4:1042 BLVRB:1967 SLCO1B3:1989
Monocarboxylic Acid Transport (GO:001571	0.11573273	70	8.208e-04	4.601e-01	SLC10A2:90 SLC10A1:122 PPARD:254 SLC16A7:295 ARID4A:319 SLC22A13:376
Positive Regulation Of DNA Metabolic Pro	0.09100158	104	1.362e-03	4.601e-01	ATAD5:166 TMEM161A:170 STON1:241 BABAM1:290 DHX36:354 GLI1:366
Protein Glycosylation (GO:0006486)	0.07936128	140	1.211e-03	4.601e-01	GCNT2:144 B3GNT7:153 POMGNT1:224 ST3GAL6:225 ALG1L2:242 GALNT6:249
Regulation Of Aldosterone Biosynthetic P	0.38356673	6	1.139e-03	4.601e-01	REST:815 WNT4:1723 CLCN2:2358 BMP5:2409 BMP6:2650 DKK3:2722
Regulation Of Neuron Projection Developm	-0.07352569	171	9.329e-04	4.601e-01	CAMSAP2:82 CDH2:167 PLPPR5:196 MINAR1:289 NDNF:340 BAG5:343
Regulation Of Substrate Adhesion–Depende	-0.13368655	49	1.213e-03	4.601e-01	CARMIL1:30 APOA1:51 LIMS2:113 CSPG5:207 DOCK1:499 CRK:580
Sensory Perception Of Light Stimulus (GO	-0.09395059	101	1.119e-03	4.601e-01	ATF6:9 CRYBA4:36 TRPM1:60 CRYGN:80 PRPH2:111 CRYGD:124
Steroid Metabolic Process (GO:0008202)	0.09750762	91	1.320e-03	4.601e-01	CYP17A1:13 LRP2:82 CYP11A1:135 CYP27A1:152 SULT2A1:165 CYP8B1:438
Chemical Synaptic Transmission (GO:00072	-0.05462672	264	2.325e-03	6.156e-01	GRID1:10 GABRA5:13 GABRR3:16 CHRM2:70 CHRM3:86 CHRNA7:104
Lymphocyte Activation Involved In Immune	-0.17997774	23	2.813e-03	6.156e-01	F2RL1:616 IFNA21:738 IFNA4:740 IFNA1:926 IFNA5:1149 IFNA6:2007
Maturation Of LSU-rRNA (GO:0000470)	0.19647401	20	2.354e-03	6.156e-01	NEDD4:7 LAS1L:200 RPL35:259 RPL7:313 RPL7L1:887 ZNHIT6:956
Mitotic Sister Chromatid Segregation (GO	0.08519772	111	1.956e-03	6.156e-01	NCAPD3:38 NCAPD2:54 DLGAP5:72 CEP192:86 SMC4:94 PIBF1:246
Porphyrin–Containing Compound Catabolic	0.24888043	12	2.834e-03	6.156e-01	SLCO1B1:646 HMOX1:650 ABCC2:752 UGT1A4:1042 BLVRB:1967 SLCO1B3:1989
Regulation Of Monoatomic Ion Transmembra	-0.10595034	67	2.728e-03	6.156e-01	PHB2:73 CHRM3:86 CRH:114 SHISA9:236 FXYD6:582 HCN1:654
Regulation Of Neuron Migration (GO:20012	-0.16295301	28	2.846e-03	6.156e-01	NSMF:756 NTNG2:895 COL3A1:1040 TNN:1084 CTNNA2:1422 PLXNB2:1628
Regulation Of Peptidyl-Serine Phosphoryl	-0.20619405	18	2.459e-03	6.156e-01	IFNA21:738 IFNA4:740 IFNA1:926 IFNA5:1149 IFNA6:2007 IFNA17:2241
Visual Perception (GO:0007601)	-0.08740090	99	2.685e-03	6.156e-01	ATF6:9 CRYBA4:36 TRPM1:60 CRYGN:80 PRPH2:111 CRYGD:124
Adenylate Cyclase–Modulating G Protein–C	-0.06683417	159	3.701e-03	7.196e-01	MC4R:24 PTH1R:35 TCP11:41 VIPR1:54 CHRM2:70 ADCY1:95
Glucocorticoid Biosynthetic Process (GO:	0.37348844	5	3.823e-03	7.196e-01	CYP17A1:13 CYP11A1:135 CYP11B1:1073 CYP21A2:1115 CYP11B2:9232 NA
Regulation Of Primary Metabolic Process	0.12991953	42	3.589e-03	7.196e-01	ADGRF1:43 CERS2:131 PPARD:254 IRS2:461 ADGRF5:963 RUBCNL:1050
Spindle Assembly (GO:0051225)	0.09657717	75	3.860e-03	7.196e-01	CEP192:86 HAUS8:197 NUMA1:222 PIBF1:246 STARD9:539 TUBGCP3:676
G-quadruplex DNA Unwinding (GO:0044806)	0.36498636	5	4.705e-03	7.277e-01	DHX36:354 DDX11:595 WRN:685 DNA2:1490 DHX9:9232 NA
T Cell Activation Involved In Immune Res	-0.15716767	27	4.711e-03	7.277e-01	F2RL1:616 IFNA21:738 IFNA4:740 IFNA1:926 IFNA5:1149 FCER1G:1520
Cardiac Conduction (GO:0061337)	-0.12204619	45	4.634e-03	7.277e-01	KCNH2:75 KCND3:500 CAV1:572 HCN1:654 KCNJ3:1004 MEF2A:1291
Metal Ion Transport (GO:0030001)	-0.06381864	169	4.285e-03	7.277e-01	SCN9A:3 SCN1A:27 CHRNA7:104 RYR2:171 KCNF1:191 ITPR1:221
Mitochondrial Gene Expression (GO:014005	0.08209163	102	4.218e-03	7.277e-01	MRPS6:107 IARS2:264 POLRMT:350 LARS2:410 FASTKD1:497 MRPS10:590
Regulation Of T Cell Cytokine Production	-0.19902933	17	4.499e-03	7.277e-01	HFE:511 HLA-F:890 TRAF6:1177 TRAF2:1228 FZD5:1399 HLA-A:1574
Cellular Response To Acetylcholine (GO:1	-0.24097440	11	5.651e-03	7.452e-01	CHRM3:86 CHRNA7:104 LY6G6D:327 SLURP2:1793 CHRNA3:2065 CHRND:2443
Cytoplasmic Translation (GO:0002181)	0.08991909	76	6.769e-03		RPL35:259 RPL7:313 RPS19:463 RPL15:744 FTSJ1:941 RPS21:1014
Endodermal Cell Differentiation (GO:0035	-0.14008587	31		7.452e-01	COL7A1:59 SETD2:512 MMP2:681 CTR9:831 MMP14:1330 ITGA4:1597
mRNA Stabilization (GO:0048255)	-0.11230747	50	6.034e-03		HNRNPU:190 IREB2:363 VIP:367 DAZ1:374 DAZ3:387 DAZ2:431
Mitotic Nuclear Division (GO:0140014)	0.11783912	44		7.452e-01	SMC4:94 ESPL1:546 NSL1:601 NCAPG2:998 SMC1A:1103 SGO1:1113

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pvai	p.aaj	gene.vais
MP0003252 abnormal bile duct	0.25182360	25	1.352e-05	6.436e-03	ABCB11:5 PKHD1:188 CYP8B1:438 AHR:645 MAP3K14:733 ABCC2:75
MP0002398 abnormal bone marrow	0.04399413	813	5.953e-05	1.417e-02	NEDD4:7 ZEB1:92 JAK3:93 MAN2A1:95 ABCG8:99 MATK:120
MP0005551 abnormal eye electrophysiolog	-0.08428508	144	5.449e-04	8.261e-02	PDE6B:22 TRPM1:60 CDHR1:64 GJA10:65 RBP3:91 PRPH2:111
MP0002429 abnormal blood cell	0.03154060	1241	6.942e-04	8.261e-02	NEDD4:7 MYO9B:11 ZEB1:92 JAK3:93 MAN2A1:95 PREX1:97
MP0002136 abnormal kidney physiology	0.05218293	286	2.910e-03	2.031e-01	CUBN:17 CLDN16:27 TRPV1:64 CLCNKA:76 LRP2:82 MAN2A1:95
MP0004019 abnormal vitamin homeostasis	0.13058466	43	3.131e-03	2.031e-01	CUBN:17 CLDN16:27 LRP2:82 CYP27A1:152 RBP7:878 CYP7A1:1173
MP0000716 abnormal immune system	0.02935683	1014	3.414e-03	2.031e-01	NEDD4:7 MYO9B:11 ZEB1:92 JAK3:93 MAN2A1:95 PREX1:97
MP0005220 abnormal exocrine pancreas	0.12850224	46	2.644e-03	2.031e-01	MAN2B1:154 PKHD1:188 INVS:444 STK11:572 SERPINF1:638 PTF1A:7
MP0004085 abnormal heartbeat	-0.06515723	160	4.902e-03	2.333e-01	CHRM2:70 KCNH2:75 CDH2:167 RYR2:171 PTS:235 NUP155:246
MP0002722 abnormal immune system	0.03467404	623	4.731e-03	2.333e-01	ZEB1:92 JAK3:93 MAN2A1:95 TCF7:128 ANK1:140 TRIM21:176
MP0000313 abnormal cell death	0.03751455	464	7.370e-03	3.189e-01	LAMA1:37 LRP2:82 LHX4:272 STIL:308 POLK:332 TERT:370
MP0005646 abnormal pituitary gland	-0.17113579	20	8.140e-03	3.229e-01	GAL:455 DRD2:507 ARNT2:696 PRL:1203 NF1:1471 PDPK1:1545
MP0000598 abnormal liver morphology	0.03528075	482	1.035e-02	3.389e-01	ABCB11:5 MAN2A1:95 PREX1:97 ANK1:140 MAN2B1:154 GOLM1:16
MP0002572 abnormal emotion/affect behav	-0.04450524	287	1.098e-02	3.389e-01	MAS1:52 B3GALT2:58 ADCY1:95 CHRNA7:104 DISC1:125 FOS:131
MP0004808 abnormal hematopoietic stem	0.09383951	62	1.093e-02	3.389e-01	MAN2A1:95 MATK:120 ARID4A:319 TCF3:452 STK11:572 IL6:789
P0002063 abnormal learning/memory/cond	-0.03996942	357	1.139e-02	3.389e-01	GABRA5:13 PTPRZ1:57 CHRM3:86 ADCY1:95 CHRNA7:104 DISC1:12
MP0005253 abnormal eye physiology	-0.07309556	95	1.442e-02	4.038e-01	BFSP2:40 TRPM1:60 PRPH2:111 CNGB3:120 FOS:131 EGFLAM:347
MP0000689 abnormal spleen morphology	0.03114279	551	1.625e-02	4.070e-01	LAMP2:42 ZEB1:92 JAK3:93 MAN2A1:95 MAN2B1:154 TRIM21:176
MP0003635 abnormal synaptic transmissio	-0.03518840	426	1.563e-02	4.070e-01	SCN9A:3 GABRA5:13 SCN1A:27 MAS1:52 SLC8A3:53 PTPRZ1:57
/IP0001845 abnormal inflammatory respons	0.03114446	508	2.047e-02	4.871e-01	TRPV1:64 JAK3:93 MAN2A1:95 IRAK2:119 NBR1:127 GOLM1:164
MP0005085 abnormal gallbladder physiolo	0.12076097	30	2.232e-02	5.059e-01	ABCB11:5 SLC10A2:90 ABCG8:99 CYP27A1:152 CYP8B1:438 ABCC2:
MP0002108 abnormal muscle morphology	-0.08175680	64	2.430e-02	5.257e-01	RPTOR:127 FGFR2:338 DCN:550 CAPN3:783 EGFR:937 IGF1R:1396
IP0002396 abnormal hematopoietic system	0.12974580	22	3.540e-02	5.480e-01	JAK3:93 MAN2A1:95 TCF3:452 CSF3R:1136 BRCA2:1297 ABCG2:142
MP0002098 abnormal vibrissa morphology	0.07685631	63	3.564e-02	5.480e-01	HR:382 TCF3:452 SPINT1:849 HOXC13:975 FOXN1:985 RBPJ:1027
MP0003868 abnormal feces composition	0.12302548	25	3.351e-02	5.480e-01	SLC10A2:90 CYP8B1:438 ITGB1:763 CYP7A1:1173 CLPS:1216 LIPE:13
MP0003136 yellow coat color	-0.23026739	7	3.495e-02	5.480e-01	OCA2:1437 EDNRB:1643 MITF:1732 EDA:2144 SOX2:9342 MC1R:934
MP0002085 abnormal embryonic tissue	0.02552713	655	3.355e-02	5.480e-01	TRPM6:12 CUBN:17 ECSIT:44 LRP2:82 ZEB1:92 NANOG:124
MP0002084 abnormal developmental patter	0.03283741	365	3.569e-02	5.480e-01	CUBN:17 LAMA1:37 ECSIT:44 NANOG:124 BPTF:150 PTPRB:182
MP0001666 abnormal nutrient absorption	0.09163406	46	3.205e-02	5.480e-01	SLC10A2:90 ABCG8:99 CYP8B1:438 ITGB1:763 PNLIPRP2:790 ABCG5
MP0003186 abnormal redox activity	0.08771361	49	3.423e-02	5.480e-01	RALBP1:285 CBS:371 XPC:516 SMN1:533 HMOX1:650 WRN:685
MP0009745 abnormal behavioral response	-0.04487522	205	2.895e-02	5.480e-01	GABRA5:13 SCN1A:27 CHRM2:70 CHRNA7:104 LYST:163 RYR2:171
MP0003195 calcinosis	0.21238739	8	3.759e-02	5.592e-01	ENPP1:116 AGXT:1077 SPP1:2286 ABCC6:2713 SOD2:9232 SLC12A1:S
MP0002135 abnormal kidney morphology	0.02876308	453	4.213e-02	6.077e-01	CUBN:17 TRPV1:64 LRP2:82 MAN2A1:95 ANK1:140 GCNT2:144
MP0004087 abnormal muscle fiber	-0.03760558	244	4.664e-02	6.276e-01	SLC8A3:53 CDH2:167 GNE:187 MYL7:346 SYNE1:434 MYOF:458
1P0002113 abnormal skeleton development	0.03046663	385	4.576e-02	6.276e-01	TRPM6:12 DMP1:80 FBN2:91 ZEB1:92 ENPP1:116 NBR1:127
MP0002723 abnormal immune serum	0.02390142	649	4.746e-02	6.276e-01	NEDD4:7 TRPV1:64 PGLYRP2:84 JAK3:93 MAN2A1:95 IRAK2:119
/IP0001545 abnormal hematopoietic system	0.09141253	35	6.186e-02	6.912e-01	MATK:120 VPS13A:566 STK11:572 NLRP3:664 RAPGEF2:1086 C8B:13
MP0005193 abnormal anterior eye	-0.03608669	245	5.576e-02	6.912e-01	BFSP2:40 BNC1:42 CHRM2:70 CHRM3:86 HSF4:103 CRYGD:124
MP0000749 muscle degeneration	-0.08955732	37	6.002e-02	6.912e-01	MYOF:458 PLEC:576 CAPN3:783 TTN:1143 IGHMBP2:1297 CACNA1S:1
MP0004197 abnormal fetal growth/weight/	0.04211565	177	5.618e-02	6.912e-01	NEDD4:7 TRPM6:12 ZEB1:92 PPARD:254 REC8:297 SIN3B:325

num.genes pval p.adj gene.va

Geneset	Stat	num.genes	pvai	p.aaj	gene.vais
testis	-0.032903636	1639	3.800e-05	2.052e-03	SCN9A:3 IQCF3:6 LOXHD1:11 CRYBA4:36 TCP11:41 BNC1:42
EBV.lymphocyte	0.042352870	752	1.276e-04	3.444e-03	TMEM131L:4 RAD51AP1:15 CDCA2:20 HJURP:25 NCAPD3:38 NCAPD2:54
pancreas	0.090990677	117	7.133e-04	1.284e-02	CPB1:9 ERP27:29 CTRB1:62 CELA3B:136 TMED6:139 CTRL:145
Brodmann.area.9	-0.060602992	184	4.879e-03	6.587e-02	SCN1A:27 MAS1:52 B3GALT2:58 DCLK1:178 PLPPR5:196 KCNQ3:324
cerebellar.hemisphere	-0.024123545	536	6.159e-02	3.396e-01	CADM3:7 SSTR4:17 SLC35F3:50 OLFM3:92 ADCY1:95 APBA2:138
cortex.kidney	0.047498253	131	6.179e-02	3.396e-01	CUBN:17 CLDN16:27 ENAM:151 TINAG:159 PKHD1:188 CLCNKB:228
liver	0.029027626	397	5.076e-02	3.396e-01	ABCB11:5 IDO2:48 PBLD:58 ACOT12:65 PGLYRP2:84 AFP:98
peyers.patch	0.038542873	199	6.288e-02	3.396e-01	MALRD1:68 SLC10A2:90 TINAG:159 REG4:163 CREB3L3:208 SLC7A9:288
stomach	0.061898610	99	3.399e-02	3.396e-01	B4GALNT3:23 CHIA:24 TMPRSS2:26 PGA4:47 PGC:69 PGA3:132
suprapubic.skin	-0.034441298	257	5.986e-02	3.396e-01	POU2F3:23 BNC1:42 COL7A1:59 KRT5:71 IL37:239 CLEC2A:328
adrenal.gland	0.045553813	116	9.156e-02	4.234e-01	CYP17A1:13 ADGRV1:40 CYP11A1:135 SULT2A1:165 SLC14A2:219 AMHR2:269
leg.skin	-0.029099368	286	9.410e-02	4.234e-01	POU2F3:23 ANKRD35:34 BNC1:42 TRPM1:60 CDHR1:64 KRT5:71
ectocervix	0.085735586	26	1.306e-01	5.424e-01	LRFN5:315 RIPOR3:914 PTHLH:1468 MATN2:1977 COL27A1:2010 SOCS2:2373
thyroid	0.028688261	175	1.935e-01	7.464e-01	PRTG:8 IDO2:48 CLCNKA:76 LRP2:82 WDR72:111 ZMAT4:195
spleen	0.019124620	366	2.156e-01	7.762e-01	MPEG1:108 DENND1C:157 AKNA:186 CD40LG:239 EXOC3L1:449 UBASH3A:456
caudate.nucleus	-0.066647796	27	2.311e-01	7.799e-01	NR2E1:383 RLBP1:1144 VAX1:1982 AQP4:2106 MLC1:2138 MAPK4:2600
transformed.skin.fibroblast	-0.020490204	276	2.465e-01	7.831e-01	ADAMTS6:5 BNC1:42 DPP4:119 CLMP:150 CEMIP:225 TARS1:243
cerebellum	-0.015715426	407	2.845e-01	8.536e-01	SSTR4:17 NOS1AP:77 MYT1:193 PCNX2:228 ZIC4:295 CLIP3:354
amygdala	-0.001729007	9	9.857e-01	9.857e-01	PTPRZ1:57 BCAN:9342 NEUROD2:9342 NEUROD6:9342 PCDH15:9342 SLC17A7:9342
aorta	0.016953420	156	4.676e-01	9.857e-01	HMCN1:22 SCRG1:130 ART4:571 ITGB1:763 PTGIS:947 ERG:960
atrium.auricle	0.013807956	95	6.431e-01	9.857e-01	CCDC141:77 TNNI3K:149 DAND5:320 MLIP:550 SHD:881 MYL4:1443
bladder	-0.002625319	29	9.610e-01	9.857e-01	SLC14A1:1817 TPSD1:2115 WFDC13:2195 ABCC4:9342 ACER2:9342 ACSM6:9342
blood	0.008924979	345	5.742e-01	9.857e-01	SLC6A6:50 BPI:78 JAK3:93 PREX1:97 GMIP:209 SLA2:434
breast	-0.022938912	20	7.227e-01	9.857e-01	KRT5:71 SCGB2A2:841 TNN:1084 ADIPOQ:9342 ALX4:9342 CIDEC:9342
Brodmann.area.24	-0.032701722	33	5.161e-01	9.857e-01	CRH:114 DRD5:160 CSPG5:207 TAC3:726 RAPGEF4:2201 UPP2:2373
C1.spinal.cord	-0.001299126	194	9.506e-01	9.857e-01	PDE6B:22 CA14:98 MMD2:220 HEPACAM:222 LHPP:252 TTYH2:270
cerebral.cortex	-0.022658189	109	4.157e-01	9.857e-01	MAS1:52 KCNF1:191 SHC3:244 C1QL2:467 RGR:585 ARNT2:696
coronary.artery	-0.002601646	15	9.722e-01	9.857e-01	CCDC190:121 CCL19:706 PLA2G2A:2016 COL4A1:2492 CCN3:9342 SPINK13:9342
endocervix	0.010301918	76	7.568e-01	9.857e-01	PTPRU:598 PLPP3:614 ADGRA2:736 MFAP2:995 COL24A1:1163 LAMC3:1272
esophagogastric.junction	0.005173245	9	9.572e-01	9.857e-01	F2RL2:361 RTL3:9232 ADCY5:9232 BARX1:9232 COL4A5:9232 GADL1:9232
esophagus.mucosa	0.001741620	261	9.236e-01	9.857e-01	ADGRF1:43 RAB11FIP1:110 SOX15:218 CRB3:278 SLC44A5:324 ZNF185:364
esophagus.muscularis.mucosa	0.048107312	28	3.787e-01	9.857e-01	PRUNE2:57 F2RL2:361 CCDC69:560 SMTN:1907 RGMB:2254 CST5:2369
fallopian.tube	-0.002778471	60	9.408e-01	9.857e-01	FOS:131 STOML3:242 TCF23:695 CDHR4:764 DTHD1:873 HOXA7:887
greater.omentum	0.003065154	38	9.479e-01	9.857e-01	ATF3:496 IL6:789 RBP7:878 SPAAR:2101 BTNL9:2507 SLC7A10:2558
hippocampus.proper	0.037679043	13	6.382e-01	9.857e-01	CNIH2:2198 NEUROD2:9232 NEUROD6:9232 SLC17A7:9232 HRK:9232 OLIG2:9232
hypothalamus	-0.024829723	78	4.497e-01	9.857e-01	SCN9A:3 MC4R:24 QRFPR:659 SYT6:947 PIRT:1391 TMEM255A:1457

TNNI3K:149 MLIP:550 HSPB7:1700 RPL3L:1709 MYPN:1788 MYBPC3:2402 A2M:79 PTPRB:182 HTR3C:298 LAMP3:349 GPRC5A:692 SHROOM4:751

BPIFB2:214 ENPP3:611 SCNN1A:622 PIP:1044 FDCSP:1365 PRSS8:1427

7.212e-01 9.857e-01 GABRA5:13 C1QTNF4:1035 KCTD4:1060 SOWAHA:1104 JAKMIP1:1127 DLL3:1129

4.511e-01 9.857e-01

8.042e-01 9.857e-01

4.515e-01 9.857e-01

left.ventricle

lung

minor.salivary.gland

nucleus.accumbens

0.026301496

0.005698226

0.022913389

-0.010166731

91