Geneset	stat	num.genes	pval	p.adj	gene.vals
Sensory Perception Of Smell (GO:0007608)	0.14618253	208	4.198e-13	2.270e-09	OR2I1P:43 OR5M3:78 OR13G1:89 OR5D3P:102 OR4E2:106 OR10Z1:121.5
Detection Of Chemical Stimulus Involved	0.14697539	129	8.613e-09	2.328e-05	OR2I1P:43 OR13G1:89 OR4E2:106 OR10Z1:121.5 OR6K3:244.5 OR2T33:304
Detection Of Chemical Stimulus Involved	0.14515771	127	1.691e-08	3.047e-05	OR2I1P:43 OR13G1:89 OR4E2:106 OR10Z1:121.5 OR6K3:244.5 OR2T33:304
Fatty Acid Metabolic Process (GO:0006631	-0.14001851	120	1.220e-07	1.649e-04	ACOT8:16 THEM4:38 GNPAT:151 LCP1:155 LPIN2:206.5 LPIN1:256
Monocarboxylic Acid Metabolic Process (G	-0.14347655	96	1.216e-06	1.315e-03	THEM4:38 LDHAL6A:64 GNPAT:151 LCP1:155 LDHAL6B:211 SCP2:390.5
Peptide Biosynthetic Process (GO:0043043	0.11155620	153	1.995e-06	1.798e-03	RPS17:34 RPS16:135 AGO2:159.5 RPL9:283 RPS19:302.5 RPL34:367
Cytoplasmic Translation (GO:0002181)	0.14136982	91	3.218e-06	2.486e-03	RPS17:34 RPS16:135 RPL9:283 RPS19:302.5 RPL34:367 RPL23A:411
Brain Development (GO:0007420)	0.10630067	157	4.473e-06	3.023e-03	NDRG4:128 ZIC1:133.5 EML1:181 GRIN2C:291 ROBO2:293.5 FLNB:383
Macromolecule Biosynthetic Process (GO:0	0.09497648	179	1.222e-05	6.005e-03	RPS17:34 RPS16:135 AGO2:159.5 RPL9:283 RPS19:302.5 GTPBP1:318.5
Sensory Perception Of Chemical Stimulus	0.12823008	98	1.176e-05	6.005e-03	OR5M3:78 OR5D3P:102 CALHM3:140 OR8K1:194 OR5I1:242.5 OR5M9:376.5
Triglyceride Metabolic Process (GO:00066	-0.19309926	43	1.189e-05	6.005e-03	APOC3:29 LCP1:155 LPIN2:206.5 LPIN1:256 GK5:558.5 PNPLA4:582
Steroid Biosynthetic Process (GO:0006694	-0.17787624	49	1.665e-05	7.503e-03	ACOT8:16 CYP8B1:163.5 OSBP:226 CYP39A1:311.5 SCP2:390.5 PRLR:536
Nitrogen Compound Transport (GO:0071705)	-0.09351927	161	4.371e-05		ABCC2:84.5 CD320:92 SLC13A1:196 SLC22A4:222 SLC38A2:260.5 SLC6A13:37
Gene Expression (GO:0010467)	0.06943954	286	5.663e-05	2.046e-02	RPS17:34 H3C1:103 HNRNPH3:123.5 RPS16:135 AGO2:159.5 ALYREF:162.5
Vitamin Transport (GO:0051180)	-0.18878962	38	5.676e-05	2.046e-02	SLC5A6:34 CD320:92 SLC25A32:128 SLC2A8:190 TCN2:388 SLC46A1:598.5
Cellular Lipid Catabolic Process (GO:004	-0.23646837	23	8.667e-05		ACOT8:16 LPIN2:206.5 LPIN1:256 ACOX1:319 PLBD1:343 PLD1:1397.5
Translation (GO:0006412)	0.07591019	228	8.207e-05	2.757e-02	RPS17:34 RPS16:135 AGO2:159.5 RPL9:283 RPS19:302.5 GTPBP1:318.5
Cell Morphogenesis Involved In Neuron Di	0.12899038	76	1.024e-04	2.915e-02	NEFH:123.5 MAP1B:188.5 DVL1:523 POU4F1:532.5 MINK1:703 APLP2:883.5
Diol Biosynthetic Process (GO:0034312)	-0.28126773	16	9.819e-05	2.915e-02	SPHK2:21 SPTSSB:40.5 ACER1:321 SPTLC1:496.5 DHFR:542.5 SPHK1:900
Neuron Projection Morphogenesis (GO:0048	0.09432961	140	1.196e-04	3.233e-02	SRGAP3:82 NEFH:123.5 MAP1B:188.5 EPHA4:251.5 SGK1:261.5 SHANK3:429
Fatty Acid Catabolic Process (GO:0009062	-0.14216875	60	1.409e-04	3.493e-02	ACOT8:16 ECHDC1:159.5 LPIN2:206.5 NUDT8:219 LPIN1:256 ACOX1:319
Serine Family Amino Acid Metabolic Proce	-0.30475009	13	1.421e-04	3.493e-02	GCLC:320 AOC1:831 SRR:1310 CTH:1712 GLYAT:1995.5 BAAT:2016.5
Lipid Biosynthetic Process (GO:0008610)	-0.13224147	68	1.643e-04	3.554e-02	LCP1:155 SCP2:390.5 MVD:534.5 PRLR:536 ACACB:624 CYP17A1:625
Sphingoid Biosynthetic Process (GO:00465	-0.31482171	12	1.593e-04	3.554e-02	SPHK2:21 SPTSSB:40.5 ACER1:321 SPTLC1:496.5 SPHK1:900 ASAH2:908
Sphingosine Biosynthetic Process (GO:004	-0.31482171	12	1.593e-04	3.554e-02	SPHK2:21 SPTSSB:40.5 ACER1:321 SPTLC1:496.5 SPHK1:900 ASAH2:908
IADH Dehydrogenase Complex Assembly (GO:	-0.15405705	49	1.922e-04	3.849e-02	ECSIT:70.5 NDUFB10:271.5 NDUFAF1:469 NUBPL:474.5 NDUFA3:606 NDUFC2:61
Mitochondrial Respiratory Chain Complex	-0.15405705	49	1.922e-04	3.849e-02	ECSIT:70.5 NDUFB10:271.5 NDUFAF1:469 NUBPL:474.5 NDUFA3:606 NDUFC2:61
Positive Regulation Of Cell Migration (G	-0.06587634	267	2.214e-04	4.127e-02	PDGFRB:27 EPHA2:60 MYADM:65 CTSH:90.5 SEMA7A:148 GRB7:295.5
Positive Regulation Of Leukocyte Activat	-0.23888495	20	2.173e-04	4.127e-02	NECTIN2:526 TSLP:612 CD226:637.5 HAVCR1:1039 WNT5A:1473.5 TLR6:2032
Embryonic Limb Morphogenesis (GO:0030326	0.18233352	34	2.347e-04	4.230e-02	INTU:217 WDPCP:625 CREBBP:877 TFAP2A:936 TBX2:1135.5 ZNF358:1164.5
Mitochondrial Respiratory Chain Complex	-0.11687195	82	2.568e-04	4.340e-02	ECSIT:70.5 NDUFB10:271.5 NDUFAF1:469 NUBPL:474.5 CHCHD7:600 NDUFA3:6
protein-RNA Complex Assembly (GO:0022618	0.08949784	141	2.494e-04	4.340e-02	AGO1:32 TARBP2:40 AGO2:159.5 SART1:195 RPS19:302.5 LUC7L2:354
Wnt Signaling Pathway (GO:0016055)	0.12170534	74	2.979e-04	4.350e-02	FZD8:59 TCF7L1:223 CCDC88C:223 WNT2B:347 FZD3:487 DVL1:523
acyl-CoA Metabolic Process (GO:0006637)	-0.19406240	28	3.800e-04		ACOT8:16 MCEE:445 ACACB:624 OGDH:631 SUCLG2:794 SUCLA2:1257
Amide Biosynthetic Process (GO:0043604)	-0.14909511	50	2.669e-04		SPTSSB:40.5 CERS3:101 CERS6:187 OSBP:226 CYP4F22:490 SPTLC1:496.5
Amide Transport (GO:0042886)	-0.18457077	31	3.768e-04		SLC5A6:34 SLC25A32:128 OSBP:226 GIPC1:313 DISP1:438 TAP1:576.5
Cholesterol Transport (GO:0030301)	-0.14404802	51	3.751e-04		APOC3:29 OSBP:226 STARD5:349 SOAT1:403 CD36:728.5 NPC1:787.5
Dicarboxylic Acid Metabolic Process (GO:	-0.14840342	49	3.279e-04		ACOT8:16 SLC25A32:128 GCLC:320 L2HGDH:442.5 DHFR:542.5 SLC46A1:598.
Import Into Cell (GO:0098657)	-0.17046163	37	3.345e-04		SLC5A6:34 SLC22A4:222 SLC16A2:242 SLC6A13:372 SLC46A1:598.5 SLC6A6:73
mRNA Processing (GO:0006397)	0.07239027	205	3.650e-04		HNRNPH3:123.5 ALYREF:162.5 SART1:195 RBMX:238.5 SNRPA1:242.5 DHX15:26

EnrichmentHsSymbolsFile2 Top pathways by permulation

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REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.16513987	390	5.512e-29	3.580e-25	OR52B2:19.5 OR52W1:29 OR2AT4:62 OR5M3:78 OR13G1:89 OR11G2:104
KEGG_OLFACTORY_TRANSDUCTION	0.15889558	380	2.536e-26	8.234e-23	OR52B2:19.5 OR52W1:29 CAMK2B:42 OR2AT4:62 OR5M3:78 OR13G1:89
REACTOME_SENSORY_PERCEPTION	0.12097937	605	3.978e-24	8.610e-21	OR52B2:19.5 OR52W1:29 OR2AT4:62 MYH9:69 OR5M3:78 OR13G1:89
REACTOME_DEVELOPMENTAL_BIOLOGY	0.08326744	1143	3.903e-21	6.337e-18	KRTAP10-1:6 SPRR2B:7 ABL2:8 RPS17:34 MAP2K2:50 MYH9:69
HOUNKPE_HOUSEKEEPING_GENES	0.06709069	1100	8.182e-14	1.063e-10	CBX1:19.5 DDX27:35 PDCD6:36.5 TSR3:39 PURB:41 MAP2K2:50
REACTOME_SIGNALING_BY_WNT	0.11693456	322	5.894e-13	6.379e-10	AGO1:32 FZD8:59 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5
HSIAO_LIVER_SPECIFIC_GENES	-0.12989976	240	4.388e-12	4.071e-09	APOC3:29 ABCC2:84.5 NR1H4:130.5 ALDH1A1:139.5 LPIN2:206.5 AZGP1:369
CARRILLOREIXACH_HEPATOBLASTOMA_VS_NORMAL	-0.06341643	1046	5.424e-12	4.403e-09	TMEM45A:15 APOC3:29 ANO5:35 SLC6A16:53 ETNPPL:59 EPHA2:60
REACTOME_INFECTIOUS_DISEASE	0.06151647	933	2.342e-10	1.690e-07	CBX1:19.5 RPS17:34 MAP2K2:50 MYH9:69 TUBA1A:71.5 IFNA14:74
REACTOME_ACTIVATION_OF_ANTERIOR_HOX_GENE	0.16697291	116	5.322e-10	3.456e-07	H3C1:103 H3C13:127 H2BC4:141 H2AC14:261.5 H2AC19:308.5 ASH2L:394
REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	0.07574312	570	7.112e-10	4.199e-07	ABL2:8 RPS17:34 MAP2K2:50 MYH9:69 TUBA1A:71.5 SRGAP3:82
REACTOME_METABOLISM_OF_LIPIDS	-0.06690441	726	9.558e-10	5.172e-07	ACOT8:16 SPHK2:21 STARD6:31 THEM4:38 SPTSSB:40.5 MTMR6:44.5
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	0.06418692	788	1.044e-09	5.214e-07	AGO1:32 RPS17:34 CAMK2B:42 TUBA1A:71.5 CALR:90 TXN2:95.5
REACTOME_RHO_GTPASES_ACTIVATE_PKNS	0.18409103	89	1.961e-09	9.096e-07	MYH9:69 YWHAQ:94 H3C1:103 H3C13:127 H2BC4:141 H2AC14:261.5
REACTOME_REGULATION_OF_EXPRESSION_OF_SLI	0.13242352	169	2.937e-09	1.271e-06	RPS17:34 RPS16:135 PSMA4:225 PSMA7:258 RPL9:283 ROBO2:293.5
HOSHIDA_LIVER_CANCER_SUBCLASS_S3	-0.10411267	260	7.793e-09	3.163e-06	GGH:50 ALDH1A1:139.5 LPIN2:206.5 SLC16A2:242 LPIN1:256 ADK:274
CAIRO_LIVER_DEVELOPMENT_DN	-0.11329995	217	9.121e-09	3.484e-06	CTSH:90.5 CAMP:104 LCP1:155 A2M:178 LPIN2:206.5 SLC16A2:242
REACTOME_SIGNALING_BY_ROBO_RECEPTORS	0.11316255	214	1.198e-08	4.322e-06	ABL2:8 RPS17:34 SRGAP3:82 RPS16:135 PSMA4:225 PSMA7:258
REACTOME_KERATINIZATION	0.11265690	214	1.391e-08	4.753e-06	KRTAP10-1:6 SPRR2B:7 KRTAP10-4:77 KRT81:91.5 KRTAP10-8:117.5 KRTAP5-8:130.5
REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SI	0.13609902	145	1.568e-08	5.092e-06	AGO1:32 FZD8:59 AGO2:159.5 PDE6G:165.5 TNRC6B:176.5 CAMK2A:192
REACTOME_METABOLISM_OF_STEROIDS	-0.13195589	152	2.006e-08	6.203e-06	ACOT8:16 STARD6:31 TM7SF2:116 NR1H4:130.5 CYP8B1:163.5 AKR1B1:213
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	0.10493804	233	3.539e-08	1.045e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5 CBX2:173
REACTOME_LEISHMANIA_INFECTION	0.12623219	158	4.448e-08	1.256e-05	MYH9:69 ACTR2:190 ARPC4:276 ARPC5:417.5 VAV1:478 FGR:498.5
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATI	-0.11969025	173	5.734e-08	1.552e-05	ETNPPL:59 CYP8B1:163.5 MYRIP:235.5 SLC16A2:242 AZGP1:369 SCP2:390.5
CAIRO_HEPATOBLASTOMA_DN	-0.09717051	262	6.362e-08	1.653e-05	ETNPPL:59 EPHA2:60 MGLL:98 LEPR:182.5 LPIN2:206.5 VIPR1:246
REACTOME_RHO_GTPASE_EFFECTORS	0.08729911	312	1.192e-07	2.848e-05	CLIP1:9 CIT:16 MYH9:69 TUBA1A:71.5 YWHAQ:94 H3C1:103
REACTOME_OXIDATIVE_STRESS_INDUCED_SENESC	0.14145624	117	1.272e-07	2.848e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 CBX2:173 TNRC6B:176.5
REACTOME_GLYOXYLATE_METABOLISM_AND_GLYCI	-0.27889902	30	1.242e-07	2.848e-05	DBT:201 DLD:242 GLDC:563.5 LIAS:566 OGDH:631 PDHA2:637.5
REACTOME_ESR_MEDIATED_SIGNALING	0.10506595	214	1.209e-07	2.848e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5 TNRC6B:176.5
REACTOME_RUNX1_REGULATES_GENES_INVOLVED_	0.15672222	92	2.061e-07	4.460e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 TNRC6B:176.5 SETD1B:246.5
REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESS	0.12340408	145	2.951e-07	5.861e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5 TNRC6B:176.5
WP_CYTOPLASMIC_RIBOSOMAL_PROTEINS	0.16018754	86	2.845e-07	5.861e-05	RPS17:34 RPS16:135 RPL9:283 RPS19:302.5 RPL34:367 RPL23A:411
HSIAO_HOUSEKEEPING_GENES	0.07661425	381	2.978e-07	5.861e-05	RPS17:34 MYH9:69 HINT1:86 YWHAQ:94 RPS16:135 SLC25A6:143
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRA	-0.22288267	44	3.137e-07	5.992e-05	DBT:201 DLD:242 ACAD8:286 HIBCH:324 MCEE:445 BCAT2:474.5
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_P	0.13893881	111	4.306e-07	7.990e-05	RPS17:34 RPS16:135 RPN2:213.5 RPL9:283 RPS19:302.5 RPL34:367
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_O	0.13040311	125	4.837e-07	8.725e-05	H3C1:103 H3C13:127 H2BC4:141 PSMA4:225 PSMA7:258 H2AC14:261.5
MARTENS_TRETINOIN_RESPONSE_DN	0.05394735	751	5.370e-07	9.425e-05	CLIP1:9 ARL6IP4:33 PURB:41 ABT1:67 HINT1:86 CALR:90
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRAN	-0.09268152	245	6.016e-07	1.002e-04	SLC22A8:8 SLC5A12:12 SLC5A6:34 SLC2A8:190 SLC13A1:196 SLC22A6:204

5.926e-07 1.002e-04

6.908e-07 1.094e-04

0.09592966

stat

-0.09003086

-0.08827839

-0.04194108

-0.06046979

512

1799

RPS17:34 CAMK2B:42 VDAC3:58 HINT1:86 YWHAQ:94 NDRG4:128

FZD8:59 H3C1:103 H3C13:127 H2BC4:141 CCDC88C:223 TCF7L1:223

gene.vals

SLC22A8:8 APOC3:29 TM6SF2:68.5 DNASE2:77 TM7SF2:116 NR1H4:130.5

SLC22A8:8 APOC3:29 TM6SF2:68.5 DNASE2:77 ABCC2:84.5 TM7SF2:116

MFAP5:1 KRIT1:13 ADAM28:22 APOC3:29 KLRF1:36 THEM4:38

IL37:66 NAA16:86 HK1:101 ITGAV:130.5 ARHGAP28:136 S100A6:180.5

KIM\_BIPOLAR\_DISORDER\_OLIGODENDROCYTE\_DEN

REACTOME\_TCF\_DEPENDENT\_SIGNALING\_IN\_RESP

Geneset

Steatohepatitis

Fatty Liver

Obesity

Endometriosis

Geneset

MP0003699 abnormal female reproductive

MP0002118 abnormal lipid homeostasis

MP0003959 abnormal lean body

MP0002161 abnormal fertility/fecundity

MP0000609 abnormal liver physiology

MP0005636 abnormal mineral homeostasis

MP0008469 abnormal protein level

stat

-0.07160620

-0.06707483

-0.14890055

-0.04044289

-0.05627103

-0.08776270

-0.05297182

num.genes

428

408

868

380

141

406

pval p.adj

4.237e-12 4.161e-08

1.571e-09 7.713e-06

8.366e-09 2.739e-05

7.350e-08 1.805e-04

DisGeNET Top pathways by permulation

	-0.00040979	094	7.3306-08		
Cardiovascular Diseases	-0.05636487	724	3.077e-07	6.023e-04	APOC3:29 GGH:50 C1QTNF9:56.5 TM6SF2:68.5 TAS2R50:83 CD320:92
Metabolic Syndrome X	-0.06606834	512	3.680e-07	6.023e-04	ADAM28:22 APOC3:29 TM6SF2:68.5 TM7SF2:116 NR1H4:130.5 LEPR:182.5
Hypertensive disease	-0.04357011	1212	4.998e-07	7.012e-04	MFAP5:1 GCM1:3 SLC22A8:8 PDGFRB:27 APOC3:29 SDHC:42
Non-alcoholic Fatty Liver Disease	-0.08190552	311	7.473e-07	9.174e-04	APOC3:29 TM6SF2:68.5 ABCC2:84.5 LAMA1:97 NR1H4:130.5 LCP1:155
Drug-Induced Liver Disease	-0.08800332	246	2.138e-06	2.100e-03	SLC22A8:8 GGH:50 ABCC2:84.5 NR1H4:130.5 ECHDC1:159.5 CYP8B1:163.5
Vomiting	-0.10445394	175	1.964e-06	2.100e-03	DBT:201 DLD:242 SLC17A5:277.5 CPOX:330.5 TCN2:388 PPOX:456.5
Lethargy	-0.13410090	104	2.359e-06	2.106e-03	DBT:201 DLD:242 SLC25A20:355 TCN2:388 DPYD:461.5 NDUFAF1:469
Atherosclerosis	-0.04379366	1033	2.653e-06	2.171e-03	PDE1A:26 APOC3:29 EPHA2:60 IL37:66 TM6SF2:68.5 CAMP:104
Hyperlipidemia	-0.09241970	210	4.124e-06	3.116e-03	APOC3:29 NR1H4:130.5 CDCP1:134 LEPR:182.5 AKR1B1:213 OLR1:223.5
Coronary Artery Disease	-0.04513434	898	5.749e-06	4.028e-03	MFAP5:1 APOC3:29 BCAS3:62.5 TM6SF2:68.5 MYO9B:84.5 ELL:95.5
Metabolic Diseases	-0.06684489	392	6.152e-06	4.028e-03	APOC3:29 OCA2:55 IL37:66 TM7SF2:116 NR1H4:130.5 LEPR:182.5
Nonalcoholic Steatohepatitis	-0.09396535	192	7.473e-06	4.587e-03	TM6SF2:68.5 LAMA1:97 NR1H4:130.5 CYP8B1:163.5 LEPR:182.5 OLR1:223.5
Hypercholesterolemia, Familial	-0.10651306	145	9.859e-06	5.379e-03	APOC3:29 OCA2:55 OLR1:223.5 ITGB3:338.5 MTTP:407.5 ABCA1:514
Hypertriglyceridemia	-0.10807565	141	9.715e-06	5.379e-03	APOC3:29 TM6SF2:68.5 NR1H4:130.5 LPIN1:256 MTTP:407.5 ABCA1:514
Liver Cirrhosis	-0.05096524	625	1.590e-05	8.216e-03	SLC22A8:8 TM6SF2:68.5 HES6:107 TM7SF2:116 NR1H4:130.5 A2M:178
Hepatitis, Toxic	-0.08725355	198	2.407e-05	1.028e-02	SLC22A8:8 GGH:50 ABCC2:84.5 NR1H4:130.5 ECHDC1:159.5 CYP8B1:163.5
Chemical and Drug Induced Liver Injury	-0.08725355	198	2.407e-05	1.028e-02	SLC22A8:8 GGH:50 ABCC2:84.5 NR1H4:130.5 ECHDC1:159.5 CYP8B1:163.5
Chemically-Induced Liver Toxicity	-0.08725355	198	2.407e-05	1.028e-02	SLC22A8:8 GGH:50 ABCC2:84.5 NR1H4:130.5 ECHDC1:159.5 CYP8B1:163.5
Drug-Induced Acute Liver Injury	-0.08725355	198	2.407e-05	1.028e-02	SLC22A8:8 GGH:50 ABCC2:84.5 NR1H4:130.5 ECHDC1:159.5 CYP8B1:163.5
Cerebral Hemorrhage	-0.15194202	64	2.656e-05	1.043e-02	KRIT1:13 SDHC:42 ITGAV:130.5 COL4A2:244 ITGB3:338.5 BAX:411.5
Coronary Arteriosclerosis	-0.04681698	706	2.655e-05	1.043e-02	APOC3:29 PRKY:114 NR1H4:130.5 LEPR:182.5 AKR1B1:213 OLR1:223.5
Liver diseases	-0.05146044	555	3.837e-05	1.449e-02	APOC3:29 TM6SF2:68.5 ABCC2:84.5 TM7SF2:116 NR1H4:130.5 ALDH1A1:139.5
Hepatitis, Drug-Induced	-0.08386215	202	4.142e-05	1.507e-02	SLC22A8:8 GGH:50 ABCC2:84.5 NR1H4:130.5 ECHDC1:159.5 CYP8B1:163.5
Arteriosclerosis	-0.03893312	988	4.317e-05	1.514e-02	APOC3:29 EPHA2:60 IL37:66 TM6SF2:68.5 CAMP:104 TM7SF2:116
Mitochondrial Diseases	-0.06208304	363	5.234e-05	1.773e-02	SDHC:42 ECSIT:70.5 NAXE:173 CERS6:187 DLD:242 NDUFB10:271.5
Pre-Eclampsia	-0.09702182	145	5.665e-05	1.854e-02	GCM1:3 TPBG:67 LEPR:182.5 OLR1:223.5 APLNR:394.5 ADM:399
Arthritis	-0.04827740	575	8.547e-05	2.708e-02	KRIT1:13 IL37:66 HK1:101 TM7SF2:116 SLC22A4:222 MRC1:225
Diabetes Mellitus, Non-Insulin-Dependent	-0.03075904	1479	1.046e-04	2.854e-02	ADAM28:22 APOC3:29 THEM4:38 OCA2:55 C1QTNF9:56.5 IL37:66
Adverse reaction to drug	-0.12570114	80	1.029e-04	2.854e-02	ABCC2:84.5 GC:258.5 B2M:315.5 TCN2:388 DHFR:542.5 NFE2L2:733.5
Drug toxicity	-0.12570114	80	1.029e-04	2.854e-02	ABCC2:84.5 GC:258.5 B2M:315.5 TCN2:388 DHFR:542.5 NFE2L2:733.5
Periodontal Diseases	-0.09998283	128	9.589e-05	2.854e-02	CAMP:104 MMP13:329 DEFB1:348 CTSD:417 BDNF:521.5 C1S:815
Vascular Diseases	-0.05852591	377	1.027e-04	2.854e-02	APOC3:29 ATXN1:95.5 TM7SF2:116 ANTXR1:153 AKR1B1:213 OLR1:223.5
Anorexia	-0.11389978	95	1.267e-04	3.191e-02	LEPR:182.5 IAPP:350.5 MAGEL2:405.5 HTR3B:509.5 BDNF:521.5 SLC46A1:598.
Hyperinsulinism	-0.05918294	361	1.203e-04	3.191e-02	APOC3:29 CTSH:90.5 OFD1:113 CRB1:177 LEPR:182.5 LPIN1:256
Myocardial Infarction	-0.03817725	899	1.239e-04	3.191e-02	APOC3:29 BCAS3:62.5 TM6SF2:68.5 ILF3:79 TAS2R50:83 TM7SF2:116
Comatose	-0.12808436	71	1.921e-04	4.716e-02	NAXE:173 DBT:201 SLC25A20:355 NDUFAF1:469 NUBPL:474.5 TMEM126B:667.

p.adj

8.186e-07 3.897e-04

6.232e-06 1.483e-03

9.326e-05 1.480e-02

1.487e-04 1.770e-02

2.444e-04 2.204e-02

3.654e-04 2.204e-02

3.705e-04 2.204e-02

gene.vals

OOEP:23 PDGFRB:27 OCA2:55 RAD51C:99 HK1:101 ANTXR1:153

APOC3:29 OCA2:55 ABCC2:84.5 MGLL:98 NR1H4:130.5 GNPAT:151

LEPR:182.5 LPIN1:256 SCP2:390.5 ANKRD26:409 GHRHR:469 BCAT2:474.5

OOEP:23 PDGFRB:27 POLL:32.5 OCA2:55 RAD51C:99 HK1:101

OCA2:55 ABCC2:84.5 HK1:101 NR1H4:130.5 ADCYAP1:161 CYP8B1:163.5

SCGB1A1:61 HK1:101 SLC13A1:196 B2M:315.5 ITGB3:338.5 GAST:352.5

ABCC2:84.5 MAGED1:105 NR1H4:130.5 ITGAV:130.5 LEPR:182.5 OLR1:223.5

MGI\_Mammalian\_Phenotype\_Level\_4 Top pathways by permulation

wir 0000409 abrioritiai protein level	-0.03297102	400	3.7036-04	2.2046-02	ABCC2.04.5 MAGED1.105 NK1114.150.5 11GAV.150.5 LEFK.162.5 OLK1.225.5
MP0002128 abnormal blood circulation	-0.05306397	410	3.402e-04	2.204e-02	PDGFRB:27 SMAD6:62.5 ITGAV:130.5 LEPR:182.5 TPH1:193 LATS2:198
MP0005334 abnormal fat pad	-0.08166510	152	5.823e-04	3.080e-02	OCA2:55 LEPR:182.5 GPR12:199 LGR4:233 LPIN1:256 LACTB2:418
MP0009763 increased sensitivity to	-0.06365150	247	7.050e-04	3.356e-02	NR1H4:130.5 LEPR:182.5 ITGB1BP2:265.5 LGALS3:335.5 ITGB3:338.5 ADM:39
MP0005376 homeostasis/metabolism phenot	-0.07082418	191	8.624e-04	3.732e-02	PDGFRB:27 TM7SF2:116 CRB1:177 LEPR:182.5 LPIN1:256 ADK:274
MP0009642 abnormal blood homeostasis	-0.02941197	1293	1.319e-03	5.233e-02	PDGFRB:27 APOC3:29 OCA2:55 SCGB1A1:61 SMAD6:62.5 MN1:72.5
MP0003121 genomic imprinting	-0.16868023	29	1.700e-03	5.779e-02	MAGEL2:405.5 CDKN1C:496.5 DIO3:634 SMCHD1:732 PEG10:766 GRB10:810.
MP0000249 abnormal blood vessel	-0.06495652	202	1.693e-03	5.779e-02	APOC3:29 SMAD6:62.5 LEPR:182.5 GJB6:191 OLR1:223.5 ITGB3:338.5
MP0003635 abnormal synaptic transmissio	0.04468974	429	2.065e-03	6.554e-02	KCNH3:11 CAMK2B:42 VDAC3:58 KCNJ10:152 LMX1B:180 CAMK2A:192
MP0002752 abnormal somatic nervous	0.03864813	583	2.220e-03	6.605e-02	GNAT1:113 NEFH:123.5 KCNJ10:152 PDE6G:165.5 PTK7:168.5 LMX1B:180
MP0003698 abnormal male reproductive	-0.04033688	522	2.370e-03	6.636e-02	CRISP1:11 PDGFRB:27 POLL:32.5 OCA2:55 RAD51C:99 GNPAT:151
MP0001486 abnormal startle reflex	0.08745316	96	3.257e-03	8.239e-02	ABL2:8 KCNJ10:152 DVL1:523 CDH23:553 TMIE:747.5 GLRA1:925.5
MP0010329 abnormal lipoprotein level	-0.09018003	90	3.289e-03	8.239e-02	APOC3:29 OCA2:55 LEPR:182.5 GPR12:199 LPIN1:256 SCP2:390.5
MP0001881 abnormal mammary gland	-0.10506080	64	3.797e-03	9.037e-02	LEPR:182.5 GHRHR:469 PRLR:536 CHEK1:825 CSF1:945 XDH:1010
MP0002419 abnormal innate immunity	-0.04409429	361	5.006e-03	9.675e-02	MYO9B:84.5 ITGAV:130.5 LCP1:155 MRC1:225 CCR1:332.5 LGALS3:335.5
MP0001119 abnormal female reproductive	-0.04755656	295	5.895e-03	9.675e-02	RAD51C:99 GNPAT:151 ANTXR1:153 LEPR:182.5 LGR4:233 ZFX:245
MP0003861 abnormal nervous system	0.03173856	723	5.812e-03	9.675e-02	SOCS7:53 CALR:90 TXN2:95.5 NEFH:123.5 SMO:125 ZIC1:133.5
MP0000627 abnormal mammary gland	-0.07167153	131	4.986e-03	9.675e-02	BECN1:242 TBX3:370.5 PRLR:536 NRG1:571 BCL2L11:584 CHEK1:825
MP0003122 maternal imprinting	-0.20528665	16	4.508e-03	9.675e-02	MAGEL2:405.5 DIO3:634 PEG10:766 IGF2:937.5 DLK1:1550.5 ARID4A:1955.5
MP0002882 abnormal neuron morphology	0.02937115	888	5.429e-03	9.675e-02	CADPS:5 ABL2:8 TUBA1A:71.5 GNAT1:113 NEFH:123.5 SMO:125
MP0005584 abnormal enzyme/coenzyme acti	-0.06785425	142	5.693e-03	9.675e-02	LEPR:182.5 SLC13A1:196 DBT:201 SLC16A2:242 LPIN1:256 ANGPTL4:524
MP0005535 abnormal body temperature	-0.07440604	124	4.541e-03	9.675e-02	MGLL:98 NR1H4:130.5 ADCYAP1:161 LEPR:182.5 ADK:274 BCAT2:474.5
MP0002111 abnormal tail morphology	-0.06072872	177	5.889e-03	9.675e-02	EPHA2:60 SLC13A1:196 DST:290 FGFR3:553 GJB2:586.5 SMN1:590
MP0000858 altered metastatic potential	-0.09943614	63	6.561e-03	1.041e-01	EPHA2:60 LEPR:182.5 CD226:637.5 LEP:869.5 MGAT5:1536.5 FGFR4:1562.5
MP0003690 abnormal glial cell	-0.12348171	40	7.030e-03	1.069e-01	ATM:598.5 CD36:728.5 NPC1:787.5 PHYH:804 LEP:869.5 PARP1:1293
MP0002063 abnormal learning/memory/cond	0.04234303	359	7.183e-03	1.069e-01	ABL2:8 KCNH3:11 VDAC3:58 TUBA1A:71.5 LMX1B:180 CAMK2A:192
MP0004883 abnormal blood vessel	-0.11795008	43	7.614e-03	1.098e-01	LEPR:182.5 PRMT2:442.5 SPP1:1037 SCPEP1:1150 ESR1:1660 IRF1:1806.5
MP0000015 abnormal ear pigmentation	-0.18062287	18	8.047e-03	1.102e-01	OCA2:55 BLOC1S3:361.5 SLC24A5:806.5 AP3B1:1744 HPS1:2721 MC1R:3006
MP0005085 abnormal gallbladder physiolo	-0.13947952	30	8.313e-03	1.102e-01	ABCC2:84.5 NR1H4:130.5 CYP8B1:163.5 SCP2:390.5 CHRM2:463 ACADL:153
MP0009643 abnormal urine homeostasis	-0.05107803	232	8.332e-03	1.102e-01	SLC22A8:8 SCGB1A1:61 ABCC2:84.5 LEPR:182.5 SLC13A1:196 DBT:201
MP0009785 altered susceptibility to	-0.08831197	74	8.951e-03	1.121e-01	CAMP:104 B2M:315.5 TAP1:576.5 PGLYRP2:635 S100A9:710 CD36:728.5
MP0000778 abnormal nervous system	0.06956628	121	8.748e-03	1.121e-01	EPHA4:251.5 ST8SIA2:302.5 TUBB3:395 FZD3:487 EBF1:724 ROBO1:837
MP0000428 abnormal craniofacial morphol	0.08510189	79	9.283e-03	1.133e-01	PKDCC:323 HAND1:669 CREBBP:877 SP8:1086.5 TBX15:1175 PDPK1:1313.5
MP0002152 abnormal brain morphology	0.02631018	974	0.750 00	1.161e-01	ABL2:8 CIT:16 SOCS7:53 MYH9:69 TUBA1A:71.5 CALR:90

tissue\_specific Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
cerebellum	0.09017416	408	7.775e-10	4.198e-08	LINC00514:2 RALGPS1:79.5 SRGAP3:82 NDRG4:128 ZIC1:133.5 CDR2L:155
cerebellar.hemisphere	0.06687893	543	1.833e-07	4.756e-06	LINC00514:2 CADPS:5 INPP5F:38 CAMK2B:42 PPFIA3:51 SOCS7:53
testis	-0.04063976	1685	2.642e-07	4.756e-06	GCM1:3 KIF15:7 CRISP1:11 CDCA2:18 OOEP:23 PRSS54:24.5
liver	-0.05782950	399	9.531e-05	1.287e-03	AGMAT:10 APOC3:29 TM6SF2:68.5 ABCC2:84.5 NR1H4:130.5 SLC22A25:149.5
subcutaneous.adipose	-0.10653859	82	8.844e-04	9.551e-03	CSN1S1:120 ACVR1C:157 TNMD:218 CMA1:521.5 ANGPTL4:524 ACACB:624
cerebral.cortex	0.07758069	111	4.925e-03	4.432e-02	KCNH3:11 CIT:16 OPRL1:329.5 LZTS1:740.5 RS1:760.5 RFPL2:841
adrenal.gland	-0.06901321	116	1.058e-02	7.140e-02	CYP2W1:4 TM7SF2:116 AKR1B1:213 QPRT:292.5 TBX3:370.5 SOAT1:403
left.ventricle	0.09009065	69	9.845e-03	7.140e-02	TNNT2:69 ASB10:76 SLC25A4:254.5 MYOM3:381 MYH7B:963 CSRP3:1012
aorta	0.05503425	156	1.837e-02	9.918e-02	HMCN1:30.5 MYH9:69 LTBP4:95.5 LOXL1:119 PXDC1:176.5 ELN:385
breast	-0.15405148	20	1.715e-02	9.918e-02	LEP:869.5 FABP4:1166 HCAR1:1239 THRSP:1987.5 GLYAT:1995.5 TNN:2086
eye.development	0.07936350	69	2.297e-02	1.128e-01	MAF:111 NRL:233.5 WNT2B:347 DLX2:467.5 VSX2:1041.5 PAX2:1438
Brodmann.area.9	0.04446780	187	3.734e-02	1.680e-01	OLFM1:52 CAMK2A:192 RAB6B:523 TAFA2:706.5 NEFM:752.5 RS1:760.5
sigmoid.colon	0.07772952	53	5.073e-02	2.107e-01	TACR2:47 ACTG2:591 HAND1:669 MAB21L2:1184.5 MYLK:1210.5 PLEKHO1:1469.5
spleen	0.02825839	367	6.687e-02	2.579e-01	OR2I1P:43 SH2D1A:83 GBA3:88 PDE6G:165.5 CD163L1:256.5 LILRB5:340
lung	-0.03908780	161	8.895e-02	3.002e-01	ADGRF5:17 SCGB1A1:61 SMAD6:62.5 A2M:178 OLR1:223.5 MRC1:225
pituitary.gland	0.03268489	234	8.785e-02	3.002e-01	CADPS:5 CHD5:196.5 VEPH1:223 BICDL1:445 GPR149:493.5 PTPRN:537.5
cortex.kidney	-0.04213762	132	9.625e-02	3.057e-01	SLC22A8:8 SLC5A12:12 SLC13A1:196 SLC22A6:204 ATP6V1G3:220.5 SLC6A13:372
minor.salivary.gland	-0.04852368	91	1.108e-01	3.150e-01	PRR4:314 DEFB1:348 AZGP1:369 AMTN:560.5 ODAM:677.5 KRTCAP3:739.5
nucleus.accumbens	0.04606611	104	1.059e-01	3.150e-01	SP9:63 RGS8:73 PTPN5:246.5 DLX6:436.5 GPR149:493.5 GNAL:755
caudate.nucleus	0.08675147	27	1.190e-01	3.197e-01	ACBD7:473 AQP4:1416 PPP1R1B:1421 MAPK4:1597.5 NR2E1:2285.5 SYNDIG1L:2836.5
peyers.patch	0.03184389	199	1.243e-01	3.197e-01	BAIAP2L2:18 GBA3:88 CACNA1F:312 TMEM253:513.5 BTNL3:635.5 FAM3D:675.5
sophagus.muscularis.mucosa	0.07836411	28	1.516e-01	3.559e-01	PGM5:285.5 KCNMB1:1182 RGMB:1752 COL4A6:2717.5 FAM83D:2946.5 CHRM3:3917.5
thyroid	-0.03160359	177	1.497e-01	3.559e-01	RNF144B:78 ITGB3:338.5 SMAD9:730.5 WDR72:800 LRP2:805 SLC26A4:810.5
endocervix	-0.04592367	79	1.594e-01	3.587e-01	PRSS12:414.5 NRG1:571 DIO3:634 GABRE:682.5 CYP27C1:926 SMPDL3A:952.5
coronary.artery	-0.08760232	15	2.403e-01	4.955e-01	COL4A1:2277 SOST:2847 SPINK13:3295 PCOLCE2:3976 MTHFD1L:4738 CCL19:5084
fallopian.tube	0.04202576	60	2.612e-01	4.955e-01	PRSS33:1409 DTHD1:1500 CRISPLD2:1929 LDLRAD1:1961.5 TUBA4B:1993 GAS2L2:2034
skeletal.muscle	0.02189719	258	2.306e-01	4.955e-01	ASB10:76 SYPL2:237 MYOM3:381 PHKA1:434.5 PDLIM3:449 SIX4:551
transformed.skin.fibroblast	-0.01965935	276	2.661e-01	4.955e-01	TPBG:67 DCBLD2:117 NAV3:119 SLC38A2:260.5 RCN1:277.5 FGF5:283.5
transverse.colon	0.02495748	170	2.647e-01	4.955e-01	GBA3:88 RXFP4:147 CEACAM7:333 BTNL3:635.5 FAM3D:675.5 MTMR11:710
Brodmann.area.24	0.05407446	33	2.829e-01	5.092e-01	DRD5:1483.5 FAM107A:1912 KCNS1:2118 DDN:2453 SHANK1:2706 CNTN5:3087
hypothalamus	0.03392891	78	3.016e-01	5.254e-01	ST8SIA2:302.5 DLX2:467.5 NGB:496 RTP1:1490 SMIM17:1628 AVP:1908
tibial.nerve	0.01994517	205		5.547e-01	ADAMTS14:23 PLEKHA7:84 LGI2:121.5 ABCA8:144 COL28A1:285.5 ITGA6:371
ectocervix	0.04627580	27		6.443e-01	SOCS2:1291 CPXM1:1756.5 ADRA1D:1985.5 PTHLH:3536.5 HOXD13:3564 ADRA2A:3693.
putamen	0.05740491	18		6.443e-01	GBX2:482 GNG7:1532 OPALIN:2514 SYNDIG1L:2836.5 GRM3:3174 HPCA:3927
bladder	-0.04245295	30		6.502e-01	VGLL1:182.5 PSCA:1097 SLC14A1:1320 ACSM6:1538 MSX2:1818 TPSD1:2383.5
atrium.auricle	0.01976622	96		7.368e-01	TNNT2:69 ASB10:76 MYOM3:381 CSRP3:1012 LRRC10:1021 PAM:1344.5
leg.skin	-0.01177097	288		7.368e-01	TMEM45A:15 IL37:66 TYR:89 CERS3:101 IL36G:109 IL1RL2:132
suprapubic.skin	-0.01094986	259		7.589e-01	SPTSSB:40.5 IL37:66 TYR:89 CERS3:101 IL36G:109 IL1RL2:132
tibial.artery	0.01681386	114		7.589e-01	MYL9:349 SMIM10:452 CLIC4:454 SPEG:627.5 ID2:1195 CRTAC1:1224
esophagogastric.junction	-0.05368098	9		7.683e-01	NKX6-1:501.5 GADL1:3084 HOXA4:4997.5 RTL3:5287 BARX1:6030 ADCY5:6166.5