Geneset	stat	num.genes	pval	p.adj	gene.vals
Fatty Acid Metabolic Process (GO:0006631	-0.15520610	120	-	2.438e-05	ACOT8:21 THEM4:38 LPIN1:237 LPIN2:293 ACOX1:299 LCP1:303
Sensory Perception Of Smell (GO:0007608)	0.11152049	208		8.649e-05	OR5M3:30 OR5D3P:65 OR8K1:67 OR5M9:104 OR4E2:167 OR13G1:177
Monocarboxylic Acid Metabolic Process (G	-0.14863473	96		8.957e-04	THEM4:38 LDHAL6A:41 SCP2:298 LCP1:303 GNPAT:343 LDHAL6B:414
Brain Development (GO:0007420)	0.11366582	157		1.105e-03	ZIC1:29 NDRG4:93 EML1:128 ROBO2:191 DLX2:222 FLNB:399
Peptide Biosynthetic Process (GO:0043043	0.11468798	153		1.105e-03	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220
Cytoplasmic Translation (GO:0002181)	0.13832859	91		3.525e-03	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293
mRNA Processing (GO:0006397)	0.09269046	205		3.525e-03	HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281
Macromolecule Biosynthetic Process (GO:0	0.09893446	179	5.215e-06	3.525e-03	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220
Triglyceride Metabolic Process (GO:00066	-0.19738527	43	7.579e-06	4.553e-03	APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765
Detection Of Chemical Stimulus Involved	0.11313734	129		4.615e-03	OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325
Regulation Of DNA-templated Transcriptio	0.03197685	1857			SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49
Detection Of Chemical Stimulus Involved	0.11290357	127		5.165e-03	OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325
Regulation Of Transcription By RNA Polym	0.03045675	1948		6.394e-03	BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29
Gene Expression (GO:0010467)	0.07410100	286		6.694e-03	RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125
Negative Regulation Of Nucleic Acid-Temp	0.05870779	444	2.474e-05	8.917e-03	TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202
RNA Splicing, Via Transesterification Re	0.09307730	171	2.783e-05		HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421
Steroid Biosynthetic Process (GO:0006694	-0.16957024	49		1.288e-02	ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717
Cellular Lipid Catabolic Process (GO:004	-0.24426022	23		1.308e-02	ACOT8:21 LPIN1:237 LPIN2:293 ACOX1:299 PLBD1:450 PLD1:806
Fatty Acid Catabolic Process (GO:0009062	-0.15035330	60	5.681e-05	1.308e-02	ACOT8:21 ECHDC1:48 NUDT8:169 LPIN1:237 LPIN2:293 SCP2:298
Lipid Biosynthetic Process (GO:0008610)	-0.14287000	68	4.677e-05	1.308e-02	SCP2:298 LCP1:303 CYP19A1:379 MVD:545 PRKAA1:625 AGPS:653
Monocarboxylic Acid Transport (GO:001571	-0.13989905	71	4.639e-05	1.308e-02	SLC5A12:11 SLC5A6:67 SLC6A13:267 SLC16A4:346 ABCC2:485 SLC10A3:5
Neuron Projection Morphogenesis (GO:0048	0.09858502	140	5.806e-05	1.308e-02	SRGAP3:15 SGK1:92 EPHA4:101 MAP1B:116 TAOK3:154 DVL1:209
Nitrogen Compound Transport (GO:0071705)	-0.09215461	161	5.642e-05	1.308e-02	SLC13A1:102 SLC22A4:123 SLC6A13:267 SLC38A2:328 CERT1:345 CD320:3
protein–RNA Complex Assembly (GO:0022618	0.09883791	141	5.230e-05	1.308e-02	AGO1:23 TARBP2:35 LUC7L2:108 RPS19:166 CPSF6:215 AGO2:220
Embryonic Limb Morphogenesis (GO:0030326	0.19705506	34	7.027e-05	1.520e-02	INTU:190 ZNF358:327 ECE1:628 TFAP2A:663 TBX2:690 CREBBP:809
Wnt Signaling Pathway (GO:0016055)	0.13316257	74	7.571e-05	1.574e-02	FZD8:87 CCDC88C:159 FZD3:194 TCF7L1:206 DVL1:209 WNT2B:319
Cell Morphogenesis Involved In Neuron Di	0.13069157	76	8.284e-05	1.578e-02	MAP1B:116 DVL1:209 NEFH:335 CELSR2:395 POU4F1:539 PAK3:558
Diol Biosynthetic Process (GO:0034312)	-0.28457400	16	8.121e-05	1.578e-02	SPHK2:101 SPTSSB:165 ACER1:431 SPTLC1:644 SPHK1:844 DHFR:932
Vitamin Transport (GO:0051180)	-0.18433388	38	8.464e-05	1.578e-02	SLC5A6:67 SLC25A32:95 CD320:351 ABCD4:534 TCN2:711 SLC2A8:821
Negative Regulation Of DNA-templated Tra	0.03655828	995	1.175e-04	2.118e-02	BMP6:7 OTUD7B:14 CBX1:19 ING2:41 TIMELESS:45 CALR:49
mRNA Splicing, Via Spliceosome (GO:00003	0.07830307	201	1.345e-04	2.346e-02	HNRNPH3:64 RBMX:164 SCNM1:179 LSM5:244 DHX15:281 SNRPA1:353
Modulation Of Chemical Synaptic Transmis	0.10041889	118		2.753e-02	CAMK2A:100 GRIK3:181 DYSF:236 SLC6A9:240 GRIA1:398 PXK:436
Translation (GO:0006412)	0.07265671	228	1.636e-04	2.753e-02	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220
Central Nervous System Development (GO:0	0.06683361	268		2.769e-02	ZIC1:29 LSR:88 NDRG4:93 EML1:128 SOX10:169 ROBO2:191
acyl-CoA Metabolic Process (GO:0006637)	-0.20315573	28		3.077e-02	ACOT8:21 MCEE:308 ACACB:663 ACSM6:715 OGDH:753 SUCLG2:937
RNA Splicing (GO:0008380)	0.11026884	95		3.108e-02	HNRNPH3:64 RRAGC:123 SCNM1:179 DHX15:281 SNRPA1:353 SNRPN:42
Acylglycerol Catabolic Process (GO:00464	-0.21780545	24		3.115e-02	APOC3:30 ABHD6:105 MGLL:122 PNPLA4:162 LCP1:303 DAGLB:840
Sphingoid Biosynthetic Process (GO:00465	-0.30706201	12		3.115e-02	SPHK2:101 SPTSSB:165 ACER1:431 SPTLC1:644 SPHK1:844 ASAH2:138
Sphingosine Biosynthetic Process (GO:004	-0.30706201	12		3.115e-02	SPHK2:101 SPTSSB:165 ACER1:431 SPTLC1:644 SPHK1:844 ASAH2:138

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

SCP2:298 ARV1:305 CYP19A1:379 CYP39A1:420 PRLR:717 RDH16:723

RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293

AGO1:23 RRAGC:123 RHEB:133 TNRC6B:151 AGO2:220 CBX8:230

Steroid Metabolic Process (GO:0008202) -0.11217652

KEGG_RIBOSOME

REACTOME_PTEN_REGULATION

Periodontal Diseases

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_DEVELOPMENTAL_BIOLOGY	0.08333348	1143		2.097e-17	RPS17:1 ABL2:9 SRGAP3:15 H3C13:18 H3C1:21 SPRR2B:34
REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.13866902	390		2.097e-17	OR52B2:27 OR5M3:30 OR52W1:53 OR8K1:67 OR56A1:79 OR5M9:104
HOUNKPE_HOUSEKEEPING_GENES	0.08182332	1100		1.831e-16	CBX1:19 PDZD11:36 PURB:37 ACTR2:47 CALR:49 YWHAQ:50
KEGG_OLFACTORY_TRANSDUCTION	0.13309674	380		9.781e-16	CAMK2B:16 OR52B2:27 OR5M3:30 OR52W1:53 OR8K1:67 OR56A1:79
REACTOME_SENSORY_PERCEPTION	0.10576950	605		1.055e-15	OR52B2:27 OR5M3:30 OR52W1:53 OR8K1:67 SNAP25:69 MYH9:72
CARRILLOREIXACH_HEPATOBLASTOMA_VS_NORMAL	-0.06988116	1046	3.035e-14	3.285e-11	APOC3:30 SLC6A16:57 TRIM35:58 TMEM45A:63 ETNPPL:66 TM6SF2:76
REACTOME_SIGNALING_BY_WNT	0.11779584	322	3.988e-13	3.700e-10	H3C13:18 H3C1:21 AGO1:23 FZD8:87 CAMK2A:100 H2BC4:109
REACTOME_INFECTIOUS_DISEASE	0.06947740	933	8.237e-13	6.686e-10	RPS17:1 H3C13:18 CBX1:19 H3C1:21 ACTR2:47 CALR:49
REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	0.08596542	570	2.645e-12	1.908e-09	RPS17:1 ABL2:9 SRGAP3:15 ACTR2:47 MAP2K2:51 RPS16:71
HSIAO_LIVER_SPECIFIC_GENES	-0.13006714	240	4.120e-12	2.676e-09	APOC3:30 ALDH1A1:233 NR1H4:276 LPIN2:293 ATP13A3:315 SOD1:383
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	0.07135570	788	1.168e-11	6.894e-09	RPS17:1 CAMK2B:16 H3C13:18 H3C1:21 AGO1:23 CALR:49
KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DEN	0.07481974	655	7.485e-11	4.051e-08	RPS17:1 CAMK2B:16 VDAC3:38 YWHAQ:50 HINT1:85 NDRG4:93
REACTOME_ACTIVATION_OF_ANTERIOR_HOX_GENE	0.16775011	116	4.427e-10	2.211e-07	H3C13:18 H3C1:21 H2BC4:109 H2AC19:238 ASH2L:305 H3-3B:402
REACTOME_REGULATION_OF_EXPRESSION_OF_SLI	0.13888108	169	4.831e-10	2.241e-07	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 ROBO2:191
REACTOME_SIGNALING_BY_ROBO_RECEPTORS	0.12246277	214	6.895e-10	2.985e-07	RPS17:1 ABL2:9 SRGAP3:15 RPS16:71 RPL37A:153 RPS19:166
REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SI	0.14200888	145	3.647e-09	1.352e-06	AGO1:23 FZD8:87 CAMK2A:100 PDE6G:141 TNRC6B:151 FZD3:194
REACTOME_METABOLISM_OF_LIPIDS	-0.06465417	726	3.402e-09	1.352e-06	ACOT8:21 MTMR6:23 CERS6:34 THEM4:38 ETNPPL:66 SCAP:96
MARTENS_TRETINOIN_RESPONSE_DN	0.06334807	751	3.955e-09	1.352e-06	CLIP1:6 H3C13:18 PURB:37 CALR:49 ARL6IP4:58 HNRNPH3:64
HSIAO_HOUSEKEEPING_GENES	0.08808260	381	3.816e-09	1.352e-06	RPS17:1 YWHAQ:50 RPS16:71 MYH9:72 HINT1:85 RPL37A:153
HOSHIDA_LIVER_CANCER_SUBCLASS_S3	-0.10599247	260	4.175e-09	1.356e-06	PNPLA4:162 ALDH1A1:233 LPIN1:237 LPIN2:293 ACOX1:299 SPARCL1:304
REACTOME_RHO_GTPASES_ACTIVATE_PKNS	0.17919402	89	5.177e-09	1.601e-06	H3C13:18 H3C1:21 YWHAQ:50 MYH9:72 H2BC4:109 H2AC19:238
REACTOME_METABOLISM_OF_RNA	0.06513104	691	6.059e-09	1.789e-06	RPS17:1 RPS16:71 RBM25:76 RAE1:105 TSEN54:110 ALYREF:125
REACTOME_ESR_MEDIATED_SIGNALING	0.11520139	214	6.525e-09	1.842e-06	H3C13:18 H3C1:21 AGO1:23 H2BC4:109 PIK3R1:118 TNRC6B:151
REACTOME_LEISHMANIA_INFECTION	0.13295812	158	8.232e-09	2.227e-06	ACTR2:47 MYH9:72 DVL1:209 GNB2:223 ARPC4:252 HSP90AB1:324
CAIRO_HEPATOBLASTOMA_DN	-0.10312635	262	9.478e-09	2.462e-06	ETNPPL:66 EPHA2:77 MGLL:122 ADM:186 LEPR:274 LPIN2:293
CAIRO_LIVER_DEVELOPMENT_DN	-0.11284772	217	1.044e-08	2.512e-06	CTSH:28 A2M:201 CAMP:234 TAPBP:251 LPIN2:293 LCP1:303
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	0.10905657	233	1.011e-08	2.512e-06	H3C13:18 H3C1:21 AGO1:23 SETD1B:61 H2BC4:109 TNRC6B:151
KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER	0.06232169	729	1.137e-08	2.637e-06	RPS17:1 CAMK2B:16 VDAC3:38 YWHAQ:50 OLFM1:56 RPS16:71
REACTOME_RHO_GTPASE_EFFECTORS	0.09384776	312	1.256e-08	2.812e-06	CLIP1:6 CIT:12 H3C13:18 H3C1:21 ACTR2:47 YWHAQ:50
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATI	-0.12360419	173	2.090e-08	4.525e-06	ETNPPL:66 MYRIP:194 SCP2:298 DHRS1:363 AMDHD1:627 RDH16:723
REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESS	0.13312341	145	3.196e-08	6.696e-06	H3C13:18 H3C1:21 AGO1:23 H2BC4:109 TNRC6B:151 AGO2:220
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRA	-0.23551324	44	6.485e-08	1.316e-05	DBT:129 ACAD8:203 HIBCH:223 DLD:257 MCEE:308 ACADSB:578
REACTOME_GLYOXYLATE_METABOLISM_AND_GLYCI	-0.28381080	30	7.438e-08	1.464e-05	DBT:129 DLD:257 LIAS:453 PDHA2:744 OGDH:753 GLDC:887
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_P	0.14751993	111	8.001e-08	1.528e-05	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293
REACTOME_OXIDATIVE_STRESS_INDUCED_SENESC	0.14287201	117	9.516e-08	1.766e-05	H3C13:18 H3C1:21 AGO1:23 H2BC4:109 TNRC6B:151 CBX8:230
REACTOME_METABOLISM_OF_STEROIDS	-0.12497443	152	1.069e-07	1.928e-05	ACOT8:21 SCAP:96 OSBP:111 STARD6:132 NR1H4:276 SCP2:298
WP_CYTOPLASMIC_RIBOSOMAL_PROTEINS	0.16483550	86	1.275e-07	2.238e-05	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293
NABA_MATRISOME	-0.04866817	1002	2.160e-07	3.609e-05	MFAP5:4 ADAM28:9 CTSH:28 IL37:88 TLL1:90 C1QTNF9:112

DisGeNET Top pathways by non-permulation

2.168e-07 3.609e-05

2.355e-07 3.824e-05

0.16272001

0.12797471

Geneset	stat	num.genes	pval	p.adj	gene.vals
Steatohepatitis	-0.08390862	512	1.062e-10	1.043e-06	APOC3:30 CERS6:34 TM6SF2:76 SLC22A8:98 GCLC:197 LPIN1:237
Fatty Liver	-0.08047223	401	3.731e-08	1.222e-04	APOC3:30 CERS6:34 TM6SF2:76 SLC22A8:98 LPIN1:237 LEPR:274
Obesity	-0.04042955	1799	2.803e-08	1.222e-04	PPM1K:3 MFAP5:4 ADAM28:9 KRIT1:27 APOC3:30 CERS6:34
Cardiovascular Diseases	-0.05610847	724	3.481e-07	6.942e-04	APOC3:30 TM6SF2:76 PDE3A:93 C1QTNF9:112 DCLK1:117 MEPE:177
Endometriosis	-0.05721276	694	3.534e-07	6.942e-04	NAA16:73 ITGAV:86 IL37:88 IAPP:161 GATA6:188 CD226:204
Hypertensive disease	-0.04344008	1212	5.404e-07	8.845e-04	MFAP5:4 GCM1:5 SDHC:26 APOC3:30 SMAD6:44 TMEM38A:56
Metabolic Syndrome X	-0.06367815	512	9.542e-07	1.339e-03	ADAM28:9 APOC3:30 TM6SF2:76 ABHD6:105 OSBP:111 ADM:186
Lethargy	-0.13789490	104	1.213e-06	1.489e-03	DBT:129 DLD:257 SLC25A20:349 ABCD4:534 ACADSB:578 DPYD:635
Drug-Induced Liver Disease	-0.08955487	246	1.411e-06	1.540e-03	ECHDC1:48 SLC22A8:98 GCLC:197 NR1H4:276 CRYZ:291 LGALS3:333
Vomiting	-0.10353350	175	2.415e-06	2.372e-03	PPOX:43 DBT:129 CPOX:235 DLD:257 SLC17A5:380 ETFA:425
Atherosclerosis	-0.04183829	1033	7.245e-06	5.882e-03	APOC3:30 TM6SF2:76 EPHA2:77 ITGAV:86 IL37:88 SCAP:96
Hyperlipidemia	-0.08999932	210	7.311e-06	5.882e-03	APOC3:30 CDCP1:173 ADM:186 LEPR:274 NR1H4:276 OLR1:292
Metabolic Diseases	-0.06610409	392	7.786e-06	5.882e-03	OCA2:25 APOC3:30 CERS6:34 PPOX:43 IL37:88 SCAP:96
Non-alcoholic Fatty Liver Disease	-0.07370420	311	8.462e-06	5.936e-03	APOC3:30 TM6SF2:76 LAMA1:142 JUND:189 GCLC:197 LEPR:274
Coronary Artery Disease	-0.04393429	898	1.011e-05	6.619e-03	MFAP5:4 BCAS3:20 APOC3:30 SIM2:75 TM6SF2:76 TLL1:90
Cerebral Hemorrhage	-0.15605216	64	1.598e-05	9.229e-03	SDHC:26 KRIT1:27 ITGAV:86 BAX:427 COL4A2:558 ITGA2B:671
Hypertriglyceridemia	-0.10542466	141	1.597e-05	9.229e-03	APOC3:30 TM6SF2:76 LPIN1:237 NR1H4:276 IL16:695 LEP:754
Hypercholesterolemia, Familial	-0.10310308	145	1.880e-05	9.303e-03	OCA2:25 APOC3:30 OLR1:292 SACS:381 COMP:503 SGCG:603
Coronary Arteriosclerosis	-0.04766163	706	1.895e-05	9.303e-03	APOC3:30 PRKY:149 GCLC:197 APLNR:228 LEPR:274 NR1H4:276
Nonalcoholic Steatohepatitis	-0.09005633	192	1.760e-05	9.303e-03	TM6SF2:76 LAMA1:142 LEPR:274 NR1H4:276 OLR1:292 LGALS3:333
Hepatitis, Toxic	-0.08597837	198	3.160e-05	1.241e-02	ECHDC1:48 SLC22A8:98 GCLC:197 NR1H4:276 LGALS3:333 SOD1:383
Chemical and Drug Induced Liver Injury	-0.08597837	198	3.160e-05	1.241e-02	ECHDC1:48 SLC22A8:98 GCLC:197 NR1H4:276 LGALS3:333 SOD1:383
Chemically-Induced Liver Toxicity	-0.08597837	198	3.160e-05	1.241e-02	ECHDC1:48 SLC22A8:98 GCLC:197 NR1H4:276 LGALS3:333 SOD1:383
Drug-Induced Acute Liver Injury	-0.08597837	198	3.160e-05	1.241e-02	ECHDC1:48 SLC22A8:98 GCLC:197 NR1H4:276 LGALS3:333 SOD1:383
Liver Cirrhosis	-0.04919206	625	3.103e-05	1.241e-02	CAVIN2:55 TM6SF2:76 SLC22A8:98 DCLK1:117 HES6:147 JUND:189
Arteriosclerosis	-0.03890266	988	4.377e-05	1.653e-02	APOC3:30 DCBLD2:47 TM6SF2:76 EPHA2:77 ITGAV:86 IL37:88
Pre-Eclampsia	-0.09786004	145	4.883e-05	1.776e-02	GCM1:5 TPBG:140 ADM:186 APLNR:228 LEPR:274 OLR1:292
Hepatitis, Drug-Induced	-0.08270928	202	5.275e-05	1.850e-02	ECHDC1:48 SLC22A8:98 GCLC:197 NR1H4:276 LGALS3:333 SOD1:383
Asthma	-0.03509834	1184	6.168e-05	2.089e-02	CRB1:40 DENND1B:45 ALLC:59 IL37:88 SCGB1A1:121 IGSF1:133
Mitochondrial Diseases	-0.06116417	363	6.746e-05	2.209e-02	SDHC:26 CERS6:34 PNPLA4:162 ASIP:170 HIBCH:223 CPOX:235
Myocardial Infarction	-0.03922563	899	8.023e-05	2.542e-02	BCAS3:20 APOC3:30 ILF3:33 TM6SF2:76 PDE3A:93 SCAP:96
Arthritis	-0.04824320	575	8.647e-05	2.654e-02	KRIT1:27 IL37:88 SLC22A4:123 NIF3L1:125 MEPE:177 JUND:189
Liver diseases	-0.04897363	555	8.925e-05	2.656e-02	APOC3:30 TM6SF2:76 DCLK1:117 ALDH1A1:233 LEPR:274 NR1H4:276
Diabetes Mellitus, Non-Insulin-Dependent	-0.03064260	1479	1.111e-04	3.210e-02	ADAM28:9 OCA2:25 CTSH:28 APOC3:30 CERS6:34 THEM4:38
Adrenal Gland Neoplasms	-0.12343027	81	1.245e-04	3.493e-02	CYP2W1:16 GATA6:188 CDKN1C:357 IGF2:411 BAX:427 ATM:572
Adverse reaction to drug	-0.12340933	80	1.374e-04	3.635e-02	B2M:347 SOD1:383 ABCC2:485 TCN2:711 NFE2L2:731 BCHE:779
Drug toxicity	-0.12340933	80	1.374e-04	3.635e-02	B2M:347 SOD1:383 ABCC2:485 TCN2:711 NFE2L2:731 BCHE:779
Functional Gastrointestinal Disorders	-0.23449355	22	1.407e-04	3.635e-02	GAST:178 NR1H4:276 ABCC2:485 BDNF:552 KEAP1:702 NFE2L2:731
Moderate mental retardation (I.Q. 35-49)	0.14539768	57	1.477e-04	3.719e-02	ZIC1:29 RBMX:164 KCNJ10:285 CC2D2A:584 TCF20:607 SHANK3:632

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

-0.09645611 128 1.678e-04 4.119e-02 CAMP:234 MMP13:325 BDNF:552 DEFB1:585 SETD2:601 IL16:695

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003699 abnormal female reproductive	-0.06936187	428	1.785e-06	8.498e-04	OCA2:25 OOEP:53 ANTXR1:91 PDE3A:93 SLC13A1:102 ADCYAP1:107
MP0002118 abnormal lipid homeostasis	-0.06576348	408	9.422e-06	2.242e-03	OCA2:25 APOC3:30 GPR12:92 SCAP:96 ADCYAP1:107 MGLL:122
MP0003959 abnormal lean body	-0.15943366	58	2.866e-05	4.547e-03	LPIN1:237 LEPR:274 SCP2:298 CYP19A1:379 GRB10:432 ANKRD26:554
MP0000609 abnormal liver physiology	-0.05917794	380	1.145e-04	8.783e-03	OCA2:25 GPR12:92 SCAP:96 ADCYAP1:107 CHKA:154 JUND:189
MP0005636 abnormal mineral homeostasis	-0.09506644	141	1.132e-04	8.783e-03	SLC13A1:102 SCGB1A1:121 GAST:178 HK1:309 B2M:347 PTH1R:409
MP0002161 abnormal fertility/fecundity	-0.04081455	868	1.292e-04	8.783e-03	OCA2:25 OOEP:53 POLL:82 ANTXR1:91 PDE3A:93 SLC13A1:102
MP0003635 abnormal synaptic transmissio	0.05621872	429	1.064e-04	8.783e-03	CAMK2B:16 KCNH3:32 VDAC3:38 SNAP25:69 CAMK2A:100 EPHA4:101
MP0009763 increased sensitivity to	-0.06584897	247	4.574e-04	1.979e-02	ADM:186 CD226:204 PARP2:271 LEPR:274 NR1H4:276 LGALS3:333
MP0002063 abnormal learning/memory/cond	0.05533216	359	4.433e-04	1.979e-02	ABL2:9 KCNH3:32 VDAC3:38 SNAP25:69 CAMK2A:100 FXR2:106
MP0002152 abnormal brain morphology	0.03587867	974	4.244e-04	1.979e-02	ABL2:9 CIT:12 ZIC1:29 KIF5C:40 CALR:49 SNAP25:69
MP0008469 abnormal protein level	-0.05312746	406	3.560e-04	1.979e-02	ITGAV:86 MAGED1:191 LEPR:274 NR1H4:276 FGF23:289 OLR1:292
MP0003861 abnormal nervous system	0.03996483	723	5.145e-04	2.041e-02	ZIC1:29 CALR:49 TXN2:86 EPHA4:101 SOCS7:132 PTK7:143
MP0002882 abnormal neuron morphology	0.03531619	888	8.282e-04	3.033e-02	CADPS:5 ABL2:9 KIF5C:40 GNAT1:75 CAMK2A:100 EPHA4:101
MP0009642 abnormal blood homeostasis	-0.03012353	1293	1.004e-03	3.186e-02	PPM1K:3 OCA2:25 APOC3:30 ILF3:33 SMAD6:44 MN1:54
MP0003698 abnormal male reproductive	-0.04367113	522	9.993e-04	3.186e-02	OCA2:25 POLL:82 OAZ3:131 PDGFRB:151 ADCY10:187 JUND:189
MP0005334 abnormal fat pad	-0.07725332	152	1.138e-03	3.187e-02	OCA2:25 GPR12:92 LPIN1:237 LGR4:249 LEPR:274 CYP19A1:379
MP0002128 abnormal blood circulation	-0.04835993	410	1.095e-03	3.187e-02	SMAD6:44 ITGAV:86 TLL1:90 E2F7:145 PDGFRB:151 ADM:186
MP0005376 homeostasis/metabolism phenot	-0.06819959	191	1.334e-03	3.529e-02	CRB1:40 PDGFRB:151 APLNR:228 LPIN1:237 LEPR:274 ADK:307
MP0000249 abnormal blood vessel	-0.06575603	202	1.482e-03	3.637e-02	APOC3:30 GJB6:36 SMAD6:44 ADM:186 JUND:189 LEPR:274
MP0002752 abnormal somatic nervous	0.04003977	583	1.528e-03	3.637e-02	KIF5C:40 GNAT1:75 CAMK2A:100 EPHA4:101 PDE6G:141 PTK7:143
MP0001486 abnormal startle reflex	0.08995919	96	2.472e-03	5.604e-02	ABL2:9 DVL1:209 KCNJ10:285 ATP2B2:596 GLRA1:893 MYO7A:1096
MP0000015 abnormal ear pigmentation	-0.20475079	18	2.664e-03	5.763e-02	OCA2:25 BLOC1S3:608 SLC24A5:981 AP3B1:1362 MC1R:2018 GNA11:2247
MP0000778 abnormal nervous system	0.07785644	121	3.344e-03	6.921e-02	EPHA4:101 FZD3:194 ST8SIA2:303 EFNB1:626 TUBB3:636 EBF1:680
MP0010329 abnormal lipoprotein level	-0.08907074	90	3.693e-03	7.325e-02	OCA2:25 APOC3:30 GPR12:92 LPIN1:237 LEPR:274 SCP2:298
MP0002419 abnormal innate immunity	-0.04468799	361	4.449e-03	7.786e-02	ITGAV:86 MEPE:177 MYO9B:265 LCP1:303 LGALS3:333 TGFB2:364
MP0001119 abnormal female reproductive	-0.04858394	295	4.907e-03	7.786e-02	ANTXR1:91 LGR4:249 LEPR:274 ZFX:283 ACOX1:299 FIGLA:300
MP0005085 abnormal gallbladder physiolo	-0.14996702	30	4.547e-03	7.786e-02	NR1H4:276 SCP2:298 ABCC2:485 CHRM2:648 CYP8B1:842 ACADL:1701
MP0003121 genomic imprinting	-0.15333664	29	4.334e-03	7.786e-02	CDKN1C:357 GRB10:432 DIO3:448 PEG10:482 MAGEL2:560 PHLDA2:1576
MP0003122 maternal imprinting	-0.20351471	16	4.867e-03	7.786e-02	IGF2:411 DIO3:448 PEG10:482 MAGEL2:560 DLK1:1799 SGCE:2499
MP0005535 abnormal body temperature	-0.07392940	124	4.806e-03	7.786e-02	ADCYAP1:107 MGLL:122 LEPR:274 NR1H4:276 ADK:307 KL:442
MP0005584 abnormal enzyme/coenzyme acti	-0.06867975	142	5.133e-03	7.882e-02	SLC13A1:102 DBT:129 LPIN1:237 LEPR:274 CCS:508 M6PR:967
MP0002111 abnormal tail morphology	-0.06030437	177	6.245e-03	9.289e-02	DST:62 EPHA2:77 SLC13A1:102 GJB2:377 BRCA1:451 VANGL1:574
MP0000428 abnormal craniofacial morphol	0.08739231	79	7.552e-03		TBX15:235 PKDCC:248 HAND1:458 SP8:472 CREBBP:809 G3BP1:976
MP0000534 abnormal ureter morphology	0.10728018	51	8.252e-03		ROBO2:191 LAMC1:517 ID2:924 ACE:955 SLIT2:1044 GATA2:1124
MP0001881 abnormal mammary gland	-0.09468609	64	9.088e-03		LEPR:274 PRLR:717 DGAT1:765 GHRHR:861 CHEK1:908 OXTR:912
MP0000627 abnormal mammary gland	-0.06559459	131	1.017e-02		BECN1:287 TBX3:344 BRCA1:451 SDC1:489 NRG1:512 BCL2L11:522
MP0004883 abnormal blood vessel	-0.11333121	43	1.034e-02		LEPR:274 PRMT2:795 SPP1:1490 ZEB1:1493 SERPIND1:1556 ESR1:1587
MP0009643 abnormal urine homeostasis	-0.04894096	232	1.147e-02		SLC22A8:98 SLC13A1:102 SCGB1A1:121 DBT:129 LEPR:274 GIPC1:312
MP0008875 abnormal xenobiotic pharmacok	-0.16317113	20		1.344e-01	
MP0001542 abnormal bone strength	-0.14130276	27	1.118e-02		FGF23:289 KLF10:376 COL1A1:1140 ALPL:1586 ESR1:1587 COL1A2:2907
000 10 12 abriorina bono otrongth	0.1.100210				. 5. 25.250 REL 10.070 COLIMITION ALL EL 1000 EUR 1.1007 COLIME.2007

tissue_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
cerebellum	0.10135726	408	4.776e-12	2.579e-10	LINC00514:10 SRGAP3:15 ZIC1:29 RALGPS1:44 NDRG4:93 MGAT3:95
testis	-0.05201174	1685	4.467e-11	1.206e-09	GCM1:5 CDCA2:39 LDHAL6A:41 OOEP:53 SLC6A16:57 ALLC:59
cerebellar.hemisphere	0.08114931	543	2.477e-10	4.459e-09	CADPS:5 LINC00514:10 CAMK2B:16 ZIC1:29 KIF5C:40 PPFIA3:43
liver	-0.06195256	399	2.909e-05	3.928e-04	AGMAT:10 APOC3:30 TM6SF2:76 GRB14:211 NR1H4:276 SLC22A25:317
subcutaneous.adipose	-0.11220056	82	4.624e-04	4.994e-03	ACVR1C:61 CSN1S1:337 TNMD:399 ACACB:663 PRG2:673 GHR:706
cerebral.cortex	0.09330727	111	7.197e-04	6.478e-03	CIT:12 KCNH3:32 OPRL1:229 KIF5A:317 RS1:572 SEMA5B:802
aorta	0.06441014	156	5.782e-03	4.461e-02	HMCN1:46 LOXL1:57 MYH9:72 LTBP4:262 PXDC1:263 PID1:552
eye.development	0.09393956	69	7.113e-03	4.802e-02	MAF:137 DLX2:222 NRL:247 WNT2B:319 VSX2:1080 PAX2:1241
left.ventricle	0.09250999	69	8.037e-03	4.822e-02	TNNT2:172 ASB10:184 SLC25A4:214 MYH7B:448 MYOM3:940 CSRP3:1395
Brodmann.area.9	0.05328140	187	1.260e-02	6.807e-02	OLFM1:56 CAMK2A:100 NEFM:378 RAB6B:509 RS1:572 HECW1:869
adrenal.gland	-0.06476611	116	1.644e-02	8.070e-02	CYP2W1:16 AKR1B1:318 QPRT:330 TBX3:344 SOAT1:456 TM7SF2:641
breast	-0.14457550	20	2.529e-02	1.138e-01	LEP:754 FABP4:899 HCAR1:1003 THRSP:1309 TNN:1942 GLYAT:2053
nucleus.accumbens	0.06069212	104	3.315e-02	1.377e-01	SP9:26 RGS8:60 POU3F4:256 NCDN:266 GNAL:290 PTPN5:306
minor.salivary.gland	-0.05548034	91	6.830e-02	2.459e-01	ODAM:294 OXGR1:538 DEFB1:585 AMTN:660 MMP27:862 AZGP1:904
pituitary.gland	0.03523471	234	6.576e-02	2.459e-01	CADPS:5 VEPH1:63 CHD5:149 PLD3:270 GPR149:331 FEV:357
sigmoid.colon	0.07000638	53	7.847e-02	2.648e-01	ACTG2:107 TACR2:197 HAND1:458 MAB21L2:519 HAND2:897 HOXD13:1342
caudate.nucleus	0.09399082	27	9.123e-02	2.737e-01	ACBD7:654 PPP1R1B:1231 NR2E1:1259 AQP4:1327 MAPK4:1757 PDE1B:1802
cortex.kidney	-0.04341786	132	8.655e-02	2.737e-01	SLC5A12:11 SLC22A8:98 SLC13A1:102 ATP6V1G3:128 SLC6A13:267 PTH1R:409
lung	-0.03674599	161	1.098e-01	3.121e-01	ADGRF5:19 SMAD6:44 SCGB1A1:121 A2M:201 OLR1:292 MRC1:370
spleen	0.02255894	367	1.435e-01	3.874e-01	SH2D1A:77 PDE6G:141 OR2I1P:196 CD163L1:207 GBA3:213 ITK:298
bladder	-0.06789683	30	1.985e-01	3.880e-01	VGLL1:519 PSCA:580 ACSM6:715 TPSD1:1445 SLC14A1:2091 DHRS2:2226
Brodmann.area.24	0.06487593	33	1.976e-01	3.880e-01	FAM107A:1020 KCNS1:1134 SHANK1:1453 DRD5:2171 NPTXR:3549 CNTN5:3999
endocervix	-0.04411267	79	1.765e-01	3.880e-01	PRSS12:116 CYP27C1:410 DIO3:448 ZNF516:498 NRG1:512 SMPDL3A:825
fallopian.tube	0.04794007	60	2.000e-01	3.880e-01	HOXC4:1193 FOSB:1365 HOXA2:1372 SOCS3:2006 CRISPLD2:2151 RARRES1:2349
leg.skin	-0.02269539	288	1.901e-01	3.880e-01	TMEM45A:63 IL37:88 IL1RL2:89 CASP14:106 CERS3:108 MPIG6B:130
skeletal.muscle	0.02453767	258	1.791e-01	3.880e-01	ASB10:184 SYPL2:195 TBX15:235 PDLIM3:301 PHKA1:420 SIX4:498
thyroid	-0.02804191	177	2.012e-01	3.880e-01	RNF144B:70 SMAD9:397 FREM2:438 SHISA2:495 ITGB3:705 IVD:761
tibial.nerve	0.02664222	205	1.920e-01	3.880e-01	ADAMTS14:80 PLEKHA7:98 ABCA8:142 LGI2:174 GRIK3:181 ITGA6:422
suprapubic.skin	-0.02129417	259	2.428e-01	4.521e-01	TNFRSF19:18 IL37:88 IL1RL2:89 CASP14:106 CERS3:108 LIPN:135
coronary.artery	-0.07441061	15	3.186e-01	4.918e-01	PCOLCE2:1538 SOST:3146 COL4A1:3312 SPINK13:4251 MTHFD1L:4356 MYO18B:4689
ectocervix	0.05539615	27	3.195e-01	4.918e-01	SOCS2:512 HOXD13:1342 ADRA1D:2384 CPXM1:2667 LRFN5:4052 ADRA2A:4318
esophagus.muscularis.mucosa	0.05894109	28	2.808e-01	4.918e-01	PGM5:261 KCNMB1:598 RGMB:1076 RGS2:3055 FAM83D:3258 CHRM3:3682
hypothalamus	0.03414467	78	2.985e-01	4.918e-01	NGB:140 DLX2:222 ST8SIA2:303 RTP1:1429 SMIM17:1627 SOX1:2263
peyers.patch	0.02127030	199	3.046e-01	4.918e-01	BAIAP2L2:28 GBA3:213 CACNA1F:437 PLB1:511 FAM3D:717 TMEM253:846

GBX2:272 HPCA:1899 GNG7:2354 GRM3:3200 OPALIN:3291 SYNDIG1L:3404

GBA3:213 RXFP4:296 FAM3D:717 SLC39A5:1168 BTNL3:1194 MTMR11:1235

NAV3:15 DCBLD2:47 TPBG:140 FGF5:184 ADM:186 ZNF281:262

FRMD7:135 PTK7:143 HOXD3:923 GATA2:1124 HOXD10:1152 TSPAN2:1366

MYL9:343 CLIC4:688 SPEG:772 ID2:924 OR51E1:1004 CRTAC1:1137 ADAM28:9 FUT1:447 PSCA:580 EPN3:594 SMIM24:813 KRTCAP3:980

18 3.279e-01 4.918e-01

3.752e-01 5.332e-01

3.666e-01 5.332e-01

3.856e-01 5.339e-01

4.397e-01 5.936e-01

0.06665165

-0.02588666

0.02821303

tibial.artery 0.02770818 114 3.089e-01 4.918e-01

276

putamen

stomach

uterus

transverse.colon 0.02020131

transformed.skin.fibroblast -0.01533983