





| A2ML1   | 0.05289031 | 134 | 5.439e-01 | 9.991e-01 | 9.999e-01 |
|---------|------------|-----|-----------|-----------|-----------|
| A3GALT2 | 0.01353791 | 132 | 8.776e-01 | 9.991e-01 | 9.999e-01 |
| A4GNT   | 0.05474929 | 151 | 5.043e-01 | 9.991e-01 | 9.999e-01 |
| AACS    | 0.01910427 | 156 | 8.129e-01 | 9.991e-01 | 9.999e-01 |
| AADACL2 | 0.01904043 | 120 | 8.365e-01 | 9.991e-01 | 9.999e-01 |
| AADACL3 | 0.02488497 | 158 | 7.563e-01 | 9.991e-01 | 9.999e-01 |
| AAK1    | 0.14011365 | 145 | 9.278e-02 | 9.991e-01 | 9.999e-01 |
| AAMDC   | 0.13809382 | 88  | 1.995e-01 | 9.991e-01 | 9.999e-01 |
| AAMP    | 0.24245174 | 95  | 1.792e-02 | 9.991e-01 | 9.999e-01 |
| AAR2    | 0.18822206 | 133 | 3.004e-02 | 9.991e-01 | 9.999e-01 |
|         |            |     |           |           |           |
|         |            |     |           |           |           |
|         |            |     |           |           |           |

Gene Rho N P p.adj qValueNoperm

| Gene    | Rho          | N   | P         | p.adj     | qValueNoperm |
|---------|--------------|-----|-----------|-----------|--------------|
| A1BG    | -0.111644190 | 123 | 2.189e-01 | 9.991e-01 | 9.999e-01    |
| A1CF    | -0.024569127 | 128 | 7.831e-01 | 9.991e-01 | 9.999e-01    |
| A2M     | -0.160699562 | 169 | 3.687e-02 | 9.991e-01 | 9.999e-01    |
| A4GALT  | -0.065096551 | 154 | 4.225e-01 | 9.991e-01 | 9.999e-01    |
| AAAS    | -0.007388264 | 132 | 9.330e-01 | 9.991e-01 | 9.999e-01    |
| AADAC   | -0.065142431 | 107 | 5.050e-01 | 9.991e-01 | 9.999e-01    |
| AADACL4 | -0.023590944 | 141 | 7.813e-01 | 9.991e-01 | 9.999e-01    |
| AADAT   | -0.058886959 | 152 | 4.711e-01 | 9.991e-01 | 9.999e-01    |
| AAGAB   | -0.010550651 | 136 | 9.030e-01 | 9.991e-01 | 9.999e-01    |
| AANAT   | -0.106992984 | 138 | 2.117e-01 | 9.991e-01 | 9.999e-01    |
|         |              |     |           |           |              |

| Fatty Acid Metabolic Process (GO:0006631 Sensory Perception Of Smell (GO:0007608) Monocarboxylic Acid Metabolic Process (G -0.148 Brain Development (GO:0007420) Peptide Biosynthetic Process (GO:0043043 Cytoplasmic Translation (GO:0002181) mRNA Processing (GO:0006397) Macromolecule Biosynthetic Process (GO:0 Triglyceride Metabolic Process (GO:0 Triglyceride Metabolic Process (GO:00066 Triglyceride Metabolic Process (GO:00066 Detection Of Chemical Stimulus Involved Regulation Of DNA-templated Transcriptio Detection Of Chemical Stimulus Involved Regulation Of Transcription By RNA Polym Gene Expression (GO:0010467) Negative Regulation Of Nucleic Acid—Temp RNA Splicing, Via Transesterification Re Steroid Biosynthetic Process (GO:0006694 Cellular Lipid Catabolic Process (GO:0006694 Cellular Lipid Catabolic Process (GO:0009062 Lipid Biosynthetic Process (GO:0008610) Monocarboxylic Acid Transport (GO:001571 Neuron Projection Morphogenesis (GO:0048 Nitrogen Compound Transport (GO:0071705) Protein—RNA Complex Assembly (GO:0022618 Nitrogen Compound Transport (GO:0030326 Unt Signaling Pathway (GO:0016055) Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) Vitamin Transport (GO:0051180) -0.184 | 049<br>473<br>582<br>798<br>859<br>046<br>446<br>4527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330 | num.genes  120 208 96 157 153 91 205 179 43 129 1857 127 1948 286 444 171 49 23 60                               | 3.199e-08<br>4.970e-07<br>9.296e-07<br>1.022e-06<br>5.208e-06<br>5.215e-06<br>7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>4.051e-05              | p.adj 2.438e-05 8.649e-05 8.957e-04 1.105e-03 1.105e-03 3.525e-03 3.525e-03 4.553e-03 4.615e-03 5.165e-03 6.394e-03 8.917e-03 9.404e-03 1.288e-02 1.308e-02                        | Gene.vals  ACOT8:21 THEM4:38 LPIN1:237 LPIN2:293 ACOX1:299 LCP1:303  OR5M3:30 OR5D3P:65 OR8K1:67 OR5M9:104 OR4E2:167 OR13G1:177  THEM4:38 LDHAL6A:41 SCP2:298 LCP1:303 GNPAT:343 LDHAL6B:414  ZIC1:29 NDRG4:93 EML1:128 ROBO2:191 DLX2:222 FLNB:399  RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220  RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293  HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281  RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220  APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765  OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325  SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49  OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325  BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29  RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125  TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202  HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421  ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  ACOT8:21 LPIN1:237 LPIN2:293 ACOX1:299 PLBD1:450 PLD1:806 |
|--|--|--|---|--|---|
| Sensory Perception Of Smell (GO:0007608)  Monocarboxylic Acid Metabolic Process (G -0.148) Brain Development (GO:0007420)  Peptide Biosynthetic Process (GO:0043043 0.1146 Cytoplasmic Translation (GO:0002181) 0.1383 mRNA Processing (GO:0006397) 0.0926 Macromolecule Biosynthetic Process (GO:0 0.0986 Triglyceride Metabolic Process (GO:0 0.0986 Detection Of Chemical Stimulus Involved 0.1133 Regulation Of DNA-templated Transcriptio 0.0315 Detection Of Chemical Stimulus Involved 0.1125 Regulation Of Transcription By RNA Polym 0.0304 Gene Expression (GO:0010467) 0.0743 Negative Regulation Of Nucleic Acid—Temp 0.0583 RNA Splicing, Via Transesterification Re 0.0936 Steroid Biosynthetic Process (GO:0006694 -0.1696 Cellular Lipid Catabolic Process (GO:000962 -0.1506) Lipid Biosynthetic Process (GO:0008610) -0.1426 Monocarboxylic Acid Transport (GO:001571 -0.1396 Neuron Projection Morphogenesis (GO:0048 0.0986 Nitrogen Compound Transport (GO:0071705) -0.092 protein—RNA Complex Assembly (GO:0022618 0.0986 Embryonic Limb Morphogenesis (GO:0030326 0.1976 Wnt Signaling Pathway (GO:0016055) 0.1336 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.2846                                     | 049<br>473<br>582<br>798<br>859<br>046<br>446<br>4527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330 | 208<br>96<br>157<br>153<br>91<br>205<br>179<br>43<br>129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49<br>23 | 3.199e-08<br>4.970e-07<br>9.296e-07<br>1.022e-06<br>5.208e-06<br>5.215e-06<br>7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>4.051e-05              | 8.649e-05<br>8.957e-04<br>1.105e-03<br>1.105e-03<br>3.525e-03<br>3.525e-03<br>4.553e-03<br>4.615e-03<br>4.615e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02 | OR5M3:30 OR5D3P:65 OR8K1:67 OR5M9:104 OR4E2:167 OR13G1:177 THEM4:38 LDHAL6A:41 SCP2:298 LCP1:303 GNPAT:343 LDHAL6B:414 ZIC1:29 NDRG4:93 EML1:128 ROBO2:191 DLX2:222 FLNB:399 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293 HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| Monocarboxylic Acid Metabolic Process (G —0.148/ Brain Development (GO:0007420) 0.1136/ Peptide Biosynthetic Process (GO:0043043 0.1146/ Cytoplasmic Translation (GO:0002181) 0.1383/ mRNA Processing (GO:0006397) 0.0926/ Macromolecule Biosynthetic Process (GO:0 0.0986/ Triglyceride Metabolic Process (GO:00066 —0.1976/ Detection Of Chemical Stimulus Involved 0.1136/ Regulation Of DNA-templated Transcriptio 0.0316/ Detection Of Chemical Stimulus Involved 0.1126/ Regulation Of Transcription By RNA Polym 0.0306/ Gene Expression (GO:0010467) 0.0747/ Negative Regulation Of Nucleic Acid—Temp 0.0587/ RNA Splicing, Via Transesterification Re 0.0936/ Cellular Lipid Catabolic Process (GO:0006694 —0.1696/ Cellular Lipid Catabolic Process (GO:0009062 —0.1506/ Lipid Biosynthetic Process (GO:0008610) —0.1426/ Monocarboxylic Acid Transport (GO:001571 —0.1396/ Neuron Projection Morphogenesis (GO:0048 0.0986/ Nitrogen Compound Transport (GO:0071705) —0.092/ protein—RNA Complex Assembly (GO:0022618 0.0986/ Embryonic Limb Morphogenesis (GO:0030326 0.1976/ Wnt Signaling Pathway (GO:0016055) 0.1336/ Cell Morphogenesis Involved In Neuron Di 0.1306/ Diol Biosynthetic Process (GO:0034312) —0.2846/  | 4473<br>582<br>798<br>859<br>046<br>446<br>6527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>6022<br>6330               | 96<br>157<br>153<br>91<br>205<br>179<br>43<br>129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49<br>23        | 4.970e-07<br>9.296e-07<br>1.022e-06<br>5.208e-06<br>5.028e-06<br>5.215e-06<br>7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05 | 8.957e-04<br>1.105e-03<br>1.105e-03<br>3.525e-03<br>3.525e-03<br>4.553e-03<br>4.615e-03<br>4.615e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02                           | THEM4:38 LDHAL6A:41 SCP2:298 LCP1:303 GNPAT:343 LDHAL6B:414 ZIC1:29 NDRG4:93 EML1:128 ROBO2:191 DLX2:222 FLNB:399 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293 HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717   |
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| Peptide Biosynthetic Process (GO:0043043  Cytoplasmic Translation (GO:0002181)  mRNA Processing (GO:0006397)  Macromolecule Biosynthetic Process (GO:0 0.0988  Triglyceride Metabolic Process (GO:00066 -0.1978  Detection Of Chemical Stimulus Involved 0.1137  Regulation Of DNA-templated Transcriptio 0.0318  Regulation Of Chemical Stimulus Involved 0.1128  Regulation Of Transcription By RNA Polym 0.0304  Gene Expression (GO:0010467) 0.0747  Negative Regulation Of Nucleic Acid-Temp 0.0587  RNA Splicing, Via Transesterification Re 0.0930  Steroid Biosynthetic Process (GO:0006694 -0.1698  Cellular Lipid Catabolic Process (GO:0009062 -0.1508  Lipid Biosynthetic Process (GO:0008610) -0.1428  Monocarboxylic Acid Transport (GO:001571 -0.1398  Neuron Projection Morphogenesis (GO:0048 0.0988  Nitrogen Compound Transport (GO:0071705) -0.092  protein-RNA Complex Assembly (GO:0022618 0.0988  Embryonic Limb Morphogenesis (GO:0030326 0.1970  Wnt Signaling Pathway (GO:0016055) 0.1336  Cell Morphogenesis Involved In Neuron Di 0.1308  Diol Biosynthetic Process (GO:0034312) -0.2848   | 798<br>859<br>046<br>446<br>3527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330                      | 153<br>91<br>205<br>179<br>43<br>129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49<br>23                     | 1.022e-06<br>5.208e-06<br>5.028e-06<br>5.215e-06<br>7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05                           | 1.105e-03<br>3.525e-03<br>3.525e-03<br>4.553e-03<br>4.615e-03<br>5.165e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02  | RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293 HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717   |
| Cytoplasmic Translation (GO:0002181)  mRNA Processing (GO:0006397)  Macromolecule Biosynthetic Process (GO:0 0.0988  Triglyceride Metabolic Process (GO:00066 -0.1978  Detection Of Chemical Stimulus Involved 0.1138  Regulation Of DNA-templated Transcriptio 0.0318  Detection Of Chemical Stimulus Involved 0.1128  Regulation Of Transcription By RNA Polym 0.0304  Gene Expression (GO:0010467) 0.0747  Negative Regulation Of Nucleic Acid-Temp 0.0587  RNA Splicing, Via Transesterification Re 0.0930  Steroid Biosynthetic Process (GO:0006694 -0.1698  Cellular Lipid Catabolic Process (GO:000962 -0.1508  Lipid Biosynthetic Process (GO:0008610) -0.1428  Monocarboxylic Acid Transport (GO:001571 -0.1398  Neuron Projection Morphogenesis (GO:00048 0.0988  Nitrogen Compound Transport (GO:0071705) -0.092  protein-RNA Complex Assembly (GO:0022618 0.0988  Embryonic Limb Morphogenesis (GO:0030326 0.1970  Wnt Signaling Pathway (GO:0016055) 0.1336  Cell Morphogenesis Involved In Neuron Di 0.1308  Diol Biosynthetic Process (GO:0034312) -0.2848  | 859<br>046<br>446<br>4527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>024<br>6022<br>6330                              | 91<br>205<br>179<br>43<br>129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49                                  | 5.208e-06<br>5.028e-06<br>5.215e-06<br>7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05  | 3.525e-03<br>3.525e-03<br>4.553e-03<br>4.615e-03<br>5.165e-03<br>6.394e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02  | RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL9:293 HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| mRNA Processing (GO:0006397)  Macromolecule Biosynthetic Process (GO:0 0.0986  Triglyceride Metabolic Process (GO:00066 -0.1976  Detection Of Chemical Stimulus Involved 0.1137  Regulation Of DNA-templated Transcriptio 0.0318  Detection Of Chemical Stimulus Involved 0.1129  Regulation Of Transcription By RNA Polym 0.0304  Gene Expression (GO:0010467) 0.0747  Negative Regulation Of Nucleic Acid-Temp 0.0587  RNA Splicing, Via Transesterification Re 0.0936  Steroid Biosynthetic Process (GO:0006694 -0.1696  Cellular Lipid Catabolic Process (GO:0004 -0.2446  Fatty Acid Catabolic Process (GO:0009062 -0.1506  Lipid Biosynthetic Process (GO:0008610) -0.1426  Monocarboxylic Acid Transport (GO:001571 -0.1396  Neuron Projection Morphogenesis (GO:0048 0.0986  Nitrogen Compound Transport (GO:0071705) -0.092  protein-RNA Complex Assembly (GO:0022618 0.0986  Embryonic Limb Morphogenesis (GO:0030326 0.1976  Wnt Signaling Pathway (GO:0016055) 0.1336  Cell Morphogenesis Involved In Neuron Di 0.1306  Diol Biosynthetic Process (GO:0034312) -0.2846   | 046<br>446<br>5527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>6024<br>6022<br>6330                                    | 205<br>179<br>43<br>129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49  | 5.028e-06<br>5.215e-06<br>7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05   | 3.525e-03<br>3.525e-03<br>4.553e-03<br>4.615e-03<br>5.165e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02   | HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281 RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717   |
| Macromolecule Biosynthetic Process (GO:0 0.0988 Triglyceride Metabolic Process (GO:00066 -0.1978 Detection Of Chemical Stimulus Involved 0.11378 Regulation Of DNA-templated Transcriptio 0.03189 Detection Of Chemical Stimulus Involved 0.11298 Regulation Of Transcription By RNA Polym 0.03049 Gene Expression (GO:0010467) 0.07479 Negative Regulation Of Nucleic Acid-Temp 0.05878 RNA Splicing, Via Transesterification Re 0.09309 Steroid Biosynthetic Process (GO:0006694 -0.16999 Cellular Lipid Catabolic Process (GO:0009062 -0.150999 Lipid Biosynthetic Process (GO:0008610) -0.14299 Monocarboxylic Acid Transport (GO:001571 -0.13999 Neuron Projection Morphogenesis (GO:00048 0.09889 Nitrogen Compound Transport (GO:0071705) -0.0929 protein-RNA Complex Assembly (GO:0022618 0.09889 Embryonic Limb Morphogenesis (GO:0030326 0.19709 Wnt Signaling Pathway (GO:0016055) 0.13369 Cell Morphogenesis Involved In Neuron Di 0.13069 Diol Biosynthetic Process (GO:0034312) -0.2848  | 446<br>3527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330   | 179<br>43<br>129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49   | 5.215e-06<br>7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05  | 3.525e-03<br>4.553e-03<br>4.615e-03<br>5.165e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02  | RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220 APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717   |
| Triglyceride Metabolic Process (GO:00066 —0.1976 Detection Of Chemical Stimulus Involved 0.1137 Regulation Of DNA-templated Transcriptio 0.0319 Detection Of Chemical Stimulus Involved 0.1129 Regulation Of Transcription By RNA Polym 0.0304 Gene Expression (GO:0010467) 0.0747 Negative Regulation Of Nucleic Acid-Temp 0.0587 RNA Splicing, Via Transesterification Re 0.0930 Steroid Biosynthetic Process (GO:0006694 —0.1690 Cellular Lipid Catabolic Process (GO:000962 —0.1500 Lipid Biosynthetic Process (GO:0008610) —0.1420 Monocarboxylic Acid Transport (GO:001571 —0.1390 Neuron Projection Morphogenesis (GO:0048 0.0980 Nitrogen Compound Transport (GO:0071705) —0.092 protein-RNA Complex Assembly (GO:0022618 0.0980 Embryonic Limb Morphogenesis (GO:0030326 0.1970 Wnt Signaling Pathway (GO:0016055) 0.13360 Cell Morphogenesis Involved In Neuron Di 0.13060 Diol Biosynthetic Process (GO:0034312) —0.2840  | 3527<br>734<br>685<br>357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330  | 43<br>129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49  | 7.579e-06<br>9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05   | 4.553e-03<br>4.615e-03<br>4.615e-03<br>5.165e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02  | APOC3:30 PNPLA4:162 LPIN1:237 LPIN2:293 LCP1:303 DGAT1:765  OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325  SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49  OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325  BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29  RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125  TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202  HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421  ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| Detection Of Chemical Stimulus Involved Regulation Of DNA-templated Transcriptio Detection Of Chemical Stimulus Involved Regulation Of Transcription By RNA Polym Gene Expression (GO:0010467) Negative Regulation Of Nucleic Acid-Temp RNA Splicing, Via Transesterification Re Steroid Biosynthetic Process (GO:0006694 Cellular Lipid Catabolic Process (GO:0004 Fatty Acid Catabolic Process (GO:0009062 Lipid Biosynthetic Process (GO:0008610) Monocarboxylic Acid Transport (GO:001571 Neuron Projection Morphogenesis (GO:0048 Nitrogen Compound Transport (GO:0071705) Protein-RNA Complex Assembly (GO:0022618 Embryonic Limb Morphogenesis (GO:0030326 Wnt Signaling Pathway (GO:0016055) Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) -0.284  | 734<br>685<br>357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330  | 129<br>1857<br>127<br>1948<br>286<br>444<br>171<br>49  | 9.388e-06<br>8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05  | 4.615e-03<br>4.615e-03<br>5.165e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02   | OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49 OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325 BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717   |
| Regulation Of DNA-templated Transcriptio  Detection Of Chemical Stimulus Involved  Regulation Of Transcription By RNA Polym  Gene Expression (GO:0010467)  Negative Regulation Of Nucleic Acid-Temp  RNA Splicing, Via Transesterification Re  Steroid Biosynthetic Process (GO:0006694  Cellular Lipid Catabolic Process (GO:0004  Fatty Acid Catabolic Process (GO:0009062  Lipid Biosynthetic Process (GO:0008610)  Monocarboxylic Acid Transport (GO:001571  Neuron Projection Morphogenesis (GO:0048  Nitrogen Compound Transport (GO:0071705)  protein-RNA Complex Assembly (GO:0022618  Embryonic Limb Morphogenesis (GO:0030326  Wnt Signaling Pathway (GO:0016055)  Cell Morphogenesis Involved In Neuron Di  Diol Biosynthetic Process (GO:0034312)  -0.284  | 685<br>357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330   | 1857<br>127<br>1948<br>286<br>444<br>171<br>49   | 8.656e-06<br>1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05   | 4.615e-03<br>5.165e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02  | SP9:26 ZIC1:29 PURB:37 ING2:41 TIMELESS:45 CALR:49  OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325  BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29  RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125  TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202  HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421  ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| Detection Of Chemical Stimulus Involved Regulation Of Transcription By RNA Polym Gene Expression (GO:0010467) Negative Regulation Of Nucleic Acid-Temp 0.0587 RNA Splicing, Via Transesterification Re Steroid Biosynthetic Process (GO:0006694 Cellular Lipid Catabolic Process (GO:0004 Fatty Acid Catabolic Process (GO:0009062 Lipid Biosynthetic Process (GO:0008610) Monocarboxylic Acid Transport (GO:001571 -0.1397 Neuron Projection Morphogenesis (GO:0048 Nitrogen Compound Transport (GO:0071705) protein-RNA Complex Assembly (GO:0022618 Embryonic Limb Morphogenesis (GO:0030326 Wnt Signaling Pathway (GO:0016055) Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) -0.284  | 357<br>675<br>100<br>779<br>730<br>7024<br>6022<br>6330  | 127<br>1948<br>286<br>444<br>171<br>49<br>23   | 1.146e-05<br>1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05  | 5.165e-03<br>6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02   | OR4E2:167 OR13G1:177 OR2I1P:196 OR2T35:264 OR6K3:288 OR2S2:325  BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29  RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125  TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202  HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421  ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| Regulation Of Transcription By RNA Polym Gene Expression (GO:0010467)  Negative Regulation Of Nucleic Acid-Temp RNA Splicing, Via Transesterification Re Steroid Biosynthetic Process (GO:0006694 Cellular Lipid Catabolic Process (GO:0004 Fatty Acid Catabolic Process (GO:0009062 Lipid Biosynthetic Process (GO:0008610) Monocarboxylic Acid Transport (GO:001571 Neuron Projection Morphogenesis (GO:0048 Nitrogen Compound Transport (GO:0071705) Protein-RNA Complex Assembly (GO:0022618 Embryonic Limb Morphogenesis (GO:0030326 Wnt Signaling Pathway (GO:0016055) Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) -0.284  | 675<br>100<br>779<br>730<br>7024<br>6022<br>6330   | 1948<br>286<br>444<br>171<br>49<br>23  | 1.537e-05<br>1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05   | 6.394e-03<br>6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02  | BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29 RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| Gene Expression (GO:0010467)  Negative Regulation Of Nucleic Acid-Temp  RNA Splicing, Via Transesterification Re  Steroid Biosynthetic Process (GO:0006694  Cellular Lipid Catabolic Process (GO:0004  Fatty Acid Catabolic Process (GO:0009062  Lipid Biosynthetic Process (GO:0008610)  Monocarboxylic Acid Transport (GO:001571  Neuron Projection Morphogenesis (GO:0048  Nitrogen Compound Transport (GO:0071705)  protein-RNA Complex Assembly (GO:0022618  Embryonic Limb Morphogenesis (GO:0030326  Wnt Signaling Pathway (GO:0016055)  Cell Morphogenesis Involved In Neuron Di  Diol Biosynthetic Process (GO:0034312)  -0.284   | 100<br>779<br>730<br>7024<br>6022<br>6330  | 286<br>444<br>171<br>49<br>23  | 1.733e-05<br>2.474e-05<br>2.783e-05<br>4.051e-05  | 6.694e-03<br>8.917e-03<br>9.404e-03<br>1.288e-02   | RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125 TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| Negative Regulation Of Nucleic Acid-Temp  RNA Splicing, Via Transesterification Re  Steroid Biosynthetic Process (GO:0006694  Cellular Lipid Catabolic Process (GO:0004  Fatty Acid Catabolic Process (GO:0009062  Lipid Biosynthetic Process (GO:0008610)  Monocarboxylic Acid Transport (GO:001571  Neuron Projection Morphogenesis (GO:0048  Nitrogen Compound Transport (GO:0071705)  protein-RNA Complex Assembly (GO:0022618  Embryonic Limb Morphogenesis (GO:0030326  Wnt Signaling Pathway (GO:0016055)  Cell Morphogenesis Involved In Neuron Di  Diol Biosynthetic Process (GO:0034312)  -0.284   | 779<br>730<br>7024<br>6022<br>6330   | 444<br>171<br>49<br>23   | 2.474e-05<br>2.783e-05<br>4.051e-05   | 8.917e-03<br>9.404e-03<br>1.288e-02  | TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202 HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717  |
| RNA Splicing, Via Transesterification Re Steroid Biosynthetic Process (GO:0006694 -0.169) Cellular Lipid Catabolic Process (GO:0004 -0.244) Fatty Acid Catabolic Process (GO:0009062 -0.150) Lipid Biosynthetic Process (GO:0008610) -0.142 Monocarboxylic Acid Transport (GO:001571 -0.139) Neuron Projection Morphogenesis (GO:0048 0.098) Nitrogen Compound Transport (GO:0071705) -0.092 protein-RNA Complex Assembly (GO:0022618 0.098) Embryonic Limb Morphogenesis (GO:0030326 0.1970) What Signaling Pathway (GO:0016055) 0.1333 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.284   | 730<br>7024<br>6022<br>6330  | 171<br>49<br>23  | 2.783e-05<br>4.051e-05  | 9.404e-03<br>1.288e-02   | HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421 ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717   |
| Steroid Biosynthetic Process (GO:0006694 -0.169) Cellular Lipid Catabolic Process (GO:0004 -0.244) Fatty Acid Catabolic Process (GO:0009062 -0.150) Lipid Biosynthetic Process (GO:0008610) -0.142 Monocarboxylic Acid Transport (GO:001571 -0.139) Neuron Projection Morphogenesis (GO:0048 0.0988) Nitrogen Compound Transport (GO:0071705) -0.092 protein–RNA Complex Assembly (GO:0022618 0.0988) Embryonic Limb Morphogenesis (GO:0030326 0.1970) Wnt Signaling Pathway (GO:0016055) 0.1333 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.284   | 024<br>022<br>330  | 49<br>23   | 4.051e-05   | 1.288e-02  | ACOT8:21 OSBP:111 SCP2:298 CYP19A1:379 CYP39A1:420 PRLR:717   |
| Cellular Lipid Catabolic Process (GO:004 -0.244) Fatty Acid Catabolic Process (GO:0009062 -0.150) Lipid Biosynthetic Process (GO:0008610) -0.142 Monocarboxylic Acid Transport (GO:001571 -0.139) Neuron Projection Morphogenesis (GO:0048 0.098) Nitrogen Compound Transport (GO:0071705) -0.092 protein–RNA Complex Assembly (GO:0022618 0.098) Embryonic Limb Morphogenesis (GO:0030326 0.1970 Wnt Signaling Pathway (GO:0016055) 0.1336 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.2844   | 330<br>330   | 23   |   |  |   |
| Fatty Acid Catabolic Process (GO:0009062 -0.150) Lipid Biosynthetic Process (GO:0008610) -0.142 Monocarboxylic Acid Transport (GO:001571 -0.139) Neuron Projection Morphogenesis (GO:0048 0.0985) Nitrogen Compound Transport (GO:0071705) -0.092 protein–RNA Complex Assembly (GO:0022618 0.0985) Embryonic Limb Morphogenesis (GO:0030326 0.1970) Wnt Signaling Pathway (GO:0016055) 0.1336 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.2845   | 330  |  | 0.0240 00   | 1.0000 02  |   |
| Lipid Biosynthetic Process (GO:0008610) -0.142 Monocarboxylic Acid Transport (GO:001571 -0.139 Neuron Projection Morphogenesis (GO:0048 0.0988 Nitrogen Compound Transport (GO:0071705) -0.092 protein–RNA Complex Assembly (GO:0022618 0.0988 Embryonic Limb Morphogenesis (GO:0030326 0.1970 Wnt Signaling Pathway (GO:0016055) 0.1337 Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) -0.284  |  | 00   | 5 681e-05   | 1.308e-02  | ACOT8:21 ECHDC1:48 NUDT8:169 LPIN1:237 LPIN2:293 SCP2:298   |
| Monocarboxylic Acid Transport (GO:001571 -0.139) Neuron Projection Morphogenesis (GO:0048 0.098) Nitrogen Compound Transport (GO:0071705) -0.092 protein–RNA Complex Assembly (GO:0022618 0.098) Embryonic Limb Morphogenesis (GO:0030326 0.1970 Wnt Signaling Pathway (GO:0016055) 0.1337 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.284   |  | 68   |   | 1.308e-02  | SCP2:298 LCP1:303 CYP19A1:379 MVD:545 PRKAA1:625 AGPS:653   |
| Neuron Projection Morphogenesis (GO:0048 0.0985) Nitrogen Compound Transport (GO:0071705) -0.092 protein-RNA Complex Assembly (GO:0022618 0.0985) Embryonic Limb Morphogenesis (GO:0030326 0.1970) Wnt Signaling Pathway (GO:0016055) 0.1337 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.2845  |  | 71   |   | 1.308e-02  | SLC5A12:11 SLC5A6:67 SLC6A13:267 SLC16A4:346 ABCC2:485 SLC10A3:54   |
| Nitrogen Compound Transport (GO:0071705) -0.092 protein-RNA Complex Assembly (GO:0022618 0.0988 Embryonic Limb Morphogenesis (GO:0030326 0.1970 Wnt Signaling Pathway (GO:0016055) 0.1337 Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) -0.284   |  | 140  |   | 1.308e-02  | SRGAP3:15 SGK1:92 EPHA4:101 MAP1B:116 TAOK3:154 DVL1:209  |
| protein–RNA Complex Assembly (GO:0022618 0.0988 Embryonic Limb Morphogenesis (GO:0030326 0.1970 Wnt Signaling Pathway (GO:0016055) 0.1333 Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) -0.2848  |  | 161  |   |  | SLC13A1:102 SLC22A4:123 SLC6A13:267 SLC38A2:328 CERT1:345 CD320:3   |
| Embryonic Limb Morphogenesis (GO:0030326 0.1970 Wnt Signaling Pathway (GO:0016055) 0.1333 Cell Morphogenesis Involved In Neuron Di 0.1306 Diol Biosynthetic Process (GO:0034312) -0.2844   |  | 141  |   | 1.308e-02  | AGO1:23 TARBP2:35 LUC7L2:108 RPS19:166 CPSF6:215 AGO2:220   |
| Wnt Signaling Pathway (GO:0016055) 0.133° Cell Morphogenesis Involved In Neuron Di Diol Biosynthetic Process (GO:0034312) -0.284   |  | 34   |   | 1.520e-02  | INTU:190 ZNF358:327 ECE1:628 TFAP2A:663 TBX2:690 CREBBP:809   |
| Cell Morphogenesis Involved In Neuron Di  Diol Biosynthetic Process (GO:0034312)  0.1306  -0.284   |  | 74   |   | 1.574e-02  | FZD8:87 CCDC88C:159 FZD3:194 TCF7L1:206 DVL1:209 WNT2B:319  |
| Diol Biosynthetic Process (GO:0034312) -0.284  |  | 76   |   | 1.574e-02<br>1.578e-02   | MAP1B:116 DVL1:209 NEFH:335 CELSR2:395 POU4F1:539 PAK3:558  |
|  |  | 16   |   | 1.578e-02  | SPHK2:101 SPTSSB:165 ACER1:431 SPTLC1:644 SPHK1:844 DHFR:932  |
|  |  | 38   |   | 1.578e-02  | SLC5A6:67 SLC25A32:95 CD320:351 ABCD4:534 TCN2:711 SLC2A8:821   |
| Negative Regulation Of DNA-templated Tra 0.0365  |  | 995  |   | 2.118e-02  | BMP6:7 OTUD7B:14 CBX1:19 ING2:41 TIMELESS:45 CALR:49  |
| mRNA Splicing, Via Spliceosome (GO:00003 0.0783  |  | 201  |   | 2.116e-02<br>2.346e-02   | HNRNPH3:64 RBMX:164 SCNM1:179 LSM5:244 DHX15:281 SNRPA1:353   |
| Modulation Of Chemical Synaptic Transmis 0.1004  |  | 118  |   | 2.753e-02  | CAMK2A:100 GRIK3:181 DYSF:236 SLC6A9:240 GRIA1:398 PXK:436  |
|  |  |  |   |  |   |
|  |  | 228  |   | 2.753e-02  | RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220  |
| Central Nervous System Development (GO:0 0.0668  |  | 268  |   | 2.769e-02<br>3.077e-02   | ZIC1:29 LSR:88 NDRG4:93 EML1:128 SOX10:169 ROBO2:191  |
| acyl-CoA Metabolic Process (GO:0006637) -0.203   |  | 28   |   |  | ACOT8:21 MCEE:308 ACACB:663 ACSM6:715 OGDH:753 SUCLG2:937   |
| RNA Splicing (GO:0008380) 0.1102   |  | 95   |   | 3.108e-02  | HNRNPH3:64 RRAGC:123 SCNM1:179 DHX15:281 SNRPA1:353 SNRPN:421   |
| Acylglycerol Catabolic Process (GO:00464 –0.217  |  | 24   |   | 3.115e-02  | APOC3:30 ABHD6:105 MGLL:122 PNPLA4:162 LCP1:303 DAGLB:840   |
| Sphingoid Biosynthetic Process (GO:00465 –0.307) Sphingosine Biosynthetic Process (GO:004 –0.307)  |  | 12   | 2.305e-04   | 3.115e-02  | SPHK2:101 SPTSSB:165 ACER1:431 SPTLC1:644 SPHK1:844 ASAH2:1381  |

## 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

| Geneset                                  | stat        | num.genes | pval      | p.adj     | gene.vals  |
|--|-------------|-----------|-----------|-----------|--|
| REACTOME_DEVELOPMENTAL_BIOLOGY           | 0.08333348  | 1143      | 3.634e-21 | 2.097e-17 | RPS17:1 ABL2:9 SRGAP3:15 H3C13:18 H3C1:21 SPRR2B:34              |
| REACTOME_OLFACTORY_SIGNALING_PATHWAY     | 0.13866902  | 390       | 6.458e-21 | 2.097e-17 | OR52B2:27 OR5M3:30 OR52W1:53 OR8K1:67 OR56A1:79 OR5M9:104        |
| HOUNKPE_HOUSEKEEPING_GENES               | 0.08182332  | 1100      | 8.459e-20 | 1.831e-16 | CBX1:19 PDZD11:36 PURB:37 ACTR2:47 CALR:49 YWHAQ:50              |
| KEGG_OLFACTORY_TRANSDUCTION              | 0.13309674  | 380       | 6.025e-19 | 9.781e-16 | CAMK2B:16 OR52B2:27 OR5M3:30 OR52W1:53 OR8K1:67 OR56A1:79        |
| REACTOME_SENSORY_PERCEPTION              | 0.10576950  | 605       | 8.123e-19 | 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             |
| LIEGO DIDOCOME                           | 0.400=000:  | 0.5       |           | 0.000 6-  | DD0454 DD04654 DD1654 456 DD046 466 DD164 465 DD164              |

## DisGeNET Top pathways by non-permulation

2.168e-07 3.609e-05

2.355e-07 3.824e-05

0.16272001

0.12797471

KEGG\_RIBOSOME

REACTOME\_PTEN\_REGULATION

Geneset

putamen

stomach

uterus

transverse.colon 0.02020131

transformed.skin.fibroblast -0.01533983

0.06665165

-0.02588666

0.02821303

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

276

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

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

p.adj

gene.vals

num.genes pval

| Geneset                                 | Stat        | num.genes | Pvai      | p.auj     | gene.vais   |
|---|-------------|-----------|-----------|-----------|---|
| 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       |           | 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       |           | 3.186e-02 | OCA2:25 POLL:82 OAZ3:131 PDGFRB:151 ADCY10:187 JUND:189         |
| MP0005334 abnormal fat pad              | -0.07725332 | 152       |           | 3.187e-02 | OCA2:25 GPR12:92 LPIN1:237 LGR4:249 LEPR:274 CYP19A1:379        |
| MP0002128 abnormal blood circulation    | -0.04835993 | 410       |           | 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 |           | CRB1:40 PDGFRB:151 APLNR:228 LPIN1:237 LEPR:274 ADK:307         |
| MP0000249 abnormal blood vessel         | -0.06575603 | 202       | 1.482e-03 |           | APOC3:30 GJB6:36 SMAD6:44 ADM:186 JUND:189 LEPR:274             |
| MP0002752 abnormal somatic nervous      | 0.04003977  | 583       |           | 3.637e-02 | KIF5C:40 GNAT1:75 CAMK2A:100 EPHA4:101 PDE6G:141 PTK7:143       |
| MP0001486 abnormal startle reflex       | 0.08995919  | 96        |           | 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 |           | OCA2:25 BLOC1S3:608 SLC24A5:981 AP3B1:1362 MC1R:2018 GNA11:224  |
| MP0000778 abnormal nervous system       | 0.07785644  | 121       |           | 6.921e-02 | EPHA4:101 FZD3:194 ST8SIA2:303 EFNB1:626 TUBB3:636 EBF1:680     |
| MP0010329 abnormal lipoprotein level    | -0.08907074 | 90        |           | 7.325e-02 | OCA2:25 APOC3:30 GPR12:92 LPIN1:237 LEPR:274 SCP2:298           |
| MP0002419 abnormal innate immunity      | -0.04468799 | 361       |           | 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        |           | 7.786e-02 | NR1H4:276 SCP2:298 ABCC2:485 CHRM2:648 CYP8B1:842 ACADL:1701    |
| MP0003121 genomic imprinting            | -0.15333664 | 29        | 4.334e-03 |           | 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       |           | 7.882e-02 | SLC13A1:102 DBT:129 LPIN1:237 LEPR:274 CCS:508 M6PR:967         |
| MP0002111 abnormal tail morphology      | -0.06030437 | 177       |           | 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 | 1.089e-01 | TBX15:235 PKDCC:248 HAND1:458 SP8:472 CREBBP:809 G3BP1:976      |
| MP0000534 abnormal ureter morphology    | 0.10728018  | 51        |           | 1.155e-01 | ROBO2:191 LAMC1:517 ID2:924 ACE:955 SLIT2:1044 GATA2:1124       |
| MP0001881 abnormal mammary gland        | -0.09468609 | 64        |           | 1.236e-01 | 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 |
| 3.1                                     |             |           |           |           |   |

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

ADAM28:9 FUT1:447 PSCA:580 EPN3:594 SMIM24:813 KRTCAP3:980

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

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