

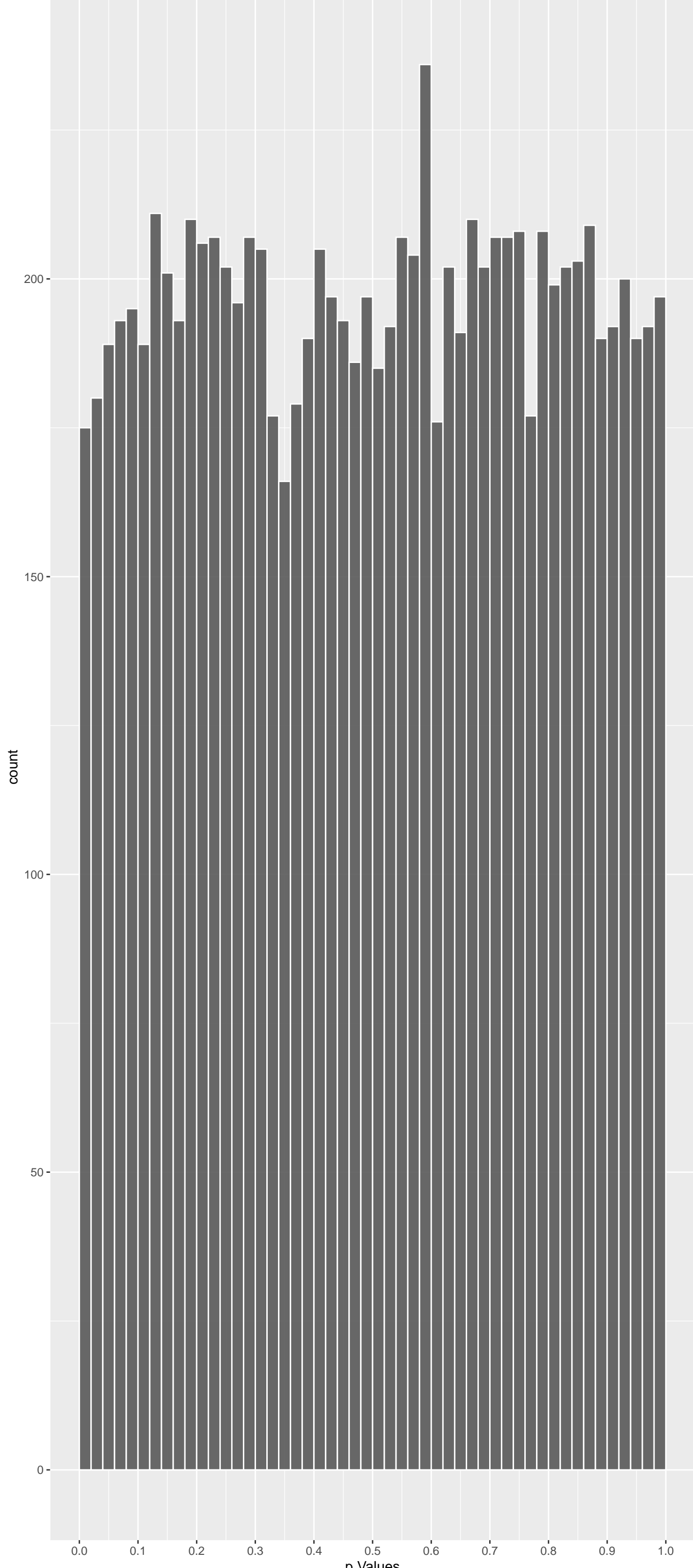
Top genes by P-value non-permuted

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
A2ML1	0.052890311	134	5.439e-01	9.991e-01	9.999e-01
A3GALT2	0.013537910	132	8.776e-01	9.991e-01	9.999e-01
A4GALT	-0.065096551	154	4.225e-01	9.991e-01	9.999e-01
A4GNT	0.054749291	151	5.043e-01	9.991e-01	9.999e-01
AAAS	-0.007388264	132	9.330e-01	9.991e-01	9.999e-01
AACS	0.019104271	156	8.129e-01	9.991e-01	9.999e-01
AADAC	-0.065142431	107	5.050e-01	9.991e-01	9.999e-01
AADACL2	0.019040428	120	8.365e-01	9.991e-01	9.999e-01
AADACL3	0.024884968	158	7.563e-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
AAK1	0.140113651	145	9.278e-02	9.991e-01	9.999e-01
AAMDC	0.138093817	88	1.995e-01	9.991e-01	9.999e-01
AAMP	0.242451740	95	1.792e-02	9.991e-01	9.999e-01
AANAT	-0.106992984	138	2.117e-01	9.991e-01	9.999e-01
AAR2	0.188222061	133	3.004e-02	9.991e-01	9.999e-01
AARD	-0.111535350	105	2.573e-01	9.991e-01	9.999e-01
AARS1	-0.068495717	145	4.130e-01	9.991e-01	9.999e-01
AARS2	-0.031408831	165	6.888e-01	9.991e-01	9.999e-01
AARSD1	0.007615327	145	9.276e-01	9.991e-01	9.999e-01
AASDH	0.090375908	165	2.483e-01	9.991e-01	9.999e-01

Top genes by Q-Value non-permuted

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
A2ML1	0.052890311	134	5.439e-01	9.991e-01	9.999e-01
A3GALT2	0.013537910	132	8.776e-01	9.991e-01	9.999e-01
A4GALT	-0.065096551	154	4.225e-01	9.991e-01	9.999e-01
A4GNT	0.054749291	151	5.043e-01	9.991e-01	9.999e-01
AAAS	-0.007388264	132	9.330e-01	9.991e-01	9.999e-01
AACS	0.019104271	156	8.129e-01	9.991e-01	9.999e-01
AADAC	-0.065142431	107	5.050e-01	9.991e-01	9.999e-01
AADACL2	0.019040428	120	8.365e-01	9.991e-01	9.999e-01
AADACL3	0.024884968	158	7.563e-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
AAK1	0.140113651	145	9.278e-02	9.991e-01	9.999e-01
AAMDC	0.138093817	88	1.995e-01	9.991e-01	9.999e-01
AAMP	0.242451740	95	1.792e-02	9.991e-01	9.999e-01
AANAT	-0.106992984	138	2.117e-01	9.991e-01	9.999e-01
AAR2	0.188222061	133	3.004e-02	9.991e-01	9.999e-01
AARD	-0.111535350	105	2.573e-01	9.991e-01	9.999e-01
AARS1	-0.068495717	145	4.130e-01	9.991e-01	9.999e-01
AARS2	-0.031408831	165	6.888e-01	9.991e-01	9.999e-01
AARSD1	0.007615327	145	9.276e-01	9.991e-01	9.999e-01
AASDH	0.090375908	165	2.483e-01	9.991e-01	9.999e-01

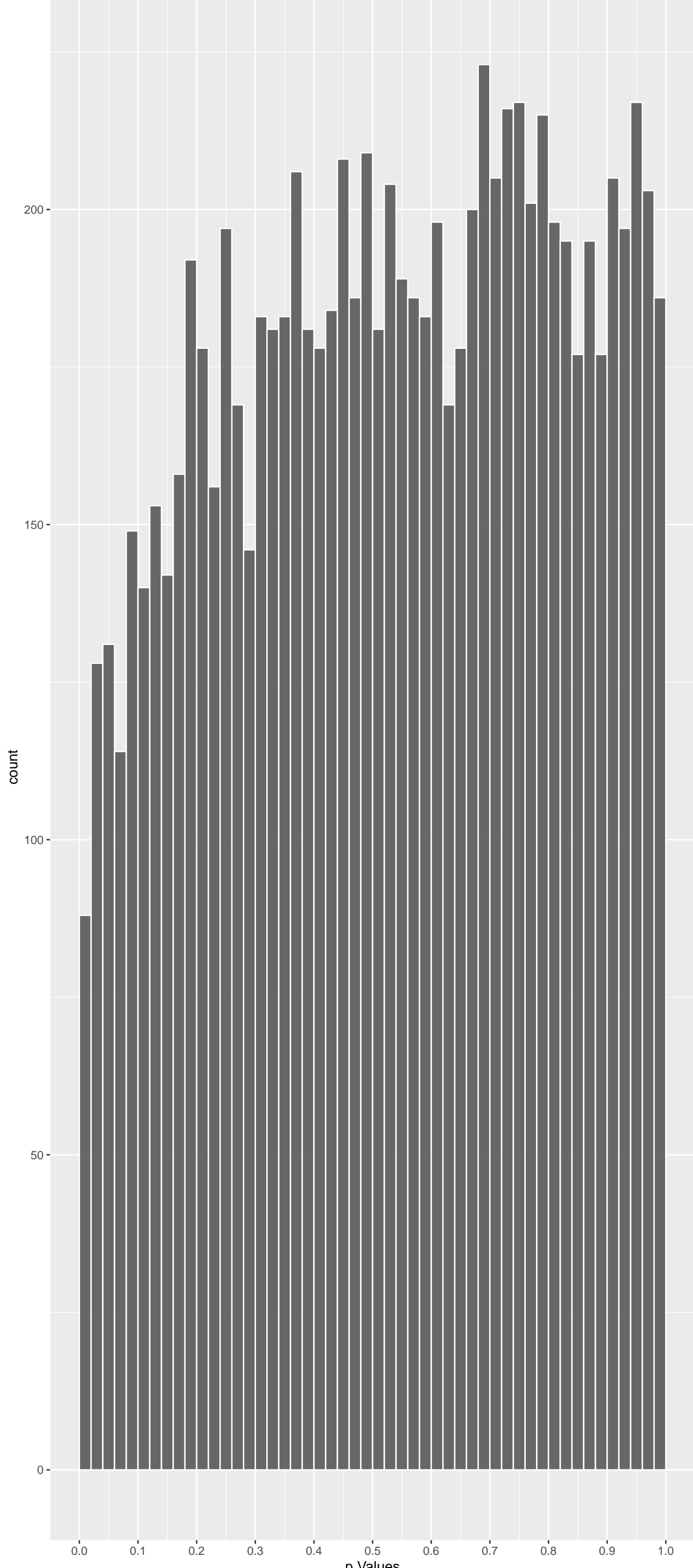
Positive Rho Non-permuted



Top Positive genes by P-value non-permuted

Gene	Rho	N	P	p.adj	qValueNoperm
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

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

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

GO\_Biological\_Process\_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Fatty Acid Metabolic Process (GO:0006631)	-0.15520610	120	4.509e-09	2.438e-05	ACOT8:21 THEM4:38 LPIN1:237 LPIN2:293 ACOX1:299 LCP1:303
Sensory Perception Of Smell (GO:0007608)	0.11152049	208	3.199e-08	8.649e-05	OR5M3:30 OR5D3P:65 OR8K1:67 OR5M9:104 OR4E2:167 OR13G1:177
Monocarboxylic Acid Metabolic Process (GO:0006631)	-0.14863473	96	4.970e-07	9.857e-04	THEM4:38 LDHAL6A:41 SCPP2:298 LCP1:303 GNPAT:343 LDHAL6B:414
Brain Development (GO:0007420)	0.11366582	157	9.296e-07	1.105e-03	ZIC1:29 NDRG4:93 EML1:128 ROBO2:191 DLX2:222 FLNB:399
Peptide Biosynthetic Process (GO:0043043)	0.11468798	153	1.022e-06	1.105e-03	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 AGO2:220
Cytoplasmic Translation (GO:0002181)	0.13832859	91	5.208e-06	3.525e-03	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL29:293
mRNA Processing (GO:0006397)	0.09289046	205	5.028e-06	3.525e-03	HNRNPH3:64 ALYREF:125 RBMX:164 CPSF6:215 LSM5:244 DHX15:281
Macromolecule Biosynthetic Process (GO:0006631)	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:0006631)	-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	0.131313734	129	9.388e-06	4.615e-03	OR4E2:167 OR13G1:177 OR21P:196 OR2T35:264 OR6K3:288 OR2S2:325
Regulation Of DNA-templated Transcription	0.031937685	1857	8.656e-06	4.615e-03	SP9:26 ZIC1:29 PURB:37 INKG:21 TIMELESS:45 CALR:49
Detection Of Chemical Stimulus Involved	0.11290357	127	1.146e-05	5.165e-03	OR4E2:167 OR13G1:177 OR21P:196 OR2T35:264 OR6K3:288 OR2S2:325
Regulation Of Transcription By RNA Polymerase	0.03045675	1948	1.537e-05	6.394e-03	BMP6:7 OTUD7B:14 CBX1:19 AGO1:23 SP9:26 ZIC1:29
Gene Expression (GO:0010467)	0.07410100	286	1.733e-05	6.694e-03	RPS17:1 H3C1:21 HNRNPH3:64 RPS16:71 RAE1:105 ALYREF:125
Negative Regulation Of Nucleic Acid-Temperature	0.05870779	444	2.474e-05	8.917e-03	TIMELESS:45 CALR:49 YWHAQ:50 PER1:90 DACH1:114 CLOCK:202
RNA Splicing, Via Transcription Factor	0.09307730	171	2.783e-05	9.404e-03	HNRNPH3:64 RBMX:164 LSM5:244 DHX15:281 SNRPA1:353 SNRPN:421
Steroid Biosynthetic Process (GO:0006694)	-0.16957024	49	4.051e-05	1.288e-02	ACOT8:21 OSBP:111 SCPP2:298 CYP19A1:379 CYP39A1:420 PRLR:717
Cellular Lipid Catabolic Process (GO:0043043)	-0.24426022	23	5.024e-05	1.308e-02	ACOT8:21 LPIN1:237 LPIN2:293 ACOX1:299 LPLBD1:450 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 SCPP2:298
Lipid Biosynthetic Process (GO:0008610)	-0.14287000	68	4.677e-05	1.308e-02	SCPP2:298 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 ABCCC2:485 SLC10A3:541
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 CD320:351
protein-RNA Complex Assembly (GO:0022618)	0.09883791	141	5.203e-05	1.308e-02	AGO1:23 TARBP2:35 EUC1:108 RPS19:166 CPSF6:215 AGO2:220
Embryonic Limb Morphogenesis (GO:0030326)	0.19705506	34	7.027e-05	1.502e-02	INTU:190 ZNF358:327 LOC1:628 TFAP2A:163 OR52W1:53 OR8K1:67 OR56A1:79
Wnt Signaling Pathway (GO:0016055)	0.13316257	74	7.571e-05	1.574e-02	FZD8:87 CDC88C:159 FZD3:194 TCFL1:206 DVL1:209 WNT2B:319
Cell Morphogenesis Involved In Neuron Development	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 SPTS5B: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 Transcription	0.07658202	995	1.175e-04	2.118e-02	BMP6:7 OTUD7B:14 CBX1:19 INKG:21 TIMELESS:45 CALR:49
mRNA Splicing, Via Spliceosome (GO:00003)	0.03830307	201	1.345e-04	2.346e-02	HNRNPH3:64 RBMX:164 SCNM1:179 LSM5:244 DHX15:281 SNRPA1:353
Modulation Of Chemical Synaptic Transmission	0.10041889	118	1.680e-04	2.753e-02	CAMK2A:100 GRIK3:181 DYF3:236 SLC6A9:240 GRIA1:398 PKX: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:0043043)	0.06683361	268	1.741e-04	2.769e-02	ZIC1:29 LSR:88 NDRG4:93 EML1:128 SXO10:169 ROBO2:191
acyl-CoA Metabolic Process (GO:0006637)	-0.20315573	28	1.992e-04	3.077e-02	ACOT8:21 MCEE:308 ACACB:663 ACSMG:715 OGDH:753 SUCLG2:937
RNA Splicing (GO:0000830)	0.11026884	95	2.069e-04	3.108e-02	HNRNPH3:64 RRAGC:123 SCNM1:179 DHX15:281 SNRPA1:353 SNRPN:421
Acylglycerol Catabolic Process (GO:00464)	-0.21780545	24	2.216e-04	3.115e-02	APOC3:30 ABHD6:105 MGLL:122 PNPLA4:162 LCP1:303 DAGLB:840
Sphingoid Biosynthetic Process (GO:00465)	-0.30706201	12	2.305e-04	3.115e-02	SPHK2:101 SPTS5B:165 ACER1:431 SPTLC1:644 SPHK1:844 ASAH2:1381
Sphingosine Biosynthetic Process (GO:0046)	-0.30706201	12	2.305e-04	3.115e-02	SPHK2:101 SPTS5B:165 ACER1:431 SPTLC1:644 SPHK1:844 ASAH2:1381
Steroid Metabolic Process (GO:0008202)	-0.11217652	91	2.200e-04	3.115e-02	SCPP2:298 ARV1:305 CYP19A1:379 CYP39A1:420 PRLR:717 RDH16:723

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

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_OLFATORY_SIGNALING_PATHWAY	0.13866902	390	6.458e-21	2.097e-17	ORS2B2:27 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_OLFATORY_TRANSDUCTION	0.13039674	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	ORS2B2:27 OR5M3:30 OR52W1:53 OR8K1:67 OR56A1:79
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 H2BCA: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 SPTLC1:643 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 VDCA3:38 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 H2BCA: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:41 TNRC6B:151 FZD3:194
REACTOME_METABOLISM_OF_LIPIDS	-0.06465417	726	3.402e-09	1.352e-06	ACOT8:21 TM6SF2:76 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_PKINS	0.17919402	89	5.177e-09	1.601e-06	H3C13:18 H3C1:21 YWHAQ:50 MYH9:72 H2BCA: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	6.252e-09	1.842e-06	H3C13:18 H3C1:21 AGO1:23 H2BCA:109 PKPC8:118 TNRC6B:151
REACTOME_LEISHMANIA_INFECTION	0.13295812	158	8.232e-09	2.227e-06	ACTR2:47 MYH9:72 DVL1:209 GNB2:239 APCCA2:252 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 AZM:201 CAMP:234 TABBP: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 SETD18:61 HNRNPH3:64 TNRC6B:151
KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER	0.06232169	729	1.137e-08	2.637e-06	RPS17:1 CAMK2B:16 VDCA3:38 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 SCPP2:298 DHR51:363 AMDHD1:627 RDH16:723
REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESS	0.13312341	145	3.196e-08	6.696e-06	H3C13:18 H3C1:21 AGO1:23 H2BCA: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_GLYCOXYLATE_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 RPL29:293
REACTOME_OXIDATIVE_STRESS_INDUCED_SENESC	0.14287201	117	9.156e-08	1.766e-05	H3C13:18 H3C1:21 AGO1:23 H2BCA:109 TNRC6B:151 CBX8:298
REACTOME_METABOLISM_OF_STEROIDS	-0.12497443	152	1.069e-07	1.928e-05	ACOT8:21 SCAP:96 OSBP:111 STARDB:132 NR1H4:276 SCPP2:298
WP_CYTOPLASMIC_RIBOSOMAL_PROTEINS	0.16483550	86	1.275e-07	2.238e-05	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL29:293
NABA_RIBOSOME	-0.04866817	1002	2.160e-07	3.609e-05	MFAP5:4 ADAM28:9 CTSH:28 LK37:88 TLL1:90 C1QTNF9:112
KEGG_RIBOSOME	0.16272001	85	2.169e-07	3.609e-05	RPS17:1 RPS16:71 RPL37A:153 RPS19:166 RPL34:189 RPL29:293
REACTOME_PTEN_REGULATION	0.12797471	137	2.355e-07	3.824e-05	AGO1:23 RRAGC:123 RHEB:133 TNRC6B:151 AGO2:220 CBX8:230

DisGeNET Top pathways by non-permutation

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	729	2.803e-08	1.222e-04	PPM1K:3 MFAP5:4 ADAM28:9 KRIT1:27 APOC3:30 CERS6:34
Cardiovascular Diseases	-0.05610847	1744	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 SLC22A8:98 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 SLC17A5:308 ETTA:425
Atherosclerosis	-0.04183829	1033	7.245e-06	5.882e-03	APOC3:30 TM6SF2:76 EPHA2:77 ITGAV:86 IL37:88 SCAP:96
Hyperlipidemia	-0.0899932	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
Hypertiglyceridemia	-0.10542466	141	1.597e-05	9.229e-03	APOC3:30 TM6SF2:76 LPIN1:237 NR1H4:276 IL16:695 LEPR:274
Hypercholesterolemia, Familial	-0.10310308	145	1.880e-05	9.303e-03	OCA2:25 APOC3:30 OLR1:292 SAC3:381 COMP:503 SGC6:603
Coronary Arteriosclerosis	-0.04766163	706	1.895e-05	9.303e-03	APOC3:30 PRKY:149 CLC1:197 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 SLC22