

Geneset		stat	num_genes	pval	padj	gene.vals
bladder		-0.160117878	24	6.677e-03	1.202e-01	UPK2:134 PLA2G2F:217 SLC14A1:306 MSX2:309 SEMA3E:1381 ACER2:2230
vagina		0.112320956	91	2.263e-04	1.222e-02	RNF222:82 EVPL:126 GJB3:257 ENDOU:339 SULT1E1:410 KRT13:492
hippocampus.proper		-0.066351284	11	4.463e-01	8.654e-01	NEUROG3:248 NTS:1086 NEUROD6:4732 GRP:5569 SLC17A7:6436 OLIG2:6778
caudate.nucleus		0.061706366	26	2.766e-01	8.654e-01	GRM3:80 GPR88:95 ANO3:334 RGS14:1114 TAC1:1338 AQP4:1961
left.ventricle		0.061445305	69	7.851e-02	6.056e-01	CKMT2:54 S100A1:123 MYH7B:181 MYL3:321 SMPX:520 ASB1:542
fallopian.tube		-0.059554967	52	1.383e-01	6.789e-01	CFAP157:73 HOXC4:332 HOXA6:415 ADAMTS3:645 EGR1:1591 CRISPLD2:1650
endocervix		0.056094196	72	1.009e-01	6.657e-01	BDKRB1:91 PLPP3:115 NXNL2:209 MSX1:350 TGM2:569 PWP2:947
leg.skin		0.055028346	217	5.693e-03	1.202e-01	ANKRD35:12 POF1B:66 RNF222:82 EVPL:126 GGT6:139 FAM83F:188
breast		0.051782294	15	4.877e-01	8.654e-01	LMXB1B:125 THRSP:2823.5 GSC:3105 NPY2R:3277 ABCB5:4003 TFAP2B:6113
suprapubic.skin		0.050664190	194	1.591e-02	1.718e-01	SLC10A6:18.5 RNF222:82 WNT4:90 EVPL:126 GGT6:139 FAM83F:188
coronary.artery		-0.049413688	15	0.578e-01	8.654e-01	HEYL:484 SOST:632 CCDC190:1096 MYO18B:2351 COL4A1:2733 MTHFD1L:3246
skeletal.muscle		0.046787336	239	1.377e-02	1.718e-01	PYGM:42 CKMT2:54 SLC2A4:160 TNNI2:186 MSS51:194.5 USP13:197
pancreas		0.044847150	94	1.346e-01	6.789e-01	CASR:8.5 PRODH2:111 CATSPERB:132.5 GCG:299 PNLP1RP1:337 ONECUT1:392
ectocervix		-0.043309474	25	5.450e-01	8.654e-01	ADRA1D:1000 TSKU:1808 ADRA2A:2027 KCNK6:2692 MATN2:3244 FGF10:3561
nucleus.accumbens		0.037904216	99	1.945e-01	8.654e-01	GPR88:95 KCNIP1:158 PTPN5:184 ANO3:334 PENK:364 GPR6:608.5
esophagus.mucosa		0.037017906	220	6.115e-02	5.504e-01	RNF222:82 BDKRB1:91 CLIC3:92.5 DENND2C:113 EVPL:126 TGM1:131
putamen		0.03691357	15	6.201e-01	9.050e-01	GRM3:80 GPR88:95 ANO3:334 KCNHA4:2081.5 RGS9:2717 LRRCL10B:3136
Brodmann.area.24		0.034009398	31	5.128e-01	8.654e-01	SLC39A12:309 SLC25A18:478 DDN:1413 SLC6A1:2491 SHANK1:2878 UPP2:3217
subcutaneous.adipose		-0.033559582	72	3.264e-01	8.654e-01	PLIN1:728 FZD4:792 PNPLA2:1203 G0S2:1241 ANGPTL4:1301 BMP6:1369
esophagogastric.junction		-0.032693923	8	7.489e-01	9.240e-01	COL4A5:2383 BARX1:5206 NKX6-1:5763 GADL1:7900 ADCY5:8233 HOKXA:9210
aorta		-0.029175763	154	2.148e-01	8.654e-01	LTBP1:125 MYO1D:185 TBXA2R:234 ART4:305 PMEP4:1368 IRAG1:428
eye.development		-0.029146938	67	4.107e-01	8.654e-01	CITED2:389 PROX1:621 FZD4:792 CDH11:879 KLF4:1015 MEIS2:1168
sigmoid.colon		-0.028927434	52	4.716e-01	8.654e-01	SLC5A7:11 TTC:453 VIP:469 HLX:1387 HAND1:1822 HMCN2:1911
greater.omentum		-0.027563112	33	5.842e-01	8.822e-01	UPK3B:519 PLIN1:728 ADAMTS4:1044 HBEGF:1150 SPRY1:2060 ATF3:2573
spleen		-0.027230574	298	1.109e-01	6.657e-01	NOX5:36 CD180:74 BLK:90 BANK1:96 TNFRSF4:204 TAS1R3:235
hypothalamus		0.027214551	66	4.459e-01	8.654e-01	SYTL5:312 DLX2:450 SCN9A:484 ENKUR:556 OXT:910 GABRG3:1163
substantia.nigra		-0.026723172	12	7.487e-01	9.240e-01	FOXB1:130 CHRMs:861 RPE65:3248 SPX:3861 SLC6A3:4464 RET:6738
cerebral.cortex		0.026592321	107	3.443e-01	8.654e-01	CALHM1:40 RIMKLA:83 PACSIN1:138 KCNF1:194.5 EIF4E1B:274 HTR3B:515
C1.spinal.cord		-0.025345457	182	2.423e-01	8.654e-01	GFAP:64 FOXB1:130 HHIP:224 SLC5A11:458 FAM222A:460 COLGALT2:599
esophagus.mucularis.mucosa		0.025039952	26	6.589e-01	9.145e-01	PRUNE2:130 KCNMB1:1064 SYNM:1698 NTN1:3444 FAM83B:3537 F2RL2:4328
ovary		0.023667029	103	4.088e-01	8.654e-01	WIPF3:20 BTNL2:53 KCNT2:403 C21orf62:422 CCDC170:436 TMEM21:747
adrenal.gland		0.020876066	108	4.558e-01	8.654e-01	ABCB1:3 SLC47A1:96 MGST1:262 CYSLTR2:305 KCNN2:612.5 MAP3K15:725
blood		-0.020364754	276	2.505e-01	8.654e-01	CTSW:6 ARHGDB123: AQP10:29 NFE2:32 RGS19:33 BLK:90
pituitary.gland		-0.019676417	213	3.272e-01	8.654e-01	NAALAD2:18 RXRG:38 OTOG:211 ZSWIM2:308 CRYBA2:455 VWAAT:461
transverse.colon		0.019482835	149	4.150e-01	8.654e-01	B3GNT6:30 EPS8L3:65 ETHE1:155 GCG:299 TMEM54:419 LGLAL59C:487
amygdala		0.018819337	9	8.450e-01	9.240e-01	LHPFL3:1480 PCDH15:1496 PTPR21:3438 NEUROD2:6882 SLC17A7:9770 TNR:10465
transformed.skin.fibroblast		-0.014560148	259	4.256e-01	8.654e-01	KDELR3:76 PRKD1:197 SPOCD1:287 SEPTIN11:382 CITED2:389 MXRA5:532
tibial.nerve		-0.013085956	192	5.355e-01	8.763e-01	GFR3A3:55.5 SCARA5:172 SLC27A6:261 GLDN:336 IL1RAPL1:443 LGI2:510
prostate		-0.012034885	38	7.977e-01	9.240e-01	NTF4:855 GLIS1:1119 TULP1:1917 SRD5A2:2029 P2RX2:2490 SP8:2704
testis		0.009100238	1381	2.972e-01	8.654e-01	DNAH2:8.5 CFAP45:13 SLAMF9:26 GSG1:37 C11orf53:41 OVOL1:46

Geneset	stat	num_genes	pval	padj	gene.vals
GOCC_9PLUS0_MOTILE_CILIUM	0.4546269	4	1.637e-03	5.422e-01	CFAP45:13 ENKUR:556 DNAH11:1124 DNAH5:1259 NA NA
GOCC_B_CELL_RECEPTOR_COMPLEX	-0.4107645	3	1.373e-02	7.190e-01	SYK:1076 CD79B:1561 CD79A:1707 NA NA NA
HP_APLASIA_CUTIS_CONGENITA_ON_TRUNK_OR_L	0.3852853	6	1.081e-03	4.775e-01	ITGB4:134 PLEC:147 KRT14:905 ITGA6:1212 ARHGAP31:1607 KRT5:7146
GOMF_ANDROGEN_BINDING	0.3768753	4	9.037e-03	7.035e-01	ALDH1A1:1092 TSPO:1523 SHBG:2329 SLC39A9:3012 NA NA
HP_BRONCHIAL_WALL_THICKENING	-0.3754813	6	1.446e-03	5.053e-01	ABCA3:608 HYDIN:1101 FNIP1:1866 SFTPC:2457 PAK2:2935 TTC26:3169
HP_TALL_CHIN	0.3750714	5	3.676e-03	9.594e-01	MYH8:382 NSD1:975 TLK2:2008 APC2:2163 OPHN1:4559 NA
GOCC_CUL4B_RING_E3_UBIQUITIN_LIGASE_COMP	0.3738549	4	9.606e-03	7.097e-01	CUL4B:583 DDB2:1421 DTL:2811 RBX1:3331 NA NA
GOMF_MELANOCORTIN_RECEPTOR_BINDING	-0.3723779	4	9.895e-03	7.097e-01	AGRP:1497 ASIP:1601 MRAP:2208 MRAP2:2994 NA NA
HP_PECTUS_EXCAVATUM_OF_INFERIOR_STERNUM	0.3709487	5	4.069e-03	5.954e-01	NF1:522 PTPN11:1349 MAP2K1:2117.5 BRAF:2370 SOS1:4070 NA
GOBP_CELL_CELL_JUNCTION_DISASSEMBLY	0.3690699	5	4.260e-03	5.954e-01	FER:751 SNAI2:1530 TGFβ3:2504 ABCC8:2629 TGFβR1:3169 NA
GOBP_NEGATIVE_REGULATION_OF_HEMATOPOIETI	0.3682289	4	1.075e-02	7.137e-01	ZFP36:1541 NFE2L2:1576 N4BP2L2:1928 TCF15:3478 NA NA
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	0.3644865	4	1.158e-02	7.137e-01	HLA-DOA:243 HLA-DOB:1690 HLA-DPA1:2852.5 HLA-DRA:3972 NA NA
GOCC_PAR_POLARITY_COMPLEX	-0.3597092	5	5.341e-03	6.152e-01	PRKCI:564 PARD6B:951 PARD6B:1738 PARD3:3725 PARD6A:4399 NA
GOCC_B_WICH_COMPLEX	0.3571460	6	2.447e-03	9.594e-01	DEK:247 ERCC6:1037 MYBBP1A:2177 DDX21:2241 SF3B1:2955 SMARCA5:5185
GOBP_RESPONSE_TO_PHEROMONE	-0.3543741	2	8.258e-02	8.580e-01	TMEM145:778 GPR180:3945 NA NA NA NA
HP_GENERALIZED_AMYLOID_DEPOSITION	0.3534351	3	3.398e-02	8.370e-01	APOA1:1827 GSN:2086 B2M:3195 NA NA NA
HP_RECURRENT_NEISSERIAL_INFECTIONS	-0.3495784	5	6.784e-03	6.687e-01	C8B:98 C6:433 C5:2207 CFB:4609 CFI:4850 NA
GOBP_POSITIVE_REGULATION_OF_EXTRACELLULA	-0.3463307	4	1.644e-02	7.377e-01	CPB2:1176.5 RGCC:2007 BMP2:2792 AGT:4003 NA NA
HP_ABNORMAL_MIDDLE_EAR_REFLEXES	0.3452500	5	7.501e-03	6.744e-01	OTOF:853 PRORP:859 AIFM1:1196 MPDU1:1595 DIAPH3:8032 NA
GOBP_PEPTIDYL_ARGININE_N_METHYLATION	0.3449578	5	7.551e-03	6.744e-01	PRMT5:1500 PRMT3:1662 PRMT8:2791 NDUFAF7:3213 PRMT6:3356 NA
HP_ELEVATED_CIRCULATING_LONG_CHAIN_FATTY	-0.3424484	5	8.000e-03	6.830e-01	ABCD1:699 PEX19:700 PEX1:1212 PEX5:4881 CPT2:5280 NA
GOBP_TRICUSPID_VALVE_MORPHOGENESIS	-0.3416423	4	1.795e-02	7.377e-01	HEY2:429 BMPR2:2367 TGFβR2:3006 BMPR1A:4473 NA NA
GOMF_INTERLEUKIN_2_RECEPTOR_BINDING	-0.3396734	5	8.524e-03	7.022e-01	GATA3:576 IL2:1880 TIMM50:3264 IL21:3460 ECM1:3839 NA
GOBP GRANULOCYTE_COLONY_STIMULATING_FACT	0.3395927	4	1.865e-02	7.377e-01	CD34:683 TSLP:709 ISL1:4083 HAVCR2:4879.5 NA NA
GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_	-0.3388384	6	4.047e-03	9.594e-01	RIPK1:578 ENDOG:1284 HDAC6:1821 ABL1:2142.5 FOXPI1:4244 PAWR:5617
GOCC_CCAAT_BINDING_FACTOR_COMPLEX	-0.3377705	6	4.165e-03	9.594e-01	NFYB:245 NFYC:1588 ATF2:1910 ING2:2021 NFYA:3378 CEBPZ:6673
GOBP_SKELETAL_MUSCLE_SATELLITE_CELL_ACTI	-0.3377407	8	9.390e-04	4.665e-01	EPHB1:69 GJD4:1079 MEGF10:2381 CAPN3:2507 WNT7A:2913 SOX15:3455
HP_APLASIA_CUTIS_CONGENITA_OVER_THE_SCAL	0.3374607	6	4.199e-03	9.594e-01	ITGB4:134 PLEC:147 MCTP2:1043 BMS1:3150 DLL4:4367 UBA2:6909
GOMF_PEROXISOME_TARGETING_SEQUENCE_BINDI	-0.3373764	5	9.891e-03	7.035e-01	PEX19:700 PEX5L:904 BABAM2:3022 PEX7:3691 PEX5:4881 NA
HP_CONGENITAL_ADRENAL_HYPERPLASIA	0.3360661	4	1.991e-02	7.450e-01	POR:1825 CYP17A1:2556 STAR:2615 HSD3B2:3596 NA NA
GOBP_ESTABLISHMENT_OF_LEFT_RIGHT_ASYMMET	0.3345227	4	2.049e-02	7.552e-01	CFAP45:13 CFAP52:173 ENKUR:556 CCDC39:9977 NA NA
GOCC_MCRD_MEDIATED_MRNA_STABILITY_COMPLE	0.3334727	5	9.807e-03	7.097e-01	PAIP1:285 SYNCNIP1:1467 CSDE1:1538 HNRNPD:3429 PABPC1:6740 NA
GOBP_PHENYLPROPANOID_METABOLIC_PROCESS	0.3331674	2	1.027e-01	8.609e-01	PON3:1308 CYP1A1:4086 NA NA NA NA
GOBP_REGULATION_OF_FAS_SIGNALING_PATHWAY	-0.3329904	3	4.575e-02	8.580e-01	ZDHHC7:789 TMBIM1:1080 SMAD5:6249 NA NA NA
GOBP_HYPOTHALAMUS_CELL_MIGRATION	-0.3326495	5	9.990e-03	7.097e-01	FOXB1:130 SEMA3E:1381 NDNF:1925 NRP2:2141 NRP1:8022 NA
GOBP_POSITIVE_REGULATION_OF_HYDROGEN_PER	-0.3326225	4	2.122e-02	7.566e-01	ENDOG:1284 HDAC6:1821 ABL1:2142.5 PAWR:5617 NA NA
GOBP_SPHINGOLIPID_TRANSLOCATION	0.3312035	4	2.178e-02	7.584e-01	ABCB1:3 ABCB4:24 ABCC1:3415 ABCA2:7474 NA NA
GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTH	0.3308770	5	1.039e-02	7.137e-01	SDS:17 BCAT2:1648 BCAT1:2244.5 SDSL:3421 ILVLB:6330 NA
GOCC_DNA_REPLICATION_FACTOR_A_COMPLEX	-0.3271269	3	4.970e-02	8.580e-01	RPA2:380 RPA1:2077 RPA3:5950 NA NA NA
GOBP_CHONDROBLAST_DIFFERENTIATION	-0.3271128	5	1.130e-02	7.137e-01	RARA:126 GDF5:1242 CCN1:1726 FGF2:5431 FGF4:5494 NA

Geneset	stat	num_genes	pval	padj	gene_vals
REACTOME_CHYLOMICRON_CLEARANCE	-0.4270646	5	9.417e-04	7.207e-01	APOB:107 APOE:246 LDLR:1315 LIPC:1642 LDLRAP1:2603 NA
REACTOME_EICOSANOIDS	-0.3748340	4	9.417e-03	9.378e-01	TBXAS1:1054 CYP8B1:1278 CYP4B1:2853 PTGIS:2929 NA NA
REACTOME_BETA_OXIDATION_OF_DECANOYL_COA_	-0.3640254	6	2.014e-03	7.730e-01	HADH:66 ACADM:388 MECR:2183 ECHS1:2401 HADHA:2626 HADHB:5554
REACTOME_BETA_OXIDATION_OF_OCTANOYL_COA_	-0.3637663	5	4.845e-03	7.730e-01	HADH:66 ACADM:388 ECHS1:2401 HADHA:2626 HADHB:5554 NA
REACTOME_ALPHA_DEFENSINS	-0.3598466	3	3.087e-02	9.398e-01	ART1:1786 CD4:2248 PRSS3:2772 NA NA NA
IBRAHIM_NRF3_UP	-0.3402808	5	8.406e-03	9.378e-01	RPN2:1382 CMAS:1464 PSMD4:1875 HMOX1:3572 GCLM:4655 NA
BAFNA_MUC4_TARGETS_UP	-0.3296240	3	4.799e-02	9.398e-01	NEK6:275 AVPR2:2798 SNAI1:5209 NA NA NA
WP_PILOCYTIC_ASTROCYTOMA	0.3220873	6	6.288e-03	8.868e-01	NF1:522 PTPN11:1349 BRAF:2370 GRB2:4051 SOS1:4070 RAF1:4951
MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP	-0.3179774	9	9.550e-04	7.207e-01	FOXN3:339 SMPD1:717 CDH11:879 PMCH:1639 SLC16A7:1851 SULF2:2927
REACTOME_BETA_OXIDATION_OF_LAURYL_COA_T	-0.3153029	5	1.461e-02	9.398e-01	HADH:66 ECHS1:2401 HADHA:2626 ACADL:4315 HADHB:5554 NA
WP_EFFECT_OF_INTESTINAL_MICROBIOME_ON_AN	0.3106366	7	4.423e-03	7.730e-01	NR12:886 VDR:1275 PPARA:2537 NPC1L1:3800 PPARD:4081 CD36:4307
REACTOME_ATORVASTATIN_ADME	0.2876818	5	2.588e-02	9.398e-01	ABCB1:3 PON3:1308 SLC01B1:2894 PON1:6359 SLC02B1:6659 NA
BIOCARTA_NPPI_PATHWAY	-0.2865456	10	1.702e-03	7.730e-01	SPP1:566 ALPL:661 COL4A2:1158 COL4A4:2014 ENPP1:2036 COL4A5:2383
SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCE	0.2848615	5	2.738e-02	9.398e-01	ZNF22:1342 SOX9:1459 CDC27:2525 PDIA4:2882 IGFB1:9251 NA
REACTOME_PREDNISONE_ADME	0.2820033	5	2.896e-02	9.398e-01	ABCB1:3 ALB:64 HSD11B1:605 SERPINI6A:7506 HSD11B2:9492 NA
MIZUKAMI_HYPOXIA_DN	-0.2779689	5	3.134e-02	9.398e-01	PDGFB:529 LRP1:745 CXCL8:3229 FGF2:5431 CXCR1:8060 NA
WP_ALTERNATIVE_PATHWAY_OF_FETAL_ANDROGEN	0.2770188	9	4.003e-03	7.730e-01	HSD17B16:150 POR:1825 HSD17B3:2212 CYB5A:2320 CYP17A1:2556 STAR:2615
MIKKELSEN_IPS_LCP_WITH_H3K4ME3_AND_H3K27	-0.2757051	5	3.274e-02	9.398e-01	CDH7:184 SLC16A8:1899 PPPIR26:3927 FUT7:5732 SLC17A7:6436 NA
REACTOME_CA2_ACTIVATED_K_CHANNELS	0.2732905	9	4.522e-03	7.730e-01	KCNN3:174 KCNN2:612.5 KCNMB1:1064 KCNN1:1408 KCNN4:2896 KCNNB4:5762
DONATO_CELL_CYCLE_TRETINOIN	-0.2726870	6	2.071e-02	9.398e-01	SKAP2:1849 ABI1:2513 BTG2:3242 TOB1:3862 ATR:5148 MNT:5488
REACTOME_LEUKOTRIENE_RECEPTORS	0.2680283	5	3.792e-02	9.398e-01	CYSLTR2:305 LTBR4:1121 LTBR4:2324 GPR7:17159 CYSLTR1:8200 NA
REACTOME_TERMINAL_PATHWAY_OF_COMPLEMENT	-0.2638915	6	2.518e-02	9.398e-01	C8B:98 C6:433 C5:2207 C8G:2879 C8A:8519 L C8:18826
REACTOME_REGULATION_OF_NP4S4_GENE_TRANSC	-0.2629308	4	6.855e-02	9.398e-01	NR3C1:1336 SRF:1407 CYP3A3:3221 NP4A:9404 NA NA NA
WILSON_PROTEASES_AT_TUMOR_BONE_INTERFAC	-0.2599469	5	4.410e-02	9.398e-01	SERPINI2:90 CTSH:3812 CTSH:4590 CTSE:4790 ADAM57:6163 NA
BYSTRYKH_TP53_TARGETS_P10EISIS_STEM_CELL_FGF3	-0.2568035	6	2.936e-02	9.398e-01	EFNB1:30 SH3RF1:34 EFNB3:1512 PKNOX1:4813 POU5F1:7550 MAP2K6:9715
GALI_TPM50_TARGETS_APOPTOTIC_UP	0.2560171	7	1.898e-02	9.398e-01	BAX:4 GADD45A:1024 CASP8:11109 BIRC3:1804 BIRC2:6062 CD40:6618
IGARASHI_ATF4_TARGETS_UP	-0.2531141	4	7.954e-02	9.398e-01	ITFG2:676 PDP1:4113 SFYN4:4437 ASB4:6782 NA NA
BIOCARTA_RAN_PATHWAY	-0.2476446	4	8.626e-02	9.430e-01	RCC1:17 RANGAP1:1865 RAN:5397 RANBP1:9078 NA NA
IKEDA_MIR1_TARGETS_DN	-0.2472354	7	2.349e-02	9.398e-01	CLCN3:1378 SMM36:1628 EIF4E:1999 ST39:2773 MTS51:3162 HSPD1:6532
ERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY	-0.2448934	6	3.775e-02	9.398e-01	PIK3R1:270 DNMI:997 SQSTM1:4525 TNFRSF1B:4594 DAP:5978 MGST3:8442
BIOCARTA_NEUTROPHIL_PATHWAY	-0.2443868	8	1.667e-02	9.398e-01	ITGB2:129 ICAM1:807 ITGAL:1308 ITGAM:1860 CD44:3352 SELT:5686
SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP	-0.2442821	6	8.323e-02	9.398e-01	CDH11:879 GALNT3:1721 SLC31A1:3765 COCH:4031 GAB:4887 AKC:9584
LIU_CD22_TARGETS_DN	0.2436449	5	5.917e-02	9.398e-01	KRT14:905 KRT15:920 KRT19:2546 SOC2:2674 HES1:13763 NA
REACTOME_COBALAMIN_CBL_METABOLISM	-0.2434498	7	2.570e-02	9.398e-01	MTR:656 MTRR:1163 MMADHC:1825 MMMA:2716 MMAB:4723 MMACHC:5597
REACTOME_SYNTHESIS_OF_5_EICOSATETRAENOIC	0.2427929	9	1.166e-02	9.378e-01	PON2:463 PON3:1308 GPX1:1447 GPX2:1556 ALOX5:2324 ALOX5AP:2391
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA	0.2427749	6	3.944e-02	9.398e-01	PGAM1:165 CALU:1887 HSPB1:3062 CTSD:3746 AKR1B1:6329 AOT:9740
BIOCARTA_SLRP_PATHWAY	-0.2420635	6	4.002e-02	9.398e-01	EPYC:925 BGN:748 KERA:1213 LUM:6609 FMOD:6666 DCM:9860
REACTOME_BETA_OXIDATION_OF_HEXANOYL_COA_	-0.2415328	5	6.141e-02	9.398e-01	HADH:66 ECHS1:2401 HADHA:2626 HADHB:5554 ACADS:10292 NA
WP_SFCA_AND_SKELETAL_MUSCLE_SUBSTRATE_ME	0.2409621	6	4.094e-02	9.398e-01	SLC2A4:160 GGC:299 FFAR2:2149 PPARD:4081 FFAR3:6844 PYY:11669
REACTOME_ARYL_HYDROCARBON_RECEPTOR_SIGNA	0.2406143	6	4.123e-02	9.398e-01	AHR:86 PTGES3:1634 ARNT:3459 AIP:3798 ARNT2:4740 HSP90AB1:11524