Oxidative Stress and Response to Thymidylate Synthase-Targeted Antimetabolites
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Supplemental Table 1. FUra-responsive genes as determined by cDNA microarray analysis

The fold change represents the extent of induction by exposure to 10 µM FUra for 24 h (see text). The p-value is corrected for multiple testing using the Benjamini-Hochberg algorithm (see Materials and Methods).

Gene Symbol	Description	Fold Change	Regulation	Corrected p-value	p-value
ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	3.98	up	0.000047	0.0000005
ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	2.58	up	0.003948	0.0008169
ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	1.59	up	0.000742	0.0000717
ABHD4	abhydrolase domain containing 4	2.02	up	0.000102	0.0000023
ABHD8	abhydrolase domain containing 8	2.80	up	0.000030	0.0000002
ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	1.52	up	0.002639	0.0004639
ACRC	acidic repeat containing	1.68	up	0.004630	0.0010282
ACSS2	acyl-CoA synthetase short-chain family member 2	1.60	up	0.001742	0.0002599
ACTA2	actin, alpha 2, smooth muscle, aorta	2.41	up	0.000263	0.0000128
ACVRL1	activin A receptor type II-like 1	2.60	up	0.003060	0.0005714
ACYP1	acylphosphatase 1, erythrocyte (common) type	1.58	up	0.003952	0.0008184
ADIRF	adipogenesis regulatory factor	1.56	up	0.004089	0.0008590
ADRB2	adrenoceptor beta 2, surface	3.42	up	0.000061	0.0000008
AEN	apoptosis enhancing nuclease	1.68	up	0.000288	0.0000151
AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4	2.69	up	0.000898	0.0000964
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	1.64	up	0.000784	0.0000784
AHR	aryl hydrocarbon receptor	1.74	up	0.001298	0.0001688
AIM1L	absent in melanoma 1-like	1.81	up	0.000164	0.0000053
AJUBA	ajuba LIM protein	1.69	up	0.004296	0.0009259
AK1	adenylate kinase 1	1.95	up	0.000130	0.0000036

AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	6.70	up	0.000022	0.0000001
AKR1B15	aldo-keto reductase family 1, member B15	6.04	up	0.000259	0.0000125
AKR1C1	aldo-keto reductase family 1, member C1	2.31	up	0.001859	0.0002856
AKR1C3	aldo-keto reductase family 1, member C3	1.91	up	0.001267	0.0001628
ALCAM	activated leukocyte cell adhesion molecule	1.57	up	0.001951	0.0003055
ALDH3A1	aldehyde dehydrogenase 3 family, member A1	2.02	up	0.001249	0.0001590
ALDH4A1	aldehyde dehydrogenase 4 family, member A1	2.56	up	0.000558	0.0000465
ALOX12P2	arachidonate 12-lipoxygenase pseudogene 2	2.01	up	0.002014	0.0003187
ALOX5	arachidonate 5-lipoxygenase	1.69	up	0.000454	0.0000323
AMDHD1	amidohydrolase domain containing 1	1.56	up	0.002121	0.0003416
AMOTL2	angiomotin like 2	1.97	up	0.000103	0.0000023
AMZ2	archaelysin family metallopeptidase 2	1.73	up	0.001129	0.0001367
AMZ2P1	archaelysin family metallopeptidase 2 pseudogene 1	1.64	up	0.000160	0.0000051
ANAPC13	anaphase promoting complex subunit 13	1.54	up	0.004966	0.0011319
ANGPTL4	angiopoietin-like 4	3.54	up	0.000034	0.0000002
ANKEF1	ankyrin repeat and EF-hand domain containing 1	1.93	up	0.000126	0.0000034
ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	2.10	up	0.000064	0.0000010
ANKRD10	ankyrin repeat domain 10	1.77	up	0.000311	0.0000173
ANKRD19P	ankyrin repeat domain 19, pseudogene	1.56	up	0.001527	0.0002147
ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	2.73	up	0.001254	0.0001600
ANKRD20A12P	ankyrin repeat domain 20 family, member A12, pseudogene	4.55	up	0.000283	0.0000147
ANKRD29	ankyrin repeat domain 29	1.56	up	0.000882	0.0000940
ANTXR2	anthrax toxin receptor 2	1.73	up	0.000210	0.0000085
ANXA8L1	annexin A8-like 1	2.51	up	0.000280	0.0000143
ANXA9	annexin A9	1.73	up	0.000297	0.0000160
AP1S2	adaptor-related protein complex 1, sigma 2 subunit	1.57	up	0.001594	0.0002275
APLP1	amyloid beta (A4) precursor-like protein 1	2.04	up	0.001394	0.0001872
APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	1.81	up	0.000017	0.0000000

APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	1.82	up	0.000147	0.0000045
APOBEC3F	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	1.98	up	0.000850	0.0000882
APOBEC3H	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3H	3.32	up	0.000301	0.0000164
APOE	apolipoprotein E	1.71	up	0.000704	0.0000658
AQP3	aquaporin 3 (Gill blood group)	3.35	up	0.000020	0.0000000
ARC	activity-regulated cytoskeleton-associated protein	1.96	up	0.000364	0.0000224
AREG	amphiregulin	1.60	up	0.001699	0.0002498
ARG2	arginase 2	3.23	up	0.000206	0.0000082
ARHGAP27	Rho GTPase activating protein 27	2.85	up	0.000468	0.0000342
ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	1.53	up	0.000965	0.0001085
ARMCX3	armadillo repeat containing, X-linked 3	1.73	up	0.002856	0.0005193
ARMCX6	armadillo repeat containing, X-linked 6	1.63	up	0.000709	0.0000664
ARRDC4	arrestin domain containing 4	1.55	up	0.000389	0.0000249
ARTN	artemin	1.79	up	0.000509	0.0000400
ARVCF	armadillo repeat gene deleted in velocardiofacial syndrome	1.69	up	0.002541	0.0004387
ASGR1	asialoglycoprotein receptor 1	2.62	up	0.000133	0.0000038
ASTN2	astrotactin 2	2.12	up	0.000716	0.0000677
ATF3	activating transcription factor 3	3.49	up	0.000064	0.0000010
ATG16L2	autophagy related 16-like 2 (S. cerevisiae)	1.66	up	0.001483	0.0002051
ATG4A	autophagy related 4A, cysteine peptidase	1.60	up	0.002062	0.0003287
ATL1	atlastin GTPase 1	1.52	up	0.001534	0.0002163
ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	1.58	up	0.003256	0.0006264
ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	7.10	up	0.000436	0.0000299
ATP6V0E2	ATPase, H+ transporting V0 subunit e2	2.36	up	0.000041	0.0000003
ATP6V0E2-AS1	ATP6V0E2 antisense RNA 1	1.55	up	0.003532	0.0006997
ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	2.04	up	0.000063	0.0000009
ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	1.52	up	0.000538	0.0000437
ATXN7L1	ataxin 7-like 1	2.27	up	0.003392	0.0006624

AVPI1	arginine vasopressin-induced 1	2.97	up	0.000102	0.0000022
BAD	BCL2-associated agonist of cell death	1.57	up	0.000184	0.0000066
BAI2	brain-specific angiogenesis inhibitor 2	1.84	up	0.000100	0.0000021
BATF2	basic leucine zipper transcription factor, ATF-like 2	2.18	up	0.000278	0.0000141
BAX	BCL2-associated X protein	1.68	up	0.000599	0.0000517
BBC3	BCL2 binding component 3	2.59	up	0.000091	0.0000017
BCAR3	breast cancer anti-estrogen resistance 3	1.92	up	0.000208	0.0000083
BCL6	B-cell CLL/lymphoma 6	1.90	up	0.000459	0.0000331
BEST4	bestrophin 4	2.88	up	0.002364	0.0003952
BHLHE40	basic helix-loop-helix family, member e40	1.83	up	0.000202	0.0000078
BIRC2	baculoviral IAP repeat containing 2	1.54	up	0.000630	0.0000559
BIRC3	baculoviral IAP repeat containing 3	2.97	up	0.000061	0.0000009
BLCAP	bladder cancer associated protein	1.62	up	0.000563	0.0000471
BLOC1S2	biogenesis of lysosomal organelles complex-1, subunit 2	1.82	up	0.000120	0.0000031
BLOC1S3	biogenesis of lysosomal organelles complex-1, subunit 3	1.50	up	0.003397	0.0006635
BLOC1S5	biogenesis of lysosomal organelles complex-1, subunit 5, muted	1.57	up	0.002550	0.0004413
BLVRB	biliverdin reductase B (flavin reductase (NADPH))	2.01	up	0.001495	0.0002076
BMS1	BMS1 ribosome biogenesis factor	1.57	up	0.000047	0.0000005
BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	1.89	up	0.004644	0.0010317
BTBD10	BTB (POZ) domain containing 10	2.23	up	0.000082	0.0000015
BTBD11	BTB (POZ) domain containing 11	1.64	up	0.000318	0.0000179
BTG1	B-cell translocation gene 1, anti-proliferative	2.04	up	0.000108	0.0000025
BTG2	BTG family, member 2	3.06	up	0.000100	0.0000020
BTG3	BTG family, member 3	1.51	up	0.000896	0.0000961
BTN2A2	butyrophilin, subfamily 2, member A2	1.63	up	0.001378	0.0001840
C10orf12	chromosome 10 open reading frame 12	2.20	up	0.000243	0.0000109
C10orf54	chromosome 10 open reading frame 54	2.10	up	0.000044	0.0000004
C11orf52	chromosome 11 open reading frame 52	1.90	up	0.000850	0.0000883
C11orf86	chromosome 11 open reading frame 86	4.44	up	0.002107	0.0003387

C12orf4	chromosome 12 open reading frame 4	1.66	up	0.001001	0.0001147
C12orf5	chromosome 12 open reading frame 5	1.59	up	0.002273	0.0003737
C17orf89	chromosome 17 open reading frame 89	1.67	up	0.004967	0.0011336
C19orf57	chromosome 19 open reading frame 57	2.34	up	0.000044	0.0000004
C1orf106	chromosome 1 open reading frame 106	2.90	up	0.000027	0.0000001
C1orf116	chromosome 1 open reading frame 116	3.99	up	0.000090	0.0000017
C1orf54	chromosome 1 open reading frame 54	2.43	up	0.000159	0.0000051
C1QTNF6	C1q and tumor necrosis factor related protein 6	1.55	up	0.000140	0.0000042
C1S	complement component 1, s subcomponent	2.26	up	0.000431	0.0000293
C21orf91	chromosome 21 open reading frame 91	1.78	up	0.000400	0.0000260
C2CD2L	C2CD2-like	1.75	up	0.004510	0.0009903
C2orf43	chromosome 2 open reading frame 43	1.55	up	0.000079	0.0000014
C4orf47	chromosome 4 open reading frame 47	1.57	up	0.002746	0.0004895
C5orf42	chromosome 5 open reading frame 42	1.83	up	0.004916	0.0011151
C6orf226	chromosome 6 open reading frame 226	1.90	up	0.000253	0.0000119
C8orf44	chromosome 8 open reading frame 44	2.02	up	0.000043	0.0000004
CA2	carbonic anhydrase II	2.49	up	0.000167	0.0000056
CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	1.74	up	0.000487	0.0000368
CALB2	calbindin 2	1.69	up	0.000477	0.0000350
CALCOCO2	calcium binding and coiled-coil domain 2	1.51	up	0.000119	0.0000030
CALHM3	calcium homeostasis modulator 3	2.41	up	0.000939	0.0001039
CAMK2B	calcium/calmodulin-dependent protein kinase II beta	4.60	up	0.002364	0.0003954
CAPG	capping protein (actin filament), gelsolin-like	1.62	up	0.001668	0.0002438
CAPN13	calpain 13	1.58	up	0.000915	0.0000992
CARHSP1	calcium regulated heat stable protein 1, 24kDa	1.52	up	0.000947	0.0001051
CASP10	caspase 10, apoptosis-related cysteine peptidase	1.69	up	0.003055	0.0005695
CASP4	caspase 4, apoptosis-related cysteine peptidase	1.92	up	0.000039	0.0000003
CASP5	caspase 5, apoptosis-related cysteine peptidase	2.11	up	0.000497	0.0000382
CAST	calpastatin	1.68	up	0.000029	0.0000002

CATSPER1	cation channel, sperm associated 1	1.97	up	0.001743	0.0002601
CBR3	carbonyl reductase 3	1.89	up	0.003410	0.0006666
CBS	cystathionine-beta-synthase	3.30	up	0.000200	0.0000077
CCDC90B	coiled-coil domain containing 90B	1.50	up	0.000250	0.0000116
CCDC96	coiled-coil domain containing 96	1.62	up	0.000102	0.0000022
CCL26	chemokine (C-C motif) ligand 26	4.94	up	0.000241	0.0000107
CCL3	chemokine (C-C motif) ligand 3	2.00	up	0.001067	0.0001258
CCND3	cyclin D3	2.23	up	0.000014	0.0000000
CCNE1	cyclin E1	1.69	up	0.001508	0.0002109
CCNE2	cyclin E2	3.06	up	0.001859	0.0002858
CCNG2	cyclin G2	2.17	up	0.004254	0.0009118
CCRL2	chemokine (C-C motif) receptor-like 2	5.08	up	0.000053	0.0000006
CD274	CD274 molecule	2.86	up	0.000116	0.0000029
CD33	CD33 molecule	1.51	up	0.000590	0.0000507
CD47	CD47 molecule	1.62	up	0.000124	0.0000033
CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	1.88	up	0.000253	0.0000118
CD68	CD68 molecule	2.27	up	0.000029	0.0000002
CD79B	CD79b molecule, immunoglobulin-associated beta	5.64	up	0.003888	0.0007965
CD82	CD82 molecule	3.54	up	0.000038	0.0000003
CD83	CD83 molecule	1.85	up	0.000495	0.0000380
CDA	cytidine deaminase	1.93	up	0.000022	0.0000001
CDC42BPG	CDC42 binding protein kinase gamma (DMPK-like)	2.12	up	0.002425	0.0004099
CDCA5	cell division cycle associated 5	1.52	up	0.000271	0.0000135
CDCP1	CUB domain containing protein 1	1.82	up	0.000044	0.0000004
CDH1	cadherin 1, type 1, E-cadherin (epithelial)	1.54	up	0.001195	0.0001480
CDIP1	cell death-inducing p53 target 1	2.60	up	0.001805	0.0002737
CDK2	cyclin-dependent kinase 2	1.55	up	0.000389	0.0000249
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	3.83	up	0.000056	0.0000007
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	2.13	up	0.000054	0.0000006

CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1.70	up	0.000106	0.0000025
CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	1.68	up	0.001232	0.0001554
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	13.86	up	0.000056	0.0000007
CENPP	centromere protein P	1.73	up	0.000938	0.0001037
CENPQ	centromere protein Q	1.87	up	0.000102	0.0000022
CENPU	centromere protein U	1.51	up	0.000614	0.0000536
CERS6	ceramide synthase 6	1.56	up	0.002558	0.0004432
CGB	chorionic gonadotropin, beta polypeptide	2.16	up	0.000509	0.0000400
CGRRF1	cell growth regulator with ring finger domain 1	1.69	up	0.003010	0.0005581
CHIC2	cysteine-rich hydrophobic domain 2	1.97	up	0.000164	0.0000054
CHM	choroideremia (Rab escort protein 1)	2.61	up	0.003329	0.0006472
CHMP1B	charged multivesicular body protein 1B	1.56	up	0.000850	0.0000883
CHRD	chordin	1.81	up	0.000742	0.0000718
CHRFAM7A	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) fusion	2.54	up	0.004040	0.0008458
CHRNA7	cholinergic receptor, nicotinic, alpha 7 (neuronal)	2.42	up	0.000074	0.0000012
CHRNB1	cholinergic receptor, nicotinic, beta 1 (muscle)	2.07	up	0.000278	0.0000141
CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	1.52	up	0.001761	0.0002639
CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	1.90	up	0.000098	0.0000020
CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	1.59	up	0.001570	0.0002225
CITED4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	1.70	up	0.000060	0.0000008
CLDN4	claudin 4	1.72	up	0.000551	0.0000456
CLEC16A	C-type lectin domain family 16, member A	2.71	up	0.002145	0.0003466
CLIC3	chloride intracellular channel 3	1.52	up	0.002290	0.0003775
CLIC4	chloride intracellular channel 4	1.66	up	0.000127	0.0000035
CLIC5	chloride intracellular channel 5	3.33	up	0.001130	0.0001370
CLK4	CDC-like kinase 4	1.53	up	0.002288	0.0003769
CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	1.58	up	0.000560	0.0000467

CMTM3	CKLF-like MARVEL transmembrane domain containing 3	1.72	up	0.000191	0.0000071
CNN1	calponin 1, basic, smooth muscle	6.13	up	0.000034	0.0000002
CNOT1	CCR4-NOT transcription complex, subunit 1	1.54	up	0.001336	0.0001755
CNST	consortin, connexin sorting protein	1.57	up	0.000037	0.0000002
COBLL1	cordon-bleu WH2 repeat protein-like 1	1.84	up	0.000289	0.0000152
COL16A1	collagen, type XVI, alpha 1	2.18	up	0.001235	0.0001559
COL4A6	collagen, type IV, alpha 6	1.55	up	0.000598	0.0000516
COL9A3	collagen, type IX, alpha 3	1.75	up	0.000442	0.0000307
COQ10B	coenzyme Q10 homolog B (S. cerevisiae)	1.52	up	0.000159	0.0000050
CORO2A	coronin, actin binding protein, 2A	1.71	up	0.004989	0.0011407
CORO6	coronin 6	1.95	up	0.000528	0.0000423
CPE	carboxypeptidase E	2.00	up	0.000022	0.0000001
CPNE8	copine VIII	1.58	up	0.001505	0.0002102
CREB3	cAMP responsive element binding protein 3	1.91	up	0.001237	0.0001565
CREB3L3	cAMP responsive element binding protein 3-like 3	1.88	up	0.000754	0.0000737
CRELD2	cysteine-rich with EGF-like domains 2	1.62	up	0.000347	0.0000209
CRIP1	cysteine-rich protein 1 (intestinal)	1.79	up	0.000163	0.0000053
CRIP2	cysteine-rich protein 2	2.08	up	0.000170	0.0000058
CRIPT	cysteine-rich PDZ-binding protein	1.60	up	0.000416	0.0000277
CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	2.35	up	0.000063	0.0000009
CRLF1	cytokine receptor-like factor 1	1.65	up	0.001293	0.0001675
CSF1R	colony stimulating factor 1 receptor	2.04	up	0.000416	0.0000276
CSF2	colony stimulating factor 2 (granulocyte-macrophage)	5.56	up	0.001739	0.0002587
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	2.27	up	0.004438	0.0009687
CSRNP1	cysteine-serine-rich nuclear protein 1	2.88	up	0.000046	0.0000005
CST6	cystatin E/M	2.11	up	0.000040	0.0000003
CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	1.59	up	0.000209	0.0000085
CTGF	connective tissue growth factor	2.96	up	0.001055	0.0001237
CTSD	cathepsin D	1.65	up	0.000247	0.0000113
CTSK	cathepsin K	1.72	up	0.001399	0.0001889

CTSV	cathepsin V	1.86	up	0.001646	0.0002379
CUL4B	cullin 4B	1.61	up	0.000046	0.0000005
CXCL16	chemokine (C-X-C motif) ligand 16	1.54	up	0.002189	0.0003560
CXCR4	chemokine (C-X-C motif) receptor 4	3.98	up	0.000039	0.0000003
CXorf40B	chromosome X open reading frame 40B	1.60	up	0.000329	0.0000191
CXorf57	chromosome X open reading frame 57	1.61	up	0.000226	0.0000096
CYB5R1	cytochrome b5 reductase 1	1.66	up	0.002679	0.0004731
CYFIP2	cytoplasmic FMR1 interacting protein 2	2.03	up	0.001676	0.0002454
CYHR1	cysteine/histidine-rich 1	1.79	up	0.000197	0.0000075
CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1	1.69	up	0.000834	0.0000850
CYP4F11	cytochrome P450, family 4, subfamily F, polypeptide 11	2.16	up	0.000444	0.0000310
CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	2.56	up	0.001262	0.0001615
CYR61	cysteine-rich, angiogenic inducer, 61	3.68	up	0.000109	0.0000026
CYSRT1	cysteine-rich tail protein 1	3.33	up	0.000029	0.0000002
CYSTM1	cysteine-rich transmembrane module containing 1	1.63	up	0.000441	0.0000305
CYTH4	cytohesin 4	3.28	up	0.000086	0.0000016
DACT3	dishevelled-binding antagonist of beta-catenin 3	2.10	up	0.000168	0.0000057
DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	8.72	up	0.000054	0.0000007
DBR1	debranching RNA lariats 1	1.51	up	0.000206	0.0000082
DDB2	damage-specific DNA binding protein 2, 48kDa	2.67	up	0.000311	0.0000173
DDIAS	DNA damage-induced apoptosis suppressor	1.69	up	0.000525	0.0000419
DDIT3	DNA-damage-inducible transcript 3	1.71	up	0.001292	0.0001674
DEF8	differentially expressed in FDCP 8 homolog (mouse)	1.77	up	0.001046	0.0001220
DENND2A	DENN/MADD domain containing 2A	2.36	up	0.000879	0.0000934
DENND2C	DENN/MADD domain containing 2C	1.79	up	0.000235	0.0000103
DENND3	DENN/MADD domain containing 3	1.52	up	0.000621	0.0000546
DES	desmin	1.53	up	0.001073	0.0001270
DGKA	diacylglycerol kinase, alpha 80kDa	2.56	up	0.000501	0.0000387
DHRS11	dehydrogenase/reductase (SDR family) member 11	1.77	up	0.003168	0.0006002
DHRS13	dehydrogenase/reductase (SDR family) member 13	1.87	up	0.001244	0.0001581

DHRS7	dehydrogenase/reductase (SDR family) member 7	1.59	up	0.000098	0.0000020
DISP1	dispatched homolog 1 (Drosophila)	2.19	up	0.000713	0.0000672
DISP2	dispatched homolog 2 (Drosophila)	2.23	up	0.000054	0.0000006
DKK1	dickkopf WNT signaling pathway inhibitor 1	1.63	up	0.001371	0.0001826
DLK2	delta-like 2 homolog (Drosophila)	1.73	up	0.000446	0.0000312
DLX2	distal-less homeobox 2	1.73	up	0.000539	0.0000439
DLX4	distal-less homeobox 4	2.00	up	0.000839	0.0000859
DMPK	dystrophia myotonica-protein kinase	1.66	up	0.003888	0.0007962
DMTF1	cyclin D binding myb-like transcription factor 1	1.50	up	0.003532	0.0006999
DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	1.59	up	0.002145	0.0003468
DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	1.62	up	0.000958	0.0001072
DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	2.00	up	0.001904	0.0002956
DOK7	docking protein 7	3.99	up	0.000551	0.0000456
DPF1	D4, zinc and double PHD fingers family 1	1.64	up	0.000269	0.0000133
DPYSL4	dihydropyrimidinase-like 4	2.66	up	0.000103	0.0000023
DRAM1	DNA-damage regulated autophagy modulator 1	2.35	up	0.000290	0.0000153
DRAXIN	dorsal inhibitory axon guidance protein	3.45	up	0.000646	0.0000583
DRICH1	aspartate-rich 1	1.52	up	0.003831	0.0007793
DSG2	desmoglein 2	1.57	up	0.000503	0.0000391
DUSP1	dual specificity phosphatase 1	1.54	up	0.000243	0.0000109
DUSP13	dual specificity phosphatase 13	2.17	up	0.000132	0.0000037
DUSP14	dual specificity phosphatase 14	2.42	up	0.000133	0.0000038
DUSP4	dual specificity phosphatase 4	1.74	up	0.000074	0.0000012
DUSP5	dual specificity phosphatase 5	2.40	up	0.000020	0.0000000
DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	1.62	up	0.000342	0.0000204
E2F7	E2F transcription factor 7	2.24	up	0.000264	0.0000129
EBI3	Epstein-Barr virus induced 3	4.18	up	0.000089	0.0000017
ECM1	extracellular matrix protein 1	4.17	up	0.000047	0.0000005
EDN2	endothelin 2	12.48	up	0.000253	0.0000119

EDRF1	erythroid differentiation regulatory factor 1	1.95	up	0.003508	0.0006915
EFEMP2	EGF containing fibulin-like extracellular matrix protein 2	1.89	up	0.003199	0.0006098
EFNB1	ephrin-B1	1.96	up	0.000858	0.0000897
EFR3B	EFR3 homolog B (S. cerevisiae)	2.19	up	0.000528	0.0000423
EGR2	early growth response 2	3.68	up	0.000477	0.0000353
EGR4	early growth response 4	2.00	up	0.003663	0.0007348
EHD2	EH-domain containing 2	1.50	up	0.000713	0.0000671
ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	1.87	up	0.000541	0.0000442
ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	2.29	up	0.000684	0.0000633
EMC7	ER membrane protein complex subunit 7	1.62	up	0.001693	0.0002487
EMX1	empty spiracles homeobox 1	1.53	up	0.001410	0.0001913
ENHO	energy homeostasis associated	1.89	up	0.000343	0.0000204
ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	1.57	up	0.003085	0.0005780
ENSA	endosulfine alpha	1.79	up	0.000672	0.0000617
EPAS1	endothelial PAS domain protein 1	1.97	up	0.000040	0.0000003
EPHA2	EPH receptor A2	2.36	up	0.000338	0.0000200
EPHB3	EPH receptor B3	2.11	up	0.001199	0.0001492
EPPK1	epiplakin 1	2.54	up	0.000135	0.0000039
EPS8L1	EPS8-like 1	1.54	up	0.001897	0.0002941
EPS8L2	EPS8-like 2	2.23	up	0.000446	0.0000312
ERAP2	endoplasmic reticulum aminopeptidase 2	2.24	up	0.000492	0.0000375
ERBB3	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	1.76	up	0.000283	0.0000147
ERICH2	glutamate-rich 2	3.26	up	0.000047	0.0000005
ERMP1	endoplasmic reticulum metallopeptidase 1	1.58	up	0.001242	0.0001575
ESAM	endothelial cell adhesion molecule	2.08	up	0.000152	0.0000048
ESPNL	espin-like	2.60	up	0.000165	0.0000054
ETNK2	ethanolamine kinase 2	1.59	up	0.001500	0.0002089
EXO1	exonuclease 1	1.74	up	0.000180	0.0000064

EXT1	exostosin glycosyltransferase 1	1.66	up	0.002299	0.0003801
F3	coagulation factor III (thromboplastin, tissue factor)	1.76	up	0.000127	0.0000035
FA2H	fatty acid 2-hydroxylase	2.07	up	0.000102	0.0000021
FAAH2	fatty acid amide hydrolase 2	1.54	up	0.000400	0.0000260
FAAHP1	fatty acid amide hydrolase pseudogene 1	3.88	up	0.000047	0.0000005
FAM105A	family with sequence similarity 105, member A	1.77	up	0.000745	0.0000725
FAM110C	family with sequence similarity 110, member C	2.40	up	0.000027	0.0000001
FAM111A	family with sequence similarity 111, member A	2.34	up	0.000441	0.0000305
FAM122B	family with sequence similarity 122B	1.65	up	0.002226	0.0003640
FAM126A	family with sequence similarity 126, member A	2.31	up	0.003928	0.0008107
FAM129A	family with sequence similarity 129, member A	2.49	up	0.000095	0.0000019
FAM174A	family with sequence similarity 174, member A	1.58	up	0.003252	0.0006231
FAM189A2	family with sequence similarity 189, member A2	2.83	up	0.000481	0.0000358
FAM199X	family with sequence similarity 199, X-linked	1.61	up	0.000150	0.0000046
FAM210B	family with sequence similarity 210, member B	2.03	up	0.000205	0.0000081
FAM212B	family with sequence similarity 212, member B	3.34	up	0.000079	0.0000014
FAM214A	family with sequence similarity 214, member A	2.70	up	0.000040	0.0000003
FAM214B	family with sequence similarity 214, member B	1.72	up	0.002834	0.0005132
FAM25A	family with sequence similarity 25, member A	3.01	up	0.000024	0.0000001
FAM27C	family with sequence similarity 27, member C	1.86	up	0.000482	0.0000360
FAM46B	family with sequence similarity 46, member B	2.96	up	0.000548	0.0000452
FAM46C	family with sequence similarity 46, member C	1.64	up	0.004263	0.0009148
FAM71E1	family with sequence similarity 71, member E1	1.52	up	0.000903	0.0000972
FAM83E	family with sequence similarity 83, member E	2.56	up	0.000217	0.0000089
FAM84B	family with sequence similarity 84, member B	1.73	up	0.000335	0.0000197
FAM8A1	family with sequence similarity 8, member A1	1.70	up	0.000104	0.0000024
FAM92B	family with sequence similarity 92, member B	5.84	up	0.000112	0.0000027
FAM98C	family with sequence similarity 98, member C	1.57	up	0.000806	0.0000813
FANCB	Fanconi anemia, complementation group B	1.62	up	0.001659	0.0002413
FAS	Fas cell surface death receptor	3.97	up	0.000215	0.0000088

FBLIM1	filamin binding LIM protein 1	3.98	up	0.003145	0.0005935
FBLN1	fibulin 1	1.89	up	0.000114	0.0000028
FBLN5	fibulin 5	2.10	up	0.001682	0.0002464
FBXO2	F-box protein 2	1.63	up	0.000631	0.0000560
FBXO22	F-box protein 22	1.53	up	0.001651	0.0002391
FDXR	ferredoxin reductase	2.27	up	0.000178	0.0000063
FER1L4	fer-1-like 4 (C. elegans), pseudogene	2.29	up	0.000926	0.0001014
FGD6	FYVE, RhoGEF and PH domain containing 6	2.28	up	0.000227	0.0000097
FGFR1OP	FGFR1 oncogene partner	1.51	up	0.002066	0.0003303
FHL2	four and a half LIM domains 2	2.80	up	0.000035	0.0000002
FICD	FIC domain containing	1.55	up	0.000684	0.0000633
FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	1.93	up	0.001513	0.0002119
FLNC	filamin C, gamma	1.76	up	0.001098	0.0001310
FLT3LG	fms-related tyrosine kinase 3 ligand	1.96	up	0.000750	0.0000731
FOLR1	folate receptor 1 (adult)	1.75	up	0.000548	0.0000451
FOSL1	FOS-like antigen 1	1.65	up	0.000083	0.0000015
FOSL2	FOS-like antigen 2	1.92	up	0.000350	0.0000212
FOXA1	forkhead box A1	1.76	up	0.000108	0.0000025
FOXD1	forkhead box D1	1.64	up	0.000742	0.0000716
FOXP1	forkhead box P1	2.39	up	0.000402	0.0000263
FOXQ1	forkhead box Q1	2.19	up	0.003296	0.0006373
FRS2	fibroblast growth factor receptor substrate 2	1.58	up	0.003260	0.0006275
FRZB	frizzled-related protein	2.55	up	0.000566	0.0000475
FST	follistatin	4.02	up	0.000102	0.0000022
FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	3.30	up	0.000042	0.0000004
FXYD3	FXYD domain containing ion transport regulator 3	5.10	up	0.000052	0.0000006
FXYD6	FXYD domain containing ion transport regulator 6	1.78	up	0.003533	0.0007013
GABARAP	GABA(A) receptor-associated protein	1.53	up	0.003009	0.0005578

GABARAPL1	GABA(A) receptor-associated protein like 1	1.68	up	0.002189	0.0003560
GAD1	glutamate decarboxylase 1 (brain, 67kDa)	1.84	up	0.000501	0.0000388
GADD45A	growth arrest and DNA-damage-inducible, alpha	2.06	up	0.000269	0.0000134
GALNT5	polypeptide N-acetylgalactosaminyltransferase 5	2.96	up	0.000039	0.0000003
GAST	gastrin	4.28	up	0.000102	0.0000021
GATA2	GATA binding protein 2	1.82	up	0.000431	0.0000293
GBE1	glucan (1,4-alpha-), branching enzyme 1	1.73	up	0.000069	0.0000011
GBX2	gastrulation brain homeobox 2	2.31	up	0.000544	0.0000445
GCH1	GTP cyclohydrolase 1	2.28	up	0.000051	0.0000006
GCHFR	GTP cyclohydrolase I feedback regulator	2.12	up	0.000253	0.0000118
GDA	guanine deaminase	1.68	up	0.000184	0.0000066
GDAP2	ganglioside induced differentiation associated protein 2	1.63	up	0.000127	0.0000035
GDI1	GDP dissociation inhibitor 1	1.60	up	0.003122	0.0005880
GEM	GTP binding protein overexpressed in skeletal muscle	1.66	up	0.000740	0.0000712
GFI1	growth factor independent 1 transcription repressor	1.73	up	0.000093	0.0000018
GFOD1	glucose-fructose oxidoreductase domain containing 1	1.72	up	0.002689	0.0004757
GGCT	gamma-glutamylcyclotransferase	1.56	up	0.002013	0.0003183
GGT1	gamma-glutamyltransferase 1	2.48	up	0.000289	0.0000152
GGT3P	gamma-glutamyltransferase 3 pseudogene	2.12	up	0.000312	0.0000174
GGTLC1	gamma-glutamyltransferase light chain 1	3.12	up	0.000040	0.0000003
GGTLC2	gamma-glutamyltransferase light chain 2	2.59	up	0.000254	0.0000121
GJB4	gap junction protein, beta 4, 30.3kDa	3.65	up	0.000022	0.0000001
GJB5	gap junction protein, beta 5, 31.1kDa	2.70	up	0.000061	0.0000008
GLRX	glutaredoxin (thioltransferase)	1.54	up	0.000476	0.0000349
GLRX2	glutaredoxin 2	1.68	up	0.000623	0.0000547
GLS	glutaminase	2.44	up	0.000184	0.0000067
GLTP	glycolipid transfer protein	1.58	up	0.001780	0.0002681
GM2A	GM2 ganglioside activator	1.88	up	0.000990	0.0001128
GNAS	GNAS complex locus	1.52	up	0.000206	0.0000082

GNGT1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	2.34	up	0.000074	0.0000012
GP1BB	glycoprotein Ib (platelet), beta polypeptide	1.87	up	0.000462	0.0000335
GPATCH11	G patch domain containing 11	1.52	up	0.000576	0.0000487
GPM6A	glycoprotein M6A	1.68	up	0.003010	0.0005585
GPR124	G protein-coupled receptor 124	1.58	up	0.002998	0.0005553
GPR137	G protein-coupled receptor 137	1.58	up	0.002380	0.0003986
GPR162	G protein-coupled receptor 162	1.97	up	0.002007	0.0003170
GPR35	G protein-coupled receptor 35	2.27	up	0.001805	0.0002731
GPR56	G protein-coupled receptor 56	2.30	up	0.000068	0.0000010
GPR87	G protein-coupled receptor 87	4.47	up	0.000014	0.0000000
GPRC5A	G protein-coupled receptor, class C, group 5, member A	2.17	up	0.000294	0.0000157
GPX1	glutathione peroxidase 1	1.65	up	0.000812	0.0000823
GRAMD1B	GRAM domain containing 1B	2.57	up	0.002219	0.0003622
GRAMD3	GRAM domain containing 3	1.69	up	0.001630	0.0002351
GRB7	growth factor receptor-bound protein 7	2.22	up	0.000147	0.0000045
GREB1	growth regulation by estrogen in breast cancer 1	1.72	up	0.003173	0.0006018
GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	1.81	up	0.004894	0.0011073
GSE1	Gse1 coiled-coil protein	1.74	up	0.004492	0.0009849
GSN	gelsolin	1.76	up	0.000836	0.0000853
GSTT2	glutathione S-transferase theta 2	1.82	up	0.001871	0.0002886
GSTT2B	glutathione S-transferase theta 2B (gene/pseudogene)	1.91	up	0.000103	0.0000023
H19	H19, imprinted maternally expressed transcript (non-protein coding)	3.04	up	0.000116	0.0000029
HAPLN3	hyaluronan and proteoglycan link protein 3	1.79	up	0.000864	0.0000907
HAUS2	HAUS augmin-like complex, subunit 2	1.79	up	0.000477	0.0000352
HBA2	hemoglobin, alpha 2	1.92	up	0.000315	0.0000176
HBEGF	heparin-binding EGF-like growth factor	3.15	up	0.000053	0.0000006
HCFC2	host cell factor C2	1.90	up	0.003302	0.0006390
HDAC11	histone deacetylase 11	1.75	up	0.000952	0.0001061

HDAC5	histone deacetylase 5	2.02	up	0.000073	0.0000012
HECA	headcase homolog (Drosophila)	1.81	up	0.000023	0.0000001
HELZ2	helicase with zinc finger 2, transcriptional coactivator	1.67	up	0.000248	0.0000113
HERC2P2	hect domain and RLD 2 pseudogene 2	1.75	up	0.000810	0.0000819
HES2	hes family bHLH transcription factor 2	2.79	up	0.000014	0.0000000
HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	1.58	up	0.003651	0.0007312
HLA-A	major histocompatibility complex, class I, A	1.81	up	0.001721	0.0002549
HLA-DPB1	major histocompatibility complex, class II, DP beta 1	1.60	up	0.001676	0.0002454
HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	2.28	up	0.002348	0.0003909
HLA-DRB1	major histocompatibility complex, class II, DR beta 1	2.33	up	0.000014	0.0000000
HLA-DRB4	major histocompatibility complex, class II, DR beta 4	2.40	up	0.000094	0.0000018
HLA-DRB5	major histocompatibility complex, class II, DR beta 5	2.19	up	0.004900	0.0011089
HMCN2	hemicentin 2	3.16	up	0.001249	0.0001589
HMGA2	high mobility group AT-hook 2	1.83	up	0.001661	0.0002418
HMOX1	heme oxygenase (decycling) 1	2.00	up	0.000014	0.0000000
HOXB4	homeobox B4	1.79	up	0.000163	0.0000053
HOXB6	homeobox B6	1.87	up	0.001296	0.0001680
HPSE	heparanase	1.56	up	0.003533	0.0007012
HRCT1	histidine rich carboxyl terminus 1	6.64	up	0.000444	0.0000309
HS1BP3	HCLS1 binding protein 3	3.13	up	0.000940	0.0001042
HS2ST1	heparan sulfate 2-O-sulfotransferase 1	1.59	up	0.002067	0.0003306
HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	1.66	up	0.002064	0.0003294
HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	1.66	up	0.000698	0.0000652
HSH2D	hematopoietic SH2 domain containing	1.96	up	0.000763	0.0000751
HSPA4L	heat shock 70kDa protein 4-like	1.65	up	0.000660	0.0000600
HSPB8	heat shock 22kDa protein 8	2.76	up	0.000436	0.0000298
HSPG2	heparan sulfate proteoglycan 2	1.93	up	0.000061	0.0000009
HTR1D	5-hydroxytryptamine (serotonin) receptor 1D, G protein-coupled	3.03	up	0.003624	0.0007246

HYAL1	hyaluronoglucosaminidase 1	2.37	up	0.000102	0.0000022
ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	1.59	up	0.000127	0.0000035
IER3	immediate early response 3	1.81	up	0.000061	0.0000008
IER5	immediate early response 5	1.99	up	0.000116	0.0000029
IFFO1	intermediate filament family orphan 1	3.28	up	0.000806	0.0000814
IFI27L1	interferon, alpha-inducible protein 27-like 1	1.75	up	0.000294	0.0000157
IFI27L2	interferon, alpha-inducible protein 27-like 2	1.79	up	0.001741	0.0002594
IFI6	interferon, alpha-inducible protein 6	2.10	up	0.000135	0.0000039
IFIH1	interferon induced with helicase C domain 1	1.78	up	0.000521	0.0000415
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	1.73	up	0.001111	0.0001335
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	2.20	up	0.001114	0.0001340
IFITM2	interferon induced transmembrane protein 2	1.63	up	0.000448	0.0000314
IFITM3	interferon induced transmembrane protein 3	1.59	up	0.001362	0.0001808
IFNGR1	interferon gamma receptor 1	1.62	up	0.001495	0.0002075
IFRD1	interferon-related developmental regulator 1	2.48	up	0.000102	0.0000021
IGF2	insulin-like growth factor 2 (somatomedin A)	2.45	up	0.000229	0.0000100
IGFBP6	insulin-like growth factor binding protein 6	1.71	up	0.000380	0.0000239
IGFL2	IGF-like family member 2	2.63	up	0.000041	0.0000003
IKBIP	IKBKB interacting protein	3.01	up	0.000441	0.0000305
IKZF5	IKAROS family zinc finger 5 (Pegasus)	1.61	up	0.004900	0.0011093
IL10RA	interleukin 10 receptor, alpha	2.73	up	0.000041	0.0000003
IL10RB	interleukin 10 receptor, beta	1.64	up	0.001421	0.0001935
IL11	interleukin 11	3.82	up	0.000150	0.0000047
IL17RB	interleukin 17 receptor B	1.73	up	0.000033	0.0000002
IL1RAP	interleukin 1 receptor accessory protein	1.83	up	0.001662	0.0002426
IL1RN	interleukin 1 receptor antagonist	5.05	up	0.000006	0.0000000
IL20RB	interleukin 20 receptor beta	1.99	up	0.002198	0.0003577
IL22RA1	interleukin 22 receptor, alpha 1	1.83	up	0.002572	0.0004468
IL4R	interleukin 4 receptor	1.59	up	0.001378	0.0001844

IL7	interleukin 7	1.98	up	0.003285	0.0006343
ILK	integrin-linked kinase	1.53	up	0.000044	0.0000004
INHBB	inhibin, beta B	2.68	up	0.000638	0.0000570
INPP1	inositol polyphosphate-1-phosphatase	2.13	up	0.001705	0.0002515
INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	1.70	up	0.001133	0.0001377
INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	2.58	up	0.000295	0.0000159
INTS7	integrator complex subunit 7	1.76	up	0.002062	0.0003287
IPP	intracisternal A particle-promoted polypeptide	1.54	up	0.000589	0.0000505
IRF7	interferon regulatory factor 7	2.89	up	0.000106	0.0000025
IRF9	interferon regulatory factor 9	2.08	up	0.001200	0.0001494
IRS2	insulin receptor substrate 2	1.52	up	0.002055	0.0003266
IRX3	iroquois homeobox 3	1.82	up	0.002468	0.0004197
ISCU	iron-sulfur cluster assembly enzyme	1.55	up	0.003901	0.0008022
ISG15	ISG15 ubiquitin-like modifier	2.46	up	0.000053	0.0000006
ISG20	interferon stimulated exonuclease gene 20kDa	2.81	up	0.000226	0.0000096
ITGA6	integrin, alpha 6	1.95	up	0.001875	0.0002895
ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	3.23	up	0.000203	0.0000079
ITGB1BP1	integrin beta 1 binding protein 1	1.55	up	0.000121	0.0000032
ITPKA	inositol-trisphosphate 3-kinase A	1.79	up	0.000164	0.0000054
ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein	1.71	up	0.000482	0.0000360
JAG1	jagged 1	1.88	up	0.000191	0.0000071
JUN	jun proto-oncogene	2.35	up	0.001594	0.0002282
JUNB	jun B proto-oncogene	1.96	up	0.000120	0.0000031
JUP	junction plakoglobin	1.94	up	0.000060	0.0000008
KALRN	kalirin, RhoGEF kinase	1.86	up	0.003827	0.0007780
KANK3	KN motif and ankyrin repeat domains 3	2.26	up	0.000217	0.0000089
KAT2B	K(lysine) acetyltransferase 2B	2.60	up	0.000463	0.0000338
KATNAL1	katanin p60 subunit A-like 1	1.58	up	0.002746	0.0004897
KCNE1L	KCNE1-like	4.32	up	0.000242	0.0000108
KCNK1	potassium channel, subfamily K, member 1	1.68	up	0.001102	0.0001317

KCNK6	potassium channel, subfamily K, member 6	1.57	up	0.000487	0.0000368
KCNK7	potassium channel, subfamily K, member 7	1.99	up	0.000741	0.0000714
KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	1.60	up	0.001204	0.0001507
KCTD21	potassium channel tetramerization domain containing 21	1.78	up	0.000621	0.0000544
KDSR	3-ketodihydrosphingosine reductase	1.72	up	0.000967	0.0001088
KIAA0040	KIAA0040	1.70	up	0.000159	0.0000050
KIAA0247	KIAA0247	2.95	up	0.000047	0.0000005
KIAA1217	KIAA1217	2.16	up	0.002558	0.0004431
KIAA1324	KIAA1324	4.86	up	0.000452	0.0000321
KIAA1683	KIAA1683	1.57	up	0.002958	0.0005429
KIAA1715	KIAA1715	1.74	up	0.004309	0.0009298
KIF16B	kinesin family member 16B	2.49	up	0.000831	0.0000846
KIF1B	kinesin family member 1B	1.84	up	0.001768	0.0002653
KIF3C	kinesin family member 3C	1.90	up	0.003463	0.0006802
KIFAP3	kinesin-associated protein 3	1.81	up	0.000204	0.0000080
KIRREL2	kin of IRRE like 2 (Drosophila)	1.81	up	0.001395	0.0001874
KLF2	Kruppel-like factor 2	2.10	up	0.000060	0.0000008
KLHL30	kelch-like family member 30	4.31	up	0.000454	0.0000323
KLHL36	kelch-like family member 36	1.54	up	0.003669	0.0007367
KLK1	kallikrein 1	1.74	up	0.003029	0.0005635
KRT13	keratin 13	2.11	up	0.004048	0.0008482
KRT15	keratin 15	3.21	up	0.000054	0.0000006
KRT18	keratin 18	1.64	up	0.001816	0.0002764
KRT18P55	keratin 18 pseudogene 55	1.63	up	0.002241	0.0003673
KRT19P2	keratin 19 pseudogene 2	1.54	up	0.004377	0.0009495
KRT32	keratin 32	1.84	up	0.000249	0.0000114
KRT34	keratin 34	2.61	up	0.000106	0.0000024
KRT8	keratin 8	1.60	up	0.001055	0.0001238
KRT80	keratin 80	2.44	up	0.000633	0.0000563

KRT83	keratin 83	1.51	up	0.000416	0.0000276
KRT9	keratin 9	2.76	up	0.001153	0.0001410
KRTAP10-12	keratin associated protein 10-12	1.65	up	0.004741	0.0010625
KRTAP2-3	keratin associated protein 2-3	2.47	up	0.000341	0.0000202
LAGE3	L antigen family, member 3	1.51	up	0.001899	0.0002945
LAMA3	laminin, alpha 3	6.09	up	0.000014	0.0000000
LAMB2	laminin, beta 2 (laminin S)	1.67	up	0.000228	0.0000098
LAMB3	laminin, beta 3	3.65	up	0.000042	0.0000004
LAMC2	laminin, gamma 2	2.36	up	0.000090	0.0000017
LAMP2	lysosomal-associated membrane protein 2	1.52	up	0.002044	0.0003240
LAMP3	lysosomal-associated membrane protein 3	4.24	up	0.000027	0.0000001
LAT2	linker for activation of T cells family, member 2	3.81	up	0.000041	0.0000003
LATS2	large tumor suppressor kinase 2	1.82	up	0.002299	0.0003798
LCAT	lecithin-cholesterol acyltransferase	1.75	up	0.002838	0.0005142
LCE1C	late cornified envelope 1C	4.99	up	0.002361	0.0003945
LCE1E	late cornified envelope 1E	3.03	up	0.002804	0.0005070
LCK	lymphocyte-specific protein tyrosine kinase	4.76	up	0.001559	0.0002209
LETM2	leucine zipper-EF-hand containing transmembrane protein 2	2.24	up	0.000387	0.0000246
LGALS7	lectin, galactoside-binding, soluble, 7	2.50	up	0.000022	0.0000001
LGALS8	lectin, galactoside-binding, soluble, 8	1.73	up	0.002972	0.0005467
LGALS9C	lectin, galactoside-binding, soluble, 9C	1.50	up	0.000492	0.0000375
LHX2	LIM homeobox 2	2.17	up	0.000031	0.0000002
LIMA1	LIM domain and actin binding 1	1.68	up	0.000765	0.0000756
LIMCH1	LIM and calponin homology domains 1	1.78	up	0.002943	0.0005393
LIMS2	LIM and senescent cell antigen-like domains 2	2.20	up	0.000528	0.0000424
LIN7A	lin-7 homolog A (C. elegans)	2.30	up	0.001048	0.0001224
LINC00337	long intergenic non-protein coding RNA 337	2.30	up	0.000180	0.0000064
LINC00618	long intergenic non-protein coding RNA 618	1.61	up	0.000103	0.0000023
LINC00857	long intergenic non-protein coding RNA 857	1.66	up	0.001314	0.0001718
LINC00937	long intergenic non-protein coding RNA 937	1.92	up	0.000844	0.0000865

LINC01137	long intergenic non-protein coding RNA 1137	2.46	up	0.001668	0.0002437
LINC01270	long intergenic non-protein coding RNA 1270	1.77	up	0.000432	0.0000295
LIPH	lipase, member H	1.94	up	0.000126	0.0000034
LNX1	ligand of numb-protein X 1, E3 ubiquitin protein ligase	4.16	up	0.004724	0.0010572
LOC101928841	collagen alpha-1(II) chain-like	9.19	up	0.000124	0.0000033
LOC388242	coiled-coil domain containing 101 pseudogene	1.72	up	0.003361	0.0006546
LOC389834	ankyrin repeat domain 57 pseudogene	2.88	up	0.001264	0.0001619
LOC645166	lymphocyte-specific protein 1 pseudogene	2.34	up	0.000063	0.0000009
LOC645638	WDNM1-like pseudogene	6.39	up	0.000368	0.0000229
LOXL2	lysyl oxidase-like 2	1.59	up	0.000106	0.0000025
LOXL4	lysyl oxidase-like 4	2.04	up	0.000887	0.0000947
LRG1	leucine-rich alpha-2-glycoprotein 1	2.19	up	0.000028	0.0000001
LRP10	low density lipoprotein receptor-related protein 10	2.36	up	0.000347	0.0000208
LRRC32	leucine rich repeat containing 32	2.84	up	0.002299	0.0003798
LRRC8C	leucine rich repeat containing 8 family, member C	1.51	up	0.003962	0.0008222
LSMEM1	leucine-rich single-pass membrane protein 1	3.01	up	0.000113	0.0000027
LY6D	lymphocyte antigen 6 complex, locus D	2.81	up	0.000150	0.0000046
LY6G6C	lymphocyte antigen 6 complex, locus G6C	2.33	up	0.001775	0.0002672
LY6K	lymphocyte antigen 6 complex, locus K	1.73	up	0.000127	0.0000035
LYNX1	Ly6/neurotoxin 1	2.16	up	0.000590	0.0000506
LYPD3	LY6/PLAUR domain containing 3	2.77	up	0.002569	0.0004459
LYPD5	LY6/PLAUR domain containing 5	3.43	up	0.000041	0.0000003
LZTS1	leucine zipper, putative tumor suppressor 1	2.23	up	0.001205	0.0001508
MACC1	metastasis associated in colon cancer 1	3.83	up	0.000907	0.0000977
MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	4.55	up	0.003308	0.0006410
MAFB	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B	3.43	up	0.000641	0.0000576
MAFF	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F	2.13	up	0.000089	0.0000017
MAMDC4	MAM domain containing 4	1.73	up	0.001763	0.0002644

MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	1.91	up	0.000073	0.0000012
MAP1LC3BP1	microtubule-associated protein 1 light chain 3 beta pseudogene 1	1.73	up	0.000380	0.0000239
MAP2	microtubule-associated protein 2	2.18	up	0.000043	0.0000004
MAP3K12	mitogen-activated protein kinase kinase kinase 12	2.15	up	0.000205	0.0000081
MAP3K13	mitogen-activated protein kinase kinase kinase 13	2.10	up	0.000294	0.0000157
MAP3K9	mitogen-activated protein kinase kinase kinase 9	1.64	up	0.000855	0.0000894
MAPK11	mitogen-activated protein kinase 11	1.80	up	0.003355	0.0006529
MAPK13	mitogen-activated protein kinase 13	1.79	up	0.000419	0.0000280
MAPKAP1	mitogen-activated protein kinase associated protein 1	1.70	up	0.000136	0.0000040
MAPRE2	microtubule-associated protein, RP/EB family, member 2	1.72	up	0.000135	0.0000039
MARCH9	membrane-associated ring finger (C3HC4) 9	1.57	up	0.000041	0.0000003
MARVELD3	MARVEL domain containing 3	1.53	up	0.000120	0.0000031
MASTL	microtubule associated serine/threonine kinase-like	1.55	up	0.000170	0.0000058
MATN2	matrilin 2	1.85	up	0.004768	0.0010700
MBD1	methyl-CpG binding domain protein 1	1.57	up	0.000566	0.0000475
MCF2L-AS1	MCF2L antisense RNA 1	1.97	up	0.000041	0.0000003
MDK	midkine (neurite growth-promoting factor 2)	1.67	up	0.000163	0.0000053
MDM2	MDM2 oncogene, E3 ubiquitin protein ligase	2.30	up	0.001836	0.0002810
MED20	mediator complex subunit 20	1.52	up	0.000858	0.0000898
MEF2BNB	MEF2B neighbor	1.71	up	0.003962	0.0008220
MEIG1	meiosis/spermiogenesis associated 1	1.54	up	0.004258	0.0009130
MFGE8	milk fat globule-EGF factor 8 protein	1.80	up	0.001756	0.0002631
MFSD4	major facilitator superfamily domain containing 4	3.13	up	0.004039	0.0008449
MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	2.45	up	0.000474	0.0000348
MGLL	monoglyceride lipase	2.18	up	0.000228	0.0000098
MGST3	microsomal glutathione S-transferase 3	1.50	up	0.003199	0.0006100
MICALL2	MICAL-like 2	1.50	up	0.003076	0.0005754
MID2	midline 2	1.80	up	0.001396	0.0001881

MIEF2	mitochondrial elongation factor 2	1.63	up	0.000304	0.0000166
MIG7	mig-7	11.78	up	0.000291	0.0000154
MIR31HG	MIR31 host gene (non-protein coding)	4.95	up	0.000204	0.0000080
MITF	microphthalmia-associated transcription factor	1.75	up	0.002707	0.0004801
MKRN1	makorin ring finger protein 1	2.11	up	0.000812	0.0000823
MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	1.64	up	0.001480	0.0002046
MLXIP	MLX interacting protein	1.62	up	0.003728	0.0007521
MNX1	motor neuron and pancreas homeobox 1	1.75	up	0.000686	0.0000635
MOAP1	modulator of apoptosis 1	1.55	up	0.000613	0.0000532
MORC3	MORC family CW-type zinc finger 3	1.52	up	0.000319	0.0000180
MORN4	MORN repeat containing 4	2.50	up	0.000160	0.0000051
MOSPD1	motile sperm domain containing 1	1.60	up	0.003852	0.0007864
MPC1	mitochondrial pyruvate carrier 1	1.99	up	0.000043	0.0000004
MPC2	mitochondrial pyruvate carrier 2	1.74	up	0.000028	0.0000001
MPND	MPN domain containing	1.55	up	0.000598	0.0000515
MPPE1	metallophosphoesterase 1	2.36	up	0.001290	0.0001669
MPRIP	myosin phosphatase Rho interacting protein	2.98	up	0.000782	0.0000779
MPZL2	myelin protein zero-like 2	2.03	up	0.000018	0.0000000
MPZL3	myelin protein zero-like 3	1.79	up	0.000514	0.0000407
MR1	major histocompatibility complex, class I-related	2.66	up	0.000450	0.0000319
MRC2	mannose receptor, C type 2	1.77	up	0.000396	0.0000256
MROH1	maestro heat-like repeat family member 1	2.64	up	0.000266	0.0000131
MSANTD2	Myb/SANT-like DNA-binding domain containing 2	1.57	up	0.002541	0.0004390
MSI2	musashi RNA-binding protein 2	2.16	up	0.000503	0.0000391
MT1B	metallothionein 1B	1.53	up	0.000483	0.0000362
MT2A	metallothionein 2A	1.73	up	0.002289	0.0003772
MUC1	mucin 1, cell surface associated	1.51	up	0.000854	0.0000890
MXD1	MAX dimerization protein 1	2.27	up	0.000116	0.0000029
MYBL1	v-myb avian myeloblastosis viral oncogene homolog-like 1	2.38	up	0.000447	0.0000313

MYBPC3	myosin binding protein C, cardiac	1.59	up	0.000676	0.0000622
MYEOV	myeloma overexpressed	2.16	up	0.000102	0.0000022
MYO1A	myosin IA	6.52	up	0.000047	0.0000005
MYO1E	myosin IE	1.95	up	0.000043	0.0000004
MYO6	myosin VI	1.65	up	0.000169	0.0000058
MYO7A	myosin VIIA	2.13	up	0.000535	0.0000434
MYOM2	myomesin 2	1.77	up	0.000866	0.0000912
MYZAP	myocardial zonula adherens protein	1.55	up	0.000899	0.0000966
N4BP2L2	NEDD4 binding protein 2-like 2	2.81	up	0.000098	0.0000020
NABP2	nucleic acid binding protein 2	1.55	up	0.001773	0.0002663
NAP1L5	nucleosome assembly protein 1-like 5	2.20	up	0.000917	0.0000995
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	1.58	up	0.002726	0.0004847
NAV3	neuron navigator 3	1.74	up	0.001924	0.0003002
NCAPH2	non-SMC condensin II complex, subunit H2	1.71	up	0.000079	0.0000013
NCEH1	neutral cholesterol ester hydrolase 1	2.39	up	0.000041	0.0000003
NCOA7	nuclear receptor coactivator 7	1.59	up	0.000135	0.0000039
NDOR1	NADPH dependent diflavin oxidoreductase 1	1.84	up	0.000445	0.0000310
NDRG1	N-myc downstream regulated 1	3.09	up	0.000014	0.0000000
NDRG4	NDRG family member 4	2.06	up	0.000097	0.0000020
NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	1.54	up	0.000022	0.0000001
NEK11	NIMA-related kinase 11	1.63	up	0.000958	0.0001072
NES	nestin	1.73	up	0.000875	0.0000926
NEU1	sialidase 1 (lysosomal sialidase)	2.09	up	0.000407	0.0000267
NEURL1B	neuralized E3 ubiquitin protein ligase 1B	1.83	up	0.000180	0.0000064
NGEF	neuronal guanine nucleotide exchange factor	1.74	up	0.000037	0.0000003
NGFR	nerve growth factor receptor	2.35	up	0.000077	0.0000013
NINJ1	ninjurin 1	2.13	up	0.000204	0.0000079
NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	1.56	up	0.002996	0.0005545
NIPAL3	NIPA-like domain containing 3	2.72	up	0.000211	0.0000086

NKX3-1	NK3 homeobox 1	1.99	up	0.000082	0.0000015
NLRP1	NLR family, pyrin domain containing 1	2.81	up	0.000364	0.0000225
NMB	neuromedin B	1.68	up	0.004102	0.0008645
NOL4L	nucleolar protein 4-like	5.77	up	0.004789	0.0010769
NOSTRIN	nitric oxide synthase trafficking	1.61	up	0.001661	0.0002419
NOTCH3	notch 3	1.86	up	0.001863	0.0002869
NOVA2	neuro-oncological ventral antigen 2	2.16	up	0.000534	0.0000432
NPNT	nephronectin	1.57	up	0.001929	0.0003012
NR1D1	nuclear receptor subfamily 1, group D, member 1	1.93	up	0.000208	0.0000083
NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	1.84	up	0.000135	0.0000039
NR4A3	nuclear receptor subfamily 4, group A, member 3	2.67	up	0.002550	0.0004411
NRP1	neuropilin 1	5.17	up	0.000417	0.0000278
NT5E	5'-nucleotidase, ecto (CD73)	1.57	up	0.000750	0.0000730
NTN4	netrin 4	1.83	up	0.002521	0.0004335
NTPCR	nucleoside-triphosphatase, cancer-related	1.72	up	0.000132	0.0000037
NUAK2	NUAK family, SNF1-like kinase, 2	2.46	up	0.000136	0.0000040
NUCB2	nucleobindin 2	1.62	up	0.000115	0.0000028
NUDT16L1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	1.68	up	0.000772	0.0000764
OASL	2'-5'-oligoadenylate synthetase-like	3.55	up	0.000044	0.0000004
OCLN	occludin	1.85	up	0.000537	0.0000436
ODF2	outer dense fiber of sperm tails 2	1.67	up	0.001919	0.0002985
OLFM1	olfactomedin 1	1.77	up	0.001576	0.0002235
OPTN	optineurin	1.97	up	0.000301	0.0000165
ORAI3	ORAI calcium release-activated calcium modulator 3	1.62	up	0.001143	0.0001395
OSBPL2	oxysterol binding protein-like 2	1.81	up	0.000253	0.0000119
OTUD1	OTU deubiquitinase 1	1.51	up	0.002988	0.0005515
OVOL1	ovo-like zinc finger 1	1.80	up	0.000281	0.0000145
P2RY2	purinergic receptor P2Y, G-protein coupled, 2	2.20	up	0.000136	0.0000040

P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	1.72	up	0.000826	0.0000840
PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	2.75	up	0.004097	0.0008619
PAPD5	PAP associated domain containing 5	4.56	up	0.002172	0.0003523
PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	1.65	up	0.001399	0.0001888
PARD6A	par-6 family cell polarity regulator alpha	2.40	up	0.000103	0.0000023
PARD6B	par-6 family cell polarity regulator beta	1.69	up	0.000900	0.0000968
PC	pyruvate carboxylase	1.52	up	0.000621	0.0000546
PCDH1	protocadherin 1	2.92	up	0.000074	0.0000012
PCGF5	polycomb group ring finger 5	1.65	up	0.002226	0.0003638
PCNA	proliferating cell nuclear antigen	1.78	up	0.000136	0.0000040
PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	1.87	up	0.001376	0.0001837
PDE2A	phosphodiesterase 2A, cGMP-stimulated	1.52	up	0.000515	0.0000408
PDE6G	phosphodiesterase 6G, cGMP-specific, rod, gamma	2.85	up	0.000159	0.0000051
PDGFB	platelet-derived growth factor beta polypeptide	1.50	up	0.000619	0.0000540
PDLIM3	PDZ and LIM domain 3	2.49	up	0.000028	0.0000001
PDLIM7	PDZ and LIM domain 7 (enigma)	2.38	up	0.000022	0.0000001
PDZD11	PDZ domain containing 11	1.68	up	0.000728	0.0000695
PEAR1	platelet endothelial aggregation receptor 1	2.41	up	0.000051	0.0000006
PERP	PERP, TP53 apoptosis effector	1.76	up	0.000531	0.0000428
PGBD2	piggyBac transposable element derived 2	1.72	up	0.001106	0.0001322
PGF	placental growth factor	2.13	up	0.000621	0.0000544
PGPEP1	pyroglutamyl-peptidase I	2.19	up	0.000206	0.0000082
PHLDA3	pleckstrin homology-like domain, family A, member 3	3.05	up	0.000115	0.0000028
PHPT1	phosphohistidine phosphatase 1	2.14	up	0.000093	0.0000018
PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein	3.39	up	0.002348	0.0003910
PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	1.75	up	0.000016	0.0000000
PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	1.56	up	0.000389	0.0000249
PIDD1	p53-induced death domain protein 1	2.13	up	0.000670	0.0000615
PIM1	pim-1 oncogene	1.93	up	0.001820	0.0002772

PINK1	PTEN induced putative kinase 1	1.95	up	0.000177	0.0000062
PLA2G10	phospholipase A2, group X	1.81	up	0.000673	0.0000619
PLA2G15	phospholipase A2, group XV	1.51	up	0.000743	0.0000722
PLA2G16	phospholipase A2, group XVI	1.69	up	0.000726	0.0000692
PLA2G4D	phospholipase A2, group IVD (cytosolic)	5.17	up	0.000195	0.0000074
PLAT	plasminogen activator, tissue	1.74	up	0.000094	0.0000019
PLAU	plasminogen activator, urokinase	4.51	up	0.000000	0.0000000
PLAUR	plasminogen activator, urokinase receptor	2.17	up	0.000033	0.0000002
PLCL2	phospholipase C-like 2	3.38	up	0.002680	0.0004735
PLCXD1	phosphatidylinositol-specific phospholipase C, X domain containing 1	1.52	up	0.002943	0.0005395
PLEC	plectin	1.66	up	0.000894	0.0000955
PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1	1.73	up	0.001210	0.0001516
PLEKHF1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	1.74	up	0.001281	0.0001655
PLIN2	perilipin 2	1.72	up	0.000663	0.0000604
PLK2	polo-like kinase 2	2.17	up	0.000054	0.0000006
PLK3	polo-like kinase 3	3.02	up	0.000163	0.0000053
PLSCR4	phospholipid scramblase 4	2.14	up	0.002517	0.0004321
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	2.29	up	0.000166	0.0000055
PMEL	premelanosome protein	2.03	up	0.002410	0.0004050
PML	promyelocytic leukemia	1.59	up	0.000119	0.0000031
PNPLA8	patatin-like phospholipase domain containing 8	1.89	up	0.000577	0.0000489
PNRC1	proline-rich nuclear receptor coactivator 1	1.58	up	0.003049	0.0005676
POLD4	polymerase (DNA-directed), delta 4, accessory subunit	1.59	up	0.000317	0.0000178
POLH	polymerase (DNA directed), eta	1.78	up	0.000219	0.0000092
PPAP2B	phosphatidic acid phosphatase type 2B	1.79	up	0.001872	0.0002889
PPL	periplakin	1.66	up	0.002804	0.0005067
PPM1A	protein phosphatase, Mg2+/Mn2+ dependent, 1A	3.10	up	0.002462	0.0004178
PPM1D	protein phosphatase, Mg2+/Mn2+ dependent, 1D	3.00	up	0.000020	0.0000000

PPM1K	protein phosphatase, Mg2+/Mn2+ dependent, 1K	1.89	up	0.002594	0.0004523
PPM1M	protein phosphatase, Mg2+/Mn2+ dependent, 1M	1.64	up	0.003280	0.0006328
PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	2.13	up	0.000183	0.0000066
PPP1R15A	protein phosphatase 1, regulatory subunit 15A	1.86	up	0.000329	0.0000190
PPP2R5B	protein phosphatase 2, regulatory subunit B', beta	1.70	up	0.002214	0.0003609
PPT2	palmitoyl-protein thioesterase 2	1.72	up	0.000548	0.0000452
PPY	pancreatic polypeptide	2.07	up	0.001876	0.0002898
PRADC1	protease-associated domain containing 1	1.89	up	0.000250	0.0000116
PRDM1	PR domain containing 1, with ZNF domain	6.10	up	0.001594	0.0002282
PRH2	proline-rich protein HaeIII subfamily 2	1.67	up	0.001504	0.0002100
PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	1.93	up	0.000281	0.0000145
PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	1.76	up	0.000167	0.0000056
PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha	1.57	up	0.001592	0.0002269
PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	1.55	up	0.004157	0.0008810
PRKCH	protein kinase C, eta	1.95	up	0.000184	0.0000067
PROCR	protein C receptor, endothelial	2.34	up	0.000080	0.0000014
PRODH	proline dehydrogenase (oxidase) 1	1.95	up	0.000208	0.0000084
PROM2	prominin 2	2.50	up	0.000108	0.0000025
PRR15L	proline rich 15-like	2.10	up	0.000185	0.0000067
PRRG1	proline rich Gla (G-carboxyglutamic acid) 1	2.74	up	0.000091	0.0000017
PRRG2	proline rich Gla (G-carboxyglutamic acid) 2	1.79	up	0.002168	0.0003511
PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	1.55	up	0.000019	0.0000000
PRSS2	protease, serine, 2 (trypsin 2)	2.27	up	0.000230	0.0000101
PRSS3	protease, serine, 3	2.11	up	0.000102	0.0000021
PRSS30P	protease, serine, 30, pseudogene	1.66	up	0.000400	0.0000260
PRSS35	protease, serine, 35	5.14	up	0.003191	0.0006066
PRSS56	protease, serine, 56	3.72	up	0.000304	0.0000166
PRSS57	protease, serine, 57	2.06	up	0.002788	0.0005022
PRSS8	protease, serine, 8	1.72	up	0.000463	0.0000336
PSAPL1	prosaposin-like 1 (gene/pseudogene)	4.09	up	0.000336	0.0000198

PSMC3IP	PSMC3 interacting protein	1.64	up	0.000507	0.0000397
PSORS1C1	psoriasis susceptibility 1 candidate 1	1.86	up	0.000135	0.0000039
PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	1.96	up	0.000211	0.0000086
PTAFR	platelet-activating factor receptor	4.27	up	0.000256	0.0000123
PTBP3	polypyrimidine tract binding protein 3	1.57	up	0.000102	0.0000022
PTPRU	protein tyrosine phosphatase, receptor type, U	1.65	up	0.000250	0.0000116
PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	2.92	up	0.000168	0.0000057
PVRL4	poliovirus receptor-related 4	4.45	up	0.000102	0.0000022
PXK	PX domain containing serine/threonine kinase	1.75	up	0.004190	0.0008925
PYCARDOS	PYCARD opposite strand	3.25	up	0.000482	0.0000361
RAB15	RAB15, member RAS oncogene family	2.02	up	0.000568	0.0000477
RAB27A	RAB27A, member RAS oncogene family	2.29	up	0.000234	0.0000103
RAB3A	RAB3A, member RAS oncogene family	1.73	up	0.001791	0.0002707
RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	1.92	up	0.001194	0.0001478
RAD1	RAD1 homolog (S. pombe)	1.90	up	0.000335	0.0000197
RAD51C	RAD51 paralog C	1.52	up	0.000094	0.0000019
RAET1E	retinoic acid early transcript 1E	2.40	up	0.001378	0.0001840
RASA4	RAS p21 protein activator 4	1.57	up	0.003892	0.0007988
RASA4B	RAS p21 protein activator 4B	2.09	up	0.000563	0.0000471
RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	2.43	up	0.000060	0.0000008
RASL10A	RAS-like, family 10, member A	2.11	up	0.000227	0.0000097
RASSF5	Ras association (RalGDS/AF-6) domain family member 5	1.83	up	0.000736	0.0000705
RBM18	RNA binding motif protein 18	1.66	up	0.000917	0.0000996
RBM4B	RNA binding motif protein 4B	1.53	up	0.002623	0.0004604
RBPMS2	RNA binding protein with multiple splicing 2	1.56	up	0.002064	0.0003295
RDX	radixin	2.39	up	0.001553	0.0002199
RECQL5	RecQ protein-like 5	2.03	up	0.000957	0.0001070
REEP2	receptor accessory protein 2	1.98	up	0.000229	0.0000100
RELL1	RELT-like 1	1.75	up	0.000852	0.0000887

RELT	RELT tumor necrosis factor receptor	1.66	up	0.001402	0.0001899
RFTN1	raftlin, lipid raft linker 1	1.96	up	0.001996	0.0003146
RFX5	regulatory factor X, 5 (influences HLA class II expression)	1.96	up	0.000102	0.0000022
RGAG4	retrotransposon gag domain containing 4	2.18	up	0.000431	0.0000292
RGCC	regulator of cell cycle	1.82	up	0.000361	0.0000220
RGS20	regulator of G-protein signaling 20	1.88	up	0.000275	0.0000138
RHBDD2	rhomboid domain containing 2	1.91	up	0.001415	0.0001922
RHBDF1	rhomboid 5 homolog 1 (Drosophila)	1.57	up	0.001741	0.0002592
RHOBTB2	Rho-related BTB domain containing 2	1.55	up	0.002750	0.0004910
RHOD	ras homolog family member D	2.05	up	0.000061	0.0000009
RHOF	ras homolog family member F (in filopodia)	1.66	up	0.001819	0.0002771
RIMBP3	RIMS binding protein 3	2.20	up	0.001342	0.0001769
RIN1	Ras and Rab interactor 1	1.64	up	0.000770	0.0000762
RINL	Ras and Rab interactor-like	2.64	up	0.000342	0.0000204
RIOK3	RIO kinase 3	2.67	up	0.000040	0.0000003
RMRP	RNA component of mitochondrial RNA processing endoribonuclease	2.50	up	0.000082	0.0000015
RNASEH2A	ribonuclease H2, subunit A	1.62	up	0.000209	0.0000084
RND3	Rho family GTPase 3	1.79	up	0.000209	0.0000084
RNF14	ring finger protein 14	1.70	up	0.000328	0.0000188
RNF146	ring finger protein 146	1.52	up	0.000421	0.0000282
RNF182	ring finger protein 182	2.36	up	0.000191	0.0000071
RNF38	ring finger protein 38	1.52	up	0.003579	0.0007128
RNU2-1	RNA, U2 small nuclear 1	2.08	up	0.000487	0.0000368
RPL23AP7	ribosomal protein L23a pseudogene 7	1.91	up	0.000498	0.0000384
RPL27A	ribosomal protein L27a	1.55	up	0.001748	0.0002612
RPS27L	ribosomal protein S27-like	2.60	up	0.000279	0.0000142
RRAD	Ras-related associated with diabetes	2.34	up	0.001755	0.0002628
RRAGC	Ras-related GTP binding C	1.61	up	0.000949	0.0001053
RRM1	ribonucleotide reductase M1	1.54	up	0.000884	0.0000943

RSRP1	arginine/serine-rich protein 1	2.43	up	0.000068	0.0000010
RUFY2	RUN and FYVE domain containing 2	2.77	up	0.000907	0.0000978
RUNX1	runt-related transcription factor 1	3.60	up	0.000219	0.0000092
RUSC1	RUN and SH3 domain containing 1	1.53	up	0.000079	0.0000014
S100A11	S100 calcium binding protein A11	2.05	up	0.000024	0.0000001
S100A13	S100 calcium binding protein A13	1.56	up	0.000449	0.0000316
S100A16	S100 calcium binding protein A16	1.76	up	0.000047	0.0000005
S100A2	S100 calcium binding protein A2	2.71	up	0.000298	0.0000161
S100A3	S100 calcium binding protein A3	1.95	up	0.000296	0.0000159
S100A6	S100 calcium binding protein A6	1.97	up	0.004309	0.0009295
SAMD4A	sterile alpha motif domain containing 4A	1.66	up	0.000493	0.0000376
SAMD5	sterile alpha motif domain containing 5	1.78	up	0.000136	0.0000040
SAP18	Sin3A-associated protein, 18kDa	1.55	up	0.002441	0.0004136
SAR1A	secretion associated, Ras related GTPase 1A	1.58	up	0.000030	0.0000002
SAT1	spermidine/spermine N1-acetyltransferase 1	2.49	up	0.000060	0.0000008
SBDS	Shwachman-Bodian-Diamond syndrome	1.54	up	0.000878	0.0000932
SBDSP1	Shwachman-Bodian-Diamond syndrome pseudogene 1	1.72	up	0.001029	0.0001193
SBSN	suprabasin	2.41	up	0.000398	0.0000258
SCPEP1	serine carboxypeptidase 1	1.73	up	0.000379	0.0000238
SDC1	syndecan 1	1.57	up	0.004621	0.0010248
SDC4	syndecan 4	2.53	up	0.000184	0.0000067
SDE2	SDE2 telomere maintenance homolog (S. pombe)	2.13	up	0.000383	0.0000242
SEC24D	SEC24 family member D	1.54	up	0.001067	0.0001258
SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	1.66	up	0.001052	0.0001230
SECTM1	secreted and transmembrane 1	1.53	up	0.003922	0.0008082
SELK	selenoprotein K	1.58	up	0.000639	0.0000572
SELM	selenoprotein M	1.51	up	0.000506	0.0000396
SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	2.71	up	0.000097	0.0000020

SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	2.28	up	0.000074	0.0000012
SEPP1	selenoprotein P, plasma, 1	1.57	up	0.003598	0.0007184
SEPT8	septin 8	1.92	up	0.004290	0.0009234
SERINC1	serine incorporator 1	1.67	up	0.000117	0.0000030
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	2.06	up	0.003266	0.0006294
SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	2.03	up	0.000039	0.0000003
SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	3.46	up	0.000094	0.0000019
SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	3.40	up	0.004304	0.0009278
SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1	2.78	up	0.000104	0.0000024
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	5.99	up	0.000074	0.0000012
SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	2.17	up	0.002965	0.0005449
SERTAD1	SERTA domain containing 1	2.88	up	0.000196	0.0000074
SESN1	sestrin 1	2.64	up	0.000097	0.0000020
SESN2	sestrin 2	1.97	up	0.000565	0.0000474
SFN	stratifin	4.48	up	0.003156	0.0005973
SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	1.63	up	0.002774	0.0004980
SGK1	serum/glucocorticoid regulated kinase 1	1.84	up	0.000254	0.0000120
SGMS2	sphingomyelin synthase 2	1.86	up	0.000664	0.0000607
SH2B3	SH2B adaptor protein 3	1.94	up	0.003968	0.0008241
SH2D3A	SH2 domain containing 3A	1.64	up	0.000129	0.0000036
SH3BGR	SH3 domain binding glutamate-rich protein	1.66	up	0.001463	0.0002011
SH3BGRL3	SH3 domain binding glutamate-rich protein like 3	1.51	up	0.000525	0.0000419
SHC1	SHC (Src homology 2 domain containing) transforming protein 1	1.74	up	0.000006	0.0000000
SHD	Src homology 2 domain containing transforming protein D	1.65	up	0.000067	0.0000010
SHROOM3	shroom family member 3	1.55	up	0.000536	0.0000434
SIRT2	sirtuin 2	1.82	up	0.000500	0.0000386
SIRT4	sirtuin 4	1.86	up	0.001402	0.0001899

SLAMF7	SLAM family member 7	3.34	up	0.000205	0.0000081
SLC10A3	solute carrier family 10, member 3	1.52	up	0.001600	0.0002293
SLC12A4	solute carrier family 12 (potassium/chloride transporter), member 4	2.69	up	0.000538	0.0000438
SLC25A42	solute carrier family 25, member 42	1.69	up	0.000489	0.0000371
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	1.57	up	0.001733	0.0002576
SLC29A3	solute carrier family 29 (equilibrative nucleoside transporter), member 3	1.54	up	0.001218	0.0001529
SLC30A1	solute carrier family 30 (zinc transporter), member 1	1.60	up	0.000171	0.0000059
SLC30A4	solute carrier family 30 (zinc transporter), member 4	1.83	up	0.000528	0.0000425
SLC31A2	solute carrier family 31 (copper transporter), member 2	1.72	up	0.000626	0.0000553
SLC44A3	solute carrier family 44, member 3	1.60	up	0.004672	0.0010432
SLC48A1	solute carrier family 48 (heme transporter), member 1	1.99	up	0.000088	0.0000016
SLC52A3	solute carrier family 52 (riboflavin transporter), member 3	1.87	up	0.000878	0.0000932
SLC6A6	solute carrier family 6 (neurotransmitter transporter), member 6	1.78	up	0.001432	0.0001955
SMIM14	small integral membrane protein 14	1.76	up	0.000069	0.0000011
SMIM22	small integral membrane protein 22	1.74	up	0.003676	0.0007386
SMIM5	small integral membrane protein 5	3.72	up	0.001520	0.0002136
SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal	4.18	up	0.000698	0.0000652
SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	1.59	up	0.003192	0.0006074
SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	2.02	up	0.001747	0.0002608
SNX2	sorting nexin 2	1.55	up	0.002525	0.0004351
SNX7	sorting nexin 7	1.68	up	0.000120	0.0000031
SOCS4	suppressor of cytokine signaling 4	1.61	up	0.000694	0.0000646
SOD2	superoxide dismutase 2, mitochondrial	1.56	up	0.000307	0.0000169
SORCS2	sortilin-related VPS10 domain containing receptor 2	4.71	up	0.000254	0.0000120
SPAG1	sperm associated antigen 1	2.85	up	0.001362	0.0001807
SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	1.58	up	0.000051	0.0000006
SPINT1	serine peptidase inhibitor, Kunitz type 1	1.53	up	0.001238	0.0001567
SPNS2	spinster homolog 2 (Drosophila)	3.21	up	0.000120	0.0000032

SPNS3	spinster homolog 3 (Drosophila)	2.37	up	0.001113	0.0001339
SPOCD1	SPOC domain containing 1	2.39	up	0.000864	0.0000908
SPP1	secreted phosphoprotein 1	3.00	up	0.000057	0.0000007
SPTSSA	serine palmitoyltransferase, small subunit A	1.55	up	0.002331	0.0003870
SQRDL	sulfide quinone reductase-like (yeast)	1.54	up	0.000185	0.0000068
SRP19	signal recognition particle 19kDa	1.97	up	0.001086	0.0001292
SSH2	slingshot protein phosphatase 2	2.51	up	0.000415	0.0000275
SSR1	signal sequence receptor, alpha	1.66	up	0.001924	0.0003001
ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	1.80	up	0.000727	0.0000694
STARD10	StAR-related lipid transfer (START) domain containing 10	1.67	up	0.001661	0.0002422
STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	1.57	up	0.000480	0.0000357
STAT4	signal transducer and activator of transcription 4	2.79	up	0.000294	0.0000158
STMN1	stathmin 1	4.04	up	0.003044	0.0005664
STOM	stomatin	2.08	up	0.000955	0.0001065
STPG1	sperm-tail PG-rich repeat containing 1	1.92	up	0.003962	0.0008227
STX11	syntaxin 11	2.20	up	0.001753	0.0002621
STYK1	serine/threonine/tyrosine kinase 1	2.27	up	0.000261	0.0000127
SULF2	sulfatase 2	3.35	up	0.000107	0.0000025
SULT2B1	sulfotransferase family, cytosolic, 2B, member 1	1.79	up	0.000228	0.0000099
SUN3	Sad1 and UNC84 domain containing 3	1.69	up	0.001199	0.0001491
SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	2.50	up	0.002014	0.0003185
SYK	spleen tyrosine kinase	1.66	up	0.000204	0.0000080
SYNE1	spectrin repeat containing, nuclear envelope 1	2.37	up	0.001269	0.0001630
SYNJ1	synaptojanin 1	1.99	up	0.000951	0.0001058
SYT17	synaptotagmin XVII	1.54	up	0.003056	0.0005698
SYTL3	synaptotagmin-like 3	1.52	up	0.002779	0.0004993
TAC3	tachykinin 3	5.10	up	0.000181	0.0000065
TACSTD2	tumor-associated calcium signal transducer 2	3.23	up	0.000277	0.0000140

TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	2.31	up	0.001140	0.0001389
TAPT1	transmembrane anterior posterior transformation 1	1.57	up	0.004519	0.0009929
TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	1.89	up	0.000288	0.0000150
TBC1D10A	TBC1 domain family, member 10A	1.67	up	0.000642	0.0000577
TBC1D2	TBC1 domain family, member 2	2.00	up	0.000063	0.0000009
TBXA2R	thromboxane A2 receptor	1.84	up	0.000135	0.0000039
TCF19	transcription factor 19	3.68	up	0.000116	0.0000029
TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	1.70	up	0.003526	0.0006977
TEP1	telomerase-associated protein 1	1.95	up	0.000116	0.0000029
TERF2IP	telomeric repeat binding factor 2, interacting protein	2.23	up	0.000219	0.0000091
TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	2.12	up	0.000244	0.0000110
TFEB	transcription factor EB	1.66	up	0.000294	0.0000157
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	1.66	up	0.001684	0.0002470
TGFA	transforming growth factor, alpha	2.84	up	0.000202	0.0000078
TGFB1	transforming growth factor, beta 1	1.63	up	0.000180	0.0000064
TGM1	transglutaminase 1	1.94	up	0.003380	0.0006594
TGM2	transglutaminase 2	2.83	up	0.000237	0.0000105
TGOLN2	trans-golgi network protein 2	1.64	up	0.000102	0.0000022
THAP10	THAP domain containing 10	1.94	up	0.000047	0.0000005
THBD	thrombomodulin	2.14	up	0.000247	0.0000113
TICAM1	toll-like receptor adaptor molecule 1	1.52	up	0.000398	0.0000258
TIMP1	TIMP metallopeptidase inhibitor 1	1.62	up	0.000280	0.0000143
TLDC1	TBC/LysM-associated domain containing 1	2.19	up	0.000359	0.0000218
TLR1	toll-like receptor 1	2.37	up	0.000389	0.0000250
TLR3	toll-like receptor 3	4.42	up	0.000042	0.0000004
TM9SF2	transmembrane 9 superfamily member 2	1.60	up	0.000086	0.0000016
TMC8	transmembrane channel-like 8	2.27	up	0.000418	0.0000279
TMCC2	transmembrane and coiled-coil domain family 2	3.04	up	0.000087	0.0000016

TMCC3	transmembrane and coiled-coil domain family 3	1.79	up	0.000047	0.0000005
TMEM106C	transmembrane protein 106C	1.54	up	0.000929	0.0001019
TMEM121	transmembrane protein 121	1.72	up	0.002638	0.0004635
TMEM125	transmembrane protein 125	1.84	up	0.000253	0.0000118
TMEM139	transmembrane protein 139	1.98	up	0.000483	0.0000362
TMEM158	transmembrane protein 158 (gene/pseudogene)	1.65	up	0.004428	0.0009656
TMEM159	transmembrane protein 159	1.53	up	0.001380	0.0001847
TMEM173	transmembrane protein 173	1.95	up	0.000059	0.0000008
TMEM185B	transmembrane protein 185B	1.84	up	0.002239	0.0003669
TMEM191A	transmembrane protein 191A (pseudogene)	1.70	up	0.000432	0.0000295
TMEM191B	transmembrane protein 191B	1.71	up	0.000309	0.0000171
TMEM194A	transmembrane protein 194A	1.76	up	0.003327	0.0006466
TMEM234	transmembrane protein 234	1.74	up	0.003145	0.0005942
TMEM255B	transmembrane protein 255B	1.63	up	0.001052	0.0001230
TMEM38B	transmembrane protein 38B	1.70	up	0.001594	0.0002280
TMEM40	transmembrane protein 40	4.37	up	0.000080	0.0000014
TMEM59	transmembrane protein 59	1.99	up	0.000053	0.0000006
TMEM59L	transmembrane protein 59-like	1.64	up	0.000103	0.0000023
TMEM61	transmembrane protein 61	2.17	up	0.000041	0.0000003
TMEM79	transmembrane protein 79	2.35	up	0.001892	0.0002932
TMEM92	transmembrane protein 92	1.81	up	0.000715	0.0000675
TMOD1	tropomodulin 1	1.96	up	0.001400	0.0001891
TMOD3	tropomodulin 3 (ubiquitous)	1.62	up	0.000683	0.0000632
TMPRSS4	transmembrane protease, serine 4	3.71	up	0.004608	0.0010200
TMPRSS7	transmembrane protease, serine 7	5.34	up	0.001061	0.0001249
TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	1.84	up	0.000601	0.0000519
TNFAIP2	tumor necrosis factor, alpha-induced protein 2	2.00	up	0.000170	0.0000058
TNFAIP8	tumor necrosis factor, alpha-induced protein 8	1.50	up	0.004547	0.0010017
TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	1.77	up	0.001156	0.0001417
TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	1.89	up	0.000384	0.0000244

TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	2.62	up	0.000865	0.0000910
TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	1.83	up	0.000216	0.0000089
TNFRSF25	tumor necrosis factor receptor superfamily, member 25	1.61	up	0.004670	0.0010418
TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy	1.80	up	0.000427	0.0000288
TNK2	tyrosine kinase, non-receptor, 2	1.54	up	0.000205	0.0000081
TNNC1	troponin C type 1 (slow)	1.78	up	0.001404	0.0001902
TNNI2	troponin I type 2 (skeletal, fast)	6.95	up	0.000456	0.0000326
TNXB	tenascin XB	1.80	up	0.001240	0.0001572
TOB1	transducer of ERBB2, 1	1.66	up	0.000268	0.0000132
TOR1B	torsin family 1, member B (torsin B)	1.68	up	0.000201	0.0000077
TP53I11	tumor protein p53 inducible protein 11	1.59	up	0.000448	0.0000315
TP53I3	tumor protein p53 inducible protein 3	5.24	up	0.000027	0.0000001
TP53INP1	tumor protein p53 inducible nuclear protein 1	3.71	up	0.000051	0.0000006
TPM1	tropomyosin 1 (alpha)	1.67	up	0.004689	0.0010475
TPST1	tyrosylprotein sulfotransferase 1	1.55	up	0.000505	0.0000394
TRAF4	TNF receptor-associated factor 4	1.75	up	0.000205	0.0000082
TRAPPC2P1	trafficking protein particle complex 2 pseudogene 1	1.61	up	0.000482	0.0000361
TRIAP1	TP53 regulated inhibitor of apoptosis 1	2.10	up	0.000136	0.0000040
TRIM15	tripartite motif containing 15	2.05	up	0.003232	0.0006176
TRIM29	tripartite motif containing 29	3.36	up	0.000630	0.0000558
TRIM68	tripartite motif containing 68	1.65	up	0.000710	0.0000666
TRIM8	tripartite motif containing 8	2.05	up	0.000046	0.0000005
TRIML2	tripartite motif family-like 2	2.33	up	0.000149	0.0000046
TRIP6	thyroid hormone receptor interactor 6	1.72	up	0.000743	0.0000722
TSC22D3	TSC22 domain family, member 3	2.14	up	0.000858	0.0000897
TSPAN1	tetraspanin 1	2.24	up	0.000026	0.0000001
TSPAN14	tetraspanin 14	1.65	up	0.000406	0.0000266
TSPAN7	tetraspanin 7	1.66	up	0.000723	0.0000688

TSPYL4	TSPY-like 4	1.56	up	0.000528	0.0000423
TTC28-AS1	TTC28 antisense RNA 1	4.99	up	0.000396	0.0000255
TTC39A	tetratricopeptide repeat domain 39A	1.63	up	0.000336	0.0000197
TUFT1	tuftelin 1	2.29	up	0.000136	0.0000040
TXNDC17	thioredoxin domain containing 17	1.61	up	0.000740	0.0000711
UBC	ubiquitin C	1.60	up	0.001959	0.0003075
UBFD1	ubiquitin family domain containing 1	2.28	up	0.000045	0.0000005
UBL3	ubiquitin-like 3	1.66	up	0.000554	0.0000460
UCK1	uridine-cytidine kinase 1	1.55	up	0.003060	0.0005715
UCN2	urocortin 2	2.02	up	0.001219	0.0001531
UFD1L	ubiquitin fusion degradation 1 like (yeast)	1.63	up	0.000298	0.0000162
UHRF2	ubiquitin-like with PHD and ring finger domains 2, E3 ubiquitin protein ligase	1.61	up	0.000089	0.0000017
ULBP2	UL16 binding protein 2	4.29	up	0.000027	0.0000001
ULK1	unc-51 like autophagy activating kinase 1	1.69	up	0.000026	0.0000001
ULK4P1	ULK4 pseudogene 1	1.64	up	0.001592	0.0002270
UNC13D	unc-13 homolog D (C. elegans)	2.08	up	0.002277	0.0003744
UNC5B-AS1	UNC5B antisense RNA 1	5.23	up	0.000041	0.0000003
UPP1	uridine phosphorylase 1	2.09	up	0.000117	0.0000030
USP11	ubiquitin specific peptidase 11	1.58	up	0.003486	0.0006860
USP18	ubiquitin specific peptidase 18	1.84	up	0.000782	0.0000780
USP35	ubiquitin specific peptidase 35	1.86	up	0.000582	0.0000495
USP53	ubiquitin specific peptidase 53	1.65	up	0.000742	0.0000717
VAMP8	vesicle-associated membrane protein 8	1.80	up	0.000228	0.0000099
VASN	vasorin	1.91	up	0.000977	0.0001105
VCAN	versican	1.70	up	0.000317	0.0000178
VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	1.57	up	0.000548	0.0000450
VEPH1	ventricular zone expressed PH domain-containing 1	1.79	up	0.004307	0.0009287
VPS37D	vacuolar protein sorting 37 homolog D (S. cerevisiae)	1.55	up	0.000309	0.0000171
WBSCR28	Williams-Beuren syndrome chromosome region 28	2.90	up	0.001121	0.0001353

WFDC1	WAP four-disulfide core domain 1	3.36	up	0.000041	0.0000003
WHAMM	WAS protein homolog associated with actin, golgi membranes and microtubules	1.75	up	0.000047	0.0000005
WIPI1	WD repeat domain, phosphoinositide interacting 1	1.50	up	0.001026	0.0001188
WLS	wntless Wnt ligand secretion mediator	1.76	up	0.001658	0.0002410
WNT7A	wingless-type MMTV integration site family, member 7A	7.33	up	0.000380	0.0000240
WNT7B	wingless-type MMTV integration site family, member 7B	2.67	up	0.000613	0.0000534
WRAP73	WD repeat containing, antisense to TP73	1.54	up	0.000750	0.0000730
WWTR1	WW domain containing transcription regulator 1	2.46	up	0.000029	0.0000002
XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	1.55	up	0.001238	0.0001568
YBX3	Y box binding protein 3	1.53	up	0.000505	0.0000395
YPEL3	yippee-like 3 (Drosophila)	4.72	up	0.000195	0.0000074
YPEL5	yippee-like 5 (Drosophila)	2.63	up	0.000020	0.0000000
ZCCHC12	zinc finger, CCHC domain containing 12	2.80	up	0.000915	0.0000992
ZFP36L2	ZFP36 ring finger protein-like 2	1.51	up	0.000162	0.0000052
ZFYVE1	zinc finger, FYVE domain containing 1	2.17	up	0.000092	0.0000018
ZNF177	zinc finger protein 177	1.50	up	0.002753	0.0004917
ZNF219	zinc finger protein 219	2.18	up	0.000060	0.0000008
ZNF226	zinc finger protein 226	1.65	up	0.001237	0.0001564
ZNF250	zinc finger protein 250	1.62	up	0.000670	0.0000614
ZNF34	zinc finger protein 34	1.85	up	0.001520	0.0002132
ZNF341	zinc finger protein 341	1.51	up	0.000301	0.0000165
ZNF354B	zinc finger protein 354B	1.85	up	0.003912	0.0008056
ZNF416	zinc finger protein 416	1.52	up	0.003985	0.0008294
ZNF430	zinc finger protein 430	1.62	up	0.003974	0.0008264
ZNF442	zinc finger protein 442	1.63	up	0.001925	0.0003003
ZNF488	zinc finger protein 488	1.74	up	0.003256	0.0006264
ZNF555	zinc finger protein 555	1.59	up	0.000347	0.0000210
ZNF564	zinc finger protein 564	1.70	up	0.002145	0.0003464

ZNF600	zinc finger protein 600	2.15	up	0.000231	0.0000101
ZNF641	zinc finger protein 641	1.55	up	0.000864	0.0000908
ZNF654	zinc finger protein 654	2.08	up	0.000217	0.0000089
ZNF672	zinc finger protein 672	1.55	up	0.001119	0.0001349
ZNF684	zinc finger protein 684	1.89	up	0.004137	0.0008731
ZNF703	zinc finger protein 703	2.57	up	0.001220	0.0001533
ZNF79	zinc finger protein 79	2.75	up	0.000014	0.0000000
ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	1.61	up	0.000261	0.0000127
ZSCAN20	zinc finger and SCAN domain containing 20	1.61	up	0.000802	0.0000808
ZSWIM3	zinc finger, SWIM-type containing 3	2.44	up	0.000515	0.0000409
A2M-AS1	A2M antisense RNA 1	1.61	down	0.003309	0.0006414
AAAS	achalasia, adrenocortical insufficiency, alacrimia	1.60	down	0.003817	0.0007749
AATK	apoptosis-associated tyrosine kinase	5.66	down	0.000014	0.0000000
ABHD11	abhydrolase domain containing 11	1.58	down	0.000803	0.0000809
ABHD14B	abhydrolase domain containing 14B	1.68	down	0.000916	0.0000994
ABLIM2	actin binding LIM protein family, member 2	7.05	down	0.000532	0.0000429
ACACA	acetyl-CoA carboxylase alpha	1.52	down	0.000366	0.0000227
ACAD9	acyl-CoA dehydrogenase family, member 9	1.62	down	0.000103	0.0000023
ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	1.64	down	0.004722	0.0010563
ACADSB	acyl-CoA dehydrogenase, short/branched chain	2.01	down	0.000376	0.0000235
ACCS	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	2.09	down	0.000442	0.0000307
ACSL3	acyl-CoA synthetase long-chain family member 3	2.58	down	0.000565	0.0000474
ACSL5	acyl-CoA synthetase long-chain family member 5	1.89	down	0.000066	0.0000010
ACSM3	acyl-CoA synthetase medium-chain family member 3	1.80	down	0.000548	0.0000451
ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	1.59	down	0.001006	0.0001155
ACTR3B	ARP3 actin-related protein 3 homolog B (yeast)	1.79	down	0.000459	0.0000330
ADCK1	aarF domain containing kinase 1	3.18	down	0.002012	0.0003180

ADCY3	adenylate cyclase 3	1.59	down	0.000656	0.0000594
AEBP2	AE binding protein 2	1.51	down	0.000074	0.0000012
AFAP1	actin filament associated protein 1	1.64	down	0.001911	0.0002971
AGFG1	ArfGAP with FG repeats 1	2.30	down	0.004440	0.0009698
AGGF1	angiogenic factor with G patch and FHA domains 1	1.79	down	0.000114	0.0000028
AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5	2.07	down	0.000028	0.0000002
AGPS	alkylglycerone phosphate synthase	2.64	down	0.000102	0.0000022
AIMP2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	1.63	down	0.001371	0.0001826
AK2	adenylate kinase 2	1.99	down	0.000259	0.0000125
AK8	adenylate kinase 8	1.63	down	0.001070	0.0001266
AKT2	v-akt murine thymoma viral oncogene homolog 2	1.71	down	0.001974	0.0003102
ALKBH3	alkB, alkylation repair homolog 3 (E. coli)	1.55	down	0.001059	0.0001245
AMD1	adenosylmethionine decarboxylase 1	1.78	down	0.000459	0.0000331
ANAPC1	anaphase promoting complex subunit 1	1.65	down	0.002028	0.0003213
ANKRD11	ankyrin repeat domain 11	1.55	down	0.003098	0.0005826
ANKRD18DP	ankyrin repeat domain 18D, pseudogene	2.49	down	0.004325	0.0009343
ANKRD28	ankyrin repeat domain 28	1.53	down	0.004395	0.0009538
ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	1.69	down	0.000206	0.0000082
ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	1.56	down	0.001170	0.0001442
AOC3	amine oxidase, copper containing 3	1.64	down	0.001775	0.0002669
AP1S3	adaptor-related protein complex 1, sigma 3 subunit	1.52	down	0.004866	0.0010984
APEH	acylaminoacyl-peptide hydrolase	1.57	down	0.000692	0.0000643
APOM	apolipoprotein M	2.87	down	0.001335	0.0001753
ARFRP1	ADP-ribosylation factor related protein 1	2.53	down	0.000664	0.0000606
ARHGAP11A	Rho GTPase activating protein 11A	2.25	down	0.000250	0.0000116
ARHGAP11B	Rho GTPase activating protein 11B	1.79	down	0.000364	0.0000225
ARHGAP19	Rho GTPase activating protein 19	2.57	down	0.000505	0.0000394
ARHGAP26	Rho GTPase activating protein 26	1.93	down	0.001230	0.0001552

ARHGAP35	Rho GTPase activating protein 35	1.50	down	0.000219	0.0000091
ARHGAP5	Rho GTPase activating protein 5	2.32	down	0.001775	0.0002673
ARHGEF39	Rho guanine nucleotide exchange factor (GEF) 39	2.52	down	0.000872	0.0000921
ARID2	AT rich interactive domain 2 (ARID, RFX-like)	1.78	down	0.000938	0.0001036
ARIH2	ariadne RBR E3 ubiquitin protein ligase 2	1.78	down	0.000022	0.0000001
ARL4A	ADP-ribosylation factor-like 4A	1.65	down	0.000049	0.0000005
ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	1.53	down	0.000057	0.0000007
ARMC3	armadillo repeat containing 3	2.70	down	0.003706	0.0007469
ARMC4	armadillo repeat containing 4	1.70	down	0.000774	0.0000768
ARMC8	armadillo repeat containing 8	1.87	down	0.003021	0.0005610
ASB13	ankyrin repeat and SOCS box containing 13	1.54	down	0.002761	0.0004937
ASIC1	acid-sensing (proton-gated) ion channel 1	1.61	down	0.001175	0.0001452
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	2.27	down	0.000569	0.0000479
ASPRV1	aspartic peptidase, retroviral-like 1	2.08	down	0.002318	0.0003843
ATAD2B	ATPase family, AAA domain containing 2B	2.04	down	0.000698	0.0000651
ATF4	activating transcription factor 4	1.59	down	0.004046	0.0008473
ATF7IP	activating transcription factor 7 interacting protein	1.62	down	0.000006	0.0000000
ATP11C	ATPase, class VI, type 11C	1.62	down	0.000253	0.0000118
ATP6V1E2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2	2.09	down	0.000297	0.0000161
ATR	ataxia telangiectasia and Rad3 related	1.51	down	0.000794	0.0000799
ATXN10	ataxin 10	1.62	down	0.000644	0.0000579
ATXN1L	ataxin 1-like	1.50	down	0.004158	0.0008814
AURKA	aurora kinase A	2.15	down	0.000280	0.0000143
AURKAPS1	aurora kinase A pseudogene 1	1.96	down	0.000121	0.0000032
AXIN2	axin 2	2.30	down	0.002618	0.0004582
AZI2	5-azacytidine induced 2	1.55	down	0.001676	0.0002455
AZIN1	antizyme inhibitor 1	1.61	down	0.000601	0.0000520
B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	1.55	down	0.001084	0.0001289
B9D1	B9 protein domain 1	1.63	down	0.000477	0.0000351

BAHCC1	BAH domain and coiled-coil containing 1	1.54	down	0.003685	0.0007410
BAIAP2	BAI1-associated protein 2	2.09	down	0.000713	0.0000671
BANK1	B-cell scaffold protein with ankyrin repeats 1	2.53	down	0.000047	0.0000005
BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide	1.54	down	0.003890	0.0007980
BCL2L12	BCL2-like 12 (proline rich)	1.50	down	0.000798	0.0000803
BCOR	BCL6 corepressor	2.86	down	0.000480	0.0000356
BCR	breakpoint cluster region	1.78	down	0.000271	0.0000135
BDNF	brain-derived neurotrophic factor	2.28	down	0.000791	0.0000793
BEND3	BEN domain containing 3	2.39	down	0.000102	0.0000022
BET1	Bet1 golgi vesicular membrane trafficking protein	1.90	down	0.001369	0.0001822
BIRC5	baculoviral IAP repeat containing 5	1.50	down	0.000362	0.0000221
BMP4	bone morphogenetic protein 4	1.67	down	0.000120	0.0000031
BORA	bora, aurora kinase A activator	1.69	down	0.000477	0.0000351
BPHL	biphenyl hydrolase-like (serine hydrolase)	1.82	down	0.000624	0.0000549
BRWD1	bromodomain and WD repeat domain containing 1	2.38	down	0.000159	0.0000051
BUB1	BUB1 mitotic checkpoint serine/threonine kinase	2.07	down	0.000103	0.0000023
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	2.26	down	0.000117	0.0000030
C17orf82	chromosome 17 open reading frame 82	1.82	down	0.001600	0.0002292
C1orf213	chromosome 1 open reading frame 213	1.56	down	0.003880	0.0007927
C1orf233	chromosome 1 open reading frame 233	1.51	down	0.003820	0.0007758
C1RL	complement component 1, r subcomponent-like	2.21	down	0.000844	0.0000867
C2orf68	chromosome 2 open reading frame 68	1.66	down	0.003029	0.0005632
C2orf69	chromosome 2 open reading frame 69	1.54	down	0.001543	0.0002180
C3AR1	complement component 3a receptor 1	1.68	down	0.001317	0.0001723
C6orf62	chromosome 6 open reading frame 62	1.55	down	0.001342	0.0001769
C7orf50	chromosome 7 open reading frame 50	1.95	down	0.002620	0.0004590
C8orf37	chromosome 8 open reading frame 37	1.73	down	0.002421	0.0004081
C9orf171	chromosome 9 open reading frame 171	2.11	down	0.000377	0.0000236
CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B subunit	2.25	down	0.001590	0.0002264
CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	1.99	down	0.000253	0.0000118

CACYBP	calcyclin binding protein	1.72	down	0.000662	0.0000602
CALML4	calmodulin-like 4	2.20	down	0.000022	0.0000001
CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	1.86	down	0.004053	0.0008497
CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	1.81	down	0.004461	0.0009764
CASC5	cancer susceptibility candidate 5	1.77	down	0.000194	0.0000073
CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	1.71	down	0.000332	0.0000194
CBX6	chromobox homolog 6	1.71	down	0.000941	0.0001043
CC2D2A	coiled-coil and C2 domain containing 2A	2.25	down	0.000786	0.0000786
CCDC106	coiled-coil domain containing 106	1.64	down	0.000548	0.0000451
CCDC121	coiled-coil domain containing 121	2.02	down	0.000335	0.0000197
CCDC146	coiled-coil domain containing 146	1.55	down	0.003652	0.0007318
CCDC167	coiled-coil domain containing 167	1.59	down	0.000345	0.0000207
CCDC18	coiled-coil domain containing 18	2.52	down	0.001020	0.0001174
CCDC88C	coiled-coil domain containing 88C	1.55	down	0.002499	0.0004279
CCNB1	cyclin B1	2.21	down	0.000022	0.0000001
CCNB2	cyclin B2	1.72	down	0.001801	0.0002723
CCNL2	cyclin L2	2.29	down	0.000141	0.0000042
CD3EAP	CD3e molecule, epsilon associated protein	1.53	down	0.000057	0.0000007
CDC20	cell division cycle 20	2.46	down	0.000197	0.0000075
CDCA7	cell division cycle associated 7	1.90	down	0.000227	0.0000098
CDCA8	cell division cycle associated 8	1.52	down	0.002155	0.0003487
CDKN3	cyclin-dependent kinase inhibitor 3	2.25	down	0.000006	0.0000000
CDPF1	cysteine-rich, DPF motif domain containing 1	1.90	down	0.000045	0.0000004
CDV3	CDV3 homolog (mouse)	1.51	down	0.002355	0.0003933
CENPA	centromere protein A	1.66	down	0.000032	0.0000002
CENPE	centromere protein E, 312kDa	1.88	down	0.000022	0.0000001
CENPF	centromere protein F, 350/400kDa	1.98	down	0.002923	0.0005337
CEP70	centrosomal protein 70kDa	1.65	down	0.000352	0.0000213
CEP83	centrosomal protein 83kDa	1.60	down	0.002516	0.0004317

CHDH	choline dehydrogenase	1.95	down	0.000515	0.0000410
CHRNA5	cholinergic receptor, nicotinic, alpha 5 (neuronal)	1.51	down	0.001696	0.0002492
CIRBP	cold inducible RNA binding protein	1.56	down	0.000091	0.0000018
CKAP5	cytoskeleton associated protein 5	1.51	down	0.000639	0.0000572
CLASP2	cytoplasmic linker associated protein 2	1.56	down	0.001267	0.0001626
CLCN2	chloride channel, voltage-sensitive 2	1.54	down	0.000958	0.0001073
CLUAP1	clusterin associated protein 1	1.75	down	0.000306	0.0000168
CLYBL	citrate lyase beta like	1.99	down	0.000372	0.0000233
CNTRL	centriolin	2.49	down	0.000152	0.0000048
COA5	cytochrome c oxidase assembly factor 5	1.88	down	0.000732	0.0000699
COQ2	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase	1.66	down	0.001805	0.0002736
COQ3	coenzyme Q3 methyltransferase	1.96	down	0.001478	0.0002041
CPOX	coproporphyrinogen oxidase	1.64	down	0.001790	0.0002704
CREB3L4	cAMP responsive element binding protein 3-like 4	1.84	down	0.000938	0.0001036
CRTC1	CREB regulated transcription coactivator 1	2.36	down	0.000305	0.0000168
CRYL1	crystallin, lambda 1	1.96	down	0.000274	0.0000137
CRYZ	crystallin, zeta (quinone reductase)	1.68	down	0.000543	0.0000444
CSE1L	CSE1 chromosome segregation 1-like (yeast)	1.54	down	0.000573	0.0000484
CSNK2A2	casein kinase 2, alpha prime polypeptide	1.60	down	0.000210	0.0000085
CTAGE5	CTAGE family, member 5	1.54	down	0.002532	0.0004366
CTPS2	CTP synthase 2	1.59	down	0.000481	0.0000359
CUTC	cutC copper transporter	2.05	down	0.000275	0.0000138
CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	2.09	down	0.000350	0.0000211
CYB5RL	cytochrome b5 reductase-like	2.30	down	0.000351	0.0000212
DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	1.83	down	0.000174	0.0000061
DCBLD2	discoidin, CUB and LCCL domain containing 2	1.57	down	0.001195	0.0001482
DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4	1.93	down	0.000502	0.0000389
DDN	dendrin	1.86	down	0.000833	0.0000849
DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	1.57	down	0.001235	0.0001561
DENND4C	DENN/MADD domain containing 4C	1.69	down	0.001242	0.0001577

DENND5B	DENN/MADD domain containing 5B	2.22	down	0.002279	0.0003752
DEPDC1	DEP domain containing 1	2.54	down	0.000054	0.0000006
DEPDC1B	DEP domain containing 1B	1.87	down	0.000336	0.0000198
DET1	de-etiolated homolog 1 (Arabidopsis)	1.53	down	0.001396	0.0001878
DHRS2	dehydrogenase/reductase (SDR family) member 2	2.94	down	0.000022	0.0000001
DHRS3	dehydrogenase/reductase (SDR family) member 3	1.61	down	0.000253	0.0000119
DHRS4-AS1	DHRS4 antisense RNA 1	1.74	down	0.003533	0.0007007
DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	1.63	down	0.000222	0.0000094
DIDO1	death inducer-obliterator 1	1.55	down	0.001501	0.0002093
DIEXF	digestive organ expansion factor homolog (zebrafish)	1.57	down	0.001026	0.0001189
DIMT1	DIM1 dimethyladenosine transferase 1 homolog (S. cerevisiae)	2.59	down	0.000305	0.0000168
DIS3L	DIS3 like exosome 3'-5' exoribonuclease	1.76	down	0.000353	0.0000214
DLEU2L	deleted in lymphocytic leukemia 2-like	1.98	down	0.000933	0.0001026
DLG1	discs, large homolog 1 (Drosophila)	1.63	down	0.002278	0.0003749
DLG5-AS1	DLG5 antisense RNA 1	1.81	down	0.002707	0.0004805
DLGAP5	discs, large (Drosophila) homolog-associated protein 5	1.95	down	0.000589	0.0000504
DNM1L	dynamin 1-like	1.51	down	0.002788	0.0005025
DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	1.64	down	0.000380	0.0000239
DOCK1	dedicator of cytokinesis 1	1.54	down	0.000062	0.0000009
DOK3	docking protein 3	1.87	down	0.000851	0.0000886
DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	1.54	down	0.001166	0.0001432
DPP8	dipeptidyl-peptidase 8	1.60	down	0.000074	0.0000012
DRD4	dopamine receptor D4	5.42	down	0.001704	0.0002513
DTD1	D-tyrosyl-tRNA deacylase 1	1.64	down	0.000495	0.0000380
DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	1.85	down	0.000254	0.0000121
EBPL	emopamil binding protein-like	2.31	down	0.000505	0.0000393
EEF2K	eukaryotic elongation factor-2 kinase	2.91	down	0.000037	0.0000002
EFCC1	EF-hand and coiled-coil domain containing 1	1.79	down	0.002990	0.0005528

EHBP1	EH domain binding protein 1	1.62	down	0.001253	0.0001596
EHMT1	euchromatic histone-lysine N-methyltransferase 1	1.86	down	0.003252	0.0006233
EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	1.74	down	0.000121	0.0000032
EIF4B	eukaryotic translation initiation factor 4B	1.77	down	0.001330	0.0001745
EIF4E	eukaryotic translation initiation factor 4E	1.82	down	0.003446	0.0006755
EIF4E2	eukaryotic translation initiation factor 4E family member 2	1.75	down	0.000458	0.0000330
EIF5	eukaryotic translation initiation factor 5	1.85	down	0.000621	0.0000545
EMC2	ER membrane protein complex subunit 2	1.50	down	0.000400	0.0000261
EML4	echinoderm microtubule associated protein like 4	1.59	down	0.000250	0.0000114
ENDOV	endonuclease V	1.52	down	0.000613	0.0000533
ENKD1	enkurin domain containing 1	2.20	down	0.000103	0.0000023
ENOX2	ecto-NOX disulfide-thiol exchanger 2	1.60	down	0.000501	0.0000389
EP400	E1A binding protein p400	1.77	down	0.003957	0.0008199
EPB41L4A-AS1	EPB41L4A antisense RNA 1	1.96	down	0.000094	0.0000019
EPHX2	epoxide hydrolase 2, cytoplasmic	1.69	down	0.000060	0.0000008
EPS15	epidermal growth factor receptor pathway substrate 15	1.75	down	0.002023	0.0003204
ERMARD	ER membrane-associated RNA degradation	1.71	down	0.000383	0.0000243
ETF1	eukaryotic translation termination factor 1	1.61	down	0.000577	0.0000490
EVI5	ecotropic viral integration site 5	1.68	down	0.004535	0.0009982
EWSR1	EWS RNA-binding protein 1	1.86	down	0.001676	0.0002453
EXD3	exonuclease 3'-5' domain containing 3	3.82	down	0.000075	0.0000013
EXOC6	exocyst complex component 6	1.59	down	0.001533	0.0002162
FAM13B	family with sequence similarity 13, member B	1.62	down	0.001349	0.0001784
FAM149B1	family with sequence similarity 149, member B1	2.61	down	0.000322	0.0000184
FAM175A	family with sequence similarity 175, member A	2.79	down	0.000036	0.0000002
FAM203A	family with sequence similarity 203, member A	2.32	down	0.000205	0.0000081
FAM216A	family with sequence similarity 216, member A	1.75	down	0.000936	0.0001031
FAM72A	family with sequence similarity 72, member A	2.08	down	0.000043	0.0000004
FAM72D	family with sequence similarity 72, member D	2.18	down	0.000103	0.0000023

FAM86FP	family with sequence similarity 86, member A pseudogene	2.00	down	0.000078	0.0000013
FASTKD2	FAST kinase domains 2	1.77	down	0.002106	0.0003382
FBRSL1	fibrosin-like 1	1.54	down	0.000415	0.0000275
FBXO18	F-box protein, helicase, 18	1.51	down	0.003884	0.0007946
FBXO24	F-box protein 24	1.97	down	0.004725	0.0010580
FBXO4	F-box protein 4	1.80	down	0.004152	0.0008787
FBXO9	F-box protein 9	1.64	down	0.000360	0.0000219
FGF9	fibroblast growth factor 9	4.09	down	0.000456	0.0000327
FGGY	FGGY carbohydrate kinase domain containing	1.64	down	0.004071	0.0008545
FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	1.93	down	0.002470	0.0004203
FJX1	four jointed box 1 (Drosophila)	1.75	down	0.000864	0.0000906
FKBP5	FK506 binding protein 5	1.63	down	0.004075	0.0008554
FLYWCH1	FLYWCH-type zinc finger 1	1.80	down	0.001059	0.0001246
FNBP4	formin binding protein 4	1.62	down	0.000990	0.0001127
FOXK2	forkhead box K2	1.57	down	0.000329	0.0000190
FRMD5	FERM domain containing 5	1.75	down	0.002895	0.0005277
FUBP3	far upstream element (FUSE) binding protein 3	1.51	down	0.000923	0.0001008
FUOM	fucose mutarotase	1.62	down	0.001594	0.0002280
FXR1	fragile X mental retardation, autosomal homolog 1	1.97	down	0.000831	0.0000847
G2E3	G2/M-phase specific E3 ubiquitin protein ligase	1.82	down	0.000390	0.0000251
G3BP1	GTPase activating protein (SH3 domain) binding protein 1	1.62	down	0.000167	0.0000056
GAS2L3	growth arrest-specific 2 like 3	2.00	down	0.000344	0.0000206
GATAD2A	GATA zinc finger domain containing 2A	1.58	down	0.000447	0.0000313
GBAS	glioblastoma amplified sequence	1.60	down	0.001020	0.0001176
GCLC	glutamate-cysteine ligase, catalytic subunit	1.81	down	0.000477	0.0000351
GCOM1	GRINL1A complex locus 1	1.51	down	0.000709	0.0000664
GDI2	GDP dissociation inhibitor 2	1.50	down	0.002521	0.0004339
GEN1	GEN1 Holliday junction 5' flap endonuclease	1.92	down	0.001167	0.0001436
GGA2	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	1.75	down	0.000159	0.0000051

GHRLOS	ghrelin opposite strand/antisense RNA	2.78	down	0.000321	0.0000182
GLT8D1	glycosyltransferase 8 domain containing 1	1.56	down	0.002992	0.0005532
GLTSCR2	glioma tumor suppressor candidate region gene 2	1.89	down	0.000409	0.0000269
GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	2.32	down	0.000037	0.0000002
GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	2.05	down	0.000242	0.0000108
GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	1.68	down	0.002959	0.0005434
GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	1.55	down	0.000244	0.0000110
GOLGA3	golgin A3	1.51	down	0.001648	0.0002386
GP9	glycoprotein IX (platelet)	1.64	down	0.001904	0.0002955
GPR180	G protein-coupled receptor 180	1.58	down	0.002040	0.0003233
GRID1	glutamate receptor, ionotropic, delta 1	1.87	down	0.000674	0.0000620
GRK6	G protein-coupled receptor kinase 6	1.53	down	0.003665	0.0007356
GSTZ1	glutathione S-transferase zeta 1	1.94	down	0.000528	0.0000423
GYLTL1B	glycosyltransferase-like 1B	1.53	down	0.002123	0.0003421
H1FX	H1 histone family, member X	1.74	down	0.000733	0.0000701
H2AFX	H2A histone family, member X	2.07	down	0.000152	0.0000048
HABP4	hyaluronan binding protein 4	1.74	down	0.000652	0.0000590
HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1	1.57	down	0.001823	0.0002785
HAUS6	HAUS augmin-like complex, subunit 6	2.76	down	0.002690	0.0004760
HDAC4	histone deacetylase 4	3.64	down	0.000057	0.0000007
HEATR3	HEAT repeat containing 3	1.76	down	0.000532	0.0000429
HEXDC	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	1.52	down	0.002232	0.0003653
HIATL1	hippocampus abundant transcript-like 1	1.50	down	0.002894	0.0005275
HIBCH	3-hydroxyisobutyryl-CoA hydrolase	1.58	down	0.004204	0.0008980
HIRA	histone cell cycle regulator	1.97	down	0.000015	0.0000000
HIST1H1C	histone cluster 1, H1c	2.29	down	0.000177	0.0000062
HIST1H1D	histone cluster 1, H1d	3.42	down	0.000091	0.0000018

HIST1H1E	histone cluster 1, H1e	3.36	down	0.000010	0.0000000
HIST1H2AB	histone cluster 1, H2ab	4.16	down	0.000087	0.0000016
HIST1H2AC	histone cluster 1, H2ac	4.16	down	0.000083	0.0000015
HIST1H2AD	histone cluster 1, H2ad	2.59	down	0.000014	0.0000000
HIST1H2AE	histone cluster 1, H2ae	2.68	down	0.000043	0.0000004
HIST1H2AH	histone cluster 1, H2ah	3.47	down	0.000006	0.0000000
HIST1H2AI	histone cluster 1, H2ai	3.64	down	0.000044	0.0000004
HIST1H2AJ	histone cluster 1, H2aj	3.07	down	0.000014	0.0000000
HIST1H2AK	histone cluster 1, H2ak	3.39	down	0.000014	0.0000000
HIST1H2AM	histone cluster 1, H2am	4.29	down	0.000033	0.0000002
HIST1H2BB	histone cluster 1, H2bb	2.23	down	0.000205	0.0000081
HIST1H2BC	histone cluster 1, H2bc	2.46	down	0.000040	0.0000003
HIST1H2BD	histone cluster 1, H2bd	1.65	down	0.000591	0.0000507
HIST1H2BF	histone cluster 1, H2bf	7.85	down	0.000459	0.0000331
HIST1H2BG	histone cluster 1, H2bg	2.45	down	0.000127	0.0000035
HIST1H2BH	histone cluster 1, H2bh	1.83	down	0.000158	0.0000050
HIST1H2BI	histone cluster 1, H2bi	1.52	down	0.000102	0.0000021
HIST1H2BJ	histone cluster 1, H2bj	3.02	down	0.000022	0.0000001
HIST1H2BK	histone cluster 1, H2bk	1.89	down	0.000228	0.0000099
HIST1H2BL	histone cluster 1, H2bl	1.80	down	0.000967	0.0001089
HIST1H2BO	histone cluster 1, H2bo	1.90	down	0.000079	0.0000014
HIST1H3B	histone cluster 1, H3b	2.77	down	0.000017	0.0000000
HIST1H3D	histone cluster 1, H3d	3.48	down	0.000015	0.0000000
HIST1H3E	histone cluster 1, H3e	1.63	down	0.001210	0.0001517
HIST1H3F	histone cluster 1, H3f	3.86	down	0.000031	0.0000002
HIST1H3H	histone cluster 1, H3h	3.95	down	0.000014	0.0000000
HIST1H3J	histone cluster 1, H3j	3.14	down	0.000177	0.0000062
HIST1H4A	histone cluster 1, H4a	3.03	down	0.000042	0.0000004
HIST1H4B	histone cluster 1, H4b	2.14	down	0.000078	0.0000013
HIST1H4C	histone cluster 1, H4c	2.02	down	0.000600	0.0000518

HIST1H4D	histone cluster 1, H4d	2.81	down	0.000106	0.0000024
HIST1H4E	histone cluster 1, H4e	3.04	down	0.000097	0.0000019
HIST1H4F	histone cluster 1, H4f	2.40	down	0.000246	0.0000112
HIST1H4H	histone cluster 1, H4h	2.93	down	0.000243	0.0000109
HIST1H4I	histone cluster 1, H4i	2.74	down	0.000075	0.0000013
HIST1H4J	histone cluster 1, H4j	2.35	down	0.000053	0.0000006
HIST1H4K	histone cluster 1, H4k	2.56	down	0.000043	0.0000004
HIST1H4L	histone cluster 1, H4l	2.99	down	0.000582	0.0000496
HIST2H2AB	histone cluster 2, H2ab	2.30	down	0.000028	0.0000001
HIST2H2AC	histone cluster 2, H2ac	3.05	down	0.000179	0.0000063
HIST2H2BE	histone cluster 2, H2be	2.50	down	0.002202	0.0003586
HIST2H2BF	histone cluster 2, H2bf	2.22	down	0.000102	0.0000021
HIST2H3A	histone cluster 2, H3a	3.55	down	0.000022	0.0000001
HIST2H4B	histone cluster 2, H4b	2.42	down	0.000820	0.0000833
HIST3H2BB	histone cluster 3, H2bb	3.02	down	0.000732	0.0000699
HMGB3	high mobility group box 3	1.74	down	0.003251	0.0006218
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	1.77	down	0.000234	0.0000103
HMMR	hyaluronan-mediated motility receptor (RHAMM)	2.63	down	0.000046	0.0000005
HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	2.06	down	0.000117	0.0000030
HNRNPA1L2	heterogeneous nuclear ribonucleoprotein A1-like 2	2.30	down	0.000064	0.0000010
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	1.53	down	0.001623	0.0002336
HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	1.80	down	0.000148	0.0000045
HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	1.60	down	0.000593	0.0000510
HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	1.92	down	0.000027	0.0000001
HNRNPK	heterogeneous nuclear ribonucleoprotein K	1.54	down	0.002838	0.0005144
HNRNPLL	heterogeneous nuclear ribonucleoprotein L-like	1.84	down	0.000116	0.0000029
HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	1.91	down	0.000287	0.0000150
HOXC4	homeobox C4	3.00	down	0.000452	0.0000320

HP1BP3	heterochromatin protein 1, binding protein 3	1.70	down	0.000490	0.0000373
HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	2.10	down	0.000211	0.0000086
HSPA4	heat shock 70kDa protein 4	1.65	down	0.000437	0.0000301
HSPA8	heat shock 70kDa protein 8	1.91	down	0.000250	0.0000115
HSPE1	heat shock 10kDa protein 1	1.52	down	0.000398	0.0000257
HSPH1	heat shock 105kDa/110kDa protein 1	1.99	down	0.000278	0.0000141
HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	1.81	down	0.003166	0.0005996
HYLS1	hydrolethalus syndrome 1	1.64	down	0.001977	0.0003110
IAPP	islet amyloid polypeptide	1.76	down	0.000068	0.0000010
ICAM5	intercellular adhesion molecule 5, telencephalin	1.55	down	0.000623	0.0000548
IDE	insulin-degrading enzyme	1.51	down	0.000743	0.0000721
IER5L	immediate early response 5-like	3.20	down	0.000060	0.0000008
IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	2.40	down	0.003325	0.0006458
IFT74	intraflagellar transport 74 homolog (Chlamydomonas)	1.67	down	0.003474	0.0006825
IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	1.62	down	0.000364	0.0000226
IL17B	interleukin 17B	1.55	down	0.002939	0.0005380
IL1R1	interleukin 1 receptor, type I	2.01	down	0.001708	0.0002523
ILF3-AS1	ILF3 antisense RNA 1 (head to head)	1.73	down	0.000227	0.0000097
ILKAP	integrin-linked kinase-associated serine/threonine phosphatase	1.56	down	0.001676	0.0002454
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	1.92	down	0.003082	0.0005768
IMPACT	impact RWD domain protein	1.76	down	0.001296	0.0001682
ING3	inhibitor of growth family, member 3	2.52	down	0.001226	0.0001545
INO80	INO80 complex subunit	1.57	down	0.001052	0.0001232
INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	2.13	down	0.000159	0.0000050
INSIG1	insulin induced gene 1	1.83	down	0.000842	0.0000863
IPO11	importin 11	1.64	down	0.000586	0.0000501
IPO4	importin 4	1.51	down	0.000983	0.0001116
IQCE	IQ motif containing E	1.68	down	0.001919	0.0002986
ISOC2	isochorismatase domain containing 2	1.51	down	0.002988	0.0005519
ITCH	itchy E3 ubiquitin protein ligase	1.75	down	0.001436	0.0001966

KAT5	K(lysine) acetyltransferase 5	1.54	down	0.000087	0.0000016
KAZALD1	Kazal-type serine peptidase inhibitor domain 1	2.33	down	0.000266	0.0000131
KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14	2.03	down	0.000487	0.0000367
KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	4.41	down	0.000147	0.0000045
KCNRG	potassium channel regulator	2.21	down	0.001719	0.0002545
KCTD15	potassium channel tetramerization domain containing 15	1.95	down	0.000359	0.0000218
KIAA0020	KIAA0020	1.69	down	0.000294	0.0000157
KIAA0368	KIAA0368	1.56	down	0.001362	0.0001806
KIAA1024	KIAA1024	1.55	down	0.001952	0.0003061
KIAA1033	KIAA1033	1.76	down	0.000074	0.0000012
KIF14	kinesin family member 14	1.94	down	0.000021	0.0000001
KIF15	kinesin family member 15	1.57	down	0.003565	0.0007095
KIF18A	kinesin family member 18A	1.87	down	0.000324	0.0000185
KIF20A	kinesin family member 20A	1.90	down	0.000061	0.0000009
KIF20B	kinesin family member 20B	1.89	down	0.000428	0.0000289
KLF10	Kruppel-like factor 10	1.53	down	0.002861	0.0005205
KLHL29	kelch-like family member 29	1.56	down	0.000147	0.0000045
KNSTRN	kinetochore-localized astrin/SPAG5 binding protein	2.13	down	0.000069	0.0000011
KNTC1	kinetochore associated 1	1.62	down	0.000298	0.0000161
KTN1-AS1	KTN1 antisense RNA 1	2.42	down	0.000170	0.0000058
L3MBTL3	l(3)mbt-like 3 (Drosophila)	2.34	down	0.001006	0.0001155
LARP1B	La ribonucleoprotein domain family, member 1B	1.74	down	0.002217	0.0003617
LARP4	La ribonucleoprotein domain family, member 4	1.57	down	0.000691	0.0000641
LARS	leucyl-tRNA synthetase	2.02	down	0.000120	0.0000032
LBR	lamin B receptor	1.63	down	0.002538	0.0004381
LEAP2	liver expressed antimicrobial peptide 2	3.05	down	0.000868	0.0000915
LENG9	leukocyte receptor cluster (LRC) member 9	2.52	down	0.000250	0.0000115
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	2.39	down	0.000276	0.0000139

LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	2.06	down	0.000157	0.0000049
LIAS	lipoic acid synthetase	1.62	down	0.001142	0.0001392
LIG3	ligase III, DNA, ATP-dependent	1.69	down	0.003530	0.0006990
LINC00115	long intergenic non-protein coding RNA 115	2.58	down	0.003882	0.0007940
LINC00263	long intergenic non-protein coding RNA 263	1.96	down	0.001298	0.0001690
LINC00482	long intergenic non-protein coding RNA 482	1.58	down	0.000318	0.0000179
LINC01003	long intergenic non-protein coding RNA 1003	2.70	down	0.001698	0.0002496
LINC01004	long intergenic non-protein coding RNA 1004	1.83	down	0.002931	0.0005358
LINC01089	long intergenic non-protein coding RNA 1089	1.89	down	0.001704	0.0002512
LINC01315	long intergenic non-protein coding RNA 1315	1.53	down	0.000353	0.0000214
LIPT2	lipoyl(octanoyl) transferase 2 (putative)	1.85	down	0.001056	0.0001240
LMNB1	lamin B1	1.58	down	0.000023	0.0000001
LNP1	leukemia NUP98 fusion partner 1	2.90	down	0.001657	0.0002406
LOC100233156	tektin 4 pseudogene	2.86	down	0.000289	0.0000152
LOC93622	Morf4 family associated protein 1-like 1 pseudogene	1.65	down	0.000291	0.0000154
LONP1	lon peptidase 1, mitochondrial	1.51	down	0.001026	0.0001186
LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	1.56	down	0.001638	0.0002367
LRPPRC	leucine-rich pentatricopeptide repeat containing	1.63	down	0.001303	0.0001700
LRRC20	leucine rich repeat containing 20	1.64	down	0.000027	0.0000001
LRRC61	leucine rich repeat containing 61	1.52	down	0.004179	0.0008882
LRRCC1	leucine rich repeat and coiled-coil centrosomal protein 1	2.03	down	0.000197	0.0000076
LRRN2	leucine rich repeat neuronal 2	1.76	down	0.000144	0.0000043
LRTOMT	leucine rich transmembrane and O-methyltransferase domain containing	1.57	down	0.001363	0.0001811
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	1.83	down	0.002023	0.0003203
LTV1	LTV1 ribosome biogenesis factor	1.51	down	0.000059	0.0000007
LUC7L3	LUC7-like 3 (S. cerevisiae)	3.27	down	0.004842	0.0010922
LYPLAL1	lysophospholipase-like 1	1.60	down	0.000343	0.0000205
LYRM4	LYR motif containing 4	1.51	down	0.003595	0.0007173

LZTFL1	leucine zipper transcription factor-like 1	1.73	down	0.003098	0.0005828
MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	1.77	down	0.000713	0.0000670
MALL	mal, T-cell differentiation protein-like	1.80	down	0.000329	0.0000192
MAP4	microtubule-associated protein 4	1.85	down	0.000389	0.0000248
MARS	methionyl-tRNA synthetase	1.66	down	0.000737	0.0000707
MAT2A	methionine adenosyltransferase II, alpha	1.58	down	0.000121	0.0000032
MBLAC2	metallo-beta-lactamase domain containing 2	2.12	down	0.000027	0.0000001
MCM7	minichromosome maintenance complex component 7	1.76	down	0.000364	0.0000224
MDC1	mediator of DNA-damage checkpoint 1	1.53	down	0.000185	0.0000067
MED22	mediator complex subunit 22	1.74	down	0.001333	0.0001751
METAP2	methionyl aminopeptidase 2	2.09	down	0.000102	0.0000022
METTL10	methyltransferase like 10	1.55	down	0.000678	0.0000625
METTL12	methyltransferase like 12	2.42	down	0.000178	0.0000062
METTL16	methyltransferase like 16	1.72	down	0.000648	0.0000586
METTL25	methyltransferase like 25	1.99	down	0.001402	0.0001895
METTL3	methyltransferase like 3	2.12	down	0.000294	0.0000158
METTL4	methyltransferase like 4	1.52	down	0.000669	0.0000613
MFSD3	major facilitator superfamily domain containing 3	1.70	down	0.000435	0.0000298
MINA	MYC induced nuclear antigen	1.58	down	0.003290	0.0006357
MIPEP	mitochondrial intermediate peptidase	1.62	down	0.000195	0.0000074
MIR4697HG	MIR4697 host gene (non-protein coding)	1.52	down	0.003773	0.0007639
MIRLET7BHG	MIRLET7B host gene (non-protein coding)	2.45	down	0.000794	0.0000797
MIS18BP1	MIS18 binding protein 1	1.57	down	0.003143	0.0005928
MKX	mohawk homeobox	3.22	down	0.004296	0.0009258
MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	1.51	down	0.000149	0.0000046
MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	1.56	down	0.000894	0.0000957
MMP11	matrix metallopeptidase 11 (stromelysin 3)	1.93	down	0.000289	0.0000151
MNX1-AS1	MNX1 antisense RNA 1 (head to head)	1.71	down	0.002084	0.0003339

MORN1	MORN repeat containing 1	2.72	down	0.000253	0.0000119
MOS	v-mos Moloney murine sarcoma viral oncogene homolog	2.06	down	0.001835	0.0002808
MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	1.66	down	0.000446	0.0000311
MRM1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	1.73	down	0.000582	0.0000495
MRPS25	mitochondrial ribosomal protein S25	2.44	down	0.000180	0.0000064
MRPS31	mitochondrial ribosomal protein S31	1.70	down	0.000533	0.0000431
MRTO4	mRNA turnover 4 homolog (S. cerevisiae)	1.76	down	0.002521	0.0004336
MSTO1	misato 1, mitochondrial distribution and morphology regulator	2.02	down	0.000124	0.0000033
MTA1	metastasis associated 1	2.04	down	0.000638	0.0000569
MTAP	methylthioadenosine phosphorylase	1.81	down	0.000915	0.0000992
MTFMT	mitochondrial methionyl-tRNA formyltransferase	1.51	down	0.000222	0.0000094
MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	1.61	down	0.000550	0.0000454
MTL5	metallothionein-like 5, testis-specific (tesmin)	2.51	down	0.000269	0.0000134
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	1.77	down	0.002690	0.0004763
MXRA7	matrix-remodelling associated 7	1.58	down	0.002344	0.0003897
MYC	v-myc avian myelocytomatosis viral oncogene homolog	1.69	down	0.001174	0.0001449
MYCL	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog	1.79	down	0.000459	0.0000332
MYCNOS	MYCN opposite strand	1.58	down	0.000295	0.0000159
MYO5C	myosin VC	1.84	down	0.000113	0.0000027
N4BP1	NEDD4 binding protein 1	1.55	down	0.000169	0.0000058
NAA15	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	2.20	down	0.002703	0.0004790
NADK	NAD kinase	1.65	down	0.000253	0.0000120
NAMPT	nicotinamide phosphoribosyltransferase	1.82	down	0.002378	0.0003983
NARS2	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	1.93	down	0.000364	0.0000225
NASP	nuclear autoantigenic sperm protein (histone-binding)	1.53	down	0.000306	0.0000168
NDE1	nudE neurodevelopment protein 1	1.87	down	0.000149	0.0000046
NECAB3	N-terminal EF-hand calcium binding protein 3	1.53	down	0.000740	0.0000710

NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	2.01	down	0.000371	0.0000231
NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	1.61	down	0.000512	0.0000405
NFYA	nuclear transcription factor Y, alpha	1.74	down	0.000751	0.0000733
NFYB	nuclear transcription factor Y, beta	1.87	down	0.000020	0.0000000
NIN	ninein (GSK3B interacting protein)	1.89	down	0.001382	0.0001853
NKRF	NFKB repressing factor	1.81	down	0.000008	0.0000000
NKX2-5	NK2 homeobox 5	1.52	down	0.004179	0.0008892
NLE1	notchless homolog 1 (Drosophila)	2.33	down	0.001273	0.0001642
NLRP2	NLR family, pyrin domain containing 2	1.63	down	0.000389	0.0000250
NMD3	NMD3 ribosome export adaptor	1.69	down	0.000290	0.0000153
NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	2.05	down	0.000027	0.0000001
NOL10	nucleolar protein 10	1.95	down	0.000640	0.0000573
NOL9	nucleolar protein 9	1.52	down	0.000061	0.0000008
NOP16	NOP16 nucleolar protein	1.52	down	0.000222	0.0000094
NOP56	NOP56 ribonucleoprotein	1.65	down	0.000458	0.0000330
NOP58	NOP58 ribonucleoprotein	1.68	down	0.000134	0.0000038
NPRL3	nitrogen permease regulator-like 3 (S. cerevisiae)	1.95	down	0.001129	0.0001367
NPTN	neuroplastin	1.54	down	0.002314	0.0003833
NR2F1-AS1	NR2F1 antisense RNA 1	1.58	down	0.003486	0.0006862
NR6A1	nuclear receptor subfamily 6, group A, member 1	1.80	down	0.000775	0.0000771
NREP	neuronal regeneration related protein	1.53	down	0.004048	0.0008483
NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)	1.71	down	0.000963	0.0001083
NSUN2	NOP2/Sun RNA methyltransferase family, member 2	1.76	down	0.000098	0.0000020
NT5M	5',3'-nucleotidase, mitochondrial	2.01	down	0.000220	0.0000093
NTHL1	nth endonuclease III-like 1 (E. coli)	1.77	down	0.000429	0.0000290
NTSR1	neurotensin receptor 1 (high affinity)	2.75	down	0.000061	0.0000009
NUDT18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	1.66	down	0.000691	0.0000642
NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	2.36	down	0.000477	0.0000353

NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	1.56	down	0.000630	0.0000557
NUP133	nucleoporin 133kDa	1.62	down	0.004418	0.0009617
NUP35	nucleoporin 35kDa	1.58	down	0.001883	0.0002915
NUP98	nucleoporin 98kDa	1.70	down	0.001451	0.0001991
OARD1	O-acyl-ADP-ribose deacylase 1	2.17	down	0.000060	0.0000008
OBSL1	obscurin-like 1	1.54	down	0.003484	0.0006853
ODF3B	outer dense fiber of sperm tails 3B	2.05	down	0.000321	0.0000183
OLA1	Obg-like ATPase 1	2.36	down	0.000753	0.0000736
OPA1	optic atrophy 1 (autosomal dominant)	1.53	down	0.001445	0.0001981
OR51B5	olfactory receptor, family 51, subfamily B, member 5	3.45	down	0.000061	0.0000009
ORC2	origin recognition complex, subunit 2	1.56	down	0.001045	0.0001219
OSBPL1A	oxysterol binding protein-like 1A	1.91	down	0.000061	0.0000008
OSBPL5	oxysterol binding protein-like 5	1.67	down	0.002152	0.0003480
OSGEPL1	O-sialoglycoprotein endopeptidase-like 1	2.35	down	0.000613	0.0000532
OTUD6B	OTU domain containing 6B	1.93	down	0.000771	0.0000763
PACS2	phosphofurin acidic cluster sorting protein 2	3.17	down	0.000539	0.0000439
PAFAH1B1	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	2.05	down	0.000426	0.0000287
PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	1.51	down	0.003907	0.0008043
PAIP1	poly(A) binding protein interacting protein 1	1.70	down	0.001402	0.0001897
PALD1	phosphatase domain containing, paladin 1	1.70	down	0.000086	0.0000016
PARPBP	PARP1 binding protein	1.58	down	0.001809	0.0002749
PARVB	parvin, beta	2.66	down	0.000070	0.0000011
PCF11	PCF11 cleavage and polyadenylation factor subunit	2.56	down	0.000022	0.0000001
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	2.04	down	0.001122	0.0001356
PCM1	pericentriolar material 1	1.75	down	0.001805	0.0002736
PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	1.57	down	0.000723	0.0000687
PCSK6	proprotein convertase subtilisin/kexin type 6	1.96	down	0.002168	0.0003512
PCSK9	proprotein convertase subtilisin/kexin type 9	1.54	down	0.000198	0.0000076

PDCD6IP	programmed cell death 6 interacting protein	1.81	down	0.001513	0.0002120
PDE3B	phosphodiesterase 3B, cGMP-inhibited	1.66	down	0.001120	0.0001351
PDE9A	phosphodiesterase 9A	1.79	down	0.000452	0.0000320
PDK1	pyruvate dehydrogenase kinase, isozyme 1	1.72	down	0.000773	0.0000766
PDP1	pyruvate dehyrogenase phosphatase catalytic subunit 1	1.66	down	0.000426	0.0000286
PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	1.77	down	0.000109	0.0000026
PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	2.84	down	0.000056	0.0000007
PECR	peroxisomal trans-2-enoyl-CoA reductase	1.54	down	0.000737	0.0000706
PEMT	phosphatidylethanolamine N-methyltransferase	1.62	down	0.000967	0.0001089
PGLS	6-phosphogluconolactonase	1.77	down	0.000108	0.0000025
PHF19	PHD finger protein 19	1.65	down	0.000304	0.0000167
PHOSPHO2	phosphatase, orphan 2	1.68	down	0.003252	0.0006224
PIF1	PIF1 5'-to-3' DNA helicase	4.26	down	0.000044	0.0000004
PIH1D1	PIH1 domain containing 1	1.55	down	0.000323	0.0000184
PINX1	PIN2/TERF1 interacting, telomerase inhibitor 1	1.84	down	0.002210	0.0003602
PITPNA	phosphatidylinositol transfer protein, alpha	1.58	down	0.000049	0.0000005
PKD1	polycystic kidney disease 1 (autosomal dominant)	1.53	down	0.000528	0.0000422
PLAC1	placenta-specific 1	1.76	down	0.001871	0.0002885
PLAGL2	pleiomorphic adenoma gene-like 2	1.59	down	0.001204	0.0001504
PLCB2	phospholipase C, beta 2	1.74	down	0.000591	0.0000508
PLCH1	phospholipase C, eta 1	2.34	down	0.002990	0.0005528
PLEKHJ1	pleckstrin homology domain containing, family J member 1	1.79	down	0.003663	0.0007348
PLK1	polo-like kinase 1	3.04	down	0.000206	0.0000082
PLK4	polo-like kinase 4	1.92	down	0.001131	0.0001374
PLXNA1	plexin A1	1.57	down	0.003927	0.0008100
PMM2	phosphomannomutase 2	1.73	down	0.000171	0.0000059
PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	1.65	down	0.000390	0.0000251
PNN	pinin, desmosome associated protein	2.15	down	0.002552	0.0004417

PNPT1	polyribonucleotide nucleotidyltransferase 1	1.55	down	0.001853	0.0002843
POLR1B	polymerase (RNA) I polypeptide B, 128kDa	2.11	down	0.004667	0.0010406
POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	1.81	down	0.003154	0.0005964
POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	1.57	down	0.000867	0.0000913
PP7080	uncharacterized LOC25845	1.87	down	0.000132	0.0000037
PPARGC1B	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	1.73	down	0.003267	0.0006299
PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	1.55	down	0.000162	0.0000052
PPHLN1	periphilin 1	1.95	down	0.001156	0.0001416
PPIEL	peptidylprolyl isomerase E-like pseudogene	1.70	down	0.000765	0.0000755
PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	1.56	down	0.000288	0.0000151
PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	1.76	down	0.001810	0.0002754
PPP2R3C	protein phosphatase 2, regulatory subunit B", gamma	1.55	down	0.004107	0.0008657
PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme	1.77	down	0.002555	0.0004424
PPP6C	protein phosphatase 6, catalytic subunit	2.65	down	0.000538	0.0000438
PPP6R2	protein phosphatase 6, regulatory subunit 2	1.86	down	0.000209	0.0000085
PPP6R3	protein phosphatase 6, regulatory subunit 3	1.97	down	0.000068	0.0000010
PRDM16	PR domain containing 16	2.40	down	0.000289	0.0000151
PRELID2	PRELI domain containing 2	1.52	down	0.001501	0.0002091
PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	1.72	down	0.003099	0.0005830
PRKACB	protein kinase, cAMP-dependent, catalytic, beta	3.82	down	0.000079	0.0000014
PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	2.04	down	0.000165	0.0000054
PRKCDBP	protein kinase C, delta binding protein	1.86	down	0.000800	0.0000805
PRMT3	protein arginine methyltransferase 3	2.08	down	0.000015	0.0000000
PRMT6	protein arginine methyltransferase 6	1.69	down	0.000014	0.0000000
PRMT7	protein arginine methyltransferase 7	1.65	down	0.001225	0.0001542
PRPF38B	pre-mRNA processing factor 38B	1.75	down	0.001298	0.0001690
PRPF4B	pre-mRNA processing factor 4B	1.61	down	0.003727	0.0007518
PRR22	proline rich 22	2.59	down	0.000073	0.0000012

PRRC2B	proline-rich coiled-coil 2B	1.53	down	0.000917	0.0000996
PSKH1	protein serine kinase H1	2.93	down	0.000197	0.0000075
PSMG4	proteasome (prosome, macropain) assembly chaperone 4	1.93	down	0.002484	0.0004241
PSRC1	proline/serine-rich coiled-coil 1	2.17	down	0.000458	0.0000329
PTCD3	pentatricopeptide repeat domain 3	1.76	down	0.003153	0.0005959
PTK2	protein tyrosine kinase 2	1.65	down	0.000329	0.0000191
PTP4A3	protein tyrosine phosphatase type IVA, member 3	1.81	down	0.002756	0.0004928
PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	1.53	down	0.004630	0.0010279
PTTG2	pituitary tumor-transforming 2	1.57	down	0.001420	0.0001932
PUS1	pseudouridylate synthase 1	1.57	down	0.002623	0.0004602
PUS7	pseudouridylate synthase 7 (putative)	2.03	down	0.000655	0.0000592
PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	1.75	down	0.000390	0.0000251
PVRL3	poliovirus receptor-related 3	1.73	down	0.001661	0.0002416
PWP1	PWP1 homolog (S. cerevisiae)	1.58	down	0.002049	0.0003251
PYCR1	pyrroline-5-carboxylate reductase 1	1.93	down	0.003262	0.0006281
PYCRL	pyrroline-5-carboxylate reductase-like	1.82	down	0.000061	0.0000009
PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	1.89	down	0.000460	0.0000333
R3HDM2	R3H domain containing 2	1.73	down	0.000192	0.0000072
RAB11A	RAB11A, member RAS oncogene family	1.53	down	0.001465	0.0002015
RAB11FIP4	RAB11 family interacting protein 4 (class II)	2.56	down	0.000191	0.0000071
RAB26	RAB26, member RAS oncogene family	1.94	down	0.000569	0.0000479
RABGAP1L	RAB GTPase activating protein 1-like	2.06	down	0.002483	0.0004236
RABL2A	RAB, member of RAS oncogene family-like 2A	1.53	down	0.000533	0.0000431
RACGAP1	Rac GTPase activating protein 1	1.59	down	0.000159	0.0000051
RAD50	RAD50 homolog (S. cerevisiae)	1.64	down	0.000022	0.0000001
RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	1.56	down	0.002462	0.0004177
RANBP2	RAN binding protein 2	1.73	down	0.002107	0.0003386
RARS2	arginyl-tRNA synthetase 2, mitochondrial	1.60	down	0.000220	0.0000093
RBBP4	retinoblastoma binding protein 4	1.57	down	0.002917	0.0005323
RBM12	RNA binding motif protein 12	2.59	down	0.000123	0.0000033

RCC2	regulator of chromosome condensation 2	1.64	down	0.001508	0.0002107
RDM1	RAD52 motif containing 1	1.62	down	0.002640	0.0004641
REEP5	receptor accessory protein 5	1.58	down	0.000959	0.0001078
RET	ret proto-oncogene	2.07	down	0.003714	0.0007490
RHOBTB1	Rho-related BTB domain containing 1	1.63	down	0.001402	0.0001897
RHOBTB3	Rho-related BTB domain containing 3	1.58	down	0.000390	0.0000251
RMDN2	regulator of microtubule dynamics 2	1.56	down	0.004490	0.0009836
RNA5-8S5	RNA, 5.8S ribosomal 5	1.85	down	0.003397	0.0006637
RNF141	ring finger protein 141	1.84	down	0.000255	0.0000122
RNF145	ring finger protein 145	1.58	down	0.000437	0.0000301
RNF207	ring finger protein 207	1.53	down	0.000971	0.0001096
RNF213	ring finger protein 213	1.74	down	0.000776	0.0000773
RNF216	ring finger protein 216	1.58	down	0.000956	0.0001068
RNF222	ring finger protein 222	1.57	down	0.004695	0.0010492
ROCK2	Rho-associated, coiled-coil containing protein kinase 2	1.82	down	0.001023	0.0001180
RPL10A	ribosomal protein L10a	2.26	down	0.002988	0.0005512
RPL22L1	ribosomal protein L22-like 1	6.99	down	0.000259	0.0000125
RPL3	ribosomal protein L3	2.10	down	0.001269	0.0001631
RPL37	ribosomal protein L37	1.62	down	0.002118	0.0003410
RPP25L	ribonuclease P/MRP 25kDa subunit-like	1.57	down	0.001470	0.0002028
RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	2.16	down	0.000598	0.0000515
RPS14	ribosomal protein S14	2.36	down	0.000125	0.0000034
RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	2.12	down	0.000060	0.0000008
RPUSD3	RNA pseudouridylate synthase domain containing 3	1.76	down	0.000548	0.0000451
RPUSD4	RNA pseudouridylate synthase domain containing 4	2.50	down	0.000044	0.0000004
RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	1.57	down	0.001153	0.0001411
RRP9	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)	1.59	down	0.000408	0.0000268
RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	1.53	down	0.000823	0.0000836
RSC1A1	regulatory solute carrier protein, family 1, member 1	1.53	down	0.004090	0.0008596

RSPH3	radial spoke 3 homolog (Chlamydomonas)	1.58	down	0.000539	0.0000440
RTDR1	rhabdoid tumor deletion region gene 1	2.68	down	0.002600	0.0004536
S100PBP	S100P binding protein	1.62	down	0.001528	0.0002150
SAPCD2	suppressor APC domain containing 2	1.80	down	0.000093	0.0000018
SBNO1	strawberry notch homolog 1 (Drosophila)	2.27	down	0.000083	0.0000015
SCAMP1	secretory carrier membrane protein 1	1.90	down	0.001546	0.0002185
SCARA3	scavenger receptor class A, member 3	1.89	down	0.000454	0.0000324
SCARNA13	small Cajal body-specific RNA 13	6.16	down	0.000010	0.0000000
SCARNA17	small Cajal body-specific RNA 17	1.97	down	0.004563	0.0010065
SCARNA9	small Cajal body-specific RNA 9	1.93	down	0.001066	0.0001256
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	1.85	down	0.000426	0.0000286
SCLY	selenocysteine lyase	1.58	down	0.000325	0.0000186
SDAD1	SDA1 domain containing 1	1.68	down	0.000150	0.0000046
SEC11A	SEC11 homolog A (S. cerevisiae)	1.51	down	0.000255	0.0000122
SEC23A	Sec23 homolog A (S. cerevisiae)	1.69	down	0.002107	0.0003384
SEC23IP	SEC23 interacting protein	1.62	down	0.000907	0.0000977
SEC24A	SEC24 family member A	1.51	down	0.003253	0.0006239
SEC63	SEC63 homolog (S. cerevisiae)	1.98	down	0.004309	0.0009294
SECISBP2	SECIS binding protein 2	1.86	down	0.000079	0.0000014
SEPT10	septin 10	1.50	down	0.003513	0.0006948
SERBP1	SERPINE1 mRNA binding protein 1	1.57	down	0.000528	0.0000422
SETD6	SET domain containing 6	1.69	down	0.001362	0.0001808
SFPQ	splicing factor proline/glutamine-rich	1.52	down	0.001264	0.0001620
SGOL2	shugoshin-like 2 (S. pombe)	1.97	down	0.000488	0.0000369
SH3PXD2B	SH3 and PX domains 2B	1.59	down	0.001276	0.0001646
SHPRH	SNF2 histone linker PHD RING helicase, E3 ubiquitin protein ligase	2.14	down	0.002070	0.0003312
SIM2	single-minded family bHLH transcription factor 2	2.59	down	0.000247	0.0000113
SIRT5	sirtuin 5	1.77	down	0.002186	0.0003552

SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 2	1.93	down	0.000722	0.0000685
SLC18B1	solute carrier family 18, subfamily B, member 1	1.97	down	0.000307	0.0000169
SLC25A13	solute carrier family 25 (aspartate/glutamate carrier), member 13	1.90	down	0.000027	0.0000001
SLC25A32	solute carrier family 25 (mitochondrial folate carrier), member 32	1.76	down	0.003090	0.0005800
SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37	1.63	down	0.000234	0.0000103
SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	1.82	down	0.000119	0.0000031
SLC30A9	solute carrier family 30 (zinc transporter), member 9	1.91	down	0.000102	0.0000022
SLC35B4	solute carrier family 35 (UDP-xylose/UDP-N-acetylglucosamine transporter), member B4	2.28	down	0.000753	0.0000735
SLC35F5	solute carrier family 35, member F5	2.23	down	0.002175	0.0003529
SLC35G1	solute carrier family 35, member G1	2.14	down	0.001496	0.0002080
SLC38A1	solute carrier family 38, member 1	1.57	down	0.000135	0.0000039
SLC39A11	solute carrier family 39, member 11	1.64	down	0.000262	0.0000127
SLC5A6	solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6	1.68	down	0.000044	0.0000004
SLC6A8	solute carrier family 6 (neurotransmitter transporter), member 8	1.53	down	0.001495	0.0002077
SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	1.67	down	0.000786	0.0000787
SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	1.56	down	0.004947	0.0011250
SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	2.78	down	0.000017	0.0000000
SLC9A8	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	1.72	down	0.002062	0.0003288
SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	1.82	down	0.000710	0.0000667
SMIM19	small integral membrane protein 19	2.15	down	0.000044	0.0000004
SNHG1	small nucleolar RNA host gene 1 (non-protein coding)	1.56	down	0.000488	0.0000370
SNHG10	small nucleolar RNA host gene 10 (non-protein coding)	2.19	down	0.000878	0.0000931

SNHG12	small nucleolar RNA host gene 12 (non-protein coding)	1.59	down	0.002471	0.0004209
SNHG15	small nucleolar RNA host gene 15 (non-protein coding)	1.57	down	0.000454	0.0000324
SNHG17	small nucleolar RNA host gene 17 (non-protein coding)	1.66	down	0.000450	0.0000317
SNHG20	small nucleolar RNA host gene 20 (non-protein coding)	1.68	down	0.004499	0.0009873
SNHG3	small nucleolar RNA host gene 3 (non-protein coding)	1.71	down	0.000219	0.0000091
SNHG7	small nucleolar RNA host gene 7 (non-protein coding)	2.55	down	0.001195	0.0001482
SOBP	sine oculis binding protein homolog (Drosophila)	1.59	down	0.000272	0.0000136
SON	SON DNA binding protein	2.37	down	0.000250	0.0000116
SORD	sorbitol dehydrogenase	1.94	down	0.002062	0.0003283
SOX4	SRY (sex determining region Y)-box 4	2.13	down	0.000282	0.0000146
SPEF2	sperm flagellar 2	3.17	down	0.001002	0.0001149
SPEN	spen family transcriptional repressor	1.67	down	0.004254	0.0009115
SPTLC2	serine palmitoyltransferase, long chain base subunit 2	2.16	down	0.000027	0.0000001
SRBD1	S1 RNA binding domain 1	1.94	down	0.000263	0.0000128
SREBF1	sterol regulatory element binding transcription factor 1	1.73	down	0.001741	0.0002595
SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	1.50	down	0.000656	0.0000594
SRPK1	SRSF protein kinase 1	1.65	down	0.000624	0.0000550
SRSF1	serine/arginine-rich splicing factor 1	2.39	down	0.000915	0.0000991
SRSF3	serine/arginine-rich splicing factor 3	1.65	down	0.001493	0.0002069
SRSF5	serine/arginine-rich splicing factor 5	1.56	down	0.002733	0.0004862
SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	1.93	down	0.002750	0.0004909
ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	1.54	down	0.000074	0.0000012
ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	2.05	down	0.000413	0.0000273
ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1.94	down	0.000014	0.0000000
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	1.86	down	0.000051	0.0000006
STAG3	stromal antigen 3	1.52	down	0.003846	0.0007830
STARD8	StAR-related lipid transfer (START) domain containing 8	2.69	down	0.000174	0.0000060
STK33	serine/threonine kinase 33	1.68	down	0.000463	0.0000336

STOX1	storkhead box 1	1.74	down	0.003784	0.0007662
STRADB	STE20-related kinase adaptor beta	1.85	down	0.000386	0.0000246
SUGP2	SURP and G patch domain containing 2	1.58	down	0.001511	0.0002115
SURF6	surfeit 6	1.96	down	0.000301	0.0000164
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	1.65	down	0.000276	0.0000139
TACC3	transforming, acidic coiled-coil containing protein 3	1.51	down	0.001078	0.0001278
TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	1.59	down	0.000163	0.0000053
TAF12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa	1.77	down	0.000081	0.0000014
TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	2.26	down	0.000062	0.0000009
TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	1.84	down	0.000850	0.0000878
TARDBP	TAR DNA binding protein	3.42	down	0.000512	0.0000404
TBC1D20	TBC1 domain family, member 20	1.64	down	0.001440	0.0001972
TBC1D22A	TBC1 domain family, member 22A	1.81	down	0.000263	0.0000128
TBC1D22B	TBC1 domain family, member 22B	1.53	down	0.001493	0.0002069
TBC1D31	TBC1 domain family, member 31	1.50	down	0.002127	0.0003429
TBCD	tubulin folding cofactor D	1.52	down	0.000438	0.0000302
TBL3	transducin (beta)-like 3	1.88	down	0.000047	0.0000005
TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	1.89	down	0.001009	0.0001161
TCFL5	transcription factor-like 5 (basic helix-loop-helix)	2.41	down	0.000014	0.0000000
TECPR2	tectonin beta-propeller repeat containing 2	1.57	down	0.000368	0.0000229
TEKT4	tektin 4	2.99	down	0.000325	0.0000186
TESPA1	thymocyte expressed, positive selection associated 1	1.52	down	0.001741	0.0002591
TEX10	testis expressed 10	1.54	down	0.000109	0.0000026
TEX19	testis expressed 19	1.86	down	0.000677	0.0000624
TFRC	transferrin receptor	1.65	down	0.000030	0.0000002
TGIF1	TGFB-induced factor homeobox 1	1.63	down	0.001111	0.0001336
THEM4	thioesterase superfamily member 4	1.92	down	0.000124	0.0000033

THEM6	thioesterase superfamily member 6	2.38	down	0.000195	0.0000074
THNSL1	threonine synthase-like 1 (S. cerevisiae)	2.01	down	0.000472	0.0000346
THOC2	THO complex 2	1.67	down	0.000851	0.0000886
TIA1	TIA1 cytotoxic granule-associated RNA binding protein	2.07	down	0.003256	0.0006260
TIMM23B	translocase of inner mitochondrial membrane 23 homolog B (yeast)	1.89	down	0.004225	0.0009041
TLE6	transducin-like enhancer of split 6	1.58	down	0.001781	0.0002684
TM4SF18	transmembrane 4 L six family member 18	2.64	down	0.000282	0.0000145
TMBIM4	transmembrane BAX inhibitor motif containing 4	2.77	down	0.001298	0.0001688
TMEM129	transmembrane protein 129	2.56	down	0.000197	0.0000075
TMEM17	transmembrane protein 17	1.61	down	0.001124	0.0001358
TMEM181	transmembrane protein 181	1.64	down	0.000846	0.0000873
TMEM187	transmembrane protein 187	2.07	down	0.000283	0.0000146
TMEM248	transmembrane protein 248	1.93	down	0.000006	0.0000000
TMEM67	transmembrane protein 67	1.73	down	0.001094	0.0001305
TMX2	thioredoxin-related transmembrane protein 2	1.65	down	0.000184	0.0000067
TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1	1.57	down	0.002345	0.0003901
TNFRSF13C	tumor necrosis factor receptor superfamily, member 13C	1.57	down	0.000294	0.0000157
TNFRSF18	tumor necrosis factor receptor superfamily, member 18	1.51	down	0.000497	0.0000382
TOLLIP-AS1	TOLLIP antisense RNA 1 (head to head)	2.19	down	0.000695	0.0000648
TRA2B	transformer 2 beta homolog (Drosophila)	1.70	down	0.001336	0.0001758
TRAPPC12	trafficking protein particle complex 12	1.83	down	0.000127	0.0000035
TRAPPC9	trafficking protein particle complex 9	1.60	down	0.000071	0.0000011
TRDMT1	tRNA aspartic acid methyltransferase 1	1.79	down	0.000108	0.0000026
TRIM33	tripartite motif containing 33	1.97	down	0.000626	0.0000553
TRIM65	tripartite motif containing 65	1.80	down	0.000449	0.0000316
TRMT10A	tRNA methyltransferase 10 homolog A (S. cerevisiae)	2.00	down	0.000179	0.0000063
TRMT10C	tRNA methyltransferase 10 homolog C (S. cerevisiae)	1.55	down	0.000022	0.0000001
TRMT61A	tRNA methyltransferase 61 homolog A (S. cerevisiae)	1.84	down	0.000770	0.0000761
TRMT61B	tRNA methyltransferase 61 homolog B (S. cerevisiae)	1.87	down	0.000783	0.0000781

TSEN2	TSEN2 tRNA splicing endonuclease subunit	2.22	down	0.001278	0.0001651
TSTD3	thiosulfate sulfurtransferase (rhodanese)-like domain containing 3	1.50	down	0.000045	0.0000004
TTC12	tetratricopeptide repeat domain 12	1.94	down	0.000417	0.0000278
TTC27	tetratricopeptide repeat domain 27	1.67	down	0.001069	0.0001262
TTC7A	tetratricopeptide repeat domain 7A	1.55	down	0.001656	0.0002404
TTF2	transcription termination factor, RNA polymerase II	1.50	down	0.000226	0.0000097
TTLL1	tubulin tyrosine ligase-like family, member 1	1.99	down	0.000199	0.0000076
TUBB4B	tubulin, beta 4B class IVb	1.54	down	0.000621	0.0000543
TUBE1	tubulin, epsilon 1	1.55	down	0.000425	0.0000285
TUBGCP5	tubulin, gamma complex associated protein 5	1.51	down	0.003411	0.0006670
TUG1	taurine up-regulated 1 (non-protein coding)	1.93	down	0.000922	0.0001006
TULP4	tubby like protein 4	1.84	down	0.000147	0.0000045
TXNDC11	thioredoxin domain containing 11	1.74	down	0.000872	0.0000921
U2SURP	U2 snRNP-associated SURP domain containing	2.30	down	0.000633	0.0000562
UBA6	ubiquitin-like modifier activating enzyme 6	2.31	down	0.001432	0.0001956
UBAP2L	ubiquitin associated protein 2-like	2.96	down	0.000803	0.0000810
UBASH3B	ubiquitin associated and SH3 domain containing B	1.94	down	0.000436	0.0000299
UBE2E1	ubiquitin-conjugating enzyme E2E 1	1.67	down	0.003068	0.0005737
UBE3B	ubiquitin protein ligase E3B	1.96	down	0.001109	0.0001329
UBE3D	ubiquitin protein ligase E3D	1.59	down	0.000512	0.0000404
UBE4B	ubiquitination factor E4B	1.58	down	0.000204	0.0000080
UBP1	upstream binding protein 1 (LBP-1a)	1.73	down	0.001019	0.0001172
UBQLN4	ubiquilin 4	1.78	down	0.000899	0.0000966
UFSP1	UFM1-specific peptidase 1 (non-functional)	1.54	down	0.003085	0.0005781
UNC5A	unc-5 homolog A (C. elegans)	1.95	down	0.001788	0.0002699
URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	1.91	down	0.000917	0.0000998
UROS	uroporphyrinogen III synthase	1.75	down	0.000412	0.0000271
USP10	ubiquitin specific peptidase 10	1.76	down	0.001823	0.0002785
USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	1.82	down	0.002255	0.0003701

USP25	ubiquitin specific peptidase 25	3.19	down	0.000166	0.0000055
USP40	ubiquitin specific peptidase 40	2.04	down	0.000459	0.0000332
USP47	ubiquitin specific peptidase 47	1.59	down	0.001733	0.0002577
USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	1.69	down	0.000389	0.0000249
UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	1.72	down	0.000949	0.0001055
UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	2.07	down	0.000081	0.0000015
VAC14	Vac14 homolog (S. cerevisiae)	1.80	down	0.000167	0.0000056
VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	3.66	down	0.002586	0.0004501
VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	2.05	down	0.002345	0.0003903
VPS9D1-AS1	VPS9D1 antisense RNA 1	1.57	down	0.003773	0.0007634
VTI1A	vesicle transport through interaction with t-SNAREs 1A	2.22	down	0.000586	0.0000501
VWA8	von Willebrand factor A domain containing 8	2.54	down	0.000723	0.0000686
WAPAL	wings apart-like homolog (Drosophila)	1.52	down	0.000716	0.0000677
WDR12	WD repeat domain 12	1.66	down	0.000992	0.0001132
WDR35	WD repeat domain 35	2.33	down	0.000917	0.0000998
WDR36	WD repeat domain 36	1.73	down	0.000321	0.0000182
WDR43	WD repeat domain 43	1.50	down	0.001126	0.0001361
WDR70	WD repeat domain 70	1.91	down	0.000079	0.0000014
WDR78	WD repeat domain 78	2.62	down	0.000257	0.0000124
WHSC1	Wolf-Hirschhorn syndrome candidate 1	1.79	down	0.000487	0.0000367
WWC3	WWC family member 3	1.86	down	0.000424	0.0000284
WWP2	WW domain containing E3 ubiquitin protein ligase 2	1.59	down	0.002635	0.0004628
XXYLT1	xyloside xylosyltransferase 1	2.05	down	0.000165	0.0000054
YARS	tyrosyl-tRNA synthetase	1.55	down	0.004255	0.0009121
YLPM1	YLP motif containing 1	1.69	down	0.002439	0.0004129
YPEL4	yippee-like 4 (Drosophila)	1.66	down	0.001437	0.0001967
YTHDC2	YTH domain containing 2	1.94	down	0.000453	0.0000322

ZBED4	zinc finger, BED-type containing 4	1.62	down	0.000250	0.0000116
ZBTB2	zinc finger and BTB domain containing 2	1.67	down	0.000786	0.0000786
ZCCHC8	zinc finger, CCHC domain containing 8	1.50	down	0.000496	0.0000381
ZCWPW1	zinc finger, CW type with PWWP domain 1	1.52	down	0.004179	0.0008876
ZDHHC3	zinc finger, DHHC-type containing 3	2.00	down	0.000450	0.0000317
ZFC3H1	zinc finger, C3H1-type containing	2.28	down	0.000180	0.0000064
ZFYVE28	zinc finger, FYVE domain containing 28	1.67	down	0.003512	0.0006941
ZMYM2	zinc finger, MYM-type 2	1.62	down	0.002421	0.0004089
ZMYM4	zinc finger, MYM-type 4	1.52	down	0.000028	0.0000001
ZNF215	zinc finger protein 215	1.81	down	0.000169	0.0000057
ZNF280D	zinc finger protein 280D	1.63	down	0.003628	0.0007259
ZNF302	zinc finger protein 302	1.88	down	0.001259	0.0001607
ZNF469	zinc finger protein 469	1.74	down	0.000484	0.0000364
ZNF485	zinc finger protein 485	1.64	down	0.000831	0.0000846
ZNF497	zinc finger protein 497	2.09	down	0.000338	0.0000200
ZNF581	zinc finger protein 581	1.84	down	0.000086	0.0000016
ZNF706	zinc finger protein 706	1.71	down	0.000168	0.0000057
ZNF775	zinc finger protein 775	1.62	down	0.001198	0.0001488
ZNF789	zinc finger protein 789	1.98	down	0.000929	0.0001020
ZNRF1	zinc and ring finger 1, E3 ubiquitin protein ligase	2.20	down	0.000205	0.0000080

Supplementary Table 2. Redox-related, FUra-responsive genes as determined by cDNA microarray analysis

Microarray data from Supplemental Table 1 were queried with regard to the GO and KEGG databases (see text) to identify genes involved in redox metabolism. The fold change represents the extent of induction by exposure to 10 µM FUra for 24 h. The p-value is corrected for multiple testing using the Benjamini-Hochberg algorithm (see Materials and Methods).

Gene Symbol	Description	Fold Change	Regulation	Corrected p-value	p-value
AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase) (AKR1B10), mRNA [NM_020299]	6.37	up	0.000054	0.000001
AKR1B15	aldo-keto reductase family 1, member B15 (AKR1B15), mRNA [NM_001080538]	6.04	up	0.000259	0.000012
AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) (AKR1C1), mRNA [NM_001353]	2.31	up	0.001859	0.000286
AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3), mRNA [NM_003739]	1.91	up	0.001267	0.000163
ALDH3A1	aldehyde dehydrogenase 3 family, member A1 (ALDH3A1), transcript variant 1, mRNA [NM_001135168]	2.02	up	0.001249	0.000159
ALDH4A1	aldehyde dehydrogenase 4 family, member A1 (ALDH4A1), nuclear gene encoding mitochondrial protein, transcript variant P5CDhS, mRNA [NM_170726]	2.56	up	0.000558	0.000046
BLVRB	biliverdin reductase B (flavin reductase (NADPH)) (BLVRB), mRNA [NM_000713]	2.01	up	0.001495	0.000208
CBR3	carbonyl reductase 3 (CBR3), mRNA [NM_001236]	1.89	up	0.003410	0.000667
CYB5R1	cytochrome b5 reductase 1 (CYB5R1), mRNA [NM_016243]	1.66	up	0.002679	0.000473
DHRS13	dehydrogenase/reductase (SDR family) member 13 (DHRS13), mRNA [NM_144683]	1.87	up	0.001244	0.000158
DHRS7	dehydrogenase/reductase (SDR family) member 7 (DHRS7), mRNA [NM_016029]	1.59	up	0.000098	0.000002
FDXR	ferredoxin reductase (FDXR), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_004110]	2.27	up	0.000178	0.000006
GLRX	glutaredoxin (thioltransferase) (GLRX), transcript variant 1, mRNA [NM_002064]	1.54	up	0.000476	0.000035
GLRX2	glutaredoxin 2 (GLRX2), transcript variant 1, mRNA [NM_016066]	1.68	up	0.000623	0.000055
GPX1	glutathione peroxidase 1 (GPX1), transcript variant 2, mRNA [NM_201397]	1.65	up	0.000812	0.000082
HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 (HSD3B7), transcript variant 2, mRNA [NM_001142777]	1.66	up	0.000698	0.000065
KDSR	3-ketodihydrosphingosine reductase (KDSR), mRNA [NM_002035]	1.72	up	0.000967	0.000109
LOXL2	lysyl oxidase-like 2 (LOXL2), mRNA [NM_002318]	1.59	up	0.000106	0.000002
LOXL4	lysyl oxidase-like 4 (LOXL4), mRNA [NM_032211]	2.04	up	0.000887	0.000095

NDOR1	NADPH dependent diflavin oxidoreductase 1 (NDOR1), transcript variant 1, mRNA [NM_001144026]	1.84	up	0.000445	0.000031
NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa (NDUFB11), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_019056]	1.54	up	0.000022	0.000000
PRODH	proline dehydrogenase (oxidase) 1 (PRODH), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_016335]	1.95	up	0.000208	0.000008
RRM1	ribonucleotide reductase M1 (RRM1), mRNA [NM_001033]	1.54	up	0.000884	0.000094
SOD2	superoxide dismutase 2, mitochondrial (SOD2), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_001024465]	1.56	up	0.000307	0.000017
SQRDL	sulfide quinone reductase-like (yeast) (SQRDL), nuclear gene encoding mitochondrial protein, mRNA [NM_021199]	1.54	up	0.000185	0.000007
TP53I3	tumor protein p53 inducible protein 3 (TP53I3), transcript variant 1, mRNA [NM_004881]	4.78	up	0.000041	0.000000
TXNDC17	thioredoxin domain containing 17 (TXNDC17), mRNA [NM_032731]	1.61	up	0.000740	0.000071
ACAD9	acyl-CoA dehydrogenase family, member 9 (ACAD9), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_014049]	1.58	down	0.003176	0.000603
ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain (ACADS), nuclear gene encoding mitochondrial protein, mRNA [NM_000017]	1.64	down	0.004722	0.001056
ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain (ACADSB), nuclear gene encoding mitochondrial protein, mRNA [NM_001609]	2.01	down	0.000376	0.000023
ALKBH3	alkB, alkylation repair homolog 3 (E. coli) (ALKBH3), mRNA [NM_139178]	1.55	down	0.001059	0.000125
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1) (AOC3), mRNA [NM_003734]	1.64	down	0.001775	0.000267
BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide (BCKDHB), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_000056]	1.54	down	0.003890	0.000798
CHDH	choline dehydrogenase (CHDH), nuclear gene encoding mitochondrial protein, mRNA [NM_018397]	1.83	down	0.000694	0.000065
CPOX	coproporphyrinogen oxidase (CPOX), mRNA [NM_000097]	1.64	down	0.001790	0.000270
CRYL1	crystallin, lambda 1 (CRYL1), mRNA [NM_015974]	1.96	down	0.000274	0.000014
CRYZ	crystallin, zeta (quinone reductase) (CRYZ), transcript variant 1, mRNA [NM_001130042]	1.68	down	0.000543	0.000044
CYB5RL	cytochrome b5 reductase-like (CYB5RL), mRNA [NM_001031672]	2.30	down	0.000351	0.000021
DHRS2	dehydrogenase/reductase (SDR family) member 2 (DHRS2), transcript variant 1, mRNA [NM_182908]	2.94	down	0.000022	0.000000
DHRS3	dehydrogenase/reductase (SDR family) member 3 (DHRS3), mRNA [NM_004753]	1.61	down	0.000253	0.000012

HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase (HMGCR), transcript variant 1, mRNA [NM_000859]	1.77	down	0.000234	0.000010
HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8 (HSD17B8), mRNA [NM_014234]	2.10	down	0.000211	0.000009
HTATIP2	HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), transcript variant 2, mRNA [NM_006410]	1.81	down	0.003166	0.000600
MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (MTHFD1L), nuclear gene encoding mitochondrial protein, mRNA [NM_015440]	1.53	down	0.000167	0.000006
PDK1	pyruvate dehydrogenase kinase, isozyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA [NM_002610]	1.72	down	0.000773	0.000077
PDP1	pyruvate dehyrogenase phosphatase catalytic subunit 1 (PDP1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_001161779]	1.66	down	0.000426	0.000029
PECR	peroxisomal trans-2-enoyl-CoA reductase (PECR), mRNA [NM_018441]	1.54	down	0.000737	0.000071
PYCR1	pyrroline-5-carboxylate reductase 1 (PYCR1), transcript variant 1, mRNA [NM_006907]	1.84	down	0.001594	0.000228
PYCRL	pyrroline-5-carboxylate reductase-like (PYCRL), mRNA [NM_023078]	1.82	down	0.000061	0.000001
PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1 (PYROXD1), mRNA [NM_024854]	1.89	down	0.000460	0.000033
SORD	sorbitol dehydrogenase (SORD), mRNA [NM_003104]	1.94	down	0.002062	0.000328
TMX2	thioredoxin-related transmembrane protein 2 (TMX2), transcript variant 1, mRNA [NM_015959]	1.63	down	0.000286	0.000015
TXNDC11	thioredoxin domain containing 11 (TXNDC11), mRNA [NM_015914]	1.74	down	0.000872	0.000092