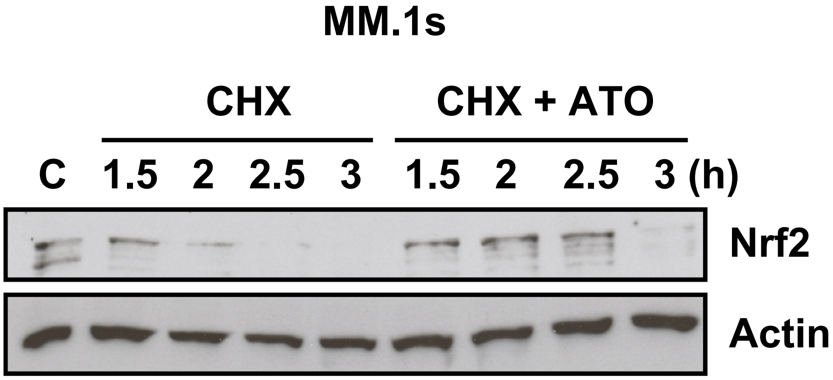
Supplemental Figure 1.

MM.1s cells were treated with 100 nM of Bortezomib for 2 h, washed with supplemented-RPMI and treated with CHX (10 µg/mL) or CHX plus ATO (2 µM) for 1.5, 2, 2.5 and 3 h. Nrf2 protein expression was analyzed by Western Blot.



Supplemental Table - 1

LogRatios for up-regulated genes at 6 h in all cell lines
Two-fold changes are in red bold

Gene Descriptor	**Symbol**	**U266 6h**	**MM.1s 6h**	**8226/S 6h**	**KMS11 6h**
3-hydroxyisobutyryl-Coenzyme A hydrolase	HIBCH	0.6	0.8	0.8	**1.1**
3-hydroxyisobutyryl-Coenzyme A hydrolase	HIBCH	0.6	0.8	0.7	**1.2**
82-kD FMRP Interacting Protein	182-FIP	0.6	0.6	0.6	0.4
82-kD FMRP Interacting Protein	182-FIP	0.5	0.5	0.7	0.3
abhydrolase domain containing 4	ABHD4	0.6	0.6	0.7	0.8
ADP-ribosylation factor guanine nucleotide-exchange factor 1	ARFGEF1	0.5	0.7	0.4	0.5
activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	AHSA1	0.7	0.8	0.4	0.8
aldo-keto reductase family 1, member C3	AKR1C3	**1.1**	**2.6**	**2.7**	**3.5**
ankyrin repeat and MYND domain containing 2	ANKMY2	0.6	0.5	0.9	0.6
AIF-like mitochondrion-associated inducer of death	AMID	**1.6**	**2.2**	**1.3**	**1.2**
ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A	0.4	**1.8**	**1.2**	**1.3**
ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A	0.5	**2.0**	0.9	**1.3**
asparagine-linked glycosylation 10 homolog (yeast)	ALG10	0.4	0.8	0.9	0.7
ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	0.8	**1.1**	0.9	**1.1**
ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	0.7	**1.2**	0.9	0.5
ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	0.4	**1.3**	0.4	0.7
ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	0.6	0.7	0.5	0.7
ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	ATP6V1A	0.6	**1.2**	0.5	0.9
ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	ATP6V1A	0.5	**1.0**	0.4	0.8
ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	ATP6V0A1	0.4	**1.2**	**1.0**	**1.3**
ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	ATP6V0A1	0.4	**1.0**	**1.0**	**1.2**
ATP-binding cassette, sub-family C (CFTR/MRP), member 5	ABCC5	0.5	**1.4**	0.3	0.7
ATP-binding cassette, sub-family G (WHITE), member 1	ABCG1	**1.2**	**1.8**	0.4	0.9
BCL2-associated athanogene 2	BAG2	0.7	0.9	0.5	0.7
BCL2-associated athanogene 3	BAG3	**2.8**	**1.3**	**1.9**	**3.1**
biogenesis of lysosome-related organelles complex-1, subunit 2	BLOC1S2	0.3	**1.4**	**1.0**	**1.5**
breast carcinoma amplified sequence 2	BCAS2	0.6	0.5	0.7	0.8
BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1	0.5	**1.6**	0.8	**2.0**
BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1	0.6	**1.4**	0.7	**1.8**
CCAAT/enhancer binding protein (C/EBP),	CEBPG	0.6	0.8	**1.2**	**1.3**

gamma					
CCAAT/enhancer binding protein (C/EBP), gamma	CEBPG	0.6	0.4	**1.1**	**1.2**
CDK2-associated protein 1	CDK2AP1	0.4	**1.1**	0.3	0.6
CDNA clone IMAGE:30349460, partial cds		**1.0**	**1.1**	0.8	**1.5**
CDNA FLJ41270 fis, clone BRAMY2036387		0.8	**1.6**	0.9	**2.1**
CDNA: FLJ22822 fis, clone KAIA3968		0.5	0.6	0.3	0.6
cell cycle progression 1	CCPG1	0.9	0.8	**1.4**	**1.9**
cell cycle progression 1	CCPG1	0.5	0.5	**1.5**	**1.6**
cell cycle progression 1	CCPG1	0.5	0.6	**1.3**	**1.6**
chondroitin sulfate glucuronyltransferase	CSGlcA-T	0.8	**1.4**	0.7	**1.0**
chondroitin sulfate glucuronyltransferase	CSGlcA-T	0.8	**1.2**	0.6	0.8
chromosome 1 open reading frame 24	C1orf24	0.5	0.8	**1.5**	**1.8**
chromosome 10 open reading frame 45	C10orf45	**1.0**	0.4	0.8	**1.7**
chromosome 10 open reading frame 45	C10orf45	**1.0**	0.3	0.7	**1.8**
chromosome 14 open reading frame 11	C14orf11	0.3	0.7	0.8	0.7
Chromosome 16 open reading frame 28	C16orf28	**1.3**	**1.5**	**1.4**	**1.0**
chromosome 20 open reading frame 139	C20orf139	**1.7**	**2.6**	**1.2**	**2.6**
chromosome 20 open reading frame 24	C20orf24	0.3	0.9	0.4	0.3
chromosome 5 open reading frame 5	C5orf5	0.8	0.9	0.8	**1.5**
chromosome 6 open reading frame 133	C6orf133	0.8	0.8	0.4	0.7
chromosome 6 open reading frame 133	C6orf133	0.7	0.7	0.4	0.9
chromosome 6 open reading frame 166	C6orf166	0.5	0.4	0.4	0.7
chromosome 9 open reading frame 55	C9orf55	0.4	0.4	0.5	0.6
Chromosome X open reading frame 39	CXorf39	0.4	0.7	0.6	0.5
claudin 12	CLDN12	0.4	0.8	0.9	0.7
Homo sapiens cDNA, 5 end /clone=IMAGE-163624		0.6	**1.4**	**1.2**	**1.6**
clusterin (complement lysis inhibitor, SP-40,40, apolipoprotein J)	CLU	0.4	**1.5**	**1.2**	**2.2**
c-Mpl binding protein	LOC113251	0.6	**1.3**	0.5	0.5
coagulation factor II (thrombin) receptor	F2R	0.5	0.8	0.4	**1.6**
COBL-like 1	COBLL1	0.9	0.6	0.6	**1.3**
COBL-like 1	COBLL1	0.6	0.9	0.5	**1.2**
collaborates/cooperates with ARF protein	CARF	0.5	0.6	0.4	0.4
CLONE=IMAGE:856163 /UG=Hs.315562 ESTs		**1.7**	**3.1**	**2.3**	**2.9**
CLONE=IMAGE:1676516 /UG=Hs.42911		0.3	0.9	0.5	0.4
CLONE=IMAGE:2330615 /UG=Hs.116586 ESTs		0.3	0.5	0.6	0.5
CLONE=IMAGE:2508169 /UG=Hs.134791 ESTs		0.5	**1.3**	0.9	**1.2**
Hs.183861 Homo sapiens cDNA FLJ20042 fis, clone COL00424		0.4	0.5	**1.0**	0.9
Hs.195822 Homo sapiens cDNA: FLJ21464 fis, clone COL04768		0.7	**1.3**	0.6	**1.0**
Human DNA sequence from clone RP5-1174N9		**4.2**	**3.2**	**3.7**	**2.0**
Hs.94 DnaJ (Hsp40) homolog, subfamily A, member 1		**1.1**	**1.0**	**1.2**	**1.4**
CLONE=CS0DF022YM06 (3 prime) /UG=Hs.201615 ESTs		**2.0**	**1.6**	**1.9**	**2.3**
CLONE=IMAGE:2815110 /UG=Hs.122113 ESTs		0.3	0.4	0.8	0.7
CLONE=IMAGE:2727178 /UG=Hs.252782 ESTs		0.7	**1.7**	**1.5**	**1.6**
DB_XREF=est:EST384381 /UG=Hs.292998 ESTs		0.5	0.5	0.6	**1.0**
CLONE=IMAGE:3084358 /UG=Hs.77496		0.4	**1.7**	**1.1**	**1.9**
CLONE=IMAGE:4347163 /UG=Hs.23248		0.5	**1.2**	0.7	0.4

CLONE=IMAGE:4346922 /UG=Hs.278614		0.4	0.3	0.5	0.8
CLONE=IMAGE:265528 /UG=Hs.155218		0.5	**1.2**	0.4	**1.0**
Hs.118786 metallothionein 2A /FL=gb:NM_005953.1		**6.0**	**6.4**	**3.4**	**6.2**
cystathionase (cystathionine gamma-lyase)	CTH	**2.0**	**1.0**	**2.4**	**1.6**
CHORD-containing, zinc binding protein 1	CHORDC1	0.9	**1.0**	0.7	0.6
cysteinyl-tRNA synthetase	CARS	0.6	0.3	0.9	**1.1**
cytochrome P450, family 2, subfamily R, polypeptide 1	CYP2R1	0.6	0.4	0.7	0.8
cytoplasmic linker associated protein 1	CLASP1	0.5	0.6	0.6	0.6
death effector domain containing 2	DEDD2	**1.2**	0.7	**1.1**	**1.4**
dihydrolipoamide dehydrogenase	DLD	0.3	0.5	0.4	0.5
DKFZP564G2022 protein	DKFZP564G2022	0.4	0.4	0.3	0.6
DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJA1	**1.0**	**1.0**	0.9	**1.2**
DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	**1.9**	**1.3**	**1.4**	**1.9**
DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	**1.7**	**1.1**	**1.5**	**1.8**
DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	**2.3**	**1.6**	**1.6**	**1.7**
DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	**2.0**	**1.5**	**1.6**	**1.8**
DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	**1.1**	0.9	**1.2**	**1.1**
DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	0.9	0.6	0.7	**1.1**
DnaJ (Hsp40) homolog, subfamily B, member 9	DNAJB9	0.4	0.5	0.5	0.5
DnaJ (Hsp40) homolog, subfamily B, member 9	DNAJB9	0.3	0.4	0.5	0.5
dual specificity phosphatase 12	DUSP12	0.7	0.4	0.5	0.5
dynactin 4 (p62)	DCTN4	0.6	**1.1**	0.9	**1.3**
echinoderm microtubule associated protein like 5	EML5	0.6	**1.1**	**1.2**	**1.3**
eukaryotic translation initiation factor 4E binding protein 1	EIF4EBP1	**1.2**	0.4	0.6	**1.3**
eukaryotic translation initiation factor 5	EIF5	0.4	**1.2**	0.8	0.6
eukaryotic translation initiation factor 5	EIF5	0.4	**1.1**	0.9	0.6
eukaryotic translation initiation factor 5	EIF5	0.3	0.8	0.8	0.6
eukaryotic translation initiation factor 5	EIF5	0.3	0.7	0.8	0.7
Exportin, tRNA (nuclear export receptor for tRNAs)	XPOT	0.7	0.6	0.5	0.4
Fas (TNFRSF6)-associated via death domain	FADD	0.6	0.7	0.4	0.5
F-box protein 30	FBXO30	0.5	**1.7**	**2.4**	**2.4**
ferritin, heavy polypeptide 1	FTH1	**2.7**	**1.3**	**2.9**	**3.4**
ferritin, heavy polypeptide 1	FTH1	**1.1**	**1.4**	0.9	**1.5**
ferritin, heavy polypeptide pseudogene 1	FTHP1	0.7	**1.1**	0.3	0.9
ferrochelatase (protoporphyria)	FECH	0.5	0.4	0.9	**1.8**
forkhead box K1	FOXK1	0.6	**1.5**	0.9	**2.1**
G protein-coupled receptor 89	GPR89	0.5	0.9	0.9	**1.1**
G protein-coupled receptor 89	GPR89	0.5	0.8	0.6	0.9
G protein-coupled receptor 89	GPR89	0.6	0.7	0.6	0.8
G protein-coupled receptor 89	GPR89	0.5	0.6	0.8	0.7
GA binding protein transcription factor, beta subunit 2, 47kDa	GABPB2	0.5	**1.0**	0.6	0.6
GABA(A) receptor-associated protein like 1	GABARAPL1	**1.3**	**2.8**	**5.4**	**3.4**
galactosidase, alpha	GLA	**2.1**	**2.2**	0.5	**1.2**
Hs.8765 RNA helicase-related protein /FL=gb:AF078844.1		**2.9**	**3.8**	**2.8**	**3.0**
Hs.326774 Homo sapiens metallothionein 1H-		**6.2**	**4.7**	**2.6**	**4.0**

like					
Hs.12102 /LL=8724 /UG_GENE=SNX3		0.4	0.8	0.7	0.9
CLONE=IMAGE:3071180 /TID=Hs2.349076.1		0.5	0.8	**1.3**	**1.5**
CLONE=IMAGE:5392477 /TID=Hs2.401218.1		0.5	0.9	0.9	**1.2**
general transcription factor IIIC, polypeptide 3, 102kDa	GTF3C3	0.9	0.4	0.9	0.7
glucosidase, beta; acid (includes glucosylceramidase)	GBA /// GBAP	0.5	0.9	0.4	0.7
glutamate-cysteine ligase, catalytic subunit	GCLC	0.6	**1.3**	0.9	**1.1**
glutamate-cysteine ligase, catalytic subunit	GCLC	0.7	**1.4**	0.9	0.9
glutamate-cysteine ligase, modifier subunit	GCLM	**1.6**	**3.0**	**2.3**	**2.6**
glutamate-cysteine ligase, modifier subunit	GCLM	**1.4**	**3.2**	**2.0**	**2.5**
glutaredoxin (thioltransferase)	GLRX	0.6	**1.2**	0.8	**1.2**
glutaredoxin 2	GLRX2	0.4	**1.0**	0.4	0.4
growth hormone inducible transmembrane protein	GHITM	0.6	0.7	0.5	0.6
heat shock 105kDa/110kDa protein 1	HSPH1	**1.9**	**1.7**	**1.4**	**1.9**
heat shock 105kDa/110kDa protein 1	HSPH1	**1.6**	**1.4**	**1.1**	**1.5**
heat shock 27kDa protein 1	HSPB1	**1.4**	**3.3**	**1.0**	**1.8**
heat shock 70kDa protein 1A /1B	HSPA1A /1B	**5.0**	**5.0**	**4.3**	**5.1**
heat shock 70kDa protein 1B	HSPA1B	**3.6**	**3.2**	**2.9**	**3.8**
heat shock 70kDa protein 4	HSPA4	0.8	0.6	0.4	**1.0**
heat shock 70kDa protein 4	HSPA4	0.9	0.5	0.5	0.8
heat shock 70kDa protein 4	HSPA4	0.8	0.6	0.5	0.6
heat shock 70kDa protein 6 (HSP70B')	HSPA6	**3.9**	**3.9**	**3.2**	**5.3**
heat shock 70kDa protein 6 (HSP70B')	HSPA6	**2.4**	**1.3**	**2.1**	**3.7**
heat shock 90kDa protein 1, alpha	HSPCA	0.4	**1.1**	0.4	0.4
heat shock 90kDa protein 1, alpha	HSPCA	0.3	**1.2**	0.3	0.3
heat shock 90kDa protein 1, alpha	HSPCA	0.3	0.7	0.2	0.3
heat shock 90kDa protein 1, beta	HSPCB	0.3	0.5	0.3	0.3
heat shock protein (hsp110 family)	APG-1	**1.0**	0.4	**1.3**	**1.0**
heme oxygenase (decycling) 1	HMOX1	**3.8**	**6.0**	**3.1**	**5.6**
HIV-1 Tat interacting protein, 60kDa	HTATIP	0.6	0.4	0.3	0.8
HIV-1 Tat interacting protein, 60kDa	HTATIP	0.4	0.6	0.4	0.7
HMG-box transcription factor 1	HBP1	0.6	0.9	0.8	**1.2**
Hypothetical LOC403340	MGC70870	0.7	0.2	**1.3**	0.6
hypothetical protein DKFZp564O0523	DKFZP564O0523	0.6	0.6	0.5	0.5
hypothetical protein FLJ10276	FLJ10276	0.3	**1.0**	0.9	**1.6**
hypothetical protein FLJ20097	FLJ20097	0.4	0.9	0.5	**1.0**
hypothetical protein FLJ20489	FLJ20489	0.6	**1.6**	**1.5**	**2.2**
hypothetical protein FLJ20716	FLJ20716	**1.6**	**1.8**	**1.1**	**1.3**
hypothetical protein FLJ31413	FLJ31413	0.3	0.8	0.7	**1.3**
Hypothetical protein FLJ32421	FLJ32421	0.4	0.3	0.3	0.5
hypothetical protein FLJ36701	FLJ36701	**4.1**	**5.6**	**4.3**	**4.5**
hypothetical protein HSPC138	HSPC138	**1.0**	0.6	0.7	0.5
hypothetical protein HSPC138	HSPC138	0.8	0.5	0.7	0.5
hypothetical protein LOC134145	LOC134145	0.9	**1.5**	0.7	**1.1**
hypothetical protein LOC339924	LOC339924	0.4	0.4	0.7	**1.3**
hypothetical protein LOC90637	LOC90637	**1.9**	**2.0**	**2.1**	**2.5**
hypothetical protein MGC11324	MGC11324	**2.8**	**3.2**	**1.7**	**4.3**
hypothetical protein MGC2747	MGC2747	0.3	0.5	0.4	0.7
hypothetical protein MGC8721	MGC8721	0.3	**1.0**	0.8	0.9

inhibitor of growth family, member 3	ING3	0.8	0.4	**1.0**	0.9
inhibitor of growth family, member 3	ING3	0.7	0.5	0.6	0.9
interferon-related developmental regulator 1	IFRD1	0.9	0.2	0.9	**1.3**
interleukin 10 receptor, alpha	IL10RA	0.8	**1.3**	0.4	**1.7**
intracellular memb.-assoc. Ca2+-indep. phospholipase A2 gamma	IPLA2(GAMMA)	0.3	0.9	**1.1**	**1.2**
KIAA0063 gene product	KIAA0063	**1.1**	0.8	0.6	**1.4**
KIAA0232 gene product	KIAA0232	0.5	0.7	0.7	**1.3**
KIAA0469 gene product	KIAA0469	**2.0**	**2.6**	**1.0**	**1.7**
kinesin family member 21A	KIF21A	0.6	**1.3**	0.5	**1.3**
LanC lantibiotic synthetase component C-like 2 (bacterial)	LANCL2	**1.0**	**1.2**	0.9	**1.2**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	0.6	**2.1**	**1.4**	**1.8**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	0.7	**1.5**	**1.7**	**1.8**
leupaxin	LPXN	**1.3**	**1.1**	0.3	0.5
LIM and senescent cell antigen-like domains 1	LIMS1	0.6	**1.0**	0.3	0.9
limkain b1	LKAP	0.8	0.6	0.8	0.6
lipopolysaccharide-induced TNF factor	LITAF	0.4	0.4	0.4	**1.9**
lipopolysaccharide-induced TNF factor	LITAF	0.3	0.3	0.3	**1.7**
Malic enzyme 1, NADP(+)-dependent, cytosolic	ME1	**1.8**	**1.8**	0.9	**2.1**
malic enzyme 1, NADP(+)-dependent, cytosolic	ME1	**1.3**	**1.5**	0.8	**2.1**
melanoma associated antigen (mutated) 1	MUM1	0.8	0.4	**1.1**	**1.4**
matrix metalloproteinase cytoplasmic tail binding protein-1	MTCBP-1	0.5	0.5	0.5	0.5
metallothionein 1E (functional)	MT1E	**7.6**	**4.5**	**4.2**	**3.6**
metallothionein 1F (functional)	MT1F	**9.5**	**8.5**	**4.0**	**8.8**
metallothionein 1F (functional)	MT1F	**5.1**	**4.9**	**3.4**	**4.2**
metallothionein 1G	MT1G	**5.5**	**5.8**	**3.6**	**3.5**
metallothionein 1H	MT1H	**7.8**	**7.5**	**3.7**	**4.9**
metallothionein 1X	MT1X	**7.5**	**9.3**	**3.5**	**5.5**
metallothionein 1X	MT1X	**7.0**	**6.6**	**3.4**	**5.4**
metallothionein 2A	MT2A	**6.0**	**6.4**	**3.4**	**6.2**
microtubule-associated protein 1 light chain 3 beta	MAP1LC3B	0.9	**1.1**	0.8	**1.3**
mitochondrial carrier homolog 1 (C. elegans)	MTCH1	0.3	0.2	0.5	0.6
mitochondrial ribosomal protein L18	MRPL18	**1.0**	**1.1**	0.7	**1.1**
Mitochondrial ribosomal protein S6	MRPS6	**1.4**	**1.0**	0.4	**1.2**
mitochondrial ribosomal protein S6	MRPS6	0.6	0.8	0.4	**1.1**
mitogen-activated protein kinase kinase 1 interacting protein 1	MAP2K1IP1	0.3	0.6	0.6	0.7
motile sperm domain containing 1	MOSPD1	0.4	0.4	0.9	0.6
muscleblind-like 2 (Drosophila)	MBNL2	**1.3**	0.8	**1.5**	**1.7**
muscleblind-like 2 (Drosophila)	MBNL2	**1.3**	0.9	**1.2**	**1.4**
muscleblind-like 2 (Drosophila)	MBNL2	**1.2**	0.5	0.6	**1.0**
NACHT, leucine rich repeat and PYD containing 7	NALP7	**1.0**	**1.6**	**1.5**	**1.8**
NAD(P)H dehydrogenase, quinone 1	NQO1	**1.4**	**5.5**	**1.9**	**2.8**
NAD(P)H dehydrogenase, quinone 1	NQO1	**1.4**	**2.8**	**2.1**	**2.4**
NAD(P)H dehydrogenase, quinone 1	NQO1	**1.2**	**3.3**	**1.4**	**2.2**
NAD(P)H dehydrogenase, quinone 2	NQO2	**1.4**	**2.2**	**1.4**	**1.7**
Nijmegen breakage syndrome 1 (nibrin)	NBS1	0.7	0.6	0.4	0.5
NSFL1 (p97) cofactor (p47)	NSFL1C	0.3	**1.1**	0.4	0.7
NTKL-binding protein 1	FLJ11752	0.5	0.7	0.4	0.5
nuclear transport factor 2-like export factor 2	NXT2	0.6	0.7	0.4	**1.0**

nucleosome assembly protein 1-like 2	NAP1L2	0.8	**2.1**	**1.7**	**1.4**
ornithine decarboxylase antizyme inhibitor	OAZIN	0.3	0.3	0.4	0.7
oxysterol binding protein-like 3	OSBPL3	0.4	**1.1**	0.5	**1.1**
pallidin homolog (mouse)	PLDN	0.3	0.6	0.3	0.7
pelota homolog (Drosophila)	PELO	0.6	**1.7**	0.9	**1.2**
peptidylprolyl isomerase D (cyclophilin D)	PPID	0.6	0.6	0.8	0.8
peptidylprolyl isomerase D (cyclophilin D)	PPID	0.5	0.3	0.7	0.5
Phosphate cytidylyltransferase 1, choline, alpha isoform	PCYT1A	0.6	**1.3**	**1.0**	**1.6**
phosphate cytidylyltransferase 1, choline, alpha isoform	PCYT1A	0.6	**1.1**	0.8	**1.5**
phosphatidylinositol glycan, class B	PIGB	0.6	0.8	**1.4**	**1.3**
phosphatidylinositol glycan, class B	PIGB	0.5	0.5	**1.3**	**1.3**
pirin (iron-binding nuclear protein)	PIR	0.9	**2.2**	**1.3**	**1.2**
prion protein (p27-30)	PRNP	0.5	0.3	0.8	**1.3**
procollagen-proline, 2-oxoglutarate 4-dioxygenase	P4HA2	0.6	**1.4**	**1.6**	**1.9**
Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	PRRG4	0.5	**1.0**	**1.0**	**1.7**
protease, serine, 16 (thymus)	PRSS16	0.8	0.5	0.9	0.9
proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	PSMD11	0.5	**1.1**	0.4	0.8
proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	PSMD12	0.4	**1.5**	0.5	**1.0**
Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	PSMD14	0.3	**1.1**	0.5	0.7
protein kinase, cAMP-dependent, catalytic, beta	PRKACB	0.5	**1.3**	**1.2**	**2.1**
protein kinase, cAMP-dependent, catalytic, beta	PRKACB	0.4	**1.1**	**1.1**	**1.6**
protein x 013	AD-020	0.7	**1.0**	0.7	0.6
proteoglycan 1, secretory granule	PRG1	0.4	0.9	0.5	0.3
PTD016 protein	LOC51136	0.5	**1.4**	0.7	**1.3**
purine-rich element binding protein B	PURB	0.4	0.7	0.4	**1.0**
quinoid dihydropteridine reductase	QDPR	0.4	0.5	0.3	0.3
rabaptin, RAB GTPase binding effector protein 2	RABEP2	0.5	0.9	0.8	0.6
RAN binding protein 2	RANBP2	0.6	0.8	0.5	0.4
reproduction 8	D8S2298E	**1.1**	**1.1**	0.7	**1.1**
Retinoblastoma-associated factor 600	RBAF600	0.6	**1.3**	0.6	**1.1**
rhomboid, veinlet-like 7 (Drosophila)	RHBDL7	0.8	0.8	0.9	0.6
rhomboid, veinlet-like 7 (Drosophila)	RHBDL7	0.8	0.7	0.7	0.6
ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	RNASEL	0.8	0.9	**1.7**	**1.5**
ribonuclease P 40kDa subunit	RPP40	0.8	**1.1**	0.5	0.8
ring finger protein 14	RNF14	0.4	0.6	0.5	0.8
ring finger protein 14	RNF14	0.5	0.5	0.5	0.5
RNA binding motif (RNP1, RRM) protein 3	RBM3	0.8	0.8	**1.1**	**1.4**
RNA binding motif protein 23	RBM23	0.7	0.7	0.4	0.4
RNA binding motif protein 30	RBM30	0.6	**1.2**	0.6	**1.0**
selenoprotein K	SELK	0.6	0.3	0.4	0.4
sequestosome 1	SQSTM1	**2.1**	**4.7**	**2.1**	**5.1**
sequestosome 1	SQSTM1	**1.1**	**2.4**	**1.8**	**2.7**
Ser/Thr-like kinase	MGC4796	**1.2**	**1.2**	**1.0**	**1.5**
Serine hydroxymethyltransferase 1 (soluble)	SHMT1	0.6	**1.0**	0.5	**1.0**
Serine hydroxymethyltransferase 1 (soluble)	SHMT1	0.6	0.7	0.6	0.9
serologically defined colon cancer antigen 33	SDCCAG33	0.9	0.8	**1.0**	**1.1**

serologically defined colon cancer antigen 33	SDCCAG33	**1.0**	0.6	**1.0**	**1.1**
sestrin 2	SESN2	**1.5**	0.4	**2.3**	**3.2**
SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	SUGT1	0.5	0.2	0.6	0.7
SHC (Src homology 2 domain containing) transforming protein 1	SHC1	0.4	0.5	0.5	0.5
Siah-interacting protein	SIP	0.7	0.6	0.4	0.8
Siah-interacting protein	SIP	0.6	0.6	0.3	0.5
Siah-interacting protein /// Siah-interacting protein	SIP	0.6	0.7	0.6	0.8
Similar to CG14903-PA		0.5	**1.1**	0.6	**1.0**
similar to F10G7.10.p	KIAA2024	0.7	**1.4**	0.6	0.9
similar to F10G7.10.p	KIAA2024	0.6	**1.3**	0.7	0.7
Similar to Hypothetical protein CBG13135		0.7	**1.4**	0.6	0.8
solute carrier family 3, member 2	SLC3A2	**1.1**	0.7	0.9	**1.3**
solute carrier family 30 (zinc transporter), member 1	SLC30A1	**3.9**	**1.8**	**2.1**	**2.7**
Solute carrier family 30 (zinc transporter), member 1	SLC30A1	**3.3**	**1.1**	**2.4**	**2.2**
solute carrier family 38, member 6	SLC38A6	0.9	**1.3**	0.5	**1.0**
solute carrier family 5 (inositol transporters), member 3	SLC5A3	**1.6**	**1.5**	0.4	**1.2**
solute carrier family 6, member 9	SLC6A9	**1.3**	0.6	**1.7**	**2.3**
solute carrier family 7, member 11	SLC7A11	**2.3**	**2.5**	**3.3**	**4.9**
solute carrier family 7, member 11	SLC7A11	**2.2**	**2.4**	**2.9**	**4.3**
solute carrier family 7, member 11	SLC7A11	**1.8**	**1.3**	**1.5**	**2.5**
sorting nexin 3	SNX3	0.4	0.8	0.6	**1.1**
sorting nexin 3	SNX3	0.3	0.7	0.5	0.8
spermidine/spermine N1-acetyltransferase	SAT	**2.3**	**2.8**	**1.0**	**1.3**
spermidine/spermine N1-acetyltransferase	SAT	**2.4**	**2.5**	0.8	**1.0**
spinster-like	SPINL	0.5	0.9	0.5	0.7
stress 70 protein chaperone, microsome-associated, 60kDa	STCH	0.4	0.4	0.4	0.9
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STIP1	0.7	0.8	0.4	0.9
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STIP1	0.7	0.8	0.4	0.8
suppression of tumorigenicity 13 (Hsp70 interacting protein)	ST13	0.5	0.6	0.6	**1.0**
suppression of tumorigenicity 13 (Hsp70 interacting protein)	ST13	0.5	0.8	0.4	0.8
suppression of tumorigenicity 13 (Hsp70 interacting protein)	ST13	0.3	0.7	0.4	0.6
syntaxin 3A	STX3A	0.6	**1.8**	0.9	**1.6**
syntaxin 3A	STX3A	0.8	**1.2**	0.6	0.8
testis derived transcript (3 LIM domains)	TES	0.7	0.6	**1.4**	**1.6**
testis derived transcript (3 LIM domains)	TES	0.7	0.4	**1.1**	**1.2**
tetratricopeptide repeat domain 14	TTC14	0.6	0.6	0.6	0.5
thioredoxin reductase 1	TXNRD1	0.9	**1.8**	0.5	**1.3**
THO complex 1	THOC1	0.3	0.8	0.6	**1.0**
weakly similar to NP_079012.2 gasdermin domain containing 1		0.5	0.6	0.4	0.6
transcription factor 8 (represses interleukin 2 expression)	TCF8	0.5	**2.1**	0.5	**1.2**
transducin (beta)-like 1X-linked	TBL1X	**1.2**	0.4	0.6	0.9

transducin (beta)-like 1X-linked	TBL1X	**1.1**	0.3	0.5	**1.0**
tribbles homolog 3 (Drosophila)	TRIB3	**1.6**	0.8	**1.4**	**2.1**
tribbles homolog 3 (Drosophila)	TRIB3	**1.7**	0.9	0.9	**1.8**
trinucleotide repeat containing 6	TNRC6	0.4	0.7	0.6	0.3
tryptophanyl-tRNA synthetase	WARS	0.6	0.8	0.4	0.8
TSPY-like 1	TSPYL1	0.6	0.5	0.3	0.6
tumor differentially expressed 2	TDE2	0.4	0.3	0.5	0.9
ubiquilin 1	UBQLN1	0.3	0.7	0.4	0.5
Ubiquitin protein ligase E3 component n-recognin 1	UBR1	0.4	0.6	0.5	0.8
ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	USP14	0.4	0.9	0.3	0.7
ubiquitin specific protease 38	USP38	0.4	0.9	0.6	0.5
ubiquitin-conjugating enzyme E2B (RAD6 homolog)	UBE2B	0.6	0.5	0.7	**1.2**
ubiquitin-conjugating enzyme E2B (RAD6 homolog)	UBE2B	0.4	0.3	0.5	0.8
ubiquitin-conjugating enzyme E2B (RAD6 homolog)	UBE2B	0.6	0.4	0.7	**1.1**
UBX domain containing 2	UBXD2	0.4	0.8	0.3	0.7
upregulated in colorectal cancer gene 1	UCC1	0.4	0.9	0.7	**1.3**
valosin-containing protein	VCP	0.6	0.8	0.5	0.9
valosin-containing protein	VCP	0.4	0.8	0.4	0.7
v-maf musculoaponeurotic fibrosarcoma oncogene homolog G	MAFG	0.8	**1.5**	0.8	**1.4**
WD repeat domain 1	WDR1	0.3	0.6	0.6	0.9
yippee-like 5 (Drosophila)	YPEL5	**1.0**	0.7	0.9	**1.5**
yippee-like 5 (Drosophila)	YPEL5	0.7	0.6	0.6	**1.7**
ZFP-36 for a zinc finger protein	HSZFP36	0.4	**1.9**	**1.3**	**1.7**
zinc finger and BTB domain containing 1	ZBTB1	0.5	**1.0**	0.6	0.6
zinc finger CCCH type, antiviral 1	ZC3HAV1	0.8	0.3	0.5	0.6
zinc finger CCCH type, antiviral 1	ZC3HAV1	0.7	0.3	0.4	0.6
zinc finger motif enhancer binding protein 2	Zep-2	0.6	**1.2**	0.4	0.9
zinc finger protein 165	ZNF165	**1.0**	**1.5**	0.5	**1.5**
zinc finger protein 184 (Kruppel-like)	ZNF184	0.4	0.8	**1.3**	**1.1**
zinc finger protein 267	ZNF267	**1.1**	**1.6**	0.4	0.8
zinc finger protein 295	ZNF295	0.4	0.9	0.7	**1.1**
zinc finger protein 3 (A8-51)	ZNF3	0.5	0.5	0.5	0.5
zinc finger protein 307	ZNF307	**1.0**	0.5	0.7	0.7
zinc finger protein 407	ZNF407	0.8	0.8	0.3	0.7
zinc finger protein 505	ZNF505	0.4	0.8	0.7	0.4
zinc finger protein 92 (HTF12)	ZNF92	0.5	**1.3**	0.9	0.5
zinc finger, A20 domain containing 2	ZA20D2	0.3	0.9	0.4	0.8
zinc finger, A20 domain containing 2	ZA20D2	0.3	0.8	0.4	0.7
Zinc finger, BED domain containing 3	ZBED3	0.9	**1.9**	**2.6**	**1.5**
zinc finger, BED domain containing 3	ZBED3	0.9	**1.1**	0.8	**1.4**

LogRatios for up-regulated genes at 24 h in all cell lines

Two-fold changes are in red bold

Gene Descriptor	Symbol	U266	MM.1s	8226/S	KMS11

		24h	24h	24h	24h
82-kD FMRP Interacting Protein	182-FIP	0.7	0.8	0.4	0.4
acylphosphatase 2, muscle type	ACYP2	0.9	**1.5**	0.9	**1.3**
ADP-ribosylation factor-like 6 interacting protein	ARL6IP	0.4	0.3	0.4	0.8
aldo-keto reductase family 1, member C3	AKR1C3	**1.6**	**3.2**	**2.9**	**5.9**
annexin A2	ANXA2	0.2	0.5	0.6	**1.4**
AIF-like mitochondrion-associated inducer of death	AMID	**1.8**	**1.9**	**1.0**	**1.1**
arachidonate 5-lipoxygenase-activating protein	ALOX5AP	**1.7**	**1.1**	0.5	**1.7**
ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A	**1.0**	**1.6**	0.6	0.9
ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A	0.8	**1.5**	0.5	0.7
biliverdin reductase B (flavin reductase (NADPH))	BLVRB	**1.4**	**2.2**	0.7	**2.9**
branched chain aminotransferase 1, cytosolic	BCAT1	**1.0**	**1.3**	0.8	**1.7**
calpain 7	CAPN7	0.5	0.3	0.5	0.3
caspase 8, apoptosis-related cysteine protease	CASP8	0.5	0.5	0.6	0.9
CCAAT/enhancer binding protein (C/EBP), gamma	CEBPG	0.5	0.6	0.5	0.8
CD63 antigen (melanoma 1 antigen)	CD63	0.4	0.4	0.3	0.3
CDK2-associated protein 1	CDK2AP1	0.8	**1.9**	0.5	**1.2**
cell cycle progression 1	CCPG1	**1.3**	0.6	0.8	**1.8**
chemokine-like factor super family 6	CKLFSF6	0.6	0.6	0.4	0.7
chloride intracellular channel 2	CLIC2	0.7	**2.6**	0.4	**1.1**
chromosome 1 open reading frame 19	C1orf19	0.6	0.4	0.4	0.3
chromosome 1 open reading frame 24	C1orf24	0.4	0.8	0.9	**1.5**
Chromosome 16 open reading frame 28	C16orf28	**1.4**	**1.1**	0.8	0.7
chromosome 20 open reading frame 139	C20orf139	**1.6**	**1.9**	0.5	**1.9**
chromosome 20 open reading frame 24	C20orf24	0.7	0.6	0.4	0.3
chromosome 20 open reading frame 24	C20orf24	0.7	0.6	0.3	0.3
chromosome 20 open reading frame 24 /// chromosome 20 open reading frame 24	C20orf24	0.7	0.6	0.4	0.2
clone=IMAGE-163624 /clone_end=5' /gb=H14241		**1.3**	**1.6**	**1.3**	**1.5**
clusterin (complement lysis inhibitor, apolipoprotein J)	CLU	**1.0**	**2.1**	**1.5**	**2.9**
clusterin (complement lysis inhibitor, apolipoprotein J)	CLU	**1.1**	**1.9**	**1.4**	**2.7**
CLONE=IMAGE:856163 /UG=Hs.315562 ESTs		**1.5**	**2.8**	**1.5**	**1.8**
Hs.306243 Homo sapiens thioredoxin delta 3 .		0.4	0.6	0.5	0.7
Homo sapiens cDNA FLJ20042 fis, clone COL00424.		0.8	0.6	0.5	0.9
Human DNA sequence from clone RP5-1174N9		**3.5**	**2.7**	**1.2**	0.9
CLONE=HTBAGB11 /UG=Hs.5461 ESTs		0.7	**1.0**	**1.0**	0.7
CLONE=IMAGE:3084358 /UG=Hs.77496		0.6	**1.2**	0.8	0.9
Hs.118786 metallothionein 2A /FL=gb:NM_005953.1		**6.0**	**6.2**	**2.9**	**5.3**
cystathionase (cystathionine gamma-lyase)	CTH	**1.5**	**1.2**	0.8	**1.3**
dimerization cofactor of hepatocyte nuclear factor 1 from muscle	DCOHM	0.6	0.9	0.7	0.9
DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJA1	0.4	0.7	0.3	0.5
DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	0.4	0.8	0.3	0.5
DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	0.4	0.7	0.3	0.5

DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	**1.6**	**2.0**	0.7	**1.2**
DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	0.8	**1.0**	0.4	0.7
dynein, cytoplasmic, heavy polypeptide 1	DNCH1	0.6	0.8	0.6	0.8
E74-like factor 4 (ets domain transcription factor)	ELF4	**1.1**	0.9	0.4	**2.3**
epoxide hydrolase 1, microsomal (xenobiotic)	EPHX1	**1.0**	0.4	**1.2**	**1.5**
esophageal cancer associated protein	MGC16824	0.3	0.6	0.8	0.8
F-box protein 30	FBXO30	**1.0**	**1.6**	**1.4**	**1.6**
ferritin, heavy polypeptide 1	FTH1	**3.0**	**1.9**	**3.2**	**3.0**
ferritin, heavy polypeptide 1	FTH1	**1.5**	**2.2**	**1.1**	**1.8**
ferritin, heavy polypeptide pseudogene 1	FTHP1	0.9	**1.5**	0.6	**1.1**
ferrochelatase (protoporphyria)	FECH	0.6	0.6	0.6	**1.2**
GABA(A) receptor-associated protein like 1	GABARAPL1	**1.7**	**2.1**	**4.3**	**2.6**
galactosidase, alpha	GLA	0.6	0.9	0.3	0.5
galectin-3 internal gene	GALIG	0.4	0.7	0.7	**1.3**
Hs.8765 RNA helicase-related protein /FL=gb:AF078844.1		**1.5**	**2.4**	**1.8**	**1.6**
Hs.326774 Homo sapiens metallothionein 1H-like protein mRNA		**5.4**	**4.6**	**2.6**	**3.1**
Hs.8173 hypothetical protein FLJ10803		0.6	0.8	0.9	**1.0**
Hs.349076 /UG_TITLE=Homo sapiens partial mRNA		0.7	0.6	0.5	0.8
general transcription factor IIIC, polypeptide 3, 102kDa	GTF3C3	0.7	0.7	0.4	0.7
glucosidase, beta; acid (includes glucosylceramidase)	GBA	**1.4**	**1.2**	0.5	0.8
glucosidase, beta; acid (includes glucosylceramidase)	GBA /// GBAP	**1.2**	**1.2**	0.4	**1.0**
glutamate-cysteine ligase, catalytic subunit	GCLC	0.9	**1.1**	0.6	0.7
glutamate-cysteine ligase, catalytic subunit	GCLC	0.9	**1.0**	0.4	0.8
glutamate-cysteine ligase, modifier subunit	GCLM	**1.3**	**2.8**	**1.3**	**1.8**
glutamate-cysteine ligase, modifier subunit	GCLM	**1.2**	**2.7**	**1.5**	**1.7**
growth hormone inducible transmembrane protein	GHITM	0.8	0.8	0.3	0.6
growth hormone inducible transmembrane protein	GHITM	0.8	0.6	0.3	0.5
growth hormone inducible transmembrane protein	GHITM	0.7	0.5	0.4	0.4
hematopoietic cell-specific Lyn substrate 1	HCLS1	0.5	0.3	0.4	0.7
heme oxygenase (decycling) 1	HMOX1	**3.8**	**6.0**	**3.2**	**5.3**
heterogeneous nuclear ribonucleoprotein A0	HNRPA0	0.5	0.7	0.4	0.5
HIV-1 Tat interactive protein 2, 30kDa	HTATIP2	**1.1**	**1.2**	0.3	0.7
Hypothetical LOC403340	MGC70870	**1.7**	**1.2**	**1.1**	0.8
hypothetical protein DKFZp761B1514	DKFZp761B1514	0.5	0.4	0.3	0.4
Hypothetical protein FLJ13611	FLJ13611	**1.1**	**1.5**	0.4	**1.2**
hypothetical protein FLJ20097	FLJ20097	0.6	0.9	0.4	0.6
hypothetical protein FLJ20489	FLJ20489	**2.0**	**2.0**	**1.6**	**2.2**
hypothetical protein FLJ20489	FLJ20489	0.7	0.9	0.6	**1.3**
hypothetical protein FLJ31413	FLJ31413	**1.0**	0.9	0.6	0.9
hypothetical protein FLJ36701	FLJ36701	**3.8**	**5.2**	**3.7**	**3.5**
hypothetical protein LOC339324	LOC339324	0.6	0.7	0.4	0.5
hypothetical protein LOC51315	LOC51315	0.3	0.5	**1.2**	0.4
hypothetical protein LOC51315	LOC51315	0.4	0.4	0.5	0.3
hypothetical protein LOC90637	LOC90637	0.6	0.9	0.4	0.7
hypothetical protein MGC11324	MGC11324	**2.5**	**3.1**	**1.1**	**4.1**

hypothetical protein MGC26717	MGC26717	0.5	0.8	0.6	0.6
inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	ID3	0.4	**5.1**	0.9	**3.0**
integrin, beta 5	ITGB5	0.7	**1.1**	0.5	0.7
jumonji domain containing 1C	JMJD1C	0.8	0.7	0.4	0.6
kelch-like ECH-associated protein 1	KEAP1	0.4	0.7	0.3	0.9
KIAA0469 gene product	KIAA0469	**2.2**	**2.4**	0.6	**1.0**
KIAA0582	KIAA0582	0.6	0.6	0.5	0.7
KIAA0738 gene product	KIAA0738	0.6	0.3	0.5	0.5
KIAA0746 protein	KIAA0746	**1.2**	0.3	0.8	**3.6**
KIAA1632 protein	KIAA1632	**1.0**	0.9	0.5	**1.2**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	**1.1**	**1.4**	0.8	**1.0**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	0.9	**1.2**	0.6	0.9
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	0.4	0.7	**1.1**	0.7
leupaxin	LPXN	**1.1**	0.8	0.6	0.7
LIM and SH3 protein 1	LASP1	0.8	0.9	0.4	0.6
limkain b1	LKAP	**1.0**	0.9	0.6	0.6
low density lipoprotein receptor-related protein 10	LRP10	0.3	0.4	0.5	0.5
major vault protein	MVP	0.5	0.9	0.8	**1.3**
malic enzyme 1, NADP(+)-dependent, cytosolic	ME1	**1.7**	**1.6**	0.5	**2.2**
metallothionein 1F (functional)	MT1F	**8.3**	**6.8**	**3.0**	**6.3**
metallothionein 1F (functional)	MT1F	**3.8**	**3.6**	**2.2**	**2.3**
metallothionein 1G	MT1G	**5.2**	**5.1**	**3.2**	**2.1**
metallothionein 1H	MT1H	**7.3**	**7.4**	**3.1**	**5.1**
metallothionein 1X	MT1X	**7.6**	**9.0**	**2.5**	**4.1**
metallothionein 1X	MT1X	**6.1**	**6.4**	**1.8**	**3.9**
metallothionein 2A	MT2A	**6.0**	**6.2**	**2.9**	**5.3**
microtubule-associated protein 1 light chain 3 beta	MAP1LC3B	**1.1**	**1.0**	0.4	**1.3**
mitogen-activated protein kinase 1	MAPK1	0.4	0.6	0.3	0.5
mitogen-activated protein kinase kinase 1 interacting protein 1	MAP2K1IP1	0.7	0.6	0.6	0.8
N-acetylglucosamine-1-phosphotransferase, gamma subunit	GNPTG	0.6	0.7	0.3	0.4
NACHT, leucine rich repeat and PYD containing 7	NALP7	0.8	**1.2**	0.8	**1.9**
NAD(P)H dehydrogenase, quinone 1	NQO1	**2.0**	**5.2**	**2.4**	**4.1**
NAD(P)H dehydrogenase, quinone 1	NQO1	**1.8**	**3.0**	**1.9**	**3.0**
NAD(P)H dehydrogenase, quinone 1	NQO1	**1.6**	**2.5**	**1.9**	**2.7**
NAD(P)H dehydrogenase, quinone 2	NQO2	**2.7**	**1.8**	**1.2**	**1.4**
N-myc (and STAT) interactor	NMI	0.7	0.8	0.4	**1.7**
nuclear receptor coactivator 7	NCOA7	0.8	0.7	0.3	**1.1**
OCIA domain containing 2	OCIAD2	0.7	0.5	0.5	0.4
optineurin	OPTN	0.4	0.3	0.8	**1.5**
origin recognition complex, subunit 3-like (yeast)	ORC3L	0.4	0.5	0.3	0.6
oxysterol binding protein-like 3	OSBPL3	0.5	**1.0**	0.3	0.8
phosphoserine aminotransferase 1	PSAT1	0.8	0.5	**1.0**	**1.3**
phosphoserine aminotransferase 1	PSAT1	0.8	0.5	0.9	**1.3**
phosphotriesterase related	PTER	0.8	**1.0**	0.5	0.6
phosphotriesterase related	PTER	0.5	0.9	0.7	0.7
pirin (iron-binding nuclear protein)	PIR	**1.6**	**2.2**	**1.4**	**1.2**
prosaposin	PSAP	0.4	0.5	0.5	0.7
prosaposin	PSAP	0.5	0.5	0.4	0.6
protein kinase C binding protein 1	PRKCBP1	0.3	0.5	0.7	0.6

protein kinase, cAMP-dependent, catalytic, beta	PRKACB	0.9	**1.4**	0.5	**1.4**
protein kinase, cAMP-dependent, catalytic, beta	PRKACB	0.8	**1.2**	0.5	0.9
RAB10, member RAS oncogene family	RAB10	0.6	0.7	0.2	0.3
RAS and EF hand domain containing	RASEF	0.8	0.9	0.5	**1.5**
Ras association (RalGDS/AF-6) domain family 2	RASSF2	**1.0**	**2.5**	0.5	0.7
Retinoblastoma-associated factor 600	RBAF600	0.9	0.7	0.5	0.5
RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)	RIOK3	0.8	0.8	0.5	0.7
sequestosome 1	SQSTM1	**2.4**	**3.9**	**2.0**	**5.6**
sequestosome 1	SQSTM1	**1.1**	**2.0**	**1.2**	**2.2**
Serine hydroxymethyltransferase 1 (soluble)	SHMT1	**1.0**	0.7	0.5	0.9
seryl-tRNA synthetase	SARS	0.5	0.3	0.3	0.8
sestrin 2	SESN2	**1.2**	**1.0**	**1.0**	**2.4**
sestrin 2	SESN2	**1.3**	**1.1**	0.9	**2.2**
Similar to CG14903-PA		0.7	**1.2**	0.5	**1.0**
similar to KIAA0592 protein /// hypothetical protein FLJ10824	FLJ10824	0.9	0.7	0.3	**1.3**
Solute carrier family 30 (zinc transporter), member 1	SLC30A1	**2.9**	0.7	0.9	**1.1**
solute carrier family 30 (zinc transporter), member 1	SLC30A1	**2.9**	**1.1**	0.5	**1.0**
solute carrier family 38, member 6	SLC38A6	**2.2**	**2.5**	0.8	**1.6**
solute carrier family 7, member 11	SLC7A11	**2.3**	**2.6**	**1.5**	**3.4**
solute carrier family 7, member 11	SLC7A11	**2.1**	**2.8**	**1.4**	**2.8**
SRB7 suppressor of RNA polymerase B homolog (yeast)	SURB7	0.4	0.8	0.3	0.6
superoxide dismutase 1, soluble	SOD1	0.3	0.5	0.2	0.4
syndecan binding protein (syntenin)	SDCBP	0.5	0.6	0.4	**1.1**
testis derived transcript (3 LIM domains)	TES	0.7	0.5	0.9	**1.2**
testis derived transcript (3 LIM domains)	TES	0.7	0.4	0.6	0.8
tetratricopeptide repeat domain 14	TTC14	**1.0**	0.7	0.8	**1.0**
tetratricopeptide repeat domain 14	TTC14	0.7	0.7	0.9	0.7
thioredoxin	TXN	0.7	0.6	0.3	0.6
benzodiazapine receptor associated protein 1 [Rattus norvegicus]		0.6	**1.4**	**1.3**	**1.2**
tribbles homolog 3 (Drosophila)	TRIB3	**1.5**	**1.0**	0.4	**1.6**
tubulin, alpha 3	TUBA3	0.6	**1.7**	0.7	**1.7**
tubulin, beta polypeptide	TUBB	**1.4**	**1.8**	0.5	**2.4**
tumor differentially expressed 2	TDE2	0.5	0.4	0.3	0.8
tumor necrosis factor receptor superfamily, member 6	TNFRSF6	0.6	**1.9**	0.5	0.8
ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	0.2	0.5	0.4	0.7
upregulated in colorectal cancer gene 1	UCC1	0.9	0.6	0.7	0.4
v-maf musculoaponeurotic fibrosarcoma oncogene homolog G	MAFG	**1.0**	**1.2**	0.7	**1.0**
zinc finger protein 262	ZNF262	0.5	0.5	0.3	0.5
zinc finger protein 302	ZNF302	0.7	0.7	0.4	0.9
zinc finger protein 364	ZNF364	0.4	0.7	0.3	0.6
zinc finger, X-linked, duplicated B	ZXDB	**1.1**	0.9	0.8	0.9

LogRatios for up-regulated genes at 48 h in all cell lines

Two-fold changes are in red bold

Gene Descriptor	Symbol	U266 48h	MM.1s 48h	8226/S 48h	KMS11 48h
actin-related protein 10 homolog (S. cerevisiae)	ACTR10	0.6	0.8	0.4	**1.2**
activating transcription factor 5	ATF5	0.5	**1.4**	0.5	0.6
acyl-Coenzyme A oxidase 1, palmitoyl	ACOX1	0.8	**1.5**	0.5	0.8
acylphosphatase 2, muscle type	ACYP2	0.6	**1.5**	0.8	**1.4**
ADP-ribosylation factor guanine nucleotide-exchange factor 1	ARFGEF1	0.7	0.5	0.6	0.6
aldo-keto reductase family 1, member C3	AKR1C3	**1.2**	**3.3**	**3.3**	**6.6**
ankyrin repeat domain 28	ANKRD28	0.9	0.4	0.4	0.6
annexin A4	ANXA4	**1.1**	**1.1**	0.6	**1.2**
annexin A4	ANXA4	0.8	**1.2**	0.6	**1.0**
AIF-like mitochondrion-associated inducer of death	AMID	**1.9**	**1.9**	0.5	**1.3**
arachidonate 5-lipoxygenase-activating protein	ALOX5AP	**2.1**	**2.1**	**1.3**	**2.9**
Ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	ARIH1	0.7	0.8	0.4	0.4
arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	ASNA1	0.2	0.5	0.3	0.5
ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A	0.7	**1.9**	0.4	**1.2**
ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 1	ATP6V0D1	0.5	0.4	0.4	0.9
ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	ATP6V0A1	0.4	0.6	0.7	0.7
B-cell CLL/lymphoma 2	BCL2	0.8	0.6	0.7	0.6
biliverdin reductase B (flavin reductase (NADPH))	BLVRB	**1.4**	**2.1**	0.8	**3.5**
BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1	**1.0**	**1.2**	0.6	**1.9**
BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1	0.7	0.7	0.6	**1.6**
CARD only protein	COP	**1.2**	**1.2**	0.5	**1.4**
caspase 8, apoptosis-related cysteine protease	CASP8	0.6	0.5	0.5	0.5
cathepsin B	CTSB	**1.2**	**1.4**	0.8	0.8
cathepsin B	CTSB	**1.0**	**1.5**	0.8	0.7
cathepsin B	CTSB	**1.0**	**1.3**	0.6	0.7
CCAAT/enhancer binding protein (C/EBP), beta	CEBPB	0.9	0.9	**1.1**	**2.3**
CCAAT/enhancer binding protein (C/EBP), gamma	CEBPG	0.4	0.7	**1.0**	**1.3**
CD63 antigen (melanoma 1 antigen)	CD63	0.5	0.5	0.5	0.7
CDNA FLJ41270 fis, clone BRAMY2036387		**1.6**	**2.1**	**1.0**	**1.7**
cell cycle progression 1	CCPG1	**1.0**	0.8	**1.8**	**2.7**
cell cycle progression 1	CCPG1	**1.0**	0.7	**1.7**	**2.7**
cell cycle progression 1	CCPG1	**1.1**	**1.1**	**1.4**	**2.3**
chemokine-like factor super family 6	CKLFSF6	0.6	0.6	0.3	0.6
chloride intracellular channel 2	CLIC2	**2.9**	**2.7**	0.4	**1.3**
chromosome 10 open reading frame 45	C10orf45	0.3	0.4	0.6	**1.7**
chromosome 10 open reading frame 45	C10orf45	0.3	0.4	0.4	**1.3**
chromosome 13 open reading frame 11	C13orf11	0.4	0.4	0.8	**1.2**
Chromosome 16 open reading frame 28	C16orf28	**1.2**	**1.5**	0.6	**1.2**
chromosome 20 open reading frame 139	C20orf139	**1.5**	**2.1**	0.6	**2.4**

chromosome 20 open reading frame 24	C20orf24	0.5	0.7	0.3	0.5
chromosome 20 open reading frame 24	C20orf24	0.4	0.5	0.3	0.3
chromosome 9 open reading frame 55	C9orf55	**1.1**	0.5	0.8	**1.2**
chromosome X open reading frame 45	CXorf45	0.6	0.8	0.6	0.4
clone=IMAGE-163624 /clone_end=5' /gb=H14241 /gi=879061		**1.4**	**1.6**	**1.5**	**2.1**
clusterin (complement lysis inhibitor, apolipoprotein J)	CLU	0.9	**1.6**	**1.2**	**2.9**
clusterin (complement lysis inhibitor, apolipoprotein J)	CLU	0.8	**1.5**	**1.4**	**2.6**
CLONE=IMAGE:856163 /UG=Hs.315562 ESTs		**1.3**	**2.7**	**1.6**	**1.9**
CLONE=IMAGE:2176544 /UG=Hs.177135 ESTs		**1.1**	**1.8**	0.8	0.6
CLONE=IMAGE:2347851 /UG=Hs.148154 ESTs		0.7	0.8	0.6	0.4
CLONE=IMAGE:2508169 /UG=Hs.134791 ESTs		**1.2**	**1.5**	0.7	**1.4**
Hs.183861 Homo sapiens cDNA FLJ20042		0.8	0.9	**1.0**	**1.5**
CLONE=IMAGE:2729211 /UG=Hs.124554 ESTs		0.9	**1.6**	0.8	0.7
Hs.118786 metallothionein 2A /FL=gb:NM_005953.1		**5.7**	**6.2**	**2.5**	**5.8**
cylindromatosis (turban tumor syndrome)	CYLD	0.2	0.7	0.7	0.7
cystathionase (cystathionine gamma-lyase)	CTH	**1.5**	**1.5**	**2.3**	**2.1**
cystathionase (cystathionine gamma-lyase)	CTH	**1.3**	**1.0**	**2.2**	0.8
DKFZP564G2022 protein	DKFZP564G2022	0.3	0.5	0.3	0.7
DKFZP564G2022 protein	DKFZP564G2022	0.3	0.5	0.3	0.6
DNA-damage-inducible transcript 4	DDIT4	0.6	**1.1**	**2.2**	0.7
DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	**1.5**	**1.5**	0.9	**1.4**
DRE1 protein	DRE1	**1.2**	**1.5**	0.8	**1.9**
dynein, cytoplasmic, heavy polypeptide 1	DNCH1	0.3	0.8	0.8	**1.3**
E74-like factor 4 (ets domain transcription factor)	ELF4	**1.2**	**1.2**	0.5	**3.0**
erbb2 interacting protein	ERBB2IP	0.6	0.6	0.4	0.8
erythrocyte membrane protein band 4.1	EPB41	0.4	0.7	0.3	0.9
ets variant gene 5 (ets-related molecule)	ETV5	0.8	0.6	**1.1**	0.4
eukaryotic translation initiation factor 4E binding protein 1	EIF4EBP1	0.6	0.7	0.6	**1.5**
Farnesyl-diphosphate farnesyltransferase 1	FDFT1	**1.4**	**1.7**	**1.2**	0.8
Farnesyl-diphosphate farnesyltransferase 1	FDFT1	**1.1**	**1.6**	**1.2**	0.8
F-box protein 30	FBXO30	**1.0**	**1.4**	**1.6**	**2.2**
ferritin, heavy polypeptide 1	FTH1	**3.0**	**2.8**	**3.7**	**3.3**
ferritin, heavy polypeptide 1	FTH1	**1.4**	**2.6**	**1.3**	**2.1**
ferritin, heavy polypeptide pseudogene 1	FTHP1	0.5	**1.8**	0.5	**1.3**
ferrochelatase (protoporphyria)	FECH	0.3	0.5	0.9	**1.4**
GABA(A) receptor-associated protein	GABARAP	0.5	0.5	0.4	**1.0**
GABA(A) receptor-associated protein like 1	GABARAPL1	**1.6**	**2.8**	**5.0**	**3.0**
gamma-glutamyltransferase 1	GGT1	**1.3**	0.9	0.3	0.5
gamma-glutamyltransferase-like 4	GGTL4 /// GGT1	0.9	0.8	0.3	0.4
Hs.8765 RNA helicase-related protein /FL=gb:AF078844.		**1.6**	**1.7**	0.9	**1.5**
Hs.326774 Homo sapiens metallothionein 1H-like protein		**5.2**	**4.4**	**2.1**	**3.2**
Hs.349076 /UG_TITLE=Homo sapiens partial mRNA		0.4	0.5	**1.1**	**1.0**

CLONE=IMAGE:4523513 /TID=Hs2.374629.1		0.4	**1.0**	0.9	**2.0**
GCIP-interacting protein p29	P29	0.5	0.7	0.4	0.9
general transcription factor IIIC, polypeptide 3, 102kDa	GTF3C3	0.5	0.6	0.6	0.7
glucosidase, beta; acid (includes glucosylceramidase)	GBA	**1.3**	**1.1**	0.5	**1.2**
glucosidase, beta; acid (includes glucosylceramidase)	GBA /// GBAP	**1.4**	**1.2**	0.4	**1.4**
glutamate-ammonia ligase (glutamine synthase)	GLUL	0.8	**1.3**	0.4	**1.5**
glutamate-ammonia ligase (glutamine synthase)	GLUL	0.7	**1.1**	0.3	**1.5**
glutamate-cysteine ligase, catalytic subunit	GCLC	0.9	**1.3**	0.9	**1.1**
glutamate-cysteine ligase, catalytic subunit	GCLC	0.9	**1.2**	0.9	**1.0**
glutamate-cysteine ligase, modifier subunit	GCLM	**1.3**	**2.8**	**1.6**	**1.8**
glutamate-cysteine ligase, modifier subunit	GCLM	**1.2**	**2.8**	**1.4**	**1.9**
glutamic pyruvate transaminase (alanine aminotransferase) 2	GPT2	0.6	0.6	**1.7**	**1.5**
granulin	GRN	**1.0**	0.3	0.5	0.6
growth hormone inducible transmembrane protein	GHITM	0.5	0.9	0.4	**1.0**
growth hormone inducible transmembrane protein	GHITM	0.6	0.7	0.5	0.9
growth hormone inducible transmembrane protein	GHITM	0.5	0.6	0.4	0.8
hematopoietic cell-specific Lyn substrate 1	HCLS1	0.4	0.5	0.5	**1.1**
heme oxygenase (decycling) 1	HMOX1	**3.6**	**5.9**	**3.2**	**6.0**
HMG-box transcription factor 1	HBP1	0.8	**1.4**	0.9	**1.7**
hypothetical protein BC004921	LOC93349	0.4	0.6	0.5	0.8
hypothetical protein FLJ11000	FLJ11000	**1.0**	**2.0**	**1.5**	**2.8**
hypothetical protein FLJ11011	FLJ11011	0.5	0.9	0.5	0.8
Hypothetical protein FLJ13611	FLJ13611	**1.5**	**1.7**	**1.0**	**1.6**
hypothetical protein FLJ20097	FLJ20097	0.8	0.9	0.5	0.9
hypothetical protein FLJ20489	FLJ20489	**2.1**	**2.0**	**1.8**	**2.9**
hypothetical protein FLJ20489	FLJ20489	0.8	**1.2**	**1.0**	**1.3**
hypothetical protein FLJ20716	FLJ20716	**1.8**	**1.6**	0.8	**1.2**
hypothetical protein FLJ21439	FLJ21439	0.6	0.5	0.3	**1.1**
hypothetical protein FLJ22405	FLJ22405	0.4	0.5	0.5	0.8
hypothetical protein FLJ22833	FLJ22833	**1.2**	0.9	0.5	0.6
hypothetical protein FLJ23749	FLJ23749	0.5	0.7	0.3	**1.4**
hypothetical protein FLJ31413	FLJ31413	**1.1**	**1.0**	0.7	**1.4**
Hypothetical protein FLJ32421	FLJ32421	0.3	0.7	0.4	0.8
hypothetical protein FLJ36701	FLJ36701	**4.0**	**5.3**	**3.9**	**3.9**
hypothetical protein LOC150271	LOC150271	0.8	**2.6**	0.8	0.8
hypothetical protein LOC201895	LOC201895	0.8	0.8	**1.1**	**1.6**
Hypothetical protein LOC201895	LOC201895	0.5	**1.2**	**1.1**	**1.3**
Hypothetical protein LOC285972	LOC285972	**2.3**	0.3	0.6	**1.1**
hypothetical protein LOC339924	LOC339924	**1.3**	**1.2**	0.9	**2.2**
hypothetical protein LOC51315	LOC51315	0.4	0.5	0.7	0.4
hypothetical protein MGC11324	MGC11324	**2.6**	**3.3**	**1.5**	**4.6**
hypothetical protein MGC4504	MGC4504	0.6	0.7	**2.4**	**2.6**
IBR domain containing 3	IBRDC3	0.7	0.9	0.7	**1.3**
inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ID2	**1.2**	**3.4**	0.9	**3.2**
inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	ID3	0.5	**4.6**	0.8	**3.4**
integrin, beta 5	ITGB5	0.5	**1.3**	0.9	0.5
interferon-related developmental regulator 1	IFRD1	**1.0**	0.9	0.8	**1.6**

Interferon-related developmental regulator 1	IFRD1	**1.0**	0.7	0.7	**1.3**
intracellular memb.-assoc. Ca2+-independent phospholipase A2 gamma	IPLA2(GAMMA)	0.4	0.7	0.6	**1.1**
intracellular memb.-assoc. Ca2+-independent phospholipase A2 gamma	IPLA2(GAMMA)	0.4	0.6	0.6	**1.0**
isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	**1.2**	0.7	0.4	**2.1**
isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	**1.0**	0.7	0.6	**2.0**
jumonji domain containing 1C	JMJD1C	0.8	0.6	0.7	0.9
jumonji domain containing 1C	JMJD1C	0.6	0.6	0.5	0.6
KIAA0469 gene product	KIAA0469	**2.2**	**2.8**	0.8	**1.9**
KIAA0582	KIAA0582	0.6	0.5	0.8	0.7
KIAA0592 protein /// KIAA0592 protein	KIAA0592	0.9	0.9	0.4	**1.5**
KIAA0746 protein	KIAA0746	**1.0**	0.3	**1.7**	**4.2**
KIAA1468	KIAA1468	0.3	0.6	0.4	0.7
KIAA1632 protein	KIAA1632	**1.3**	**1.2**	0.8	**1.7**
KIAA1632 protein	KIAA1632	**1.1**	0.6	0.3	**1.6**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	**1.3**	**1.3**	**2.5**	**1.1**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	**1.3**	**1.4**	**1.4**	**1.4**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	**1.0**	**1.2**	**1.0**	**1.1**
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	0.7	0.8	**1.1**	0.8
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	0.6	0.9	0.7	0.9
leucine rich repeat (in FLII) interacting protein 2	LRRFIP2	0.5	0.9	0.6	**1.3**
leupaxin	LPXN	**1.3**	0.8	0.8	0.9
LIM and SH3 protein 1	LASP1	0.8	0.9	0.7	0.8
limkain b1	LKAP	**1.0**	**1.4**	0.8	0.9
lysosomal-associated membrane protein 1	LAMP1	0.3	0.4	0.4	0.7
lysosomal-associated membrane protein 2	LAMP2	0.6	0.7	0.7	0.7
lysosomal-associated membrane protein 2	LAMP2	0.4	0.7	0.7	0.8
major histocompatibility complex, class I-related	MR1	0.9	**1.4**	**1.0**	0.8
major histocompatibility complex, class I-related	MR1	0.5	**1.2**	0.3	0.7
major vault protein	MVP	**1.1**	**1.1**	**1.2**	**1.4**
malic enzyme 1, NADP(+)-dependent, cytosolic	ME1	**1.5**	**1.7**	**1.0**	**2.8**
Malic enzyme 1, NADP(+)-dependent, cytosolic	ME1	**1.5**	**1.8**	0.9	**2.5**
membrane component, chromosome 17, surface marker 2	M17S2	0.5	**1.0**	0.4	0.9
membrane component, chromosome 17, surface marker 2	M17S2	0.3	0.8	0.7	0.6
metallothionein 1E (functional)	MT1E	**6.9**	**3.6**	**2.9**	**2.2**
metallothionein 1F (functional)	MT1F	**7.5**	**6.9**	**1.4**	**6.3**
metallothionein 1F (functional)	MT1F	**3.2**	**3.4**	**1.1**	**2.5**
metallothionein 1G	MT1G	**4.8**	**5.1**	**2.5**	**2.6**
metallothionein 1H	MT1H	**7.8**	**7.4**	**2.6**	**5.5**
metallothionein 1X	MT1X	**7.3**	**9.1**	**2.1**	**4.6**
metallothionein 1X	MT1X	**5.7**	**6.3**	**1.9**	**4.4**
metallothionein 2A	MT2A	**5.7**	**6.2**	**2.5**	**5.8**
methionine sulfoxide reductase B	MSRB	0.6	0.8	0.5	0.3
microtubule-associated protein 1 light chain 3 beta	MAP1LC3B	0.9	0.9	0.8	**1.9**
microtubule-associated protein 1 light chain 3 beta	MAP1LC3B	0.9	0.9	0.6	**1.6**
mitogen-activated protein kinase kinase 1 interacting protein 1	MAP2K1IP1	0.8	0.6	0.6	**1.0**
N-acetylglucosamine kinase /// N-acetylglucosamine kinase	NAGK	0.6	0.6	0.7	**1.0**
N-acetylglucosamine-1-phosphotransferase,	GNPTG	0.8	0.9	0.9	0.8

gamma subunit					
NACHT, leucine rich repeat and PYD containing 7	NALP7	0.6	**1.1**	0.9	**1.9**
NAD(P)H dehydrogenase, quinone 1	NQO1	**2.4**	**5.5**	**3.0**	**4.2**
NAD(P)H dehydrogenase, quinone 1	NQO1	**1.9**	**3.1**	**2.1**	**3.2**
NAD(P)H dehydrogenase, quinone 1	NQO1	**1.8**	**2.6**	**2.3**	**3.0**
NAD(P)H dehydrogenase, quinone 2	NQO2	**2.7**	**2.2**	**1.1**	**2.1**
N-myc (and STAT) interactor	NMI	**1.1**	0.8	0.5	**1.9**
nuclear factor (erythroid-derived 2)-like 1	NFE2L1	0.5	**1.1**	0.6	**1.8**
nuclear factor (erythroid-derived 2)-like 2	NFE2L2	0.6	0.6	0.4	0.6
nuclear receptor coactivator 4	NCOA4	0.4	0.3	0.3	0.4
nuclear receptor coactivator 7	NCOA7	0.5	0.7	0.8	**1.6**
OCIA domain containing 2	OCIAD2	0.9	0.7	0.6	0.5
phosphatidylinositol glycan, class B	PIGB	**1.0**	**1.0**	**1.8**	**2.1**
phosphatidylinositol glycan, class B	PIGB	**1.0**	0.7	**1.6**	**2.4**
phosphoenolpyruvate carboxykinase 2 (mitochondrial)	PCK2	0.5	0.7	0.9	**2.0**
phosphoserine aminotransferase 1	PSAT1	0.3	0.7	**2.0**	**2.1**
phosphoserine aminotransferase 1	PSAT1	0.3	0.7	**1.7**	**2.0**
phosphoserine phosphatase	PSPH	0.5	0.5	0.5	0.8
phosphotriesterase related	PTER	0.9	0.9	0.6	0.9
pirin (iron-binding nuclear protein)	PIR	**1.6**	**2.4**	**1.4**	**1.5**
presenilin 1 (Alzheimer disease 3)	PSEN1	0.4	0.6	0.4	0.7
prion protein (p27-30)	PRNP	0.8	0.4	0.5	**1.5**
prion protein (p27-30)	PRNP	0.5	0.4	0.6	**1.0**
programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	0.6	**1.3**	0.3	**1.9**
prosaposin	PSAP	0.3	0.6	0.9	**1.1**
protein kinase C binding protein 1	PRKCBP1	0.4	0.6	0.7	0.6
protein kinase, cAMP-dependent, catalytic, beta	PRKACB	0.8	0.8	0.4	**1.9**
protein kinase, cAMP-dependent, catalytic, beta	PRKACB	0.6	**1.1**	0.4	**1.5**
RAB GTPase activating protein 1	RABGAP1	0.4	0.6	0.5	0.5
RAB GTPase activating protein 1-like	RABGAP1L	0.6	**4.1**	0.6	**1.0**
RAB10, member RAS oncogene family	RAB10	0.5	0.5	0.4	0.4
RAP2B, member of RAS oncogene family	RAP2B	0.7	0.6	0.3	0.7
RAS and EF hand domain containing	RASEF	0.7	**1.1**	0.4	**2.2**
regulating synaptic membrane exocytosis 3	RIMS3	**1.5**	**1.5**	0.6	**1.2**
restin	RSN	0.8	0.6	0.5	**1.4**
Retinoblastoma-associated factor 600	RBAF600	0.5	0.8	0.7	**1.0**
Ribosomal protein S24	RPS24	**1.1**	**1.4**	0.7	0.8
ribosomal protein S6 kinase, 52kDa, polypeptide 1	RPS6KC1	0.5	0.5	0.9	**1.3**
ring finger and KH domain containing 2	RKHD2	**1.2**	0.9	0.5	0.5
ring finger protein 153	RNF153	0.5	**1.1**	0.5	**1.0**
RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)	RIOK3	0.8	0.7	0.6	0.9
RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)	RIOK3	0.7	0.7	0.5	0.8
RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)	RIOK3	0.6	0.9	0.4	0.6
S100 calcium binding protein A6 (calcyclin)	S100A6	0.9	**1.6**	0.5	**1.9**
sequestosome 1	SQSTM1	**2.5**	**3.3**	**2.1**	**5.1**
sequestosome 1	SQSTM1	0.9	**1.8**	**1.7**	**2.6**
Ser/Thr-like kinase	MGC4796	**1.2**	**1.0**	0.4	**1.2**
Serine hydroxymethyltransferase 1 (soluble)	SHMT1	**1.1**	**1.3**	0.5	**1.0**
Serine hydroxymethyltransferase 1 (soluble)	SHMT1	0.9	**1.0**	0.5	**1.0**
serine/threonine kinase 17a (apoptosis-inducing)	STK17A	0.3	**1.7**	0.4	**1.0**

seryl-tRNA synthetase	SARS	0.5	0.7	**1.1**	**1.2**
sestrin 2	SESN2	0.9	**1.3**	**2.1**	**2.8**
sestrin 2	SESN2	0.8	**1.3**	**1.9**	**3.1**
SHC (Src homology 2 domain containing) transforming protein 1	SHC1	0.6	0.6	0.4	0.5
similar to hypothetical protein FLJ10883	LOC115294	0.4	0.8	0.4	**1.0**
similar to KIAA0592 protein	LOC387680	**1.0**	**1.1**	0.5	**1.5**
similar to KIAA0592 protein /// hypothetical protein FLJ10824	FLJ10824	0.9	**1.0**	0.4	**1.7**
solute carrier family 3, member 2	SLC3A2	**1.0**	0.8	0.8	**1.3**
solute carrier family 30 (zinc transporter), member 1	SLC30A1	**2.6**	**1.2**	0.7	**1.0**
Solute carrier family 30 (zinc transporter), member 1	SLC30A1	**2.5**	0.7	0.9	**1.2**
solute carrier family 38, member 6	SLC38A6	**2.5**	**2.1**	**1.1**	**2.2**
solute carrier family 43, member 1	SLC43A1	**1.2**	**1.1**	0.8	**1.1**
solute carrier family 7, member 11	SLC7A11	**1.7**	**2.5**	**2.7**	**4.2**
solute carrier family 7, member 11	SLC7A11	**1.6**	**2.5**	**2.5**	**3.4**
solute carrier family 7, member 11	SLC7A11	**1.7**	**1.2**	**1.0**	**1.5**
special AT-rich sequence binding protein 1	SATB1	**2.9**	0.9	0.6	**1.9**
spermidine/spermine N1-acetyltransferase	SAT	0.9	**1.4**	**1.4**	**2.2**
spermidine/spermine N1-acetyltransferase	SAT	0.7	**1.3**	**1.1**	**2.0**
sulfatase modifying factor 1	SUMF1	0.9	**1.0**	0.7	**1.1**
suppressor of hairy wing homolog 3 (Drosophila)	SUHW3	**1.2**	**1.1**	0.8	0.8
synaptotagmin-like 1	SYTL1	**1.0**	**1.0**	**1.0**	**2.1**
syndecan binding protein (syntenin)	SDCBP	0.6	0.6	0.8	**1.5**
syntaxin 3A	STX3A	**1.4**	**1.0**	0.6	**1.2**
syntaxin 4A (placental)	STX4A	0.9	0.9	0.4	0.6
Tax1 (human T-cell leukemia virus type I) binding protein 1	TAX1BP1	0.5	0.8	0.4	**1.4**
testis derived transcript (3 LIM domains)	TES	0.4	0.8	**1.2**	**1.4**
testis derived transcript (3 LIM domains)	TES	0.5	0.6	**1.0**	**1.4**
tetratricopeptide repeat domain 14	TTC14	**1.2**	**1.0**	0.9	**1.0**
thioredoxin	TXN	0.7	0.8	0.4	**1.0**
tribbles homolog 3 (Drosophila)	TRIB3	**1.2**	**1.2**	**1.5**	**2.6**
tribbles homolog 3 (Drosophila)	TRIB3	0.9	**1.0**	**1.4**	**1.8**
tryptophanyl-tRNA synthetase	WARS	0.5	0.7	0.5	**1.6**
tubulin, alpha 3	TUBA3	0.4	**1.6**	0.4	**1.8**
tubulin, epsilon 1	TUBE1	0.4	0.5	**1.6**	**1.4**
tumor differentially expressed 1	TDE1	0.3	0.4	0.5	0.8
tumor differentially expressed 2	TDE2	0.6	0.6	0.7	**1.1**
tumor necrosis factor receptor superfamily, member 6	TNFRSF6	0.5	**1.4**	0.6	0.5
ubiquitin specific protease 11	USP11	0.6	**1.0**	0.5	0.7
ubiquitination factor E4B (UFD2 homolog, yeast)	UBE4B	0.5	0.5	0.4	0.8
vacuolar protein sorting 26 (yeast)	VPS26	0.8	0.7	0.5	**1.5**
vacuolar protein sorting 4B (yeast)	VPS4B	0.4	0.5	0.4	0.6
v-maf musculoaponeurotic fibrosarcoma oncogene homolog G	MAFG	**1.0**	**1.3**	0.5	**1.3**
YTH domain family 3	YTHDF3	0.9	0.5	0.4	0.6
zinc finger protein 226	ZNF226	0.7	0.8	0.4	0.8
zinc finger protein 258	ZNF258	0.6	0.9	0.4	0.7
zinc finger protein 304	ZNF304	0.9	0.8	0.6	0.6

Zinc finger, BED domain containing 3	ZBED3	0.7	**2.2**	**2.3**	**1.5**
zinc finger, FYVE domain containing 26	ZFYVE26	0.7	0.5	0.8	0.4

Supplemental Table - 2

LogRatios for down-regulated genes at 6 h in all cell lines

Two-fold changes are in green bold

Gene Descriptor	Symbol	U266 6h	MM.1s 6h	8226/S 6h	KMS11 6h
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	**-1.7**	**-1.0**	-0.3	-0.7
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	**-1.5**	**-1.8**	-0.3	**-1.0**
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	**-1.6**	**-1.4**	-0.4	-0.9
7-dehydrocholesterol reductase	DHCR7	-0.5	**-1.6**	-0.3	-0.5
a disintegrin and metalloproteinase domain 10	ADAM10	-0.5	-0.8	-0.3	-0.8
a disintegrin and metalloproteinase domain 10	ADAM10	-0.4	-0.7	-0.3	-0.7
acyl-CoA synthetase long-chain family member 4	ACSL4	-0.4	-0.7	-0.6	-0.8
adaptor protein with pleckstrin homology and src homology 2 domains	APS	**-1.1**	**-1.3**	-0.7	**-1.2**
adenylate kinase 3	AK3	**-1.5**	**-1.5**	-0.5	**-1.0**
Aminoacylase 1-like 2	ACY1L2	**-1.0**	**-1.6**	-0.7	**-1.3**
Aminoacylase 1-like 2	ACY1L2	-0.7	**-1.1**	-0.7	**-1.0**
arginine-rich, mutated in early stage tumors	ARMET	-0.4	-0.6	-0.5	**-1.0**
AT rich interactive domain 5A (MRF1-like)	ARID5A	-0.5	-0.4	-0.6	-0.7
ATP citrate lyase	ACLY	-0.4	**-1.0**	-0.6	-0.7
ATP citrate lyase	ACLY	-0.3	-0.9	-0.4	-0.6
ATPase type 13A	ATP13A	-0.3	-0.4	-0.3	-0.6
ATPase, Class I, type 8B, member 2	ATP8B2	-0.5	-0.8	-0.6	**-1.1**
barren homolog (Drosophila)	BRRN1	-0.5	-0.7	-0.4	-0.4
BCL2-like 1	BCL2L1	**-1.2**	-0.6	-0.6	**-1.6**
BCL2-like 1	BCL2L1	**-1.2**	-0.6	-0.5	**-1.4**
BCL2-like 1 /// BCL2-like 1	BCL2L1	**-1.0**	-0.8	-0.3	**-1.3**
BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	-0.8	-0.5	-0.3	-0.7
Butyrophilin, subfamily 3, member A2	**BTN3A2**	**-1.1**	-1.1	-1.2	-1.2
butyrophilin, subfamily 3, member A2	BTN3A2	**-1.0**	-0.8	**-1.0**	**-1.5**
butyrophilin, subfamily 3, member A3	BTN3A3	-0.9	-0.7	-0.9	**-1.6**
carbohydrate (chondroitin 4) sulfotransferase 12	CHST12	**-1.5**	**-1.4**	-0.4	**-1.3**
carbohydrate (chondroitin) synthase 1	CHSY1	-0.7	**-1.0**	-0.4	-0.7
casein kinase 1, epsilon	CSNK1E	-0.7	-0.9	-0.6	**-1.0**
caveolin 1, caveolae protein, 22kDa	CAV1	-0.8	**-1.0**	-0.6	-0.7
caveolin 1, caveolae protein, 22kDa	CAV1	-0.7	-0.9	-0.6	-0.7
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-0.7	**-1.0**	**-1.6**	**-1.2**
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-0.6	-0.7	**-1.3**	**-1.1**
CDC20 cell division cycle 20 homolog (S. cerevisiae)	CDC20	-0.5	-0.6	-0.4	-0.7
ceroid-lipofuscinosis, neuronal 6, late infantile, variant	CLN6	-0.3	-0.9	-0.3	-0.5

chemokine (C-C motif) receptor 1	CCR1	-0.9	-0.7	-0.5	**-1.6**
chemokine (C-C motif) receptor 1	CCR1	**-1.1**	-0.6	-0.6	**-1.5**
chromosome 12 open reading frame 14	C12orf14	-0.4	**-1.0**	-0.8	**-1.4**
chromosome 12 open reading frame 14	C12orf14	-0.4	**-1.0**	-0.8	**-1.4**
chromosome 18 open reading frame 19	C18orf19	-0.5	-0.4	-0.3	-0.9
chromosome 20 open reading frame 30	C20orf30	-0.3	-0.2	-0.2	-0.3
chromosome 22 open reading frame 9	C22orf9	-0.6	**-1.2**	-0.7	**-1.1**
chromosome 22 open reading frame 9	C22orf9	-0.5	-0.9	-0.4	**-1.1**
chromosome 7 open reading frame 21	C7orf21	-0.8	-0.5	-0.5	-0.6
chromosome 9 open reading frame 140	C9orf140	-0.6	**-1.1**	-0.3	**-1.0**
chromosome 9 open reading frame 86	C9orf86	-0.3	-0.4	-0.5	-0.5
CLONE=IMAGE:981825 /UG=Hs.103135 ESTs		-0.2	**-1.0**	-0.7	**-1.2**
CLONE=IMAGE:2432978 /UG=Hs.66666 ESTs		-0.4	-0.6	-0.6	-0.6
CLONE=IMAGE:2722673 /UG=Hs.211198 ESTs		-0.6	-0.7	-0.6	-0.9
CLONE=IMAGE:4657001 /UG=Hs.127264 ESTs		-0.7	-0.9	-0.6	-0.8
CLONE=IMAGE:4718390 /UG=Hs.40034 integrin, alpha 4		-0.6	**-1.6**	-0.8	**-1.4**
c-src tyrosine kinase	CSK	-0.6	-0.7	-0.5	-0.8
CSRP2 binding protein	CSRP2BP	-0.5	-0.6	-0.5	-0.7
CTD, RNA polymerase II, polypeptide A small phosphatase 1	**CTDSP1**	**-1.0**	**-1.4**	**-1.2**	**-1.3**
CTD, RNA polymerase II, polypeptide A small phosphatase 2	CTDSP2	-0.4	-0.6	-0.4	-0.6
cyclin A2	CCNA2	-0.7	-0.3	-0.3	-0.4
cyclin D1 (PRAD1: parathyroid adenomatosis 1)	**CCND1**	**-1.3**	**-3.0**	**-1.5**	**-2.1**
cytoskeleton-associated protein 4	CKAP4	-0.4	-0.8	-0.3	-0.8
DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	-0.3	-0.7	-0.4	-0.7
deleted in lymphocytic leukemia, 1	DLEU1	-0.5	**-1.1**	-0.9	**-1.7**
deoxyhypusine synthase	DHPS	-0.5	-0.7	-0.3	-0.7
deoxyhypusine synthase	DHPS	-0.4	-0.7	-0.7	-0.6
deoxyhypusine synthase	DHPS	-0.4	-0.7	-0.5	-0.6
DEP domain containing 6	DEPDC6	-0.5	**-1.3**	-0.4	-0.7
Der1-like domain family, member 3	DERL3	-0.6	-0.8	-0.4	**-1.1**
disrupter of silencing 10	SAS10	-0.6	-0.8	-0.7	**-1.6**
DKFZP564I1171 protein	DKFZP564I1171	-0.4	**-1.5**	-0.6	**-1.1**
E2F transcription factor 5, p130-binding	E2F5	-0.5	**-1.2**	-0.7	**-1.3**
ELLP3030	UNQ3030	-0.5	-0.5	-0.5	**-1.6**
elongation of very long chain fatty acids -like 1	ELOVL1	-0.4	-0.3	-0.6	-0.3
emopamil binding protein (sterol isomerase)	EBP	-0.4	-0.8	-0.2	-0.3
ERO1-like (S. cerevisiae)	ERO1L	-0.4	**-1.1**	-0.4	-0.9
family with sequence similarity 46, member C	FAM46C	-0.8	-0.5	-0.8	**-1.5**
family with sequence similarity 46, member C	FAM46C	-0.6	-0.4	-0.8	**-1.5**
farnesyl-diphosphate farnesyltransferase 1	FDFT1	**-1.3**	**-2.1**	-0.7	-0.7
farnesyl-diphosphate farnesyltransferase 1	FDFT1	**-1.5**	**-2.0**	-0.6	-0.7
fatty acid synthase	**FASN**	**-1.2**	**-1.8**	**-1.6**	**-1.7**
flotillin 1	FLOT1	-0.6	-0.5	-0.4	-0.7
flotillin 1	FLOT1	-0.7	-0.4	-0.3	-0.6
forkhead box O3A	FOXO3A	-0.7	-0.6	-0.7	-0.5
forkhead box O3A	FOXO3A	-0.4	-0.6	-0.6	-0.5
forkhead box O3A	FOXO3A	-0.3	-0.5	-0.6	-0.5
general transcription factor IIE, polypeptide 2, beta	GTF2E2	-0.9	-0.5	-0.5	-0.3

34kDa					
glucocorticoid induced transcript 1	GLCCI1	**-1.3**	**-1.5**	-0.5	**-1.1**
glucocorticoid induced transcript 1	GLCCI1	**-1.3**	**-1.4**	-0.4	**-1.2**
glucosidase I	GCS1	-0.4	-0.7	-0.6	**-1.2**
glutaminase	GLS	-0.3	-0.5	-0.5	-0.4
glutaminase	GLS	-0.4	-0.4	-0.3	-0.5
glycosyltransferase 25 domain containing 1	GLT25D1	-0.6	-0.7	-0.4	-0.9
glycosyltransferase AD-017	AD-017	-0.9	**-1.9**	-0.5	-0.8
GTP binding protein 3 (mitochondrial)	GTPBP3	-0.4	-0.4	-0.4	-0.8
guanine monphosphate synthetase	GMPS	-0.6	-0.8	-0.4	-0.4
H1 histone family, member X	H1FX	-0.7	**-1.2**	-0.8	-0.3
heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	-0.3	**-1.0**	-0.6	-0.6
heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	-0.3	-0.9	-0.4	-0.5
heterogeneous nuclear ribonucleoprotein H3 (2H9)	HNRPH3	-0.4	-0.4	-0.6	-0.6
heterogeneous nuclear ribonucleoprotein H3 (2H9)	HNRPH3	-0.4	-0.4	-0.4	-0.5
hexokinase 2	HK2	**-2.7**	**-1.6**	-0.9	**-2.7**
high mobility group nucleosomal binding domain 4	HMGN4	-0.2	-0.4	-0.4	-0.7
high-mobility group 20B	HMG20B	-0.5	-0.9	-0.3	-0.6
histone deacetylase 9	HDAC9	-0.4	**-2.5**	-0.9	-0.9
HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	HRMT1L2	-0.2	-0.6	-0.3	-0.7
Homo sapiens, clone IMAGE:3894337, mRNA		-0.3	-0.7	-0.6	-0.8
Homo sapiens, clone IMAGE:5274897, mRNA		-0.5	-0.8	-0.5	-0.7
Hypothetical LOC389362		-0.4	-0.8	-0.7	**-1.0**
hypothetical protein BC007882	LOC152217	-0.3	-0.5	-0.6	-0.9
hypothetical protein FLJ10656	P15RS	-0.3	-0.5	-0.5	-0.8
hypothetical protein FLJ11164	FLJ11164	-0.4	-0.3	-0.4	-0.9
hypothetical protein FLJ35036	FLJ35036	-0.9	**-1.2**	-0.7	-0.6
Hypothetical protein FLJ35036	FLJ35036	-0.8	-0.7	-0.7	-0.7
hypothetical protein FLJ35036	FLJ35036	-0.5	-0.6	-0.8	-0.7
hypothetical protein LOC202781	LOC202781	-0.4	**-1.3**	-0.5	-0.9
hypothetical protein LOC221362	LOC221362	-0.9	**-1.1**	-0.9	**-1.1**
hypothetical protein LOC286167	LOC286167	-0.9	-0.5	-0.6	-0.5
hypothetical protein LOC339287	LOC339287	-0.6	**-1.1**	-0.6	-0.6
hypothetical protein LOC51061	LOC51061	-0.4	**-1.1**	-0.6	-0.6
hypothetical protein MGC15416	MGC15416	-0.2	**-1.0**	-0.6	-0.9
hypothetical protein MGC22793	MGC22793	-0.7	**-1.4**	-0.5	**-1.3**
hypothetical protein MGC3196	MGC3196	-0.3	-0.7	-0.3	**-1.1**
hypothetical protein MGC4172	MGC4172	-0.7	**-1.6**	-0.7	-0.9
hypoxia-inducible protein 2	HIG2	-0.8	-0.9	-0.3	**-1.0**
Inositol polyphosphate-4-phosphatase, type I, 107kDa	INPP4A	-0.7	**-1.0**	-0.4	-0.8
Inositol polyphosphate-4-phosphatase, type I, 107kDa	INPP4A	-0.6	**-1.0**	-0.3	-0.7
insulin induced gene 1	**INSIG1**	**-2.0**	**-2.6**	**-1.3**	**-1.2**
insulin induced gene 1	**INSIG1**	**-1.9**	**-2.6**	**-1.2**	**-1.3**
insulin induced gene 1	INSIG1	**-1.6**	**-2.1**	-0.8	**-1.2**
interferon regulatory factor 2	IRF2	-0.4	-0.8	-0.6	**-1.3**
interferon regulatory factor 4	IRF4	-0.9	**-1.5**	-0.8	**-1.4**
interferon regulatory factor 4	**IRF4**	**-1.0**	**-1.4**	**-1.0**	**-1.8**
ischemia/reperfusion inducible protein	FLJ23476	-0.4	-0.6	-0.4	**-1.3**
ischemia/reperfusion inducible protein	FLJ23476	-0.3	-0.6	-0.7	**-1.5**

isopentenyl-diphosphate delta isomerase	IDI1	**-1.7**	**-1.8**	-0.6	**-1.0**
isopentenyl-diphosphate delta isomerase	IDI1	**-1.6**	**-1.7**	-0.6	**-1.0**
KIAA0186 gene product	KIAA0186	-0.5	-0.6	-0.3	-0.5
KIAA0877 protein	KIAA0877	-0.5	-0.6	-0.4	-0.4
KIAA1196 protein	KIAA1196	-0.3	-0.9	-0.4	**-1.0**
Kruppel-like factor 16	KLF16	**-1.3**	-0.6	**-1.8**	**-3.0**
lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	LSS	-0.6	**-2.3**	-0.7	-0.8
lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	LSS	-0.6	**-2.0**	-0.5	-0.7
likely ortholog of yeast ARV1	ARV1	-0.6	-0.8	-0.4	-0.6
low density lipoprotein receptor	**LDLR**	**-2.2**	**-2.8**	**-1.0**	**-2.1**
low density lipoprotein receptor	LDLR	**-2.5**	**-2.3**	-0.7	**-2.0**
low density lipoprotein receptor	LDLR	**-2.5**	**-2.3**	-0.8	**-1.3**
MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	-0.5	-0.6	-0.7	-0.8
MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	-0.3	-0.6	-0.5	-0.6
MADS box transcription enhancer factor 2, polypeptide C	MEF2C	-0.8	-0.5	-0.6	-0.8
mannosidase, alpha, class 2A, member 1	MAN2A1	-0.4	-0.9	-0.4	**-1.0**
mannosidase, alpha, class 2A, member 1	MAN2A1	-0.2	-0.8	-0.5	**-1.0**
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7	-0.9	**-1.4**	-0.6	-0.7
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7	-0.8	**-1.3**	-0.4	-0.6
CD46, trophoblast-lymphocyte cross-reactive antigen	MCP	-0.4	-0.5	-0.3	-0.5
metastasis associated 1 /// metastasis associated 1	MTA1	-0.3	**-1.3**	-0.6	-0.9
MID1 interacting protein 1, gastrulation specific G12-like	MID1IP1	-0.5	-0.8	-0.6	-0.3
minor histocompatibility antigen HA-1	HA-1	-0.7	-0.4	-0.9	**-1.0**
mitochondrial isoleucine tRNA synthetase	FLJ10326	-0.4	-0.8	-0.2	-0.7
mitochondrial ribosomal protein 63	MRP63	-0.3	-0.5	-0.4	-0.5
mitochondrial ribosomal protein L34	MRPL34	-0.4	-0.5	-0.5	**-1.1**
mitogen-activated protein kinase kinase kinase kinase 1	MAP4K1	-0.6	-0.9	-0.8	-0.8
mitogen-activated protein kinase kinase kinase kinase 1	MAP4K1	-0.5	-0.9	-0.5	-0.7
MRNA; cDNA DKFZp564C0762 (from clone DKFZp564C0762)		-0.4	-0.7	-0.6	**-1.2**
N-acylaminoacyl-peptide hydrolase	APEH	-0.5	-0.9	-0.5	-0.7
NAD(P) dependent steroid dehydrogenase-like	NSDHL	-0.7	-0.6	-0.7	-0.7
NAD(P) dependent steroid dehydrogenase-like	NSDHL	-0.8	-0.4	-0.4	-0.5
nuclear autoantigenic sperm protein (histone-binding)	NASP	-0.5	-0.6	-0.3	-0.5
nuclear factor (erythroid-derived 2)-like 3	NFE2L3	-0.7	**-1.0**	-0.4	**-1.9**
nuclear protein E3-3	DKFZP564J0123	-0.3	-0.4	-0.3	-0.5
nucleoporin 210	NUP210	**-1.2**	-0.5	-0.4	-0.8
nucleoporin 210	NUP210	-0.9	-0.5	-0.3	-0.8
nucleoporin 88kDa	NUP88	-0.4	-0.3	-0.3	-0.4
opioid receptor, sigma 1	OPRS1	-0.2	-0.9	-0.2	-0.6
opioid receptor, sigma 1	OPRS1	-0.4	-0.7	-0.6	-0.9
opsin 3 (encephalopsin, panopsin)	OPN3	-0.6	**-1.3**	-0.6	**-1.3**
opsin 3 (encephalopsin, panopsin)	OPN3	**-1.0**	**-1.3**	-0.5	**-1.6**

oxidation resistance 1	OXR1	-0.5	**-1.1**	-0.5	-0.6
oxidation resistance 1	OXR1	-0.4	**-1.0**	-0.4	-0.6
oxidative-stress responsive 1	OSR1	-0.5	-0.5	-0.3	-0.4
PAI-1 mRNA-binding protein	PAI-RBP1	-0.2	-0.3	-0.4	-0.5
PALM2-AKAP2 protein	PALM2-AKAP2	**-1.2**	**-1.7**	-0.5	**-1.1**
PALM2-AKAP2 protein	PALM2-AKAP2	**-1.0**	**-1.5**	-0.6	**-1.2**
PALM2-AKAP2 protein	PALM2-AKAP2	**-1.1**	**-1.4**	-0.7	**-1.2**
Pantothenate kinase 3	PANK3	-0.8	-0.8	-0.3	**-1.0**
PAX transcription activation domain interacting protein 1 like	PAXIP1L	-0.7	**-1.1**	-0.7	-0.8
phosphatidylinositol glycan, class F	PIGF	-0.5	**-1.2**	-0.4	-0.8
phosphoribosyl pyrophosphate synthetase 2	PRPS2	-0.3	-0.8	-0.4	-0.7
phosphoribosylaminoimidazole carboxylase	PAICS	-0.5	-0.7	-0.4	-0.8
phosphoribosylaminoimidazole carboxylase	PAICS	-0.4	-0.7	-0.5	-0.7
pim-2 oncogene	PIM2	-0.4	-0.3	-0.8	**-1.0**
plakophilin 2	PKP2	**-1.3**	**-1.5**	-0.9	**-1.1**
plakophilin 4	PKP4	-0.3	-0.5	-0.3	-0.4
PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	PMS1	-0.5	-0.7	-0.5	**-1.0**
poly(A) binding protein, cytoplasmic 4 (inducible form)	PABPC4	-0.5	**-1.1**	-0.3	-0.6
polymerase (RNA) I polypeptide D, 16kDa	POLR1D	-0.4	-0.9	-0.4	-0.5
polymerase (RNA) II (DNA directed) polypeptide H	POLR2H	-0.4	-0.7	-0.5	**-1.0**
PR domain containing 1, with ZNF domain	PRDM1	**-1.0**	-0.8	-0.4	**-1.0**
presenilin 2 (Alzheimer disease 4)	PSEN2	-0.6	-0.7	-0.3	-0.6
protease, serine, 7 (enterokinase)	PRSS7	**-1.1**	**-3.7**	-0.9	**-1.1**
proteasome (prosome, macropain) subunit, beta type, 8	PSMB8	**-1.4**	**-2.0**	-0.7	**-1.5**
proteasome (prosome, macropain) subunit, beta type, 8	PSMB8	**-2.4**	**-1.4**	-0.8	**-1.4**
protein phosphatase 1, catalytic subunit, gamma isoform	PPP1CC	-0.2	-0.5	-0.2	-0.5
protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52)	PPP2R2A	-0.6	-0.6	-0.4	-0.6
protein predicted by clone 23733	HSU79274	-0.6	-0.5	-0.4	**-1.2**
protein tyrosine phosphatase type IVA, member 3	PTP4A3	**-1.1**	-0.3	-0.6	**-1.5**
PTK2B protein tyrosine kinase 2 beta	PTK2B	**-1.0**	**-1.0**	-0.7	**-1.2**
purinergic receptor P2X, ligand-gated ion channel, 7	P2RX7	-0.8	**-2.1**	-0.4	-0.8
RAD50 homolog (S. cerevisiae)	RAD50	-0.3	-0.6	-0.4	-0.6
RAS p21 protein activator 4	RASA4	-0.8	**-1.1**	-0.3	**-1.0**
ras-related C3 botulinum toxin substrate 2	RAC2	**-1.0**	-0.8	-0.9	**-1.1**
ras-related C3 botulinum toxin substrate 2	RAC2	-0.7	-0.5	-0.5	-0.7
regulator of G-protein signalling 19	RGS19	-0.8	**-1.0**	-0.4	**-1.6**
retinoic acid receptor, alpha	RARA	-0.8	-0.9	-0.6	-0.8
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	-0.3	-0.3	-0.4	-0.3
Rho GTPase activating protein 4	ARHGAP4	-0.5	-0.3	-0.4	-0.6
Rho guanine nucleotide exchange factor (GEF) 3	ARHGEF3	-0.8	-0.6	-0.5	-0.9
rho/rac guanine nucleotide exchange factor (GEF) 2	ARHGEF2	-0.6	-0.5	-0.7	-0.5

ribosomal protein L10	RPL10	-0.9	-0.8	-0.6	-0.8
SAM domain and HD domain 1	SAMHD1	-0.9	-0.8	-0.4	-0.4
SAM domain and HD domain 1	SAMHD1	-0.5	-0.7	-0.6	-0.6
scribbled homolog (Drosophila)	SCRIB	-0.3	-0.6	-0.6	-0.7
serologically defined colon cancer antigen 3	SDCCAG3	-0.6	**-1.1**	-0.9	**-1.5**
sialyltransferase 8D (alpha-2, 8-polysialyltransferase)	SIAT8D	-0.5	**-1.5**	-0.4	-0.9
sialyltransferase 8D (alpha-2, 8-polysialyltransferase)	SIAT8D	-0.5	**-1.3**	-0.4	**-1.3**
similar to cyclin-E binding protein 1 (H. sapiens)	MGC14386	-0.3	-0.5	-0.4	-0.5
similar to ribosomal protein L22	LOC200916	-0.2	-0.4	-0.4	-0.5
Similar to SRR1-like protein		-0.5	-0.4	-0.4	**-1.0**
Similar to TSG118.1		-0.4	-0.3	-0.7	**-1.1**
small nuclear ribonucleoprotein polypeptide A'	SNRPA1	-0.2	-0.2	-0.6	-0.6
small optic lobes homolog (Drosophila)	SOLH	-0.4	-0.7	-0.8	**-1.1**
solute carrier family 25, member 11	SLC25A11	-0.4	-0.7	-0.5	-0.7
solute carrier family 25, member 11	SLC25A11	-0.3	-0.5	-0.5	-0.7
solute carrier family 29, member 1	SLC29A1	-0.6	-0.9	-0.6	**-1.0**
solute carrier family 29, member 1	SLC29A1	-0.4	-0.9	-0.8	**-1.0**
solute carrier family 35, member B2	SLC35B2	-0.5	-0.9	**-1.0**	**-1.0**
squalene epoxidase	**SQLE**	**-1.4**	**-2.6**	**-1.2**	**-1.1**
squalene epoxidase	SQLE	**-1.1**	**-1.4**	-0.7	-0.9
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	-0.7	**-2.7**	-0.4	-0.7
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	-0.9	**-2.5**	-0.5	-0.7
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	-0.7	**-2.2**	-0.5	-0.6
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	**-1.0**	**-2.4**	-0.4	-0.6
sterol regulatory element binding transcription factor 2	SREBF2	-0.5	**-1.4**	-0.4	-0.6
sterol-C4-methyl oxidase-like	**SC4MOL**	**-1.5**	**-2.0**	**-1.1**	**-1.8**
synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	-0.3	-0.3	-0.6	**-1.0**
syndecan 1	SDC1	-0.5	-0.8	-0.7	**-1.6**
TATA box binding protein (TBP)-associated factor, 105kDa	TAF4B	-0.6	-0.8	-0.7	**-1.2**
THO complex 3	THOC3	-0.2	-0.2	-0.3	-0.7
three prime repair exonuclease 2	TREX2	-0.3	-0.5	-0.4	-0.5
thymine-DNA glycosylase	TDG	-0.3	-0.6	-0.5	-0.8
TNF receptor-associated factor 7	TRAF7	-0.3	-0.7	-0.7	-0.9
TP53 regulating kinase	TP53RK	-0.3	-0.3	-0.3	-0.9
E2A immunoglobulin enhancer binding factors E12/E47	TCF3	-0.8	-0.6	-0.8	-0.8
E2A immunoglobulin enhancer binding factors E12/E47	TCF3	-0.8	-0.5	-0.3	-0.4
transcription factor Dp-1	TFDP1	-0.3	-0.7	-0.3	-0.5
transcription factor Dp-1	TFDP1	-0.6	-0.5	-0.7	-0.8
transforming, acidic coiled-coil containing protein 3	TACC3	-0.8	-0.7	-0.3	**-1.2**
translocation associated membrane protein 2	TRAM2	-0.9	**-1.2**	-0.3	-0.4
transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	TAP2	-0.6	-0.6	-0.6	-0.4
tripartite motif-containing 14	TRIM14	**-1.4**	-0.8	-0.5	**-1.0**
tripeptidyl peptidase II	TPP2	-0.4	-0.6	-0.5	-0.7
tripeptidyl peptidase II	TPP2	-0.4	-0.4	-0.3	-0.6

tubulin, gamma 1	TUBG1	**-1.0**	-0.9	-0.6	**-1.2**
tumor necrosis factor receptor superfamily, member 17	TNFRSF17	-0.7	-0.9	-0.4	-0.7
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UQCRFS1	-0.3	-0.4	-0.5	-0.5
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	-0.8	**-1.4**	-0.6	-0.7
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	-0.5	**-1.1**	-0.6	-0.6
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	-0.7	**-1.0**	**-1.0**	-0.6
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	-0.6	-0.8	-0.7	-0.5
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	-0.5	-0.8	-0.8	-0.5
ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)	UBE2E1	-0.3	-0.5	-0.2	-0.4
ubiquitin-conjugating enzyme E2S	UBE2S	**-1.0**	**-1.1**	-0.6	-0.9
UDP-glucose ceramide glucosyltransferase	UGCG	-0.3	-0.5	-0.5	-0.8
UDP-N-acteylglucosamine pyrophosphorylase 1	UAP1	-0.6	**-1.3**	-0.5	**-1.3**
unc-13 homolog C (C. elegans)	UNC13C	**-1.4**	-0.8	-0.9	**-1.4**
unc-13 homolog C (C. elegans)	UNC13C	**-1.2**	-0.7	-0.9	**-1.2**
unc-13 homolog C (C. elegans)	UNC13C	**-1.2**	-0.7	-0.7	**-1.4**
unc-84 homolog B (C. elegans)	UNC84B	-0.5	-0.5	-0.7	-0.7
unc-93 homolog B1 (C. elegans)	UNC93B1	-0.4	-0.6	-0.3	-0.9
v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	ETS1	-0.4	-0.7	-0.5	-0.9
vitamin K epoxide reductase complex, subunit 1	VKORC1	-0.4	-0.8	-0.2	-0.5
v-myb myeloblastosis viral oncogene homolog (avian)	MYB	-0.5	-0.8	-0.7	-0.9
wingless-type MMTV integration site family, member 10A	WNT10A	-0.5	-0.5	-0.7	**-1.7**
Wolf-Hirschhorn syndrome candidate 1	WHSC1	-0.4	-0.5	-0.4	**-1.1**
YY1 associated protein	YAP	-0.5	-0.2	-0.3	-0.3
zinc finger CCCH type domain containing 1	ZC3HDC1	-0.7	**-1.0**	-0.4	-0.7
zinc finger protein 22 (KOX 15)	ZNF22	-0.4	-0.5	-0.4	-0.5

LogRatios for down-regulated genes at 24 h in all cell lines

Two-fold changes are in green bold

Gene Descriptor	**Symbol**	**U266 24h**	**MM.1s 24h**	**8226/S 24h**	**KMS11 24h**
24-dehydrocholesterol reductase	DHCR24	**-2.6**	**-2.0**	-0.4	**-1.7**
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	**-1.7**	**-1.5**	-0.6	**-1.5**
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	**-1.5**	**-1.3**	-0.5	**-1.3**
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	**-1.8**	**-2.0**	-0.3	**-1.9**
3-oxoacid CoA transferase 1	OXCT1	-0.6	-0.4	-0.1	-0.4
7-dehydrocholesterol reductase	DHCR7	**-1.9**	**-2.9**	-0.6	**-2.0**
7-dehydrocholesterol reductase	DHCR7	**-1.6**	**-2.5**	-0.6	**-1.6**

8D6 antigen	8D6A	**-1.5**	**-1.3**	-0.7	**-1.8**
a disintegrin and metalloproteinase domain 10	ADAM10	-0.4	**-1.2**	-0.5	-0.9
activated RNA polymerase II transcription cofactor 4	PC4	-0.8	**-1.2**	-0.6	-0.8
acyl-CoA synthetase long-chain family member 3	ACSL3	-0.5	-0.9	-0.2	-0.3
adaptor protein with pleckstrin homology and src homology 2 domains	APS	**-1.4**	-0.9	-0.4	-0.8
adenosine monophosphate deaminase 1 (isoform M)	AMPD1	**-1.1**	**-2.7**	-0.7	**-1.5**
Aminoacylase 1-like 2	ACY1L2	-0.6	**-1.2**	-0.4	**-1.2**
Aminoacylase 1-like 2	ACY1L2	-0.5	-0.8	-0.3	**-1.0**
arginine-rich, mutated in early stage tumors	ARMET	**-1.1**	**-1.6**	-0.2	**-1.5**
ATP citrate lyase	ACLY	-0.4	-0.6	-0.2	-0.6
ATP citrate lyase	ACLY	-0.4	-0.4	-0.2	-0.3
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	ATP5D	-0.4	-0.6	-0.5	-0.9
ATPase type 13A	ATP13A	-0.6	-0.6	-0.3	**-1.1**
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	-0.7	-0.9	-0.4	-0.5
ATPase, Class I, type 8B, member 2	ATP8B2	-0.5	**-1.0**	-0.2	**-1.0**
BCL2-like 1	BCL2L1	**-1.5**	**-1.0**	-0.7	**-1.7**
BCL2-like 1	BCL2L1	**-1.3**	**-1.0**	-0.5	**-1.3**
BCL2-like 1 /// BCL2-like 1	BCL2L1	**-1.1**	**-1.1**	-0.6	**-1.3**
bicaudal D homolog 2 (Drosophila)	BICD2	-0.7	-0.3	-0.5	-0.7
bicaudal D homolog 2 (Drosophila)	BICD2	-0.6	-0.3	-0.4	-0.6
BTB (POZ) domain containing 3	BTBD3	**-1.1**	**-1.1**	-0.9	**-1.1**
butyrophilin, subfamily 3, member A1	BTN3A1	-0.7	-0.8	-0.3	-0.4
Butyrophilin, subfamily 3, member A2	BTN3A2	**-2.3**	**-1.6**	-0.8	**-4.0**
butyrophilin, subfamily 3, member A2	BTN3A2	**-1.7**	**-1.4**	-0.7	**-1.7**
butyrophilin, subfamily 3, member A3	BTN3A3	**-1.7**	**-1.4**	-0.7	**-1.5**
calmodulin-like 4	CALML4	**-1.2**	**-1.8**	-0.4	-0.5
calreticulin	CALR	-0.7	**-1.1**	-0.6	**-1.5**
calreticulin	CALR	-0.3	-0.5	-0.3	-0.8
Casein kinase 1, epsilon	CSNK1E	-0.8	-0.8	-0.6	-0.5
casein kinase 1, epsilon	CSNK1E	-0.4	-0.7	-0.4	-0.6
caveolin 1, caveolae protein, 22kDa	CAV1	-0.5	**-1.0**	-0.8	**-1.5**
caveolin 1, caveolae protein, 22kDa	CAV1	-0.4	-0.8	-0.9	**-1.3**
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-0.6	**-1.0**	**-1.1**	-0.4
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-0.7	-0.9	**-1.1**	-0.5
ceroid-lipofuscinosis, neuronal 6, late infantile, variant	CLN6	-0.7	**-1.0**	-0.3	**-1.3**
CGI-100 protein	CGI-100	-0.8	**-1.0**	-0.3	-0.9
chemokine (C-C motif) ligand 3	CCL3 /// CCL3L1 /// MGC12815	-0.2	**-2.0**	**-2.1**	**-1.1**
chemokine (C-C motif) receptor 1	CCR1	-0.7	-0.7	-0.6	**-1.6**
chemokine (C-C motif) receptor 1	CCR1	-0.7	-0.7	-0.5	**-1.2**
chromosome 1 open reading frame 22	C1orf22	-0.3	**-1.0**	-0.2	-0.7
Chromosome 10 open reading frame 75	C10orf75	**-1.0**	**-1.5**	-0.9	-0.9
chromosome 14 open reading frame 147	C14orf147	-0.5	-0.3	-0.2	-0.3
chromosome 15 open reading frame 22	C15orf22	-0.6	-0.5	-0.3	-0.9

chromosome 19 open reading frame 10	C19orf10	-0.8	**-1.0**	-0.5	**-1.0**
chromosome 19 open reading frame 10	C19orf10	-0.4	-0.7	-0.4	-0.8
chromosome 2 open reading frame 30	C2orf30	-0.4	-0.7	-0.3	-0.3
chromosome 3 open reading frame 6	C3orf6	-0.9	-0.6	-0.3	-0.8
chromosome 5 open reading frame 13	C5orf13	-0.9	-0.7	-0.7	-0.4
cisplatin resistance related protein CRR9p	CRR9	**-1.0**	-0.9	-0.3	**-1.0**
Hs.80305 /len=1196		-0.4	-0.5	-0.7	-0.5
coenzyme Q4 homolog (yeast)	COQ4	-0.4	-0.4	-0.5	-0.6
CLONE=IMAGE:2273535 /UG=Hs.123370 ESTs		-0.9	**-1.0**	-0.8	-0.8
CLONE=IMAGE:2383109 /UG=Hs.20300 ESTs		**-1.4**	**-1.0**	-0.5	**-1.0**
CLONE=CS0DI031YP04 (3 prime) /UG=Hs.173705		-0.6	-0.6	-0.5	**-1.1**
CLONE=BMFBGA04 /UG=Hs.13323		-0.7	-0.8	-0.2	-0.8
CLONE=IMAGE:3272383 /UG=Hs.40328 ESTs		-0.4	-0.4	-0.5	-0.4
CLONE=IMAGE:3071091 /UG=Hs.22627 ESTs		**-1.7**	**-1.1**	**-1.2**	**-2.4**
CLONE=IMAGE:261468 /UG=Hs.251865 ESTs		-0.7	**-1.5**	-0.4	-0.6
CLONE=IMAGE:111468 /UG=Hs.308800 ESTs		**-1.3**	**-1.0**	-0.5	-0.7
Core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	C1GALT1	-0.7	-0.5	-0.8	-0.7
cryptochrome 1 (photolyase-like)	CRY1	-0.8	**-1.9**	-0.7	**-1.0**
CSRP2 binding protein	CSRP2BP	-0.5	-0.7	-0.3	-0.7
C-type lectin, superfamily member 12	CLECSF12	-0.3	**-1.9**	-0.4	**-1.3**
C-type lectin, superfamily member 12	CLECSF12	-0.4	**-1.6**	-0.3	**-1.3**
C-type lectin, superfamily member 12	CLECSF12	-0.3	**-2.4**	-0.4	**-1.6**
cutC copper transporter homolog (E.coli)	CUTC	-0.5	-0.3	-0.5	-0.3
cyclin D2	CCND2	-0.9	-0.4	-0.5	**-1.0**
cyclin D2	CCND2	-0.9	-0.3	-0.4	-0.6
cytochrome P450, family 51, subfamily A, polypeptide 1	CYP51A1	**-1.3**	**-1.9**	-0.3	**-1.5**
cytochrome P450, family 51, subfamily A, polypeptide 1	CYP51A1	**-1.4**	**-1.8**	-0.5	**-1.4**
cytoplasmic polyadenylation element binding protein 4	CPEB4	-0.6	-0.4	-0.5	-0.6
cytoskeleton-associated protein 4	CKAP4	**-1.0**	**-1.3**	-0.4	**-1.2**
cytoskeleton-associated protein 4	CKAP4	-0.9	**-1.3**	-0.4	**-1.1**
deleted in lymphocytic leukemia, 1	DLEU1	-0.7	-0.9	-0.6	**-1.2**
Der1-like domain family, member 3	DERL3	**-1.6**	**-1.0**	**-1.0**	**-2.6**
dicarbonyl/L-xylulose reductase	DCXR	-0.8	-0.4	-0.2	**-1.1**
DKFZP564I1171 protein	DKFZP564I1171	-0.5	**-1.3**	-0.5	-0.3
dolichyl-phosphate mannosyltransferase polypeptide 3	DPM3	**-1.0**	**-1.2**	-0.6	-0.9
dual specificity phosphatase 22	DUSP22	-0.5	**-1.0**	-0.3	-0.6
dUTP pyrophosphatase	DUT	-0.7	-0.3	-0.3	-0.9
E2F transcription factor 5, p130-binding	E2F5	-0.4	**-1.0**	-0.3	-0.9
elongation factor, RNA polymerase II, 2	ELL2	-0.7	-0.4	-0.7	-0.9
emopamil binding protein (sterol isomerase)	EBP	**-1.0**	**-1.6**	-0.2	**-1.1**
endoplasmic reticulum to nucleus signalling 1	ERN1	-0.8	**-1.7**	**-1.1**	-0.6
eukaryotic translation initiation factor 1A, X-linked	EIF1AX	-0.8	-0.5	-0.2	-0.7
family with sequence similarity 46, member C	FAM46C	**-1.5**	**-1.9**	-0.4	**-1.4**
family with sequence similarity 46, member C	FAM46C	**-1.4**	**-1.6**	-0.5	**-1.2**
farnesyl-diphosphate farnesyltransferase 1	FDFT1	**-1.7**	**-2.0**	-0.5	**-1.4**
farnesyl-diphosphate farnesyltransferase 1	FDFT1	**-1.7**	**-1.9**	-0.4	**-1.6**

fatty acid desaturase 1	FADS1	**-1.9**	**-3.6**	-0.4	**-1.5**
fatty acid desaturase 1	FADS1	**-2.0**	**-3.0**	-0.5	**-2.1**
fatty acid desaturase 1	FADS1	**-1.5**	**-1.7**	-0.5	**-1.1**
fatty acid synthase	FASN	**-2.3**	**-1.6**	-0.9	**-2.3**
FK506 binding protein 11, 19 kDa	FKBP11	**-1.6**	**-1.7**	-0.4	**-2.3**
FK506 binding protein 11, 19 kDa	FKBP11	**-1.6**	**-1.6**	-0.5	**-2.4**
for protein disulfide isomerase-related	PDIR	**-1.1**	**-1.0**	-0.4	**-1.7**
Friend leukemia virus integration 1	FLI1	-0.5	-0.6	-0.5	-0.4
FtsJ homolog 1 (E. coli)	FTSJ1	-0.7	-0.4	-0.5	-0.9
G protein-coupled receptor 160	GPR160	**-1.7**	-0.7	-0.4	-0.3
Hs.119597 stearoyl-CoA desaturase		**-1.3**	**-2.8**	-0.4	**-1.4**
general transcription factor IIIA	GTF3A	-0.6	-0.5	-0.5	-0.6
general transcription factor IIIA	GTF3A	-0.6	-0.5	-0.4	-0.6
glucocorticoid induced transcript 1	GLCCI1	**-1.7**	**-1.3**	-0.6	**-1.3**
glucocorticoid induced transcript 1	GLCCI1	**-1.8**	**-1.3**	-0.4	**-1.3**
Glucocorticoid induced transcript 1	GLCCI1	**-2.3**	**-1.2**	-0.3	**-1.6**
glutaminase	GLS	-0.4	-0.7	-0.2	-0.7
glycosyltransferase AD-017	AD-017	**-1.1**	**-1.4**	-0.6	-0.9
golgi associated, gamma adaptin ear containing, ARF binding protein 2	GGA2	-0.4	-0.6	-0.4	-0.4
H1 histone family, member X	H1FX	-0.5	**-1.7**	-0.6	-0.5
H3 histone, family 3B (H3.3B)	H3F3B	**-1.9**	**-3.0**	-0.9	-0.4
heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	HSPA5	-0.8	-0.8	-0.4	**-1.1**
hepatitis delta antigen-interacting protein A	DIPA	-0.5	-0.6	-0.5	-0.9
heterogeneous nuclear ribonucleoprotein C (C1/C2)	HNRPC	-0.9	-0.8	-0.6	-0.9
heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	-0.4	-0.8	-0.5	-0.6
High density lipoprotein binding protein (vigilin)	HDLBP	-0.7	-0.5	-0.5	-0.6
high mobility group AT-hook 1	HMGA1	-0.5	-0.7	-0.5	**-1.1**
high-mobility group box 1	HMGB1	-0.9	**-1.5**	-0.5	-0.6
histone deacetylase 9	HDAC9	-0.8	-0.9	**-1.6**	**-1.0**
HLA-G histocompatibility antigen, class I, G	HLA-G	-0.7	-0.3	-0.3	-0.5
HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	HRMT1L2	-0.5	-0.8	-0.4	-0.7
hydroxysteroid (17-beta) dehydrogenase 8	HSD17B8	-0.6	**-1.0**	-0.5	**-1.1**
Hypothetical LOC402578		**-1.3**	-0.6	-0.6	-0.8
hypothetical protein DKFZp762C1112	DKFZp762 C1112	-0.4	-0.5	-0.3	-0.9
hypothetical protein FLJ10154	FLJ10154	-0.6	-0.6	-0.3	-0.4
hypothetical protein FLJ10204	FLJ10204	-0.6	-0.5	-0.6	-0.6
Hypothetical protein FLJ20254	FLJ20254	-0.7	-0.9	-0.4	-0.7
Hypothetical protein FLJ35036	FLJ35036	-0.8	-0.4	-0.4	-0.7
hypothetical protein FLJ35036	FLJ35036	-0.3	-0.3	-0.5	-0.6
hypothetical protein HSPC268	HSPC268	-0.4	-0.8	-0.4	-0.6
hypothetical protein HSPC268	HSPC268	-0.4	-0.7	-0.4	-0.7
hypothetical protein LOC202781	LOC202781	-0.7	**-1.2**	-0.5	-0.9
hypothetical protein LOC339287	LOC339287	-0.8	**-1.0**	-0.6	-0.7
hypothetical protein LOC51061	LOC51061	-0.7	**-1.5**	-0.5	-0.9
hypothetical protein MGC4172	MGC4172	-0.5	**-1.1**	-0.6	**-1.8**
hypothetical protein MGC5508	MGC5508	-0.3	-0.4	-0.3	-0.8
hypoxia up-regulated 1	HYOU1	-0.7	**-1.3**	-0.3	**-1.0**
immunoglobulin superfamily, member 4	IGSF4	-0.8	**-1.8**	-0.3	**-1.0**

Immunoglobulin superfamily, member 4	IGSF4	-0.5	**-1.5**	-0.3	**-1.0**
insulin induced gene 1	INSIG1	**-3.0**	**-3.1**	**-1.1**	**-1.6**
insulin induced gene 1	INSIG1	**-2.9**	**-3.0**	**-1.3**	**-1.7**
insulin induced gene 1	INSIG1	**-3.0**	**-2.9**	**-1.0**	**-1.9**
interferon regulatory factor 4	IRF4	**-1.5**	**-1.6**	-0.7	**-1.6**
interferon regulatory factor 4	IRF4	**-1.4**	**-1.5**	-0.8	**-1.1**
interferon stimulated gene 20kDa	ISG20	**-1.4**	-0.8	-0.7	-0.4
interleukin enhancer binding factor 3, 90kDa	ILF3	-0.3	-0.3	-0.3	-0.7
interleukin-1 receptor-associated kinase 1	IRAK1	-0.3	-0.4	-0.3	**-1.2**
Intermediate filament protein syncoilin	SYNCOILIN	**-1.2**	-0.9	-0.5	-0.8
ischemia/reperfusion inducible protein	FLJ23476	-0.6	-0.6	-0.6	**-1.1**
isopentenyl-diphosphate delta isomerase	IDI1	**-1.8**	**-1.9**	-0.3	**-1.3**
isopentenyl-diphosphate delta isomerase	IDI1	**-1.7**	**-1.9**	-0.4	**-1.3**
KDEL endoplasmic reticulum protein retention receptor 2	KDELR2	-0.4	-0.7	-0.3	-0.7
KH-type splicing regulatory protein (FUSE binding protein 2)	KHSRP	-0.5	-0.5	-0.4	-0.6
lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	LSS	**-1.4**	**-2.4**	-0.7	**-1.4**
lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	LSS	**-1.2**	**-2.0**	-0.6	**-1.4**
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	**-2.6**	**-3.6**	-0.6	**-1.7**
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	**-1.8**	**-3.2**	-0.6	**-1.8**
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	**-2.3**	**-3.0**	-0.6	**-1.4**
LYRIC/3D3	LYRIC	-0.8	-0.5	-0.5	-0.7
major histocompatibility complex, class I, B	HLA-B	**-1.0**	-0.5	-0.5	-0.5
major histocompatibility complex, class I, C	HLA-C /// HLA-B	-0.9	-0.3	-0.4	-0.4
major histocompatibility complex, class I, E	HLA-E	**-1.4**	**-2.3**	-0.5	**-1.3**
major histocompatibility complex, class I, E	HLA-E	-0.8	**-1.5**	-0.3	-0.7
major histocompatibility complex, class I, F	HLA-F	**-1.1**	-0.4	-0.4	-0.7
major histocompatibility complex, class I, F	HLA-F	-0.9	-0.4	-0.4	-0.6
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7	**-1.3**	**-1.7**	-0.5	**-1.3**
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7	**-1.1**	**-1.5**	-0.6	**-1.2**
mitochondrial ribosomal protein L23	MRPL23	-0.8	-0.5	-0.3	-0.9
M-phase phosphoprotein 9	MPHOSPH9	**-1.1**	-0.4	-0.3	-0.3
MRNA; cDNA DKFZp564C0762 (from clone DKFZp564C0762)		**-1.1**	-0.8	-0.4	**-1.0**
myosin regulatory light chain interacting protein	MYLIP	-0.9	-0.9	**-1.6**	-0.9
NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NDUFV2	-0.2	-0.6	-0.2	-0.5
nuclear autoantigenic sperm protein (histone-binding)	NASP	-0.6	-0.9	-0.5	-0.6
nuclear factor (erythroid-derived 2)-like 3	NFE2L3	-0.5	**-1.0**	-0.5	-0.8
nuclear factor, interleukin 3 regulated	NFIL3	-0.6	**-1.7**	-0.6	**-1.0**
nucleostemin	NS	-0.8	-0.3	-0.3	-0.8
PAI-1 mRNA-binding protein	PAI-RBP1	-0.3	-0.6	-0.6	-0.9

PALM2-AKAP2 protein	PALM2-AKAP2	**-1.3**	-0.9	-0.4	-0.9
PALM2-AKAP2 protein	PALM2-AKAP2	**-1.2**	-0.7	-0.2	-0.9
Paternally expressed 10	PEG10	-0.8	**-1.1**	-0.6	-0.6
Paternally expressed 10	PEG10	-0.7	**-1.0**	-0.7	-0.6
PAX transcription activation domain interacting protein 1 like	PAXIP1L	-0.6	**-1.0**	-0.4	-0.8
peroxiredoxin 4	PRDX4	**-1.0**	**-1.2**	-0.2	**-1.0**
phosphatidylinositol glycan, class F	PIGF	-0.7	-0.6	-0.3	-0.7
phosphatidylinositol glycan, class F	PIGF	-0.4	-0.5	-0.4	-0.4
phosphoribosylaminoimidazole carboxylase	PAICS	-0.5	-0.6	-0.3	-0.9
phosphoribosylaminoimidazole carboxylase	PAICS	-0.6	-0.6	-0.2	-0.8
plakophilin 2	PKP2	**-1.5**	**-1.5**	-0.4	-0.7
POU domain, class 2, associating factor 1	POU2AF1	**-1.4**	-0.8	**-1.1**	-0.9
PR domain containing 1, with ZNF domain	PRDM1	**-1.0**	**-1.1**	-0.9	**-1.3**
proapoptotic caspase adaptor protein	PACAP	**-1.9**	**-1.9**	-0.8	**-3.3**
proapoptotic caspase adaptor protein	PACAP	**-3.4**	**-1.8**	-0.6	**-2.9**
protease, serine, 7 (enterokinase)	PRSS7	-0.7	**-3.5**	-0.6	**-3.3**
proteasome (prosome, macropain) subunit, beta type, 8	PSMB8	**-1.0**	-0.8	-0.2	**-1.1**
protein disulfide isomerase related protein	ERP70	**-1.1**	**-1.8**	-0.6	**-1.8**
protein disulfide isomerase related protein	ERP70	**-1.3**	**-1.9**	-0.5	**-1.8**
protein kinase D3	PRKD3	-0.7	-0.9	-0.4	-0.3
protein kinase D3 /// protein kinase D3	PRKD3	**-1.1**	**-1.0**	-0.4	-0.4
putative dimethyladenosine transferase	HSA9761	-0.3	-0.6	-0.5	-0.6
putative nuclear protein ORF1-FL49	ORF1-FL49	-0.4	**-1.3**	-0.4	-0.6
RAB36, member RAS oncogene family	RAB36	**-1.1**	**-2.0**	-0.5	**-1.4**
ras-related C3 botulinum toxin substrate 2	RAC2	-0.9	-0.9	-0.2	-0.6
ras-related C3 botulinum toxin substrate 2	RAC2	-0.6	-0.5	-0.2	-0.3
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	**-1.0**	-0.7	-0.6	-0.7
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	**-1.2**	-0.6	-0.4	-0.6
ribosomal protein S6 kinase, 70kDa, polypeptide 1	RPS6KB1	**-1.0**	-0.5	-0.6	-0.5
S-adenosylhomocysteine hydrolase	AHCY	-0.1	-0.6	-0.2	-0.6
SAM domain and HD domain 1	SAMHD1	-0.7	-0.6	-0.4	-0.5
SAM domain and HD domain 1	SAMHD1	-0.8	-0.3	-0.6	-0.5
SEC24 related gene family, member D (S. cerevisiae)	SEC24D	-0.5	-0.6	-0.6	**-1.4**
Sec61 alpha 1 subunit (S. cerevisiae)	SEC61A1	-0.3	-0.6	-0.2	-0.4
SEH1-like (S. cerevisiae)	SEH1L	-0.3	-0.4	-0.3	-0.9
selenoprotein T	SELT	-0.8	**-1.3**	-0.8	-0.8
selenoprotein T	SELT	-0.3	**-1.0**	**-1.0**	-0.6
sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	SIAT1	-0.9	-0.6	-0.8	**-1.8**
signal recognition particle 72kDa	SRP72	-0.3	-0.4	-0.3	-0.3
signal sequence receptor, alpha	SSR1	-0.4	**-1.0**	-0.2	**-1.2**
signal sequence receptor, alpha	SSR1	-0.3	-0.8	-0.2	**-1.0**
signal sequence receptor, gamma	SSR3	-0.5	-0.9	-0.5	-0.7
signal sequence receptor, gamma	SSR3	-0.3	-0.8	-0.4	-0.8
Similar to 0610010D24Rik protein		-0.4	**-1.0**	-0.7	-0.9
similar to RIKEN cDNA 2700047N05	LOC134492	-0.4	-0.7	-0.4	-0.6
small optic lobes homolog (Drosophila)	SOLH	-0.5	-0.5	-0.4	-0.7
solute carrier family 29 (nucleoside transporters),	SLC29A1	-0.6	-0.6	-0.3	-0.9

member 1					
solute carrier family 29 (nucleoside transporters), member 1	SLC29A1	-0.6	-0.6	-0.5	-0.7
solute carrier family 39 (zinc transporter), member 4	SLC39A4	-0.9	-0.6	-0.3	-0.7
squalene epoxidase	SQLE	**-1.8**	**-1.5**	-0.7	**-1.8**
squalene epoxidase	SQLE	**-1.5**	**-1.3**	-0.6	**-1.6**
START domain containing 4, sterol regulated	STARD4	**-1.5**	**-1.8**	-0.6	**-1.6**
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	**-1.9**	**-3.1**	-0.8	**-2.2**
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	**-1.6**	**-3.0**	-0.8	**-2.6**
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	**-1.6**	**-2.8**	-0.8	**-2.0**
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	**-1.8**	**-3.1**	-0.7	**-2.5**
sterol regulatory element binding transcription factor 2	SREBF2	**-1.6**	**-2.2**	-0.4	**-1.5**
sterol regulatory element binding transcription factor 2	SREBF2	**-1.5**	**-2.0**	-0.3	**-1.7**
sterol-C4-methyl oxidase-like	SC4MOL	**-2.1**	**-2.2**	-0.5	**-1.8**
stromal cell-derived factor 2-like 1	SDF2L1	**-1.5**	**-1.2**	-0.8	**-1.8**
Synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	-0.9	-0.6	-0.6	-0.9
synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	-0.3	-0.3	-0.2	-0.5
syndecan 1	SDC1	**-1.0**	**-1.0**	-0.5	**-2.4**
syndecan 1	SDC1	-0.5	-0.6	-0.3	**-2.1**
thioredoxin domain containing 5	TXNDC5	-0.5	-0.6	-0.4	-0.8
thioredoxin domain containing 7 (protein disulfide isomerase)	TXNDC7	**-1.0**	**-1.4**	-0.5	**-1.4**
thioredoxin domain containing 7 (protein disulfide isomerase)	TXNDC7	-0.9	**-1.4**	-0.3	**-1.4**
thioredoxin domain containing 7 (protein disulfide isomerase)	TXNDC7	-0.8	**-1.2**	-0.3	**-1.1**
thioredoxin domain containing 7 (protein disulfide isomerase)	TXNDC7	-0.7	**-1.2**	-0.3	**-1.1**
thymine-DNA glycosylase	TDG	-0.5	-0.6	-0.4	-0.5
tissue inhibitor of metalloproteinase 2	TIMP2	-0.9	-0.6	-0.4	-0.4
tissue inhibitor of metalloproteinase 2	TIMP2	-0.9	-0.4	-0.3	-0.3
hypothetical protein LOC283585		-0.5	**-1.3**	-0.5	**-1.3**
transcription factor Dp-1	TFDP1	**-1.3**	**-1.9**	-0.5	**-1.1**
translocation associated membrane protein 2	TRAM2	**-1.4**	**-1.2**	-0.5	-0.8
translocation associated membrane protein 2	TRAM2	**-1.1**	**-1.1**	-0.5	-0.7
tribbles homolog 1 (Drosophila)	TRIB1	**-1.3**	**-2.0**	**-1.0**	-0.5
tubulin, gamma 1	TUBG1	-0.9	**-1.0**	-0.3	-0.4
tumor necrosis factor receptor superfamily, member 17	TNFRSF17	-0.9	**-1.8**	**-1.5**	**-2.5**
tumor necrosis factor, alpha-induced protein 8	TNFAIP8	-0.4	**-1.1**	-0.3	-0.4
tumor protein D52	TPD52	-0.5	-0.9	-0.3	-0.5
tumor protein D52	TPD52	-0.5	-0.8	-0.4	-0.6
tumor protein D52	TPD52	-0.5	-0.7	-0.2	-0.7
tumor rejection antigen (gp96) 1	TRA1	**-1.4**	-0.9	-0.4	**-1.1**
tumor rejection antigen (gp96) 1	TRA1	-0.7	-0.3	-0.3	-0.5
tumor suppressor deleted in oral cancer-related 1	DOC-1R	-0.7	-0.8	-0.3	-0.9
tyrosylprotein sulfotransferase 2	TPST2	**-1.2**	-0.3	-0.3	-0.9
ubiquitin-conjugating enzyme E2, J1	UBE2J1	**-1.8**	**-1.2**	**-1.0**	**-1.5**

ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	**-1.5**	**-1.0**	-0.6	**-1.2**
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	**-1.2**	-0.7	-0.3	**-1.1**
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	**-1.3**	-0.6	-0.5	**-1.2**
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	**-1.1**	-0.4	-0.4	-0.9
UDP-N-acteylglucosamine pyrophosphorylase 1	UAP1	-0.6	**-1.6**	-0.3	-0.9
unc-13 homolog C (C. elegans)	UNC13C	**-1.1**	**-1.6**	-0.7	**-1.3**
unc-13 homolog C (C. elegans)	UNC13C	**-1.1**	**-1.3**	-0.6	**-1.3**
unc-13 homolog C (C. elegans)	UNC13C	-0.8	**-1.1**	-0.5	**-1.1**
valyl-tRNA synthetase 2	VARS2	-0.5	-0.7	-0.5	**-1.1**
valyl-tRNA synthetase 2	VARS2	-0.5	-0.6	-0.4	-0.8
vascular endothelial growth factor B	VEGFB	-0.4	-0.7	-0.4	-0.9
vitamin K epoxide reductase complex, subunit 1	VKORC1	-0.7	**-1.0**	-0.3	**-1.0**
v-myb myeloblastosis viral oncogene homolog (avian)	MYB	-0.8	**-1.4**	-0.5	**-1.0**
WD repeat domain 4	WDR4	-0.6	-0.7	-0.5	**-1.2**
X-box binding protein 1	XBP1	-0.4	-0.9	-0.3	-0.9

LogRatios for down-regulated genes at 48 h in all cell lines
Two-fold changes are in green bold

Gene Descriptor	**Symbol**	**U266 48h**	**MM.1s 48h**	**8226/S 48h**	**KMS11 48h**
3-oxoacid CoA transferase 1	OXCT1	-0.6	-0.5	-0.2	-0.7
8D6 antigen	8D6A	**-1.4**	**-2.3**	-0.8	**-2.2**
activated RNA polymerase II transcription cofactor 4	PC4	**-1.2**	**-1.5**	-0.5	**-1.2**
acylphosphatase 1, erythrocyte (common) type	ACYP1	**-1.8**	**-1.2**	-0.4	-0.4
adenosine deaminase	ADA	**-1.0**	-0.2	-0.3	**-1.7**
Aminoacylase 1-like 2	ACY1L2	-0.9	**-1.8**	-0.6	**-1.8**
Aminoacylase 1-like 2	ACY1L2	-0.9	**-1.3**	-0.3	**-1.7**
AT rich interactive domain 2 (ARID, RFX-like)	ARID2	-0.5	-0.7	-0.8	**-1.4**
Atherin	LOC90378	-0.9	-0.8	-0.3	**-1.0**
ATP citrate lyase	ACLY	-0.3	-0.7	-0.3	-0.9
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	ATP5D	-0.6	-0.7	-0.5	-0.9
ATPase type 13A	ATP13A	-0.8	-0.5	-0.3	-0.9
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	-0.6	-0.8	-0.4	-0.7
ATPase, Class I, type 8B, member 2	ATP8B2	-0.4	**-1.4**	-0.5	**-1.7**
baculoviral IAP repeat-containing 5 (survivin)	BIRC5	**-1.0**	**-1.7**	-0.6	-0.3
baculoviral IAP repeat-containing 5 (survivin)	BIRC5	**-1.2**	**-1.6**	-0.2	-0.3
BCL2-like 1	BCL2L1	**-1.0**	**-1.8**	-0.6	**-1.8**
BCL2-like 1	BCL2L1	**-1.3**	**-1.8**	-0.5	**-1.4**
BCL2-like 1 /// BCL2-like 1	BCL2L1	-0.9	**-1.5**	-0.6	**-1.4**
bicaudal D homolog 2 (Drosophila)	BICD2	-0.8	-0.5	-0.5	**-1.5**
bicaudal D homolog 2 (Drosophila)	BICD2	-0.7	-0.3	-0.8	-0.9
brain acyl-CoA hydrolase	BACH	-0.9	**-1.5**	-0.4	-0.6

BTB (POZ) domain containing 3	BTBD3	-0.8	**-1.0**	**-1.1**	**-1.5**
BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	**-1.0**	**-1.9**	-0.3	-0.3
Butyrophilin, subfamily 3, member A2	BTN3A2	**-2.3**	**-2.0**	-0.7	**-4.5**
butyrophilin, subfamily 3, member A2	BTN3A2	**-1.9**	**-1.1**	-0.6	**-2.5**
butyrophilin, subfamily 3, member A3	BTN3A3	**-2.3**	**-1.0**	-0.7	**-2.6**
Casein kinase 1, epsilon	CSNK1E	-0.6	**-1.0**	-0.6	-0.8
casein kinase 1, epsilon	CSNK1E	-0.4	-0.5	-0.4	-0.6
caveolin 1, caveolae protein, 22kDa	CAV1	**-1.2**	**-1.5**	-0.9	**-2.4**
caveolin 1, caveolae protein, 22kDa	CAV1	**-1.2**	**-1.3**	**-1.0**	**-2.2**
caveolin 2	CAV2	-0.6	-0.7	**-1.0**	**-1.7**
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-0.5	**-1.0**	-0.7	-0.8
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-0.2	-0.6	-0.8	-0.5
CDNA: FLJ22198 fis, clone HRC01218		-0.5	**-1.0**	-0.6	-0.5
cell division cycle 25A	CDC25A	**-1.5**	**-1.5**	-0.3	**-1.6**
cell division cycle associated 4	CDCA4	-0.5	-0.5	-0.4	-0.7
ceroid-lipofuscinosis, neuronal 6, late infantile, variant	CLN6	-0.6	**-1.3**	-0.5	**-2.1**
CGI-100 protein	CGI-100	**-1.1**	-0.8	-0.4	**-1.3**
CGI-146 protein	PNAS-4	-0.3	-0.5	-0.4	-0.4
chromosome 14 open reading frame 147	C14orf147	-0.6	-0.5	-0.3	-0.8
chromosome 16 open reading frame 34	C16orf34	-0.4	-0.7	-0.2	-0.3
chromosome 19 open reading frame 13	C19orf13	-0.5	-0.3	-0.4	-0.6
Chromosome 19 open reading frame 6	C19orf6	-0.4	-0.4	**-1.0**	-0.9
chromosome 19 open reading frame 6	C19orf6	-0.3	-0.5	**-1.0**	-0.4
chromosome 21 open reading frame 56	C21orf56	-0.4	-0.4	-0.5	-0.8
chromosome 22 open reading frame 9	C22orf9	**-1.3**	**-1.3**	-0.3	**-2.8**
chromosome 7 open reading frame 19	C7orf19	-0.8	-0.6	-0.5	**-1.3**
chromosome 9 open reading frame 86	C9orf86	-0.4	-0.4	-0.5	-0.7
chromosome condensation 1	CHC1	-0.3	**-1.0**	-0.5	-0.9
cisplatin resistance related protein CRR9p	CRR9	**-1.4**	-0.7	-0.5	**-1.2**
cisplatin resistance related protein CRR9p	CRR9	**-1.2**	-0.5	-0.3	-0.7
Cleavage and polyadenylation specific factor 6, 68kDa	CPSF6	-0.5	**-1.1**	-0.7	-0.8
Hs.80305 /len=1196		-0.6	-0.7	-0.6	-0.7
coenzyme Q4 homolog (yeast)	COQ4	-0.7	-0.1	-0.4	-0.4
CLONE=IMAGE:981825 /UG=Hs.103135 ESTs		-0.4	**-1.0**	**-1.0**	-0.6
CLONE=IMAGE:1407864 /UG=Hs.180446 karyopherin (importin) beta 1		**-1.2**	-0.5	-0.7	**-1.1**
CLONE=IMAGE:1407864 /UG=Hs.180446 karyopherin (importin) beta 1		**-1.0**	-0.4	-0.5	**-1.2**
Hs.283906 Homo sapiens BAC clone RP11-244E6 from 2		-0.7	-0.7	-0.3	-0.6
CLONE=IMAGE:2108389 /UG=Hs.2910 phosphoribosyl pyrophosphate synthetase 2		**-1.1**	**-1.2**	-0.5	**-1.4**
CLONE=IMAGE:2273535 /UG=Hs.123370 ESTs		-0.8	**-1.1**	-0.5	**-1.0**
Human DNA sequence from clone RP11-16H23 on chromosome 10.		-0.4	-0.4	-0.4	-0.3
Hs.173705 Homo sapiens cDNA: FLJ22050 fis, clone HEP09454		-0.8	-0.6	-0.6	-0.7
CLONE=IMAGE:3219006 /UG=Hs.145020 ESTs		-0.6	-0.5	-0.5	-0.8

CLONE=IMAGE:4277696 /UG=Hs.5181		**-1.2**	**-1.2**	-0.7	**-2.2**
CLONE=IMAGE:4701118 /UG=Hs.180446		**-1.1**	-0.5	-0.8	**-1.3**
CLONE=IMAGE:261468 /UG=Hs.251865 ESTs		-0.6	**-1.5**	-0.2	**-1.0**
CLONE=IMAGE:308683 /UG=Hs.26425 ESTs		-0.6	-0.6	-0.6	**-1.1**
CSE1 chromosome segregation 1-like (yeast)	CSE1L	**-1.1**	**-1.0**	-0.3	-0.5
CSE1 chromosome segregation 1-like (yeast)	CSE1L	-0.8	-0.9	-0.2	-0.4
CSRP2 binding protein	CSRP2BP	-0.4	-0.5	-0.6	-0.8
CTP synthase	CTPS	-0.7	-0.5	-0.2	-0.9
C-type lectin, superfamily member 12	CLECSF12	-0.3	**-1.1**	-0.7	**-1.2**
cyclin A2	CCNA2	**-1.4**	**-1.8**	-0.2	-0.3
cyclin D1 (PRAD1: parathyroid adenomatosis 1)	CCND1	**-1.9**	**-2.6**	-0.5	**-2.0**
cyclin D2	CCND2	-0.9	**-1.4**	**-1.3**	**-2.0**
cyclin D2	CCND2	-0.6	**-1.0**	**-1.0**	**-1.0**
cyclin D2	CCND2	-0.6	-0.5	-0.3	-0.7
cyclin F	CCNF	-0.9	**-4.8**	-0.4	**-1.1**
cytoskeleton-associated protein 4	CKAP4	-0.6	**-1.4**	-0.5	**-1.2**
cytoskeleton-associated protein 4	CKAP4	-0.7	**-1.1**	-0.4	-0.9
DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	DDX46	-0.6	-0.8	-0.3	-0.8
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11	DDX11	-0.8	**-1.2**	-0.7	**-1.6**
DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	-0.4	-0.8	-0.2	**-1.0**
deleted in lymphocytic leukemia, 1	DLEU1	-0.3	**-1.2**	-0.9	**-1.5**
Der1-like domain family, member 3	DERL3	**-1.7**	-0.9	-0.5	**-2.1**
dihydrofolate reductase	DHFR	**-1.4**	**-1.5**	-0.4	-0.5
DKFZP586L0724 protein	DKFZP586 L0724	-0.4	-0.2	-0.4	-0.6
DNA replication complex GINS protein PSF2	Pfs2	**-2.2**	**-1.4**	-0.4	-0.7
DnaJ (Hsp40) homolog, subfamily C, member 10	DNAJC10	-0.8	-0.9	-0.6	**-1.1**
dolichyl-phosphate mannosyltransferase polypeptide 3	DPM3	**-1.5**	-0.7	-0.4	-0.9
dUTP pyrophosphatase	DUT	**-1.1**	**-1.3**	-0.5	**-1.1**
E2F transcription factor 2	E2F2	**-3.7**	**-1.6**	-0.7	**-1.6**
Elongation factor, RNA polymerase II, 2	ELL2	**-3.0**	**-1.3**	**-1.5**	**-3.1**
elongation factor, RNA polymerase II, 2	ELL2	**-1.0**	-0.4	-0.7	**-1.3**
eukaryotic translation elongation factor 1 epsilon 1	EEF1E1	-0.5	-0.6	-0.4	-0.8
eukaryotic translation initiation factor 1A, X-linked	EIF1AX	**-1.1**	-0.7	-0.3	**-1.1**
fatty acid binding protein 5 (psoriasis-associated)	FABP5	-0.5	**-1.6**	-0.5	**-1.0**
fatty acid synthase	FASN	**-1.5**	**-1.9**	-0.7	**-3.0**
F-box protein 45	FBXO45	-0.4	-0.3	-0.3	**-1.0**
F-box protein 9	FBXO9	-0.3	-0.5	-0.9	-0.6
F-box protein 9	FBXO9	-0.3	-0.4	-0.9	-0.4
F-box protein 9	FBXO9	-0.3	-0.3	-0.9	-0.5
FK506 binding protein 11, 19 kDa	FKBP11	**-2.3**	**-1.6**	-0.5	**-2.7**
FK506 binding protein 11, 19 kDa	FKBP11	**-2.3**	**-1.5**	-0.5	**-2.2**
fumarate hydratase	FH	-0.4	-0.8	-0.3	-0.9
fumarate hydratase	FH	-0.5	-0.7	-0.2	-0.6
GAJ protein	GAJ	**-2.1**	**-2.6**	-0.6	-0.7
general transcription factor IIIA	GTF3A	-0.8	-0.7	-0.8	**-1.0**
general transcription factor IIIA	GTF3A	-0.8	-0.7	-0.7	**-1.0**
glucocorticoid induced transcript 1	GLCCI1	**-2.3**	**-1.7**	-0.4	**-2.0**
glucocorticoid induced transcript 1	GLCCI1	**-1.9**	**-1.1**	-0.6	**-1.7**
glucocorticoid induced transcript 1	GLCCI1	**-1.9**	**-1.0**	-0.5	**-1.7**

glutaminase	GLS	-0.3	-0.8	-0.4	-0.7
glycosyltransferase 25 domain containing 1	GLT25D1	-0.7	**-1.0**	-0.4	-0.9
glycosyltransferase AD-017	AD-017	**-1.1**	-0.9	-0.6	-0.5
golgi associated, gamma adaptin ear containing, ARF binding protein 2	GGA2	-0.4	-0.4	-0.3	-0.6
growth and transformation-dependent protein	E2IG5	-0.4	-0.4	-0.2	**-1.2**
H3 histone, family 3B (H3.3B)	H3F3B	**-2.2**	**-2.3**	-0.8	**-1.1**
heat shock 70kDa protein 14	HSPA14	-0.4	-0.4	-0.3	-0.6
Helicase, lymphoid-specific	HELLS	**-2.2**	**-2.4**	-0.5	**-1.8**
Helicase, lymphoid-specific	HELLS	**-1.7**	**-2.2**	-0.4	**-1.4**
heterogeneous nuclear ribonucleoprotein A3	HNRPA3	-0.7	-0.5	-0.2	-0.8
heterogeneous nuclear ribonucleoprotein C (C1/C2)	HNRPC	**-1.0**	**-1.2**	-0.7	**-1.3**
high mobility group AT-hook 1	HMGA1	**-1.2**	**-1.8**	-0.9	**-1.8**
high mobility group AT-hook 1	HMGA1	**-1.0**	-0.9	-0.6	**-1.1**
high-mobility group box 1	HMGB1	-0.5	**-1.1**	-0.4	-0.9
HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	HRMT1L2	-0.4	-0.7	-0.5	**-1.2**
hydroxysteroid (17-beta) dehydrogenase 8	HSD17B8	-0.5	**-1.0**	-0.6	-0.9
Hypothetical LOC388796		-0.5	-0.5	-0.5	-0.7
Hypothetical LOC388796		-0.3	-0.4	-0.3	-0.7
Hypothetical LOC402578		**-1.1**	-0.7	-0.7	**-1.6**
Hypothetical LOC402578		**-1.1**	**-1.1**	-0.3	**-1.5**
hypothetical protein	LOC387882	**-1.0**	**-2.3**	-0.9	-0.9
hypothetical protein DKFZp434K1815	DKFZp434 K1815	-0.8	-0.3	-0.5	-0.8
hypothetical protein FLJ10154	FLJ10154	-0.4	-0.4	-0.5	-0.3
hypothetical protein FLJ12953 similar to Mus musculus D3Mm3e	FLJ12953	-0.7	**-1.1**	-0.5	-0.6
hypothetical protein FLJ20364	FLJ20364	-0.9	**-1.2**	-0.4	-0.3
hypothetical protein FLJ20425	LYAR	-0.5	-0.9	-0.3	**-1.5**
hypothetical protein FLJ35036	FLJ35036	**-1.0**	-0.6	-0.4	**-1.1**
Hypothetical protein FLJ35036	FLJ35036	-0.8	-0.4	-0.4	**-1.0**
hypothetical protein FLJ35036	FLJ35036	-0.6	-0.3	-0.6	-0.6
hypothetical protein H41	H41	-0.5	**-1.1**	-0.5	**-1.3**
hypothetical protein H41	H41	-0.3	-0.9	-0.5	-0.9
hypothetical protein H41	H41	-0.3	-0.4	-0.4	-0.6
hypothetical protein HSPC268	HSPC268	**-2.3**	-0.6	-0.8	-0.5
hypothetical protein HSPC268	HSPC268	-0.8	-0.3	-0.6	-0.5
hypothetical protein LOC124512	LOC124512	-0.4	-0.5	-0.3	-0.6
hypothetical protein LOC202781	LOC202781	-0.5	-0.8	-0.6	-0.3
hypothetical protein LOC221362	LOC221362	-0.7	-0.5	-0.5	-0.4
hypothetical protein LOC339287	LOC339287	-0.7	-0.6	-0.7	-0.8
hypothetical protein LOC348094	LOC348094	-0.2	-0.8	-0.4	**-1.5**
hypothetical protein MAC30	MAC30	**-2.1**	**-2.1**	-0.3	**-1.1**
hypothetical protein MAC30	MAC30	**-1.9**	**-2.2**	-0.3	**-1.1**
hypothetical protein MGC33867	MGC33867	-0.6	-0.9	-0.4	**-1.2**
hypothetical protein MGC4172	MGC4172	-0.8	**-1.3**	-0.7	**-2.8**
hypothetical protein MGC5508	MGC5508	-0.5	-0.5	-0.5	**-1.1**
hypoxia-inducible protein 2	HIG2	**-1.2**	**-1.7**	-0.4	**-1.7**
immunoglobulin superfamily, member 4	IGSF4	-0.8	**-1.6**	-0.4	**-1.1**
Immunoglobulin superfamily, member 4	IGSF4	-0.6	**-1.5**	-0.4	**-1.2**
insulin induced gene 1	INSIG1	**-2.3**	**-3.7**	-0.3	**-1.9**

insulin induced gene 1	INSIG1	**-2.4**	**-3.5**	-0.2	**-1.7**
insulin induced gene 1	INSIG1	**-2.3**	**-3.3**	-0.4	**-1.5**
interferon regulatory factor 4	IRF4	**-1.5**	**-1.1**	-0.3	-0.9
interleukin enhancer binding factor 3, 90kDa	ILF3	-0.3	-0.9	-0.7	**-1.7**
interleukin enhancer binding factor 3, 90kDa	ILF3	-0.3	-0.7	-0.5	**-1.0**
Intermediate filament protein syncoilin	SYNCOILIN	**-1.3**	-0.8	-0.6	**-1.0**
jun D proto-oncogene	JUND	**-1.3**	**-1.7**	-0.8	-0.9
KH-type splicing regulatory protein (FUSE binding protein 2)	KHSRP	-0.7	-0.7	**-1.3**	**-1.7**
KIAA0152 gene product	KIAA0152	-0.7	-0.3	-0.4	**-1.2**
KIAA0186 gene product	KIAA0186	**-1.8**	**-2.3**	-0.2	**-1.0**
KIAA0877 protein	KIAA0877	-0.4	**-2.0**	-0.2	**-1.1**
lamin B1	LMNB1	-0.5	**-1.7**	-0.7	-0.7
LYRIC/3D3	LYRIC	**-1.0**	-0.3	-0.6	-0.9
LYRIC/3D3	LYRIC	-0.4	-0.4	-0.3	-0.7
MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	**-1.3**	**-2.1**	-0.5	-0.7
MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	**-1.5**	**-2.0**	-0.4	-0.7
MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	MCM4	**-2.0**	**-2.7**	-0.4	**-1.4**
MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	MCM4	**-1.8**	**-2.1**	-0.4	**-1.1**
MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	MCM4	**-1.3**	**-2.1**	-0.3	-0.9
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7	**-1.4**	**-2.2**	-0.8	**-1.7**
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7	**-1.3**	**-1.8**	-0.8	**-1.2**
mesoderm development candidate 2	MESDC2	-0.5	-0.9	-0.2	-0.8
methylenetetrahydrofolate dehydrogenase (NADP+ dependent)	MTHFD1	-0.7	-0.8	-0.3	**-1.0**
mitochondrial ribosomal protein L23	MRPL23	-0.7	-0.7	-0.4	-0.8
mitochondrial ribosomal protein L24	MRPL24	-0.4	-0.5	-0.7	-0.5
mitochondrial ribosomal protein L38	MRPL38	-0.6	-0.5	-0.3	-0.8
mitochondrial ribosomal protein S15	MRPS15	-0.3	-0.4	-0.2	-0.4
M-phase phosphoprotein 9	MPHOSPH9	**-1.2**	-0.6	-0.2	-0.9
MRNA; cDNA DKFZp564C0762 (from clone DKFZp564C0762)		**-1.0**	**-1.2**	-0.7	**-1.0**
mutS homolog 6 (E. coli)	MSH6	-0.6	**-1.0**	-0.2	-0.7
MYC-associated zinc finger protein	MAZ	**-1.0**	**-1.5**	-0.6	**-2.3**
MYC-associated zinc finger protein	MAZ	-0.8	-0.8	-0.2	**-1.4**
Myosin VA (heavy polypeptide 12, myoxin)	MYO5A	-0.3	-0.5	-0.6	-0.3
NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NDUFV2	-0.3	-0.5	-0.4	-0.4
nuclear factor (erythroid-derived 2)-like 3	NFE2L3	-0.7	-0.7	-0.8	**-1.1**
nuclear mitotic apparatus protein 1	NUMA1	-0.7	-0.4	-0.2	-0.7
nucleolar protein 5A (56kDa with KKE/D repeat)	NOL5A	-0.6	-0.4	-0.5	**-1.4**
nucleostemin	NS	-0.9	-0.4	-0.4	**-1.2**
Nudix (nucleoside diphosphate linked moiety X)-type motif 3	NUDT3	-0.5	-0.5	-0.3	-0.9
Nudix (nucleoside diphosphate linked moiety X)-type motif 5	NUDT5	**-1.0**	-0.4	-0.5	**-1.7**
Opa-interacting protein 5	OIP5	-0.8	**-1.7**	-0.3	-0.4

PAI-1 mRNA-binding protein	PAI-RBP1	-0.8	**-1.0**	-0.6	**-1.7**
Paternally expressed 10	PEG10	**-1.5**	**-2.3**	-0.7	**-1.7**
Paternally expressed 10	PEG10	**-1.3**	**-1.9**	-0.8	**-1.2**
phosphatidylinositol glycan, class F	PIGF	**-1.0**	-0.6	-0.6	**-1.0**
phosphatidylinositol glycan, class F	PIGF	-0.8	-0.2	-0.6	-0.5
phospholipase A2, group XIIA /// phospholipase A2, group XIIA	PLA2G12A	**-1.0**	**-1.0**	-0.3	-0.9
phosphoribosyl pyrophosphate amidotransferase	PPAT	-0.3	-0.5	-0.3	**-1.1**
phosphoribosylaminoimidazole carboxylase	PAICS	-0.4	-0.9	-0.4	**-1.1**
phosphoribosylaminoimidazole carboxylase	PAICS	-0.5	-0.8	-0.3	**-1.2**
POU domain, class 2, associating factor 1	POU2AF1	**-1.4**	-0.9	-0.5	**-1.4**
PR domain containing 1, with ZNF domain	PRDM1	**-1.0**	**-1.0**	-0.6	**-1.1**
primase, polypeptide 1, 49kDa	PRIM1	-0.6	**-1.1**	-0.4	-0.8
proapoptotic caspase adaptor protein	PACAP	**-4.0**	**-1.4**	-0.4	**-2.8**
proapoptotic caspase adaptor protein	PACAP	**-2.7**	**-1.6**	-0.6	**-3.2**
processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	POP5	-0.4	-0.6	-0.6	-0.6
proliferation-associated 2G4, 38kDa	PA2G4	-0.5	-0.7	-0.4	**-1.3**
protease, serine, 7 (enterokinase)	PRSS7	**-1.1**	**-4.5**	**-1.1**	**-3.8**
proteasome (prosome, macropain) subunit, beta type, 8	PSMB8	-0.9	-0.5	-0.4	**-1.7**
protein disulfide isomerase related protein	ERP70	-0.8	**-1.3**	-0.2	**-1.6**
protein disulfide isomerase related protein	ERP70	**-1.0**	**-1.1**	-0.3	**-1.2**
protein kinase D3	PRKD3	**-1.0**	-0.7	-0.5	-0.3
protein kinase D3	PRKD3	**-1.1**	-0.7	-0.3	-0.4
protein kinase D3 /// protein kinase D3	PRKD3	**-1.3**	-0.9	-0.4	-0.7
putative dimethyladenosine transferase	HSA9761	-0.3	-0.9	-0.6	**-1.2**
R3H domain (binds single-stranded nucleic acids) containing	R3HDM	-0.4	-0.5	-0.5	-0.7
RAN binding protein 5	RANBP5	-0.4	-0.9	-0.3	**-1.0**
RAN binding protein 5	RANBP5	-0.5	-0.7	-0.4	-0.5
replication factor C (activator 1) 3, 38kDa	RFC3	**-1.2**	**-1.3**	-0.3	-0.8
replication factor C (activator 1) 4, 37kDa	RFC4	**-1.3**	**-1.3**	-0.2	-0.3
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	-0.7	**-1.4**	**-1.0**	**-1.7**
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	-0.7	**-1.4**	**-1.0**	**-1.4**
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	-0.5	-0.7	-0.4	-0.6
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	-0.3	-0.6	-0.4	-0.5
Ribonuclease H1	RNASEH1	-0.7	-0.6	-0.4	**-1.5**
ribosomal protein L15	RPL15	-0.6	-0.4	-0.2	-0.5
RNA binding motif protein 14	RBM14	-0.5	-0.9	-0.6	-0.8
RNA binding motif protein, X-linked	RBMX	-0.7	-0.4	-0.4	-0.6
SAM domain and HD domain 1	SAMHD1	**-1.0**	-0.6	-0.4	**-1.2**
SAM domain and HD domain 1	SAMHD1	-0.8	-0.4	-0.3	**-1.1**
SEC14-like 1 (S. cerevisiae)	SEC14L1	-0.6	-0.6	-0.3	**-1.1**
SEH1-like (S. cerevisiae)	SEH1L	-0.5	-0.9	-0.5	**-1.4**
selenoprotein T	SELT	-0.8	**-1.0**	-0.7	-0.8
selenoprotein T	SELT	-0.5	-0.9	-0.8	-0.7
SET translocation (myeloid leukemia-associated)	SET	-0.2	-0.4	-0.7	**-1.2**
seven in absentia homolog 2 (Drosophila)	SIAH2	-0.5	**-1.0**	-0.2	**-1.4**
SFRS protein kinase 1	SRPK1	-0.4	-0.4	-0.3	-0.7
sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	SIAT1	**-1.1**	-0.5	-0.9	**-1.7**
sialyltransferase 7D	SIAT7D	**-1.1**	-0.9	-0.3	**-1.4**

sialyltransferase 7D	SIAT7D	-0.7	-0.9	-0.3	**-1.7**
signal sequence receptor, gamma	SSR3	-0.4	**-1.1**	-0.7	**-1.2**
signal sequence receptor, gamma	SSR3	-0.4	-0.6	-0.2	-0.9
Similar to 0610010D24Rik protein		-0.8	**-1.2**	-0.4	-0.4
similar to ribosomal protein L22	LOC200916	-0.3	-0.3	-0.4	-0.6
similar to RIKEN cDNA 2700047N05	LOC134492	-0.4	-0.8	-0.4	-0.4
Similar to RIKEN cDNA 2700049P18 gene	MGC57827	-0.5	**-2.3**	-0.3	-0.3
small nuclear ribonucleoprotein polypeptides B and B1	SNRPB	-0.6	-0.7	-0.2	-0.6
solute carrier family 16, member 3	SLC16A3	**-1.7**	**-1.5**	-0.7	**-1.4**
solute carrier family 16, member 3	SLC16A3	**-1.6**	**-1.4**	-0.6	-0.8
solute carrier family 29 (nucleoside transporters), member 1	SLC29A1	-0.8	**-1.3**	-0.5	**-1.9**
solute carrier family 29 (nucleoside transporters), member 1	SLC29A1	-0.7	**-1.0**	-0.5	**-1.4**
solute carrier family 39 (zinc transporter), member 4	SLC39A4	**-1.0**	-0.8	-0.4	-0.8
spermidine synthase	SRM	-0.5	-0.7	-0.4	**-1.7**
splicing factor, arginine/serine-rich 2	SFRS2	-0.4	-0.8	-0.4	-0.7
splicing factor, arginine/serine-rich 2	SFRS2	-0.3	-0.6	-0.4	-0.6
splicing factor, arginine/serine-rich 3	SFRS3	-0.4	-0.4	-0.3	-0.4
splicing factor, arginine/serine-rich 6	SFRS6	-0.8	-0.3	-0.6	-0.6
squalene epoxidase	SQLE	**-1.4**	**-2.6**	-0.2	**-1.9**
stem-loop (histone) binding protein	SLBP	-0.6	-0.7	-0.3	**-1.1**
stromal cell-derived factor 2-like 1	SDF2L1	**-1.6**	-0.7	-0.9	**-1.3**
structure specific recognition protein 1	SSRP1	-0.5	-0.8	-0.2	**-1.1**
Synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	-0.7	-0.9	-0.4	**-1.4**
synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	-0.5	-0.6	-0.4	**-1.0**
syndecan 1	SDC1	**-1.7**	-0.9	-0.3	**-3.3**
TATA box binding protein (TBP)-associated factor, 28kDa	TAF11	-0.3	-0.6	-0.5	-0.4
TEA domain family member 1 (SV40 transcriptional enhancer factor)	TEAD1	-0.4	-0.5	-0.3	-0.5
tetratricopeptide repeat domain 3	TTC3	-0.3	-0.4	-0.4	-0.5
thioredoxin domain containing 7 (protein disulfide isomerase)	TXNDC7	**-1.2**	**-1.2**	-0.3	**-1.3**
thymine-DNA glycosylase	TDG	-0.5	-0.4	-0.6	-0.8
tissue inhibitor of metalloproteinase 2	TIMP2	**-1.4**	-0.9	-0.5	-0.6
tissue inhibitor of metalloproteinase 2	TIMP2	**-1.2**	-0.6	-0.5	-0.4
Transcribed locus, moderately similar to NP_689672.2		-0.4	-0.6	-0.5	-0.5
Transcribed locus, moderately similar to NP_689672.2		-0.4	-0.6	-0.6	-0.3
transcription elongation regulator 1	TCERG1	-0.5	-0.4	-0.2	-0.7
E2A immunoglobulin enhancer binding factors E12/E47	TCF3	**-1.8**	**-1.1**	-0.3	**-1.3**
E2A immunoglobulin enhancer binding factors E12/E47	TCF3	-0.9	-0.4	-0.3	-0.3
transcription factor Dp-1	TFDP1	**-1.3**	**-3.7**	-0.6	**-2.1**
transcription factor Dp-1	TFDP1	**-1.0**	**-2.0**	-0.3	**-1.2**
translocation associated membrane protein 2	TRAM2	**-2.0**	**-1.5**	-0.6	**-1.1**
translocation associated membrane protein 2	TRAM2	**-1.4**	**-1.3**	-0.8	**-1.0**

translocation protein 1	TLOC1	-0.3	-0.7	-0.5	-0.8
tribbles homolog 1 (Drosophila)	TRIB1	**-1.3**	**-1.6**	**-1.3**	-0.3
tubulin, gamma 1	TUBG1	**-1.4**	**-1.0**	-0.7	-0.8
tumor necrosis factor receptor superfamily, member 17	TNFRSF17	**-1.8**	**-1.5**	**-1.0**	**-2.7**
Tyr 3-monooxygenase/tryptophan 5-monooxygenase activation protein	YWHAH	-0.8	**-1.6**	-0.3	-0.7
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UQCRFS1	-0.3	-0.3	-0.3	-0.5
ubiquitin-conjugating enzyme E2 variant 1	UBE2V1 /// Kua-UEV	-0.2	-0.5	-0.4	-0.5
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	**-1.9**	-0.6	-0.4	**-1.8**
ubiquitin-like, containing PHD and RING finger domains, 1	UHRF1	**-2.0**	**-2.2**	-0.3	-0.6
UDP-N-acteylglucosamine pyrophosphorylase 1	UAP1	-0.7	**-1.4**	-0.3	**-1.3**
unc-13 homolog C (C. elegans)	UNC13C	**-1.2**	**-1.9**	**-1.0**	**-2.2**
unc-13 homolog C (C. elegans)	UNC13C	**-1.1**	**-1.6**	**-1.1**	**-1.9**
unc-13 homolog C (C. elegans)	UNC13C	**-1.1**	**-1.5**	**-1.1**	**-1.8**
uracil-DNA glycosylase	UNG	-0.5	**-2.1**	-0.6	**-1.4**
valyl-tRNA synthetase 2	VARS2	-0.5	**-1.1**	-0.6	**-1.5**
valyl-tRNA synthetase 2	VARS2	-0.4	-0.7	-0.4	**-1.2**
vitamin K epoxide reductase complex, subunit 1	VKORC1	-0.9	-0.7	-0.2	**-1.0**
v-myb myeloblastosis viral oncogene homolog (avian)	MYB	**-1.2**	**-1.4**	-0.7	**-1.8**
V-myb myeloblastosis viral oncogene homolog (avian)-like 1	MYBL1	**-1.8**	**-1.4**	-0.6	**-1.4**
v-myc myelocytomatosis viral oncogene homolog (avian)	MYC	**-1.3**	-0.4	-0.4	**-1.4**
WD repeat domain 4	WDR4	-0.5	-0.8	-0.8	**-1.4**
WD repeat domain 4	WDR4	-0.5	-0.7	-0.7	**-1.5**
Wolf-Hirschhorn syndrome candidate 1	WHSC1	-0.7	**-1.8**	-0.2	**-1.4**
YEATS domain containing 4	YEATS4	-0.6	**-1.2**	-0.5	-0.5
zinc finger protein 580	ZNF580	-0.7	**-1.3**	-0.3	-0.9
Zinc finger protein, subfamily 1A, 1 (Ikaros)	ZNFN1A1	-0.7	-0.4	-0.3	**-1.0**
zinc finger protein, subfamily 1A, 1 (Ikaros)	ZNFN1A1	-0.7	-0.3	-0.3	-0.9