

Table A. Genes significantly influenced by Cobalt and Hypoxia in HIF1a -/- Cells

ID	Gene Name	Abbr
	Nuclear (GO = 0005634)	
H3014H11	DNA segment, Chr 15, ERATO Doi 417, expressed	
H3017F05	lamin A	Lmna
H3100G09	requiem	Req
H3110H03	Btg3 associated nuclear protein	Banp
H3118B02	prothymosin alpha	Ptma
H3135G01	myeloid ecotropic viral integration site-related gene 1	Mrg1
	Membrane Proteins (GO = 0016021)	
H3029C03	podocalyxin-like	Podxl
H3035F09	Ras and a-factor-converting enzyme 1 homolog	Rce1
H3090D12	mannose-P-dolichol utilization defect 1	Mpdu1
H3112F03	degenerative spermatocyte homolog (Drosophila)	Degs
H3140C05	tumor necrosis factor receptor superfamily	Tnfrsf12a
H3151H12	RIKEN cDNA 1110025J15 gene	
	Enzymes (Various GO)	
H3013B02	ATPase, H+ transporting, V1 subunit B, isoform 2	Atp6v1b2
H3021E11	ATPase, H+ transporting, V1 subunit A, isoform 1	Atp6v1a1
H3028F05	ornithine decarboxylase, structural	Odc
H3042F09	dual specificity phosphatase 19	Dusp19
H3048G11	biliverdin reductase B (flavin reductase (NADPH))	Blvrb
H3095F09	brain-specific ang. Inh. 1-associated protein 2	Baiap2
H3157A06	PET112-like (yeast)	Pet112l
H3157D12	microsomal glutathione S-transferase 3	Mgst3
	Misc Functions (Various GO)	
H3002F06	eukaryotic translation initiation factor 3	Eif3
H3003H10	actinin, alpha 1	Actn1
H3042H12	expressed sequence A1840044	
H3078C09	oxysterol binding protein-like 2	Osbpl2
H3108H07	cortactin	Cttn
H3138G07	vacuolar protein sorting 26 (yeast)	Vps26
H3151F07	procollagen, type VI, alpha 1	Col6a1
	Function Unknown	
H3008B08	RIKEN cDNA 6330411E07 gene	
H3014E12	signal recognition particle 72	Srp72
H3038G11	translocase of outer mitochondrial membrane	Tomm20
H3043F08	protein phosphatase 1, regulatory subunit 2	Ppp1r2
H3057G09	RIKEN cDNA 6030440G05 gene	
H3060C11	spermine oxidase	Smox
H3071D02	kelch domain containing 2	Klhdc2
H3094E02	RIKEN cDNA A230106A15 gene	
H3098D04	RIKEN cDNA 1300004C11 gene	
H3103E10	Rho GTPase activating protein 18	Arhgap18
H3106H11	RIKEN cDNA 2400001E08 gene	
H3110E06	RIKEN cDNA 9130011E15 gene	
H3139F07	RIKEN cDNA 2410066K11 gene	
H3144B07	H19 fetal liver mRNA	H19
H3146A07	RIKEN cDNA C130083N04 gene	
H3156C11	RIKEN cDNA 1700052N19 gene	
	Unknown	
H3010B02		

Table A. Genes significantly influenced by Cobalt and Hypoxia in HIF1a ^{-/-} Cells (cont.)

H3014F03		
H3014G11		
H3017C01		
H3017D04		
H3034H05		
H3049F11		
H3051E02		
H3056B11		
H3065B07		
H3094E01		
H3096C07		
H3098B01		
H3101A07		
H3101A11		
H3107B03		
H3111B07		
H3115G07		
H3118H04		
H3150D07		
H3154E06		
H3159A07		

**Table B. Genes significantly influenced by Hypoxia treatment in □
WT and HIF1a -/- cells**

ID	Name	Abbr.
H3003H10	Rattus norvegicus non-muscle alpha-actin	Actn1
H3016D10	lectin, galactose binding, soluble 3	Lgals3
H3024B04	Mus musculus chaperonin subunit 3 (gamma)	Cct3
H3028F03	Mus musculus cell-line LXB2 cathepsin L	Ctsl
H3030D10	Mus musculus pyruvate kinase, muscle	Pkm2
H3030D11	Mus musculus pyruvate kinase, muscle	Pkm2
H3045G06	translocated promoter region (TPR) NM_003292.1	
H3048G11	Similar to biliverdin reductase B	Blvrb
H3059H07	clone RP23-20N14 on chromosome 11	
H3067C04	Homo sapiens small nuclear ribonucleoprotein	Snrpb2
H3088G10	Similar to Absent in melanoma 1 protein	Mina
H3094E01	RP23-32O9 on chromosome 2	
H3103C03	Similar to R13F6.10.p [Caenorhabditis elegans]	
H3103G04	ras association (RalGDS/AF-6) domain family	Rassf1
H3116A06	Mus musculus, clone IMAGE:4024675	
H3118B01	Mouse mRNA for prothymosin alpha	Ptma
H3128C03	RIKEN cDNA 5430419M09 gene (5430419M09Rik)	
H3129G12	protease, serine, 15	Prss15
H3137C05	RAB14, member RAS oncogene family	Rab14
H3145H03	mitogen activated protein kinase 3	Mapk3
H3146D12	clone RP23-135F6 on chromosome 11	
H3147H11	tissue specific transplantation antigen P35B	Tsta3
H3148E03	capping protein (actin filament) muscle Z-line, beta	Capzb
H3151F07	procollagen, type VI, alpha 1 (Col6a1)	Col6a1
H3153B03	Mus musculus chromosome 8 clone RP24-324M11	
H3157D03	clone RP23-384K10 on chromosome 2	

Table C. Genes significantly influenced by Cobalt treatment in WT and HIF1a -/- □ cells

ID	Gene Name	Abbr.
A-2031	Metallothionein-I (image 1052401)	Mt1
H3020E11	M.musculus mRNA for cyclin F	Ccnf
H3024G12	clone RP23-407M20 on chromosome 11	
H3028F05	Mouse kidney ornithine decarboxylase mRN	Odc
H3029B11	Mouse chromatin nonhistone high mobility	Hmga1
H3049F11	RIKEN cDNA 9930116P15 gene (9930116P15Rik)	
H3067E01	eukaryotic translation elongation factor 1 alpha 1	Eef1a1
H3098B01	Unknown	
H3131A07	Mus musculus peroxisomal/mitochondrial d	Ech1
H3132E03	Homo sapiens chromosome 17, clone hRPK.1	
H3137C06	Mouse transglutaminase (TGase) mRNA, com	Tgm2
H3140C11	Homo sapiens ATPase, H+ transporting, ly	Atp6v0b
H3144B07	Mus musculus H19 and muscle-specific Nct	H19
H3151H12	NMDA receptor glutamate-binding subunit	Lag

Table D. Genes significantly influenced by Hypoxia in WT cells

Name	ID	Fold Changes				TTEST			
		W-Co	W-H	N-Co	N-H	W-Co	W-H	N-Co	N-H
Mus musculus lactate dehydrogenase 1, A	H3023H12	2.71	3.93	0.86	0.89	0.01	0.00	0.43	0.55
Mus musculus phosphoglycerate kinase (Pg	H3023D06	2.31	3.67	0.69	0.93	0.01	0.00	0.12	0.74
Mouse mRNA for alpha-enolase (2-phospho-	H3027E08	2.12	3.02	0.98	1.10	0.01	0.01	0.94	0.69
Mus musculus procollagen-proline, 2-oxog	H3003D12	1.29	2.61	0.97	1.05	0.01	0.00	0.68	0.69
Mouse mRNA for alpha-enolase (2-phospho-	H3027E09	1.76	2.48	0.87	0.75	0.01	0.01	0.54	0.12
Homo sapiens Xq28 genomic DNA in the reg	H3022H02	1.83	2.43	1.00	0.82	0.08	0.01	0.98	0.37
Mus musculus pyruvate kinase 3 (PK3), mR	H3030D11	1.93	2.36	0.87	0.65	0.00	0.00	0.53	0.03
Rat 37 kd protein mRNA, partial cds	H3101C10	1.37	2.30	0.81	0.83	0.16	0.01	0.29	0.44
Homo sapiens cDNA FLJ10500 fis, clone NT	H3030G02	1.77	2.20	1.12	1.12	0.00	0.00	0.18	0.27
Mus musculus triosephosphate isomerase (H3149C10	2.06	2.18	0.82	0.81	0.00	0.01	0.29	0.24
Mouse gene for basigin, complete cds (ex	H3020G04	1.30	2.10	0.72	0.91	0.09	0.01	0.09	0.54
GAPDH	H3012A11	1.42	2.09	0.91	0.85	0.18	0.03	0.75	0.57
Homo sapiens 12p21 BAC RPC11-259O18 (Ro	H3123A12	1.95	2.07	0.78	0.95	0.00	0.01	0.14	0.72
Arabidopsis thaliana chromosome II secti	H3017G08	1.59	2.05	0.93	0.96	0.00	0.00	0.55	0.64
Mus musculus pyruvate kinase 3 (Pk3), mR	H3030D10	1.62	2.02	0.86	0.69	0.01	0.01	0.38	0.00
Homo sapiens mRNA; cDNA DKFZp434B0920 (f	H3118B12	1.49	1.96	0.90	0.90	0.10	0.02	0.53	0.65
Mouse growth factor-induced delayed earl	H3019C07	1.69	1.95	1.21	1.05	0.00	0.00	0.16	0.77
Arabidopsis thaliana chromosome I BAC F2	H3022E07	1.43	1.94	0.79	0.82	0.00	0.00	0.11	0.18
Mus musculus aldolase 1, A isoform (Aldo	H3031D03	1.35	1.92	0.88	0.92	0.00	0.00	0.20	0.34
Unknown	H3013E11	1.40	1.87	0.82	1.08	0.13	0.01	0.38	0.74
Human DNA sequence from clone RP5-876B10	H3145B03	1.24	1.86	0.83	0.70	0.26	0.00	0.55	0.18
Homo sapiens mRNA; cDNA DKFZp566E034 (fr	H3103B07	1.26	1.86	1.03	0.87	0.08	0.00	0.80	0.37
45S rRNA	H3079C09	1.03	1.83	0.76	0.75	0.90	0.00	0.29	0.26
Mouse mRNA for alpha-enolase (2-phospho-	H3027E07	1.94	1.82	0.75	0.92	0.03	0.02	0.23	0.72
Homo sapiens mRNA for KIAA1139 protein,	H3016G08	1.64	1.82	1.17	1.28	0.03	0.01	0.44	0.13
Homo sapiens chromosome 14 clone RP11-23	H3035F10	1.46	1.79	2.02	1.04	0.19	0.04	0.40	0.90
Mus musculus histone H1(0) gene, complet	H3110G08	1.21	1.78	0.85	1.54	0.17	0.00	0.54	0.11
Metallothionein-I (image 1052401)	A-2031	2.81	1.78	2.13	1.56	0.00	0.00	0.02	0.07
Mus musculus keratin complex 1, acidic,	H3022G09	0.90	1.78	0.93	1.09	0.10	0.01	0.42	0.56
bNIP3 (BCL2 adenovirus interacin protei	H3136C07	1.38	1.78	0.91	0.99	0.14	0.01	0.46	0.93
Mus musculus glucose phosphate isomerase	H3125B04	1.64	1.76	1.15	1.23	0.03	0.03	0.40	0.33
Mouse mRNA for fibronectin receptor beta	H3019E08	1.45	1.75	0.90	0.86	0.00	0.00	0.55	0.38
IgM	H3085G01	1.11	1.74	0.88	0.78	0.53	0.05	0.60	0.37
Homo sapiens BAC clone RP11-196O16 from	H3150A01	1.36	1.73	0.88	1.00	0.02	0.00	0.27	0.98
Mus musculus N-myc downstream regulated	H3031C12	1.16	1.71	0.93	1.21	0.19	0.00	0.57	0.09
Homo sapiens cDNA FLJ20122 fis, clone CO	H3128G06	1.47	1.70	1.09	1.22	0.00	0.00	0.16	0.09
Mouse hexokinase mRNA, complete cds	H3134D04	1.23	1.67	0.91	0.75	0.13	0.01	0.77	0.44
Mus musculus unknown mRNA, complete cds	H3125C10	1.32	1.67	0.94	1.18	0.06	0.00	0.61	0.15
Homo sapiens genomic DNA, chromosome 22q	H3058G01	1.03	1.67	1.03	1.33	0.87	0.01	0.82	0.06
Rattus norvegicus mRNA for MIPP65, compl	H3142F07	1.31	1.65	1.03	1.19	0.16	0.01	0.86	0.37
Caenorhabditis elegans cosmid Y6B3B, com	H3012A11	1.36	1.63	0.79	0.82	0.00	0.00	0.15	0.17
Murine mRNA for L-34 galactoside-binding	H3016D10	1.46	1.62	1.07	1.32	0.01	0.00	0.47	0.02
Homo sapiens mRNA for KIAA0585 protein,	H3142H08	1.27	1.61	1.06	0.94	0.20	0.04	0.70	0.74
Homo sapiens protease, serine, 15 (PRSS1	H3129G12	1.32	1.60	1.18	1.48	0.06	0.00	0.24	0.03
Rat mRNA for ribosomal protein L5	H3028D04	1.23	1.60	0.66	1.11	0.47	0.04	0.17	0.67
Cricetulus griseus (chinese hamster) mRN	H3024D01	1.45	1.58	1.23	1.14	0.12	0.03	0.45	0.39
Mus musculus BCL2/adenovirus E1B 19 kDa-	H3016D08	1.39	1.58	0.91	0.95	0.00	0.01	0.25	0.48
Mus musculus domesticus mitochondrial ca	H3143D12	1.45	1.55	1.05	1.21	0.01	0.03	0.77	0.28
M.musculus tex264 mRNA (3'region)	H3132D05	1.27	1.55	1.00	1.13	0.26	0.05	1.00	0.52
Mus musculus cell-line LXB2 cathepsin L	H3028F03	2.17	1.54	1.28	2.92	0.02	0.04	0.37	0.00
human STS WI-11792	H3149G05	1.13	1.50	0.81	1.48	0.38	0.01	0.20	0.10
Homo sapiens chromosome 17, clone hRPK.3	H3153F08	1.18	1.49	0.96	0.96	0.24	0.02	0.71	0.88
mouse mRNA for megakaryocyte potentiatin	H3134A02	1.25	1.49	0.85	1.15	0.12	0.03	0.48	0.49
Mus musculus procollagen, type VI, alpha	H3151F07	0.89	1.48	0.53	0.73	0.60	0.01	0.00	0.02
Homo sapiens zinc finger protein 220 (ZN	H3031D12	1.43	1.48	0.76	0.84	0.12	0.02	0.13	0.21
Influenza A/Memphis/8/88 (H3N2), PB2 pol	H3147H11	1.73	1.47	1.26	1.45	0.04	0.04	0.11	0.04
Human DNA sequence from clone 717M23 on	H3025G08	1.08	1.47	0.86	0.68	0.75	0.03	0.73	0.37
Mouse calpactin I heavy chain (p36) mRNA	H3126C03	1.08	1.47	0.76	0.81	0.65	0.02	0.12	0.22
Mouse elongation factor 2 (ef-2) mRNA, 3	H3129B11	1.49	1.45	0.97	1.38	0.12	0.02	0.89	0.26
Human BAC clone CTA-385F2 from 7p15, com	H3158F12	1.52	1.44	0.96	1.17	0.06	0.04	0.87	0.48

Table D. Genes significantly influenced by Hypoxia in WT cells (cont.)

Tapa-1=integral membrane protein TAPA-1	H3151C09	1.49	1.44	0.96	1.25		0.02	0.04	0.79	0.25
Mus musculus scavenger receptor type A S	H3056C09	1.02	1.44	0.98	1.02		0.87	0.00	0.92	0.90
Mus musculus matrix metalloproteinase 23	H3058D07	0.71	1.43	0.49	0.55		0.04	0.01	0.13	0.09
Chlamydia pneumoniae section 35 of 103 o	H3030B07	1.07	1.40	0.62	1.22		0.80	0.02	0.08	0.51
Mus musculus gelsolin (Gsn), mRNA	H3120B07	1.13	1.38	0.86	1.04		0.32	0.03	0.20	0.76
Rattus norvegicus proline rich protein m	H3116A06	1.24	1.35	1.08	1.30		0.01	0.01	0.46	0.05
Mus musculus UCP2 mRNA, complete cds	H3136E12	1.14	1.35	0.83	1.21		0.39	0.04	0.25	0.23
Mus musculus nidogen 2 (Nid2), mRNA	H3115F11	1.40	1.35	0.76	1.05		0.01	0.04	0.06	0.75
M.musculus mRNA for mitogen activated pr	H3145H03	1.23	1.35	0.93	1.60		0.08	0.02	0.27	0.00
Hamster apt gene for adenine phosphorib	H3022F10	1.17	1.35	0.94	0.93		0.45	0.04	0.64	0.68
Homo sapiens cDNA FLJ10879 fis, clone NT	H3148E03	1.14	1.34	1.02	1.39		0.24	0.03	0.92	0.04
Mus musculus mRNA for GANP protein	H3031B12	1.42	1.33	0.92	0.96		0.01	0.03	0.52	0.77
Mus musculus mini chromosome maintenance	H3146C08	1.22	1.32	1.06	0.98		0.12	0.03	0.64	0.85
Fugu rubripes cosmid 151J19 covering the	H3157C12	0.99	1.32	0.89	0.99		0.94	0.01	0.29	0.90
Mus musculus 123F2 protein mRNA, complet	H3103G04	1.40	1.31	1.28	0.70		0.11	0.02	0.29	0.03
Phaseolus vulgaris clone pPERB5 peroxid	H3110G03	1.11	1.30	0.80	1.07		0.44	0.04	0.08	0.64
cloning vector pSport1, complete cds	H3020C02	2.07	1.27	1.25	1.11		0.01	0.02	0.38	0.68
Mus musculus lymphocyte antigen 6 comple	H3027D05	0.78	1.26	0.88	0.84		0.01	0.05	0.38	0.16
Homo sapiens conserved gene amplified in	H3132C02	0.85	1.25	0.74	0.89		0.31	0.02	0.20	0.40
Homo sapiens cDNA FLJ10078 fis, clone HE	H3097B10	1.24	1.25	0.91	1.04		0.11	0.03	0.75	0.87
Homo sapiens PAC clone RP4-673M15 from 7	H3025G12	1.13	1.25	0.96	0.85		0.16	0.02	0.77	0.35
Homo sapiens chromosome 17, clone hRPC.5	H3017H10	1.13	1.24	0.96	1.01		0.13	0.04	0.68	0.95
Rattus norvegicus gene for selenium-depe	H3074A08	1.12	1.23	0.85	1.09		0.49	0.03	0.28	0.64
Mus musculus GLUT4 vesicle protein mRNA,	H3022E01	1.24	1.22	1.01	1.04		0.01	0.05	0.96	0.68
Rattus norvegicus SPA-1 like protein p12	H3151E06	1.08	1.22	0.91	0.98		0.44	0.04	0.35	0.89
BAC sequence from the SPG4 candidate reg	H3029D11	1.15	1.21	1.20	1.45		0.34	0.01	0.34	0.12
Homo sapiens YEAF1 mRNA for YY1 and E4TF	H3021H08	1.07	1.21	1.08	1.15		0.22	0.04	0.37	0.23
Mus musculus ribosomal protein L23 (Rp12)	H3101A08	1.13	1.20	0.92	1.10		0.54	0.04	0.66	0.65
Homo sapiens genomic DNA, chromosome 8p1	H3126F04	0.82	1.20	0.99	1.23		0.15	0.03	0.95	0.35
Homo sapiens chromosome 17, clone HRPC29	H3142E06	0.74	0.90	0.83	1.13		0.00	0.02	0.37	0.41
Homo sapiens MUM2 (MUM2) gene, complete	H3118D07	0.77	0.90	1.01	0.97		0.04	0.02	0.93	0.88
Homo sapiens mRNA for type II membrane p	H3003H02	0.94	0.88	1.12	1.02		0.34	0.03	0.21	0.85
Homo sapiens clone HQ0189 PRO0189 mRNA,	H3076F07	1.30	0.88	1.29	0.96		0.15	0.01	0.19	0.78
Homo sapiens 3q26.2-27 BAC RPC111-436A20	H3005F02	0.95	0.88	0.89	1.03		0.46	0.03	0.09	0.79
H.sapiens mRNA (clone ICRFp507L1876)	H3059H09	0.89	0.88	0.88	0.99		0.18	0.02	0.21	0.87
Methanosarcina barkeri fhm a, d, g, b ge	H3016H06	1.16	0.88	0.88	0.93		0.28	0.04	0.18	0.57
Homo sapiens genomic DNA, chromosome 21q	H3096E05	1.20	0.87	1.08	1.29		0.21	0.03	0.56	0.15
Mus musculus CRIPT protein mRNA, complet	H3137A04	0.98	0.87	1.23	1.04		0.86	0.03	0.14	0.77
Caenorhabditis elegans cosmid C13D9	H3016F11	0.97	0.86	0.92	1.01		0.64	0.03	0.28	0.89
Human DNA sequence from PAC 196E23 on ch	H3016E06	0.94	0.86	0.96	0.96		0.31	0.04	0.69	0.49
No Hits Found	H3072E04	1.21	0.85	0.88	1.06		0.02	0.04	0.51	0.71
Homo sapiens mRNA; cDNA DKFZp434G0972 (f	H3134C01	0.90	0.85	0.84	0.91		0.42	0.04	0.30	0.33
Mouse transglutaminase (TGase) mRNA, com	H3137C06	0.63	0.85	0.56	0.88		0.02	0.01	0.01	0.41
Human mRNA for KIAA0020 gene, complete c	H3016H05	0.97	0.84	1.08	1.12		0.59	0.03	0.27	0.23
Human DNA sequence from clone RP5-839B4	H3146B04	1.19	0.84	0.94	1.05		0.30	0.03	0.54	0.60
Homo sapiens chromosome 19, fosmid 37308	H3142B09	0.90	0.84	0.95	1.07		0.24	0.05	0.77	0.66
Human DNA sequence from PAC 42616 on chr	H3075G07	1.03	0.84	0.79	1.11		0.79	0.04	0.22	0.59
Human Xp22 BAC CT-285115 (from CalTech/R	H3016H04	1.11	0.84	0.88	0.90		0.33	0.03	0.32	0.40
Mus musculus eukaryotic translation init	H3016F05	0.89	0.83	0.99	0.91		0.04	0.00	0.85	0.22
Homo sapiens clone PAC 270M7 chromosome	H3011D06	1.11	0.83	0.88	0.95		0.50	0.04	0.39	0.72
Human DNA sequence from clone RP3-467K16	H3001B10	0.91	0.83	0.89	1.00		0.32	0.04	0.36	1.00
Homo sapiens EST00098 gene, last exon	H3009G09	0.97	0.83	1.43	0.90		0.83	0.03	0.38	0.41
Homo sapiens chromosome 17, clone hRPC.3	H3015H04	1.01	0.83	0.88	1.04		0.94	0.03	0.26	0.79
Homo sapiens cDNA FLJ10154 fis, clone HE	H3111G04	0.86	0.82	1.08	0.98		0.16	0.01	0.61	0.85
Homo sapiens cDNA FLJ11144 fis, clone PL	H3017D08	0.92	0.82	1.01	0.94		0.31	0.05	0.90	0.44
Homo sapiens BAC clone RP11-445A14 from	H3115F02	1.01	0.82	1.47	1.05		0.94	0.03	0.14	0.77
Neospora caninum thrombospondin-related	H3051H10	0.92	0.82	0.87	0.96		0.42	0.04	0.10	0.62
Mus musculus MHC class III region RD gen	H3003F05	1.06	0.81	0.85	1.10		0.44	0.04	0.56	0.69
Homo sapiens full length insert cDNA clo	H3071C08	0.97	0.81	0.81	0.83		0.80	0.05	0.10	0.10
Mus musculus ribosomal protein S6 (Rps6)	H3113A04	0.99	0.80	2.02	1.00		0.92	0.04	0.42	0.98
Mus musculus adenosine deaminase (ADA) g	H3017G11	0.92	0.80	0.83	0.92		0.36	0.04	0.03	0.35
Mus musculus B6D2F1 clone 2C4D mRNA	H3100E08	1.13	0.80	1.23	0.83		0.19	0.03	0.20	0.23

Table D. Genes significantly influenced by Hypoxia in WT cells (cont.)

Homo sapiens, clone RP11-44O2, complete	H3004F06	0.96	0.80	0.89	0.94		0.55	0.01	0.09	0.39
Human DNA sequence from clone 653C5 on c	H3011E02	0.67	0.80	0.81	0.82		0.00	0.03	0.49	0.52
Mus musculus transcription factor Sp3 mR	H3008H04	1.00	0.80	0.83	0.89		0.98	0.04	0.26	0.36
Neurospora crassa gene for adenylate cyc	H3142H11	1.04	0.80	1.03	0.82		0.79	0.01	0.93	#####
Mus musculus glutathione-S-transferase,	H3119G08	1.08	0.80	0.83	1.17		0.55	0.04	0.15	0.25
Human acidic 82 kDa protein mRNA, comple	H3120A06	1.08	0.80	1.32	0.93		0.68	0.02	0.22	0.59
M.musculus mRNA for adenine nucleotide t	H3028B03	0.87	0.80	0.83	0.91		0.17	0.04	0.33	0.65
Homo sapiens chromosome 5 clone CITB-H1_	H3041D03	0.84	0.80	0.84	0.92		0.14	0.04	0.33	0.69
Homo sapiens chromosome 21 PAC LLNLP704M	H3103C03	0.96	0.79	0.85	0.65		0.76	0.02	0.38	0.01
Mus musculus ribosomal protein L29 (Rpl2	H3115H06	1.31	0.79	1.22	1.21		0.08	0.02	0.29	0.23
Mycobacterium tuberculosis H37Rv complet	H3125G08	1.04	0.79	0.90	0.91		0.77	0.03	0.60	0.67
Mus musculus mRNA for ubiquitin-conjugat	H3140B06	1.13	0.79	0.90	0.82		0.36	0.05	0.67	0.42
R.norvegicus mRNA for microtubule associ	H3146D12	0.93	0.79	0.74	0.65		0.56	0.05	0.23	0.04
Human hypervariable fragment g	H3119B05	0.92	0.79	1.03	0.96		0.45	0.02	0.71	0.82
Sprague-Dawley (clone LRB13) RAB14 mRNA,	H3137C05	1.25	0.79	0.69	0.56		0.46	0.04	0.08	0.04
Homo sapiens putative DNA dependent ATPa	H3132E05	1.31	0.79	0.87	0.81		0.02	0.02	0.51	0.38
Homo sapiens BAC clone CTB-118P15 from 8	H3132F07	0.85	0.78	0.81	0.93		0.29	0.05	0.26	0.70
Homo sapiens mRNA; cDNA DKFZp564C2163 (f	H3100C04	1.18	0.78	1.35	1.07		0.08	0.03	0.18	0.63
Homo sapiens cDNA FLJ10005 fis, clone HE	H3153F11	0.87	0.78	1.03	0.83		0.34	0.02	0.86	0.33
Human DNA sequence from clone 931E15 on	H3014F08	1.01	0.77	0.90	1.02		0.93	0.00	0.16	0.81
Human mRNA for KIAA0094 gene, partial cd	H3109E11	1.07	0.77	1.08	0.92		0.63	0.05	0.68	0.45
Mus musculus chaperonin subunit 3 (gamma	H3024B04	0.85	0.77	0.90	0.79		0.16	0.04	0.46	0.04
Human DNA sequence from clone RP4-592A1	H3135G09	0.83	0.77	0.98	0.81		0.23	0.03	0.90	0.32
Mus musculus nucleosome binding protein	H3132F05	1.19	0.77	1.18	0.97		0.26	0.02	0.46	0.80
Mus musculus nuclear protein 220 (Np220)	H3029A07	1.08	0.77	1.01	0.94		0.64	0.03	0.94	0.69
Homo sapiens chromosome 19, BC335474 (Cl	H3048C09	0.89	0.77	1.20	0.99		0.43	0.03	0.18	0.93
Human DNA sequence from clone RP4-746H2	H3029D09	0.81	0.77	1.40	0.86		0.05	0.01	0.05	0.33
Homo sapiens chromosome 4 clone B266E3 m	H3010C04	0.96	0.76	0.93	1.12		0.81	0.04	0.69	0.43
M.musculus 94kb genomic sequence encodin	H3035C01	0.86	0.76	1.04	0.71		0.26	0.01	0.79	0.14
Homo sapiens 12q15 BAC RPC11-444B24 (Ro	H3022H03	1.11	0.76	0.97	0.98		0.25	0.02	0.85	0.90
Homo sapiens Chromosome 22q11.2 BAC Clon	H3070A01	0.98	0.76	0.64	0.77		0.89	0.04	0.01	0.13
Genomic sequence for Arabidopsis thalian	H3057A03	0.96	0.75	1.04	0.87		0.79	0.03	0.82	0.27
Mus musculus MHC class III region RD gen	H3140F01	0.81	0.75	1.25	0.98		0.19	0.01	0.33	0.92
R.norvegicus (Sprague-Dawley) ribosomal	H3139H05	0.96	0.75	0.76	1.08		0.71	0.04	0.16	0.58
Rat glycine methyltransferase gene (EC 2	H3011C08	1.03	0.75	0.85	0.99		0.85	0.05	0.34	0.94
Mus musculus putative serine/threonine p	H3010H08	0.91	0.74	0.81	0.98		0.44	0.04	0.20	0.88
Homo sapiens protein phosphatase 2A regu	H3153C10	0.86	0.74	0.65	0.83		0.49	0.05	0.00	0.27
Homo sapiens nuclear cap binding protein	H3007D12	0.93	0.74	0.85	0.92		0.40	0.01	0.37	0.60
Mus musculus mRNA for adenylate kinase i	H3052D11	0.74	0.74	0.93	0.96		0.02	0.05	0.73	0.84
Mouse Murr1 mRNA, exon	H3137G06	0.77	0.74	0.81	0.98		0.07	0.03	0.43	0.93
Homo sapiens chromosome 11 open reading	H3133C11	0.99	0.74	0.85	0.86		0.94	0.02	0.28	0.54
Homo sapiens tetratricopeptide repeat do	H3124H03	0.88	0.73	1.02	0.92		0.27	0.05	0.90	0.55
Homo sapiens zyxin-related protein 1 gen	H3117G10	0.92	0.73	1.16	1.04		0.41	0.02	0.09	0.63
Homo sapiens Xp22 GSHB-314C4 (Genome Sys	H3157D03	0.91	0.73	0.85	0.71		0.41	0.05	0.22	0.05
Mus musculus galectin-4 (Lgals4) mRNA, p	H3034E11	0.95	0.73	0.80	1.02		0.59	0.03	0.20	0.86
Caenorhabditis elegans cosmid C08G5	H3108H01	0.80	0.73	1.08	0.99		0.03	0.04	0.67	0.92
Homo sapiens, clone hRPK.25_A_1, complet	H3131C01	0.86	0.73	0.73	0.73		0.30	0.03	0.45	0.46
Mus musculus Na+/H+ exchanger (NHE-1) mR	H3140A02	0.89	0.73	1.06	1.07		0.41	0.04	0.83	0.84
Homo sapiens mRNA; cDNA DKFZp564O243 (fr	H3156A06	0.91	0.73	0.97	1.06		0.39	0.03	0.80	0.57
Homo sapiens mRNA for KIAA0660 protein,	H3150C01	0.80	0.73	1.09	0.95		0.09	0.03	0.57	0.74
M.musculus mRNA for TAF148	H3109C11	1.03	0.72	0.89	0.89		0.85	0.03	0.57	0.54
Mus musculus major histocompatibility lo	H3117H11	0.78	0.72	0.96	1.11		0.10	0.02	0.82	0.55
rae-28=polyhomeotic gene homolog {clone	H3105A03	0.93	0.72	0.58	0.55		0.78	0.05	0.15	0.18
Homo sapiens carboxylesterase 3 (brain)	H3111D10	0.83	0.72	0.77	1.00		0.22	0.04	0.13	0.99
Caenorhabditis elegans cosmid F59B10, co	H3076E09	0.99	0.72	0.95	1.02		0.96	0.05	0.80	0.94
Drosophila melanogaster (P1 DS01219 (D12	H3040C05	0.95	0.72	0.97	1.09		0.81	0.04	0.83	0.86
Human mRNA for NADPH-flavin reductase, c	H3048G11	0.75	0.71	0.53	0.50		0.10	0.03	0.03	0.03
Novel human mRNA from chromosome 1, whic	H3054E02	0.95	0.71	0.96	0.70		0.75	0.04	0.87	0.16
Mus musculus TIMELESS protein mRNA, comp	H3022A12	0.84	0.71	0.69	0.71		0.21	0.05	0.02	0.16
Rattus norvegicus liver nuclear protein	H3128C03	1.08	0.71	0.69	0.62		0.51	0.04	0.07	0.04
Homo sapiens cDNA FLJ20479 fis, clone KA	H3027C01	0.88	0.71	1.22	0.84		0.34	0.03	0.13	0.18
Homo sapiens nuclear phosphoprotein simi	H3116F07	0.76	0.70	1.21	1.09		0.11	0.03	0.29	0.59

Table D. Genes significantly influenced by Hypoxia in WT cells (cont.)

Mus musculus prolactin-like protein E (P	H3008F06	0.96	0.70	0.71	0.91		0.74	0.04	0.03	0.42
Homo sapiens cDNA FLJ10690 fis, clone NT	H3088G02	0.77	0.70	1.10	0.91		0.22	0.02	0.60	0.37
Mus musculus tropomodulin 3 (Tmod3) mRNA	H3084H05	0.90	0.70	0.92	1.20		0.66	0.02	0.74	0.51
R.rattus pyruvate dehydrogenase E1 alpha	H3068G07	0.89	0.70	0.86	0.76		0.39	0.01	0.35	0.17
Rattus norvegicus brain mRNA for cystein	H3075C12	0.85	0.70	0.88	0.90		0.38	0.01	0.52	0.72
Mus musculus Chetk-alpha gene for cholin	H3065C11	0.61	0.70	0.80	0.90		0.01	0.02	0.33	0.55
Homo sapiens cDNA FLJ10700 fis, clone NT	H3154B06	0.98	0.70	0.73	0.85		0.87	0.04	0.45	0.69
Arabidopsis thaliana DNA chromosome 3, B	H3005C10	0.89	0.70	0.97	0.88		0.30	0.02	0.88	0.39
Homo sapiens Chromosome 22q13 Cosmid Clo	H3012B03	0.97	0.70	0.79	0.83		0.86	0.02	0.13	0.28
Homo sapiens vacuolar proton pump delta	H3041B05	0.95	0.70	0.97	0.87		0.63	0.02	0.87	0.48
Homo sapiens translocated promoter regio	H3045G06	1.10	0.70	0.67	0.55		0.48	0.05	0.08	0.05
Homo sapiens BAC clone RP11-518G12 from	H3001B07	0.87	0.70	0.83	0.98		0.32	0.04	0.36	0.92
Homo sapiens 3 BAC RP11-154F9 (Roswell P	H3143B11	1.03	0.69	0.95	1.01		0.87	0.02	0.80	0.98
Mus sp. gene for PIN1, complete cds	H3065F01	1.27	0.69	0.90	0.65		0.21	0.04	0.59	0.13
Cu-Zn SOD	H3130B11	0.99	0.69	0.94	1.01		0.97	0.03	0.80	0.98
Homo sapiens mRNA; cDNA DKFZp586H1823 (f	H3159E12	0.82	0.69	0.77	0.80		0.06	0.00	0.34	0.35
Ehrlichia canis 28 kDa major surface ant	H3118C09	0.88	0.69	0.64	0.57		0.64	0.04	0.08	0.06
Homo sapiens mannosidase, beta A, lysoso	H3047B05	1.06	0.69	0.96	0.73		0.74	0.02	0.82	0.19
Homo sapiens CGI-22 protein mRNA, comple	H3033G10	0.86	0.69	1.26	1.04		0.30	0.02	0.57	0.91
Human DNA sequence from clone RP4-799G3	H3094G09	0.96	0.69	1.05	0.83		0.65	0.02	0.71	0.17
human STS WI-11595	H3118C11	0.86	0.69	0.93	1.17		0.30	0.05	0.62	0.35
Homo sapiens chromosome X sequence from	H3037C01	0.97	0.68	0.72	0.65		0.86	0.02	0.35	0.28
Mus musculus genomic DNA sequence from c	H3022A09	0.74	0.68	0.53	0.47	#####	0.02	0.06	#####	
Arabidopsis thaliana DNA chromosome 4, B	H3148A12	1.56	0.68	1.00	0.85		0.31	0.03	0.99	0.73
R.norvegicus mRNA for ubiquitin and ribo	H3074C04	0.81	0.68	0.87	1.09		0.23	0.04	0.47	0.62
Homo sapiens transcription factor IGHM e	H3113H05	0.95	0.68	0.97	0.95		0.74	0.01	0.89	0.80
Arabidopsis thaliana chromosome I BAC T2	H3088G10	0.99	0.68	0.77	0.75		0.97	0.03	0.21	0.04
Homo sapiens unknown protein IT1 mRNA, p	H3137F09	0.92	0.68	1.12	0.90		0.69	0.03	0.53	0.75
Homo sapiens PAC clone RP4-572A3, comple	H3099G08	0.92	0.68	0.95	0.81		0.41	0.01	0.71	0.46
Mus musculus histone H2A.Z (H2A.Z) mRNA,	H3027E01	0.91	0.68	0.78	0.74		0.52	0.04	0.38	0.34
Homo sapiens mRNA; cDNA DKFZp761G1824 (f	H3022G11	1.05	0.68	0.91	0.86		0.69	0.01	0.63	0.52
Eptaretus burgeri mRNA for calreticulin	H3073E09	0.84	0.67	1.26	0.94		0.23	0.03	0.15	0.66
Mus musculus Ccte gene for chaperonin co	H3148A03	0.76	0.67	0.86	0.88		0.04	0.01	0.16	0.47
Homo sapiens small nuclear ribonucleopro	H3067C04	0.74	0.67	0.96	0.69		0.17	0.05	0.78	0.05
Caenorhabditis elegans cosmid Y73B6A, co	H3121E12	1.11	0.67	1.07	1.09		0.65	0.05	0.79	0.77
M.musculus mRNA for heat stable antigen	H3109A05	0.71	0.67	0.59	0.62		0.01	0.01	#####	#####
Homo sapiens huntingtin interacting prot	H3125G12	0.72	0.67	1.08	1.06		0.09	0.04	0.71	0.76
Homo sapiens chromosome 22q11 clone b461	H3136E06	0.81	0.66	1.07	0.74		0.55	0.03	0.84	#####
Human BAC clone RG021N08 from 7q21-q22,	H3035E09	0.91	0.66	1.55	0.82		0.61	0.01	0.09	0.43
Homo sapiens clone RP11-511111, complete	H3014B12	0.86	0.66	0.75	0.85		0.39	0.03	0.13	0.12
Homo sapiens Chromosome 11q13 BAC Clone	H3008G12	0.80	0.66	0.78	0.82		0.16	0.04	0.18	0.12
Human DNA sequence from clone 1111N9 on	H3111H10	0.88	0.66	0.91	1.05		0.23	0.01	0.68	0.80
Human DNA sequence from clone 797M17 on	H3080G05	0.90	0.66	1.12	1.02		0.50	0.02	0.58	0.94
Caenorhabditis elegans cosmid T10B11	H3153A09	0.80	0.66	1.19	0.91		0.15	0.04	0.61	0.61
Homo sapiens chromosome 4 clone C0481P14	H3017G10	0.82	0.66	0.77	1.04		0.22	0.03	0.24	0.77
R. norvegicus mRNA for 22kDa integral pe	H3124F10	0.84	0.65	1.02	1.04		0.29	0.03	0.94	0.84
Caenorhabditis elegans cosmid F27C1	H3153B03	1.06	0.65	0.65	0.80		0.65	0.01	0.05	0.05
Homo sapiens N-ethylmaleimide-sensitive	H3154G05	0.72	0.65	0.63	0.74		0.06	0.05	0.13	0.07
Homo sapiens chromosome 5 clone CITB-H1_	H3014H09	0.76	0.65	0.73	0.89		0.12	0.05	0.08	0.30
Homo sapiens 3q26.2-27 BAC RPC111-379K17	H3135F12	1.01	0.65	1.03	1.08		0.96	0.03	0.91	0.76
Homo sapiens cosmid from Xq28, complete	H3005G09	0.86	0.65	0.71	0.96		0.16	0.00	0.03	0.79
Mus musculus P450 (cytochrome) oxidoredu	H3090A06	0.84	0.65	0.59	0.63		0.42	0.05	0.26	0.28
b326h7, complete sequence [Homo sapiens]	H3145G05	1.01	0.65	0.95	0.67		0.96	0.03	0.75	#####
Homo sapiens mRNA; cDNA DKFZp586A1023 (f	H3032A03	0.89	0.65	0.91	1.02		0.22	0.04	0.59	0.91
Caenorhabditis elegans cosmid ZK970, com	H3059H07	0.79	0.65	0.71	0.81		0.10	0.02	0.08	0.05
Homo sapiens protein with polyglutamine	H3076G02	5.28	0.65	1.85	0.51		0.50	0.05	#####	#####
Homo sapiens cDNA FLJ10242 fis, clone HE	H3120F04	0.90	0.65	0.76	0.55		0.45	0.02	0.23	0.09
Mouse mRNA for nuclear pore-targeting co	H3043A09	0.78	0.64	0.88	0.84		0.20	0.03	0.42	0.15
Mus musculus retinoic acid-responsive pr	H3041D01	0.95	0.64	0.81	0.76		0.67	0.02	0.16	0.09
Mouse mRNA for prothymosin alpha	H3118B01	0.79	0.64	0.79	0.66		0.13	0.00	0.26	0.04
Homo sapiens clone NH0569I24, complete s	H3020A09	0.91	0.64	1.03	0.93		0.58	0.03	0.91	0.81
Rattus norvegicus non-muscle alpha-actin	H3003H10	1.06	0.64	0.52	0.75		0.81	0.01	0.00	0.04

Table D. Genes significantly influenced by Hypoxia in WT cells (cont.)

Homo sapiens 12p13 BAC RPCI11-1092P21 (R	H3073G05	0.50	0.64	0.50	0.53		#####	0.02	0.14	#####
Homo sapiens chromosome 7q22 sequence, c	H3116F04	0.77	0.64	0.95	1.21		0.09	0.02	0.78	0.26
Homo sapiens mRNA; cDNA DKFZp434L1850 (f	H3146D06	1.03	0.63	0.79	1.04		0.92	0.04	0.25	0.85
Human DNA sequence from clone RP3-402G11	H3017D11	0.74	0.63	0.88	0.92		0.05	0.00	0.67	0.69
Homo sapiens CST gene for cerebroside su	H3007D11	0.84	0.63	0.80	0.92		0.19	0.02	0.33	0.66
Homo sapiens cDNA FLJ10305 fis, clone NT	H3044B11	0.80	0.63	0.98	0.94		0.03	0.00	0.93	0.67
Human HepG2 3' region Mbol cDNA, clone h	H3105C09	0.99	0.62	1.26	0.91		0.92	0.03	0.22	0.62
Homo sapiens motor protein (P87/89), mRN	H3144H01	0.78	0.62	0.89	0.92		0.24	0.05	0.71	0.77
Mus musculus extracellular matrix protei	H3135F07	0.96	0.61	0.91	0.56		0.81	0.04	0.77	0.19
Human clone 53BP2 p53-binding protein mR	H3123H05	0.83	0.61	0.86	0.74		0.24	0.03	0.38	0.38
Human DNA sequence from clone 1100E15 on	H3149C09	0.95	0.61	0.82	0.75		0.69	0.01	0.22	0.10
Rattus norvegicus clone N27 mRNA	H3128D02	0.73	0.61	0.85	0.56		0.15	0.05	0.78	#####
Human DNA sequence from clone RP5-976O13	H3048E07	1.07	0.60	1.11	1.45		0.61	0.01	0.68	0.06
Homo sapiens kelch (Drosophila)-like 2 (H3131E05	0.94	0.60	0.86	0.90		0.68	0.03	0.33	0.69
Homo sapiens 12p13 BAC RPCI11-439G16 (Ro	H3068E02	0.92	0.60	1.20	1.05		0.63	0.04	0.44	0.69
Human DNA sequence from clone RP4-657D16	H3131H03	0.75	0.60	1.00	1.03		0.19	0.05	0.98	0.89
Homo sapiens PAC clone RP5-1106E3 from 7	H3137G05	0.55	0.60	1.03	0.77		0.00	0.00	0.89	0.17
Pisum sativum gibberellin c20-oxidase ge	H3094E01	0.77	0.60	0.57	0.61		0.09	0.01	0.02	0.02
Homo sapiens DNA for immunoglobulin heav	H3015B12	0.80	0.59	0.82	0.75		0.23	0.02	0.36	0.23
Mus musculus hydroxysteroid 17-beta dehy	H3137G10	0.87	0.59	1.14	1.03		0.54	0.03	0.45	0.89
Homo sapiens clone NH0427G18, complete s	H3021F06	0.99	0.59	0.85	0.99		0.92	0.01	0.45	0.98
Homo sapiens polymerase (RNA) II (DNA di	H3089E01	1.02	0.58	1.08	0.79		0.84	0.02	0.66	0.36
M.musculus gene for MUC18 glycoprotein (H3146E06	0.73	0.58	0.94	0.91		0.15	0.03	0.72	0.53
Homo sapiens Xp22 BAC GSHB-590J6 (Genome	H3146B08	0.96	0.58	0.83	1.02		0.89	0.04	0.29	0.93
Meriones unguiculatus alpha-tubulin mRNA	H3078E04	0.44	0.58	0.60	0.45		#####	0.01	0.23	#####
Homo sapiens Xp22 BAC GSHB-45N23 (Genome	H3094B11	0.96	0.58	0.90	0.90		0.81	0.01	0.60	0.75
Homo sapiens, clone RP11-9B17, complete	H3142C07	0.68	0.57	0.70	0.84		0.08	0.01	0.19	0.33
Homo sapiens ribonuclease 6 precursor (R	H3045A05	1.00	0.57	1.06	1.08		0.99	0.03	0.78	0.72
Mus musculus augmenter of liver regenera	H3122H03	0.87	0.57	1.06	1.09		0.22	0.00	0.79	0.64
Caenorhabditis elegans cosmid F45E4	H3008B09	0.81	0.57	0.77	0.79		0.15	0.01	0.34	0.24
Mus musculus chromosome 17 BAC citb20h22	H3146H09	0.74	0.57	0.90	1.05		0.05	0.03	0.60	0.48
Drosophila melanogaster, chromosome 2L,	H3150G05	0.82	0.57	0.55	0.58		0.23	0.02	0.08	0.14
Homo sapiens HSPC290 mRNA, partial cds	H3015H12	0.82	0.56	0.82	0.86		0.17	0.01	0.48	0.07
Homo sapiens SSX4 protein gene, partial	H3032C11	0.84	0.55	0.96	0.86		0.56	0.00	0.86	0.58
Geobacter sp. 16S rRNA gene, strain CdA-	H3159A02	0.67	0.55	0.70	0.64		0.09	0.04	0.39	0.10
No Hits Found	H3020F01	0.76	0.55	0.77	0.41		0.15	0.03	0.66	0.11
Mus musculus synaptosomal-associated pro	H3148B07	0.68	0.55	0.62	1.04		0.12	0.04	0.20	0.88
Arabidopsis thaliana chromosome III BAC	H3015D12	0.79	0.55	0.62	0.68		0.18	0.01	0.32	0.17
Mus musculus ets variant gene 6 (TEL onc	H3134C05	0.67	0.54	0.71	0.53		0.04	0.02	0.36	#####
Human p67 mRNA, complete cds	H3130A05	0.50	0.51	0.60	0.57		0.00	0.00	#####	#####

Table E. Genes significantly influenced by Cobalt in WT Cells

Name	ID	Fold Changes				TTEST			
		W-Co	W-H	N-Co	N-H	W-Co	W-H	N-Co	N-H
Homo sapiens cDNA FLJ10097 fis, clone HE	H3086C08	2.94	1.87	1.04	0.93	0.02	0.52	0.87	0.78
Metallothionein-I (image 1052401)	A-2031	2.81	1.78	2.13	1.56	0.00	0.00	0.02	0.07
Mus musculus glyceraldehyde-3-phosphate	H3031E11	2.77	3.23	1.11	1.02	0.05	0.12	0.81	0.92
Mus musculus lactate dehydrogenase 1, A	H3023H12	2.71	3.93	0.86	0.89	0.01	0.00	0.43	0.55
Homo sapiens chromosome 9q34, clone 63G1	H3123F02	2.49	1.66			0.05	0.20	#DIV/0!	#DIV/0!
Mus musculus phosphoglycerate kinase (Pg	H3023D06	2.31	3.67	0.69	0.93	0.01	0.00	0.12	0.74
Homo sapiens cyclin D2 (CCND2) mRNA	H3117B01	2.23	2.24	1.69	1.39	0.05	#DIV/0!	0.14	0.16
Mus musculus H19 and muscle-specific Nct	H3144B07	2.20	2.42	0.35	0.33	0.03	0.10	0.00	0.00
Mus musculus B6D2F1 clone 2A-1 mRNA	H3086F12	2.20	3.24	1.89	1.89	0.02	#DIV/0!	0.12	0.02
Mus musculus cell-line LXB2 cathepsin L	H3028F03	2.17	1.54	1.28	2.92	0.02	0.04	0.37	0.00
Mouse mRNA for alpha-enolase (2-phospho-	H3027E08	2.12	3.02	0.98	1.10	0.01	0.01	0.94	0.69
Mus musculus Kruppel-like factor 4 (gut)	H3075C08	2.10	1.83	1.28	0.99	0.02	0.24	#DIV/0!	#DIV/0!
cloning vector pSport1, complete cds	H3020C02	2.07	1.27	1.25	1.11	0.01	0.02	0.38	0.68
Mus musculus triosephosphate isomerase (H3149C10	2.06	2.18	0.82	0.81	0.00	0.01	0.29	0.24
Mus musculus Fc receptor, IgG, high affi	H3109H04	2.05	1.51			0.01	0.41	#DIV/0!	#DIV/0!
Mus musculus imidazoline receptor I-1-li	H3127C11	2.04	1.41	1.34	1.36	0.01	0.15	0.15	0.09
Mus musculus biglycan (Bgn), mRNA	H3127D03	1.99		0.64	0.86	0.01	#DIV/0!	0.15	0.61
Rickettsia prowazekii strain Madrid E, c	H3093D05	1.97	1.10	0.77	0.51	0.05	0.73	#DIV/0!	#DIV/0!
Homo sapiens 12p21 BAC RPC11-259O18 (Ro	H3123A12	1.95	2.07	0.78	0.95	0.00	0.01	0.14	0.72
Mouse mRNA for alpha-enolase (2-phospho-	H3027E07	1.94	1.82	0.75	0.92	0.03	0.02	0.23	0.72
Mus musculus pyruvate kinase 3 (Pk3), mR	H3030D11	1.93	2.36	0.87	0.65	0.00	0.00	0.53	0.03
Homo sapiens signal sequence receptor, a	H3107F10	1.91	1.01	0.99	1.18	0.04	0.97	0.96	0.48
Homo sapiens chromosome 22q11 clone b476	H3141F10	1.89	1.39	1.19	1.72	0.03	0.60	0.28	0.01
Mouse metallothionein-I (MT-I) gene, 5'	H3020C02	1.88	1.07	1.22	1.11	0.00	0.68	0.38	0.66
Metallothionein II	H3013D11	1.85	0.89	0.79	0.84	0.03	0.43	0.55	0.64
Mouse locus RPII215 polymerase II large	H3036C03	1.82	1.03	1.16	1.06	0.00	0.87	0.30	0.69
R.norvegicus nonerythroid alpha-spectrin	H3118C03	1.82	1.43	1.33	1.11	0.00	0.05	0.12	0.55
Mus musculus translation repressor NAT1	H3027A06	1.81	1.24	1.07	1.75	0.00	0.29	0.79	0.02
Homo sapiens mRNA; cDNA DKFZp434D222 (fr	H3107B08	1.79	0.92	1.22	0.93	0.04	0.64	0.25	0.48
C.griseus epsilon-COP mRNA	H3155F09	1.79	1.78	1.46	1.40	0.02	0.13	0.06	0.02
Homo sapiens HSPC026 mRNA, complete cds	H3114B06	1.78	1.20	1.35	0.88	0.05	0.39	0.16	0.56
Homo sapiens cDNA FLJ10500 fis, clone NT	H3030G02	1.77	2.20	1.12	1.12	0.00	0.00	0.18	0.27
Mouse mRNA for alpha-enolase (2-phospho-	H3027E09	1.76	2.48	0.87	0.75	0.01	0.01	0.54	0.12
Mus musculus nucleolar RNA helicase II/G	H3048F06	1.75	1.66	1.16	1.36	0.04	0.12	0.77	0.27
Homo sapiens cDNA FLJ11223 fis, clone PL	H3108H08	1.75	1.02	0.91	0.79	0.04	0.95	#DIV/0!	#DIV/0!
Homo sapiens Xp22 BAC GSHB 526D21 (Genom	H3128H11	1.74	1.31	0.95	0.79	0.03	0.15	0.75	0.18
Influenza A/Memphis/8/88 (H3N2), PB2 pol	H3147H11	1.73	1.47	1.26	1.45	0.04	0.04	0.11	0.04
Mouse growth factor-induced delayed earl	H3019C07	1.69	1.95	1.21	1.05	0.00	0.00	0.16	0.77
Homo sapiens ATPase, H+ transporting, ly	H3140C11	1.68	0.98	1.62	1.29	0.00	0.90	0.01	0.05
Campylobacter jejuni NCTC11168 complete	H3024G12	1.68	1.18	1.52	1.51	0.04	0.52	0.04	0.29
Rattus norvegicus DCoH gene	H3135D04	1.67	1.28	1.51	1.14	0.05	0.31	0.06	0.54
Homo sapiens mRNA; cDNA DKFZp564P046 (fr	H3132C11	1.66	1.19	1.12	1.10	0.01	0.30	0.60	0.61
Mus musculus fibroblast growth factor in	H3018G01	1.65	1.02	1.23	1.04	0.03	0.94	0.46	0.86
Mus musculus glucose phosphate isomerase	H3125B04	1.64	1.76	1.15	1.23	0.03	0.03	0.40	0.33
Homo sapiens mRNA for KIAA1139 protein,	H3016G08	1.64	1.82	1.17	1.28	0.03	0.01	0.44	0.13
Mus musculus pyruvate kinase 3 (Pk3), mR	H3030D10	1.62	2.02	0.86	0.69	0.01	0.01	0.38	0.00
Homo sapiens chromosome 4q25, BAC clone	H3010E09	1.61	0.88	1.12	1.22	0.00	0.49	0.35	0.24
Homo sapiens cDNA FLJ20528 fis, clone KA	H3028G09	1.61	1.03			0.01	#DIV/0!	#DIV/0!	#DIV/0!
Saccharomyces cerevisiae chromosome XIII	H3058H12	1.61	1.17	0.98	1.18	0.00	0.39	0.87	0.16
Human BAC clone GS1-165I4 from 7q21, com	H3057C09	1.60	0.99	1.22	0.88	0.04	0.92	0.44	0.27
Homo sapiens BAC clone RP11-359K10 from	H3069D01	1.60	1.01	1.19	1.07	0.02	0.96	0.09	0.67
Arabidopsis thaliana chromosome II secti	H3017G08	1.59	2.05	0.93	0.96	0.00	0.00	0.55	0.64
Human DNA sequence from PAC 260J9 on chr	H3113B04	1.59	0.98	1.13	1.43	0.03	0.88	0.67	0.12
Mus musculus heme oxygenase (decycling)	H3019A12	1.58	0.99	1.56	1.22	0.01	0.94	0.07	0.30
Mus musculus GM2 activator protein (Gm2a	H3035D04	1.58	1.26	1.02	1.48	0.02	0.13	0.92	0.08
Mus musculus Sui1 homolog mRNA, complete	H3133C01	1.58	1.07	1.27	1.05	0.04	0.68	0.19	0.77
Homo sapiens clone RP11-333O1, complete	H3125H02	1.55	1.28	0.83	1.05	0.01	0.24	0.36	0.72
Homo sapiens chromosome 17, clone hRPK.6	H3130C09	1.53	1.26	1.26	1.86	0.01	0.38	0.52	0.02
Homo sapiens Chromosome 22q11 Pac Clone	H3016B03	1.53	1.00	1.19	0.91	0.03	0.99	0.30	0.48
Arabidopsis thaliana DNA chromosome 3, B	H3156G09	1.53	1.11	1.09	1.62	0.02	0.59	0.60	0.04

Table E. Genes significantly influenced by Cobalt in WT Cells (cont.)

	H3118C04	1.52	1.22	1.33	1.11		0.03	0.35	0.07	0.54
Homo sapiens small nuclear RNA activatin	H3125H12	1.51	1.17	0.87	1.02		0.03	0.41	0.64	0.92
Rattus norvegicus microtubule-associated	H3082B10	1.50	1.24	1.10	1.07		0.03	0.26	0.54	0.74
Mus musculus DNA topoisomerase IIalpha m	H3139A05	1.49	1.18	0.97	1.09		0.01	0.30	0.90	0.66
Tapa-1=integral membrane protein TAPA-1	H3151C09	1.49	1.44	0.96	1.25		0.02	0.04	0.79	0.25
Homo sapiens cDNA FLJ10888 fis, clone NT	H3100C05	1.49	1.15	0.95	1.02		0.01	0.16	0.75	0.90
Mouse stathmin gene sequence	H3122C07	1.49	1.09	0.84	1.10		0.00	0.49	0.40	0.64
Mus musculus mitochondrial DNA, complete	H3126C07	1.48	1.08	0.86	1.02		0.03	0.55	0.55	0.92
Mus musculus MHC class I heavy chain pre	H3141B11	1.48	1.25	1.89	1.36		0.03	0.42	0.07	0.11
Homo sapiens mRNA for KIAA0226 protein,	H3058E06	1.48	1.20	1.31	1.33		0.02	0.08	0.14	0.02
Mus musculus arsenical resistance ATPase	H3105D06	1.48	1.23	1.11	1.08		0.03	0.43	0.62	0.76
Mus musculus WW domain binding protein 5	H3127H02	1.48	1.91	1.16	1.28		0.03	0.12	0.74	0.51
Mouse placental lactogen I (PL-I) mRNA,	H3011H02	1.48	1.08	2.80	1.04		0.02	0.60	0.42	0.89
Homo sapiens mitogen-activated protein k	H3011F01	1.47	0.99	1.20	1.24		0.02	0.92	0.52	0.07
Homo sapiens cDNA FLJ20122 fis, clone CO	H3128G06	1.47	1.70	1.09	1.22		0.00	0.00	0.16	0.09
Murine PCNA II pseudogene	H3021F12	1.47	1.23	1.03	0.93		0.02	0.44	0.90	0.75
Mus musculus mRNA for ENP, complete cds	H3102A05	1.47	0.99	1.02	0.89		0.01	0.92	0.92	0.48
human STS WI-16536	H3147F11	1.46	1.59	1.05	1.16		0.03	0.11	0.81	0.41
Mus musculus synovial sarcoma, transloca	H3096H08	1.46	1.01	1.26	1.09		0.05	0.95	0.33	0.77
Murine mRNA for L-34 galactoside-binding	H3016D10	1.46	1.62	1.07	1.32		0.01	0.00	0.47	0.02
Human DNA sequence from clone RP3-351K20	H3121D08	1.45	0.81	0.85	0.78		0.04	0.28	0.44	0.27
Mus musculus domesticus mitochondrial ca	H3143D12	1.45	1.55	1.05	1.21		0.01	0.03	0.77	0.28
Mouse mRNA for fibronectin receptor beta	H3019E08	1.45	1.75	0.90	0.86		0.00	0.00	0.55	0.38
Caenorhabditis elegans cosmid W01C8	H3144F01	1.44	0.95	1.22	1.13		0.05	0.72	0.19	0.34
Arabidopsis thaliana chromosome I BAC F2	H3022E07	1.43	1.94	0.79	0.82		0.00	0.00	0.11	0.18
Human DNA sequence from clone LUCA11 on	H3144B05	1.43	0.99	1.00	1.41		0.03	0.96	0.99	0.04
Mus musculus ferritin light chain 1 (Ftl)	H3020B08	1.43	0.95	1.09	1.25		0.01	0.71	0.74	0.14
Mus musculus mRNA for GANP protein	H3031B12	1.42	1.33	0.92	0.96		0.01	0.03	0.52	0.77
Homo sapiens chromosome 4 clone C0483I23	H3107E04	1.42	1.03	1.23	1.44		0.03	0.85	0.12	0.01
Mus musculus adenine nucleotide transloc	H3125H05	1.41	1.07	0.72	1.08		0.05	0.75	0.16	0.49
Rat 24-kDa subunit of mitochondrial NADH	H3133D04	1.41	0.90	1.24	1.55		0.03	0.63	0.24	0.03
Homo sapiens chromosome 14 clone CTD-254	H3140G09	1.41	1.10	1.00	0.77		0.03	0.46	0.98	0.18
Human DNA sequence from clone 486I3 on c	H3021F04	1.40	1.18	1.06	0.97		0.03	0.23	0.55	0.85
Mouse kidney ornithine decarboxylase mRN	H3028F05	1.40	0.98	1.40	1.68		0.01	0.88	0.00	0.02
Homo sapiens px19-like protein (PX19), m	H3116A11	1.40	1.35	0.89	0.87		0.05	0.10	0.46	0.37
Homo sapiens chromosome 17, clone hRPK.6	H3049F11	1.40	1.16	1.33	1.43		0.00	0.30	0.05	0.01
Mus musculus nidogen 2 (Nid2), mRNA	H3115F11	1.40	1.35	0.76	1.05		0.01	0.04	0.06	0.75
Homo sapiens mRNA for Centrosome- and Go	H3042D09	1.39	0.97	1.05	1.15		0.02	0.64	0.50	0.04
Mus musculus BCL2/adenovirus E1B 19 kDa-	H3016D08	1.39	1.58	0.91	0.95		0.00	0.01	0.25	0.48
Homo sapiens mRNA, clone:PO2ST9	H3018C09	1.39	1.15	1.06	0.96		0.03	0.19	0.66	0.72
Mus musculus TERF1-interacting nuclear p	H3129H07	1.38	1.45	0.85	1.26		0.03	0.15	0.63	0.32
Mus musculus mRNA for ATF4, partial cds	H3124E06	1.38	0.91	1.26	1.31		0.04	0.61	0.24	0.23
saposin=sphingolipid activator protein [H3151D11	1.37	1.27	0.90	1.44		0.02	0.21	0.61	0.04
Rattus norvegicus bHLH transcription fac	H3094E11	1.37	1.01	1.10	1.09		0.04	0.96	0.59	0.43
human STS SHGC-36320	H3097B05	1.37	0.99	0.90	0.79		0.02	0.96	0.73	0.49
Homo sapiens chromosome 4 clone B71M12 m	H3077F05	1.37	0.82	0.96	0.73		0.04	0.42	0.91	0.45
Homo sapiens cDNA FLJ10330 fis, clone NT	H3019F09	1.37	0.85	0.78	0.62		0.02	0.22	0.18	0.03
Homo sapiens BAC clone RP11-196O16 from	H3150A01	1.36	1.73	0.88	1.00		0.02	0.00	0.27	0.98
Mus musculus ribosomal protein S4, X-lin	H3120D10	1.36	1.05	0.81	1.24		0.03	0.72	0.37	0.01
Caenorhabditis elegans cosmid Y6B3B, com	H3012A11	1.36	1.63	0.79	0.82		0.00	0.00	0.15	0.17
Rattus norvegicus mRNA for GEF-2, comple	H3030E02	1.35	1.12	0.99	0.95		0.04	0.33	0.97	0.72
Homo sapiens mRNA for KIAA0397 protein,	H3139D09	1.35	0.81	0.78	1.00		0.05	0.25	0.50	1.00
Mouse hexokinase mRNA, complete cds	H3114D09	1.35	1.15	0.86	1.41		0.03	0.31	0.49	0.03
Mus musculus aldolase 1, A isoform (Aldo	H3031D03	1.35	1.92	0.88	0.92		0.00	0.00	0.20	0.34
Homo sapiens PTP11-associated RhoGAP 1 (H3133F07	1.34	1.09	0.91	1.09		0.03	0.57	0.49	0.61
NMDA receptor glutamate-binding subunit	H3151H12	1.34	1.06	1.35	1.78		0.03	0.55	0.00	0.00
Homo sapiens mRNA; cDNA DKFZp566F2124 (f	H3142A03	1.34	0.92	1.16	0.86		0.01	0.56	0.28	0.27
Homo sapiens RNA polymerase III subunit	H3083H08	1.34	1.22	1.05	1.00		0.04	0.42	0.40	0.99
Homo sapiens PAC 126N20 derived from chr	H3125B09	1.33	1.23	1.03	0.90		0.03	0.47	0.90	0.66
Caenorhabditis elegans cosmid F19B10	H3034D02	1.33	0.88	1.04	0.79		0.01	0.34	0.84	0.11
H.sapiens CpG island DNA genomic Mse1 fr	H3081C09	1.33	0.86	1.09	0.70		0.03	0.24	0.72	0.05
Mus musculus mRNA for chromatin assembly	H3087E05	1.32	1.13	1.07	0.95		0.05	0.47	0.63	0.70

Table E. Genes significantly influenced by Cobalt in WT Cells (cont.)

M.musculus mRNA for ribosomal protein S2	H3145D12	1.32	1.00	0.95	1.39		0.05	0.99	0.82	0.05
Homo sapiens ribosomal protein L13 mRNA,	H3030A04	1.31	1.07	1.15	1.44		0.04	0.61	0.46	0.04
Homo sapiens putative DNA dependent ATPa	H3132E05	1.31	0.79	0.87	0.81		0.02	0.02	0.51	0.38
Homo sapiens testis enhanced gene transc	H3021E03	1.31	1.09	1.04	1.03		0.00	0.20	0.64	0.75
Mus musculus protective protein for beta	H3114C10	1.31	1.21	1.08	1.15		0.04	0.06	0.68	0.44
Mus musculus succinate dehydrogenase Fp	H3153F01	1.30	1.11	1.18	1.45		0.01	0.44	0.14	0.01
Mouse laminin B2 chain mRNA, complete cd	H3113E11	1.30	1.19	0.84	1.37		0.02	0.10	0.11	0.01
Mus musculus procollagen-proline, 2-oxog	H3003D12	1.29	2.61	0.97	1.05		0.01	0.00	0.68	0.69
Mus musculus ferritin light chain 1 (Ftl)	H3012B07	1.29	1.03	1.23	1.10		0.02	0.78	0.26	0.39
Mus musculus p162 protein mRNA, complete	H3004D10	1.29	1.05	0.99	0.97		0.01	0.50	0.95	0.86
Oryctolagus cuniculus endooligopeptidase	H3111B12	1.28	1.12	1.13	1.07		0.02	0.13	0.38	0.60
Caenorhabditis elegans cosmid C08D8	H3118D03	1.28	1.10	0.85	1.07		0.02	0.44	0.46	0.56
Human DNA sequence from cosmid L25A3, Hu	H3139C02	1.27	1.31	0.78	1.00		0.03	0.08	0.36	0.99
Mus musculus glucosidase, alpha, acid (G	H3109C03	1.27	1.07	1.07	1.49		0.02	0.34	0.55	0.00
M.musculus mRNA sequence	H3079H11	1.27	0.96	0.83	1.22		0.03	0.79	0.25	0.09
Homo sapiens chromosome 5, BAC clone 8e5	H3062G06	1.27	1.18	1.02	1.31		0.01	0.07	0.84	0.02
Mus domesticus strain MilP mitochondrion	H3129E07	1.26	0.99	0.92	1.27		0.03	0.96	0.64	0.10
Mus musculus GLUT4 vesicle protein mRNA,	H3022E01	1.24	1.22	1.01	1.04		0.01	0.05	0.96	0.68
Human DNA sequence from clone RP4-622L5	H3020E08	1.24	1.13	1.07	1.00		0.01	0.12	0.53	0.98
Rattus norvegicus proline rich protein m	H3116A06	1.24	1.35	1.08	1.30		0.01	0.01	0.46	0.05
No Hits Found	H3072E04	1.21	0.85	0.88	1.06		0.02	0.04	0.51	0.71
Mus musculus peptidylprolyl isomerase A	H3028A06	1.20	0.95	1.11	1.12		0.04	0.66	0.59	0.46
Homo sapiens PAC clone RP5-1159C10 from	H3014F04	1.18	1.04	1.08	1.11		0.05	0.45	0.58	0.43
Rattus norvegicus mRNA for Nogo-C protei	H3017F12	1.18	1.13	1.06	1.07		0.02	0.19	0.55	0.55
H.sapiens mRNA for unknown antigen	H3079D07	1.15	1.07	1.23	1.25		0.05	0.68	0.06	0.10
Mus musculus eukaryotic translation init	H3016F05	0.89	0.83	0.99	0.91		0.04	0.00	0.85	0.22
Homo sapiens A kinase (PRKA) anchor prot	H3149A04	0.86	1.02	1.05	0.96		0.05	0.85	0.83	0.72
Ureaplasma urealyticum section 37 of 59	H3022E02	0.85	0.99	0.90	0.92		0.02	0.91	0.32	0.46
Homo sapiens chromosome 19, cosmid R2644	H3020F09	0.85	0.96	0.98	1.07		0.01	0.69	0.92	0.67
Homo sapiens mRNA; cDNA DKFZp761M1112 (f	H3003B05	0.84	0.84	1.03	1.00		0.02	0.08	0.71	0.99
Homo sapiens tetracycline transporter-li	H3010D04	0.84	0.94	0.99	1.07		0.01	0.35	0.95	0.44
Homo sapiens genomic DNA, chromosome 21q	H3098G10	0.83	0.94	1.02	1.19		0.04	0.60	0.90	0.20
	H3011E12	0.83	1.01	0.72	0.86		0.01	0.96	#DIV/0!	0.04
Homo sapiens cleavage stimulation factor	H3134H11	0.83	1.02	1.12	0.97		0.05	0.83	0.37	0.79
Homo sapiens chromosome 17, clone hRPK.1	H3132E03	0.82	0.87	0.67	0.90		0.04	0.18	0.02	0.37
Mus musculus protein phosphatase 5 (PP5)	H3158H01	0.82	0.89	1.05	1.05		0.04	0.26	0.58	0.53
Human DNA sequence from clone XX-PRYR7CC	H3004F01	0.81	0.94	0.92	1.15		0.05	0.59	0.61	0.44
Human DNA sequence from clone RP4-746H2	H3029D09	0.81	0.77	1.40	0.86		0.05	0.01	0.05	0.33
Caenorhabditis elegans cosmid C08G5	H3108H01	0.80	0.73	1.08	0.99		0.03	0.04	0.67	0.92
Homo sapiens cDNA FLJ10305 fis, clone NT	H3044B11	0.80	0.63	0.98	0.94		0.03	0.00	0.93	0.67
Mus musculus syndecan 1 (Sdc1), mRNA	H3013F05	0.80	1.01	1.04	1.10		0.02	0.95	0.70	0.41
Homo sapiens genomic DNA, chromosome 3p2	H3016G03	0.80	0.90	0.86	0.91		0.02	0.41	0.24	0.39
Homo sapiens chromosome 22q11 clone p108	H3146G12	0.79	0.87	1.02	1.00		0.00	0.27	0.84	1.00
Human BAC clone RG072E11 from 7q21-7q22,	H3029G06	0.79	0.85	0.88	0.88		0.03	0.16	0.17	0.11
Human DNA sequence from clone 1118D24 on	H3067E01	0.79	0.75	0.59	0.89		0.05	0.09	0.04	0.54
Homo sapiens chromosome 16 clone RPCI-11	H3110B07	0.79	0.90	0.80	0.88		0.04	0.23	0.37	0.57
Homo sapiens chromosome 9, clone hRPK.35	H3154C05	0.79	1.06	1.06	0.91		0.03	0.72	0.88	0.75
No Hits Found	H3125F09	0.78	1.05	1.11	0.98		0.04	0.65	0.67	0.91
Mus musculus myristoylated alanine rich	H3113D09	0.78	0.88	0.91	0.56		0.04	0.26	0.69	0.01
M.musculus mRNA for cyclin F	H3020E11	0.78	0.95	0.77	1.04		0.04	0.57	0.02	0.77
Mus musculus lymphocyte antigen 6 comple	H3027D05	0.78	1.26	0.88	0.84		0.01	0.05	0.38	0.16
Homo sapiens DNA sequence from PAC 434O1	H3131C07	0.78	0.89	0.80	1.18		0.00	0.08	0.47	0.52
Mouse chromatin nonhistone high mobility	H3029B11	0.78	0.94	1.22	1.16		0.02	0.45	0.02	0.12
Homo sapiens MUM2 (MUM2) gene, complete	H3118D07	0.77	0.90	1.01	0.97		0.04	0.02	0.93	0.88
Homo sapiens chromosome 17, clone hRPK.5	H3002C06	0.77	0.98	1.09	1.04		0.04	0.87	0.54	0.77
Homo sapiens genomic DNA, chromosome 21q	H3049C12	0.77	0.82	0.95	0.93		0.05	0.16	0.81	0.69
Rattus norvegicus uk mRNA for uridine ki	H3015D10	0.77	0.70	0.95	0.76		0.02	0.05	0.88	0.08
Human DNA sequence from clone 55110 on c	H3004H07	0.77	0.81	0.78	1.01		0.04	0.17	0.12	0.97
Mus musculus Ccte gene for chaperonin co	H3148A03	0.76	0.67	0.86	0.88		0.04	0.01	0.16	0.47
Homo sapiens cDNA FLJ10745 fis, clone NT	H3001B09	0.76	0.92	0.88	0.95		0.03	0.60	0.43	0.74
Homo sapiens PAC clone RP5-1006K12 from	H3031E06	0.76	0.83	0.86	0.99		0.01	0.08	0.54	0.96
Homo sapiens HRIHFB2411 mRNA, partial cd	H3140F06	0.76	0.98	0.79	1.17		0.03	0.87	0.38	0.52

Table E. Genes significantly influenced by Cobalt in WT Cells (cont.)

Homo sapiens mRNA; cDNA DKFZp434I0721 (f	H3057E04	0.76	0.97	0.84	0.91		0.04	0.74	0.17	0.44
Mus musculus serpentine receptor (Cyt28)	H3149F11	0.76	0.90	0.76	0.80		0.01	0.32	0.23	0.12
Homo sapiens clone RP5-111214, complete	H3010F11	0.75	0.82	0.69	0.72		0.04	0.22	0.17	0.19
Homo sapiens Kruppel-type zinc finger (C	H3013F09	0.75	0.74	0.70	0.80		0.03	0.07	0.18	0.18
Homo sapiens ataxin 2 related protein (A	H3149B07	0.75	0.79	0.89	0.92		0.02	0.24	0.51	0.67
M.sativa Rbcsk-1A gene	H3153H10	0.75	0.86	0.77	0.60		0.04	0.17	0.42	0.00
Mus musculus mRNA for adenylate kinase i	H3052D11	0.74	0.74	0.93	0.96		0.02	0.05	0.73	0.84
Homo sapiens chromosome 17, clone HRPC29	H3142E06	0.74	0.90	0.83	1.13		0.00	0.02	0.37	0.41
Mus musculus chromosome 17 BAC citb20h22	H3146H09	0.74	0.57	0.90	1.05		0.05	0.03	0.60	0.48
M.musculus red-1 gene	H3098G04	0.74	1.11	0.94	1.12		0.00	0.24	0.27	0.32
Human DNA sequence from clone RP3-402G11	H3017D11	0.74	0.63	0.88	0.92		0.05	0.00	0.67	0.69
Mus musculus hybrid receptor gp250 precu	H3146F06	0.74	0.71	1.29	0.99		0.04	0.09	0.43	0.97
Mouse gene for reticulocalbin, exon5, ex	H3027B09	0.73	0.96	0.94	1.10		0.02	0.78	0.64	0.49
Rattus norvegicus LIM-domain protein LMP	H3082E06	0.73	0.78	1.08	1.04		0.04	0.05	0.68	0.81
Homo sapiens mRNA; cDNA DKFZp566B213 (fr	H3015G11	0.73	0.59	0.83	0.66		0.02	0.18	0.46	0.02
Human DNA sequence from clone CTA-221G9	H3012C11	0.73	0.93	1.01	0.95		0.05	0.64	0.96	0.54
Homo sapiens genomic DNA, chromosome 21q	H3156E05	0.73	0.70	0.66	0.56		0.03	0.06	#DIV/0!	#DIV/0!
Cafeteria roenbergensis mitochondrial DN	H3121H05	0.72	0.95	0.76	1.18		0.05	0.81	0.07	0.28
Homo sapiens clone DJ0764O12, complete s	H3150H03	0.72	0.87	1.06	1.10		0.04	0.48	0.69	0.40
Mus musculus chromosome 16 clone ct7-581	H3146A12	0.72	0.85	0.81	0.88		0.03	0.51	0.34	0.49
Homo sapiens PAC clone RP5-1093G23 from	H3149G10	0.72	1.03	0.86	0.77		0.01	0.76	0.57	0.12
Mus musculus peroxisomal/mitochondrial d	H3131A07	0.72	1.06	0.68	1.11		0.02	0.74	0.01	0.51
S.pombe chromosome III cosmid c1672	H3157A09	0.72	0.61	0.91	0.82		0.03	0.14	0.75	0.43
Homo sapiens transducin (beta)-like 3 (T	H3034C10	0.71	0.84	0.95	0.87		0.05	0.33	0.73	0.33
M.musculus mRNA for heat stable antigen	H3109A05	0.71	0.67	0.59	0.62		0.01	0.01	#DIV/0!	#DIV/0!
Arabidopsis thaliana chromosome III P1 M	H3054A12	0.71	1.15	0.76	1.01		0.03	0.31	0.14	0.96
Mus musculus Pcdh7 mRNA for BH-protocadh	H3067F12	0.71	1.04	0.64	1.00		0.03	0.72	0.12	0.99
Mus musculus matrix metalloproteinase 23	H3058D07	0.71	1.43	0.49	0.55		0.04	0.01	0.13	0.09
Rat mRNA for calcineurin A	H3110H11	0.71	0.96	0.97	1.14		0.04	0.69	0.77	0.46
Human chromosome 14 DNA sequence *** IN	H3096C06	0.71	0.91	1.06	0.75		0.03	0.53	0.73	0.05
Homo sapiens cDNA FLJ10700 fis, clone NT	H3040G11	0.71	0.79	1.01	1.09		0.05	0.13	0.95	0.62
Caenorhabditis elegans cosmid W03A5	H3001F09	0.70	0.69	0.78	0.95		0.03	0.07	0.23	0.77
Mus musculus groucho-related gene produc	H3159C02	0.70	0.92	0.72	0.77		0.01	0.48	0.19	0.07
Mus musculus membrane component, surface	H3098B01	0.70	0.79	0.60	0.42		0.00	0.05	0.04	0.01
Mus musculus ubiquitin-activating enzyme	H3135E07	0.69	0.99	0.74	0.97		0.03	0.97	0.22	0.88
Mus musculus bone morphogenetic protein-	H3033E11	0.69	1.05	0.82	1.01		0.02	0.68	0.15	0.97
Mouse mRNA for protein tyrosine phosphat	H3118G02	0.68	0.84	0.95	0.94		0.01	0.15	0.80	0.68
Mus musculus vertebrate homolog of C. el	H3050G09	0.68	0.87	0.88	0.77		0.01	0.08	0.31	0.11
R.norvegicus mRNA for synaptonemal compl	H3150E03	0.68	0.89	0.69	0.74		0.04	0.56	0.10	0.12
Mus musculus ets variant gene 6 (TEL onc	H3134C05	0.67	0.54	0.71	0.53		0.04	0.02	0.36	#DIV/0!
No Hits Found	H3032G12	0.67	0.82	0.76	0.83		0.00	0.19	0.16	0.30
C.familiaris mRNA for TRAM-protein	H3100D02	0.67	1.08	1.02	1.11		0.04	0.66	0.93	0.71
Human DNA sequence from clone 653C5 on c	H3011E02	0.67	0.80	0.81	0.82		0.00	0.03	0.49	0.52
Human chromosome 14 DNA sequence *** IN	H3034B08	0.66	1.06	0.82	0.62		0.04	0.72	0.55	0.03
Homo sapiens clone snt1 breast cancer as	H3132A02	0.66	1.22	0.75	0.92		0.00	0.05	0.07	0.44
Mus musculus transforming growth factor,	H3114E06	0.66	1.00	0.62	0.73		0.01	0.98	#DIV/0!	0.32
Mouse chromosome 6 BAC-284H12 (Research	H3025H05	0.65	1.11	0.71	0.82		0.03	0.52	0.13	0.62
Homo sapiens clone 25023 mRNA sequence	H3125F02	0.65	0.84	1.27	1.05		0.00	0.14	0.29	0.79
Novel human gene mapping to chosome 22	H3146F09	0.65	0.79	1.24	0.83		0.01	0.39	#DIV/0!	0.41
Arabidopsis thaliana chromosome II secti	H3125F05	0.65	0.72	0.89	0.57		0.02	0.14	0.25	0.20
Mouse Cx43 gene, exon 2, and 5' and 3' u	H3113A06	0.64	0.94	0.69	0.72		0.02	0.69	0.21	0.14
Mouse transglutaminase (TGase) mRNA, com	H3137C06	0.63	0.85	0.56	0.88		0.02	0.01	0.01	0.41
Homo sapiens PAC clone RP5-1090P18 from	H3139C05	0.63	0.67	0.69	0.65		0.05	0.06	0.14	0.10
Mus musculus E2F transcription factor 5	H3136D10	0.63	0.75	0.69	0.71		0.02	0.38	0.52	0.57
Mus musculus Chetk-alpha gene for cholin	H3065C11	0.61	0.70	0.80	0.90		0.01	0.02	0.33	0.55
Mouse mRNA for tenascin, complete cds	H3124A01	0.61	0.80	0.59			0.02	0.16	#DIV/0!	#DIV/0!
Homo sapiens cDNA FLJ10504 fis, clone NT	H3029C12	0.60	0.72	0.87			0.03	0.09	0.73	#DIV/0!
Homo sapiens, clone hRPK.1_A_1, complete	H3086B11	0.58	1.17	1.05	0.70		0.01	0.15	#DIV/0!	#DIV/0!
Canis familiaris KIT (c-kit) mRNA, compl	H3026B10	0.57	0.84	0.69	0.74		0.03	0.68	0.14	0.41
Mus musculus dihydroliipoamide branched c	H3150E04	0.57	0.84	0.39			0.01	0.66	#DIV/0!	#DIV/0!
Rattus norvegicus steroid sensitive gene	H3131D09	0.56	0.82	0.88	0.78		0.02	0.23	0.61	0.27
M.musculus of PCTAIRE-1 mRNA encoding pr	H3118F06	0.56	1.13	0.83	1.25		0.00	0.27	0.42	0.35

Table E. Genes significantly influenced by Cobalt in WT Cells (cont.)

Human DNA sequence from PAC 257A7 on chr	H3018G12	0.55	0.67	1.55	1.35		0.04	0.18	#DIV/0!	0.34
Homo sapiens PAC clone RP5-1106E3 from 7	H3137G05	0.55	0.60	1.03	0.77		0.00	0.00	0.89	0.17
Human p67 mRNA, complete cds	H3130A05	0.50	0.51	0.60	0.57		0.00	0.00	#DIV/0!	#DIV/0!
Homo sapiens transcription factor 7 (T-c	H3021D12	0.49	0.48	0.69	0.54		0.05	#DIV/0!	#DIV/0!	#DIV/0!
Cricetulus griseus adenosine kinase mRNA	H3028C09	0.42	0.78	1.15	1.11		0.00	#DIV/0!	0.56	0.68
Escherichia coli K-12 MG1655 section 365	H3146A10	0.29	0.86	0.46	0.50		0.02	0.74	0.26	0.27

Table F. Genes significantly influenced by Hypoxia treatment in HIF1a -/- cells

Name	ID	Fold Changes				TTEST	W-Co	W-H	N-Co	N-H
		W-Co	W-H	N-Co	N-H					
Mus musculus cell-line LXB2 cathepsin L	H3028F03	2.17	1.54	1.28	2.92	0.02	0.04	0.37	0.00	
Mus musculus mannosidase 2, alpha 1 (Man	H3114D03	1.13	1.34	1.11	2.25	0.52	0.11	0.62	0.03	
Homo sapiens phosphoenolpyruvate carboxy	H3026F06	0.98	1.06	0.98	1.99	0.94	0.67	0.91	0.01	
Mus musculus asparagine synthetase mRNA,	H3154F02	0.91	0.85	1.15	1.97	0.66	0.56	0.64	0.01	
Mouse mRNA for nucleosome assembly prote	H3094E07	1.43	1.09	1.27	1.89	0.12	0.75	0.38	0.03	
Mus musculus B6D2F1 clone 2A-1 mRNA	H3086F12	2.20	3.24	1.89	1.89	0.02	#DIV/0!	0.12	0.02	
Homo sapiens chromosome 17, clone hRPK.6	H3130C09	1.53	1.26	1.26	1.86	0.01	0.38	0.52	0.02	
Mus musculus arf-like protein 2 (ARL2) m	H3135B11	1.34	1.17	1.35	1.84	0.08	0.46	0.10	0.01	
Mus musculus lysosomal membrane glycopro	H3109D03	1.38	1.06	1.45	1.82	0.05	0.49	0.06	0.02	
Homo sapiens cDNA FLJ10595 fis, clone NT	H3026C04	0.92	1.03	1.13	1.82	0.61	0.89	0.60	0.00	
Mus musculus chaperonin subunit 5 (epsil	H3023F07	1.58	1.01	1.05	1.79	0.10	0.91	0.79	0.01	
Homo sapiens Chromosome 16 BAC clone CIT	H3039C09	1.62	1.24	1.42	1.79	#DIV/0!	#DIV/0!	0.22	0.04	
NMDA receptor glutamate-binding subunit	H3151H12	1.34	1.06	1.35	1.78	0.03	0.55	0.00	0.00	
Homo sapiens clone RG036G02, complete se	H3137F01	1.41	1.04	1.09	1.77	0.10	0.67	0.62	0.02	
Mus musculus translation repressor NAT1	H3027A06	1.81	1.24	1.07	1.75	0.00	0.29	0.79	0.02	
Rat clathrin heavy chain mRNA, complete	H3026F01	1.33	1.30	0.96	1.73	0.24	0.24	0.82	0.01	
Homo sapiens chromosome 22q11 clone b476	H3141F10	1.89	1.39	1.19	1.72	0.03	0.60	0.28	0.01	
Homo sapiens glutamyl-prolyl-tRNA synthe	H3001H07	1.01	0.95	0.75	1.71	0.96	0.85	0.37	0.04	
Mus musculus nucleophosmin 1 (Npm1), mRN	H3136B07	1.11	0.85	0.81	1.68	0.54	0.44	0.48	0.02	
Mouse kidney ornithine decarboxylase mRN	H3028F05	1.40	0.98	1.40	1.68	0.01	0.88	0.00	0.02	
Fugu rubripes rara gene, exons 4-10	H3145F11	1.15	0.96	1.16	1.68	0.41	0.87	0.53	0.03	
Mus musculus DEBT-91 mRNA, complete cds	H3067A07	1.19	1.08	1.14	1.66	0.23	0.57	0.16	0.00	
Homo sapiens clone HQ0518 PRO0518 mRNA,	H3120D12	1.18	1.17	1.15	1.66	0.22	0.35	0.33	0.01	
Mouse alpha-tubulin gene M-alpha-2, 3' e	H3123G01	1.06	0.91	1.26	1.66	0.75	0.50	0.12	0.01	
Human DNA sequence from clone RP1-102D24	H3117H12	0.88	0.71	1.03	1.64	0.49	0.09	0.90	0.01	
Human mRNA for KIAA0381 gene, partial cd	H3154E03	1.09	0.98	0.94	1.64	0.65	0.95	0.84	0.04	
Mus musculus junctional adhesion molecul	H3121F06	1.28	1.45	1.24	1.63	0.38	0.31	0.31	0.01	
Mus musculus Int6-ps1 pseudogene	H3032B05	0.92	0.90	1.39	1.63	0.65	0.55	0.21	0.02	
Mus musculus microtubule-associated prot	H3058E07	1.29	1.33	1.16	1.63	0.23	0.07	0.45	0.01	
Human DNA sequence *** SEQUENCING IN PRO	H3109F01	1.02	1.06	0.97	1.63	0.86	0.67	0.87	0.05	
Rat mRNA for ribosomal protein L5	H3028D05	1.24	0.91	1.13	1.62	0.21	0.59	0.52	0.03	
Arabidopsis thaliana DNA chromosome 3, B	H3156G09	1.53	1.11	1.09	1.62	0.02	0.59	0.60	0.04	
Human DNA sequence from clone RP4-629F1	H3058F01	0.99	1.11	0.89	1.61	#DIV/0!	#DIV/0!	0.59	0.03	
Mus musculus ribosomal protein L26 (Rpl2	H3030E07	0.97	0.87	1.11	1.60	0.86	0.35	0.62	0.03	
M.musculus Hexa mRNA for beta-N-acetylhe	H3024C07	1.01	1.02	1.21	1.60	0.95	0.94	0.24	0.03	
M.musculus mRNA for mitogen activated pr	H3145H03	1.23	1.35	0.93	1.60	0.08	0.02	0.27	0.00	
Homo sapiens Chromosome 16 BAC clone CIT	H3118C12	1.07	1.13	0.87	1.59	0.80	0.64	0.56	0.05	
H.sapiens CpG island DNA genomic Mse1 fr	H3055F08	1.25	0.78	0.95	1.58	0.37	0.15	0.74	0.03	
Homo sapiens chromosome 19, cosmid R2817	H3126B06	1.04	1.29	1.59	1.57	0.89	#DIV/0!	0.21	0.02	
Homo sapiens chromosome 5 clone CIT-HSPC	H3101H03	1.23	1.07	1.24	1.57	0.33	0.76	0.30	0.02	
Rat 24-kDa subunit of mitochondrial NADH	H3133D04	1.41	0.90	1.24	1.55	0.03	0.63	0.24	0.03	
Homo sapiens glycyl-tRNA synthetase (GAR	H3134C11	1.16	0.99	1.02	1.55	0.39	0.97	0.94	0.02	
Cu-Zn SOD (image 1512393)	A-2053	1.11	1.06	1.13	1.55	0.60	0.82	0.48	0.03	
Homo sapiens BAC clone RP11-519H15 from	H3140D05	1.13	0.91	1.21	1.54	0.38	0.47	0.20	0.01	
Mus musculus tumor differentially expres	H3135D01	1.17	1.14	1.00	1.53	0.27	0.47	0.99	0.05	
Mus musculus vacuolar adenosine triphosp	H3021E11	1.20	1.01	1.49	1.52	0.20	0.94	0.00	0.01	
Oryza sativa genomic DNA, chromosome 2,	H3128B12	0.90	0.86	0.98	1.52	0.53	0.35	0.94	0.04	
Mus musculus junctional adhesion molecul	H3151D05	1.02	1.36	0.97	1.52	0.88	0.13	0.88	0.03	
Murine mRNA for integrin beta subunit	H3134H10	1.38	1.18	1.17	1.51	0.08	0.63	0.36	0.01	
Mus musculus alcohol dehydrogenase 5 (Ad	H3024A06	1.16	1.08	1.11	1.50	0.32	0.56	0.55	0.02	
R.norvegicus mRNA for ribosomal protein	H3046F11	0.92	0.93	1.12	1.50	0.56	0.69	0.57	0.01	
Mus musculus silica-induced gene 81 (Sil	H3024F03	1.23	1.33	0.99	1.49	0.21	0.20	0.97	0.05	
Mus musculus glucosidase, alpha, acid (G	H3109C03	1.27	1.07	1.07	1.49	0.02	0.34	0.55	0.00	
Mus musculus adaptor-related protein com	H3018B01	0.97	0.93	1.32	1.48	0.79	0.46	0.06	0.01	
Mus musculus telomeric repeat binding fa	H3121F09	0.86	0.98	1.33	1.48	0.41	0.93	0.07	0.03	
Mus musculus zipper (leucine) protein ki	H3150H08	1.17	0.96	1.10	1.48	0.38	0.83	0.42	0.03	
Homo sapiens protease, serine, 15 (PRSS1	H3129G12	1.32	1.60	1.18	1.48	0.06	0.00	0.24	0.03	
H.sapiens initiation factor 4B cDNA	H3050G08	0.83	1.10	1.07	1.47	0.29	0.63	0.64	0.02	
Human DNA sequence from clone RP4-695O20	H3158G09	1.17	0.99	1.09	1.46	0.10	0.85	0.52	0.00	
Mus musculus ubiquitin-specific protease	H3140A01	1.07	1.02	1.19	1.46	0.54	0.91	0.30	0.01	
Clostridium acetobutylicum mannitol-spec	H3070B12	0.83	0.83	1.22	1.46	0.40	0.33	0.39	0.05	
Mus musculus actin-related protein compl	H3019A08	1.02	1.09	1.11	1.46	0.88	0.60	0.37	0.01	
Arabidopsis thaliana chromosome II secti	H3107E10	1.13	1.04	1.08	1.46	0.57	0.90	0.69	0.03	

Table F. Genes significantly influenced by Hypoxia treatment in HIF1a -/- cells (cont.)

Mus musculus chaperonin subunit 7 (eta)	H3026F08	1.10	0.99	1.02	1.45		0.57	0.93	0.87	0.00
Homo sapiens 12p BAC RPC11-75L1 (Roswel	H3149A10	1.17	1.27	0.79	1.45		0.27	0.06	0.26	0.03
Mus musculus succinate dehydrogenase Fp	H3153F01	1.30	1.11	1.18	1.45		0.01	0.44	0.14	0.01
Mus musculus major histocompatibility lo	H3107B03	1.07	1.00	1.48	1.45		0.73	0.98	0.04	0.03
Influenza A/Memphis/8/88 (H3N2), PB2 pol	H3147H11	1.73	1.47	1.26	1.45		0.04	0.04	0.11	0.04
Homo sapiens chromosome 5 clone CITB-H1_	H3144C11	1.06	1.33	0.92	1.44		0.66	0.13	0.65	0.02
No Hits Found	H3019D11	1.03	0.80	1.23	1.44		0.88	0.34	0.32	0.02
Homo sapiens chromosome 8 BAC clone 402H	H3115E10	0.96	1.04	1.00	1.44		0.81	0.81	0.97	0.03
Arabidopsis thaliana chromosome III BAC	H3034H05	1.35	1.13	1.61	1.44		0.18	0.58	0.04	0.02
saposin=sphingolipid activator protein [H3151D11	1.37	1.27	0.90	1.44		0.02	0.21	0.61	0.04
Homo sapiens ribosomal protein L13 mRNA,	H3030A04	1.31	1.07	1.15	1.44		0.04	0.61	0.46	0.04
Homo sapiens chromosome 4 clone C0483I23	H3107E04	1.42	1.03	1.23	1.44		0.03	0.85	0.12	0.01
Rattus norvegicus outer mitochondrial me	H3038G11	1.07	0.78	1.44	1.43		0.76	0.33	0.04	0.03
Homo sapiens chromosome 17, clone hRPK.6	H3049F11	1.40	1.16	1.33	1.43		0.00	0.30	0.05	0.01
Homo sapiens clone GS096J14, complete se	H3130H12	1.13	1.12	0.82	1.43		0.54	0.61	0.21	0.04
Mus musculus protein synthesis elongatio	H3040C12	0.75	1.07	1.03	1.42		0.05	0.53	0.85	0.02
Human DNA sequence from PAC 106B9 on chr	H3128E05	1.06	1.04	1.13	1.42		0.72	0.78	0.35	0.03
Homo sapiens cDNA FLJ20625 fis, clone KA	H3106H11	1.39	1.27	1.35	1.42		0.06	0.25	0.05	0.04
Mouse skeletal muscle beta tropomyosin m	H3135D11	0.95	1.34	0.84	1.42		0.73	0.17	0.35	0.03
Mus musculus hexosaminidase B (Hexb), mR	H3078E09	1.49	1.01	1.06	1.42		0.05	0.96	0.74	0.04
Human mRNA for KIAA0212 gene, complete c	H3020D08	1.12	1.05	1.28	1.41		0.34	0.71	0.09	0.03
S.pombe chromosome II cosmid c25H2	H3036C07	1.21	1.15	0.81	1.41		0.18	0.30	0.24	0.03
Mouse hexokinase mRNA, complete cds	H3114D09	1.35	1.15	0.86	1.41		0.03	0.31	0.49	0.03
Human DNA sequence from clone LUCA11 on	H3144B05	1.43	0.99	1.00	1.41		0.03	0.96	0.99	0.04
Human mRNA for KIAA0217 gene, partial cd	H3145G10	1.24	1.13	1.22	1.41		0.30	0.47	0.31	0.03
Mus musculus mRNA for erythroid differen	H3158G06	1.01	0.99	1.36	1.40		0.93	0.95	0.10	0.03
C.griseus epsilon-COP mRNA	H3155F09	1.79	1.78	1.46	1.40		0.02	0.13	0.06	0.02
Homo sapiens cDNA FLJ10622 fis, clone NT	H3076A07	1.26	1.21	1.06	1.40		0.19	0.29	0.70	0.00
Homo sapiens mRNA; cDNA DKFZp434F1126 (f	H3153B06	1.44	1.12	1.25	1.40		0.05	0.52	0.21	0.03
Mus musculus mitochondrial DNA, complete	H3126D01	0.87	1.04	0.93	1.39		0.39	0.77	0.72	0.03
Homo sapiens cDNA FLJ10879 fis, clone NT	H3148E03	1.14	1.34	1.02	1.39		0.24	0.03	0.92	0.04
Rattus rattus mRNA for neurodegeneration	H3149G04	1.00	1.04	1.16	1.39		0.96	0.74	0.32	0.01
M.musculus mRNA for ribosomal protein S2	H3145D12	1.32	1.00	0.95	1.39		0.05	0.99	0.82	0.05
Mus musculus major histocompatibility lo	H3058A11	2.76	2.31	1.39	1.39		0.10	0.10	0.11	0.03
Caenorhabditis elegans cosmid Y105C5B, c	H3108H07	1.17	1.40	1.27	1.39		0.39	0.13	0.04	0.01
Mus musculus mRNA for cartilage-associat	H3044A03	1.18	1.23	1.06	1.38		0.28	0.16	0.63	0.02
Homo sapiens mRNA; cDNA DKFZp586B0918 (f	H3159B11	1.14	1.06	1.23	1.37		0.19	0.48	0.22	0.02
Cricetulus griseus PxF mRNA, complete cd	H3030F12	1.03	1.06	0.94	1.37		0.80	0.70	0.73	0.03
Mouse laminin B2 chain mRNA, complete cd	H3113E11	1.30	1.19	0.84	1.37		0.02	0.10	0.11	0.01
Homo sapiens 12p21.3 BAC RPC11-69M1 (Ro	H3144E08	1.11	0.99	1.24	1.36		0.41	0.94	0.13	0.03
Mus musculus beta-site APP cleaving enzy	H3098E11	1.04	0.94	1.08	1.36		0.86	0.78	0.65	0.03
Mus musculus MEK kinase 3, mRNA, partial	H3120D01	1.12	0.97	1.01	1.36		0.55	0.86	0.95	0.04
Homo sapiens glutaminase isoform C mRNA,	H3143H12	1.21	1.27	1.29	1.35		0.48	0.30	0.28	0.02
Homo sapiens Chromosome 12 BAC RP11-478B	H3159C12	1.10	1.24	1.03	1.35		0.21	0.13	0.85	0.02
Mus musculus ribosomal protein S26 (RPS2	H3035A02	0.87	0.91	1.29	1.35		0.42	0.57	0.05	0.03
Homo sapiens clone 24667 mRNA sequence	H3076A06	0.88	0.66	1.15	1.35		0.54	0.12	0.43	0.03
Rattus norvegicus mRNA for protein kinas	H3150C08	1.12	0.98	1.13	1.34		0.25	0.80	0.23	0.01
Mouse S16 ribosomal protein processed ps	H3112H10	1.17	1.15	1.09	1.34		0.34	0.53	0.62	0.05
Homo sapiens CGI-102 protein mRNA, compl	H3112E04	1.01	1.09	1.06	1.34		0.96	0.57	0.52	0.04
Homo sapiens genomic DNA, chromosome 21q	H3060A04	0.75	0.82	0.89	1.33		0.18	0.26	0.38	0.02
H beta 58=essential for embryogenesis [m	H3138G07	1.38	0.85	1.59	1.33		0.12	0.31	0.05	0.03
Mus musculus isocitrate dehydrogenase 3	H3149D06	1.24	1.15	0.99	1.33		0.28	0.35	0.91	0.04
Human DNA sequence from clone RP4-702J19	H3148H12	1.13	0.94	1.47	1.33		0.69	0.80	0.18	0.02
Rattus norvegicus mRNA for DA41, complet	H3049H11	0.99	1.04	1.07	1.33		0.92	0.78	0.58	0.02
Mus musculus zinc finger protein 207 (Zf	H3134G10	1.12	0.87	1.22	1.33		0.34	0.31	0.22	0.04
Homo sapiens mRNA for KIAA0226 protein,	H3058E06	1.48	1.20	1.31	1.33		0.02	0.08	0.14	0.02
Murine mRNA for L-34 galactoside-binding	H3016D10	1.46	1.62	1.07	1.32		0.01	0.00	0.47	0.02
Human DNA sequence from clone RP11-541N1	H3123B08	1.18	1.20	0.82	1.32		0.33	0.23	0.24	0.01
Mus musculus nuclear receptor coactivato	H3129G07	0.91	1.08	0.90	1.32		0.46	0.59	0.51	0.05
Rattus norvegicus hfb2 mRNA, complete cd	H3018H03	0.96	1.09	1.02	1.32		0.75	0.66	0.90	0.03
Homo sapiens clone NH0166O04, complete s	H3123E03	0.91	1.05	1.04	1.31		0.63	0.80	0.75	0.03
Homo sapiens chromosome 5, BAC clone 8e5	H3062G06	1.27	1.18	1.02	1.31		0.01	0.07	0.84	0.02
Mus musculus D6MM5e protein (D6Mm5e) and	H3146F03	0.98	0.99	1.11	1.31		0.86	0.90	0.35	0.02
Rattus norvegicus proline rich protein m	H3116A06	1.24	1.35	1.08	1.30		0.01	0.01	0.46	0.05
Mus musculus TGF-beta receptor binding p	H3025D04	1.04	0.83	0.92	1.29		0.84	0.42	0.61	0.02

Table F. Genes significantly influenced by Hypoxia treatment in HIF1a -/- cells (cont.)

Homo sapiens clone 24797 mRNA sequence	H3014D05	1.09	1.04	0.93	1.29		0.58	0.61	0.49	0.02
Homo sapiens clone RP11-357E16, complete	H3003D09	1.12	0.89	1.43	1.29		0.39	0.35	0.06	0.04
Rat PMSG-induced ovarian mRNA, 3' sequenc	H3010B06	1.04	0.88	0.91	1.29		0.75	0.28	0.39	0.02
Rattus norvegicus Smad4 protein (Smad4)	H3128C04	1.02	1.04	0.95	1.28		0.87	0.73	0.64	0.04
Mus musculus transforming growth factor,	H3062E02	1.04	1.09	0.93	1.28		0.66	0.40	0.44	0.02
Mus musculus mRNA for CtBP1 protein	H3108G09	1.15	1.05	1.16	1.28		0.34	0.73	0.17	0.03
Homo sapiens BAC clone GS1-77A9 from 7p1	H3020A08	1.11	0.91	1.20	1.28		0.13	0.13	0.23	0.02
Mus musculus procollagen-lysine, 2-oxogl	H3060C03	1.27	1.16	1.13	1.26		0.13	0.40	0.30	0.04
Mus musculus ribosomal protein L12 (Rpl1	H3079A02	1.15	1.13	0.90	1.26		0.32	0.27	0.68	0.05
Homo sapiens far upstream element bindin	H3020A11	0.85	0.94	1.00	1.24		0.08	0.43	0.98	0.04
Homo sapiens methionine-tRNA synthetase	H3005G12	0.92	0.88	1.00	1.24		0.47	0.22	0.99	0.04
Homo sapiens BAC clone GS1-115E6 from 7p	H3150A05	0.99	0.98	1.10	1.24		0.92	0.87	0.41	0.03
Mus musculus ribosomal protein S4, X-lin	H3120D10	1.36	1.05	0.81	1.24		0.03	0.72	0.37	0.01
Human chromosome 14 DNA sequence *** IN	H3026B05	0.78	0.99	0.97	1.20		0.18	0.95	0.77	0.02
Mus musculus cdc2/CDC28-like protein kin	H3154B09	0.94	0.98	1.16	1.20		0.42	0.93	0.12	0.04
Homo sapiens mRNA for Centrosome- and Go	H3042D09	1.39	0.97	1.05	1.15		0.02	0.64	0.50	0.04
Mus musculus ribosomal protein S6 kinase	H3002D07	0.98	1.05	0.92	0.87		0.66	0.26	0.40	0.03
Unknown	H3011E12	0.83	1.01	0.72	0.86		0.01	0.96	#DIV/0!	0.04
Homo sapiens cDNA FLJ10962 fis, clone PL	H3004E04	1.10	0.98	0.86	0.85		0.38	0.77	0.18	0.03
Human BAC clone GS1-330J10 from 5p15.2,	H3153E02	0.72	0.64	0.68	0.84		0.24	0.06	0.25	0.04
Homo sapiens HSPC117 mRNA, complete cds	H3017G09	0.98	0.93	1.03	0.84		0.84	0.58	0.85	0.04
Mus musculus annexin A5 (Anxa5), mRNA	H3016C05	1.04	1.18	0.86	0.83		0.69	0.15	0.06	0.02
Arabidopsis thaliana chromosome 1 BAC F5	H3002D01	0.93	0.95	0.86	0.83		0.30	0.48	0.11	0.02
Human mRNA for KIAA0179 gene, partial cd	H3020A05	0.89	0.86	0.97	0.83		0.20	0.20	0.80	0.05
Mus musculus zinc finger protein X-linke	H3153B04	1.04	1.04	0.89	0.82		0.72	0.81	0.49	0.03
Arabidopsis thaliana genomic DNA, chromo	H3059B10	1.01	0.98	0.98	0.82		0.96	0.88	0.93	0.03
H.sapiens mRNA for pur alpha extended 3'	H3008B08	0.99	0.92	0.83	0.82		0.95	0.24	0.04	0.04
Mus musculus heterogeneous nuclear ribon	H3111H11	0.95	0.95	0.91	0.82		0.60	0.62	0.21	0.00
Human DNA sequence from clone RP3-347H13	H3159E05	1.01	0.91	1.11	0.82		0.92	0.35	0.33	0.05
Mus musculus BAC GSMB-407A4 (Genome Sys	H3093G01	1.15	0.98	0.96	0.82		0.36	0.91	0.81	0.03
Caenorhabditis elegans cosmid ZK970, com	H3059H07	0.79	0.65	0.71	0.81		0.10	0.02	0.08	0.05
Human DNA sequence from clone RP4-742C19	H3014H11	0.87	0.90	0.78	0.81		0.21	0.50	0.04	0.03
Homo sapiens cDNA FLJ10909 fis, clone OV	H3071D02	1.01	0.90	0.75	0.81		0.83	0.26	0.01	0.04
Homo sapiens mRNA; cDNA DKFZp434E146 (fr	H3011D03	1.01	0.92	0.82	0.81		0.85	0.16	0.08	0.02
Homo sapiens mRNA; cDNA DKFZp434L0130 (f	H3014G11	0.76	0.70	0.56	0.81		0.09	0.25	0.00	0.04
Mus musculus mRNA for NEFA protein, comp	H3012H05	0.99	0.97	0.72	0.81		0.94	0.95	0.05	0.02
Mus musculus DNA from BAC 10818 containi	H3017C01	0.88	0.72	0.65	0.81		0.32	0.17	0.01	0.02
Mus musculus vacuolar adenosine triphosp	H3013B02	0.92	0.94	0.67	0.80		0.65	#DIV/0!	0.02	0.02
Homo sapiens mRNA; cDNA DKFZp434A179 (fr	H3011D05	0.94	0.83	0.82	0.80		0.50	0.06	0.06	0.03
Caenorhabditis elegans cosmid F27C1	H3153B03	1.06	0.65	0.65	0.80		0.65	0.01	0.05	0.05
Mus musculus TXNRD1 mRNA for thioredoxin	H3005B03	0.97	0.81	1.01	0.79		0.86	0.08	0.91	0.04
Mus musculus chaperonin subunit 3 (gamma	H3024B04	0.85	0.77	0.90	0.79		0.16	0.04	0.46	0.04
Homo sapiens chromosome 17, clone hRPK.6	H3149G08	1.10	1.10	1.07	0.79		0.35	0.39	0.54	0.05
Mus musculus MARCKS-like protein (Mlp),	H3016C07	0.93	1.07	0.83	0.78		0.46	0.52	0.06	0.03
Human DNA sequence *** SEQUENCING IN PRO	H3019B09	1.13	0.87	0.89	0.78		0.46	0.42	0.38	0.03
Mus musculus ankyrin repeat-containing p	H3154E05	0.98	0.96	0.88	0.78		0.87	0.79	0.36	0.04
Human DNA sequence from clone RP5-1185N5	H3001C05	1.02	1.01	0.91	0.77		0.89	0.96	0.49	0.04
Mus musculus chaperonin subunit 3 (gamma	H3024B03	0.87	0.80	0.85	0.77		0.15	0.07	0.16	0.04
Mouse mRNA for germ cell specific lamin	H3017F05	1.00	1.02	0.72	0.77		1.00	0.91	0.05	0.04
Mus musculus flap structure specific end	H3009B04	1.08	0.98	0.92	0.77		0.55	0.86	0.45	0.01
Mus musculus ubiquitin conjugating enzym	H3014G12	0.93	0.84	0.74	0.76		0.60	0.29	0.05	0.05
Human chromosome 14 DNA sequence *** IN	H3159A07	0.92	0.99	0.78	0.76		0.39	0.93	0.05	0.03
Mus musculus purine-selective Na+ nucleo	H3014C12	0.81	0.79	0.90	0.76		0.13	0.25	0.57	0.03
Homo sapiens 3q26.2-27 BAC RPC11-469J4	H3113A03	1.10	0.99	0.94	0.76		0.58	0.92	0.63	0.05
Mus musculus mRNA for erythroid differen	H3101A07	1.03	0.90	0.83	0.76		0.86	0.48	0.05	0.04
Human mRNA for KIAA0250 gene, complete c	H3140H11	1.03	0.88	0.92	0.76		0.86	0.36	0.54	0.05
Mus musculus villin 2 (Vil2), mRNA	H3014F03	1.02	1.04	0.82	0.76		0.88	0.79	0.03	0.00
R.norvegicus mRNA for alpha initiation f	H3120A01	0.97	0.59	0.92	0.76		0.88	0.09	0.53	0.04
Mouse mRNA for prothymosin alpha	H3118B02	0.88	0.78	0.62	0.75		0.32	0.17	0.03	0.05
Arabidopsis thaliana chromosome I BAC T2	H3088G10	0.99	0.68	0.77	0.75		0.97	0.03	0.21	0.04
Homo sapiens full length insert cDNA clo	H3124A10	0.82	0.88	0.81	0.75		0.06	0.37	0.06	0.03
Rattus norvegicus non-muscle alpha-actin	H3003H10	1.06	0.64	0.52	0.75		0.81	0.01	0.00	0.04
Human DNA sequence from clone RP3-382I10	H3051D07	1.07	1.00	0.84	0.75		0.55	0.97	0.13	0.01
Homo sapiens TNF-alpha stimulated ABC pr	H3015E12	0.86	0.85	0.72	0.74		0.28	0.40	0.07	0.04
Homo sapiens mRNA; cDNA DKFZp434P1215 (f	H3010B04	0.82	0.98	0.87	0.74		0.09	0.73	0.23	0.00

Table F. Genes significantly influenced by Hypoxia treatment in HIF1a -/- cells (cont.)

Rattus norvegicus mRNA for catalytic sub	H3021G03	1.05	1.04	0.74	0.74		0.78	0.81	0.07	0.04
Homo sapiens 12q13-62.7-72 BAC RPC111-66	H3018D03	0.77	1.36	0.93	0.74		#DIV/0!	#DIV/0!	0.74	0.04
Human DNA sequence from clone RP1-80N2 o	H3020G06	0.90	0.79	0.79	0.74		0.47	0.14	0.16	0.04
Mus musculus tyrosine kinase TXK (tkk) m	H3012B12	0.90	0.72	0.74	0.74		0.55	0.08	0.20	0.03
Mus musculus mRNA for chemokine receptor	H3051E02	0.87	0.85	0.63	0.73		0.57	0.56	0.03	0.03
Mus musculus procollagen, type VI, alpha	H3151F07	0.89	1.48	0.53	0.73		0.60	0.01	0.00	0.02
Rattus norvegicus clone UV123Sp6 ultravi	H3015G06	0.95	0.91	0.87	0.73		0.62	0.35	0.35	0.04
Homo sapiens Xq28 BAC PAC and cosmid clo	H3146A07	1.08	0.95	0.76	0.73		0.60	0.78	0.02	0.03
Homo sapiens SCG10 like-protein, helicas	H3151B10	1.60	1.04	0.87	0.73		0.29	0.92	0.38	0.05
Human clone iota unknown protein mRNA, c	H3013F12	0.91	0.82	0.79	0.73		0.42	0.29	0.18	0.04
Homo sapiens 12q seeder BAC RP11-202H2 (H3017B03	0.94	0.85	0.80	0.73		0.73	0.50	0.20	0.05
Mus musculus major histocompatibility lo	H3119A06	1.36	0.89	0.92	0.73		0.06	0.48	0.59	0.03
Homo sapiens clone DJ0856O24, complete s	H3062E11	1.29	0.97	0.95	0.72		0.23	0.90	0.73	0.03
H.sapiens PRM1 gene, PRM2 gene and TNP2	H3026A12	0.83	0.69	0.74	0.72		0.14	0.08	0.20	0.04
Homo sapiens genomic DNA, chromosome 8p1	H3156C11	0.75	0.76	0.58	0.72		0.24	0.12	0.01	0.03
Homo sapiens hepatocyte nuclear factor 4	H3059C01	1.00	0.92	0.74	0.72		1.00	0.57	0.07	0.03
Homo sapiens chromosome 9, clone RP11-52	H3011H01	0.95	0.89	0.73	0.72		0.74	0.50	0.06	0.03
Homo sapiens signal recognition particle	H3014E12	0.85	0.87	0.71	0.72		0.14	0.37	0.04	0.01
Mus musculus myristoylated alanine rich	H3112E12	0.84	1.17	0.86	0.71		0.48	0.54	0.38	0.03
Homo sapiens Xp22 GSHB-314C4 (Genome Sys	H3157D03	0.91	0.73	0.85	0.71		0.41	0.05	0.22	0.05
Mus musculus transforming growth factor	H3112G06	1.07	1.16	0.92	0.71		0.72	0.33	0.50	0.02
Mus musculus degenerative spermatocyte h	H3112F03	1.37	0.77	0.63	0.71		0.30	0.39	0.00	0.04
Human DNA sequence from clone RP4-621F18	H3150D11	0.97	0.98	1.15	0.71		0.85	0.91	0.57	0.03
Human DNA sequence from clone RP1-262C15	H3035A11	0.98	0.88	0.82	0.71		0.88	0.40	0.37	0.04
Fugu rubripes neural cell adhesion molec	H3021D09	1.14	0.75	0.80	0.71		0.56	0.11	0.12	0.03
Homo sapiens genomic DNA, chromosome 3p2	H3025A04	0.93	0.69	1.36	0.71		0.70	0.10	0.18	0.03
Homo sapiens 12p13.3 PAC RPC15-1180D12 (H3119G09	0.99	1.10	0.88	0.71		0.93	0.30	0.46	0.00
Mus musculus 123F2 protein mRNA, complet	H3103G04	1.40	1.31	1.28	0.70		0.11	0.02	0.29	0.03
S.pombe chromosome I cosmid c26F1	H3088A07	1.02	1.06	0.84	0.70		0.89	0.68	0.43	0.03
H.sapiens CpG island DNA genomic Mse1 fr	H3081C09	1.33	0.86	1.09	0.70		0.03	0.24	0.72	0.05
Mus musculus Treacher Collins Francesche	H3076H12	0.85	0.88	0.85	0.70		0.43	0.60	0.31	0.02
Homo sapiens Chromosome 11q12.2 PAC clon	H3031E12	1.06	1.27	1.00	0.70		0.71	0.06	0.99	0.03
Homo sapiens cDNA FLJ11144 fis, clone PL	H3017A04	0.67	0.69	0.99	0.69		0.23	0.27	0.95	0.04
Mus musculus pyruvate kinase 3 (Pk3), mR	H3030D10	1.62	2.02	0.86	0.69		0.01	0.01	0.38	0.00
Rat mRNA for p34 protein, complete cds	H3025B06	0.97	1.07	0.94	0.69		0.78	0.61	0.64	0.03
Homo sapiens 12 BAC RP11-438N16 (Roswell	H3011H04	1.13	0.96	1.10	0.69		0.63	0.88	0.63	0.03
Homo sapiens genomic DNA, chromosome 21,	H3153G03	0.98	0.83	0.96	0.69		0.88	0.21	0.88	0.02
Mouse mRNA for elongation factor 1-alpha	H3079A06	0.82	0.86	0.59	0.69		0.11	0.32	0.07	0.04
Homo sapiens small nuclear ribonucleopro	H3067C04	0.74	0.67	0.96	0.69		0.17	0.05	0.78	0.05
Caenorhabditis elegans cosmid Y116A8C, c	H3001F11	0.83	0.95	0.72	0.68		0.36	0.85	0.09	0.04
Mouse metallothionein II (MT-II) gene	H3013D11	1.20	1.03	0.72	0.68		0.22	0.90	0.10	0.02
Human DNA sequence from clone CTA-250D10	H3124D03	0.63	0.60	0.73	0.68		0.12	0.10	0.42	0.03
Homo sapiens clone 24519 unknown mRNA, p	H3017F03	0.84	1.02	0.52	0.68		0.40	0.73	0.14	0.00
Subacute sclerosing panencephalitis (SSP	H3010B02	0.88	0.81	0.68	0.68		0.34	0.30	0.01	0.01
Alcaligenes sp. KUFA-1 dmfA1 and dmfA2 g	H3106A03	0.98	0.89	0.83	0.68		0.93	0.18	0.34	0.05
Mus musculus Cbp/p300-interacting transa	H3135G01	0.92	0.72	0.66	0.68		0.77	0.30	0.04	0.01
Sclerotium cepivorum strain DE-1 anonymo	H3015F10	0.84	0.77	0.71	0.67		0.19	0.42	0.24	0.05
Mus musculus transforming growth factor	H3097C06	0.78	0.97	0.93	0.67		0.10	0.81	0.71	0.04
Human mRNA for myoblast cell surface ant	H3131A02	0.86	0.81	0.87	0.67		0.25	0.16	0.34	0.00
Mus musculus glutathione peroxidase 1 (G	H3026F02	1.22	0.75	1.13	0.67		0.42	0.26	0.57	0.03
Mus musculus spindlin (Spin), mRNA	H3101A11	0.89	1.10	0.65	0.67		0.82	0.34	0.01	0.01
Human DNA sequence from clone SC22CB-13C	H3137B03	1.18	0.94	0.61	0.67		0.73	0.81	0.12	0.05
Homo sapiens 12p12 BAC RPC111-320J20 (Ro	H3065B07	1.32	0.86	0.64	0.67		0.21	0.57	0.04	0.05
Homo sapiens mRNA for serine/threonine p	H3090C12	0.99	1.05	0.92	0.67		0.96	0.70	0.41	0.02
Mus musculus putative transcription fact	H3110H03	1.01	0.91	0.59	0.67		0.96	0.61	0.00	0.02
Homo sapiens cDNA FLJ20115 fis, clone CO	H3098D04	1.19	0.81	0.65	0.66		0.51	0.50	0.04	0.03
Mus musculus mesoderm specific transcrip	H3137B11	0.78	0.97	0.87	0.66		0.25	0.93	0.65	0.05
Mus musculus ribonucleotide reductase M2	H3024A11	1.13	1.12	0.86	0.66		0.55	0.61	0.40	0.03
Homo sapiens cDNA FLJ10334 fis, clone NT	H3078C04	1.02	0.84	0.57	0.66		0.94	0.48	0.14	0.05
Homo sapiens mRNA, cDNA DKFZp566B213 (fr	H3015G11	0.73	0.59	0.83	0.66		0.02	0.18	0.46	0.02
Mouse mRNA for prothymosin alpha	H3118B01	0.79	0.64	0.79	0.66		0.13	0.00	0.26	0.04
Mus musculus mRNA for nuclear protein ZA	H3134F07	1.01	0.81	0.75	0.65		0.91	0.19	0.10	0.02
R. norvegicus mRNA for Mss4 protein	H3118B06	0.91	1.00	0.88	0.65		0.50	1.00	0.47	0.03
R.norvegicus mRNA for microtubule associ	H3146D12	0.93	0.79	0.74	0.65		0.56	0.05	0.23	0.04
Human DNA sequence from clone 122O8 on c	H3011A10	0.97	0.81	0.97	0.65		0.81	0.21	0.84	0.00

Table F. Genes significantly influenced by Hypoxia treatment in HIF1a -/- cells (cont.)

Mus musculus cyclin-dependent kinase 5 (H3111B07	0.92	0.94	0.45	0.65		0.77	0.84	0.01	0.05
Mus musculus pyruvate kinase 3 (Pk3), mR	H3030D11	1.93	2.36	0.87	0.65		0.00	0.00	0.53	0.03
Homo sapiens chromosome 21 PAC LLNLP704M	H3103C03	0.96	0.79	0.85	0.65		0.76	0.02	0.38	0.01
Homo sapiens cDNA FLJ10885 fis, clone NT	H3119B10	0.70	0.77	0.97	0.65		0.34	0.46	0.93	0.05
Homo sapiens hect (homologous to the E6-	H3017D04	0.96	0.84	0.67	0.64		0.77	0.35	0.02	0.01
Human Chromosome X PAC RPC11-290C9 from	H3094F06	1.01	0.70	0.96	0.64		0.97	0.45	0.85	0.01
Homo sapiens clone DJ0548K24, complete s	H3113A05	0.97	1.10	0.85	0.64		0.87	0.66	0.38	0.03
Homo sapiens Sad1 unc-84 domain protein	H3102F06	1.01	0.89	0.65	0.64		0.99	0.75	0.05	0.03
No Hits Found	H3159D09	0.78	0.69	0.77	0.63		0.24	0.16	0.38	0.01
Butyrivibrio fibrisolvens butyrivibrioci	H3012B08	0.89	0.92	0.76	0.63		0.58	0.74	0.27	0.02
Human DNA sequence from clone RP5-976O13	H3056B11	0.86	0.85	0.63	0.63		0.31	0.34	0.03	0.04
Novel human gene mapping to chromosome 1	H3105G05	1.02	0.86	0.95	0.63		0.93	0.32	0.81	0.03
Mus musculus inhibitor of DNA binding 3	H3154E06	1.25	1.03	0.66	0.63		0.18	0.88	0.05	0.02
Homo sapiens, complete sequence	H3082G06	1.02	1.09	1.11	0.63		0.91	0.33	0.67	0.03
Rattus norvegicus Lnk4 mRNA, complete cd	H3158D06	0.95	1.06	0.94	0.63		0.76	0.69	0.84	0.00
Homo sapiens cDNA FLJ20746 fis, clone HE	H3060C11	0.97	0.83	0.57	0.62		0.90	0.52	0.01	0.00
Homo sapiens 2,3-bisphosphoglycerate mut	H3142C11	1.11	0.89	0.99	0.62		0.50	0.42	0.93	0.00
Homo sapiens clone UWGC:djs228 from 7q31	H3071F07	0.99	0.80	0.94	0.62		0.89	0.09	0.67	0.00
Homo sapiens cDNA FLJ10330 fis, clone NT	H3019F09	1.37	0.85	0.78	0.62		0.02	0.22	0.18	0.03
Mus musculus tetratricopeptide repeat do	H3121G11	0.81	0.88	0.97	0.62		0.40	0.58	0.89	0.03
Human chromosome 14 DNA sequence *** IN	H3034B08	0.66	1.06	0.82	0.62		0.04	0.72	0.55	0.03
Rattus norvegicus liver nuclear protein	H3128C03	1.08	0.71	0.69	0.62		0.51	0.04	0.07	0.04
Homo sapiens DNA segment on chromosome X	H3041B09	0.89	0.89	0.71	0.62		0.54	0.46	0.13	0.04
Homo sapiens cDNA FLJ10858 fis, clone NT	H3059E06	1.01	1.06	0.87	0.62		0.97	0.83	0.57	0.03
Mus musculus SH3 domain-containing prote	H3078F12	0.68	1.18	0.46	0.62		0.50	0.58	0.12	0.02
Homo sapiens 12q15 BAC RPC111-444B24 (Ro	H3088C01	0.88	0.60	0.86	0.62	#DIV/0!	#DIV/0!		0.26	0.04
Homo sapiens clone DJ0635B05, complete s	H3150D07	0.84	0.70	0.58	0.62		0.54	0.12	0.00	0.01
Homo sapiens DNA from chromosome 19-cosm	H3001D03	0.83	0.83	0.77	0.62		0.38	0.41	0.20	0.01
Mus musculus stannin gene, complete cds	H3116B06	0.77	1.00	1.00	0.61		0.11	0.97	1.00	0.05
Pisum sativum gibberellin c20-oxidase ge	H3094E01	0.77	0.60	0.57	0.61		0.09	0.01	0.02	0.02
Mouse delta/YY1/NF-E1/UCRBP transcriptio	H3090G09	1.06	0.97	0.81	0.61		0.51	0.58	0.12	0.04
Rattus norvegicus podocalyxin mRNA, comp	H3029C03	0.82	1.04	0.60	0.61		0.17	0.76	0.05	0.05
Human chromosome 14 DNA sequence *** IN	H3139F07	1.02	0.82	0.62	0.60		0.91	0.33	0.01	0.01
Campylobacter jejuni NCTC11168 complete	H3094E02	0.68	0.79	0.57	0.60		0.36	0.27	0.01	0.01
M.sativa Rbcsk-1A gene	H3153H10	0.75	0.86	0.77	0.60		0.04	0.17	0.42	0.00
Homo sapiens BAC clone RP11-364H22 from	H3150D04	0.95	0.61	0.87	0.60		0.79	0.09	0.58	0.02
Human mRNA for KIAA0205 gene, complete c	H3088F09	1.04	1.01	0.82	0.60		0.71	0.87	0.10	0.02
Homo sapiens mRNA for farnesylated-prote	H3035F09	1.05	0.81	0.65	0.60		0.81	0.28	0.00	0.00
Human BAC clone GS1-552A1 from 7q21-q22,	H3051F06	1.01	0.97	0.56	0.60		0.96	0.89	0.08	0.02
Mus musculus ubi-d4/requiem gene, exons	H3100G09	0.88	0.91	0.79	0.59		0.23	0.42	0.03	0.00
Mus musculus splicing factor, arginine/s	H3075D05	0.94	0.76	0.80	0.59		0.68	0.06	0.20	0.00
Homo sapiens chromosome 16, cosmid clone	H3140C05	0.95	1.04	0.75	0.59		0.57	0.72	0.03	0.00
Mus musculus selenoprotein W, muscle 1 (H3118A07	0.93	0.67	1.02	0.58		0.75	0.06	0.92	0.05
phosphatase inhibitor-2=cytosolic regula	H3043F08	1.33	0.96	0.58	0.58		0.39	0.90	0.02	0.04
Mus musculus eukaryotic translation init	H3002F06	0.81	0.92	0.58	0.58		0.54	0.79	0.01	0.02
Homo sapiens mRNA; cDNA DKFZp564B0371 (f	H3057G09	1.03	0.89	0.68	0.58		0.90	0.45	0.01	0.01
REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CH	H3012C10	0.71	0.84	0.76	0.57		0.07	0.32	0.20	0.02
M.musculus mRNA for p80 Ku autoantigen	H3027G11	0.89	0.81	0.88	0.57		0.29	0.05	0.53	0.02
Human DNA sequence from clone 705O1 on c	H3022C07	0.72	0.88	0.64	0.57		0.07	0.76	0.23	0.02
Homo sapiens splicing factor, arginine/s	H3046B09	0.99	0.74	0.79	0.57		0.96	0.25	0.15	0.05
Mus musculus Tousled-like kinase (Arabid	H3137A01	1.30	0.76	0.70	0.57		0.47	0.45	0.12	0.00
Human DNA sequence from clone RP4-667H12	H3118H04	0.90	0.66	0.59	0.56		0.84	0.49	0.03	0.00
Homo sapiens disabled-2 gene, complete c	H3112G10	1.28	1.20	0.86	0.56		0.07	0.10	0.26	0.01
Mus musculus myristoylated alanine rich	H3113D09	0.78	0.88	0.91	0.56		0.04	0.26	0.69	0.01
Sprague-Dawley (clone LRB13) RAB14 mRNA,	H3137C05	1.25	0.79	0.69	0.56		0.46	0.04	0.08	0.04
Unknown	H3041B12	1.07	0.88	0.91	0.56		0.71	0.60	0.56	0.01
Homo sapiens cDNA FLJ11333 fis, clone PL	H3103E10	1.06	0.96	0.54	0.56		0.72	0.70	0.01	0.00
Homo sapiens mRNA, expressed in fibrobla	H3157A06	1.03	0.66	0.58	0.56		0.90	0.25	0.03	0.03
M.musculus gene encoding endonuclease G	H3021D08	1.03	0.74	0.68	0.56		0.91	0.34	0.17	0.00
Mus musculus natural resistance associat	H3029B01	1.06	0.90	0.73	0.56		0.78	0.75	0.16	0.05
Mus musculus mitochondrion, complete gen	H3096C07	1.02	0.85	0.77	0.56		0.89	0.16	0.04	0.02
Homo sapiens chromosome 17, clone 297N7,	H3029B06	1.24	0.90	0.58	0.55		0.18	0.49	0.09	0.05
Homo sapiens transferrin receptor (TFRC)	H3060A09	1.07	0.72	0.98	0.55		0.76	0.08	0.93	0.05
Homo sapiens translocated promoter regio	H3045G06	1.10	0.70	0.67	0.55		0.48	0.05	0.08	0.05
human STS WI-14908	H3020B11	0.91	0.83	0.73	0.55		0.52	0.27	0.14	0.01

Table F. Genes significantly influenced by Hypoxia treatment in HIF1a -/- cells (cont.)

Human DNA sequence from clone RP4-718P11	H3037D03	0.93	0.74	0.75	0.55		0.80	0.31	0.15	0.04
Mus musculus suppressor of Lec15 homolog	H3090D12	0.92	0.70	0.66	0.55		0.88	0.50	0.05	0.01
human STS SHGC-32238	H3107C05	1.21	1.01	0.75	0.55		0.16	0.94	0.16	0.03
Homo sapiens retinoic acid repressible p	H3046A01	1.11	1.04	0.88	0.55		0.34	0.66	0.49	0.05
Mus musculus phosphatase and tensin homo	H3086A07	1.00	0.69	0.89	0.55		0.98	0.10	0.66	0.01
Homo sapiens dystonia 1, torsion (autoso	H3143F02	1.26	1.03	0.73	0.54		0.62	0.95	#DIV/0!	0.00
Mus musculus chaperonin 10 mRNA, complet	H3005A04	1.03	1.00	0.69	0.54		0.88	1.00	0.30	0.02
Homo sapiens *** SEQUENCING IN PROGRESS	H3078C09	0.81	0.66	0.57	0.54		0.54	0.27	0.02	0.02
Human DNA sequence from 4PTEL, Huntingto	H3063B03	1.19	1.04	0.76	0.54		#DIV/0!	0.87	#DIV/0!	0.02
Homo sapiens cullin 3 (CUL3) mRNA	H3104A12	1.31	0.88	0.59	0.53		0.42	0.57	0.10	0.04
Rat tryptophan-2,3-dioxygenase mRNA, com	H3008C07	0.69	0.97	0.62	0.53		0.14	#DIV/0!	0.10	0.02
N.tabacum mRNA for elongation factor 1-a	H3042F09	0.80	0.64	0.63	0.53		0.48	0.24	0.03	0.02
Mus musculus glycosyl-phosphatidyl-inosi	H3106B06	1.01	0.85	0.67	0.53		0.98	0.55	0.06	0.03
Mus musculus platelet derived growth fac	H3140C02	0.75	0.89	0.69	0.52		0.17	0.54	0.41	0.01
Mus musculus H19 and muscle-specific Nct	H3144B06	1.13	0.99	0.62	0.52		0.64	0.98	0.17	0.03
Homo sapiens microsomal glutathione S-tr	H3157D12	0.84	0.99	0.48	0.52		0.40	0.96	0.03	0.02
Homo sapiens cDNA FLJ11345 fis, clone PL	H3042H12	0.91	0.97	0.55	0.52		0.76	0.92	0.03	0.03
Genomic sequence for Arabidopsis thalian	H3120B12	0.89	0.75	0.60	0.52		0.69	0.46	0.08	0.04
H.sapiens gene for U5 snRNP-specific 200	H3142C08	0.94	0.84	0.70	0.51		0.65	0.20	0.07	0.02
Human hVps41p (HVPS41) mRNA, complete cd	H3097C08	0.94	0.74	0.56	0.50		0.89	0.47	0.11	0.05
Cricetinae gen. sp. insulin receptor tyr	H3095F09	0.90	0.76	0.55	0.50		0.59	0.14	0.02	0.03
Caenorhabditis elegans cosmid T23F2	H3135C05	1.28	0.80	0.69	0.50		0.60	0.37	0.08	0.04
CREB-binding protein [mice, brain, mRNA	H3075G02	0.97	0.77	0.63	0.50		0.74	0.08	0.12	0.04
Mus musculus scmh1 mRNA for sex comb on	H3113B01	1.05	0.72	0.84	0.50		0.85	0.31	0.60	0.04
Human mRNA for NADPH-flavin reductase, c	H3048G11	0.75	0.71	0.53	0.50		0.10	0.03	0.03	0.03
Unknown	H3093B08	1.32	0.67	0.44	0.49		#DIV/0!	0.31	0.18	0.01
Homo sapiens BAC clone CTA-242D1 from 7q	H3095E03	0.98	0.55	0.83	0.49		#DIV/0!	#DIV/0!	#DIV/0!	0.05
Mus musculus tuftelin 1 (Tuft1), mRNA	H3101F11	1.14	0.71	0.57	0.49		0.62	0.12	0.07	0.05
Homo sapiens cyclin-dependent kinase inh	H3115G07	0.84	0.64	0.55	0.49		0.48	0.12	0.01	0.01
Human autoantigen mRNA, complete cds	H3066G06	1.24	0.83	0.74	0.49		0.09	0.24	0.27	0.01
Human DNA from chromosome 19-specific PA	H3038F04	0.91	0.79	0.74	0.48		0.70	0.40	0.29	0.05
Mus musculus protein tyrosine phosphatas	H3129A06	0.67	0.68	0.67	0.48		0.13	0.15	0.10	0.03
Homo sapiens clone NH0032P22, complete s	H3073G01	0.93	0.80	0.71	0.48		0.74	0.20	0.12	0.01
Mus musculus tumor-suppressing subchromo	H3022A10	0.78	0.73	0.40	0.48		0.39	0.37	0.07	0.01
Vitis vinifera cultivar Danuta VINE-1 re	H3153B09	1.04	0.89	0.86	0.47		0.74	0.56	0.65	0.05
Homo sapiens chromosome 17, clone RP11-4	H3081C11	0.82	0.75	0.59	0.47		0.39	0.20	0.08	0.05
Homo sapiens Putative prostate cancer tu	H3093G07	0.89	0.69	0.53	0.47		0.79	0.43	0.08	0.03
Caenorhabditis elegans cosmid Y53H1C, co	H3110E06	1.01	0.76	0.63	0.47		0.94	0.13	0.02	0.04
Mus musculus talin (Tln), mRNA	H3130H06	0.69	0.63	0.67	0.47		#DIV/0!	0.69	0.47	0.02
Mus musculus BTB and CNC homology 2 (Bac	H3135A04	0.91	0.74	0.52	0.46		0.81	0.44	0.06	0.02
Homo sapiens choline/ethanolaminephospho	H3069G01	1.14	0.79	0.61	0.46		0.81	0.66	0.14	0.05
Fugu rubripes transcription factor (SLP-	H3133B12	0.71	0.79	0.81	0.45		0.12	0.19	0.50	0.03
Homo sapiens cDNA FLJ10747 fis, clone NT	H3093B11	1.03	0.82	0.67	0.44		0.91	0.36	0.07	0.02
Heme oxygenase II	H3109G11	1.03	0.76	0.54	0.43		0.96	0.60	0.05	0.05
Mus musculus cysteine rich intestinal pr	H3108G04	0.91	0.93	0.52	0.43		0.33	0.34	0.10	0.05
Mus musculus glyceraldehyde-3-phosphate	H3072A08	1.14	3.11	0.57	0.43		0.73	0.14	0.10	0.01
Homo sapiens nuclear body protein Sp140	H3140G12	1.46	1.35	0.59	0.43		0.16	0.49	0.12	0.01
Mus musculus membrane component, surface	H3098B01	0.70	0.79	0.60	0.42		0.00	0.05	0.04	0.01
Homo sapiens 12p12-27.2-31.7 BAC RPC11-	H3020F03	0.69	0.65	0.77	0.42		0.66	#DIV/0!	0.28	0.03
Rattus norvegicus prostaglandin F2a rece	H3056D11	0.80	1.04	0.69	0.41		0.18	0.84	0.31	0.03
Drosophila melanogaster genomic scaffold	H3064A10	1.01	0.86	0.89	0.41		0.97	0.53	0.72	0.04
Homo sapiens clone UWGC:djs124 from 7p14	H3140A03	0.87	1.05	0.80	0.38		0.47	0.80	0.51	0.03
Mus musculus H19 and muscle-specific Nct	H3144B07	2.20	2.42	0.35	0.33		0.03	0.10	0.00	0.00

Table G. Genes significantly influenced by Cobalt in HIF1a -/- cells

Name	ID	Fold Changes				TTEST			
		W-Co	W-H	N-Co	N-H	W-Co	W-H	N-Co	N-H
R.norvegicus mRNA for RNA polymerase II-	H3136B02	1.15	0.89	2.25	1.41	0.49	0.60	0.02	0.17
Metallothionein-I (image 1052401)	A-2031	2.81	1.78	2.13	1.56	0.00	0.00	0.02	0.07
Mouse normal c-myc gene and translocated	H3076D10	1.12	1.07	1.97	1.12	0.32	0.64	0.00	0.43
Homo sapiens PAC clone RP4-791C19 from 7	H3084A12	1.55	1.27	1.80	1.38	0.14	0.17	0.03	0.25
Homo sapiens PAC B39I12 derived from chr	H3019E03	1.38	0.78	1.76	1.02	0.14	0.26	0.03	0.91
Caenorhabditis elegans cosmid F17C8, com	H3139E10	0.89	0.91	1.63	1.31	0.33	0.49	0.04	0.19
Homo sapiens ATPase, H+ transporting, ly	H3140C11	1.68	0.98	1.62	1.29	0.00	0.90	0.01	0.05
Arabidopsis thaliana chromosome III BAC	H3034H05	1.35	1.13	1.61	1.44	0.18	0.58	0.04	0.02
H beta 58=essential for embryogenesis [m	H3138G07	1.38	0.85	1.59	1.33	0.12	0.31	0.05	0.03
Homo sapiens Smad6 protein (SMAD6) gene,	H3104B08	1.33	0.82	1.56	1.07	0.08	0.26	0.05	0.41
Homo sapiens cDNA FLJ20579 fis, clone RE	H3021B06	1.32	1.41	1.56	1.21	0.12	0.09	0.00	0.08
Campylobacter jejuni NCTC11168 complete	H3024G12	1.68	1.18	1.52	1.51	0.04	0.52	0.04	0.29
human STS SHGC-31539	H3157D09	1.19	0.84	1.52	0.94	0.36	0.48	0.00	0.63
Human DNA sequence *** SEQUENCING IN PRO	H3081A11	0.89	0.92	1.51	1.08	0.50	0.61	0.04	0.68
M.musculus mRNA for cellular nucleic aci	H3117E04	1.12	0.88	1.51	1.34	0.36	0.25	0.02	0.08
Mus musculus disabled homolog 1 (Drosoph	H3036B09	0.91	0.95	1.50	1.15	0.61	0.79	0.04	0.51
Mus musculus vacuolar adenosine triphosp	H3021E11	1.20	1.01	1.49	1.52	0.20	0.94	0.00	0.01
Mus musculus major histocompatibility lo	H3107B03	1.07	1.00	1.48	1.45	0.73	0.98	0.04	0.03
Homo sapiens chromosome 4 clone C0162P16	H3132B08	1.15	1.09	1.47	1.27	0.43	0.69	0.03	0.21
Rattus norvegicus mRNA for cystathionine	H3103D05	2.64		1.46	2.11	#DIV/0!	#DIV/0!	0.00	0.06
Rattus norvegicus outer mitochondrial me	H3038G11	1.07	0.78	1.44	1.43	0.76	0.33	0.04	0.03
Homo sapiens KIAA0396 mRNA, partial cds	H3029F04	1.03	0.97	1.43	1.09	0.83	0.75	0.01	0.44
Human mRNA for KIAA0110 gene, complete c	H3125H04	1.43	1.21	1.42	1.06	0.10	0.42	0.05	0.77
Mus musculus solute carrier family 30 (z	H3157E05	1.00	0.87	1.42	1.07	1.00	0.28	0.02	0.69
Mus musculus nuclear factor of kappa lig	H3026A08	1.23	1.11	1.41	0.99	0.10	0.30	0.03	0.97
Homo sapiens Xp22-83 BAC GSHB-324M7 (Gen	H3130C12	0.87	0.85	1.41	1.11	0.60	0.49	0.05	0.52
Rattus norvegicus non-muscle alpha-actin	H3018E09	1.05	1.01	1.41	1.01	0.77	0.94	0.03	0.91
Mus musculus crystallin, alpha 2 (Crya2)	H3143B04	1.38	1.37	1.40	0.95	0.06	0.08	0.05	0.80
Mouse kidney ornithine decarboxylase mRN	H3028F05	1.40	0.98	1.40	1.68	0.01	0.88	0.00	0.02
Mus musculus metastasis associated 1-lik	H3021B10	1.14	0.99	1.38	0.97	0.48	0.97	0.03	0.87
Mus musculus transforming growth factor	H3066H08	0.59	0.89	1.38	0.91	#DIV/0!	0.72	0.04	#DIV/0!
Mus musculus chromosome 7, clone 19K5, c	H3094D03	1.14	0.94	1.37	1.05	0.42	0.59	0.02	0.69
Human DNA sequence from PAC 211D12 on ch	H3080D05	1.32	0.83	1.36	0.98	0.09	0.28	0.02	0.86
Campylobacter jejuni NCTC11168 complete	H3010G10	0.95	0.96	1.36	1.02	0.61	0.67	0.03	0.82
Mus musculus DBCCR1 (DBCCR1) mRNA, compl	H3155E12	0.87	0.87	1.35	1.08	0.25	0.36	0.05	0.50
NMDA receptor glutamate-binding subunit	H3151H12	1.34	1.06	1.35	1.78	0.03	0.55	0.00	0.00
Homo sapiens cDNA FLJ20625 fis, clone KA	H3106H11	1.39	1.27	1.35	1.42	0.06	0.25	0.05	0.04
Homo sapiens PAC clone RP4-630F1 from 7q	H3021A06	1.05	0.97	1.34	1.08	0.62	0.70	0.02	0.34
Homo sapiens chromosome 17, clone hRPK.6	H3049F11	1.40	1.16	1.33	1.43	0.00	0.30	0.05	0.01
Mus musculus synectin mRNA, complete cds	H3122F05	1.41	1.08	1.33	1.42	0.06	0.78	0.03	0.06
Homo sapiens chromosome 16 BAC clone CIT	H3114E05	0.79	0.75	1.32	1.33	0.36	0.17	0.01	0.25
Dictyostelium discoideum HIV1 TAT-bindin	H3095B11	1.25	1.02	1.32	1.11	0.17	0.87	0.02	0.39
Homo sapiens cDNA FLJ10968 fis, clone PL	H3093F01	1.06	1.03	1.31	1.30	0.72	0.86	0.03	0.10
Mus musculus myeloblastosis oncogene-lik	H3144E01	1.20	1.09	1.31	1.08	0.22	0.62	0.04	0.54
Mus musculus POU domain, class 2, transc	H3058B08	1.18	0.95	1.30	1.16	0.23	0.73	0.04	0.33
Mus musculus androgen regulated vas defe	H3029F03	0.89	0.94	1.30	1.08	0.20	0.61	0.02	0.57
Caenorhabditis elegans cosmid Y105C5B, c	H3108H07	1.17	1.40	1.27	1.39	0.39	0.13	0.04	0.01
Mus wagneri mRNA for heat shock protein	H3049B07	1.05	0.77	1.27	1.15	0.79	0.25	0.03	0.37
Human DNA sequence from clone CTA-206C7	H3143H05	1.02	0.99	1.27	1.42	0.93	0.98	0.01	0.13
Mus musculus ATPase-like vacuolar proton	H3027A11	1.14	0.95	1.27	1.26	0.53	0.77	0.04	0.06
Caenorhabditis elegans cosmid T12F5	H3002C03	1.16	0.94	1.24	1.20	0.34	0.59	0.04	0.12
Homo sapiens MVP gene, promoter region	H3029A09	0.88	0.91	1.23	0.91	0.20	0.40	0.02	0.23
Mouse chromatin nonhistone high mobility	H3029B11	0.78	0.94	1.22	1.16	0.02	0.45	0.02	0.12
Mus musculus mRNA for neural specific sr	H3029G08	1.18	0.94	1.22	1.16	0.07	0.63	0.05	0.23
Homo sapiens genomic DNA, chromosome 21,	H3060F08	1.12	1.13	1.20	1.04	0.54	0.44	0.04	0.79
Human PC6A protease (hPC6) mRNA, complet	H3001B01	0.93	0.88	1.13	0.89	0.60	0.41	0.04	0.09
Homo sapiens chromosome 16, cosmid clone	H3141B10	1.33	1.02	0.90	0.64	0.53	0.94	0.03	0.12
Human chromosome 14 DNA sequence *** IN	H3150C11	0.82	1.07	0.88	1.04	0.24	0.61	0.04	0.68
Drosophila melanogaster DNA sequence (P1	H3031B02	1.11	1.07	0.86	0.97	0.09	0.38	0.04	0.61
Mouse mRNA for TBPIP, complete cds	H3111B08	1.07	1.02	0.85	0.83	0.36	0.86	0.04	0.08
{clone E572, estrogen induced gene} [rat	H3091D04	1.01	0.86	0.84	0.92	0.88	0.07	0.04	0.21
Homo sapiens mRNA; cDNA DKFZp434P231 (fr	H3016H12	0.98	0.90	0.84	0.90	0.58	0.19	0.04	0.12
Mus musculus mRNA for erythroid differen	H3101A07	1.03	0.90	0.83	0.76	0.86	0.48	0.05	0.04

Table G. Genes significantly influenced by Cobalt in HIF1a -/- cells (cont.)

Mus musculus (clone C7/B9) S-adenosyl ho	H3014E01	0.92	0.91	0.83	0.92		0.46	0.27	0.04	0.30
Mus musculus mRNA for mtrpd, complete cd	H3004A06	0.86	0.98	0.83	1.00		0.21	0.87	0.05	0.98
Mus musculus adenosine deaminase (ADA) g	H3017G11	0.92	0.80	0.83	0.92		0.36	0.04	0.03	0.35
H.sapiens mRNA for pur alpha extended 3'	H3008B08	0.99	0.92	0.83	0.82		0.95	0.24	0.04	0.04
Mus musculus hydroxylacyl-Coenzyme A deh	H3129H03	0.93	1.01	0.82	0.94		0.52	0.93	0.04	0.55
Human mRNA for KIAA0253 gene, partial cd	H3012F08	1.03	1.00	0.82	1.03		0.73	0.96	0.04	0.76
Homo sapiens 3q25-26 BAC CITB-371O18 (Ca	H3051D06	1.07	0.89	0.82	0.92		0.57	0.29	0.04	0.38
Mus musculus villin 2 (Vil2), mRNA	H3014F03	1.02	1.04	0.82	0.76		0.88	0.79	0.03	0.00
Homo sapiens genomic DNA, chromosome 21q	H3051G11	0.97	0.83	0.81	0.82		0.84	0.17	0.03	0.08
Homo sapiens ATPase, Cu++ transporting,	H3114A07	1.06	1.07	0.81	0.81		0.62	0.58	0.04	0.08
Homo sapiens chromosome 22q11 clone b48,	H3013G01	0.99	1.04	0.81	0.94		0.90	0.72	0.05	0.77
Homo sapiens 12 seeders BAC RP11-19E18 (H3015B02	0.93	0.92	0.81	0.91		0.50	0.46	0.02	0.30
Arabidopsis thaliana BAC T1N24	H3011D09	1.13	1.04	0.81	1.03		0.31	0.59	0.01	0.66
Rattus norvegicus mRNA for 26S proteasom	H3031D07	0.94	0.91	0.80	0.87		0.53	0.38	0.01	0.05
Mus musculus domesticus transcription fa	H3026B01	0.83	0.72	0.80	0.82		0.42	0.06	0.04	0.21
Clostridium sticklandii ORFX' (partial),	H3003B07	0.95	0.84	0.80	0.93		0.70	0.26	0.05	0.41
Mus musculus kinesin family member 3a (K	H3111B02	0.95	0.89	0.79	1.06		0.54	0.19	0.02	0.61
Mus musculus ubi-d4/requiem gene, exons	H3100G09	0.88	0.91	0.79	0.59		0.23	0.42	0.03	0.00
Homo sapiens mRNA for KIAA0516 protein,	H3156H02	1.04	1.12	0.79	1.17		0.71	0.28	0.04	0.16
H.sapiens mitogen inducible gene mig-2,	H3011B01	1.14	1.13	0.79	0.98		0.17	0.24	0.04	0.81
Homo sapiens chromosome 5, P1 clone 1308	H3059D01	0.86	0.89	0.79	0.89		0.27	0.48	0.04	0.27
Caenorhabditis elegans cosmid T21E8, com	H3010H07	0.88	0.88	0.79	0.95		0.21	0.40	0.03	0.54
Human DNA sequence from clone 654H19 on	H3012B05	0.85	0.88	0.79	1.00		0.17	0.33	0.05	0.96
Mus musculus inner centromere protein IN	H3008C04	0.92	0.89	0.79	0.83		0.37	0.27	0.04	0.08
Hamster (clone pBH21) RCC1 mRNA, complet	H3014B08	0.98	0.91	0.78	0.95		0.76	0.23	0.02	0.59
Human DNA sequence from clone RP11-150A6	H3071F04	1.05	0.92	0.78	0.83		0.66	0.49	0.02	0.05
Human DNA sequence from clone RP4-742C19	H3014H11	0.87	0.90	0.78	0.81		0.21	0.50	0.04	0.03
Mus musculus calmodulin synthesis (CaM)	H3006H07	1.01	0.96	0.78	0.90		0.86	0.53	0.01	0.08
Human chromosome 14 DNA sequence *** IN	H3159A07	0.92	0.99	0.78	0.76		0.39	0.93	0.05	0.03
rat carboxypeptidase-a: 5' gene flank(dn	H3051B02	1.06	0.89	0.78	0.83		0.62	0.34	0.03	0.08
Mus cookii linear IgA disease antigen ho	H3002A06	0.84	1.04	0.78	0.96		0.07	0.73	0.02	0.71
Oryctolagus cuniculus mannosyl-oligosacc	H3013H03	0.95	0.98	0.78	0.96		0.66	0.86	0.02	0.78
Mouse mRNA for stromal cell derived prot	H3003G06	0.96	0.92	0.78	1.00		0.56	0.30	0.00	0.99
Rattus norvegicus calcium- and integrin-	H3051F03	1.03	0.90	0.77	1.40		0.87	0.30	0.02	0.15
Homo sapiens Chromosome 16 BAC clone CIT	H3014D07	0.68	0.59	0.77	0.88		0.14	0.09	0.05	0.18
Rattus norvegicus guanosine monophosphat	H3051G07	1.00	0.95	0.77	0.90		0.99	0.38	0.03	0.28
Mus musculus mitochondrion, complete gen	H3096C07	1.02	0.85	0.77	0.56		0.89	0.16	0.04	0.02
Homo sapiens cDNA FLJ10771 fis, clone NT	H3011D04	0.96	0.95	0.77	1.03		0.65	0.54	0.01	0.72
M.musculus mRNA for cyclin F	H3020E11	0.78	0.95	0.77	1.04		0.04	0.57	0.02	0.77
Mouse N-acetylglucosamine galactosyltran	H3014F06	1.05	0.98	0.76	0.95		0.50	0.76	0.02	0.51
Homo sapiens Chromosome 16 BAC clone CIT	H3071F06	1.03	0.95	0.76	0.82		0.78	0.67	0.05	0.10
Drosophila melanogaster genomic scaffold	H3002H01	0.94	0.88	0.76	0.96		0.74	0.49	0.03	0.71
Human chromosome 14 DNA sequence *** IN	H3111G08	0.88	0.89	0.76	1.02		0.31	0.48	0.03	0.86
Mus musculus hairy-related transcription	H3010G03	0.44	0.41	0.76	0.94		0.37	0.35	0.05	0.66
Drosophila melanogaster, chromosome 2R,	H3014F09	1.02	1.24	0.76	0.99		0.89	0.58	0.02	0.91
Homo sapiens Xq28 BAC PAC and cosmid clo	H3146A07	1.08	0.95	0.76	0.73		0.60	0.78	0.02	0.03
Drosophila melanogaster BAC clone BACR25	H3016F10	1.17	0.99	0.76	1.02		0.19	0.87	0.01	0.83
Caenorhabditis elegans cosmid B0399, com	H3012A08	0.95	0.85	0.75	0.89		0.66	0.17	0.03	0.35
Arabidopsis thaliana genomic DNA, chromo	H3010F02	0.95	0.93	0.75	0.91		0.64	0.58	0.03	0.30
Mus musculus protocadherin 2C mRNA, comp	H3151G09	0.97	0.96	0.75	0.64		0.88	0.90	0.01	0.05
Mus musculus chromosome 17 BAC citb20h22	H3059B08	0.96	0.95	0.75	1.01		0.69	0.71	0.03	0.98
Arabidopsis thaliana chromosome III BAC	H3034B06	0.88	0.93	0.75	0.70		0.70	0.79	0.01	0.18
Homo sapiens chromosome 16, cosmid clone	H3140C05	0.95	1.04	0.75	0.59		0.57	0.72	0.03	0.00
Homo sapiens cDNA FLJ10909 fis, clone OV	H3071D02	1.01	0.90	0.75	0.81		0.83	0.26	0.01	0.04
Homo sapiens PEA15 protein (PEA15) gene,	H3012H06	0.93	0.90	0.75	0.82		0.49	0.30	0.05	0.12
Homo sapiens cDNA FLJ20591 fis, clone KA	H3010G01	0.99	0.79	0.75	0.79		0.96	0.18	0.04	0.14
Homo sapiens 12p BAC RPC111-75L1 (Roswel	H3011G10	0.89	0.92	0.74	1.02		0.31	0.36	0.02	0.89
Cricetulus griseus arsenite-resistance p	H3039B01	0.99	0.72	0.74	0.53		0.87	0.05	0.04	0.13
Human BAC clone CTB-13L3 from 7q21, comp	H3071B03	0.94	0.88	0.74	0.89		0.63	0.25	0.01	0.23
Homo sapiens cDNA FLJ20339 fis, clone HE	H3017H06	0.91	0.88	0.74	1.02		0.55	0.47	0.03	0.85
S.pombe chromosome II cosmid c30B4	H3117D10	1.05	1.00	0.74	0.79		0.70	0.98	0.01	0.25
Drosophila melanogaster DNA sequence (P1	H3135C09	0.90	1.03	0.74	0.91		0.26	0.79	0.04	0.53
Campylobacter jejuni NCTC11168 complete	H3070D10	1.17	0.98	0.74	1.26		0.10	0.93	0.02	0.65
Mus musculus glycerol-3-phosphate acyltr	H3071H04	0.97	0.80	0.74	0.84		0.78	0.12	0.01	0.11
Mouse mRNA for N-ras protein (exons 1 -	H3132C10	0.70	0.85	0.74	0.74		#DIV/0!	0.44	0.02	#DIV/0!

Table G. Genes significantly influenced by Cobalt in HIF1a -/- cells (cont.)

Mus musculus transcription factor SP1 (S	H3100E07	1.00	1.02	0.73	0.84		1.00	0.90	0.00	0.19
Homo sapiens cDNA FLJ10177 fis, clone HE	H3051D12	0.98	0.84	0.73	0.85		0.85	0.22	0.04	0.17
Homo sapiens genomic DNA, chromosome 21q	H3111G10	1.02	0.97	0.73	1.05		0.86	0.85	0.03	0.78
Mus musculus cysteine-rich repeat-contai	H3007D06	0.97	0.94	0.73	0.89		0.76	0.59	0.03	0.36
Human DNA sequence from clone 112K5 on c	H3010F06	0.84	0.99	0.73	0.95		0.31	0.98	0.01	0.59
Rat c-erbA-alpha-2 protein mRNA, complet	H3129H04	0.96	1.04	0.73	0.98		0.50	0.70	0.00	0.88
Homo sapiens spliceosome-associated fact	H3151G01	1.28	1.29	0.73	0.88		0.18	0.09	0.04	0.42
Homo sapiens plexin B1 (PLXNB1), mRNA	H3015D06	0.94	1.01	0.73	0.91		0.66	0.94	0.02	0.41
Human DNA sequence from clone 423B22 on	H3003F03	0.90	0.85	0.73	0.85		0.44	0.20	0.03	0.20
Mus musculus protein kinase C, delta (Pk	H3059B03	0.89	0.86	0.72	0.99		0.33	0.17	0.02	0.91
Chlamydomonas eugametos mitochondrion, c	H3014G05	0.96	1.02	0.72	1.02		0.65	0.88	0.03	0.86
Rattus norvegicus unknown mRNA	H3006A03	1.08	0.95	0.72	1.06		0.58	0.75	0.04	0.75
Caenorhabditis elegans cosmid Y106G6H, c	H3111F06	0.99	0.95	0.72	0.89		0.91	0.78	0.04	0.48
Homo sapiens cDNA FLJ10092 fis, clone HE	H3014A10	0.79	0.83	0.72	0.80		0.11	0.36	0.03	0.08
Mus musculus small inducible cytokine A2	H3159A01	0.79	0.77	0.72	0.78		0.66	0.61	0.05	0.32
Homo sapiens clone 24416 mRNA sequence	H3059A08	0.97	0.92	0.72	0.95		0.86	0.64	0.03	0.77
Mus musculus early development regulator	H3014D10	0.99	0.86	0.72	0.95		0.91	0.34	0.02	0.63
Homo sapiens integral type I protein (P2	H3114C02	1.10	0.91	0.72	1.22		0.67	0.64	0.01	0.27
Arabidopsis thaliana DNA chromosome 3, B	H3017D06	0.85	0.90	0.72	0.90		0.32	0.59	0.04	0.38
Mus musculus secretory carrier membrane	H3015G07	1.07	0.82	0.72	0.90		0.72	0.09	0.05	0.35
Human DNA sequence from clone RP1-186O1	H3006G08	0.89	0.83	0.72	0.92		0.37	0.28	0.05	0.58
human STS SHGC-33056	H3138C09	1.12	1.01	0.72	0.80		0.77	0.99	0.03	0.09
Mouse mRNA for germ cell specific lamin	H3017F05	1.00	1.02	0.72	0.77		1.00	0.91	0.05	0.04
glyoxalase I [human, HeLa cells, mRNA Pa	H3012F03	0.97	0.98	0.71	0.82		0.78	0.83	0.03	0.13
Mus musculus hypermethylated in cancer 1	H3004D11	0.87	0.76	0.71	0.95		0.30	0.10	0.03	0.71
Homo sapiens signal recognition particle	H3014E12	0.85	0.87	0.71	0.72		0.14	0.37	0.04	0.01
Mouse DNA for lamin B1, exon 11, complet	H3008H09	0.89	0.93	0.71	0.92		0.31	0.44	0.01	0.44
Homo sapiens cosmid from Xq28, complete	H3005G09	0.86	0.65	0.71	0.96		0.16	0.00	0.03	0.79
Mus musculus prolactin-like protein E (P	H3008F06	0.96	0.70	0.71	0.91		0.74	0.04	0.03	0.42
Mus musculus capping protein beta-subuni	H3020A01	0.94	0.84	0.71	0.79		0.56	0.08	0.01	0.12
Homo sapiens PAC clone RP5-847G17 from 7	H3051A09	0.87	0.86	0.71	0.89		0.37	0.36	0.04	0.45
Zea mays mRNA for cysteine protease comp	H3059B05	0.74	0.81	0.71	0.98		0.08	0.25	0.03	0.89
Homo sapiens cDNA FLJ10273 fis, clone HE	H3114G01	1.05	0.50	0.71	0.86	#DIV/0!		0.20	0.04	0.55
Mus musculus opioid receptor, delta 1 (O	H3004F10	0.87	0.72	0.71	0.76		0.43	0.09	0.05	0.08
Mus musculus (clone pVZmSin3A) mSin3A mR	H3086E04	0.88	0.69	0.70	0.86		0.56	0.06	0.04	0.44
Arabidopsis thaliana chromosome II secti	H3059G01	0.89	0.81	0.70	0.90		0.53	0.34	0.03	0.44
Homo sapiens genomic DNA, chromosome 21q	H3117A09	0.78	0.57	0.70	0.82		0.37	0.05	0.05	0.29
Homo sapiens chromosome 19, overlapping	H3008D09	0.88	0.82	0.70	0.74		0.43	0.43	0.05	0.05
Homo sapiens DNA sequence from PAC 333H9	H3002E03	0.90	1.04	0.70	0.76		0.65	0.86	0.03	0.14
Mus musculus deoxyribonuclease 1-like 3	H3016H03	1.14	1.08	0.70	0.91		0.48	0.71	0.01	0.25
Mus musculus delta-aminolevulinate dehyd	H3013F01	0.82	1.04	0.69	0.80		0.27	0.81	0.02	0.11
Mus musculus BAC GSMB-407A4 (Genome Sys	H3159C07	0.97	0.74	0.69	0.84		0.83	0.12	0.04	0.28
M.musculus 45S pre rRNA gene	H3004H10	0.90	0.75	0.69	0.88		0.41	0.11	0.04	0.33
Mus musculus TIMELESS protein mRNA, comp	H3022A12	0.84	0.71	0.69	0.71		0.21	0.05	0.02	0.16
Mus musculus mRNA for AMY-1, complete cd	H3006A10	0.85	0.77	0.69	0.80		0.33	0.18	0.03	0.07
Mus musculus cyclin-dependent kinase 5 a	H3059G02	0.92	0.87	0.69	0.88		0.51	0.40	0.04	0.35
Homo sapiens thyroid receptor interactor	H3071D04	1.03	0.99	0.69	0.81		0.83	0.94	0.01	0.06
Clostridium botulinum P-21, P-47 ntinh, b	H3022D07	0.86	0.93	0.69	1.10		0.31	0.65	0.03	0.66
Homo sapiens ferritin-like pseudogene, p	H3016D01	0.90	0.81	0.69	0.94		0.41	0.24	0.03	0.65
Homo sapiens expressed in human embryoni	H3135C10	0.88	1.06	0.69	0.94		0.23	0.62	0.01	0.65
Rattus norvegicus cca1 mRNA, complete cd	H3007A08	0.90	0.86	0.69	0.81		0.30	0.30	0.02	0.13
Mus musculus focal adhesion kinase (Fadk	H3027G04	0.92	0.97	0.69	1.11		0.63	0.61	0.02	0.76
Homo sapiens chromosome 8 clone PAC 87.2	H3051B08	1.04	0.94	0.69	0.80		0.82	0.65	0.02	0.14
Homo sapiens cDNA FLJ20693 fis, clone KA	H3079C12	1.15	0.99	0.69	0.59		0.47	0.97	0.05	0.07
Homo sapiens genomic DNA, chromosome 21q	H3071G04	1.02	0.93	0.69	0.80		0.91	0.64	0.05	0.18
Homo sapiens mRNA for KIAA0546 protein,	H3153E10	0.85	0.74	0.68	0.98		0.39	0.07	0.02	0.87
Homo sapiens mRNA; cDNA DKFZp564B0371 (f	H3057G09	1.03	0.89	0.68	0.58		0.90	0.45	0.01	0.01
Mus musculus peroxisomal/mitochondrial d	H3131A07	0.72	1.06	0.68	1.11		0.02	0.74	0.01	0.51
human STS WI-15054	H3071H12	0.96	0.84	0.68	0.93		0.77	0.14	0.01	0.51
Homo sapiens polyamine modulated factor	H3012D03	1.19	1.01	0.68	0.83		0.33	0.96	0.03	0.16
Mus musculus ral guanine nucleotide diss	H3142C03	0.96	0.81	0.68	0.58		0.78	0.19	0.03	#DIV/0!
Homo sapiens chromosome 14 BAC containin	H3016D03	0.86	0.83	0.68	0.82		0.38	0.23	0.05	0.24
Human DNA sequence from clone 1103G7 on	H3117F08	1.01	0.78	0.68	0.57		0.97	0.27	0.01	0.07
Subacute sclerosing panencephalitis (SSP	H3010B02	0.88	0.81	0.68	0.68		0.34	0.30	0.01	0.01
Drosophila melanogaster (P1 DS07473 (D11	H3051H07	0.91	0.82	0.68	0.92		0.58	0.20	0.03	0.61

Table G. Genes significantly influenced by Cobalt in HIF1a -/- cells (cont.)

Mus musculus vacuolar adenosine triphosp	H3013B02	0.92	0.94	0.67	0.80		0.65	#DIV/0!	0.02	0.02
Homo sapiens mRNA for KIAA1137 protein,	H3017B04	0.92	1.02	0.67	0.77		0.43	0.86	0.05	0.12
Mus musculus secreted acidic cysteine ri	H3024A05	1.05	1.02	0.67	0.97		0.85	0.88	0.04	0.85
R.norvegicus (Sprague Dawley) ribosomal	H3027H07	1.02	0.94	0.67	1.04		0.90	0.68	0.03	0.81
Mouse ribosomal protein L30 gene, comple	H3030F06	1.65	0.76	0.67	0.73		#DIV/0!	0.24	0.02	0.30
Homo sapiens hect (homologous to the E6-	H3017D04	0.96	0.84	0.67	0.64		0.77	0.35	0.02	0.01
Human DNA sequence from clone RP1-181C24	H3007H05	0.90	0.92	0.67	0.81		0.47	0.67	0.02	0.13
Human DNA sequence from clone RP1-41P2 o	H3058C11	0.73	0.97	0.67	0.95		0.35	0.83	0.02	0.66
Mus musculus MAP kinase-activated protei	H3016F01	0.92	0.82	0.67	0.78		0.52	0.34	0.04	0.13
Rattus norvegicus clone C201 intestinal	H3011G08	1.00	0.75	0.67	0.91		1.00	0.17	0.04	0.45
Homo sapiens chromosome 17, clone hRPK.1	H3132E03	0.82	0.87	0.67	0.90		0.04	0.18	0.02	0.37
Rattus norvegicus protein associating wi	H3014A06	1.03	1.01	0.66	0.88		0.83	0.97	0.04	0.49
Homo sapiens chromosome 14 clones CTD-22	H3116D04	0.99	0.63	0.66	0.97		0.97	0.18	0.03	0.84
Mus musculus suppressor of Lec15 homolog	H3090D12	0.92	0.70	0.66	0.55		0.88	0.50	0.05	0.01
Mus musculus inhibitor of DNA binding 3	H3154E06	1.25	1.03	0.66	0.63		0.18	0.88	0.05	0.02
Homo sapiens ubiquitous TPR motif, X iso	H3062H04	1.39	0.88	0.66	0.60		#DIV/0!	0.83	0.05	0.26
Mus musculus Ena-vasodilator stimulated	H3133H01	0.98	1.12	0.66	1.40		0.92	0.36	0.03	0.06
Mus musculus evectin-2 (Evt2) mRNA, comp	H3146C11	0.95	1.11	0.66	0.93		0.59	0.21	0.00	0.53
Rattus norvegicus syntaxin 13 mRNA, comp	H3008A01	0.92	0.78	0.66	0.86		0.57	0.11	0.01	0.25
Homo sapiens chromosome 16 clone CIT978S	H3147H01	0.84	0.85	0.66	0.93		0.36	0.32	0.04	0.70
Mus musculus Cbp/p300-interacting transa	H3135G01	0.92	0.72	0.66	0.68		0.77	0.30	0.04	0.01
Human BAC clone CTB-191D16, complete seq	H3016E07	0.74	0.81	0.66	1.01		0.37	0.52	0.01	0.93
Homo sapiens PAC clone RP4-613I23 from 7	H3097A01	0.86	0.96	0.66	0.56		0.21	0.60	0.02	0.17
Homo sapiens chromosome 21 segment HS21C	H3005F05	0.98	0.89	0.66	0.90		0.91	0.57	0.03	0.52
Human chromosome 14 DNA sequence *** IN	H3139E03	0.86	1.16	0.66	1.08		0.27	0.09	0.04	0.61
Homo sapiens cDNA FLJ20423 fis, clone KA	H3095A06	1.10	1.10	0.66	1.18		0.55	0.43	0.05	0.38
Mus musculus signal transducer and activ	H3004E09	0.91	0.84	0.66	0.89		0.59	0.34	0.03	0.50
Rattus norvegicus mRNA for NaPi-2 beta,	H3159E08	0.75	0.73	0.66	1.12		0.26	0.24	0.05	0.50
Mus musculus adenylosuccinate lyase (Ads	H3008C12	0.90	0.82	0.66	0.96		0.49	0.65	0.01	0.83
Homo sapiens mRNA for KIAA1076 protein,	H3013E11	0.80	1.07	0.65	0.86		0.10	0.36	0.02	0.22
Homo sapiens cDNA FLJ20115 fis, clone CO	H3098D04	1.19	0.81	0.65	0.66		0.51	0.50	0.04	0.03
Mus musculus DNA from BAC 10818 containi	H3017C01	0.88	0.72	0.65	0.81		0.32	0.17	0.01	0.02
No Hits Found	H3139D03	0.82	0.92	0.65	0.94		0.26	0.61	0.05	0.75
Homo sapiens mRNA for farnesylated-prote	H3035F09	1.05	0.81	0.65	0.60		0.81	0.28	0.00	0.00
Rattus norvegicus caveolae-associated pr	H3036C12	1.25	1.33	0.65	1.12		0.30	0.12	0.02	0.60
Homo sapiens 12p13 PAC RPC111-726G1 (Ros	H3017H11	0.78	0.84	0.65	0.70		0.09	0.39	0.04	0.05
Mus musculus Bce-1 protein (Bce-1) mRNA,	H3103G12	1.10	0.76	0.65	0.58		#DIV/0!	0.48	0.05	#DIV/0!
Human clone 23867 mRNA sequence	H3083E01	0.88	0.99	0.65	0.84		0.42	0.95	0.02	0.33
Rattus norvegicus mRNA for BAT3, complet	H3005F09	0.94	0.88	0.65	0.97		0.68	0.49	0.01	0.84
Homo sapiens protein phosphatase 2A regu	H3153C10	0.86	0.74	0.65	0.83		0.49	0.05	0.00	0.27
Human inositol 1,3,4-trisphosphate 5/6-k	H3151B03	1.11	1.29	0.65	0.62		0.61	0.37	0.04	0.09
Homo sapiens GCN5 (general control of am	H3096E01	0.94	0.98	0.65	0.87		0.70	0.89	0.03	0.38
Human DNA sequence from clone 890O15 on	H3027G06	1.07	0.78	0.65	0.98		0.89	0.47	0.01	0.93
Homo sapiens genomic DNA, chromosome 21q	H3001D06	0.93	0.93	0.65	0.88		0.57	0.52	0.05	0.38
Mus musculus spindlin (Spin), mRNA	H3101A11	0.89	1.10	0.65	0.67		0.82	0.34	0.01	0.01
Homo sapiens chromosome 22q11 clone b461	H3036H06	1.19	0.97	0.64	0.56		0.41	0.91	0.01	0.19
Mus musculus nucleolar protein (MSP58) m	H3100H01	1.21	0.77	0.64	0.45		0.52	0.39	0.02	0.12
Homo sapiens 12p12 BAC RPC111-320J20 (Ro	H3065B07	1.32	0.86	0.64	0.67		0.21	0.57	0.04	0.05
Gallus gallus ovocleidin-116 mRNA, compl	H3094G03	0.97	0.81	0.64	0.63		0.86	0.27	0.04	#DIV/0!
No Hits Found	H3071H05	0.96	0.84	0.64	0.81		0.85	0.39	0.05	0.29
Arabidopsis thaliana BAC F6N23	H3155H03	1.05	1.17	0.64	1.22		0.74	0.26	0.02	0.18
Drosophila melanogaster, chromosome 3R,	H3141D04	1.09	0.95	0.64	0.94		0.64	0.80	0.03	0.76
Rat mRNA for cdc25A, complete cds	H3004B08	1.03	0.75	0.64	0.81		0.89	0.18	0.03	0.19
Homo sapiens dimethylglycine dehydrogena	H3158D01	0.79	1.28	0.64	0.76		0.09	0.24	0.03	0.09
Homo sapiens Chromosome 22q11.2 BAC Clon	H3070A01	0.98	0.76	0.64	0.77		0.89	0.04	0.01	0.13
Mus musculus leucine rich repeat (in FLI)	H3112H04	1.22	0.83	0.63	0.81		0.59	0.47	0.04	0.45
N.tabacum mRNA for elongation factor 1-a	H3042F09	0.80	0.64	0.63	0.53		0.48	0.24	0.03	0.02
Human DNA sequence from clone RP5-976O13	H3056B11	0.86	0.85	0.63	0.63		0.31	0.34	0.03	0.04
Homo sapiens mRNA for zinc finger protei	H3014D06	0.98	0.92	0.63	0.85		0.88	0.61	0.02	0.20
Saccharomyces cerevisiae chromosome VII,	H3102B06	1.38	0.91	0.63	0.65		0.36	0.70	0.01	0.30
Mus musculus mRNA for chemokine receptor	H3051E02	0.87	0.85	0.63	0.73		0.57	0.56	0.03	0.03
Caenorhabditis elegans cosmid Y53H1C, co	H3110E06	1.01	0.76	0.63	0.47		0.94	0.13	0.02	0.04
No Hits Found	H3107F07	0.99	0.98	0.63	1.06		0.94	0.90	0.02	0.73
Mus musculus Tnf receptor-associated fac	H3015E06	0.94	0.93	0.63	0.77		0.65	0.68	0.04	0.21
Mus musculus degenerative spermatocyte h	H3112F03	1.37	0.77	0.63	0.71		0.30	0.39	0.00	0.04

Table G. Genes significantly influenced by Cobalt in HIF1a -/- cells (cont.)

Rattus norvegicus beta-1,2-N-acetylgluco	H3010C12	0.97	0.99	0.63	0.68		0.83	0.95	0.05	0.06
Human DNA sequence from clone 1054A22 on	H3004E12	0.86	0.82	0.62	0.95		0.46	0.39	0.03	0.77
Homo sapiens T-cell, immune regulator 1	H3008B10	0.90	0.83	0.62	0.80		0.52	0.41	0.03	0.14
Rattus norvegicus mRNA for peroxisome as	H3156A09	0.84	1.04	0.62	0.96		0.70	0.91	0.01	0.92
Human DNA sequence from clone 162O13 on	H3135D03	0.96	0.93	0.62	0.54		0.91	0.84	0.04	0.06
Human chromosome 14 DNA sequence *** IN	H3139F07	1.02	0.82	0.62	0.60		0.91	0.33	0.01	0.01
Mus musculus iroquois related homeobox 3	H3006F12	0.96	0.80	0.62	0.78		0.77	0.31	0.01	0.10
Mus musculus ets variant gene 6 (TEL onc	H3154D06	0.98	0.98	0.62	0.79		0.90	0.96	0.00	0.40
Homo sapiens genomic DNA, chromosome 6p2	H3029D06	0.99	0.99	0.62	0.82		0.94	0.94	0.01	0.18
Mouse mRNA for prothymosin alpha	H3118B02	0.88	0.78	0.62	0.75		0.32	0.17	0.03	0.05
Homo sapiens PAC clone RP5-1093G23 from	H3065C09	1.26	0.76	0.62	0.53		0.48	0.13	0.01	0.09
Human DNA sequence from clone LA16-380F5	H3135F08	0.96	1.02	0.62	0.64		0.77	0.92	0.02	0.06
Mus musculus tyrosine 3-monooxygenase/tr	H3019H06	1.02	1.06	0.61	0.93		0.87	0.68	0.01	0.63
Rat mRNA for ribosomal protein L17	H3029F12	0.85	0.79	0.61	1.00		0.34	0.23	0.02	0.99
Arabidopsis thaliana chromosome II secti	H3155A08	0.74	1.51	0.61	0.84	#DIV/O!	#DIV/O!		0.01	0.37
Homo sapiens Rho GDP dissociation inhibi	H3131H01	0.77	1.00	0.61	0.88		0.15	0.98	0.02	0.42
NonO=non-POU domain-containing octamer-b	H3014D09	0.84	0.85	0.61	0.75		0.13	0.22	0.01	0.09
Mus musculus mitochondrion, complete gen	H3134H02	0.89	0.70	0.61	0.56		0.76	0.28	0.04	0.18
Homo sapiens 3q26.2-27 BAC RPC11-379K17	H3022B11		0.70	0.61	0.49	#DIV/O!	0.13	0.01	#DIV/O!	
Mus musculus transposon ETn, SWV/nude-Bc	H3116F10	0.91	0.78	0.61	1.31		0.64	0.20	0.02	0.07
Homo sapiens clone NH0506C08, complete s	H3071D11	0.82	0.75	0.60	0.69		0.35	0.20	0.03	0.07
Homo sapiens mRNA; cDNA DKFZp564B213 (fr	H3100D08	1.19	0.86	0.60	0.42		0.40	0.55	0.04	0.11
Mus musculus odd Oz/ten-m homolog 3 (Dro	H3071H08	0.91	0.80	0.60	0.94		0.57	0.21	0.03	0.74
Rattus norvegicus podocalyxin mRNA, comp	H3029C03	0.82	1.04	0.60	0.61		0.17	0.76	0.05	0.05
Mus musculus membrane component, surface	H3098B01	0.70	0.79	0.60	0.42		0.00	0.05	0.04	0.01
Homo sapiens chromosome 5, PAC clone 45L	H3055B06	1.20	1.08	0.60	0.65		0.54	0.83	0.05	0.28
Human DNA sequence from cosmid L241B9, H	H3034F01	0.85	0.92	0.60	0.55		0.41	0.71	0.04	0.07
Homo sapiens pericentrin (PCNT) mRNA	H3140F07	0.75	0.84	0.60	1.00		0.17	0.36	0.04	0.99
Mus musculus putative transcription fact	H3110H03	1.01	0.91	0.59	0.67		0.96	0.61	0.00	0.02
Homo sapiens BAC clone RP11-187G20 from	H3119B04	0.89	0.82	0.59	1.07		0.47	0.22	0.04	0.75
M.musculus 45S pre rRNA gene	H3001E09	0.96	0.89	0.59	0.93		0.78	0.53	0.03	0.67
No Hits Found	H3001D05	0.92	0.97	0.59	0.85		0.62	0.88	0.02	0.23
Oryctolagus cuniculus anion exchanger 3	H3012D11	0.74	0.67	0.59	0.73		0.39	0.28	0.02	0.06
Human DNA sequence from clone RP4-667H12	H3118H04	0.90	0.66	0.59	0.56		0.84	0.49	0.03	0.00
Mus musculus Ash2l mRNA, complete cds, s	H3148F02	0.81	0.94	0.59	1.00		0.43	0.78	0.03	1.00
Pyrococcus abyssi complete genome; segme	H3032H07	1.03	0.96	0.59	0.78		0.84	0.74	0.03	0.28
Mus musculus cell division cycle 25 homo	H3041B01	1.18	0.68	0.59	0.47		0.76	0.59	0.01	0.06
Arabidopsis thaliana chromosome II secti	H3074E02	1.28	0.71	0.59	0.75		0.44	0.42	0.03	0.22
Human DNA sequence from clone 1118D24 on	H3067E01	0.79	0.75	0.59	0.89		0.05	0.09	0.04	0.54
Homo sapiens cDNA FLJ20516 fis, clone KA	H3013F06	0.76	0.70	0.58	0.78		0.15	0.33	0.02	0.07
Homo sapiens clone DJ0635B05, complete s	H3150D07	0.84	0.70	0.58	0.62		0.54	0.12	0.00	0.01
phosphatase inhibitor-2=cytosolic regula	H3043F08	1.33	0.96	0.58	0.58		0.39	0.90	0.02	0.04
Homo sapiens mRNA, expressed in fibrobla	H3157A06	1.03	0.66	0.58	0.56		0.90	0.25	0.03	0.03
Homo sapiens genomic DNA, chromosome 8p1	H3156C11	0.75	0.76	0.58	0.72		0.24	0.12	0.01	0.03
Caenorhabditis elegans cosmid F23F12	H3124D08	0.78	0.79	0.58	0.49		0.35	0.19	0.02	0.08
Homo sapiens cDNA FLJ10628 fis, clone NT	H3024F10	1.35		0.58		#DIV/O!	#DIV/O!		0.01	#DIV/O!
Mus musculus melanoma X-actin (Actx), mR	H3041F03	0.82	0.83	0.58	0.77		0.09	0.13	0.02	0.27
Homo sapiens PAC clone RP4-759N11 from 7	H3076A10	1.00	1.00	0.58	0.79		1.00	1.00	0.01	0.16
Mus musculus eukaryotic translation init	H3002F06	0.81	0.92	0.58	0.58		0.54	0.79	0.01	0.02
Pisum sativum gibberellin c20-oxidase ge	H3094E01	0.77	0.60	0.57	0.61		0.09	0.01	0.02	0.02
BAC sequence from the SPG4 candidate reg	H3051F09	1.04	0.91	0.57	0.77		0.91	0.74	0.02	0.22
Homo sapiens mRNA for KIAA1036 protein,	H3158G07	1.13	1.20	0.57	0.92		0.41	#DIV/O!	0.02	0.48
Homo sapiens *** SEQUENCING IN PROGRESS	H3078C09	0.81	0.66	0.57	0.54		0.54	0.27	0.02	0.02
Campylobacter jejuni NCTC11168 complete	H3094E02	0.68	0.79	0.57	0.60		0.36	0.27	0.01	0.01
Homo sapiens cDNA FLJ20746 fis, clone HE	H3060C11	0.97	0.83	0.57	0.62		0.90	0.52	0.01	0.00
Human DNA sequence from cosmid V311G7, b	H3139D02	0.94	0.98	0.57	0.82		0.62	0.85	0.00	0.09
human STS A006C44	H3114C05	0.65	0.85	0.56	0.71	#DIV/O!	#DIV/O!	0.35	0.03	0.20
Mouse transglutaminase (TGase) mRNA, com	H3137C06	0.63	0.85	0.56	0.88		0.02	0.01	0.01	0.41
Homo sapiens mRNA; cDNA DKFZp434L0130 (f	H3014G11	0.76	0.70	0.56	0.81		0.09	0.25	0.00	0.04
Homo sapiens chromosome 19, cosmid R2994	H3108A08		1.21	0.56	0.62	#DIV/O!	#DIV/O!	0.65	0.03	#DIV/O!
Homo sapiens cDNA FLJ11345 fis, clone PL	H3042H12	0.91	0.97	0.55	0.52		0.76	0.92	0.03	0.03
Homo sapiens chromosome 17, clone 289A8,	H3019G04			0.55	1.27	#DIV/O!	#DIV/O!	#DIV/O!	0.04	0.35
Cricetinae gen. sp. insulin receptor tyr	H3095F09	0.90	0.76	0.55	0.50		0.59	0.14	0.02	0.03
	H3114G03	1.03	0.93	0.55	0.72	#DIV/O!	#DIV/O!	0.84	0.02	#DIV/O!
Homo sapiens cyclin-dependent kinase inh	H3115G07	0.84	0.64	0.55	0.49		0.48	0.12	0.01	0.01

Table G. Genes significantly influenced by Cobalt in HIF1a -/- cells (cont.)

Rattus norvegicus SH3 domain-containing	H3108H02		0.73	0.55	0.73		#DIV/0!	0.58	0.04	#DIV/0!
Homo sapiens cDNA FLJ11333 fis, clone PL	H3103E10	1.06	0.96	0.54	0.56		0.72	0.70	0.01	0.00
Human DNA sequence from clone RP5-117715	H3130F06		2.26	0.54	1.34		#DIV/0!	#DIV/0!	0.04	#DIV/0!
Mus musculus vanin 1 (Vnn1), mRNA	H3036H03	1.32	0.66	0.53	0.61		0.09	0.09	0.03	#DIV/0!
Mus musculus procollagen, type VI, alpha	H3151F07	0.89	1.48	0.53	0.73		0.60	0.01	0.00	0.02
Mus musculus X chromosome: L1cam locus,	H3153G10	0.86	0.79	0.53	0.80		0.75	0.36	0.01	0.32
Human mRNA for NADPH-flavin reductase, c	H3048G11	0.75	0.71	0.53	0.50		0.10	0.03	0.03	0.03
Rattus norvegicus alpha-actinin 4 mRNA,	H3133G03	0.94	1.04	0.52	0.87		0.69	0.72	0.01	0.38
Mus musculus ribosomal protein L30 (Rpl3	H3030B06	1.08	1.08	0.52	1.69		0.76	0.65	0.05	0.13
Rattus norvegicus non-muscle alpha-actin	H3003H10	1.06	0.64	0.52	0.75		0.81	0.01	0.00	0.04
Mus musculus chromosome X, clone RP21-30	H3135F04	0.74	1.04	0.51	0.59		0.08	0.80	0.03	0.10
Human DNA sequence from clone RP3-382110	H3071A06	0.94	0.77	0.51	0.61		0.84	0.50	0.03	0.11
Ureaplasma urealyticum section 18 of 59	H3020D07	0.79	0.91	0.49	0.77		0.15	0.49	0.02	0.18
ribosomal protein L37 [rats, myoblast L6	H3133F06	0.88	1.02	0.49	1.00		0.52	0.93	0.03	1.00
Homo sapiens microsomal glutathione S-tr	H3157D12	0.84	0.99	0.48	0.52		0.40	0.96	0.03	0.02
Homo sapiens 12q24.2 PAC RPCI5-1135M4 (R	H3125A02	0.77	1.22	0.48	0.77		0.38	0.44	0.01	0.22
Homo sapiens DNA sequence from P1 p373c6	H3026H06	0.85	0.68	0.48	0.47		0.64	0.39	0.04	0.08
Homo sapiens chromosome 8 clone HPAC24 m	H3154B08	0.67	0.58	0.47	0.74		0.41	0.32	0.01	0.27
Mus musculus protein synthesis elongatio	H3119H02	0.87	0.71	0.46	0.76		0.38	0.14	0.03	0.25
Homo sapiens ubiquitin carrier protein E	H3024A07	0.71	0.68	0.46	0.93		0.23	0.20	0.01	0.86
Mus musculus cyclin-dependent kinase 5 (H3111B07	0.92	0.94	0.45	0.65		0.77	0.84	0.01	0.05
O.cuniculus mRNA for cytosolic serine hy	H3024F06	0.92	0.67	0.43	0.48		#DIV/0!	#DIV/0!	0.03	#DIV/0!
Rattus norvegicus unknown mRNA	H3003E03	0.73	0.64	0.42	0.62		0.32	0.16	0.01	0.08
Rattus norvegicus unknown mRNA	H3006C08	0.73	0.66	0.40	0.58		0.34	0.23	0.04	0.12
Mus musculus ligatin (Lgtn) mRNA, partia	H3138F09	1.17	0.99	0.35	0.34		0.73	#DIV/0!	0.00	0.07
Mus musculus H19 and muscle-specific Nct	H3144B07	2.20	2.42	0.35	0.33		0.03	0.10	0.00	0.00

Table H. Genes significantly influenced by the loss of HIF1a (WT ctrl vs HIF1a -/- ctrl) □

ID	Name	Fold Change W-Ctrl/N-Ctrl	T-Test
H3108G04	Crip1: cysteine-rich protein 1	2.572	0.000
H3140H02	Homo sapiens BAC clone GS1-146J4 from 7q	2.416	0.004
H3134F05	Mus musculus glutathione-S-transferase,	2.242	0.013
H3140F12	Homo sapiens chromosome 4 clone C0473M13	2.174	0.004
H3084E06	Mus musculus chromosome 7, clone 19K5, c	2.126	0.049
A-2031	Metallothionein-I (image 1052401)	1.840	0.007
H3131A03	Homo sapiens TATA box binding protein (T	1.808	0.005
H3154G07	Rattus norvegicus Insulin-like growth fa	1.802	0.020
H3103C08	Homo sapiens clone UWGC:rg020I24 from 7q	1.768	0.032
H3087H09	Mus musculus calcium binding protein A6	1.747	0.006
H3024C11	Mus musculus heat shock protein, 86 kDa	1.739	0.006
H3146A04	Homo sapiens cDNA FLJ10463 fis, clone NT	1.724	0.013
H3113F07	Mus musculus cyclin-dependent kinase inh	1.715	0.039
H3134D01	Homo sapiens mRNA for KIAA0573 protein,	1.697	0.004
H3103F12	human STS SHGC-31509	1.696	0.014
H3124H10	M.musculus COL3A1 gene for collagen alph	1.686	0.008
H3115F11	Mus musculus nidogen 2 (Nid2), mRNA	1.666	0.001
H3148D05	Mus musculus MGA protein mRNA, complete	1.664	0.002
H3130B11	Cu-Zn SOD	1.623	0.016
H3120E02	Mus musculus integral membrane protein 2	1.584	0.040
H3030G02	Homo sapiens cDNA FLJ10500 fis, clone NT	1.583	0.009
H3128A11	Mus musculus heterogeneous nuclear ribon	1.577	0.015
H3149A01	Mus musculus cyclin D3 (Ccnd3), mRNA	1.568	0.018
H3041D03	Homo sapiens chromosome 5 clone CITB-H1_	1.566	0.008
H3086D02	Mus musculus mRNA for SHD-1 protein	1.565	0.019
A-2062	Mn SOD (image 3468203)	1.564	0.038
H3110B07	Homo sapiens chromosome 16 clone RPCI-11	1.562	0.024
H3029C03	Rattus norvegicus podocalyxin mRNA, comp	1.554	0.023
H3133G03	Rattus norvegicus alpha-actinin 4 mRNA,	1.552	0.009
H3125G12	Homo sapiens huntingtin interacting prot	1.549	0.039
H3019D01	Mouse calmodulin (Cam I) mRNA, complete	1.533	0.001
H3021E08	Mus musculus calmodulin (Calm), mRNA	1.531	0.008
H3152C12	Homo sapiens mRNA for KIAA0847 protein,	1.526	0.001
H3040G11	Homo sapiens cDNA FLJ10700 fis, clone NT	1.525	0.022
H3019E08	Mouse mRNA for fibronectin receptor beta	1.522	0.007
H3153F04	Homo sapiens chromosome 4 clone C0201M04	1.513	0.009
H3100H03	Human DNA sequence from clone 12M9 on ch	1.511	0.034
H3118D07	Homo sapiens MUM2 (MUM2) gene, complete	1.509	0.018
H3119G08	Mus musculus glutathione-S-transferase,	1.490	0.001
H3037A03	Mus musculus actinin, alpha 1 (Actn1), mRNA	1.490	0.043
H3026F04	Mus musculus similar to protein kinase, lysine deficient	1.489	0.031
H3146C02	Mus musculus platelet derived growth fac	1.488	0.015
H3022H02	Homo sapiens Xq28 genomic DNA in the reg	1.487	0.046
H3044G08	Homo sapiens chromosome 17, clone hRPK.1	1.481	0.033
H3114E05	Homo sapiens Chromosome 16 BAC clone CIT	1.480	0.036
H3139E03	Human chromosome 14 DNA sequence *** IN	1.478	0.009
H3132H05	XPBC/ERCC-3=DNA repair gene [mice, mRNA,	1.471	0.032
H3027A08	Human mRNA for KIAA0076 gene, complete c	1.468	0.039
H3142E06	Homo sapiens chromosome 17, clone HRPC29	1.456	0.008

Table H. Genes significantly influenced by the loss of HIF1a (WT ctrl vs HIF1a -/- ctrl) □
(cont.)

H3114F01	Mus musculus mRNA for Guanine Nucleotide	1.453	0.020
H3137C06	Mouse transglutaminase (TGase) mRNA, com	1.453	0.006
H3146D07	Homo sapiens, complete sequence	1.451	0.018
H3022F02	Mus musculus general transcription facto	1.439	0.025
H3108A10	Homo sapiens CGI-94 protein mRNA, comple	1.434	0.033
H3019F11	Caenorhabditis elegans cosmid F58E2	1.433	0.022
H3150H03	Homo sapiens clone DJ0764O12, complete s	1.433	0.028
H3150B05	Homo sapiens chromosome 8 clone HPAC24 m	1.428	0.007
A-2049	Catalase (image 1068861)	1.426	0.006
H3098G10	Homo sapiens genomic DNA, chromosome 21q	1.413	0.020
H3044B11	Homo sapiens cDNA FLJ10305 fis, clone NT	1.412	0.030
H3034C10	Homo sapiens transducin (beta)-like 3 (T	1.406	0.029
H3102A09	Rattus norvegicus outer membrane protein	1.404	0.034
H3140A11	Homo sapiens BAC clone CTA-252K19 from 7	1.402	0.003
H3156D01	Mus musculus presenilin 1 (Psen1), mRNA	1.400	0.033
H3108H01	Caenorhabditis elegans cosmid C08G5	1.392	0.018
H3116F07	Homo sapiens nuclear phosphoprotein simi	1.390	0.040
H3122H03	Mus musculus augmenter of liver regenera	1.386	0.034
H3142B09	Homo sapiens chromosome 19, fosmid 37308	1.384	0.023
H3118F06	M.musculus of PCTAIRE-1 mRNA encoding pr	1.384	0.031
H3120D03	Human mRNA for KIAA0077 gene, partial cd	1.379	0.022
H3154D02	Mus musculus CD82 antigen (Cd82), mRNA	1.376	0.041
H3159G05	Mus musculus glutathione-S-transferase,	1.366	0.021
H3016D10	Murine mRNA for L-34 galactoside-binding	1.356	0.003
H3134A11	Homo sapiens chromosome 9, clone hRPK.53	1.356	0.029
H3128G11	human STS A001X12	1.355	0.039
H3145E02	Mus musculus WW-domain binding protein 1	1.351	0.033
H3156C10	Homo sapiens clone NH0309N08, complete s	1.351	0.048
H3020H06	Mus musculus ELKL motif kinase (Emk), mR	1.347	0.032
H3143A06	Leishmania donovani kinetoplast minirc	1.347	0.041
H3052C11	Mus musculus clathrin light chain 2 mRNA	1.347	0.023
H3117C12	Homo sapiens cDNA FLJ20571 fis, clone RE	1.343	0.047
H3022A02	Homo sapiens genomic DNA, chromosome 21q	1.343	0.043
H3131C12	Homo sapiens chromosome 21 segment HS21C	1.339	0.008
H3028A06	Mus musculus peptidylprolyl isomerase A	1.335	0.023
H3149E08	Mus musculus annexin A7 (Anxa7), mRNA	1.332	0.013
H3150C01	Homo sapiens mRNA for KIAA0660 protein,	1.322	0.047
H3130B11	Mouse Cu-Zn superoxide dismutase mRNA, c	1.321	0.040
H3026E06	H.sapiens mRNA for APRIL protein	1.319	0.041
H3123A12	Homo sapiens 12p21 BAC RPC11-259O18 (Ro	1.318	0.033
H3109C03	Mus musculus glucosidase, alpha, acid (G	1.317	0.010
H3022E07	Arabidopsis thaliana chromosome I BAC F2	1.312	0.031
H3098F10	Mus musculus spinocerebellar ataxia 2 ho	1.308	0.044
H3027D05	Mus musculus lymphocyte antigen 6 comple	1.305	0.017
H3003H01	Arabidopsis thaliana chromosome II secti	1.304	0.021
H3134H11	Homo sapiens cleavage stimulation factor	1.300	0.032
H3151E06	Rattus norvegicus SPA-1 like protein p12	1.296	0.012
H3054B09	Homo sapiens cDNA mapping to 22q13	1.294	0.019
H3029H03	Mus musculus eukaryotic translation init	1.292	0.015
H3051F10	MUS musculusGRO1 oncogene (Gro1), mRNA(n	1.290	0.040
H3158G09	Human DNA sequence from clone RP4-695O20	1.289	0.024

Table H. Genes significantly influenced by the loss of HIF1a (WT ctrl vs HIF1a -/- ctrl) (cont.)

H3137A04	Mus musculus CRIPT protein mRNA, complet	1.287	0.027
H3012F11	Homo sapiens chromosome 14 BAC containin	1.286	0.021
H3124B01	Caenorhabditis elegans cosmid Y38E10A, c	1.279	0.050
H3007C09	Sorghum bicolor BAC clone 25.M18, comple	1.270	0.035
H3078C02	Drosophila melanogaster c11.1 gene, part	1.268	0.023
H3003D12	Mus musculus procollagen-proline, 2-oxog	1.261	0.010
H3154H09	Homo sapiens clone DJ0935K16, complete s	1.258	0.045
H3022G10	Unidentified low G+C gram-positive bacte	1.257	0.010
H3027G01	Mus musculus MHC class III region RD gen	1.255	0.038
H3158A06	Human DNA sequence from clone RP5-1123D4	1.249	0.009
H3029G08	Mus musculus mRNA for neural specific sr	1.243	0.036
H3013A08	Rattus norvegicus plakoglobin mRNA, comp	1.242	0.028
H3146D01	Homo sapiens phosphorylase kinase, alpha	1.238	0.039
H3018B01	Mus musculus adaptor-related protein com	1.238	0.041
H3020E04	Mus musculus unknown mRNA, clone A1.2	1.234	0.004
H3031H12	Homo sapiens cDNA FLJ10654 fis, clone NT	1.221	0.026
H3017D11	Human DNA sequence from clone RP3-402G11	1.220	0.001
H3159C03	Homo sapiens 3',5'-cyclic AMP phosphodie	1.218	0.029
H3030A10	Homo sapiens 12p BAC RPC11-434C1 (Roswe	1.218	0.033
H3020A08	Homo sapiens BAC clone GS1-77A9 from 7p1	1.217	0.045
H3146H01	Z.mays cyp71c4 gene	1.206	0.024
H3146C11	Mus musculus evectin-2 (Evt2) mRNA, comp	1.206	0.049
H3002F12	Mus musculus COP9 (constitutive photomor	1.197	0.017
H3021E12	Mus musculus nucleotide binding protein	1.186	0.037
H3155G01	Homo sapiens mRNA; cDNA DKFZp434K0926 (f	1.186	0.047
H3149A04	Homo sapiens A kinase (PKA) anchor prot	1.185	0.022
H3153E03	Homo sapiens genomic DNA, chromosome 22q	1.182	0.029
H3002B06	Mus musculus EH domain-containing protei	1.162	0.044
H3151B09	Homo sapiens PAC clone RP1-130H16 from 2	1.161	0.041
H3017F06	Homo sapiens mRNA; cDNA DKFZp434A115 (fr	1.153	0.027
H3010B05	Rattus norvegicus mRNA for brain 4.1(S),	1.144	0.035
H3002D01	Arabidopsis thaliana chromosome 1 BAC F5	1.138	0.042
H3005D02	M.musculus NRF1 mRNA	0.870	0.029
H3017F03	Homo sapiens clone 24519 unknown mRNA, p	0.864	0.046
H3111B08	Mouse mRNA for TBPIP, complete cds	0.862	0.040
H3014B01	Leishmania tarentolae kinetoplast pre-ed	0.858	0.041
H3006C10	Rat ribosomal protein L18 mRNA, complete	0.836	0.040
H3051G07	Rattus norvegicus guanosine monophospat	0.829	0.029
H3094A03	Human DNA sequence from clone 1103G7 on	0.828	0.012
H3156H02	Homo sapiens mRNA for KIAA0516 protein,	0.812	0.033
H3006H07	Homo sapiens chromosome 1 clone RP5-837M10	0.808	0.006
H3004E04	Homo sapiens cDNA FLJ10962 fis, clone PL	0.798	0.006
H3019B01	M.musculus mRNA for sodium/potassium ATP	0.798	0.041
H3005E10	Rat Na+, K+ -ATPase beta subunit protein	0.798	0.016
H3003A03	M.musculus bgbp gene, exons 2 & 3	0.791	0.020
H3029B11	Mouse chromatin nonhistone high mobility	0.790	0.018
H3009F01	Homo sapiens ES/130-related protein mRNA	0.790	0.047
H3008C02	Mus musculus PKCq-interacting protein PI	0.787	0.025
H3079A02	Mus musculus ribosomal protein L12 (Rpl1	0.779	0.048
H3111C04	Homo sapiens BAC clone 1D9 from 2p21, co	0.776	0.014
H3100C04	Homo sapiens mRNA; cDNA DKFZp564C2163 (f	0.772	0.041

Table H. Genes significantly influenced by the loss of HIF1a (WT ctrl vs HIF1a -/- ctrl) (cont.)

H3148G02	Human DNA sequence from clone 581F7 on c	0.771	0.028
H3146D12	R.norvegicus mRNA for microtubule associ	0.770	0.041
H3071G05	Mus musculus mRNA for DBF4-related prote	0.766	0.020
H3112B03	M.musculus mRNA for TIF1 beta protein	0.763	0.023
H3122F02	Rat mRNA for ribosomal protein L38	0.762	0.046
H3111C08	Homo sapiens PRO0530 mRNA, complete cds	0.760	0.039
H3112A10	Mus musculus ribosomal protein L28 (Rpl2	0.756	0.004
H3112G04	M.musculus mRNA for ribosomal protein S5	0.753	0.034
H3159B08	Homo sapiens BAC clone CTB-114B19 from 7	0.747	0.015
H3069D01	Homo sapiens BAC clone RP11-359K10 from	0.744	0.039
H3022B11	Homo sapiens 3q26.2-27 BAC RPC111-379K17	0.742	0.045
H3115B08	Mus musculus ATPase inhibitor (Atpi), mR	0.737	0.005
H3131B01	Mus musculus NIPI-like protein (NIPIL(A3	0.737	0.044
H3010D10	Mus musculus tumor necrosis factor alpha	0.736	0.027
H3129B09	Mus musculus HepA-related protein Harp m	0.731	0.030
H3112G01	M.musculus mRNA for ribosomal protein S5	0.727	0.006
H3097D09	Arabidopsis thaliana chromosome I BAC F2	0.725	0.035
H3149G09	Homo sapiens DNA sequence from PAC 329E2	0.725	0.033
H3102G02	R.norvegicus mRNA for ribosomal protein	0.720	0.041
H3041H07	Arabidopsis thaliana AAO4 mRNA for aldeh	0.720	0.033
H3121C03	Homo sapiens PAC clone RP1-74M20 from X,	0.715	0.003
H3126C03	Mouse calpactin I heavy chain (p36) mRNA	0.713	0.050
H3112G03	M.musculus mRNA for ribosomal protein S5	0.713	0.039
H3134G05	Homo sapiens mRNA; cDNA DKFZp564O1863 (f	0.712	0.005
H3011B06	Homo sapiens mRNA; cDNA DKFZp434A179 (fr	0.711	0.009
H3124F08	Mus musculus acidic ribosomal phosphopro	0.707	0.018
H3031H05	Albinaria xanthostoma isolate xan.Kol1.1	0.707	0.008
H3126H04	Human DNA sequence from clone 23K20 on c	0.702	0.041
H3014G01	Homo sapiens HSPC061 mRNA, complete cds	0.700	0.017
H3124H06	Mus musculus ribosomal protein S3 (Rps3)	0.699	0.015
H3112H11	Mouse S16 ribosomal protein processed ps	0.693	0.010
H3075G08	Mus musculus P40-8, functional (P40-8),	0.691	0.016
H3120C12	Mycobacterium tuberculosis H37Rv complet	0.688	0.010
H3115D03	Mus musculus P40-8, functional (P40-8),	0.685	0.004
H3036E04	Homo sapiens PAC 704H1777 chromosome 8 m	0.685	0.025
H3130A12	R.norvegicus mRNA for ribosomal protein	0.684	0.016
H3129A01	Mouse aldehyde dehydrogenase II mRNA, co	0.682	0.046
H3030D11	Mus musculus pyruvate kinase 3 (Pk3), mR	0.677	0.025
H3115D01	Mus musculus P40-8, functional (P40-8),	0.676	0.028
H3125H06	Drosophila melanogaster genomic scaffold	0.674	0.017
H3149G02	Homo sapiens HSPC193 mRNA, complete cds	0.665	0.012
H3124F09	Mus musculus acidic ribosomal phosphopro	0.664	0.004
H3104F04	Mus musculus cyclin B2 (Ccnb2), mRNA	0.660	0.049
H3074A08	Rattus norvegicus gene for selenium-depe	0.657	0.015
H3118H01	Homo sapiens chromosome CITB-H1_2291F22,	0.653	0.015
H3134E06	No Hits Found	0.651	0.020
H3120G06	Mouse tropomyosin isoform 2 mRNA, comple	0.649	0.004
H3019H06	Mus musculus tyrosine 3-monooxygenase/tr	0.649	0.013
H3115D02	Mus musculus P40-8, functional (P40-8),	0.642	0.001
H3125H02	Homo sapiens clone RP11-333O1, complete	0.641	0.031
H3140H04	Homo sapiens mRNA for epsilon-sarcoglyca	0.640	0.042

Table H. Genes significantly influenced by the loss of HIF1a (WT ctrl vs HIF1a -/- ctrl) (cont.)

H3151C09	Tapa-1=integral membrane protein TAPA-1	0.636	0.036
H3075G10	M.musculus genes encoding histone H4, hi	0.631	0.022
H3029B01	Mus musculus natural resistance associat	0.629	0.049
H3126A06	Genomic sequence from Human 9q34, comple	0.628	0.034
H3028D10	Mus musculus synapsin Ib (SynI) mRNA, co	0.622	0.016
H3115D04	Mus musculus P40-8, functional (P40-8),	0.620	0.003
H3150C12	Mus musculus intersectin-EH binding prot	0.620	0.003
H3060D09	Rattus norvegicus NADH ubiquinone oxidor	0.617	0.032
H3091E10	Mus musculus p8 protein (p8) gene, compl	0.612	0.032
H3148F02	Mus musculus Ash2I mRNA, complete cds, s	0.589	0.022
H3111E08	Homo sapiens mRNA; cDNA DKFZp586O1224 (f	0.584	0.044
H3028D04	Rat mRNA for ribosomal protein L5	0.581	0.026
H3048F06	Mus musculus nucleolar RNA helicase II/G	0.568	0.017
H3007G06	Mus musculus keratin complex 1, acidic,	0.567	0.011
H3137B11	Mus musculus mesoderm specific transcrip	0.564	0.007
H3109C02	Mus musculus tissue inhibitor of metallo	0.562	0.007
H3157C12	Fugu rubripes cosmid 151J19 covering the	0.551	0.001
H3138F09	Mus musculus ligatin (Lgtn) mRNA, partia	0.551	0.030
H3058G01	Homo sapiens genomic DNA, chromosome 22q	0.545	0.003
H3114C12	Mus musculus cytosolic class 3 aldehyde	0.544	0.000
H3125A07	Mus musculus collagen binding protein 1	0.518	0.006
H3120D05	Homo sapiens unknown mRNA (ALEX3, armidillo cance	0.492	0.027
H3126A04	Mouse mRNA encoding alpha-fetoprotein (a	0.435	0.044
H3058A11	Mus musculus major histocompatibility lo	0.421	0.007
H3079H10	Mus musculus eukaryotic translation initiation factor 2, s	0.400	0.020
H3136A07	Mus musculus procollagen, type I, alpha	0.391	0.024
H3104F03	Rattus norvegicus potassium channel regu	0.380	0.001
H3005A04	Mus musculus chaperonin 10 mRNA, complet	0.366	0.005
H3144B06	Mus musculus H19 and muscle-specific Nct	0.211	0.003
H3127D03	Mus musculus biglycan (Bgn), mRNA	0.187	0.019
H3140G12	H19 fetal liver	0.131	0.001
H3144B07	Mus musculus H19 and muscle-specific Nct	0.067	0.001

Table I. Comparison of genes in Table 2 with those presented in Jiang et al (ref. 52)

	Identical	Homologous
Fig 1A	metallothionein	L26 (L17)
	p35 (H3147H11)	L15 (L17)
	eIF3	L29 (L17)
		L13 (L17)
Fig 1b	enolase	L21 (L17)
Fig 1		Chronic sommatatropin2 (csh1)
		L13 (L17)
		L37 (L17)
		L22 (L17)
		L39 (L17)
		L41 (L17)
		L3 (L17)
		L12 (L17)
FIG 2C	Fibronectin receptor Beta	GLut1 (Glut4)
	lactate dehydrogenase	eIF2 (eIF 3)
	GAPDH	eIF1a (eIF 3)
	P4H	MMP7 (MMP23)
	eIF3	L9 (L17)
		L21 (L17)
		L37 (L17)
		L13 (L17)
		L28 (L17)
		L41 (L17)
		L22 (L17)
Fig 2D	lactate dehydrogenase	eIF1a (eIF 3)
	Fibronectin receptor Beta	eIF4 (eIF 3)
	Macropain 26S	eIF2 (eIF 3)
		MMP28 (MMP23)
		MMP25 (MMP23)
		L13 (L17)
		L28 (L17)
		L20 (L17)
		L15 (L17)
		L18 (L17)
		L7 (L17)
Fig 2e	enolase	L7 (L17)
	galactoside binding	L30 (L17)
	proline rich (H3116A06)	eIF2 (eIF 3)
	eIF3	L5 (L17)
		L3 (L17)
Fig 3F		Chronic sommatatropin2 (csh1)
		L22 (L17)
		L3 (L17)
		L12 (L17)
		L13 (L17)
		L37 (L17)
		L39 (L17)
		L21 (L17)

Table I. Comparison of genes in Table 2 with those presented in Jiang et al (ref. 52) (cont.)

		L41 (L17)
Fig 3G	enolase	
Fig 3	Cathepsin L	GLut1 (Glut4)
	pyruvate kinase	GLut2 (Glut4)
	p35 (H3147H11)	eIF1 (Eif3)
	GPI	eIF2 (eIF 3)
	galactoside binding	eIF4 (eIF 3)
	BNIP3	AdenylateKinase 3 (ADK2)
	BNIP3L	27a (L17)
	GAPDH	L12 (L17)
	aldolase	L29 (L17)
	P4H	L30 (L17)
	ADK2	L9 (L17)
	Transglutaminase 2	L10 (L17)
		L30 (L17)
		L27 (L17)
Fig 4H	enolase	lymphocyte ant 1 (lymA 3)
	MUM2	
	Transglutaminase 2	
	Macropain 26s	
Fig 4	enolase	Chronic sommatatropin2 (csh1)
	mitochondrial carrier	L3 (L17)
	GAPDH	L12 (L17)
		L13 (L17)
		L37 (L17)
		L39 (L17)
		L21 (L17)
		L41 (L17)