Gene name	Acc#	Gene Symbol	ChIP-enrichment	Fold-induced expression
hypothetical protein FLJ13063	BC014945	FLJ13063	12.68	89.65
heat shock 70kDa protein 1A	NM_005345	HSPA1A	245.65	58.54
DnaJ (Hsp40) homolog, subfamily C, member 3	NM_006260	DNAJC3	0.52	49.76
DnaJ (Hsp40) homolog, subfmaily B, member 1	NM_006145	DNAJB1	17.12	38.72
heat shock 27kDa protein 2	NM_001541	HSPB2	22.12	34.90
serine proteinase inhibitor, clade H (hsp47), member 2	NM_001235	SERPINH2	111.29	21.53
heat shock 70kDa protein 6 (HSP70B')	NM_002155	HSPA6	312.89	20.59
hypothetical protein DKFZp564I0422	NM_031435	DKFZP564I0422	1.83	18.86
mitochondrial ribosomal protein L18	NM_014161	MRPL18	67.66	17.16
chromosome 6 open reading frame 37	NM_017633	C6orf37	16.75	17.09
cDNA FLJ37360 fis, clone BRAMY2023358	AK094679	Data not found		15.33
DnaJ (Hsp40) homolog, subfamily B, member 4	NM_007034	DNAJB4	0.76	14.67
heat shock protein (hsp110 family)	NM_014278	APG-1	23.07	14.45
heat shock 105kD	NM_006644	HSP105B	653.34	13.40
N-acetylated alpha-linked acidic dipeptidase 2	NM_005467	NAALAD2	0.33	12.29
cDNA DKFZp434B102	BC030800		0.39	11.68
tumor necrosis factor receptor superfamily, member 21	BC005192	TNFRSF21	31.39	10.63
heat shock 27kDa protein 1	NM_001540	HSPB1	174.23	10.11
relaxin 1 (H1)	BC005956	RLN1	58.72	9.96
Homo sapiens cDNA: FLJ21243 fis, clone COL01164	AK024896			7.74
solute carrier family 28, member 1	NM_004213	SLC28A1	0.20	6.56
death effector domain-containing DNA binding protein 2	BC013372	DEDD2	13.98	6.44
Homo sapiens clone 24627 mRNA sequence	AF070618			6.18
tripartite motif-containing 26	BC032297	TRIM26		6.10
DKFZP434I1735 protein	AB037737	DKFZP434I1735	0.30	5.88
collagen, type IV, alpha 6	NM_033641	COL4A6	6.07	5.69
crystallin, mu	NM_001888	CRYM	4.37	5.60
FK506 binding protein 4, 59kDa	NM_002014	FKBP4	6.28	5.24
hypothetical protein FLJ22693	NM_022750	FLJ22693	9.26	4.95
crystallin, beta A4	NM_001886	CRYBA4	29.57	4.68
ubiquitin B	BC015127	UBB	347.68	4.46
DnaJ (Hsp40) homolog, subfamily B, member 6	AL832124	DNAJB6		4.37
protein kinase anchoring protein GKAP42	NM_025211	GKAP42	0.24	4.14
ribosomal protein S14	BC006784	RPS14	6.54	3.85
cDNA FLJ39749 fis, clone SMINT2017599	AK097068			3.81
p21 (CDKN1A)-activated kinase 2	NM_002577	PAK2		3.81
hypothetical protein MGC10814	NM_032671	MGC10814	16.49	3.79
GPI anchored molecule like protein	NM_002066	GML	55.60	3.75
DnaJ (Hsp40) homolog, subfamily B, member 6	NM_005494	DNAJB6	70.75	3.68
heat shock 70kDa protein 1-like	NM_005527	HSPA1L	238.60	3.47
wingless-type MMTV integration site family, member 4	NM_030761	WNT4		3.45
ESTs	AI023475			3.44
glioblastoma amplified sequence	BC001837	GBAS	35.49	3.42
MHC class I polypeptide-related sequence A	NM_000247	MICA	45.89	3.34
G protein-coupled receptor 4	NM_005282	GPR4	44.42	3.29
fucosyltransferase 1	NM_000148	FUT1	0.65	3.24
heat shock 27kDa protein 3	NM_006308	HSPB3	0.32	3.19
cysteine-rich, angiogenic inducer, 61	BC009199	CYR61	1.70	3.18
protein kinase C, alpha	NM_002737	PRKCA	0.35	3.16
hypothetical protein LOC63929	NM_022098	LOC63929	159.88	3.14
hypothetical protein FLJ20558	NM_017880	FLJ20558	1.04	3.04
heat shock 90kDa protein 1, beta	NM_007355	HSPCB	220.28	2.96
Siah-interacting protein	BC005975	SIP	60.99	2.94
ESTs, Weakly similar to L1 repeat, [Mus musculus]	AI741106			2.94
hypothetical protein P15-2	NM_018698	NXT2	241.38	2.92
Homo sapiens cDNA FLJ13997 fis, clone Y79AA1002220	AK024059			2.92
TAF7, TBP-associated factor, 55kDa	NM_005642	TAF7	116.50	2.81
AF464140	NM_145034	LOC163590		2.79
suppressor of G2 allele of SKP1, S. cerevisiae, homolog of	NM_006704	SUGT1	13.18	2.72
hypothetical protein MGC8721	NM_016127	MGC8721	41.74	2.66
nuclear receptor coactivator 3	NM_006534	NCOA3	1.63	2.62
brain-specific protein p25 alpha	NM_007030	p25	0.62	2.62
ESTs, similar to hypothetical FLJ11220 [Homo sapiens]	BM546166	NR0B1		2.60
ESTs	W88881	Data not found		2.56
chromosome 14 open reading frame 3	NM_012111	C14orf3	36.45	2.56
ESTs, similar to 2109260A B cell growth factor [Homo sapiens]	BM016400	GRP58		2.55
ESTs	BF724210			2.54
myotubularin related protein 8	BC012399	MTMR8	5.92	2.52
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	BC002987	STIP1	226.45	2.48
ESTs	N50733			2.46
hypothetical protein BC009514	AK098237	LOC127253		2.38
PR domain containing 2, with ZNF domain	NM_012231	PRDM2	0.47	2.38
CDC-like kinase 4	NM_020666	CLK4	0.36	2.32
Homo sapiens cDNA FLJ11174 fis, clone PLACE1007367	AK002036			2.29
Homo sapiens cDNA FLJ32453 fis, clone SKMUS2001703	AK057015			2.29
ESTs	BE787384			2.25
coagulation factor VIII, procoagulant component (hemophilia A)	NM_000132	F8	21.39	2.19
ESTs	BQ025398			2.19
VCY2 interacting protein 1	BC008806	VCY2IP1	0.47	2.18
suppression of tumorigenicity 13 (Hsp70 interacting protein)	NM_003932	ST13	174.17	2.17
hypothetical protein FLJ10830	BC003176	FLJ10830	21.30	2.15
heat shock 10kDa protein 1 (chaperonin 10)	NM_002157	HSPE1	154.26	2.14
ESTs, similar to hypothetical protein FLJ20378 [Homo sapiens]	BF679873			2.09
crystallin, gamma D	NM_006891	CRYGD	3.76	2.06
fragile X mental retardation, autosomal homolog 1	NM_005087	FXR1	26.53	2.06
crystallin, beta A1	NM_005208	CRYBA1	0.74	2.06
crystallin, beta B3	NM_004076	CRYBB3	0.28	2.04
fibroblast growth factor 18	BC006245	FGF18	8.01	2.03
CHORD-containing, zinc binding protein 1	NM_012124	CHORDC1	104.88	2.03
crystallin, gamma A	NM_014617	CRYGA	1.18	1.99
frizzled homolog 4 (Drosophila)	NM_012193	FZD4	15.20	1.97
clone MGC:15478 IMAGE:2967661, mRNA	BC010426		1.11	1.97
ESTs, similar to hypothetical protein FLJ20489 [Homo sapiens]	BQ186420			1.96
heat shock 60kDa protein 1 (chaperonin)	NM_002156	HSPD1	415.79	1.95
MORF-related gene X	NM_012286	MRGX	11.75	1.94
TEA domain family member 1 (SV40 transcriptional enhancer factor)	AL833289	TEAD1	0.18	1.93
retinoblastoma binding protein 2	NM_005056	RBBP2	72.94	1.89
carboxypeptidase E	NM_001873	CPE	19.95	1.89
SBBI26 protein	NM_018846	SBBI26	0.24	1.87
carbohydrate (chondroitin 6) sulfotransferase 3	NM_004273	CHST3	0.46	1.87
TAL1 (SCL) interrupting locus	NM_003035	SIL	0.52	1.87
crystallin, beta B2	NM_000496	CRYBB2	0.94	1.86
peptidylprolyl isomerase D (cyclophilin D)	NM_005038	PPID	8.93	1.85
hypothetical protein FLJ13936	AK096157	FLJ25416		1.84
heat shock 70kDa protein 8	NM_006597	HSPA8	191.34	1.83
EST	AI149051			1.83
crystallin, zeta (quinone reductase)	NM_001889	CRYZ		1.82
WEE1+ homolog (S. pombe)	NM_003390	WEE1	0.35	1.80
chaperonin containing TCP1, subunit 4 (delta)	NM_006430	CCT4	108.93	1.77
ATPase, Ca++ transporting, type 2C, member 1	NM_014382	ATP2C1	33.12	1.77
DnaJ (Hsp40) homolog, subfamily A, member 1	NM_001539	DNAJA1	325.10	1.76

cDNA FLJ25921, similar to Tandem PH Domain Containing Protein-2	AK098787	PLEKHA2		1.73
cDNA DKFZp761B128	AL834266	DKFZp761B128		1.71
ESTs, similar to zinc finger protein 91 (HPF7, HTF10) [Homo sapiens	AA169259			1.70
homeodomain interacting protein kinase 3	NM_005734	HIPK3	0.26	1.70
similar to BLAST-1 precursor (BCM1 surface antigen), clone MGC:34	BC030224			1.69
Homo sapiens, clone IMAGE:4617948, mRNA	AK095225			1.67
forkhead box J1	NM_001454	FOXJ1	9.76	1.67
serine hydrolase-like	NM_014509	dJ222E13.1	54.05	1.67
WD-repeat protein	NM_005828	HAN11	0.35	1.66
zinc finger protein 184 (Kruppel-like)	BC022992	ZNF184		1.62
ESTs	BG252605			1.62
heterogeneous nuclear ribonucleoprotein A2/B1	NM_002137	HNRPA2B1	55.24	1.60
KIAA0721 protein	BC009116	KIAA0721	16.37	1.60
ethanolamine kinase	NM_018638	EKI1		1.60
crystallin, gamma S	NM_017541	CRYGS	0.56	1.55
cDNA DKFZp434J1313	AL137262			1.54
KIAA0999 protein	NM_025164	KIAA0999	12.69	1.54
unactive progesterone receptor, 23 kD	BC003005	TEBP	80.55	1.50
heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	NM_005347	HSPA5	1.07	1.49
KIAA0931 protein	AB023148	KIAA0931		1.47
hypothetical protein My014	AB007957	MY014		1.43
thioredoxin	NM_003329	TXN	0.60	1.43
Homo sapiens cDNA FLJ39218 fis, clone OCBBF2006660	AK096537			1.42
KIAA0630 protein	AB014530	Nbak2		1.41
Wolf-Hirschhorn syndrome candidate 1-like 1	NM_023034	WHSC1L1		1.41
PI-3-kinase-related kinase SMG-1	NM_015092	SMG1		1.41
synaptosomal-associated protein, 23kDa	BC000148	SNAP23	30.44	1.41
SR rich protein	NM_032870	DKFZp564B0769		1.40
Homo sapiens cDNA FLJ37789 fis, clone BRHIP3000081	AK095108			1.39
protein phosphatase 1, catalytic subunit, gamma isoform	NM_002710	PPP1CC		1.39
ESTs	H28794			1.36
tumor necrosis factor (ligand) superfamily, member 13	NM_003808	TNFSF13		1.36
crystallin, lambda 1	NM_015974	CRYL1		1.35
crystallin, gamma C	NM_020989	CRYGC		1.35
PTD002 protein	NM_016144	PTD002		1.35
DnaJ (Hsp40) homolog, subfamily B, member 9	NM_012328	DNAJB9	0.70	1.33
heat shock protein 75	NM_016292	TRAP1	0.45	1.31
nucleolar protein NOP5/NOP58	NM_015934	NOP5/NOP58	158.68	1.30
cell division cycle 25A	NM_001789	CDC25A		1.30
hypothetical protein BC008988	BC008988	LOC91937	0.57	1.29
hypothetical protein FLJ33282	AB053301	FLJ33282		1.29
DnaJ (Hsp40) homolog, subfamily C, member 6	NM_014787	DNAJC6	0.79	1.28
Homo sapiens cDNA FLJ40369 fis, clone TESTI2034847	AK097688			1.28
hypothetical protein FLJ10482	NM_018107	RNPC4	87.16	1.28
KIAA1970 protein	AL832489	KIAA1970		1.27
diacylglycerol kinase, epsilon 64kDa	NM_003647	DGKE	124.74	1.26
clone MGC:9852 IMAGE:3865825, mRNA	BC009051	Data not found	0.01	1.26
CD48 antigen (B-cell membrane protein)	BC016182	CD48	196.45	1.26
hypothetical protein FLJ20422	BC005210	FLJ20422	17.37	1.26
mitochondrial carrier homolog 1	NM_014341	MTCH1		1.25
clone MGC:27375 IMAGE:4688423, mRNA	BC017422		46.55	1.24
hypothetical protein BC013949	NM_138442	LOC115098		1.24
formin-binding protein 17	AL049935	FNBP1		1.24
eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	BC013590	EIF2B5	26.71	1.24
heat shock 70kDa protein 2	NM_021979	HSPA2	0.47	1.24
ribosomal protein L10a	BC006791	RPL10A	10.56	1.23
apoptotic chromatin condensation inducer in the nucleus	NM_014977	ACINUS		1.23
ribosomal protein L34	NM_033625	RPL34	45.91	1.22
tumor-associated calcium signal transducer 1	NM_002354	TACSTD1	12.80	1.22
heat shock 70kDa protein 9B (mortalin-2)	BC000478	HSPA9B	48.40	1.22
EST	AA127063			1.20
hypothetical protein MGC4308	NM_032359	MGC4308	7.29	1.20
crystallin, beta A2	NM_057094	CRYBA2		1.19
CD47 antigen (integrin-associated signal transducer)	NM_001777	CD47		1.19
phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	NM_003557	PIP5K1A		1.19
kelch-like protein C3IP1	BC004175	C3IP1	0.37	1.17
DnaJ (Hsp40) homolog, subfamily B, member 11	NM_016306	DNAJB11	1.01	1.17
tubby like protein 3	BC032587	TULP3		1.17
MBD2 (methyl-CpG-binding protein)-interacting zinc finger protein	BC001073	MIZF	1.05	1.17
F-box and WD-40 domain protein 1B	NM_012300	FBXW1B		1.15
cDNA FLJ10023, moderately similar to KIAA0411	AK057565			1.15
catenin, beta interacting protein 1	BC014300		4.92	1.14
adaptor-related protein complex 2, beta 1 subunit	NM_001282	AP2B1		1.14
crystallin, beta B1	NM_001887	CRYBB1		1.13
MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	X74794	MCM4		1.13
hypothetical protein FLJ10404	BC008784	FLJ10404	0.92	1.12
chromosome 22 open reading frame 2	BC016139	C22orf2	5.15	1.11
amplified in osteosarcoma	BC007254	OS-9	0.91	1.11
guanine nucleotide binding protein 4	NM_004485	GNG4	18.65	1.10
Similar to histamine N-methyltransferase, clone MGC:14500	BC005907		23.00	1.08
unactive progesterone receptor, 23 kD	NM_006601	TEBP		1.08
ATPase inhibitor precursor	BC001867	ATPIF1	1.21	1.07
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Dros	BC005898	SFRS10	70.26	1.07
hypothetical protein MGC3036	BC001354	MGC3036	1.56	1.05
tRNA isopentenylpyrophosphate transferase	NM_017646	IPT	16.14	1.05
CD2 antigen (cytoplasmic tail) binding protein 2	AB033004	CD2BP2		1.04
v-crk sarcoma virus CT10 oncogene homolog (avian)	NM_016823	CRK		1.03
heat shock factor binding protein 1	BC007515	HSBP1	0.13	1.03
mannosidase, alpha, class 2B, member 1	BC007362			1.03
C-terminal PDZ domain ligand of neuronal nitric oxide synthase	AB007933	CAPON		1.03
hypothetical protein MGC2474	BC001361	MGC2474	19.18	1.02
Huntingtin interacting protein K	NM_016400	HYPK	85.42	1.01
hypothetical protein FLJ22369	NM_032221	CHD5	7.72	1.01
chaperonin containing TCP1, subunit 3 (gamma)	BC008019	CCT3		1.00
ferritin, light polypeptide	BC004245	FTL	70.46	1.00
hypothetical protein MGC10814	BC004943	MGC10814	18.44	1.00
chromosome 9 open reading frame 16	BC008887	C9orf16	0.72	0.99
DnaJ (Hsp40) homolog, subfamily B, member 5	NM_012266	DNAJB5	0.50	0.99
peroxisomal membrane protein 2, 22kDa	BC009836	PXMP2	0.70	0.99
hypothetical protein HSPC219	BC002863	HSPC219	1.51	0.99
cleavage and polyadenylation specific factor 2, 100kDa	AK001627	Data not found		0.98
DnaJ (Hsp40) homolog, subfamily C, member 8	NM_014280	DNAJC8	0.88	0.97
hypothetical protein FLJ20360	AL832762	FLJ20360		0.97
EST, Highly similar to densin-180 [Homo sapiens]	AA609242			0.96
kallikrein 10	NM_002776	KLK10		0.96
benzodiazapine receptor (peripheral)	BC001110	BZRP	0.27	0.95
KIAA1948 protein	AB075828	KIAA1948		0.95
KIAA0261 protein	D87450	KIAA0261		0.95
proliferation-associated 2G4, 38kDa	BC001951	PA2G4	0.07	0.94
microsomal glutathione S-transferase 1	BC005923	MGST1	17.70	0.94
eukaryotic translation initiation factor 5	BC007728	EIF5	38.47	0.94
mitotic phosphoprotein 44	NM_138285	LOC129401		0.94

sarcolemma associated protein	AB046821	SLMAP		0.93
ribosomal protein S6	BC009427	RPS6	0.11	0.93
hypothetical protein MGC4701	BC003648	MGC4701		0.93
signal recognition particle 54kDa	BC003389	SRP54	1.64	0.93
torsin family 1, member B (torsin B)	BC015578	TOR1B	0.61	0.91
tumor rejection antigen (gp96) 1	BC009195	TRA1	0.52	0.90
hypothetical protein HSPC228	BC005937	HSPC228	2.46	0.89
hypothetical protein FLJ10482	BC002566	RNPC4	0.96	0.89
serine proteinase inhibitor, clade B (ovalbumin), member 1	BC009015	SERPINB1	0.19	0.88
hypothetical protein PRO1853	BC004548	PRO1853	0.77	0.87
nucleoporin 88kDa	BC000335	NUP88	28.71	0.86
crystallin, zeta (quinone reductase)-like 1	NM_005111	CRYZL1		0.86
H19, imprinted maternally expressed untranslated mRNA	BC007513	H19	8.19	0.84
DnaJ (Hsp40) homolog, subfamily C, member 4	NM_005528	DNAJC4	0.94	0.84
similar to arginyl-tRNA synthetase	BC010420	LOC57038	0.93	0.84
aconitase 2, mitochondrial	NM_001098	ACO2	14.67	0.84
ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E-like 2 isofc	BC008981	ATP6V1E2	0.45	0.82
karyopherin (importin) beta 1	L38951	KPNB1		0.82
stromal cell-derived factor 2	BC001406	SDF2	0.53	0.81
DNA (cytosine-5-)-methyltransferase 2	NM_004412	DNMT2	19.35	0.81
BBP-like protein 2	BC008873	BLP2	60.77	0.80
hypothetical protein MGC21990	BC015422	ANKRD9	45.95	0.79
hypothetical protein FLJ10352	NM_032142	FLJ10352	11.47	0.79
DnaJ (Hsp40) homolog, subfamily B, member 12	NM_017626	DNAJB12	1.30	0.78
Homo sapiens EST from clone 37208, full insert	AL355686			0.78
excision repair cross-complementing, group 2 (x. pigmentosum D)	BC008346	ERCC2	0.57	0.78
ceramide kinase	NM_022766	CERK		0.77
cytochrome b5 reductase b5R.2	NM_016229	CYB5R2		0.76
zinc finger protein 359	BC007256	ZNF23	0.88	0.75
cutaneous T-cell lymphoma tumor antigen se70-2	BC000791	SE70-2	0.43	0.75
interferon, alpha 16	NM_002173	IFNA16	19.22	0.75
chromosome 21 open reading frame 51	NM_058182	C21orf51	55.88	0.74
protease, serine, 12 (neurotrypsin, motopsin)	NM_003619	PRSS12		0.71
hypothetical protein FLJ10468	BC001651	FLJ10468	0.61	0.69
interleukin 8	NM_000584	IL8	0.52	0.68
inhibitor of growth family, member 3	BC009777	ING3	2.40	0.67
peroxiredoxin 3	BC008038	PRDX3	6.34	0.66
putative N6-DNA-methyltransferase	NM_013240	N6AMT1		0.66
mutS homolog 5 (E. coli)	BC001358	MSH5	1.22	0.65
dystonia 1, torsion (autosomal dominant; torsin A)	BC000674	DYT1	1.14	0.65
tripartite motif-containing 39	BC007661	TRIM39	0.37	0.60
ESTs	H08304			0.60
activating transcription factor 5	BC005174	ATF5	2.64	0.59
ESTs	BF038515			0.57
serine/threonine kinase 35	AK024394	STK35		0.57
Homo sapiens clone 23556 mRNA sequence	AF035290			0.54
component of oligomeric golgi complex 7	BC000549	COG7		0.53
KIAA1387 protein	AB037808	KIAA1387		0.51
RAS p21 protein activator (GTPase activating protein) 1	NM_002890	RASA1		0.51
ESTs, similar to hypothetical protein FLJ20489 [Homo sapiens]	BM909488			0.51
hypothetical protein FLJ22570	BC004867	FLJ22570	0.39	0.50
hypothetical protein MGC4606	BC003640	MGC4606	0.80	0.49
ESTs	BG564282			0.46
ESTs	BI020159			0.44
DKFZP434D1335 protein	AK027643	DKFZP434D1335		0.38
ESTs	N46723	Data not found		0.37
KIAA0449 protein	AB007918	KIAA0449		0.35
sphingosine-1-phosphate lyase 1	AB033078	SGPL1		0.32
crystallin, alpha B	BC007008	CRYAB	4.31	-239.40
abhydrolase domain containing 3	NM_138340	ABHD3	0.77	
ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like :	NM_006437	ADPRTL1	2.93	
aldehyde dehydrogenase 6 family, member A1	BC004909	ALDH6A1	0.63	
adaptor-related protein complex 3, mu 2 subunit	NM_006803	AP3M2	0.83	
ADP-ribosylation factor 5	BC003043	ARF5	0.77	
actin related protein M1	BC007289	ARPM1	8.72	
acetylserotonin O-methyltransferase	NM_004043	ASMT	0.76	
ATPase, Na+/K+ transporting, beta 3 polypeptide	BC011835	ATP1B3	1.18	
ATPase, Ca++ transporting, plasma membrane 3	NM_021949	ATP2B3	22.63	
B7 homolog 3	NM_025240	B7-H3	1.21	
BCL2-associated athanogene 3	NM_004281	BAG3	23.37	
beta-carotene dioxygenase 2	NM_031938	BCDO2	3.36	
chromosome 17 open reading frame 1A	NM_031456	C17orf1A	2.95	
chromosome 1 open reading frame 2	NM_006589	C1orf2	1.27	
chromosome 21 open reading frame 62	NM_019596	C21orf62	3.86	
chromosome 4 open reading frame 6	NM_005750	C4orf6	8.87	
chromosome 6 open reading frame 10	NM_006781	C6orf10	1.86	
chromosome 6 open reading frame 37	BC007351	C6orf37	0.28	
calcium channel, voltage-dependent, L type, alpha 1C subunit	NM_000719	CACNA1C		
calneuron 1	NM_031468	CALN1	0.46	
calpain 3, (p94)	BC003169	CAPN3	0.37	
calcium-sensing receptor	NM_000388	CASR	3.01	
chemokine (C-C motif) ligand 20	NM_004591	CCL20	5.55	
cyclin D3	BC011616	CCND3	0.62	
CD69 antigen (p60, early T-cell activation antigen)	BC007037	CD69	1.13	
cyclin-dependent kinase 5, regulatory subunit 2 (p39)	NM_003936	CDK5R2		
centromere protein A, 17kDa	BC000881	CENPA	0.56	
hypothetical protein from BCRA2 region	BC010643	CG005	1.02	
CGI-31 protein	NM_015959	CGI-31	4.13	
choroideremia-like (Rab escort protein 2)	NM_001821	CHML	0.49	
CDC28 protein kinase 2	BC006458	CKS2	0.48	
C-type lectin-like receptor-1	NM_016511	CLEC1	0.52	
collagen, type VI, alpha 3	NM_004369	COL6A3	1.93	
cystatin SN	NM_001898	CST1	3.63	
cystatin SA	NM_001322	CST2	6.13	
cystatin S	NM_001899	CST4	2.33	
catenin (cadherin-associated protein), delta 1	NM_001331	CTNND1	0.70	
cytochrome P450, subfamily XXXIX, polypeptide 1	BC010358	CYP39A1	0.40	
ESTs	BE928544	Data not found		
ESTs	R55848	Data not found		
ESTs, Weakly similar to endogenous retroviral family W, env(C7), m	BE883514	Data not found		
tetraspanin similar to TM4SF9	BC002920	DC-TM4F2	1.59	
KIAA1885 protein	BC008844	DKFZP434L1435	0.24	
hypothetical protein DKFZp434N0650	BC009497	DKFZp434N0650	2.04	
DKFZP564D116 protein	BC009494	DKFZP564D116	0.77	
DKFZP586G1517 protein	BC017477	DKFZP586G1517	1.34	
hypothetical protein DKFZp761F2014	NM_020215	DKFZp761F2014	3.52	
similar to MRJ gene for a member of the DNAJ protein family (H. sap	NM_058246	DNAJB6	1.70	
down-regulator of transcription 1, TBP-binding (negative cofactor 2)	AL833729	DR1		
ectodysplasin 1, anhidrotic receptor	NM_022336	EDAR		
Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	NM_000569	FCGR3A	0.51	
complement factor H related 3	NM_021023	FHR-3	1.82	
hypothetical protein FKSG44	NM_031904	FKSG44	0.54	

cDNA FLJ00103	BC012332	FLJ00103	29.18
hypothetical protein FLJ11078	NM_018316	FLJ11078	2.12
hypothetical protein FLJ11715	NM_024564	FLJ11715	1.00
hypothetical protein FLJ13441	NM_023924	FLJ13441	5.23
hypothetical protein FLJ13881	NM_024729	FLJ13881	0.04
hypothetical protein FLJ14126	NM_024849	FLJ14126	7.77
hypothetical protein FLJ14981	NM_032868	FLJ14981	2.08
hypothetical protein FLJ20323	NM_019005	FLJ20323	0.97
hypothetical protein FLJ20333	AB037754	FLJ20333	
hypothetical protein FLJ20417	NM_017810	FLJ20417	0.59
hypothetical protein FLJ20950	NM_024952	FLJ20950	1.47
hypothetical protein FLJ21616	BC009259	FLJ21616	0.15
hypothetical protein FLJ23018	NM_024810	FLJ23018	0.52
hypothetical protein FLJ23594	NM_024781	FLJ23594	0.53
FXYD domain containing ion transport regulator 2	BC013289	FXYD2	9.65
guanine deaminase	NM_004293	GDA	0.75
gap junction protein, beta 3, 31kDa (connexin 31)	BC012918	GJB3	0.27
golgi phosphoprotein 2	NM_016548	GOLPH2	0.74
G protein-coupled receptor 7	NM_005285	GPR7	0.19
G protein-coupled receptor, family C, group 5, member B	NM_016235	GPRC5B	2.96
heme oxygenase (decycling) 1	NM_002133	HMOX1	5.83
heterogeneous nuclear ribonucleoprotein K	BC000355	HNRPK	1.44
hypothetical protein HSPC111	NM_016391	HSPC111	4.62
hypothetical protein HSPC138	BC015991	HSPC138	0.53
islet amyloid polypeptide	NM_000415	IAPP	0.68
interferon, gamma-inducible protein 16	BC017059	IFI16	0.49
interferon gamma receptor 2 (interferon gamma transducer 1)	BC003624	IFNGR2	0.49
interleukin 18 binding protein	NM_005699	IL18BP	3.67
inactivation escape 1	NM_003669	INE1	0.32
integrin, alpha M	NM_000632	ITGAM	5.70
potassium voltage-gated channel, shaker-related subfamily, beta me	NM_003636	KCNAB2	3.17
potassium voltage-gated channel, subfamily G, member 2	NM_012283	KCNG2	0.57
KIAA0102 gene product	BC008063	KIAA0102	0.30
KIAA0410 gene product	NM_014778	KIAA0410	0.49
KIAA0663 gene product	NM_014827	KIAA0663	0.40
KIAA0971 protein	BC001544	KIAA0971	0.38
KIAA1049 protein	BC011884	KIAA1049	12.59
densin-180	NM_020794	KIAA1365	2.26
lymphocyte-specific protein tyrosine kinase	BC013200	LCK	0.28
leukocyte receptor cluster (LRC) member 4	BC002512	LENG4	0.30
lectin, galactoside-binding, soluble, 3 (galectin 3)	NM_002306	LGALS3	0.26
hypothetical protein LOC51061	NM_015914	LOC51061	0.60
similar to prokaryotic-type class I peptide chain release factors	BC014428	LOC54516	3.79
KIAA1634 protein	AB046854	MAGI-3	
mastermind-like 1 (Drosophila)	NM_014757	MAML1	
microtubule-associated protein 2	NM_002374	MAP2	2.09
hypothetical protein MGC10820	BC004269	MGC10820	0.26
hypothetical protein MGC13183	NM_032358	MGC13183	0.48
hypothetical gene MGC16733 similar to CG12113	BC009995	MGC16733	0.39
hypothetical protein MGC4189	BC004451	MGC4189	2.46
hypothetical protein MGC5309	BC003353	MGC5309	0.61
hypothetical protein MGC5370	BC006795	MGC5370	0.28
hypothetical protein MGC5590	NM_024058	MGC5590	0.45
hypothetical protein MGC8721	BC015012	MGC8721	106.35
microrchidia homolog (mouse)	NM_014429	MORC	0.28
mitochondrial ribosomal protein L30	NM_016503	MRPL30	0.59
mitochondrial ribosomal protein L51	NM_016497	MRPL51	0.70
mitochondrial ribosomal protein S6	NM_032476	MRPS6	0.57
membrane-spanning 4-domains, subfamily A, member 6A	NM_022349	MS4A6A	2.52
microsomal triglyceride transfer protein (large polypeptide, 88kDa)	NM_000253	MTP	1.01
myeloid differentiation primary response gene (88)	BC013589	MYD88	0.87
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	BC000855	NDUFB4	46.70
nuclear factor I/B	BC001283	NFIB	0.78
putative small membrane protein NID67	BC009719	NID67	0.51
neuronatin	NM_005386	NNAT	3.87
putative nucleolar RNA helicase	NM_019082	NOH61	
ovarian carcinoma immunoreactive antigen	BC003409	OCIA	2.54
oxysterol binding protein-like 2	NM_014835	OSBPL2	0.58
hypothetical protein P1 p373c6	BC014031	P1P373C6	0.74
prostate cancer associated protein 7	AL137559	PCANAP7	
protocadherin gamma subfamily A, 4	NM_018917	PCDHGA4	0.79
hypothetical protein MGC1346	NM_032758	PHF5A	2.92
plasminogen-like	BC005379	PLGL	3.64
phosphomevalonate kinase	BC007694	PMVK	5.58
PR domain containing 4	NM_012406	PRDM4	2.05
protein kinase C substrate 80K-H	NM_002743	PRKCSH	32.82
protein kinase, cGMP-dependent, type II	NM_006259	PRKG2	2.27
pleiotrophin (heparin binding growth factor 8, neurite growth-promo	NM_002825	PTN	2.56
RNA binding motif protein 3	BC006825	RBM3	0.36
putative c-Myc-responsive	BC011683	RCL	0.55
replication initiation region protein (60kD)	BC001760	RIP60	0.23
ribosomal protein L10a	BC011366	RPL10A	0.40
serum amyloid A4, constitutive	NM_006512	SAA4	
sterol-C4-methyl oxidase-like	BC010653	SC4MOL	1.52
splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate spli	BC010264	SFRS1	0.53
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Dros	BC000160	SFRS10	0.34
sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltrar	NM_003896	SIAT9	3.06
solute carrier family 25 (mitochondrial deoxynucleotide carrier), mer	BC005120	SLC25A19	0.19
NS1-associated protein 1	BC005110	SNX14	0.16
taste receptor, type 2, member 14	NM_023922	TAS2R14	0.34
TBC1 domain family, member 5	NM_014744	TBC1D5	
tumor necrosis factor receptor superfamily, member 6	BC012479	TNFRSF6	0.26
testis specific protein 1 (probe H4-1 p3-1)	NM_003296	TPX1	0.50
ubiquitin D	BC012472	UBD	4.06
ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	BC006305	UCHL1	2.18
WD repeat domain 4	BC006341	WDR4	0.35
ribosomal protein, large, P0	BC000673		2.33
Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete	BC009447		0.51
Homo sapiens, clone MGC:10077 IMAGE:3896690, mRNA, complete	BC010732		0.26
ESTs	AI125564		
ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapier	AI733650		
ESTs, Weakly similar to PIHUB6 salivary proline-rich protein precurs	BG538389		

	Gene Name	Acc#	ChIP enrich	Induced Expression	Highest Scoring HSE
BOUND & INDUCED	hypothetical protein FLJ13063	BC014945	12.68	89.65	TTCTGGGCTGTTCG
46	heat shock 70kDa protein 1A	NM_005345	245.65	58.54	TACTGGAAAGTTCC
	DnaJ (Hsp40) homolog, subfmaily B, member 1	NM_006145	17.12	38.72	CTCTGGAAGCTTCC
	heat shock 27kDa protein 2	NM_001541	22.12	34.90	TCCTGGAAACTTCT
	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2	NM_001235	111.29	21.53	TTCCAGAAGTTTCT
	heat shock 70kDa protein 6 (HSP70B')	NM_002155	312.89	20.59	TTCGCGAAAGTTCG
	mitochondrial ribosomal protein L18	NM_014161	67.66	17.16	TTCTAGAAGGCACT
	chromosome 6 open reading frame 37	NM_017633	16.75	17.09	TTCTCGAAACCTCG
	heat shock protein (hsp110 family)	NM_014278	23.07	14.45	TTCGAGAAAGATCT
	heat shock 105kD	NM_006644	653.34	13.40	TTCTGGAAAGTTCT
	tumor necrosis factor receptor superfamily, member 21	BC005192	31.39	10.63	TTCTGGAAATTACT
	heat shock 27kDa protein 1	NM_001540	174.23	10.11	ATCTGGAAACCTTCT
	relaxin 1 (H1)	BC005956	58.72	9.96	ACCCTGAAACAACT
	death effector domain-containing DNA binding protein 2	BC013372	13.98	6.44	TTCTGGCACCTTCT
	collagen, type IV, alpha 6	NM_033641	6.07	5.69	TTCTTGAAGATTCT
	FK506 binding protein 4, 59kDa	NM_002014	6.28	5.24	CTCTAGAAAGTTCT
	hypothetical protein FLJ22693	NM_022750	9.26	4.95	TTCTGGAAGATTCC
	crystallin, beta A4	NM_001886	29.57	4.68	ACCTGGGACTTACC
	ubiquitin B	BC015127	347.68	4.46	CTCTGGAAACTTCC
	ribosomal protein S14	BC006784	6.54	3.85	CCCCAGAAACTACC
	hypothetical protein MGC10814	NM_032671	16.49	3.79	TTCTAGAAAGTTCT
	GPI anchored molecule like protein	NM_002066	55.60	3.75	TTCTAGAACATTCC
	DnaJ (Hsp40) homolog, subfamily B, member 6	NM_005494	70.75	3.68	TTCGCGAAGGTTCT
	heat shock 70kDa protein 1-like	NM_005527	238.60	3.47	TACTGGAAAGTTCC
	glioblastoma amplified sequence	BC001837	35.49	3.42	CTCTGGACAGCTCT
	MHC class I polypeptide-related sequence A	NM_000247	45.89	3.34	CACTGGAATTTTCT
	G protein-coupled receptor 4	NM_005282	44.42	3.29	TTCCAGAACCTTCT
	hypothetical protein LOC63929	NM_022098	159.88	3.14	
	heat shock 90kDa protein 1, beta	NM_007355	220.28	2.96	TTCTGGAAGCTTCT
	Siah-interacting protein	BC005975	60.99	2.94	ATCTCGAACCTTCG
	hypothetical protein P15-2	NM_018698	241.38	2.92	TTCTGGAACGTTCT
	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	NM_005642	116.50	2.81	TTCTGGAAACATCT
	suppressor of G2 allele of SKP1, S. cerevisiae, homolog of	NM_006704	13.18	2.72	CTCCAGAAGTTTCC
	hypothetical protein MGC8721	NM_016127	41.74	2.66	TTCGGGAAGCTTCT
	chromosome 14 open reading frame 3	NM_012111	36.45	2.56	TTCTAGTAGTTTCC
	myotubularin related protein 8	BC012399	5.92	2.52	CTCTTGGCTCCTCC
	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	BC002987	226.45	2.48	TTCTGGAAATTTCC
	coagulation factor VIII, procoagulant component (hemophilia A)	NM_000132	21.39	2.19	TTCTAGAATCTTCG
	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	NM_003932	174.17	2.17	TTCTAGAAGATTCT
	hypothetical protein FLJ10830	BC003176	21.30	2.15	ATCTCGAAGGTTCT
	heat shock 10kDa protein 1 (chaperonin 10)	NM_002157	154.26	2.14	TTCTGGAAAGTTCT
	fragile X mental retardation, autosomal homolog 1	NM_005087	26.53	2.06	CTCTTGCATTTTCC
	fibroblast growth factor 18	BC006245	8.01	2.03	
	cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	NM_012124	104.88	2.03	TTCGCGAAGGTTCC
	frizzled homolog 4 (Drosophila)	NM_012193	15.20	1.97	CCCCGGGACGCTCG
	heat shock 60kDa protein 1 (chaperonin)	NM_002156	415.79	1.95	TTCTGGAAAGTTCT
INDUCED NOT BOUND	DnaJ (Hsp40) homolog, subfamily C, member 3	NM_006260	0.52	49.76	TTCCAGGAAATTCA
24	hypothetical protein DKFZp564I0422	NM_031435	1.83	18.86	ACCCAGCAGCTACC
	DnaJ (Hsp40) homolog, subfamily B, member 4	NM_007034	0.76	14.67	TACCGGAAGGTACC
	N-acetylated alpha-linked acidic dipeptidase 2	NM_005467	0.33	12.29	TTGTGGAATGTTCC
	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKFZp434B102)	BC030800	0.39	11.68	TTTGTGGAGGTTCT
	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	NM_004213	0.20	6.56	CTCCTGGACTTTCC
	DKFZP434I1735 protein	AB037737	0.30	5.88	
	crystallin, mu	NM_001888	4.37	5.60	TTCCAGGAGTTTTT
	protein kinase anchoring protein GKAP42	NM_025211	0.24	4.14	CTCCAGAAATTTCC
	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype incluc	NM_000148	0.65	3.24	TACTGGACTCTTCC
	heat shock 27kDa protein 3	NM_006308	0.32	3.19	ATCTTGGAGATTCT
	cysteine-rich, angiogenic inducer, 61	BC009199	1.70	3.18	
	protein kinase C, alpha	NM_002737	0.35	3.16	CTCGTGCACGTTCT
	hypothetical protein FLJ20558	NM_017880	1.04	3.04	TCCCGGCATCCTCC
	nuclear receptor coactivator 3	NM_006534	1.63	2.62	TTCTGGGACGCACG
	brain-specific protein p25 alpha	NM_007030	0.62	2.62	CTCTGGGAAGGTCC
	PR domain containing 2, with ZNF domain	NM_012231	0.47	2.38	TTCCACCAAGTTCT
	CDC-like kinase 4	NM_020666	0.36	2.32	TTCTCAAATTCTCC
	VCY2 interacting protein 1	BC008806	0.47	2.18	CTCCGGAACCTTCT
	crystallin, gamma D	NM_006891	3.76	2.06	TCCCAGCACTTTCG
	crystallin, beta A1	NM_005208	0.74	2.06	CCCTAGAAGGCTCT
	crystallin, beta B3	NM_004076	0.28	2.04	TCCCAGAATGAACC
	crystallin, gamma A	NM_014617	1.18	1.99	TTCTGGCATTTTCG
	Homo sapiens, clone MGC:15478 IMAGE:2967661, mRNA, complete cds	BC010426	1.11	1.97	CCCTCGGAGCTTCT
BOUND NOT INDUCED	DnaJ (Hsp40) homolog, subfamily A, member 1	NM_001539	325.10	1.76	TTCTGGAAAGTTCC
48	CD48 antigen (B-cell membrane protein)	BC016182	196.45	1.26	TTCCAGCCTCTTCT
	heat shock 70kDa protein 8	NM_006597	191.34	1.83	TTCTGGAAGGTTCT
	nucleolar protein NOP5/NOP58	NM_015934	158.68	1.30	TTCCAGAATGTTCC
	diacylglycerol kinase, epsilon 64kDa	NM_003647	124.74	1.26	TTCCAGAATTTTCT
	chaperonin containing TCP1, subunit 4 (delta)	NM_006430	108.93	1.77	TTCTGGAAGGTTCG
	hypothetical protein FLJ10482	NM_018107	87.16	1.28	TTCCAGAACCTTCC
	Huntingtin interacting protein K	NM_016400	85.42	1.01	TCCCTGAAGCTTCT
	unactive progesterone receptor, 23 kD	BC003005	80.55	1.50	CCCCAGAATGCACC
	retinoblastoma binding protein 2	NM_005056	72.94	1.89	TTCCGGAAGTTACC
	ferritin, light polypeptide	BC004245	70.46	1.00	CTCTGGAACCCTCC
	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	BC005898	70.26	1.07	TTCTAGAACTTTCC
	BBP-like protein 2	BC008873	60.77	0.80	TTCCAGAAAGTTCC
	chromosome 21 open reading frame 51	NM_058182	55.88	0.74	TTCTTGAAGGTTCT
	heterogeneous nuclear ribonucleoprotein A2/B1	NM_002137	55.24	1.60	TTCTAGAACCTTCC
	serine hydrolase-like	NM_014509	54.05	1.67	TTCTAGAAGGTTCT
	heat shock 70kDa protein 9B (mortalin-2)	BC000478	48.40	1.22	TTCTGGAAACCTCC
	Homo sapiens, clone MGC:27375 IMAGE:4688423, mRNA, complete cds	BC017422	46.55	1.24	ATCTTGAAATTTCT
	hypothetical protein MGC21990	BC015422	45.95	0.79	CCCCTGGAGCCTCT
	ribosomal protein L34	NM_033625	45.91	1.22	TTCAAGAACCTTCC
	eukaryotic translation initiation factor 5	BC007728	38.47	0.94	

	ATPase, Ca++ transporting, type 2C, member 1	NM_014382	33.12	1.77	TTCTAGAAACTTCC
	synaptosomal-associated protein, 23kDa	BC000148	30.44	1.41	TTCTGGAAATTTCT
	nucleoporin 88kDa	BC000335	28.71	0.86	ATCCAGAACTTTCC
	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	BC013590	26.71	1.24	
	Homo sapiens, Similar to histamine N-methyltransferase, clone MGC:14500 IMAGE:4249	BC005907	23.00	1.08	
	carboxypeptidase E	NM_001873	19.95	1.89	TTCTGGAATATTCT
	DNA (cytosine-5-)-methyltransferase 2	NM_004412	19.35	0.81	TTCTGGAATCTTCT
	interferon, alpha 16	NM_002173	19.22	0.75	TTCATGAAGATTCC
	hypothetical protein MGC2474	BC001361	19.18	1.02	TTCTGGGAGCTTCT
	guanine nucleotide binding protein 4	NM_004485	18.65	1.10	TTCTGGAACCTTCT
	microsomal glutathione S-transferase 1	BC005923	17.70	0.94	TTCTCGAACATTTC
	hypothetical protein FLJ20422	BC005210	17.37	1.26	
	KIAA0721 protein	BC009116	16.37	1.60	TTCCAGACCTTTCG
	tRNA isopentenylpyrophosphate transferase	NM_017646	16.14	1.05	TTCTAGAACTTTCT
	aconitase 2, mitochondrial	NM_001098	14.67	0.84	TTCCCGAAGCTTCC
	tumor-associated calcium signal transducer 1	NM_002354	12.80	1.22	TTCTGGAAGGTTCT
	KIAA0999 protein	NM_025164	12.69	1.54	TACCAGAACCTTCC
	MORF-related gene X	NM_012286	11.75	1.94	CACGTGAACATTCT
	hypothetical protein FLJ10352	NM_032142	11.47	0.79	TTCTGGAATTTTCC
	ribosomal protein L10a	BC006791	10.56	1.23	CTCTCGAAGGTTCC
	forkhead box J1	NM_001454	9.76	1.67	TTCCAGAACCTTCC
	peptidylprolyl isomerase D (cyclophilin D)	NM_005038	8.93	1.85	TTCTGGAAATTTCT
	H19, imprinted maternally expressed untranslated mRNA	BC007513	8.19	0.84	
	hypothetical protein FLJ22369	NM_032221	7.72	1.01	TTCTAGAATTTTCT
	hypothetical protein MGC4308	NM_032359	7.29	1.20	TTCTAGAAGGTTCT
	peroxiredoxin 3	BC008038	6.34	0.66	TCCGGGAAGGTTCC
	chromosome 22 open reading frame 2	BC016139	5.15	1.11	TACTAGAAAATTCC
NOT BOUND NOT INDUCED	catenin, beta interacting protein 1	BC014300	4.92	1.14	CTCTAGGAACCACC
58	crystallin, alpha B	BC007008	4.31		TCCTGGAAACTTCT
	activating transcription factor 5	BC005174	2.64	0.59	
	hypothetical protein HSPC228	BC005937	2.46	0.89	CCCCAGAAGAAACC
	inhibitor of growth family, member 3	BC009777	2.40	0.67	AACTGGCAGCCTCG
	signal recognition particle 54kDa	BC003389	1.64	0.93	CCCCCGGAGTCTCT
	hypothetical protein MGC3036	BC001354	1.56	1.05	TTCCGGAAGATTCT
	hypothetical protein HSPC219	BC002863	1.51	0.99	TTCTGGACAGCTCT
	DnaJ (Hsp40) homolog, subfamily B, member 12	NM_017626	1.30	0.78	CTCCAGACGGCTCG
	mutS homolog 5 (E. coli)	BC001358	1.22	0.65	CTCTAGCACTCACT
	ATPase inhibitor precursor	BC001867	1.21	1.07	
	dystonia 1, torsion (autosomal dominant; torsin A)	BC000674	1.14	0.65	TCCCTGCAATTTCC
	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	NM_005347	1.07	1.49	CCCGAGGCATTTCC
	MBD2 (methyl-CpG-binding protein)-interacting zinc finger protein	BC001073	1.05	1.17	TTCTAGGCTCATCT
	DnaJ (Hsp40) homolog, subfamily B, member 11	NM_016306	1.01	1.17	TCCTCGGACTTTCC
	DnaJ (Hsp40) homolog, subfamily C, member 4	NM_005528	0.94	0.84	ACCTGGGAGCCTCC
	crystallin, beta B2	NM_000496	0.94	1.86	TTCCAGGCTTTTCT
	similar to arginyl-tRNA synthetase	BC010420	0.93	0.84	TTACAGAAAGTTCT
	hypothetical protein FLJ10404	BC008784	0.92	1.12	TCCTAGTACCTTCT
	amplified in osteosarcoma	BC007254	0.91	1.11	ACCTTGGAGCCACG
	DnaJ (Hsp40) homolog, subfamily C, member 8	NM_014280	0.88	0.97	CCCGAGACGTTTCT
	zinc finger protein 359	BC007256	0.88	0.75	TCCCTGACTCTACC
	hypothetical protein MGC4606	BC003640	0.80	0.49	TCCTCGGCCTTACC
	DnaJ (Hsp40) homolog, subfamily C, member 6	NM_014787	0.79	1.28	TACTTGAATCCTCC
	hypothetical protein PRO1853	BC004548	0.77	0.87	ACCTTGAAGGTACC
	chromosome 9 open reading frame 16	BC008887	0.72	0.99	TTCGGGGACACTCG
	peroxisomal membrane protein 2, 22kDa	BC009836	0.70	0.99	
	DnaJ (Hsp40) homolog, subfamily B, member 9	NM_012328	0.70	1.33	CTCGGGCAGCTTCT
	torsin family 1, member B (torsin B)	BC015578	0.61	0.91	CTCGCGGCAGCACT
	hypothetical protein FLJ10468	BC001651	0.61	0.69	TCCCCGCAGCCTCC
	thioredoxin	NM_003329	0.60	1.43	CTCCGGAATTTACC
	excision repair cross-complementing rodent repair deficiency, complementation group 2 (	BC008346	0.57	0.78	CACGCGCAGTATCC
	hypothetical protein BC008988	BC008988	0.57	1.29	CTCTGGAAACTTCT
	crystallin, gamma S	NM_017541	0.56	1.55	ATCTTGAACCTTTC
	stromal cell-derived factor 2	BC001406	0.53	0.81	TCCCAGACCACACT
	tumor rejection antigen (gp96) 1	BC009195	0.52	0.90	TTCCAGGAGTCTCC
	TAL1 (SCL) interrupting locus	NM_003035	0.52	1.87	ACCTTGAATGCTCG
	interleukin 8	NM_000584	0.52	0.68	TTCCTGAATATTCT
	DnaJ (Hsp40) homolog, subfamily B, member 5	NM_012266	0.50	0.99	CTCCGGAAAGCTCC
	heat shock 70kDa protein 2	NM_021979	0.47	1.24	CTCGTGAATTTTCC
	carbohydrate (chondroitin 6) sulfotransferase 3	NM_004273	0.46	1.87	CTCCTGCACTTTCC
	heat shock protein 75	NM_016292	0.45	1.31	CTCCTGGAGCTTCG
	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E-like 2 isoform 2	BC008981	0.45	0.82	CTCTAGAACTTTTT
	cutaneous T-cell lymphoma tumor antigen se70-2	BC000791	0.43	0.75	AACCTGAATTTTCC
	hypothetical protein FLJ22570	BC004867	0.39	0.50	TTCTGGCCACTTCC
	tripartite motif-containing 39	BC007661	0.37	0.60	
	kelch-like protein C3IP1	BC004175	0.37	1.17	TTCAGGAAAATTCT
	WD-repeat protein	NM_005828	0.35	1.66	TCCCTGCACCTTCC
	WEE1+ homolog (S. pombe)	NM_003390	0.35	1.80	CTCGGGACCTTTCT
	benzodiazapine receptor (peripheral)	BC001110	0.27	0.95	ATCTGGACTGTTCT
	homeodomain interacting protein kinase 3	NM_005734	0.26	1.70	TCCTTTAAACTTCC
	SBBI26 protein	NM_018846	0.24	1.87	TTCTAGAAATCTTC
	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	BC009015	0.19	0.88	TACTGGAACTTTGG
	TEA domain family member 1 (SV40 transcriptional enhancer factor)	AL833289	0.18	1.93	
	heat shock factor binding protein 1	BC007515	0.13	1.03	TTCTGGAAGCGTCT
	ribosomal protein S6	BC009427	0.11	0.93	TCCGTGGCGCCTCG
	proliferation-associated 2G4, 38kDa	BC001951	0.07	0.94	ACCTGGAAGCTTCT
	Homo sapiens, clone MGC:9852 IMAGE:3865825, mRNA, complete cds	BC009051	0.01	1.26	

ACC#	Gene name	Induced expression	bp separating TSS	ACC#	Gene name	Induced expression	chr
NM_003932	suppression of tumorigenicity 13 (colon carcinoma)	2.17	414	NM_022098	hypothetical protein LOC63929	3.14	chr22
BC000665	t-complex 1	1.63	880	NM_014161	mitochondrial ribosomal protein L18	17.16	chr6
AK022769	hypothetical protein FLJ12707	1.82	470	NM_012111	chromosome 14 open reading frame 3	2.56	chr14
AK056363	hypothetical protein MGC20983	1.81	566	NM_002743	protein kinase C substrate 80K-H		chr19
BC015679	hypothetical protein MGC23401		145	NM_031435	hypothetical protein DKFZp564I0422	18.86	chr12
NM_031435	hypothetical protein DKFZp564I0422	18.86	145	NM_144982	hypothetical protein MGC23401	1.32	chr3

Supplemental Table 1 – Complete data set of all genes considered for this study. The first column is the gene name. The second column is the accession number of the mRNA sequence used to measure the expression of the gene and to predict the promoter for the ChIP and luciferase experiments. The third column is the gene symbol. The fourth column is the HSF1 ChIP fold-enrichment measurement, and the last column is the fold-induced expression measurement as measured by real-time RT-PCR.

Supplemental Table 2 – Complete data set for the 176 genes assayed for both induced expression and HSF1 binding. The first column is the name of the category. The second column is the gene name. The third column is the accession number of the gene. The fourth column is the ChIP-enrichment measurement. The fifth column is the fold-induced expression measurement, and the last column is the highest scoring HSE in the promoter region of the gene as determined by the HSE PSSM evaluation.

Supplemental Table 3 – Heat shock genes arranged in an head-to-head orientation in the genome. This table describes the heat shock genes that use a potential bidirectional promoter. Included are the gene names, the induced expression measurements of each gene, the estimated distance between transcription start sites and the chromosome on which the pair is located.