Table S8. Common genes downregulated by live *Borrelia burgdorferi* (Bb) alone or combined with IL-10 at 24 h post-stimulation

		Fold Change		
Gene number	Annotation	Live Bb	Live Bb + IL-10	Description/function
				Enzyme
AK160524	PDPR	-1.38	-2.03	pyruvate dehydrogenase phosphatase regulatory subunit
NM_009662	ALOX5	-2.9	-1.98	arachidonate 5-lipoxygenase
NM_177305	ARL4C	-2.18	-2.06	ADP-ribosylation factor-like 4C
NM_007550	BLM	-1.7	-1.38	Bloom syndrome, RecQ helicase-like
NM_178309	BRIP1	-1.6	-1.23	BRCA1 interacting protein C-terminal helicase 1
NM_016803	CHST3	-1.69	-2.13	carbohydrate (chondroitin 6) sulfotransferase 3
NM_013495	CPT1A	-1.6	-1.38	carnitine palmitoyltransferase 1A (liver)
NM_010049	DHFR	-1.72	-1.17	dihydrofolate reductase
NM_023595	DUT (includes EG:1854)	-2.18	-1.66	deoxyuridine triphosphatase
NM_028013	ENDOD1	-1.89	-1.19	endonuclease domain containing 1
NM_012012	EXO1	-2.45	-2.39	exonuclease 1
NM_025995	FBXO5	-1.96	-2.11	F-box protein 5
NM_021891	FIGNL1	-2.51	-1.94	fidgetin-like 1
NM_010401	HAL	-1.71	-2.25	histidine ammonia-lyase
NM_008234	HELLS	-1.24	-1.2	helicase, lymphoid-specific
NM_133815	LBR	-1.99	-1.47	lamin B receptor
NM_010715	LIG1	-2.02	-1.35	ligase I, DNA, ATP-dependent
NM_010764	MAN2B1	-1.8	-1.39	mannosidase, alpha, class 2B, member 1
NM_008563	MCM3	-1.86	-1.37	minichromosome maintenance complex component 3
NM_008567	MCM6	-2.35	-1.54	minichromosome maintenance complex component 6
NM_008568	MCM7	-2.42	-1.48	minichromosome maintenance complex component 7
AK008211	MGST3	-1.57	-1.49	microsomal glutathione S-transferase 3
NM_138315	MICAL1	-1.86	-1.09	microtubule associated monoxygenase, calponin and LIM domain containing 1
XM_193936	KIF20B	-1.48	-2.73	kinesin family member 20B
NM_146208	NEIL3	-2.54	-2.05	nei endonuclease VIII-like 3 (E. coli)
NM_011131	POLD1	-1.79	-1.19	polymerase (DNA directed), delta 1, catalytic subunit 125kDa
NM_011132	POLE	-2.33	-1.85	polymerase (DNA directed), epsilon
XM_979374	PPIL5	-2.41	-1.96	peptidylprolyl isomerase (cyclophilin)-like 5
NM_008969	PTGS1	-2.38	-1.55	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
NM_011226	RAB19	-1.97	-1.27	RAB19, member RAS oncogene family
NM_011234	RAD51	-2.76	-2.14	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
BC089001	RFC5	-1.97	-1.22	replication factor C (activator 1) 5, 36.5kDa
NM_023275	RHOJ	-1.44	-1.42	ras homolog gene family, member J
NM_021472	RNASE4	-1.78	-1.34	ribonuclease, RNase A family, 4
NM_009104	RRM2	-3.42	-2.13	ribonucleotide reductase M2
NM_018822	SGSH	-1.67	-1.09	N-sulfoglucosamine sulfohydrolase
NM_009183	ST8SIA4	-3.2	-2.09	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4

NM_009405	TNNI2	-1.48	-1.19	troponin I type 2 (skeletal, fast)
NM_011623	TOP2A	-2.06	-1.59	topoisomerase (DNA) II alpha 170kDa
NM_021288	TYMS	-1.1	-1.65	thymidylate synthetase
NM_026785	UBE2C	-2.5	-2.54	ubiquitin-conjugating enzyme E2C
NM_026024	UBE2T	-2.97	-2.36	ubiquitin-conjugating enzyme E2T (putative)
BC066035	ZRANB3	-1.34	-1.07	zinc finger, RAN-binding domain containing 3
				G-protein coupled receptor
NM_009910	CXCR3	-2.1	-1.61	chemokine (C-X-C motif) receptor 3
NM_009911	CXCR4	-1.82	-1.59	chemokine (C-X-C motif) receptor 4
NM_007901	S1PR1	-1.53	-1.36	sphingosine-1-phosphate receptor 1
				Growth factor
NM_027950	OSGIN1	-1.34	-1.17	oxidative stress induced growth inhibitor 1
NM_019521	GAS6	-2.46	-2.06	growth arrest-specific 6
NM_013598	KITLG	-2.16	-2.71	KIT ligand
NM_009368	TGFB3	-1.11	-1.26	transforming growth factor, beta 3
				Kinase
NM_011497	AURKA	-2.09	-1.77	aurora kinase A
NM_011496	AURKB	-2.84	-2.18	aurora kinase B
NM_009772	BUB1	-2.2	-1.95	budding uninhibited by benzimidazoles 1 homolog (yeast)
NM_009773	BUB1B	-1.48	-1.22	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
NM_007659	CDK1	-1.7	-1.73	cyclin-dependent kinase 1
NM_016904	CKS1B	-1.75	-1.52	CDC28 protein kinase regulatory subunit 1B
NM_025415	CKS2	-1.99	-1.83	CDC28 protein kinase regulatory subunit 2
NM_010353	GSG2	-2.11	-2.13	germ cell associated 2 (haspin)
NM_025979	MASTL	-1.22	-2.19	microtubule associated serine/threonine kinase-like
NM_010790	MELK	-2.46	-2.09	maternal embryonic leucine zipper kinase
NM_010892	NEK2	-2.39	-2.56	NIMA (never in mitosis gene a)-related kinase 2
AK037833	NUCKS1	-1.18	-1.13	nuclear casein kinase and cyclin-dependent kinase substrate 1
NM_080850	PASK	-1.9	-1.86	PAS domain containing serine/threonine kinase
NM_023209	PBK	-3.31	-2.91	PDZ binding kinase
NM_011121	PLK1	-2.75	-2.58	polo-like kinase 1
XM_620516	MEX3B	-2.45	-2.41	mex-3 homolog B (C. elegans)
NM_009387	TK1	-2.25	-1.19	thymidine kinase 1, soluble
				Peptidase
AK030860	RNF150	-1.82	-1.38	ring finger protein 150
NM_007610	CASP2	-1.32	-1.07	caspase 2, apoptosis-related cysteine peptidase
NM_176913	DPEP2	-1.19	-1.42	dipeptidase 2
NM_007930	ENC1	-1.63	-1.59	ectodermal-neural cortex 1 (with BTB-like domain)
NM_001014976	ESPL1	-1.16	-1.12	extra spindle pole bodies homolog 1 (S. cerevisiae)
NM_008873	PLAU	-2.02	-1.65	plasminogen activator, urokinase
NM_017407	SPAG5	-2.1	-2.23	sperm associated antigen 5
NM_029012	SPPL3	-1.08	-2.19	signal peptide peptidase 3
NM_146144	USP1	-1.11	-1.17	ubiquitin specific peptidase 1

				Phosphatase
NM_023117	CDC25B	-1.77	-1.68	cell division cycle 25 homolog B (S. pombe)
BC049694	CDKN3	-2.43	-2.13	cyclin-dependent kinase inhibitor 3
NM_026268	DUSP6	-2.31	-1.86	dual specificity phosphatase 6
NM_011216	PTPRO	-1.5	-1.23	protein tyrosine phosphatase, receptor type, O
				Transcription regulator
NM_007496	ZFHX3	-1.28	-1.77	zinc finger homeobox 3
NM_009764	BRCA1	-1.78	-1.59	breast cancer 1, early onset
NM_007891	E2F1	-1.49	-1.15	E2F transcription factor 1
NM_177733	E2F2	-2.3	-1.65	E2F transcription factor 2
NM_178609	E2F7	-1.6	-1.59	E2F transcription factor 7
NM_007971	EZH2	-2.04	-1.44	enhancer of zeste homolog 2 (Drosophila)
NM_008021	FOXM1	-2.78	-1.93	forkhead box M1
NM_134250	MED7	-1.4	-1.6	mediator complex subunit 7
NM_008252	HMGB2	-2.19	-2.04	high-mobility group box 2
AK138228	HMX2	-1.03	-1.89	H6 family homeobox 2
XM_284454	IRF2BP2	-1.42	-1.72	interferon regulatory factor 2 binding protein 2
NM_017405	LSR	-2.04	-1.34	lipolysis stimulated lipoprotein receptor
NM_008652	MYBL2	-2.12	-1.72	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
NM_183091	NFKBIL2	-1.58	-1.28	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2
NM_013917	PTTG1	-1.11	-1.26	pituitary tumor-transforming 1
NM_025674	TCF19	-2.2	-1.34	transcription factor 19
S79780	TFDP2	-2.06	-1.6	transcription factor Dp-2 (E2F dimerization partner 2)
NM_019551	TDP2	-1.24	-1.25	tyrosyl-DNA phosphodiesterase 2
NM_010931	UHRF1	-2.41	-1.74	ubiquitin-like with PHD and ring finger domains 1
NM_175494	ZNF367	-2.51	-2.55	zinc finger protein 367
				Translation regulator
AK017827	EIF2C4	-1.44	-1.36	eukaryotic translation initiation factor 2C, 4
				Transmembrane receptor
NM_007650	CD5	-1.37	-1.22	CD5 molecule
NM_020008	CLEC7A	-2.9	-2.16	C-type lectin domain family 7, member A
AK088666	IGHM	-2.33	-1.86	immunoglobulin heavy constant mu
NM_001025602	IL1RL1	-1.98	-1.76	interleukin 1 receptor-like 1
NM_031254	TREM2	-1.44	-1.41	triggering receptor expressed on myeloid cells 2
				Transporter
NM_020332	ANKH	-1.44	-1.36	ankylosis, progressive homolog (mouse)
AK045558	AP1S2	-3	-1.85	adaptor-related protein complex 1, sigma 2 subunit
NM_008035	FOLR2	-1.56	-1.8	folate receptor 2 (fetal)
NM_009004	KIF20A	-2.57	-2.54	kinesin family member 20A
NM_010655	KPNA2	-1.06	-1.12	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
NM_012025	RACGAP1	-2.97	-2.18	Rac GTPase activating protein 1
NM_012032	SERINC3	-1.11	-1.3	serine incorporator 3
NM_016917	SLC40A1	-1.84	-2.09	solute carrier family 40 (iron-regulated transporter), member 1

NM_008017	SMC2	-1.91	-1.96	structural maintenance of chromosomes 2
NM_133786	SMC4	-1.61	-1.68	structural maintenance of chromosomes 4
NM_133977	TF	-1.52	-1.39	transferrin
				Other
NM_025411	C1ORF128	-1.34	-1.23	chromosome 1 open reading frame 128
AK138072	1190002F15RIK	-1.93	-1.95	RIKEN cDNA 1190002F15 gene
AK162197	C3ORF58	-1.55	-1.11	chromosome 3 open reading frame 58
BC036300	C1ORF96	-2.08	-2.2	chromosome 1 open reading frame 96
AK003102	C8ORF4	-1.48	-1.44	chromosome 8 open reading frame 4
NM_026931	C8ORF4	-2.25	-2.04	chromosome 8 open reading frame 4
BC070477	C9ORF140	-4.19	-3.69	chromosome 9 open reading frame 140
BC046968/XM_149712	2210010N04Rik	-1.21	-1.55	Unknown
XM_133876	NSMCE4A	-1.56	-1.12	non-SMC element 4 homolog A (S. cerevisiae)
NM_183089	DSCC1	-2.97	-2.62	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
XM_131720	C1ORF135	-2.45	-2.02	chromosome 1 open reading frame 135
NM_028131	CENPN	-1.9	-1.49	centromere protein N
NM_146171	NCAPD2	-2.51	-2.17	non-SMC condensin I complex, subunit D2
NM_026515	KIAA0101	-3.03	-2.39	KIAA0101
NM_025581	SKA1	-2.86	-2.32	spindle and kinetochore associated complex subunit 1
AK013380	NCAPD2	-1.77	-1.8	non-SMC condensin I complex, subunit D2
NM_197959	KIF18B	-2.69	-2.23	kinesin family member 18B
NM_198654	NSL1	-3.25	-2.84	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)
BC003498	PSD3	-1.71	-1.45	pleckstrin and Sec7 domain containing 3
XM_974899	5730405I09Rik	-1.59	-1.34	Unknown
AJ237585	NCAPG	-2.66	-2.13	non-SMC condensin I complex, subunit G
NM_198652	HJURP	-1.14	-1.18	Holliday junction recognition protein
NM_144526	FAM64A	-2.57	-3.11	family with sequence similarity 64, member A
NM_183224	FAM19A3	-1.73	-2.72	family with sequence similarity 19 (chemokine (C-C motif)-like), member A3
NM_145980	C10ORF10	-1.8	-3.96	chromosome 10 open reading frame 10
NM_009643	AHNAK	-1.2	-1.13	AHNAK nucleoprotein
NM_172714	LIN54	-1.3	-1.36	lin-54 homolog (C. elegans)
AK198605	AK198605	-1.58	-1.45	Unknown
NM_001039562	ANKRD37	-2.05	-1.37	ankyrin repeat domain 37
AK083552	ANKLE1	-1.64	-1.7	ankyrin repeat and LEM domain containing 1
NM_181416	ARHGAP11A	-1.28	-1.67	Rho GTPase activating protein 11A
NM_009707	ARHGAP6	-1.69	-1.7	Rho GTPase activating protein 6
NM_024184	ASF1B	-2.39	-2	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)
NM_027435	ATAD2	-2.22	-1.57	ATPase family, AAA domain containing 2
NM_178113	NCAPD3	-1.92	-1.46	non-SMC condensin II complex, subunit D3
XM_283903	FAM102B	-1.64	-1.27	family with sequence similarity 102, member B
BC013561	BC013561	-1.29	-1.14	Unknown
NM_145946	FANCI	-1.98	-1.72	Fanconi anemia, complementation group I
NM_009689	BIRC5	-3.05	-2.74	baculoviral IAP repeat-containing 5

NM_144818	NCAPH	-1.46	-1.89	non-SMC condensin I complex, subunit H
BU554808	BU554808	-2.64	-2.11	Unknown
NM_001039579		-1.53	-1.37	Unknown
NM_001029856	ATAD5	-2.21	-2.05	ATPase family, AAA domain containing 5
NM_176995	NEURL1B	-2.29	-1.94	neuralized homolog 1B (Drosophila)
NM_145974	N4BP3	-3.66	-2.2	Nedd4 binding protein 3
NM_172578	C14ORF106	-1.53	-2.08	chromosome 14 open reading frame 106
XM_001000807	CBX5	-1.69	-1.2	chromobox homolog 5
NM_009828	CCNA2	-3.4	-3	cyclin A2
NM_172301	CCNB1	-2.4	-2.71	cyclin B1
NM_007630	CCNB2	-2.51	-2.87	cyclin B2
NM_007631	CCND1	-2.94	-2.22	cyclin D1
NM_007634	CCNF	-2.06	-2.46	cyclin F
NM_007642	CD28	-1.37	-1.63	CD28 molecule
NM_027987	CD300LG	-2.87	-1.57	CD300 molecule-like family member g
NM_009856	CD83	-1.18	-2.04	CD83 molecule
NM_023223	CDC20	-2.05	-2.1	cell division cycle 20 homolog (S. cerevisiae)
NM_011799	CDC6	-2.59	-2	cell division cycle 6 homolog (S. cerevisiae)
NM_023284	NUF2	-3.2	-2.94	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
NM_175384	CDCA2	-2.39	-1.84	cell division cycle associated 2
NM_013538	CDCA3	-1.92	-1.61	cell division cycle associated 3
NM_026410	CDCA5	-2.02	-1.59	cell division cycle associated 5
NM_025866	CDCA7	-1.39	-1.54	cell division cycle associated 7
NM_026560	CDCA8	-1.74	-1.53	cell division cycle associated 8
NM_007671/U19596	Cdkn2c	-2.29	-1.7	Unknown
NM_007681	CENPA	-1.85	-2.09	centromere protein A
BC059032	CENPE	-2.5	-2.37	centromere protein E, 312kDa
XM_899897	CENPF	-2.99	-2.87	centromere protein F, 350/400kDa (mitosin)
NM_021886	CENPH (includes EG:64946)	-1.52	-1.57	centromere protein H
NM_021790	CENPK	-1.84	-1.91	centromere protein K
NM_027429	CENPL	-1.37	-1.35	centromere protein L
NM_031863	CENPQ	-2.04	-2.09	centromere protein Q
NM_028760	CEP55	-3.05	-2.27	centrosomal protein 55kDa
NM_145409	CHTF18	-1.68	-1.36	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)
NM_001004140	CKAP2	-1.2	-1.86	cytoskeleton associated protein 2
NM_007791	CSRP1	-1.61	-1.18	cysteine and glycine-rich protein 1
NM_025795	NCAPH2	-1.24	-1.34	non-SMC condensin II complex, subunit H2
NM_033075	D17H6S56E-5	-2.11	-1.83	DNA segment, Chr 17, human D6S56E 5
NM_026412	C15ORF23	-1.62	-2.22	chromosome 15 open reading frame 23
NM_153574	FAM13A	-1.48	-1.67	family with sequence similarity 13, member A
NM_134147	MACROD1	-1.68	-1.92	MACRO domain containing 1
NM_029523	DEPDC1	-1.67	-2.03	DEP domain containing 1
NM_178683	DEPDC1B	-3.07	-3.29	DEP domain containing 1B

NM_018769	DFNA5	-1.1	-1.02	deafness, autosomal dominant 5
NM_134081	DNAJC9	-2.11	-1.6	DnaJ (Hsp40) homolog, subfamily C, member 9
NM_029766	DTL	-3.14	-2.01	denticleless homolog (Drosophila)
NM_198249	ARHGEF40	-1.74	-1.47	Rho guanine nucleotide exchange factor (GEF) 40
NM_001013377	C9ORF100	-2.18	-2.65	chromosome 9 open reading frame 100
NM_001013368	E2F8	-3.24	-3.62	E2F transcription factor 8
NM_007900	ECT2	-2.93	-2.42	epithelial cell transforming sequence 2 oncogene
ENSMUST00000090782	ENSMUST00000090782	-1.79	-1.75	Unknown
ENSMUST00000091560	ENSMUST00000091560	-1.12	-1.27	Unknown
ENSMUST00000101051	ENSMUST00000101051	-2.17	-1.91	Unknown
NM_198605	SKA3	-1.55	-1.81	spindle and kinetochore associated complex subunit 3
BC094429	C6ORF167	-1.61	-1.23	chromosome 6 open reading frame 167
NM_016925	FANCA	-1.67	-1.35	Fanconi anemia, complementation group A
NM_011711	FMNL3	-1.46	-1.38	formin-like 3
NM_133236	GLCCI1	-2.35	-1.99	glucocorticoid induced transcript 1
NM_020567	GMNN	-1.89	-1.11	geminin, DNA replication inhibitor
XM_986527	Gna12	-1.17	-1.12	Unknown
NM_029522	GPSM2	-1.51	-1.7	G-protein signaling modulator 2
NM_146120	GSN	-1.36	-1.1	gelsolin
NM_008197	H1F0	-1.86	-1.77	H1 histone family, member 0
BC028539	H2AFV	-2.31	-1.84	H2A histone family, member V
NM_010436	H2AFX	-2.55	-2.39	H2A histone family, member X
NM_020034	HIST1H1B	-1.72	-2.18	histone cluster 1, H1b
NM_015786	HIST1H1C	-1.13	-1.33	histone cluster 1, H1c
NM_015787	HIST1H1E	-2.08	-2.16	histone cluster 1, H1e
NM_175660	HIST1H2AE (includes EG:3012)	-1.63	-1.91	histone cluster 1, H2ae
NM_175661	HIST1H2AI	-1.66	-2.12	histone cluster 1, H2ai
NM_178182	HIST1H2AE (includes EG:3012)	-3.34	-2.49	histone cluster 1, H2ae
NM_178183	HIST1H2AD	-3.08	-2.46	histone cluster 1, H2ad
NM_178192	HIST4H4	-1.88	-1.81	histone cluster 4, H4
NM_175654	HIST4H4	-2	-2.13	histone cluster 4, H4
NM_175655	HIST4H4	-2.05	-2.05	histone cluster 4, H4
NM_175662	HIST2H2AC	-1.62	-1.45	histone cluster 2, H2ac
NM_033596	HIST4H4	-1.93	-2.08	histone cluster 4, H4
AK015962	HIST3H2A	-2.05	-2.17	histone cluster 3, H2a
NM_175652	HIST4H4	-1.98	-1.71	histone cluster 4, H4
NM_010439	HMGB1L1	-1.56	-1.25	high-mobility group box 1-like 1
NM_008253	HMGB3	-1.75	-1.65	high-mobility group box 3
NM_016957	LOC729505	-2.35	-2.2	high-mobility group nucleosomal binding domain 2 pseudogene
NM_207676	CADM1	-1.8	-1.76	cell adhesion molecule 1
NM_016692	INCENP	-1.68	-1.56	inner centromere protein antigens 135/155kDa
BC068159	IQGAP3	-1.79	-2.07	IQ motif containing GTPase activating protein 3

BC024571	ITGA6	-1.55	-1.14	integrin, alpha 6
BC080858	KBTBD11	-2.43	-1.49	kelch repeat and BTB (POZ) domain containing 11
NM_010615	KIF11	-2.64	-5.1	kinesin family member 11
XM_619672	KIF14	-2.12	-1.87	kinesin family member 14
NM_139303	KIF18A	-1.37	-1.68	kinesin family member 18A
NM_145588	KIF22	-3.15	-2.62	kinesin family member 22
NM_024245	KIF23	-2.03	-1.86	kinesin family member 23
NM_008446	KIF4A	-2.71	-2.22	kinesin family member 4A
NM_010722	LMNB2	-1.44	-1.17	lamin B2
XR_003516	LOC619863	-2.88	-2.28	Unknown
XM_001004490	EFR3B	-1.69	-1.55	EFR3 homolog B (S. cerevisiae)
NM_019391	LSP1	-1.52	-1.57	lymphocyte-specific protein 1
NM_133762	NCAPG2	-2.68	-2.38	non-SMC condensin II complex, subunit G2
NM_019499	MAD2L1	-1.8	-1.71	MAD2 mitotic arrest deficient-like 1 (yeast)
NM_027290	MCM10	-2.42	-1.51	minichromosome maintenance complex component 10
BC082308	MFHAS1	-1.41	-1.31	malignant fibrous histiocytoma amplified sequence 1
BC090402	MGC73635	-2.3	-2.15	Unknown
NM_010796	CLEC10A	-1.36	-1.23	C-type lectin domain family 10, member A
NM_145137	CLEC10A	-2.67	-3.03	C-type lectin domain family 10, member A
X82786	MKI67	-3.31	-3.02	antigen identified by monoclonal antibody Ki-67
NM_026178	MMD	-1.88	-1.85	monocyte to macrophage differentiation-associated
NM_029797	MND1	-1.49	-1.3	meiotic nuclear divisions 1 homolog (S. cerevisiae)
NM_028021	MYH14	-1.55	-1.68	myosin, heavy chain 14, non-muscle
NM_016701	NES	-1.33	-1.21	nestin
NM_134122	NRM	-1.8	-1.39	nurim (nuclear envelope membrane protein)
NM_133947	NUMA1	-1.47	-1.24	nuclear mitotic apparatus protein 1
NM_133851	NUSAP1	-2.91	-3.16	nucleolar and spindle associated protein 1
NM_011045	PCNA	-1.1	-1.11	proliferating cell nuclear antigen
NM_008787	PCNT	-1.27	-1.26	pericentrin
NM_145150	PRC1	-3.42	-3.36	protein regulator of cytokinesis 1
NM_139200	CYTIP	-2	-1.98	cytohesin 1 interacting protein
NM_019976	PSRC1	-1.76	-2.19	proline/serine-rich coiled-coil 1
NM_021424	PVRL1	-1.58	-1.31	poliovirus receptor-related 1 (herpesvirus entry mediator C)
NM_009009	RAD21	-1.28	-1.31	RAD21 homolog (S. pombe)
NM_009013	RAD51AP1	-2.18	-1.67	RAD51 associated protein 1
NM_207246	RASGRP3	-3.23	-2.45	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
NM_138956	RASSF3	-1.34	-1.28	Ras association (RalGDS/AF-6) domain family member 3
NM_011249	RBL1	-1.75	-1.44	retinoblastoma-like 1 (p107)
NM_025654	RDM1	-2.2	-1.86	RAD52 motif 1
NM_173402	RGS12	-1.62	-1.53	regulator of G-protein signaling 12
NM_022881	RGS18	-1.99	-1.43	regulator of G-protein signaling 18
NM_009061	RGS2	-3.03	-2.98	regulator of G-protein signaling 2, 24kDa
NM_026653	RPA1	-1.5	-1.27	replication protein A1, 70kDa
NM_011284	RPA2	-1.3	-1.11	replication protein A2, 32kDa

NM_028232	SGOL1	-2.63	-2.3	shugoshin-like 1 (S. pombe)
NM_199007	SGOL2	-2.25	-2.18	shugoshin-like 2 (S. pombe)
NM_011369	SHCBP1	-3.44	-2.37	SHC SH2-domain binding protein 1
NM_009193	SLBP	-1.41	-1.3	stem-loop binding protein
NM_207213	SNX25	-1.81	-1.18	sorting nexin 25
NM_026282	SPC24	-2.88	-3.06	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)
NM_025565	SPC25	-2.39	-2.41	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)
NM_153070	Srgap3	-1.61	-1.7	Unknown
NM_019641	STMN1	-2.35	-2.06	stathmin 1
NM_011513	MED22	-1.41	-1.52	mediator complex subunit 22
TC1429930	TC1429930	-2.17	-1.53	Unknown
TC1434027	TC1434027	-2.61	-2.49	Unknown
TC1502405	TC1502405	-1.16	-1.76	Unknown
NM_011589	TIMELESS	-1.72	-1.22	timeless homolog (Drosophila)
NM_177260	TMEM154	-2.69	-1.86	transmembrane protein 154
AK009669	TMEM158	-2.18	-2.6	transmembrane protein 158 (gene/pseudogene)
U39074	TMPO	-1.37	-1.4	thymopoietin
NM_028109	TPX2	-1.57	-1.45	TPX2, microtubule-associated, homolog (Xenopus laevis)
NM_027763	TREML1	-1.72	-1.53	triggering receptor expressed on myeloid cells-like 1
NM_019634	TSPAN7	-1.28	-1.41	tetraspanin 7
NM_028639	TTC7A	-1.28	-1.4	tetratricopeptide repeat domain 7A
NM_028006	TUBE1	-1.52	-1.52	tubulin, epsilon 1
M30774	Tyms-ps	-1.4	-1.47	Unknown
NM_194342	SUN2	-1.17	-1.57	Sad1 and UNC84 domain containing 2
NM_172598	WDHD1	-1.47	-1.43	WD repeat and HMG-box DNA binding protein 1
AK050869	WHSC1	-1.65	-1.68	Wolf-Hirschhorn syndrome candidate 1
NM_026507	ZWILCH	-1.39	-1.34	Zwilch, kinetochore associated, homolog (Drosophila)

A corrected one-way analysis of variance was used to analyze the microarray data. Genes whose expression levels changed by at least 1.5-fold or more down-regulated genes ($P < 0.05$) as compared to unstimulated cells were considered to be differentially expressed in a statistically significant manner.