Table S2. Selected gene transcripts altered in macrophages at 24 h after exposure to live *Borrelia burgdorferi* (Bb) as compared to those exposed to live Bb in the presence of added IL-10

		Fold change		Ratio	
Gene number	Annotation	Live Bb	Live Bb + IL-10	Live Bb/ Live Bb + IL-10	Description/function
					Cytokine
NM_011337	Ccl3	10.63	9.25	1.15	Chemokine (C-C motif) ligand 3
NM_031167	Il1rn	4.43	4.63	0.96	Interleukin 1 receptor antagonist
NM_010548	Il10	4.07	4.71	0.86	Interleukin 10
					Enzyme
NM_025278	Gng12	2.68	2.33	1.15	Guanine nucleotide binding protein (G protein), gamma 12
NM_018851	Samhd1	2.88	2.55	1.13	SAM domain and HD domain, 1
NM_012054	Aoah	2.82	2.65	1.06	Acyloxyacyl hydrolase
NM_023141	Tor3a	2.38	2.57	0.93	Torsin family 3, member A
NM_027959	Pdia6	2.35	2.56	0.92	Protein disulfide isomerase associated 6
NM_012021	Prdx5	2.53	2.86	0.88	Peroxiredoxin 5
					G-protein coupled receptor
NM_008773	P2ry2	2.29	2.46	0.93	Purinergic receptor P2Y, G-protein coupled 2
					Ion channel
NM_177715	Kctd12	3.63	3.09	1.18	Potassium channel tetramerisation domain containing 12
NM_134133	2010002N04Rik	2.28	2.62	0.87	RIKEN cDNA 2010002N04 gene
					Kinase
NM_013820	Hk2	3.01	2.75	1.1	Hexokinase 2
NM_177320	Pik3r5	2.58	2.9	0.89	Phosphoinositide-3-kinase, regulatory subunit 5, p101
NM_010407	Hck	4.45	5.16	0.86	Hemopoietic cell kinase
NM_019777	Ikbke	2.72	3.2	0.85	Inhibitor of kappaB kinase epsilon
					Peptidase
NM_007609	Casp4	4.02	3.63	1.11	Caspase 4, apoptosis-related cysteine peptidase
AK134736	Cpd	2.92	2.98	0.98	Carboxypeptidase D
					Phosphatase
NM_176919	Ppm1h	2.8	2.43	1.15	Protein phosphatase 1H (PP2C domain containing
					Transcription regulator
NM_030612	Nfkbiz	10.21	9.48	1.08	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
NM_009883	Cebpb	2.37	2.62	0.9	CCAAT/enhancer binding protein (C/EBP), beta
NM_008416	Junb	2.51	2.83	0.89	Jun-B oncogene
NM_007679	Cebpd	2.53	2.97	0.85	CCAAT/enhancer binding protein (C/EBP), delta
					Transmembrane receptor
NM_011610	Tnfrsf1b	5.46	4.88	1.12	Tumor necrosis factor receptor superfamily, member 1b
BC008626	Icam1	2.4	2.19	1.1	Intercellular adhesion molecule
NM_030691	Igsf6	3.23	3.28	0.98	Immunoglobulin superfamily, member 6
NM_031195	Msr1	2.7	2.83	0.95	Macrophage scavenger receptor 1
					Transporter

NM_011638	Tfrc	4.72	4.15	1.14	Transferrin receptor
BC031452	Rrbp1	2.61	2.53	1.03	Ribosome binding protein 1
					Other
NM_021327	Tnip1	3.03	2.55	1.19	TNFAIP3 interacting protein 1
NM_001025156	Ccdc93	2.71	2.3	1.18	Coiled-coil domain containing 93
NM_010708	Lgals9	3.32	2.93	1.13	Lectin, galactose binding, soluble 9
NM_010104	Edn1	3	2.74	1.09	Endothelin 1
NM_021893	Cd274	4.65	4.26	1.09	CD274 antigen
ENSMUST00000042692	ENSMUST00000042692	2.67	2.46	1.08	Unknown
NM_009058	Ralgds	3.08	2.85	1.08	Ral guanine nucleotide dissociation stimulator
NM_029803	Ifi27	2.59	2.41	1.08	Interferon, alpha-inducible protein 27
BY715385	4930519F09Rik	2.21	2.13	1.04	RIKEN cDNA 4930519F09 gene
NM_001024932	LOC545812	2.13	2.1	1.02	Paired immunoglobin-like type 2 receptor beta 2
NM_133209	Pilrb	2.78	2.76	1.01	Paired immunoglobin-like type 2 receptor beta 1
NM_007707	Socs3	6.15	6.15	1	Suppressor of cytokine signaling 3
NM_172722	C330023M02Rik	2.64	2.63	1	RIKEN cDNA C330023M02 gene
NM_025465	1810029B16Rik	3.8	3.89	0.98	RIKEN cDNA 1810029B16 gene
AT_ssM_TR_5	AT_ssM_TR_5	2.91	3.08	0.95	Unknown
NM_027836	Ms4a7	6	6.31	0.95	Membrane-spanning 4-domains, subfamily A, member 7
NM_153510	Pilra	3.8	4.05	0.94	Paired immunoglobin-like type 2 receptor alpha
AK083254	Diap2	2.81	3.13	0.9	Diaphanous homolog 2 (Drosophila)
NM_001039692	Arhgap12	3.84	4.29	0.89	Rho GTPase activating protein 12
NM_001029841	Sla	2.81	3.19	0.88	Src-like adaptor
NM_020001	Clec4n	4.3	5.08	0.85	C-type lectin domain family 4, member n
NM_023380	Samsn1	2.53	3.03	0.84	SAM domain, SH3 domain and nuclear localization signals, 1

A corrected one-way analysis of variance was used to analyze the microarray data. Genes whose expression levels changed by at least 2-fold or more up-regulated genes ($P < 0.05$) as compared to unstimulated cells were considered to be differentially expressed in a statistically significant manner. The underlined genes are common to both the 4 and 24 h time-points.