Table 3. List of genes with similar expression profiles in the CNS and heart of steroid treated and untreated *B. burgdorferi*-infected NHPs

Gene*	Genetic element*	Paralogous family*	Functional group*	Gene description*	Dexa-treated medulla†	Dexa-treated heart†	Competent medulla‡	Competent heart‡
BB0013	Chromosome	None	U	BB0013 hypothetical protein	3	2	3	2
BB0016	Chromosome	None	IM	BB0016 glpE protein (glpE) {Haemophilus influenzae}	3	1	3	1
BB0017	Chromosome	None	HX	BB0017 conserved hypothetical integral membrane protein {Bacillus subtilis}	3	0.5	2	0.5
BB0020	Chromosome	PF6	IM	BB0020 pyrophosphate-fructose 6-phosphate 1-phosphotransferase, beta subunit (pfpB) {Borrelia burgdorferi}	3	1	2	1
BB0028	Chromosome	None	U	BB0028 hypothetical protein	2	0	1	0
BB0035	Chromosome	None	R	BB0035 DNA topoisomerase IV (parC) {Borrelia burgdorferi}	2	1	3	1
BB0051	Chromosome	PF47	HX	BB0051 conserved hypothetical integral membrane protein {Bacillus subtilis}	3	2	3	2
BB0058	Chromosome	PF123	U	BB0058 hypothetical protein	2	1	1	0.5
BB0070	Chromosome	None	HX	BB0070 conserved hypothetical protein {Synechocystis PCC6803}	0	2	0	2
BB0074	Chromosome	PF43	TF	BB0074 peptide chain release factor 2 (prfB) {Salmonella choleraesuis}	1	0.5	3	0.5
BB0104	Chromosome	None	PD	BB0104 periplasmic serine protease DO (htrA) {Haemophilus influenzae}	2	0	2	1
BB0115	Chromosome	None	RP	BB0115 ribosomal protein S6 (rpsF) {Odontella sinensis}	3	0	2	1
BB0116	Chromosome	PF16	TP	BB0116 PTS system, maltose and glucose-specific II ABC component (malX) {Escherichia coli}	3	0	2	0.5
BB0117	Chromosome	None	HE	BB0117 hemolysin III (yplQ) {Bacillus subtilis}	3	0	1	0.5
BB0131	Chromosome	None	R	BB0131 recA protein (recA) {Borrelia burgdorferi}	3	0.5	1	0.5
BB0137	Chromosome	PF25	FM	BB0137 long-chain-fatty-acid CoA ligase {Synechocystis PCC6803}	3	1	1	0
BB0174	Chromosome	None	U	BB0174 hypothetical protein	1	0.5	2	0.5
BB0181	Chromosome	None	F	BB0181 flagellar hook-associated protein (flgK) {Borrelia burgdorferi}	1	0.5	2	0.5
BB0196	Chromosome	PF43	TF	BB0196 peptide chain release factor 1 (prfA) {Haemophilus influenzae}	1	0	1	0
BB0209	Chromosome	None	U	BB0209 hypothetical protein	3	1	1	0.5
BB0210	Chromosome	None	CE	BB0210 surface-located membrane protein 1 (lmp1) {Mycoplasma hominis}	3	0.5	3	0.5
BB0217	Chromosome	PF41	TP	BB0217 phosphate ABC transporter, permease protein (pstA) {Synechocystis PCC6803}	3	1	1	0
BB0220	Chromosome	None	ARS	BB0220 alanyl-tRNA synthetase (alaS) {Escherichia coli}	3	2	2	0.5
BB0228	Chromosome	None	HX	BB0228 conserved hypothetical protein {Saccharomyces cerevisiae}	3	0	1	0
BB0243	Chromosome	None	IM	BB0243 glycerol-3-phosphate dehydrogenase, anaerobic (glpA) {Haemophilus influenzae}	2	0	3	0.5
BB0252	Chromosome	None	HX	BB0252 conserved hypothetical integral membrane protein {Methanococcus jannaschii}	2	1	2	0.5
BB0253	Chromosome	PF22	PD	BB0253 ATP-dependent protease LA (lon-1) {Borrelia burgdorferi}	3	2	3	2
BB0257	Chromosome	None	D	BB0257 cell division protein, putative {Escherichia coli}	2	1	1	0.5

Gene*	Genetic element*	Paralogous family*	Functional group*	Gene description*	Dexa-treated medulla†	Dexa-treated heart†	Competent medulla‡	Competent heart‡
BB0264	Chromosome	PF9	HS	BB0264 heat shock protein 70 (dnaK-1) {Borrelia burgdorferi}	3	1	2	1
BB0277	Chromosome	None	F	BB0277 flagellar motor switch protein (fliN) {Borrelia burgdorferi}	1	0.5	2	0.5
BB0290	Chromosome	PF38	F	BB0290 flagellar motor switch protein (fliG-2) {Borrelia burgdorferi}	1	0.5	3	0.5
BB0308	Chromosome	None	U	BB0308 hypothetical protein	3	0.5	1	0.5
BB0310	Chromosome	None	U	BB0310 hypothetical protein	3	0.5	3	0.5
BB0311	Chromosome	None	HX	BB0311 conserved hypothetical protein {Haemophilus influenzae}	3	0.5	3	0.5
BB0324	Chromosome	None	U	BB0324 hypothetical protein	3	1	2	1
BB0333	Chromosome	PF41	TP	BB0333 oligopeptide ABC transporter, permease protein (oppC-1) {Haemophilus influenzae}	3	2	2	0.5
BB0334	Chromosome	PF4	TP	BB0334 oligopeptide ABC transporter, ATP-binding protein (oppD) {Bacillus subtilis}	3	0.5	1	0.5
BB0351	Chromosome	None	U	BB0351 hypothetical protein	2	1	0.5	0
BB0354	Chromosome	None	U	BB0354 hypothetical protein	2	0	1	0
BB0356	Chromosome	None	U	BB0356 hypothetical protein	2	1	2	0.5
BB0362	Chromosome	None	PE	BB0362 prolipoprotein diacylglyceryl transferase (lgt) {Escherichia coli}	1	0.5	0.5	0
BB0372	Chromosome	None	ARS	BB0372 glutamyl-tRNA synthetase (gltX) {Rhizobium meliloti}	2	0.5	1	0.5
BB0373	Chromosome	None	U	BB0373 hypothetical protein	3	1	3	1
BB0374	Chromosome	None	U	BB0374 hypothetical protein	3	1	2	0.5
BB0377	Chromosome	None	HX	BB0377 conserved hypothetical protein {Haemophilus influenzae}	0.5	1	0	1
BB0405	Chromosome	PF35	U	BB0405 hypothetical protein	3	0.5	1	0
BB0419	Chromosome	PF14	GM	BB0419 response regulatory protein (rrp-1) {Synechocystis PCC6803}	0.5	3	0.5	3
BB0420	Chromosome	PF14	GM	BB0420 sensory transduction histidine kinase/response regulator {Synechocystis PCC6803}	1	2	0.5	1
BB0447	Chromosome	None	TP	BB0447 Na+/H+ antiporter (napA) {Enterococcus hirae}	2	0	1	0
BB0464	Chromosome	None	HX	BB0464 hypothetical	1	2	0.5	1
BB0482	Chromosome	None	RP	BB0482 ribosomal protein S19 (rpsS) {Borrelia burgdorferi}	1	0.5	1	0.5
BB0517	Chromosome	PF15	HS	BB0517 heat shock protein (dnaJ-1) {Borrelia burgdorferi}	3	0.5	3	0.5
BB0518	Chromosome	None	HS	BB0518 heat shock protein 70 (dnaK-2) {Borrelia burgdorferi}	3	0	2	0
BB0544	Chromosome	None	NM	BB0544 phosphoribosyl pyrophosphate synthetase (prs) {Mycoplasma pneumoniae}	2	0	1	0
BB0546	Chromosome	None	U	BB0546 hypothetical protein	2	0	1	0
BB0560	Chromosome	None	HS	BB0560 heat shock protein 90 (htpG) {Borrelia burgdorferi}	2	0.5	2	0.5
BB0575	Chromosome	None	NM	BB0575 CTP synthase (pyrG) {Methanococcus jannaschii}	1	0	0.5	0

Gene*	Genetic element*	Paralogous family*	Functional group*	Gene description*	Dexa-treated medulla†	Dexa-treated heart†	Competent medulla‡	Competent heart‡
BB0580	Chromosome	None	HX	BB0580 conserved hypothetical integral membrane protein {Synechocystis PCC6803}	0	0.5	0.5	1
BB0581	Chromosome	PF20	R	BB0581 DNA recombinase (recG) {Synechocystis PCC6803}	3	1	3	1
BB0591	Chromosome	None	X	BB0591 competence locus E, putative {Bacillus subtilis}	1	0.5	1	0.5
BB0600	Chromosome	None	U	BB0600 hypothetical protein	2	1	1	0
BB0602	Chromosome	None	HS	BB0602 chaperonin, putative {Coxiella burnetti}	3	0.5	1	0
BB0616	Chromosome	None	HX	BB0616 conserved hypothetical integral membrane protein {Bacillus subtilis}	3	0.5	1	0.5
BB0625	Chromosome	None	CE	BB0625 N-acetylmuramoyl-L-alanine amidase, putative {Enterococcus faecalis}	3	2	2	1
BB0627	Chromosome	PF131	PD	BB0627 vacuolar X-prolyl dipeptidyl aminopeptidase I (pepX) {Mycobacterium leprae}	3	1	1	0.5
BB0640	Chromosome	PF41	TP	BB0640 spermidine/putrescine ABC transporter, permease protein (potC) {Escherichia coli}	3	1	1	0
BB0643	Chromosome	PF122	HX	BB0643 conserved hypothetical GTP-binding protein {Mycoplasma genitalium}	3	0.5	1	0.5
BB0644	Chromosome	None	HX	BB0644 conserved hypothetical protein {Haemophilus influenzae}	3	1	1	0
BB0651	Chromosome	None	HX	BB0651 conserved hypothetical protein {Haemophilus influenzae}	2	0.5	0.5	0.5
BB0666	Chromosome	None	U	BB0666 hypothetical protein	2	1	0.5	0
BB0680	Chromosome	PF13	CH	BB0680 methyl-accepting chemotaxis protein (mcp-4) {Escherichia coli}	3	2	3	1
BB0687	Chromosome	None	FM	BB0687 phosphomevalonate kinase, putative {Saccharomyces cerevisiae}	1	0.5	2	0.5
BB0688	Chromosome	None	FM	BB0688 mevalonate kinase {Methanococcus jannaschii}	3	2	3	2
BB0724	Chromosome	None	TP	BB0724 K+ transport protein (ntpJ) {Enterococcus hirae}	3	2	2	1
BB0726	Chromosome	PF32	TP	BB0726 minD-related ATP-binding protein (ylxH-3) {Bacillus subtilis}	3	1	1	0
BB0731	Chromosome	None	HX	BB0731 conserved hypothetical protein {Leptospira interrogans serovar lai}	3	0.5	2	0.5
BB0732	Chromosome	None	CE	BB0732 penicillin-binding protein (pbp-3) {Neisseria gonorrhoeae}	3	0.5	2	0.5
BB0738	Chromosome	PF34	ARS	BB0738 valyl-tRNA synthetase (valS) {Bacillus stearothermophilus}	3	0.5	3	0.5
BB0740	Chromosome	None	HX	BB0740 conserved hypothetical protein {Escherichia coli}	2	1	1	0.5
BB0742	Chromosome	PF4	TP	BB0742 ABC transporter, ATP-binding protein {Synechocystis PCC6803}	3	0.5	3	0.5
BB0743	Chromosome	None	U	BB0743 hypothetical protein	2	1	1	0
BB0747	Chromosome	PF41	TP	BB0747 oligopeptide ABC transporter, permease protein (oppB-2) {Bacillus subtilis}	2	1	2	1
BB0752	Chromosome	None	U	BB0752 hypothetical protein	3	2	3	2
BB0757	Chromosome	PF3	PD	BB0757 ATP-dependent Clp protease proteolytic component (clpP-2) {Haemophilus influenzae}	2	0	3	0.5
BB0768	Chromosome	None	B	BB0768 pyridoxal kinase (pdxK) {Salmonella choleraesuis}	2	0	1	0
BB0774	Chromosome	PF78	F	BB0774 flagellar basal-body rod protein (flgG) {Salmonella choleraesuis}	1	0.5	2	0.5

Gene*	Genetic element*	Paralogous family*	Functional group*	Gene description*	Dexa-treated medulla†	Dexa-treated heart†	Competent medulla‡	Competent heart‡
BB0781	Chromosome	None	CH	BB0781 GTP-binding protein (obg) {Synechocystis PCC6803}	3	2	3	2
BB0789	Chromosome	None	D	BB0789 cell division protein (ftsH) {Bacillus subtilis}	3	2	3	2
BB0827	Chromosome	None	R	BB0827 ATP-dependent helicase (hrpA) {Escherichia coli}	3	2	2	0
BB0828	Chromosome	None	R	BB0828 DNA topoisomerase I (topA) {Synechocystis PCC6803}	3	2	2	0
BB0829	Chromosome	None	R	BB0829 exonuclease SbcD (sbcD) {Escherichia coli}	3	2	3	2
BB0832	Chromosome	None	U	BB0832 hypothetical protein	3	1	1	0
BB0834	Chromosome	PF23	PD	BB0834 ATP-dependent Clp protease, subunit C (clpC) {Porphyra purpurea}	3	0.5	2	0.5
BBA01	lp54	PF48	HX	BBA01 conserved hypothetical protein {Borrelia burgdorferi}	1	0	0.5	0
BBA04	lp54	PF44	CE	BBA04 antigen, S2 {Borrelia burgdorferi}	3	2	2	1
BBA15	lp54	PF53	CE	BBA15 outer surface protein A (ospA) {Borrelia burgdorferi}	1	0.5	1	0.5
BBA16	lp54	PF53	CE	BBA16 outer surface protein B (ospB) {Borrelia burgdorferi}	3	0	2	0
BBA33	lp54	None	U	BBA33 hypothetical protein	1	2	0.5	2
BBA57	lp54	None	HX	BBA57 hypothetical protein	1	2	1	2
BBB07	cp26	None	CE	BBB07 outer surface protein, putative {Borrelia burgdorferi}	3	0.5	1	0.5
BBB16	cp26	PF37	TP	BBB16 oligopeptide ABC transporter, periplasmic oligppeptide-binding protein (oppAIV) {Escherichia coli}	2	1	1	0.5
BBB19	cp26	None	CE	BBB19 outer surface protein C (ospC)	3	2	3	2
BBC11	cp9	PF96	HX	BBC11 conserved hypothetical protein {Borrelia burgdorferi}	1	0	`1	0
BBE08	lp25	None	U	BBE08 hypothetical protein	2	0	1	0
BBG03	lp28-2	PF48	HX	BBG03 conserved hypothetical protein, authentic frameshift {Borrelia burgdorferi}	3	2	2	1
BBG10	lp28-2	PF101	U	BBG10 hypothetical protein	1	0.5	0.5	0
BBG17	lp28-2	None	U	BBG17 hypothetical protein	1	0.5	1	0.5
BBG25	lp28-2	PF143	HX	BBG25 conserved hypothetical protein {Borrelia burgdorferi}	3	1	2	1
BBG27	lp28-2	None	HX	BBG27 conserved hypothetical protein {Borrelia burgdorferi}	3	2	3	2
BBH15	lp28-3	None	U	BBH15 hypothetical protein	2	1	2	1
BBI16	lp28-4	PF60	U	BBI16 hypothetical protein	1	0.5	1	0.5
BBJ02.1	lp38	PF48	HX	BBJ02.1 conserved hypothetical protein, pseudogene {Borrelia burgdorferi}	1	0	1	0
BBK49	lp36	PF69	U	BBK49 hypothetical protein	3	1	2	0
BBK52	lp36	PF44	CE	BBK52 protein p23 {Borrelia burgdorferi}	1	0.5	1	0.5
BBL03	cp32-8	PF148	U	BBL03 hypothetical protein	1	0	1	0

Gene*	Genetic element*	Paralogous family*	Functional group*	Gene description*	Dexa-treated medulla†	Dexa-treated heart†	Competent medulla‡	Competent heart‡
BBL07	cp32-8	PF150	HX	BBL07 conserved hypothetical protein {Borrelia burgdorferi}	1	0	1	0
BBL34	cp32-8	PF49	HX	BBL34 conserved hypothetical protein {Borrelia burgdorferi}	1	0	1	0
BBM12	cp32-6	PF153	U	BBM12 hypothetical protein	3	1	2	0
BBN20	cp32-9	PF140	HX	BBN20 conserved hypothetical protein {Borrelia burgdorferi}	2	0.5	2	0.5
BBN21	cp32-9	PF141	U	BBN21 hypothetical protein, paralogous family 141, authentic frameshift {Borrelia burgdorferi}	2	0.5	1	0
BBN26	cp32-9	PF143	HX	BBN26 outer surface protein, putative {Borrelia burgdorferi}	0.5	0	0.5	0
BBO07	cp32-7	PF150	HX	BBO07 conserved hypothetical protein {Borrelia burgdorferi}	3	1	2	0.5
BBP07	cp32-1	PF150	HX	BBP07 conserved hypothetical protein {Borrelia burgdorferi}	3	2	0.5	0
BBP15	cp32-1	PF156	U	BBP15 hypothetical protein	1	0	0.5	0
BBP17	cp32-1	PF159	U	BBP17 hypothetical protein	1	0	1	0
BBP22	cp32-1	PF142	HX	BBP22 conserved hypothetical protein {Borrelia burgdorferi}	1	0.5	1	0
BBQ52	lp56	PF147	U	BBQ52 hypothetical protein	2	0.5	1	0
BBR13	cp32-4	PF154	U	BBR13 hypothetical protein	3	2	1	0.5
BBR14	cp32-4	PF155	U	BBR14 hypothetical protein	1	0	1	0
BBR15	cp32-4	PF156	U	BBR15 hypothetical protein	3	0.5	3	0.5
BBR17	cp32-4	PF159	U	BBR17 hypothetical protein	2	0.5	1	0
BBR21	cp32-4	PF141	HX	BBR21 conserved hypothetical protein {Borrelia burgdorferi}	2	0	1	0
BBR22	cp32-4	PF142	HX	BBR22 conserved hypothetical protein {Borrelia burgdorferi}	2	0.5	1	0
BBR27	cp32-4	PF80	HX	BBR27 conserved hypothetical protein {Borrelia burgdorferi}	0.5	0	0.5	0
BBS04	cp32-3	PF148	U	BBS04 hypothetical protein	2	1	1	0
BBS07	cp32-3	PF150	HX	BBS07 conserved hypothetical protein {Borrelia burgdorferi}	1	0.5	1	0.5
BBS12	cp32-3	PF153	U	BBS12 hypothetical protein	2	0.5	0.5	0

*All designations used are according to *B. burgdorferi* genome database (http://www.tigr.org/tigr-scripts/CMR2/GenomePage3.spl?database=gbb)

†DECAL performed on medulla and heart tissue samples taken from dexamethosone-treated NHPs.

‡DECAL performed on medulla and heart tissue samples taken from immunocompetent NHPs. The functional categories are: ARS, amino acid biosynthesis; B, biosynthesis; CE, cell envelope; CH, chemotaxis proteins, D, cell division; F, flagellar biosynthesis; FM, fatty acid metabolism; GM, general metabolism; HE, hemolysins; HS, heat shock proteins; HX, conserved hypothetical proteins; IM, intermediary metabolism; NM, nucleotide metabolism; PD, protein degradation; PE, protein export; R, replication; RP, ribosomal proteins; TF, translation factors; TP, transport proteins; TR, transcription; U, hypothetical proteins; X, other.