Supporting information for Revel *et al*. (2002) *Proc. Natl. Acad. Sci. USA* **99** (3), 1562–1567. (10.1073/pnas.032667699)

Table 5. Gene expression variations greater than 1.8-fold comparing *in vitro* 23°C, pH 7.5 (unfed tick) to dialysis membrane chambers

TIGR gene no. and annotation	Fold change	Uncertainty	Gene function	Paralogous family
BB0191 hypothetical protein	–21.57	0.37		
BBA16 outer surface protein B (ospB)	–15.31	0.4	Cell Envelope/Other	53
BBA15 outer surface protein A (ospA)	–12.48	0.38	Cell Envelope/Other	53
BBB29 PTS system, maltose and glucose-specific IIABC component (malX)	–10.56	0.42	Transport and binding proteins/Carbohydrates, organic alcohols, and acids	16
BB0070 conserved hypothetical protein	–7.6	0.41		---
BB0684 carotenoid biosynthesis protein, putative	–5.68	0.38	Unknown Function/General	---
BB0690 neutrophil activating protein (napA)	–5.24	0.4	Cellular Processes/Detoxification	---
BB0423 hypothetical protein	–4.82	0.46		---
BB0424 hypothetical protein	–4.78	0.46		---
BB0533 phnP protein (phnP)	–4.62	0.36	Central Intermediary Metabolism/Phosphorus compounds	---
BB0137 long-chain-fatty-acid CoA ligase	–4.41	0.38	Fatty Acid and Phospholipid Metabolism/Degradation	25
BB0366 aminopeptidase I (yscI)	–4.37	0.36	Protein Fate/Degradation of proteins, peptides, and glycopeptides	131
BB0691 translation elongation factor G (fus-2)	–4.28	0.38	Protein Synthesis/Translation factors	11
BBA62 lipoprotein	–4.26	0.36	Cell Envelope/Other	---
BB0144 glycine betaine, L-proline ABC transporter, glycine/betaine/L-proline-binding protein (proX)	–4.22	0.4	Transport and binding proteins/Amino acids, peptides and amines	---
BBQ36 hypothetical protein	–3.84	0.39		---
BB0789 cell division protein (ftsH)	–3.57	0.38	Cellular Processes/Cell division	---
BB0269 minD-related ATP-binding protein (ylxH-1)	–3.33	0.36	Cellular Processes/Cell division	32
BB0683 3-hydroxy-3-methylglutaryl-CoA	–3.31	0.39	Fatty Acid and Phospholipid Metabolism/Biosynthesis	---

synthase				
BBK45 immunogenic protein P37, putative	–3.27	0.36	Cell Envelope/Biosynthesisand degradation of surface polysaccharides	75
BBA38 hypothetical protein	–3.26	0.4		146
BBQ42 conserved hypothetical protein	–3.26	0.4		80
BB0149 flagellar hook-associated protein 2 (fliD)	–3.26	0.38	Cellular Processes/Chemotaxis and motility	---
BB0271 flagellar biosynthesis protein (flhA)	–3.25	0.38	Cellular Processes/Chemotaxis and motility	---
BB0592 hypothetical protein	–3.15	0.4		---
BB0061 thioredoxin (trxA)	–3.08	0.37	Energy Metabolism/Electrontransport	---
BB0662 hypothetical protein	–3.03	0.4		---
BB0156 hypothetical protein	–2.95	0.42		---
BB0724 K+ transport protein (ntpJ)	–2.93	0.4	Transport and binding proteins/Cations	---
BB0545 xylulokinase (xylB)	–2.91	0.4	Energy Metabolism/Sugars	---
BB0067 peptidase, putative	–2.89	0.36	Protein Fate/Degradation of proteins, peptides, and glycopeptides	---
BB0241 glycerol kinase (glpK)	–2.74	0.38	Energy Metabolism/Other	---
BB0466 ABC transporter, ATP-binding protein	–2.67	0.34	Transport and binding proteins/Unknown substrate	4
BBB22 conserved hypothetical protein	–2.65	0.37		94
BB0805 polyribonucleotide nucleotidyltransferase (pnpA)	–2.6	0.36	Transcription/Degradation of RNA	---
BB0824 hypothetical protein	–2.48	0.4		---
BB0141 membrane fusion protein (mtrC)	–2.45	0.35	Cellular Processes/Toxinproduction and resistance	---
BB0236 hypothetical protein	–2.36	0.39		---

BBL15 hypothetical protein	2.32	0.39		156
BB0036 DNA topoisomerase IV (parE)	2.41	0.35	DNA Metabolism/DNA replication, recombination, and repair	30
BB0134 hypothetical protein	2.57	0.36		---
BBA72 hypothetical protein	2.8	0.38		---
BBL40 erpB2 protein (erpB2)	2.85	0.38	Cell Envelope/Other	163
BB0741 chaperonin (groES)	2.94	0.4	Protein Fate/Protein folding and stabilization	---

BB0096 V-type ATPase, subunit E, putative	3.03	0.35	Energy Metabolism/ATP-proton motive force interconversion	---
BB0567 chemotaxis histidine kinase (cheA-1)	3.19	0.39	Cellular Processes/Chemotaxis and motility	134
BB0681 methyl-accepting chemotaxis protein (mcp-5)	3.66	0.36	Cellular Processes/Chemotaxis and motility	13
BBA73 antigen, P35, putative	3.68	0.41	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	54
BB0669 chemotaxis histidine kinase (cheA-2)	3.71	0.38	Cellular Processes/Chemotaxis and motility	134
BBJ23 hypothetical protein	4.09	0.41		106
BBJ31 hypothetical protein	4.42	0.42		59
BBA25 decorin binding protein B (dbpB)	4.73	0.46	Cell Envelope/Other	74
BB0565 purine-binding chemotaxis protein (cheW-2)	5.72	0.4	Cellular Processes/Chemotaxis and motility	33
BBJ51 vlsE1 protein, authentic frameshift (vlsE1)	8.46	0.48	Cell Envelope/Other	170
BBA36 lipoprotein	9.18	0.4	Cell Envelope/Other	---
BB0844 hypothetical protein	14.42	0.39		12
BBB19 outer surface protein C (ospC)	119.37	0.42	Cell Envelope/Other	---