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

Table 3. Gene expression variations greater than 1.8-fold comparing *in vitro* 23°C, pH 7.5 (unfed tick) to *in vito* 37°C, pH 6.8 (fed tick)

TIGR gene no. and annotation	Fold change	Uncertainty	Gene function	Paralogous family
BBL29 conserved hypothetical protein	–10.11	0.47		161
BB0191 hypothetical protein	–7.63	0.36		---
BB0385 basic membrane protein D (bmpD)	–5.96	0.42	Cell Envelope/Other	36
BB0684 carotenoid biosynthesis protein, putative	–5.42	0.36	Unknown Function/General	---
BB0070 conserved hypothetical protein	–5.23	0.4		---
BB0545 xylulokinase (xylB)	–3.89	0.36	Energy Metabolism/Sugars	---
BB0466 ABC transporter, ATP-binding protein	–3.54	0.34	Transport and binding proteins/Unknown substrate	4
BB0683 3-hydroxy-3-methylglutaryl-CoA synthase	–3.22	0.38	Fatty Acid and Phospholipid Metabolism/Biosynthesis	---
BB0686 mevalonate pyrophosphate decarboxylase	–2.93	0.37	Fatty Acid and Phospholipid Metabolism/Biosynthesis	---
BB0423 hypothetical protein	–2.84	0.4		---
BBF07 hypothetical protein	–2.79	0.4		100
BB0533 phnP protein (phnP)	–2.7	0.37	Central Intermediary Metabolism/Phosphorus compounds	---
BBB23 conserved hypothetical protein	–2.64	0.39		94
BB0269 minD-related ATP-binding protein (ylxH-1)	–2.59	0.36	Cellular Processes/Cell division	32
BB0384 basic membrane protein C (bmpC)	–2.57	0.34	Cell Envelope/Other	36

BBO28 lipoprotein (mlpG)	2.21	0.39	Cell Envelope/Other	113
BB0351 hypothetical protein	2.47	0.43		---
BB0135 histidyl-tRNA synthetase (hisS)	2.51	0.38	Protein Synthesis/tRNA aminoacylation	---
BB0151 N-acetylglucosamine-6-phosphate deacetylase (nagA)	2.51	0.39	Energy Metabolism/Sugars	---
BB0195 conserved hypothetical protein	2.55	0.36		123
BBA61 conserved hypothetical protein	2.55	0.39		---
BB0397 hypothetical protein	2.66	0.42		---
BB0216 phosphate ABC transporter, permease protein (pstC)	2.66	0.42	Transport and binding proteins/Anions	41
BB0561 phosphogluconate dehydrogenase, decarboxylating (gnd)	2.69	0.38	Energy Metabolism/Pentose phosphate pathway	---
BB0689 hypothetical protein	2.7	0.36		---
BBA03 outer membrane protein	2.72	0.35	Cell Envelope/Other	---
BB0365 lipoprotein LA7	2.74	0.4	Cell Envelope/Other	---
BBK13 conserved hypothetical protein	2.83	0.37		40
BBM29 conserved hypothetical protein	2.91	0.36		161
BBR36 conserved hypothetical protein	2.93	0.37		165
BBN29 hypothetical protein, paralogous family 161, authentic point mutation	3.03	0.35		161

TIGR gene no. and annotation	Fold change	Uncertainty	Gene function	Paralogous family
BB0601 serine hydroxymethyltransferase (glyA)	3.03	0.39	Amino Acid Biosynthesis/Serine family	---
BB0037 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC)	3.06	0.35	Fatty Acid and Phospholipid Metabolism/Biosynthesis	---
BBP39 erpB2 protein (erpB2)	3.08	0.38	Cell Envelope/Other	163
BB0330 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-3)	3.11	0.42	Transport and binding proteins/Aminoacids, peptides and amines	37
BBO40 erpM protein (erpM)	3.16	0.35	Cell Envelope/Other	163
BB0296 heat shock protein (hslV)	3.2	0.37	Protein Fate/Protein folding and stabilization	---
BB0741 chaperonin (groES)	3.2	0.41	Protein Fate/Protein folding and stabilization	---
BBA74 outer membrane porin (oms28)	3.32	0.4	Transport and binding proteins/Porins	171
BB0036 DNA topoisomerase IV (parE)	3.35	0.37	DNA Metabolism/DNA replication, recombination, and repair	30
BB0588 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase, putative (pfs-2)	3.35	0.36	Purines, Pyrimidines, Nucleosides, and Nucleotides/Salvage of nucleosides and nucleotides	26
BBS30 lipoprotein (mlpC)	3.38	0.36	Cell Envelope/Other	113
BB0257 cell division protein, putative	3.47	0.43	Cellular Processes/Cell division	---
BBA71 hypothetical protein	3.48	0.39		54
BB0646 hypothetical protein	3.57	0.35		---
BBI42 outer membrane protein, putative	3.61	0.4	Cell Envelope/Other	52
BBJ34 hypothetical protein	3.62	0.37		92
BB0096 V-type ATPase, subunit E, putative	3.66	0.38	Energy Metabolism/ATP-proton motive force interconversion	---
BB0518 heat shock protein 70 (dnaK-2)	3.83	0.39	Protein Fate/Protein folding and stabilization	9
BB0677 ribose/galactose ABC transporter, ATP-binding protein (mglA)	3.88	0.41	Transport and binding proteins/Carbohydrates, organic alcohols, and acids	4
BBK53 outer membrane protein	3.95	0.4	Cell Envelope/Other	52
BBN35 conserved hypothetical protein	4.09	0.4		165
BBK07 hypothetical protein	4.1	0.37		59
BBP35 conserved hypothetical protein	4.2	0.34		165
BB0668 flagellar filament outer layer protein (flaA)	4.22	0.36	Cellular Processes/Chemotaxis and motility	---
BBQ47 erpX protein (erpX)	4.23	0.4	Cell Envelope/Other	163
BBO36 conserved hypothetical protein	4.29	0.37		165
BB0669 chemotaxis histidine kinase (cheA-2)	4.58	0.39	Cellular Processes/Chemotaxis and motility	134
BB0094 V-type ATPase, subunit A (atpA)	4.58	0.46	Energy Metabolism/ATP-proton motive force interconversion	39
BB0329 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2)	4.77	0.41	Transport and binding proteins/Aminoacids, peptides and amines	37
BBR29 conserved hypothetical protein	4.99	0.37		161
BBJ23 hypothetical protein	5.12	0.37		106
BB0563 hypothetical protein	5.19	0.35		35

TIGR gene no. and annotation	Fold change	Uncertainty	Gene function	Paralogous family
BBC12 conserved hypothetical protein	5.22	0.39		165
BBQ03 outer membrane protein, putative	5.29	0.42	Cell Envelope/Other	52
BBM38 erpK protein (erpK)	5.33	0.35	Cell Envelope/Other	164
BBJ45 hypothetical protein	5.33	0.39		59
BBL40 erpB2 protein (erpB2)	5.58	0.41	Cell Envelope/Other	163
BBA04 antigen, S2	5.69	0.39	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	44
BB0565 purine-binding chemotaxis protein (cheW-2)	5.72	0.45	Cellular Processes/Chemotaxis and motility	33
BB0567 chemotaxis histidine kinase (cheA-1)	5.74	0.4	Cellular Processes/Chemotaxis and motility	134
BB0671 chemotaxis operon protein (cheX)	6.46	0.41	Unknown Function/General	---
BBA72 hypothetical protein	6.56	0.39		---
BB0323 hypothetical protein	6.8	0.35		---
BB0680 methyl-accepting chemotaxis protein (mcp-4)	7.14	0.39	Cellular Processes/Chemotaxis and motility	13
BBC05 conserved hypothetical protein	7.25	0.38		161
BBA05 antigen, S1	9.22	0.4	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	---
BBJ31 hypothetical protein	9.26	0.39		59
BBM28 lipoprotein (mlpF)	10.61	0.43	Cell Envelope/Other	113
BBA73 antigen, P35, putative	11.05	0.39	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	54
BBA07 chpAI protein, putative	11.11	0.45	Regulatory Functions/Other	---
BBM27 rev protein (rev)	12.25	0.48	Unknown Function/General	63
BB0844 hypothetical protein	15.1	0.39		12
BB0681 methyl-accepting chemotaxis protein (mcp-5)	15.15	0.41	Cellular Processes/Chemotaxis and motility	13
BBA64 antigen, P35	15.35	0.4	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	54
BBK17 adenine deaminase (adeC)	16.02	0.37	Purines, Pyrimidines, Nucleosides, and Nucleotides/Salvage of nucleosides and nucleotides	61
BBA34 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppAV)	16.1	0.44	Transport and binding proteins/Aminoacids, peptides and amines	37
BBA65 hypothetical protein	19.52	0.42		54
BBK32 immunogenic protein P35	28	0.41	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	
BBA24 decorin binding protein A (dbpA)	46.68	0.38	Cell Envelope/Other	74
BBA36 lipoprotein	58.08	0.37	Cell Envelope/Other	---
BBA66 antigen, P35, putative	75.22	0.41	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	54
BBA25 decorin binding protein B (dbpB)	85.69	0.41	Cell Envelope/Other	74
BBB19 outer surface protein C (ospC)	196.29	0.43	Cell Envelope/Other	---