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

Table 4. Gene expression variations greater than 1.8-fold comparing *in vitro* 37°C, pH 6.8 (fed tick) to dialysis membrane chambers

TIGR gene no. and annotation	Fold change	Uncertainty	Gene function	Paralogous family
BBA66 antigen, P35, putative	–31.02	0.43	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	54
BBK32 immunogenic protein P35	–19.31	0.42	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	---
BBA65 hypothetical protein	–18.22	0.43		54
BBA25 decorin binding protein B (dbpB)	–18.11	0.47	Cell Envelope/Other	74
BBA16 outer surface protein B (ospB)	–16.01	0.43	Cell Envelope/Other	53
BBA24 decorin binding protein A (dbpA)	–14.77	0.42	Cell Envelope/Other	74
BBA34 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppAV)	–10.57	0.44	Transport and binding proteins/Aminoacids, peptides and amines	37
BBA07 chpAI protein, putative	–9.05	0.44	Regulatory Functions/Other	---
BBA15 outer surface protein A (ospA)	–8.86	0.42	Cell Envelope/Other	53
BBK17 adenine deaminase (adeC)	–7.58	0.39	Purines, Pyrimidines, Nucleosides, and Nucleotides/Salvage of nucleosides and nucleotides	61
BBA05 antigen, S1	–7.04	0.39	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	---
BBA36 lipoprotein	–6.33	0.41	Cell Envelope/Other	---
BBA74 outer membrane porin (oms28)	–6.07	0.4	Transport and binding proteins/Porins	171
BBA64 antigen, P35	–6.04	0.41	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	54
BBC05 conserved hypothetical protein	–5.87	0.4		161
BBM28 lipoprotein (mlpF)	–5.77	0.43	Cell Envelope/Other	113
BBK07 hypothetical protein	–5.67	0.43		59
BBJ08 hypothetical protein	–5.48	0.4		12
BBQ03 outer membrane protein, putative	–5.41	0.41	Cell Envelope/Other	52
BB0323 hypothetical protein	–5.4	0.39		---
BBB29 PTS system, maltose and glucose-specific IIABC component (malX)	–5.01	0.44	Transport and binding proteins/Carbohydrates, organic alcohols, and acids	16
BBI42 outer membrane protein, putative	–4.81	0.45	Cell Envelope/Other	52
BB0563 hypothetical protein	–4.81	0.4		35
BB0631 hypothetical protein	–4.31	0.42		---
BB0681 methyl-accepting chemotaxis protein	–4.14	0.4	Cellular Processes/Chemotaxis and motility	13

TIGR gene no. and annotation	Fold change	Uncertainty	Gene function	Paralogous family
(mcp-5)				
BBA04 antigen, S2	–4.08	0.4	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	44
BBK12 hypothetical protein	–4.07	0.39		59
BB0629 PTS system, fructose-specific IIABC component (fruA-2)	–4.07	0.36	Transport and binding proteins/Carbohydrates, organic alcohols, and acids	19
BBK47 hypothetical protein	–4.05	0.4		69
BB0680 methyl-accepting chemotaxis protein (mcp-4)	–3.83	0.39	Cellular Processes/Chemotaxis and motility	13
BB0678 ribose/galactose ABC transporter, permease protein (rbsC-1)	–3.78	0.43	Transport and binding proteins/Carbohydrates, organic alcohols, and acids	130
BB0238 hypothetical protein	–3.76	0.39		---
BB0729 glutamate transporter (gltP)	–3.71	0.46	Transport and binding proteins/Amino acids, peptides and amines	---
BB0329 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2)	–3.63	0.42	Transport and binding proteins/Aminoacids, peptides and amines	37
BBA67 hypothetical protein	–3.62	0.36		---
BBC12 conserved hypothetical protein	–3.56	0.4		165
BB0558 phosphoenolpyruvate-protein phosphatase (ptsI)	–3.49	0.41	Transport and binding proteins/Carbohydrates, organic alcohols, and acids	---
BBA62 lipoprotein	–3.49	0.37	Cell Envelope/Other	---
BB0603 membrane-associated protein p66	–3.48	0.42	Cell Envelope/Other	---
BB0366 aminopeptidase I (yscI)	–3.37	0.38	Protein Fate/Degradation of proteins, peptides, and glycopeptides	131
BB0144 glycine betaine, L-proline ABC transporter, glycine/betaine/L-proline-binding protein (proX)	–3.1	0.37	Transport and binding proteins/Amino acids, peptides and amines	---
BB0299 cell division protein (ftsZ)	–3.09	0.41	Cellular Processes/Cell division	---
BB0418 hypothetical protein	–3.04	0.36		---
BBA73 antigen, P35, putative	–3	0.43	Cell Envelope/Biosynthesis and degradation of surface polysaccharide	54
BB0694 signal recognition particle protein (ffh)	–2.99	0.4	Protein Fate/Protein and peptide secretion and trafficking	10
BB0056 phosphoglycerate kinase (pgk)	–2.93	0.36	Energy Metabolism/Glycolysis & gluconeogenesis	---
BBJ09 outer surface protein D (ospD)	–2.88	0.38	Cell Envelope/Other	---
BB0057 glyceraldehyde 3-phosphate dehydrogenase (gap)	–2.87	0.4	Energy Metabolism/Glycolysis & gluconeogenesis	---
BBR29 conserved hypothetical protein	–2.85	0.38		161

TIGR gene no. and annotation	Fold change	Uncertainty	Gene function	Paralogous family
BB0786 general stress protein (ctc)	–2.85	0.38	Cellular Processes/Celldivision	---
BBK45 immunogenic protein P37, putative	–2.75	0.35	Cell Envelope/Biosynthesisand degradation of surface polysaccharides	75
BBK48 immunogenic protein P37, putative	–2.68	0.38	Cell Envelope/Biosynthesisand degradation of surface polysaccharides	75
BBP28 lipoprotein	–2.67	0.41	Cell Envelope/Other	113
BB0668 flagellar filament outer layer protein (flaA)	–2.66	0.39	Cellular Processes/Chemotaxis and motility	---
BBK13 conserved hypothetical protein	–2.63	0.37		40
BB0691 translation elongation factor G (fus-2)	–2.58	0.39	Protein Synthesis/Translation factors	11
BB0588 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase, putative (pfs-2)	–2.47	0.39	Purines, Pyrimidines, Nucleosides, and Nucleotides/Salvage of nucleosides and nucleotides	26
BB0789 cell division protein (ftsH)	–2.43	0.38	Cellular Processes/Cell division	---
BB0241 glycerol kinase (glpK)	–2.43	0.38	Energy Metabolism/Other	---
BBJ34 hypothetical protein	–2.3	0.38		92

BBS25 conserved hypothetical protein	2.82	0.41		112
BBH13 conserved hypothetical protein	2.83	0.39		80
BBE16 hypothetical protein	2.9	0.51		99
BBF33 surface antigen lipoprotein at right end of				---
lp28-1 (vlsE)"	2.99	0.41		170
BBF03 conserved hypothetical protein	3.34	0.39		80
BBJ51 vlsE1 protein, authentic frameshift (vlsE1)	4.3	0.44	Cell Envelope/Other	170