Table S2. Temperature responsive genes in *S. Typhimurium* LT2 and JH4000 and identification of those genes dependent upon H-NS for regulation. The entire complement of temperature responsive genes was identified as those showing an expression ratio of ≥3 – fold in *S. Typhimurium* LT2 between 37°C and 25°C. Table S2a contains all genes that were more highly expressed at 37°C than at 25°C. Table S2b shows all genes that were more highly expressed at 25°C than at 37°C. Temperature responsive genes identified in S2a and S2b that responded by less than 3-fold in JH4000 were defined as being dependent upon H-NS for temperature regulation. Table S2c shows H-NS – regulated genes that were more highly expressed in LT2 at 37°C than 25°C. Table S2d represents H-NS – regulated genes that were more highly expressed at 25°C than at 37°C. Genes showing less than a 1-fold difference in expression ratio between LT2 and JH4000 were excluded**.**

Table S2a. All genes expressed ≥3x more at 37°C than at 25°C in LT2a (FDR=0.01%). N.B. Includes H-NS - independent genes

Gene	**LT2a 37°C**	**LT2a 25°C**	**Ratio 37/25°C**	**JH4000 37°C**	**JH4000 25°C**	**Ratio 37/25°C**	**Function**
aceE	13.620	1.269	10.729	5.270	1.247	4.226	pyruvate dehydrogenase, decarboxylase component
aceF	10.050	1.521	6.607	4.047	1.029	3.931	pyruvate dehydrogenase, dihydrolipoyltransacetylase component
ackA	12.421	1.443	8.607	1.412	0.617	2.289	acetate kinase A (propionate kinase 2)
acnB	26.529	7.541	3.518	8.434	3.116	2.707	aconitate hydratase 2
adhE	3.023	0.499	6.053	1.691	0.651	2.599	iron-dependent alcohol dehydrogenase of the multifunctional alcohol dehydrogenase AdhE
aer	8.341	1.311	6.362	0.269	0.167	1.606	aerotaxis sensor receptor, senses cellular redox state or proton motive force
agp	5.041	1.213	4.157	1.274	0.422	3.020	glucose-1-phosphatase
alaS	8.463	2.471	3.425	2.467	1.392	1.773	alanyl-tRNA synthetase
ansB	30.756	6.143	5.007	0.470	0.387	1.214	periplasmic L-asparaginase II
araC	2.088	0.676	3.090	1.130	0.266	4.254	transcriptional regulator (AraC/XylS family) for ara operon
artI	5.163	0.800	6.455	1.085	0.440	2.462	ABC superfamily (bind_prot), arginine transport system
aspA	106.382	13.780	7.720	3.907	1.952	2.001	aspartate ammonia-lyase (aspartase)
atpA	52.096	16.067	3.242	21.503	9.236	2.328	membrane-bound ATP synthase, F1 sector, alpha-subunit
atpD	28.871	7.672	3.763	12.825	3.871	3.313	membrane-bound ATP synthase, F1 sector, beta-subunit
atpG	31.288	8.442	3.706	10.919	4.931	2.214	membrane-bound ATP synthase, F1 sector, gamma-subunit
atpH	51.301	14.342	3.577	17.127	7.844	2.183	membrane-bound ATP synthase, F1 sector, delta-subunit
avrA	4.456	0.289	15.427	8.791	4.691	1.874	putative inner membrane protein
basR	2.616	0.771	3.393	3.460	1.413	2.449	response regulator in two-component regulatory system with BasS (OmpR family)
cadA	8.740	0.241	36.235	0.736	0.227	3.241	lysine decarboxylase 1
cadB	3.984	0.321	12.419	1.771	0.799	2.216	APC family, lysine/cadaverine transport protein
cbiC	2.263	0.566	4.001	2.324	4.746	0.490	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiD	3.387	0.589	5.748	2.745	3.974	0.691	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiE	2.411	0.531	4.539	2.581	4.650	0.555	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiF	4.446	0.402	11.063	3.175	5.457	0.582	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiG	3.569	0.338	10.563	2.936	4.907	0.598	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiH	3.986	0.320	12.461	3.365	4.064	0.828	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiJ	2.733	0.387	7.069	1.502	3.050	0.493	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiK	3.682	0.289	12.748	2.827	2.908	0.972	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiL	3.201	0.405	7.908	2.844	4.035	0.705	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiM	2.150	0.549	3.913	2.285	5.235	0.437	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiN	1.987	0.438	4.538	2.405	4.810	0.500	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiO	1.404	0.400	3.508	1.135	2.011	0.565	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiT	2.710	0.484	5.598	2.086	3.287	0.635	synthesis of vitamin B12 adenosyl cobalamide precursor
cboQ	1.661	0.407	4.077	1.835	3.148	0.583	synthesis of vitamin B12 adenosyl cobalamide precursor
cheA	14.059	3.528	3.985	0.221	0.126	1.755	sensory histitine protein kinase, transduces signal between chemo- signal receptors and CheB and CheY
cheW	21.256	5.436	3.910	0.335	0.177	1.897	purine-binding chemotaxis protein; regulation
clpB	4.316	1.034	4.173	8.169	2.179	3.749	ATP-dependent protease, Hsp 100, part of novel multi-chaperone system with DnaK, DnaJ, and GrpE
crp	14.241	3.647	3.905	2.146	0.855	2.510	catabolite activator protein (CAP), cyclic AMP receptor protein (CRP family)
cydA	48.283	1.472	32.803	2.520	2.349	1.073	cytochrome d terminal oxidase, polypeptide subunit I
cydB	45.421	2.005	22.655	3.319	2.481	1.338	cytochrome d terminal oxidase polypeptide subunit II
dcuA	3.113	0.905	3.440	0.611	0.352	1.735	Dcu family, anaerobic dicarboxylate transport protein
dcuB	5.049	0.965	5.232	1.237	2.180	0.567	Dcu family, anaerobic C4-dicarboxylate transporter
deoB	5.418	1.468	3.692	4.187	1.831	2.286	phosphopentomutase
deoD	4.531	1.391	3.258	2.824	0.975	2.897	purine-nucleoside phosphorylase
dmsA	4.913	0.173	28.442	0.195	0.144	1.352	anaerobic dimethyl sulfoxide reductase, subunit A
dmsB	4.158	0.205	20.244	0.188	0.117	1.611	anaerobic dimethyl sulfoxide reductase, subunit B
dnaK	9.148	1.764	5.185	25.177	3.865	6.514	chaperone Hsp70 in DNA biosynthesis/cell division
eno	20.451	6.485	3.154	4.833	2.050	2.358	enolase
fabB	29.977	1.991	15.058	6.561	1.909	3.437	3-oxoacyl-[acyl-carrier-protein] synthase I
fdnG	10.470	0.903	11.594	1.590	0.572	2.780	putative molybdopterin oxidoreductases
fdnH	11.053	0.640	17.266	1.016	0.330	3.076	formate dehydrogenase-N, Fe-S beta subunit, nitrate-inducible

fdnI	6.156	0.462	13.323	0.660	0.493	1.341	formate dehydrogenase-N, cytochrome B556(Fdn) gamma subunit, nitrate-inducible
flgA	11.190	2.101	5.327	0.419	0.278	1.504	flagellar biosynthesis; assembly of basal-body periplasmic P ring
flgB	14.352	4.009	3.580	0.580	0.399	1.455	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgC	25.654	3.951	6.492	0.228	0.116	1.961	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgD	30.569	3.941	7.757	0.221	0.146	1.509	flagellar biosynthesis, initiation of hook assembly
flgE	49.796	4.189	11.888	0.248	0.129	1.920	flagellar biosynthesis, hook protein
flgF	32.494	3.936	8.255	0.334	0.180	1.858	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgG	29.543	3.112	9.494	0.245	0.195	1.253	flagellar biosynthesis, cell-distal portion of basal-body rod
flgH	11.670	2.333	5.003	0.194	0.099	1.967	flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein
flgI	8.778	1.792	4.899	0.187	0.089	2.110	putative flagella basal body protein
flgJ	7.747	1.314	5.893	0.213	0.210	1.015	flagellar biosynthesis
flgK	15.040	1.286	11.692	0.213	0.098	2.174	flagellar biosynthesis, hook-filament junction protein 1
flgL	23.051	2.647	8.707	0.286	0.135	2.121	flagellar biosynthesis; hook-filament junction protein
fliA	45.442	6.002	7.571	0.329	0.243	1.356	sigma F (sigma 28) factor of RNA polymerase, transcription of late flagellar genes (class 3a and 3b operons)
fliB	5.829	1.179	4.946	0.312	0.196	1.591	N-methylation of lysine residues in flagellin
fliC	72.576	12.541	5.787	0.513	0.202	2.543	flagellar biosynthesis; flagellin, filament structural protein
fliD	31.808	2.193	14.506	0.614	0.250	2.460	flagellar biosynthesis; filament capping protein; enables filament assembly
fliE	5.600	1.439	3.892	0.658	0.279	2.355	putative Flagellar hook-basal body protein
fliJ	6.972	0.944	7.384	0.243	0.103	2.364	flagellar fliJ protein
fliK	12.982	1.182	10.981	0.343	0.128	2.672	flagellar hook-length control protein
fliL	17.026	3.135	5.432	0.251	0.191	1.317	flagellar biosynthesis
fliM	10.933	2.384	4.586	0.240	0.182	1.319	flagellar biosynthesis, component of motor switch and energizing
fliS	19.838	3.520	5.636	0.247	0.170	1.454	flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)
fliT	12.192	3.652	3.338	0.453	0.361	1.253	flagellar biosynthesis; possible export chaperone for FliD
fliY	8.970	1.210	7.415	1.115	0.948	1.177	putative periplasmic binding transport protein
fliZ	33.925	2.613	12.982	0.416	0.270	1.540	putative regulator of FliA
fljA	7.380	1.428	5.167	0.408	0.240	1.700	Flagellar synthesis: repressor of fliC
fljB	164.070	16.050	10.223	1.008	0.265	3.801	Flagellar synthesis: phase 2 flagellin (filament structural protein)
frdA	44.011	3.484	12.632	2.319	1.419	1.634	fumarate reductase, anaerobic, flavoprotein subunit
frdB	39.053	2.669	14.630	1.847	1.143	1.615	fumarate reductase, anaerobic, Fe-S protein subunit
frdC	25.871	3.737	6.923	1.588	1.788	0.888	fumarate reductase, anaerobic, membrane anchor polypeptide
frdD	22.769	4.890	4.656	1.920	2.633	0.729	fumarate reductase, anaerobic, membrane anchor polypeptide
fumB	9.006	1.595	5.646	1.306	1.014	1.288	fumarase B (fumarate hydratase class I), anaerobic isozyme
fusA	45.514	10.890	4.180	13.579	6.112	2.222	protein chain elongation factor EF-G, GTP-binding
galU	3.728	0.525	7.100	3.004	2.802	1.072	glucose-1-phosphate uridylyltransferase
gldA	4.376	1.432	3.055	1.173	0.769	1.526	glycerol dehydrogenase, NAD
glnS	5.690	1.544	3.684	1.719	0.886	1.939	glutamine tRNA synthetase
glpA	3.232	0.393	8.231	0.555	0.180	3.082	sn-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit
glpB	6.081	0.464	13.094	0.514	0.167	3.070	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit
glpC	5.548	0.292	19.009	0.566	0.224	2.524	sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit
glpF	6.378	1.906	3.345	3.684	0.265	13.890	MIP channel, glycerol diffusion
glpQ	29.336	4.286	6.846	1.287	0.209	6.160	glycerophosphodiester phosphodiesterase, periplasmic
glpT	18.182	4.849	3.749	1.287	0.258	4.999	MFS family, sn-glycerol-3-phosphate transport protein
glyA	15.312	3.702	4.136	3.485	1.651	2.111	serine hydroxymethyltransferase
glyQ	6.306	1.163	5.420	2.422	0.880	2.753	glycine tRNA synthetase, alpha subunit
glyS	7.121	2.300	3.097	4.077	1.636	2.492	glycine tRNA synthetase, beta subunit
gudD	1.625	0.492	3.305	0.364	0.145	2.507	d-glucarate dehydratase
hcp	2.181	0.359	6.069	0.233	0.174	1.341	hybrid cluster protein; similar to prismane-protein homolog
hcr	2.141	0.426	5.028	0.356	0.211	1.691	NADH oxidoreductase for hcp gene product
hilA	7.306	0.405	18.021	1.563	0.789	1.980	invasion genes transcription activator
hilC	10.201	1.565	6.519	8.792	10.217	0.861	bacterial regulatory helix-turn-helix proteins, araC family
hilD	13.267	0.884	15.015	5.801	5.242	1.107	regulatory helix-turn-helix proteins, araC family
hisB	1.627	0.508	3.202	0.603	0.366	1.647	bifunctional: imidazoleglycerol-phosphate dehydratase; histidinol-phosphatase
hmpA	2.362	0.520	4.540	0.621	0.235	2.646	dihydropteridine reductase 2 and nitric oxide dioxygenase activity
htpG	8.404	1.268	6.628	7.512	1.381	5.441	chaperone Hsp90, heat shock protein C 62.5
hybA	5.160	0.366	14.085	0.428	0.154	2.776	function unknown, intitally thought to be hydrogenase-2 small subunit which now identified as hybO
hybB	4.083	0.464	8.804	0.290	0.242	1.199	putative cytochrome Ni/Fe component of hydrogenase-2

hybC	7.808	0.856	9.122	1.002	0.500	2.003	hydrogenase-2, large subunit
hybD	7.581	1.239	6.118	1.060	0.700	1.516	putative processing element for hydrogenase-2
hybE	3.612	0.879	4.108	0.584	0.490	1.192	putative hydrogenase
hybF	2.763	0.872	3.168	0.762	0.749	1.017	putative hydrogenase expression/formation protein
hybG	1.573	0.510	3.083	0.488	0.380	1.282	hydrogenase-2 operon protein
hypA	1.579	0.465	3.395	0.404	0.438	0.922	guanine-nucleotide binding protein in formate-hydrogenlyase system, functions as nickel donor for HycE of hydrogenlyase 3
hypB	7.116	0.735	9.681	4.139	1.417	2.921	hydrogenase-3 accessory protein, assembly of metallocenter
hypC	4.960	0.735	6.746	3.258	1.986	1.640	putative hydrogenase expression/formation protein
hypD	4.234	0.832	5.089	2.992	1.848	1.619	putative hydrogenase expression/formation protein
hypE	4.277	0.955	4.477	2.883	1.450	1.988	putative hydrogenase expression/formation protein
hypO	6.866	0.453	15.156	0.381	0.180	2.109	putative Ni/Fe hydrogenases, small subunit
iagB	5.092	0.363	14.030	2.259	1.806	1.251	cell invasion protein
invA	3.477	0.516	6.737	4.450	5.055	0.880	invasion protein
invB	7.005	0.764	9.173	9.270	7.102	1.305	surface presentation of antigens; secretory proteins
invC	9.746	0.691	14.113	9.967	6.150	1.621	surface presentation of antigens; secretory proteins
invE	3.905	0.340	11.481	4.127	2.619	1.576	invasion protein
invF	9.101	0.602	15.120	6.536	3.545	1.844	invasion protein
invG	6.203	0.359	17.267	4.286	1.950	2.198	invasion protein; outer membrane
invH	2.863	0.414	6.908	3.873	7.185	0.539	invasion protein
invI	8.481	0.284	29.835	4.852	1.426	3.402	surface presentation of antigens; secretory proteins
invJ	8.546	0.297	28.808	9.615	2.291	4.197	surface presentation of antigens; secretory proteins
ispD	17.957	4.692	3.827		2.692	0.000	4-phosphocytidyl-2C-methyl-D-erythritol synthase
katG	4.253	0.653	6.512	0.579	0.323	1.791	catalase; hydroperoxidase HPI(I)
leuS	5.526	1.686	3.278	1.751	1.367	1.281	leucine tRNA synthetase
manX	14.804	3.895	3.800	6.547	4.953	1.322	Sugar Specific PTS family, mannose-specific enzyme IIAB
manY	20.686	3.159	6.548	5.859	4.146	1.413	Sugar Specific PTS family, mannose-specific enzyme IIC
manZ	10.556	2.982	3.540	3.313	5.300	0.625	Sugar Specific PTS family, mannose-specific enzyme IID
mdoG	5.063	1.500	3.375	1.853	1.204	1.539	periplasmic glucans biosynthesis protein
mopA	42.131	8.817	4.779	75.297	13.775	5.466	chaperone Hsp60 with peptide-dependent ATPase activity, affects cell division
mopB	20.619	6.043	3.412	28.901	9.033	3.199	chaperone Hsp10, affects cell division
motB	8.767	2.103	4.168	0.216	0.175	1.232	enables flagellar motor rotation, linking torque machinery to cell wall
nanK	13.293	2.997	4.435	2.907	0.300	9.686	putative ManNAc kinase
napB	22.150	0.671	33.022	1.179	0.858	1.374	periplasmic nitrate reductase, small subunit, cytochrome C550, in complex with NapA
napD	5.605	0.315	17.812	0.422	0.126	3.359	periplasmic nitrate reductase
napF	3.854	0.378	10.210	0.209	0.164	1.270	ferredoxin-type protein: electron transfer
napH	11.510	0.470	24.504	0.589	0.792	0.744	ferredoxin-type protein: electron transfer
narH	5.684	0.151	37.717	0.669	0.167	4.004	nitrate reductase 1, FeS (beta) subunit
narI	4.729	0.282	16.741	0.700	0.188	3.731	nitrate reductase 1, cytochrome b(NR), gamma subunit
narJ	7.624	0.254	30.043	0.598	0.124	4.835	nitrate reductase 1, delta subunit, chaperone required for molybdenum cofactor assembly in nitrate reductase 1
Not LT2a67	5.843	0.401	14.571	16.123	3.968	4.063	ribonucleoside diphosphate reductase 1, alpha subunit
Not LT2a81	14.164	2.614	5.419	5.543	2.006	2.763	anaerobic ribonucleoside-triphosphate reductase
nrdA	5.704	1.534	3.719	2.296	1.064	2.158	nitrite reductase periplasmic cytochrome c(552)
nrdD	2.460	0.284	8.655	0.232	0.175	1.323	formate-dependent nitrite reductase; a penta-haeme cytochrome c
nrfA	4.413	0.423	10.428	0.244	0.128	1.914	putative nitrite reductase; formate-dependent, Fe-S centers
nrfB	3.126	0.308	10.157	0.219	0.099	2.209	putative nitrate reductase, formate dependent
nrfC	3.146	0.385	8.176	0.299	0.167	1.794	formate-dependent nitrite reductase; involved in attachment of haem c to cytochrome c552
nrfD	2.920	0.466	6.267	0.342	0.170	2.016	putative hydrogenase, membrane component
nrfE	1.311	0.281	4.658	0.217	0.140	1.551	outer membrane protein W; colicin S4 receptor; putative transporter
ompA	52.264	13.939	3.750	36.507	8.525	4.282	putative cytoplasmic protein
ompW	31.967	0.483	66.193	1.044	0.926	1.127	putative flagellar biosynthesis/type III secretory pathway protein
orfX	1.966	0.369	5.325	1.270	0.788	1.611	phosphoenolpyruvate carboxykinase
orgA	9.223	1.194	7.725	13.633	10.311	1.322	transcriptional repressor for pyruvate dehydrogenase complex (GntR family)
pckA	62.680	16.454	3.809	11.588	4.740	2.444	aminoacyl-histidine dipeptidase (peptidase D)
pdhR	3.116	0.437	7.125	1.031	0.362	2.844	putative peptidase T(aminotripeptidase)
pepD	9.322	1.798	5.183	2.724	1.163	2.342	pyruvate formate lyase I, induced anaerobically
pepT	2.345	0.671	3.496	0.700	0.676	1.035	phosphoglycerate kinase
pflB	37.967	1.579	24.045	8.841	3.843	2.301	phenylalanine tRNA synthetase, alpha-subunit

pgk	21.147	3.760	5.625	6.680	2.173	3.074	response regulator in two-component regulatory system with PhoQ, transcribes genes expressed under low Mg+ concentration (OmpR family)
pheS	4.342	1.452	2.990	2.951	1.514	1.949	Hydrogen sulfide production: membrane anchoring protein
phoP	10.586	2.808	3.770	11.778	7.424	1.587	Hydrogen sulfide production: iron- sulfur subunit; electron transfer
phsA	3.962	0.363	10.900	0.336	0.137	2.455	Hydrogen sulfide production: membrane anchoring protein
phsB	3.156	0.497	6.355	0.401	0.197	2.030	phosphoglyceromutase
phsC	2.261	0.751	3.012	0.458	0.406	1.129	cell invasion protein
pmgI	3.195	0.586	5.454	0.687	0.340	2.023	cell invasion protein; cytoplasmic
prgH	8.401	0.296	28.427	4.325	1.910	2.264	cell invasion protein; cytoplasmic
prgI	35.734	0.849	42.110	24.601	6.875	3.578	cell invasion protein; lipoprotein, may link inner and outer membranes
prgJ	29.962	0.718	41.755	21.266	6.349	3.349	proline tRNA synthetase
prgK	29.425	1.352	21.771	27.172	9.844	2.760	
proS	4.276	1.301	3.288	1.694	0.793	2.136	phosphotransacetylase
PSLT103	10.890	0.997	10.925	11.075	3.054	3.627	PTS family, Hpr protein, phosphohistidinoprotein-hexose phosphotransferase
pta	18.538	1.112	16.673	1.795	0.570	3.149	sugar specific PTS family, enzyme IIA, also regulates N metabolism
ptsH	14.637	2.670	5.482	5.157	1.963	2.628	pyruvate kinase II, glucose stimulated
ptsN	7.779	2.060	3.775	3.427	1.280	2.676	pyruvate kinase I (formerly F), fructose stimulated
pykA	11.604	1.615	7.183	3.647	1.068	3.414	50S ribosomal subunit protein L2
pykF	4.144	1.274	3.254	3.176	1.870	1.698	50S ribosomal subunit protein L5
rplB	70.832	22.009	3.218	18.979	11.563	1.641	50S ribosomal subunit protein L6
rplE	58.105	15.292	3.800	16.066	15.246	1.054	50S ribosomal subunit protein L9
rplF	50.203	15.869	3.164	22.615	17.833	1.268	50S ribosomal subunit protein L18
rplI	18.553	5.920	3.134	4.715	4.160	1.133	RNA polymerase, alpha subunit
rplR	64.233	12.407	5.177	15.500	9.360	1.656	30S ribosomal subunit protein S4
rpoA	68.896	14.694	4.689	14.900	6.370	2.339	30S ribosomal subunit protein S5
rpsD	63.666	15.324	4.155	13.046	7.750	1.683	30S ribosomal subunit protein S8, and regulator
rpsE	58.561	12.001	4.880	14.066	7.947	1.770	30S ribosomal subunit protein S14
rpsH	50.002	14.287	3.500	18.755	14.814	1.266	30S ribosomal subunit protein S18
rpsN	67.823	14.352	4.726	20.317	15.618	1.301	anti sigma E (sigma 24) factor, negative regulator
rpsR	17.789	5.835	3.049	4.970	4.180	1.189	putative AraC-type DNA-binding domain-containing protein
rseA	47.772	12.452	3.837	12.983	7.594	1.710	putative bacterial regulatory proteins, luxR family
rtsA	7.320	0.747	9.798	1.274	0.779	1.635	succinate dehydrogenase, flavoprotein subunit
rtsB	4.220	0.698	6.046	0.937	0.900	1.040	succinate dehydrogenase, cytochrome b556
sdhA	57.242	17.160	3.336	14.776	8.744	1.690	preprotein translocase; secretion protein of IISP family
sdhC	32.955	10.084	3.268	5.571	3.940	1.414	surface presentation of antigens; secretory proteins
secA	5.727	1.826	3.136	3.561	1.596	2.231	cell invasion protein
sicA	5.224	0.396	13.187	14.540	3.798	3.829	cell invasion protein
sipA	4.194	0.407	10.304	19.185	3.909	4.908	cell invasion protein
sipB	7.683	1.431	5.371	35.331	9.000	3.926	cell invasion protein
sipC	8.653	0.864	10.019	53.896	8.971	6.008	surface presentation of antigens; secretory proteins
sipD	6.629	0.604	10.969	23.518	5.506	4.271	surface presentation of antigens; secretory proteins
spaP	3.125	0.501	6.231	7.869	6.268	1.256	surface presentation of antigens; secretory proteins
spaQ	2.205	0.722	3.055	6.740	7.822	0.862	surface presentation of antigens; secretory proteins
spaR	1.559	0.318	4.908	4.603	3.600	1.279	ornithine decarboxylase isozyme, inducible
spaS	1.099	0.233	4.719	2.276	1.570	1.450	transcriptional regulator
speF	14.578	0.249	58.660	0.291	0.283	1.028	ssrAB activated gene
sprB	9.709	0.642	15.118	15.081	7.763	1.943	ssrAB activated gene
srfA	7.113	0.826	8.609	0.220	0.124	1.776	ssrAB activated gene: predicted coiled-coil structure
srfB	7.542	1.321	5.708	0.447	0.344	1.297	putative cytoplasmic protein
srfC	6.391	0.837	7.635	0.355	0.284	1.251	homologous to secreted protein sopD
STM0699	4.733	0.431	10.992	0.306	0.296	1.035	putative ABC transporter periplasmic binding protein
STM0972	1.501	0.377	3.981	7.341	9.787	0.750	putative periplasmic protein
STM1255	2.940	0.885	3.323	0.627	0.671	0.935	putative outer membrane protein
STM1300	4.332	1.074	4.032	0.385	0.339	1.136	putative dimethyl sulphoxide reductase
STM1328	3.319	0.639	5.196	5.797	4.801	1.207	putative dimethyl sulphoxide reductase, chain A1
STM1498	1.130	0.160	7.075	0.147	0.191	0.767	putative hydrogenase-1 large subunit
STM1499	1.033	0.247	4.178	0.192	0.152	1.262	putative hydrogenase-1 small subunit
STM1538	1.029	0.300	3.433	1.734	0.467	3.715	putative catalase
STM1539	0.766	0.216	3.550	1.931	0.394	4.899	putative 50S ribosomal protein
STM1731	2.099	0.262	8.012	15.771	13.756	1.146	
STM1967	1.553	0.491	3.164	1.312	1.626	0.807	

STM2248	5.490	0.437	12.561	0.682	0.736	0.926	
STM2250	10.256	0.708	14.486	1.171	1.093	1.071	putative transketolase
STM2252	7.641	0.704	10.849	0.915	1.090	0.839	putative inner membrane protein
STM2340	8.842	1.178	7.505	0.901	0.537	1.676	putative cytoplasmic protein
STM2342	5.943	1.401	4.241	0.569	0.350	1.628	putative cytoplasmic protein
STM2343	4.213	1.237	3.405	0.520	0.402	1.292	putative nucleoside-diphosphate-sugar epimerase
STM2868	8.182	0.821	9.962	10.246	6.631	1.545	putative uronate isomerase
STM2914	1.463	0.289	5.060	0.228	0.163	1.403	putative methyl-accepting chemotaxis protein
STM3137	2.997	0.891	3.362	0.577	0.370	1.560	putative methyl-accepting chemotaxis protein
STM3138	8.742	0.485	18.042	1.813	2.462	0.736	transcriptional regulator of sugar metabolism
STM3216	21.944	1.056	20.784	0.355	0.248	1.430	putative cytochrome c peroxidase
STM3262	3.145	1.046	3.006	0.623	0.353	1.764	putative anaerobic dimethyl sulfoxide reductase, subunit A
STM3820	2.745	0.253	10.851	0.527	0.427	1.233	putative anaerobic dimethyl sulfoxide reductase, subunit B
STM4305	0.865	0.195	4.429	0.399	0.189	2.115	putative phage protein
STM4306	0.957	0.224	4.270	0.378	0.162	2.329	putative cytoplasmic protein
STM4312	1.755	0.483	3.636	0.505	1.287	0.392	putative cytoplasmic protein
STM4313	2.390	0.502	4.764	0.530	1.002	0.530	putative ATPase involved in DNA repair
STM4492	1.794	0.592	3.029	0.987	0.424	2.326	transaldolase B
STM4496	1.674	0.500	3.346	0.804	0.406	1.981	threonine dehydratase, catabolic
talB	21.026	1.837	11.447	4.793	0.929	5.158	HAAAP family, L-threonine/ L-serine permease, anaerobically inducible
tdcB	3.745	0.401	9.332	2.254	1.476	1.527	propionate kinase/acetate kinase II, anaerobic
tdcC	3.697	0.315	11.721	2.231	1.166	1.914	pyruvate formate-lyase 4/ 2-ketobutyrate formate-lyase
tdcD	3.036	0.249	12.184	1.200	1.042	1.151	transketolase 1 isozyme
tdcE	2.890	0.356	8.122	1.358	1.391	0.976	outer membrane channel; specific tolerance to colicin E1; segregation of daughter chromosomes, role in organic solvent tolerance
tktA	26.347	4.252	6.196	5.139	1.849	2.780	trehalose- 6-P hydrolase, alternative inducer of maltose system, cytoplasmic
tolC	4.832	1.084	4.457	4.142	1.118	3.705	methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor
treC	3.271	0.899	3.637	0.383	0.222	1.724	protein chain elongation factor EF-Tu (duplicate of tufA)
trg	5.879	1.349	4.358	0.243	0.201	1.210	ABC superfamily (peri_perm), sn-glycerol 3-phosphate transport protein
tufB	106.579	32.446	3.285	39.574	16.331	2.423	putative outer membrane antigen
ugpB	1.661	0.404	4.110	1.188	0.215	5.522	putative inner membrane lipoprotein
yaeT	11.769	3.257	3.613	3.373	3.016	1.118	putative outer membrane lipoprotein
ybgE	6.766	1.218	5.556	1.056	1.181	0.894	putative outer membrane lipoprotein
ybgT	28.247	1.421	19.874	2.445	1.973	1.239	putative transcriptional repressor (TetR/AcrR family)
ycfJ	0.999	0.308	3.242	0.692	0.443	1.563	putative cytoplasmic protein
ycfQ	1.955	0.450	4.347	0.802	0.334	2.400	putative transcriptional regulator
ydfZ	4.552	0.485	9.392	0.530	0.406	1.304	putative esterase
yebK	1.770	0.528	3.354	0.635	0.237	2.681	putative formate acetyltransferase
yeiG	7.126	1.472	4.841	12.881	2.388	5.394	3-hydroxyisobutyrate dehydrogenase
yfiD	13.108	0.462	28.356	0.501	0.332	1.508	paral putative tRNA synthase
ygbJ	4.859	0.450	10.789	0.274	0.223	1.230	putative fuculose phosphate aldolase
ygbK	5.377	0.430	12.504	0.336	0.151	2.227	putative endonuclease
ygbL	2.977	0.276	10.785	0.246	0.153	1.608	putative P-loop-containing kinase
ygbM	3.422	0.395	8.669	0.257	0.152	1.696	
yhbJ	3.392	1.046	3.244	2.015	0.715	2.816	putative cytoplasmic protein
yhbU	1.639	0.337	4.858	0.308	1.017	0.303	putative POT family, di-/tripeptide transport protein
yjbR	1.648	0.475	3.473	0.824	0.204	4.048	putative cytoplasmic protein
yjdL	1.788	0.578	3.093	0.401	0.304	1.321	putative periplasmic protein
yjjI	2.067	0.322	6.430	0.453	0.165	2.737	paral putative periplasmic protein
ymdA	2.988	0.948	3.151	0.465	0.447	1.040	glucose-6-phosphate dehydrogenase
yraP	9.546	1.579	6.044	6.082	1.559	3.902	
zwf	2.961	0.851	3.481	1.310	0.500	2.622	

Table S2b. All genes expressed ≥3x more at 25°C than at 37°C in LT2a (FDR=0.01%). N.B. Includes H-NS - independent genes

Gene	LT2a 37°C	LT2a 25°C	Ratio 25/37°C	JH4000 37°C	JH4000 25°C	Ratio 25/37°C	Function
ais	1.015	5.220	5.144	2.583	9.466	3.664	aluminum inducible protein
ansP	0.259	1.430	5.515	0.333	0.657	1.975	APC family, L-asparagine transport protein
apt	0.930	4.204	4.521	1.135	3.999	3.524	adenine phosphoribosyltransferase
astA	0.475	2.809	5.909	0.502	0.732	1.460	arginine succinyltransferase
astB	0.179	0.872	4.870	0.391	0.591	1.510	succinylarginine dihydrolase
astC	0.956	5.585	5.844	0.869	0.997	1.147	succinylornithine transaminase, also has acetylornitine transaminase activity
astD	0.321	1.613	5.029	0.555	0.833	1.500	succinylglutamic semialdehyde dehydrogenase
astE	0.173	0.573	3.314	0.528	0.822	1.559	succinylglutamate desuccinylase
atpI	6.185	24.399	3.945	4.799	9.707	2.023	membrane-bound ATP synthase subunit, F1-F0-type proton-ATPase
avtA	0.397	1.629	4.098	0.686	0.596	0.868	valine-pyruvate aminotransferase
bioH	0.848	2.986	3.519	1.077	0.995	0.924	putative hydrolase, biotin biosynthesis; reaction prior to pimeloyl CoA
brnQ	0.872	3.058	3.509	1.215	1.632	1.343	LIVCS family, branched chain amino acid transporter system II (LIV-II)
chaA	0.790	2.523	3.192	1.764	7.322	4.150	CaCA family, sodium-calcium/proton antiporter
cspB	1.177	6.241	5.305	1.209	5.493	4.544	putative cold-shock protein
cspC	28.310	121.067	4.276	21.663	72.530	3.348	cold shock protein, multicopy suppresses mukB mutants, putative regulator
cutC	1.046	3.050	2.914	0.818	1.538	1.882	copper homeostasis protein
cybC	1.546	6.759	4.371	4.244	5.899	1.390	cytochrome b(562)
cyoC	10.988	36.743	3.344	23.168	24.591	1.061	cytochrome o ubiquinol oxidase subunit III
cyoD	5.522	33.136	6.001	22.223	18.888	0.850	cytochrome o ubiquinol oxidase subunit IV
cyoE	2.570	30.652	11.926	15.141	14.628	0.966	protohaeme IX farnesyltransferase (haeme O biosynthesis)
dadX	3.105	11.473	3.695	2.364	2.067	0.874	alanine racemase 2, catabolic
ddlA	1.697	6.499	3.830	1.299	2.161	1.663	D-alanine-D-alanine ligase A
deaD	1.048	3.235	3.086	0.520	4.561	8.765	cysteine sulfinate desulfinase
dgoT	0.119	0.355	2.983	0.220	0.130	0.590	MFS family, D-galactonate transport protein
dlhH	1.212	5.350	4.413	2.613	3.419	1.309	putative dienelactone hydrolase family
dppB	0.216	0.861	3.979	0.351	0.211	0.601	ABC superfamily (membrane), dipeptide transport protein 1
dppC	0.228	0.745	3.274	0.336	0.217	0.646	ABC superfamily (membrane), dipeptide transport protein 2
exbB	0.400	1.660	4.152	0.875	0.662	0.756	uptake of enterochelin; tonB-dependent uptake of B colicins
fabI	3.860	16.533	4.284	5.996	13.179	2.198	enoyl-[acyl-carrier-protein] reductase (NADH)
feoA	0.468	6.831	14.584	0.899	0.854	0.950	ferrous iron transport protein A
fepB	0.170	0.536	3.162	0.289	0.157	0.544	ABC superfamily (peri_perm), ferric enterobactin (enterochelin) tranporter
fepD	0.148	1.005	6.794	0.247	0.165	0.667	ABC superfamily (membrane), ferric enterobactin (enterochelin) transporter
fepG	0.154	0.948	6.168	0.288	0.202	0.702	ABC superfamily (membrane), ferric enterobactin transporter
fhuA	0.126	0.514	4.076	0.274	0.148	0.542	outer membrane protein receptor / transporter for ferrichrome, colicin M, and phages T1, T5, and phi80
fhuB	0.227	0.717	3.164	0.304	0.206	0.678	ABC superfamily (membrane), hydroxamate-dependent iron uptake
fhuC	0.135	0.621	4.587	0.279	0.176	0.629	ABC superfamily (atp_bind), hydroxymate-dependent iron transport
fhuD	0.109	0.634	5.795	0.295	0.192	0.650	ABC superfamily (bind _prot), hydroxamate-dependent iron uptake
fimZ	0.129	0.393	3.044	0.522	3.566	6.835	fimbrial protein Z, putative transcriptional regulator (LuxR/UhpA family)
gabT	0.200	0.628	3.136	1.570	0.556	0.354	4-aminobutyrate aminotransferase
gcd	0.336	1.286	3.823	1.444	1.244	0.861	glucose dehydrogenase
gltP	1.772	6.390	3.606	1.738	1.395	0.802	DAACS family, glutamate:aspartate symport protein
gltS	1.836	8.494	4.626	1.048	1.518	1.448	GltS family, glutamate transport protein
hcaT	0.758	3.494	4.610	0.821	2.047	2.492	putative MFS family transport protein
hemC	4.433	13.828	3.119	4.430	6.299	1.422	porphobilinogen deaminase (hydroxymethylbilane synthase)
hemD	4.009	12.245	3.055	3.785	7.468	1.973	uroporphyrinogen III synthase
hpt	1.560	10.680	6.847	1.443	3.938	2.730	hypoxanthine phosphoribosyltransferase
ilvG	0.483	1.591	3.294	0.807	1.328	1.644	acetolactate synthase II, large subunit, fragment 1, cryptic
ilvL	1.339	5.728	4.277	2.700	5.579	2.066	ilvGEDA operon leader peptide
ilvM	1.236	4.137	3.347	1.987	4.169	2.098	acetolactate synthase II, small subunit
infA	1.906	10.886	5.711	1.708	11.067	6.480	protein chain initiation factor IF-1
leuA	0.190	0.579	3.047	0.599	0.536	0.895	2-isopropylmalate synthase
lgt	1.655	5.698	3.444	1.465	5.780	3.945	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase
livJ	0.545	1.662	3.047	0.524	0.479	0.912	ABC superfamily (bind_prot), branched-chain amino acid transporter, high-affinity
lysA	0.324	1.040	3.209	0.644	0.718	1.114	diaminopimelate decarboxylase
lysP	0.493	1.660	3.368	0.686	1.406	2.049	APC family, lysine-specific permease
malG	0.271	1.856	6.849	0.525	0.761	1.451	ABC superfamily (membrane), maltose transport protein

metB	0.862	3.286	3.814	0.762	1.197	1.570	cystathionine gamma-synthase
metE	0.451	1.883	4.177	0.567	2.218	3.909	5-methyltetrahydropteroyltriglutamate- homocysteine S-methyltransferase
metR	0.742	4.346	5.854	1.121	3.265	2.913	regulator for metE and metH (LysR family)
mioC	1.324	8.465	6.394	1.440	3.537	2.455	initiation of chromosome replication
mntH	0.345	1.100	3.190	0.314	0.529	1.682	Nramp family, manganese/divalent cation transport prortein
mreD	0.709	4.009	5.654	0.743	3.527	4.749	rod shape-determining protein
mscL	1.742	5.685	3.263	3.179	4.594	1.445	mechanosensitive channel
mtr	0.236	0.838	3.543	0.320	0.518	1.617	HAAAP family, tryptophan-specific transport protein
ndk	11.126	50.722	4.559	7.862	14.602	1.857	nucleoside diphosphate kinase
nikR	1.020	3.631	3.560	0.930	1.181	1.270	nickel-responsive transcriptional regulator
oafA	0.771	2.626	3.404	2.189	5.761	2.632	O-antigen five: acetylation of the O-antigen (LPS)
ompX	7.036	37.301	5.301	27.205	28.598	1.051	outer membrane protease, receptor for phage OX2
orfB	3.753	12.887	3.433	7.576	10.318	1.362	putative cytoplasmic protein
pgsA	1.368	5.268	3.852	1.470	1.904	1.295	phosphatidylglycerophosphate synthetase (CDP-1,2-diacyl-sn-glycero-3-phosphate phosphatidyl transferase)
pheP	0.377	1.696	4.494	0.640	1.278	1.997	APC family, phenylalanene transporter
phoU	0.914	3.712	4.061	1.246	1.268	1.018	regulatory gene for high affinity phosphate uptake
pldB	1.348	5.234	3.883	1.173	4.443	3.786	lysophospholipase L(2)
ppiC	1.446	6.689	4.625	1.643	3.376	2.054	peptidyl-prolyl cis-trans isomerase C (rotamase C)
proP	0.606	2.106	3.478	1.812	2.024	1.117	MFS family, low-affinity proline transporter (proline permease II)
proV	0.913	3.783	4.144	5.302	5.537	1.044	ABC superfamily (atp_bind), glycine/betaine/proline transport protein
proW	1.095	7.507	6.859	12.100	13.180	1.089	ABC superfamily (membrane), glycine/betaine/proline transport protein
PSLT003	0.923	3.203	3.471	1.039	2.128	2.047	
PSLT015	0.262	0.785	3.000	1.062	0.612	0.576	
PSLT064	0.175	0.680	3.890	0.517	0.687	1.328	
PSLT073	0.171	0.638	3.730	2.568	5.497	2.141	
pstB	0.694	2.119	3.055	1.295	1.317	1.017	ABC superfamily (atp_bind), high-affinity phosphate transporter
rarD	1.038	5.062	4.878	1.717	3.240	1.887	chloramphenicol resistance
rbsA	0.297	1.068	3.595	0.545	0.171	0.314	ABC superfamily (atp_bind), D-ribose high-affinity transport protein
rbsD	0.373	2.999	8.047	0.702	0.238	0.339	D-ribose high-affinity transport system; membrane-associated protein
rfaI	0.951	3.716	3.909	2.612	5.138	1.967	UDP-D-galactose:(glucosyl)lipopolysaccharide- alpha-1,3-D-galactosyltransferase
rfaJ	0.741	3.321	4.484	1.832	4.162	2.271	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase
rfaY	0.675	2.952	4.374	1.321	2.981	2.257	lipopolysaccharide core biosynthesis; modification of heptose region of the core
rfaZ	0.563	4.462	7.922	1.429	6.250	4.373	lipopolysaccharide core biosynthesis
rfbN	1.634	6.634	4.059	3.342	9.462	2.831	LPS side chain defect: rhamnosyl transferase
rfbU	1.171	6.203	5.296	3.038	9.055	2.980	LPS side chain defect: mannosyl transferase
rfbV	1.756	10.886	6.201	4.715	16.619	3.525	LPS side chain defect: abequosyltransferase
rfbX	0.968	4.196	4.333	2.922	7.172	2.455	LPS side chain defect: putative O-antigen transferase
rfc	0.686	2.091	3.050	0.867	1.779	2.052	O-antigen polymerase
rfe	1.458	7.496	5.141	2.099	5.530	2.635	undecaprenyl-phosphate N-acetylglucosaminyltransferase
rhlE	0.251	1.010	4.017	0.459	1.372	2.988	putative ATP-dependent RNA helicase
rhtC	0.660	3.430	5.196	1.053	2.528	2.400	RhtB family, threonine efflux protein
ribB	0.989	4.543	4.591	3.339	3.204	0.959	3,4 dihydroxy-2-butanone-4-phosphate synthase
rimK	0.733	2.271	3.098	0.654	1.608	2.458	ribosomal protein S6 modification protein
rpmH	5.513	30.249	5.487	2.816	13.923	4.945	50S ribosomal subunit protein L34
rthB	0.602	4.779	7.936	0.877	3.170	3.615	homoserine/homoserine lactone efflux protein
scsA	0.955	2.952	3.091	1.024	3.396	3.316	Suppression of copper sensitivity: putative copper binding protein
sdiA	1.128	3.497	3.099	1.001	0.538	0.538	transcriptional regulator of ftsQAZ gene cluster (LuxR/UhpA family)
secG	5.311	16.389	3.086	3.919	11.102	2.833	preprotein translocase IISP family, auxillary membrane component
sfbB	0.243	0.752	3.094	0.303	0.204	0.675	putative ABC-type transport system ATPase component/cell division protein
sitA	0.245	0.794	3.236	0.511	0.374	0.731	Salmonella iron transporter: fur regulated
sodA	1.394	23.912	17.150	6.619	7.190	1.086	superoxide dismutase, manganese
speB	2.413	9.612	3.984	3.701	8.054	2.176	agmatinase
stfC	0.100	0.349	3.486	0.243	0.282	1.161	
stfG	0.113	0.386	3.409	0.226	0.308	1.365	putative minor fimbrial subunit; putative adhesin
STM0327	4.146	16.648	4.015	0.575	1.213	2.111	putative cytoplasmic protein
STM0334	0.115	0.361	3.136	0.313	0.617	1.972	putative cytoplasmic protein
STM0381	0.227	0.696	3.069	0.417	0.423	1.016	putative inner membrane protein
STM0559	0.138	0.872	6.307	0.242	0.685	2.833	
STM0651	0.180	0.747	4.150	0.464	1.413	3.042	putative permease

STM0764	0.152	0.882	5.816	0.526	1.237	2.352	transcriptional regulator, lysR family
STM0954	1.163	3.994	3.434	1.413	5.927	4.195	putative inner membrane protein
STM1012	0.542	1.929	3.561	0.443	0.647	1.462	Gifsy-2 prophage; probable regulatory protein
STM1129	11.130	50.027	4.495	1.143	0.385	0.337	putative inner membrane protein
STM1267	0.630	2.354	3.734	5.878	10.898	1.854	putative cytoplasmic protein
STM1554	0.349	1.288	3.688	0.702	1.000	1.425	putative coiled-coil protein
STM1586	0.303	2.004	6.612	0.481	0.481	1.000	putative periplasmic protein
STM1623	0.703	3.178	4.521	1.187	1.538	1.296	putative carboxylesterase
STM1624	0.550	2.303	4.185	0.711	1.098	1.546	putative cytoplasmic protein
STM1697	0.616	6.044	9.815	1.047	3.887	3.714	putative Diguanylate cyclase/phosphodiesterase domain 2
STM1872	0.866	2.673	3.087	1.238	4.378	3.538	putative cytoplasmic protein
STM1988	0.508	1.668	3.283	0.645	2.072	3.213	putative cytoplasmic protein
STM2179	0.135	0.429	3.178	0.229	0.194	0.845	putative sugar transporter
STM2400	0.373	1.187	3.186	0.549	1.112	2.024	putative inner membrane protein
STM2722	0.099	0.367	3.711	0.156	0.232	1.491	Fels-2 prophage: similar to gpP, ATP charging, in phage P2
STM2726	3.001	11.631	3.876	0.798	1.916	2.401	Fels-2 prophage: hypothetical protein
STM2747	0.643	3.380	5.260	0.562	2.081	3.703	putative cytoplasmic protein
STM2762	0.112	0.375	3.345	0.377	0.834	2.208	putative inner membrane protein
STM2766	0.630	3.015	4.785	0.905	2.910	3.217	putative cytoplasmic protein
STM2767	1.698	6.765	3.985	3.055	5.970	1.954	putative Superfamily I DNA and RNA helicase
STM3021	0.280	0.886	3.162	0.368	0.575	1.563	putative inner membrane protein
STM3022	0.338	1.329	3.937	0.565	1.348	2.385	putative transport protein
STM3026	0.094	0.361	3.829	0.501	0.478	0.953	putative outer membrane protein
STM3124	0.941	4.293	4.563	0.627	0.510	0.814	putative response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain
STM3253	0.221	1.926	8.714	0.223	0.184	0.825	putative fructose/tagatose biphosphate aldolase
STM3254	0.196	1.319	6.738	0.273	0.203	0.743	putative fructose-1-phosphate kinase
STM3255	0.121	1.118	9.243	0.494	0.511	1.035	putative phosphotransferase system fructose-specific component IIB
STM3256	0.119	0.704	5.934	0.325	0.289	0.887	putative phosphotransferase system mannitol/fructose-specific IIA domain
STM3333	0.477	1.533	3.214	0.376	0.408	1.085	putative purine-cytosine permease
STM3516	0.805	2.879	3.574	0.698	0.944	1.351	putative cytoplasmic protein
STM3745	1.185	6.518	5.500	0.718	0.906	1.262	putative cytoplasmic protein
STM3844	0.353	1.093	3.091	0.266	0.375	1.412	
STM3906	1.253	3.784	3.020	2.221	4.365	1.966	putative cytoplasmic protein
STM3907	1.419	7.904	5.572	2.885	5.187	1.798	putative cytoplasmic protein
STM3927	1.371	4.466	3.257	2.467	4.373	1.772	putative inner membrane protein
STM3940	0.748	3.493	4.667	1.194	3.594	3.009	putative inner membrane protein
STM3941	0.950	3.064	3.224	1.966	6.481	3.297	putative inner membrane protein
STM3944	0.920	3.244	3.525	1.422	3.258	2.291	putative inner membrane protein
STM3966	0.593	2.529	4.262	0.925	4.154	4.490	putative arylsulfatase regulator
STM4041	0.171	1.058	6.197	0.538	0.428	0.797	putative inner membrane protein
STM4042	0.467	2.362	5.059	0.836	0.788	0.943	putative branched-chain amino acid permease
STM4054	0.145	0.481	3.309	0.321	0.210	0.656	putative dicarboxylate-binding periplasmic protein
STM4204	0.164	0.670	4.095	1.474	4.270	2.897	putative inner membrane protein
STM4205	0.158	0.549	3.467	1.142	2.999	2.626	putative phage glycosyltransferase
STM4272	0.203	0.774	3.809	0.369	0.324	0.879	putative inner membrane protein
STM4427	0.260	0.786	3.022	0.712	0.537	0.754	putative endonuclease
STM4457	1.756	5.641	3.212	0.780	1.627	2.085	putative transposase
STM4562	0.674	3.215	4.771	3.557	9.499	2.671	putative inner membrane protein
suhB	0.920	5.193	5.643	0.944	3.915	4.146	inositol monophosphatase
tldD	1.686	7.990	4.738	1.999	3.458	1.730	suppresses inhibitory activity of CsrA
trpR	1.436	4.494	3.129	1.339	1.618	1.208	transcriptional repressor for trp operon and aroH (TrpR family)
tyrB	1.303	8.289	6.364	1.187	2.143	1.806	tyrosine aminotransferase, tyrosine repressible
wecB	2.684	8.170	3.044	3.303	6.228	1.886	UDP-N-acetyl glucosamine -2-epimerase
wecF	0.830	2.850	3.433	2.141	2.537	1.185	TDP-Fuc4NAc:lipidII transferase
wecG	0.987	5.548	5.624	1.937	4.422	2.282	putative UDP-N-acetyl-D-mannosaminuronic acid transferase
wzxE	1.346	5.982	4.444	2.189	5.411	2.472	O-antigen translocase in LPS biosyntesis
wzzE	2.067	9.710	4.699	3.559	6.084	1.709	modulator of enterobacterial common antigen (ECA) polysaccharide chain length
xerC	1.508	5.326	3.532	1.684	4.173	2.478	putative integrase/recombinase, site-specific
yabK	0.426	1.400	3.285	0.441	1.250	2.835	putative binding-protein-dependent transport system inner membrane component
yacC	0.683	3.814	5.588	0.639	1.480	2.314	putative periplasmic protein

yadR	1.084	7.781	7.176	2.878	4.888	1.698	putative HesB-like domain
yafV	0.864	2.769	3.204	1.409	1.621	1.151	putative amidohydrolase
yaiZ	1.382	10.395	7.524	0.801	1.398	1.745	putative inner membrane protein
ybaN	0.358	1.430	3.999	0.688	0.838	1.219	putative phage gene 58
ybaO	0.320	0.998	3.122	0.363	0.626	1.726	putative transcriptional regulator (AsnC familiy)
ybaY	1.884	5.842	3.100	11.020	14.026	1.273	glycoprotein/polysaccharide metabolism
ybdA	0.116	0.713	6.137	0.223	0.140	0.627	putative POT family transport protein
ybdJ	0.496	1.718	3.464	0.458	0.834	1.820	putative inner membrane protein
ybhE	1.249	3.709	2.969	2.359	2.001	0.848	putative 3-carboxymuconate cyclase
ybjO	0.374	1.203	3.215	0.487	0.864	1.774	putative inner membrane protein
ybjX	3.173	10.507	3.311	5.180	19.320	3.730	Homolog of virK
ycdZ	0.551	2.120	3.847	0.541	1.458	2.698	putative inner membrane protein
yceA	0.326	1.212	3.720	0.804	1.764	2.193	putative enzyme related to sulfurtransferases
yceD	20.546	64.854	3.156	15.710	40.828	2.599	putative metal-binding
ycgO	0.658	2.895	4.401	0.777	1.216	1.565	putative CPA1 family, Na:H transport protein
yciM	0.979	3.110	3.177	1.361	2.464	1.811	putative N-acetylglucosaminyl transferase
yciS	0.983	7.440	7.571	1.979	5.874	2.968	putative inner membrane protein
ydcZ	0.951	3.461	3.637	0.690	0.812	1.177	putative inner membrane protein
ydgC	0.307	0.946	3.084	0.467	0.720	1.544	putative inner membrane protein
ydgR	3.037	14.321	4.716	2.827	2.899	1.025	putative POT family, peptide transport protein
ydhF	1.388	4.645	3.347	0.596	1.116	1.874	putative aldo/keto reductase
ydhL	0.307	0.942	3.066	0.239	0.432	1.809	putative oxidoreductase
ydiE	0.221	0.916	4.150	0.394	0.653	1.657	putative cytoplasmic protein
ydiQ	0.136	0.431	3.176	0.272	0.251	0.922	putative electron transfer flavoprotein
ydiU	0.419	3.073	7.336	0.806	2.020	2.508	putative cytoplasmic protein
yeaN	0.317	1.283	4.045	0.539	0.762	1.413	putative MFS family transport protein (amino acid/amine transport)
yeaS	1.034	4.819	4.662	3.299	7.040	2.134	paral putative transport protein
yedA	0.238	0.860	3.614	0.318	0.469	1.474	putative permease
yegB	0.177	0.651	3.690	0.409	0.644	1.576	putative MFS family transport protein
yehS	0.456	1.892	4.146	0.565	1.669	2.954	putative cytoplasmic protein
yehY	0.352	1.318	3.740	1.392	1.791	1.287	putative ABC-type proline/glycine betaine transport systems, permease component
yehZ	0.571	1.824	3.198	1.969	2.072	1.052	putative ABC superfamily (bind_prot) transport protein (possibly glycine betaine choline transport for osmoprotection)
yejL	1.461	5.391	3.689	1.304	3.219	2.469	putative cytoplasmic protein
yejM	0.846	3.351	3.962	0.996	2.104	2.113	putative hydrolase of alkaline phosphatase superfamily
yfaO	0.863	3.588	4.157	0.871	1.420	1.630	putative NTP pyrophosphohydrolases including oxidative damage repair enzymes
yfaZ	1.031	3.483	3.378	1.267	3.157	2.491	putative inner membrane protein
yfcL	0.929	2.988	3.217	0.810	1.137	1.404	putative cytoplasmic protein
yfdH	0.133	0.529	3.984	0.235	0.471	2.007	putative glycosyltransferase
yfdZ	1.916	7.251	3.784	1.583	2.822	1.783	putative aminotransferase
yfhP	1.272	4.232	3.327	5.873	4.429	0.754	believed to be involved in assembly of Fe-S clusters
ygaM	0.739	2.442	3.304	1.534	3.047	1.987	putative inner membrane protein
ygbE	0.632	2.958	4.681	1.408	5.045	3.584	putative inner membrane protein
ygbQ	2.925	9.141	3.125	2.286	4.794	2.097	putative Septum formation initiator
ygdQ	0.521	1.627	3.127	0.908	3.337	3.673	putative integral membrane transport protein
ygfY	2.123	7.592	3.576	1.453	2.280	1.569	putative cytoplasmic protein
ygiE	0.539	1.958	3.629	0.740	0.857	1.158	putative divalent heavy-metal cations transporter
ygjO	0.474	1.737	3.666	0.395	1.120	2.839	paral putative methyltransferase
yheR	0.806	2.657	3.295	1.936	1.803	0.931	putative NAD(P)H oxidoreductase
yhgG	0.371	1.333	3.599	1.005	1.787	1.778	putative cytoplasmic protein
yhgI	1.723	6.073	3.524	2.866	4.706	1.642	putative Thioredoxin-like proteins and domain
yhhK	0.748	2.619	3.503	0.888	1.247	1.403	putative acetyltransferase
yiaG	0.477	1.498	3.139	0.980	2.108	2.152	putative transcriptional regulator
yiaK	0.189	0.630	3.338	0.275	0.209	0.758	putative malate dehydrogenase
yibK	1.691	4.825	2.853	0.751	0.808	1.076	putative tRNA/rRNA methyltransferase
yicL	0.474	1.489	3.139	1.656	3.807	2.299	putative permease, integral membrane protein
yicM	0.164	0.691	4.212	0.321	0.435	1.354	putative MFS family tranport protein (1st mdule)
yicN	0.572	3.516	6.148	0.640	1.163	1.816	putative inner membrane protein
yieG	0.618	2.035	3.295	0.629	0.670	1.065	putative xanthine/uracil permeases family

yieH	0.850	4.020	4.729	1.118	0.885	0.792	putative phosphatase/phosphohexomutase
yifB	0.535	2.846	5.317	0.941	3.958	4.206	putative magnesium chelatase, subunit ChlI
yifK	0.743	4.237	5.700	1.039	3.101	2.986	putative APC family, amino-acid transport protein, permease protein
yigA	3.021	11.317	3.746	3.346	6.154	1.839	putative cytoplasmic protein
yigB	1.301	5.204	3.999	1.676	4.445	2.652	putative hydrolase of the HAD superfamily
yigF	0.727	3.389	4.661	1.273	4.643	3.648	putative inner membrane protein
yigG	0.944	3.433	3.638	1.702	5.838	3.430	putative inner membrane protein
yigI	2.182	11.078	5.077	2.376	5.794	2.438	putative protein PaaI, possibly involved in aromatic compounds catabolism
yigL	1.075	4.340	4.037	1.391	4.171	2.999	putative hydrolase of the HAD superfamily
yigM	0.545	3.303	6.058	0.858	2.283	2.661	paral putative transport protein
yiiG	0.125	0.953	7.631	0.288	0.574	1.998	putative cytoplasmic protein
yijC	4.468	15.433	3.454	2.605	3.740	1.436	putative transcriptional repressor (TetR/AcrR family)
yjaD	1.414	4.683	3.312	1.890	3.212	1.700	putative NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding
yjcD	0.384	1.818	4.728	0.499	1.002	2.008	putative xanthine/uracil permease family
yjcG	0.389	1.616	4.151	0.521	0.351	0.674	putative SSS family transport protein
yjdC	1.422	4.941	3.475	1.906	3.133	1.644	putative bacterial regulatory protein, merR family
yjeO	0.442	1.710	3.867	0.931	3.650	3.922	putative inner membrane protein
yjgM	0.484	1.528	3.158	2.754	7.870	2.858	putative acetyltransferase
yjiJ	0.681	3.271	4.800	0.742	0.376	0.506	putative sugar transporter
yjjU	1.020	3.426	3.360	1.384	2.091	1.511	putative phosphoesterase
yjjY	8.916	29.804	3.343	11.194	16.484	1.472	putative inner membrane protein
yliA	0.901	3.231	3.586	1.023	0.958	0.937	putative ATPase components of ABC-type transport system, contain duplicated ATPase domain
yncA	1.250	5.026	4.020	1.208	1.110	0.918	putative acyltransferase
yniB	0.673	2.103	3.123	0.948	1.571	1.657	putative regulator
yoaB	1.484	5.799	3.908	0.812	1.933	2.380	putative translation initiation inhibitor
yobF	24.519	148.009	6.037	29.495	88.950	3.016	putative cytoplasmic protein
yohD	0.230	0.904	3.935	0.496	0.609	1.227	putative DedA family, membrane protein
yojI	0.251	0.923	3.675	0.313	0.406	1.297	putative ABC-type multidrug/protein/lipid transport system, ATPase component
yqeF	4.029	12.283	3.049	1.463	1.330	0.909	putative acetyl-CoA acetyltransferase
yqgA	0.214	0.860	4.027	0.384	0.637	1.658	putative inner membrane protein

Table S2c. Genes showing a ≥3-fold higher expression at 37°C than 25°C in LT2a but no significant change in expression in JH4000

Genes showing less than a 1-fold difference between expression ratios of LT2a and JH4000 were excluded

Gene	**LT2a 37°C**	**LT2a 25°C**	**Ratio 37/25°C**	**JH4000 37°C**	**JH4000 25°C**	**Ratio 37/25°C**	**Function**
ackA	12.421	1.443	8.607	1.412	0.617	2.289	acetate kinase A (propionate kinase 2)
adhE	3.023	0.499	6.053	1.691	0.651	2.599	iron-dependent alcohol dehydrogenase of the multifunctional alcohol dehydrogenase AdhE
aer	8.341	1.311	6.362	0.269	0.167	1.606	aerotaxis sensor receptor, senses cellular redox state or proton motive force
alaS	8.463	2.471	3.425	2.467	1.392	1.773	alanyl-tRNA synthetase
ansB	30.756	6.143	5.007	0.470	0.387	1.214	periplasmic L-asparaginase II
artI	5.163	0.800	6.455	1.085	0.440	2.462	ABC superfamily (bind_prot), arginine transport system
aspA	106.382	13.780	7.720	3.907	1.952	2.001	aspartate ammonia-lyase (aspartase)
atpG	31.288	8.442	3.706	10.919	4.931	2.214	membrane-bound ATP synthase, F1 sector, gamma-subunit
atpH	51.301	14.342	3.577	17.127	7.844	2.183	membrane-bound ATP synthase, F1 sector, delta-subunit
avrA	4.456	0.289	15.427	8.791	4.691	1.874	putative inner membrane protein
cadB	3.984	0.321	12.419	1.771	0.799	2.216	APC family, lysine/cadaverine transport protein
cbiC	2.263	0.566	4.001	2.324	4.746	0.490	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiD	3.387	0.589	5.748	2.745	3.974	0.691	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiE	2.411	0.531	4.539	2.581	4.650	0.555	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiF	4.446	0.402	11.063	3.175	5.457	0.582	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiG	3.569	0.338	10.563	2.936	4.907	0.598	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiH	3.986	0.320	12.461	3.365	4.064	0.828	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiJ	2.733	0.387	7.069	1.502	3.050	0.493	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiK	3.682	0.289	12.748	2.827	2.908	0.972	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiL	3.201	0.405	7.908	2.844	4.035	0.705	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiM	2.150	0.549	3.913	2.285	5.235	0.437	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiN	1.987	0.438	4.538	2.405	4.810	0.500	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiO	1.404	0.400	3.508	1.135	2.011	0.565	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiT	2.710	0.484	5.598	2.086	3.287	0.635	synthesis of vitamin B12 adenosyl cobalamide precursor
cboQ	1.661	0.407	4.077	1.835	3.148	0.583	synthesis of vitamin B12 adenosyl cobalamide precursor
cheA	14.059	3.528	3.985	0.221	0.126	1.755	sensory histitine protein kinase, transduces signal between chemo- signal receptors and CheB and CheY
cheW	21.256	5.436	3.910	0.335	0.177	1.897	purine-binding chemotaxis protein; regulation
crp	14.241	3.647	3.905	2.146	0.855	2.510	catabolite activator protein (CAP), cyclic AMP receptor protein (CRP family)
cydA	48.283	1.472	32.803	2.520	2.349	1.073	cytochrome d terminal oxidase, polypeptide subunit I
cydB	45.421	2.005	22.655	3.319	2.481	1.338	cytochrome d terminal oxidase polypeptide subunit II
dcuA	3.113	0.905	3.440	0.611	0.352	1.735	Dcu family, anaerobic dicarboxylate transport protein
dcuB	5.049	0.965	5.232	1.237	2.180	0.567	Dcu family, anaerobic C4-dicarboxylate transporter
dmsA	4.913	0.173	28.442	0.195	0.144	1.352	anaerobic dimethyl sulfoxide reductase, subunit A
dmsB	4.158	0.205	20.244	0.188	0.117	1.611	anaerobic dimethyl sulfoxide reductase, subunit B
fdnG	10.470	0.903	11.594	1.590	0.572	2.780	putative molybdopterin oxidoreductases
fdnI	6.156	0.462	13.323	0.660	0.493	1.341	formate dehydrogenase-N, cytochrome B556(Fdn) gamma subunit, nitrate-inducible
flgA	11.190	2.101	5.327	0.419	0.278	1.504	flagellar biosynthesis; assembly of basal-body periplasmic P ring
flgB	14.352	4.009	3.580	0.580	0.399	1.455	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgC	25.654	3.951	6.492	0.228	0.116	1.961	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgD	30.569	3.941	7.757	0.221	0.146	1.509	flagellar biosynthesis, initiation of hook assembly
flgE	49.796	4.189	11.888	0.248	0.129	1.920	flagellar biosynthesis, hook protein
flgF	32.494	3.936	8.255	0.334	0.180	1.858	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgG	29.543	3.112	9.494	0.245	0.195	1.253	flagellar biosynthesis, cell-distal portion of basal-body rod
flgH	11.670	2.333	5.003	0.194	0.099	1.967	flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein
flgI	8.778	1.792	4.899	0.187	0.089	2.110	putative flagella basal body protein
flgJ	7.747	1.314	5.893	0.213	0.210	1.015	flagellar biosynthesis
flgK	15.040	1.286	11.692	0.213	0.098	2.174	flagellar biosynthesis, hook-filament junction protein 1
flgL	23.051	2.647	8.707	0.286	0.135	2.121	flagellar biosynthesis; hook-filament junction protein
fliA	45.442	6.002	7.571	0.329	0.243	1.356	sigma F (sigma 28) factor of RNA polymerase, transcription of late flagellar genes (class 3a and 3b operons)
fliB	5.829	1.179	4.946	0.312	0.196	1.591	N-methylation of lysine residues in flagellin
fliC	72.576	12.541	5.787	0.513	0.202	2.543	flagellar biosynthesis; flagellin, filament structural protein
fliD	31.808	2.193	14.506	0.614	0.250	2.460	flagellar biosynthesis; filament capping protein; enables filament assembly

fliE	5.600	1.439	3.892	0.658	0.279	2.355	putative Flagellar hook-basal body protein
fliJ	6.972	0.944	7.384	0.243	0.103	2.364	flagellar fliJ protein
fliK	12.982	1.182	10.981	0.343	0.128	2.672	flagellar hook-length control protein
fliL	17.026	3.135	5.432	0.251	0.191	1.317	flagellar biosynthesis
fliM	10.933	2.384	4.586	0.240	0.182	1.319	flagellar biosynthesis, component of motor switch and energizing
fliS	19.838	3.520	5.636	0.247	0.170	1.454	flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)
fliT	12.192	3.652	3.338	0.453	0.361	1.253	flagellar biosynthesis; possible export chaperone for FliD
fliY	8.970	1.210	7.415	1.115	0.948	1.177	putative periplasmic binding transport protein
fliZ	33.925	2.613	12.982	0.416	0.270	1.540	putative regulator of FliA
fljA	7.380	1.428	5.167	0.408	0.240	1.700	Flagellar synthesis: repressor of fliC
frdA	44.011	3.484	12.632	2.319	1.419	1.634	fumarate reductase, anaerobic, flavoprotein subunit
frdB	39.053	2.669	14.630	1.847	1.143	1.615	fumarate reductase, anaerobic, Fe-S protein subunit
frdC	25.871	3.737	6.923	1.588	1.788	0.888	fumarate reductase, anaerobic, membrane anchor polypeptide
frdD	22.769	4.890	4.656	1.920	2.633	0.729	fumarate reductase, anaerobic, membrane anchor polypeptide
fumB	9.006	1.595	5.646	1.306	1.014	1.288	fumarase B (fumarate hydratase class I), anaerobic isozyme
fusA	45.514	10.890	4.180	13.579	6.112	2.222	protein chain elongation factor EF-G, GTP-binding
galU	3.728	0.525	7.100	3.004	2.802	1.072	glucose-1-phosphate uridylyltransferase
gldA	4.376	1.432	3.055	1.173	0.769	1.526	glycerol dehydrogenase, NAD
glnS	5.690	1.544	3.684	1.719	0.886	1.939	glutamine tRNA synthetase
glpC	5.548	0.292	19.009	0.566	0.224	2.524	sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit
glyA	15.312	3.702	4.136	3.485	1.651	2.111	serine hydroxymethyltransferase
glyQ	6.306	1.163	5.420	2.422	0.880	2.753	glycine tRNA synthetase, alpha subunit
hcp	2.181	0.359	6.069	0.233	0.174	1.341	hybrid cluster protein; similar to prismane-protein homolog
hcr	2.141	0.426	5.028	0.356	0.211	1.691	NADH oxidoreductase for hcp gene product
hilA	7.306	0.405	18.021	1.563	0.789	1.980	invasion genes transcription activator
hilC	10.201	1.565	6.519	8.792	10.217	0.861	bacterial regulatory helix-turn-helix proteins, araC family
hilD	13.267	0.884	15.015	5.801	5.242	1.107	regulatory helix-turn-helix proteins, araC family
hisB	1.627	0.508	3.202	0.603	0.366	1.647	bifunctional: imidazoleglycerol-phosphate dehydratase; histidinol-phosphatase
hmpA	2.362	0.520	4.540	0.621	0.235	2.646	dihydropteridine reductase 2 and nitric oxide dioxygenase activity
hybA	5.160	0.366	14.085	0.428	0.154	2.776	function unknown, intitally thought to be hydrogenase-2 small subunit which now identified as hybO
hybB	4.083	0.464	8.804	0.290	0.242	1.199	putative cytochrome Ni/Fe component of hydrogenase-2
hybC	7.808	0.856	9.122	1.002	0.500	2.003	hydrogenase-2, large subunit
hybD	7.581	1.239	6.118	1.060	0.700	1.516	putative processing element for hydrogenase-2
hybE	3.612	0.879	4.108	0.584	0.490	1.192	putative hydrogenase
hybF	2.763	0.872	3.168	0.762	0.749	1.017	putative hydrogenase expression/formation protein
hybG	1.573	0.510	3.083	0.488	0.380	1.282	hydrogenase-2 operon protein
hypA	1.579	0.465	3.395	0.404	0.438	0.922	guanine-nucleotide binding protein in formate-hydrogenlyase system, functions as nickel donor for HycE of hydrogenlyase 3
hypB	7.116	0.735	9.681	4.139	1.417	2.921	hydrogenase-3 accessory protein, assembly of metallocenter
hypC	4.960	0.735	6.746	3.258	1.986	1.640	putative hydrogenase expression/formation protein
hypD	4.234	0.832	5.089	2.992	1.848	1.619	putative hydrogenase expression/formation protein
hypE	4.277	0.955	4.477	2.883	1.450	1.988	putative hydrogenase expression/formation protein
hypO	6.866	0.453	15.156	0.381	0.180	2.109	putative Ni/Fe hydrogenases, small subunit
iagB	5.092	0.363	14.030	2.259	1.806	1.251	cell invasion protein
invA	3.477	0.516	6.737	4.450	5.055	0.880	invasion protein
invB	7.005	0.764	9.173	9.270	7.102	1.305	surface presentation of antigens; secretory proteins
invC	9.746	0.691	14.113	9.967	6.150	1.621	surface presentation of antigens; secretory proteins
invE	3.905	0.340	11.481	4.127	2.619	1.576	invasion protein
invF	9.101	0.602	15.120	6.536	3.545	1.844	invasion protein
invG	6.203	0.359	17.267	4.286	1.950	2.198	invasion protein; outer membrane
invH	2.863	0.414	6.908	3.873	7.185	0.539	invasion protein
katG	4.253	0.653	6.512	0.579	0.323	1.791	catalase; hydroperoxidase HPI(I)
leuS	5.526	1.686	3.278	1.751	1.367	1.281	leucine tRNA synthetase
manX	14.804	3.895	3.800	6.547	4.953	1.322	Sugar Specific PTS family, mannose-specific enzyme IIAB
manY	20.686	3.159	6.548	5.859	4.146	1.413	Sugar Specific PTS family, mannose-specific enzyme IIC
manZ	10.556	2.982	3.540	3.313	5.300	0.625	Sugar Specific PTS family, mannose-specific enzyme IID
mdoG	5.063	1.500	3.375	1.853	1.204	1.539	periplasmic glucans biosynthesis protein
motB	8.767	2.103	4.168	0.216	0.175	1.232	enables flagellar motor rotation, linking torque machinery to cell wall
napB	22.150	0.671	33.022	1.179	0.858	1.374	periplasmic nitrate reductase, small subunit, cytochrome C550, in complex with NapA

napF	3.854	0.378	10.210	0.209	0.164	1.270	ferredoxin-type protein: electron transfer
napH	11.510	0.470	24.504	0.589	0.792	0.744	ferredoxin-type protein: electron transfer
narH	0.911	34.344	37.717	1.376	5.511	4.004	nitrate reductase 1, FeS (beta) subunit
nrdA	5.704	1.534	3.719	2.296	1.064	2.158	ribonucleoside diphosphate reductase 1, alpha subunit
nrdD	2.460	0.284	8.655	0.232	0.175	1.323	anaerobic ribonucleoside-triphosphate reductase
nrfA	4.413	0.423	10.428	0.244	0.128	1.914	nitrite reductase periplasmic cytochrome c(552)
nrfB	3.126	0.308	10.157	0.219	0.099	2.209	formate-dependent nitrite reductase; a penta-haeme cytochrome c
nrfC	3.146	0.385	8.176	0.299	0.167	1.794	putative nitrite reductase; formate-dependent, Fe-S centers
nrfD	2.920	0.466	6.267	0.342	0.170	2.016	putative nitrate reductase, formate dependent
nrfE	1.311	0.281	4.658	0.217	0.140	1.551	formate-dependent nitrite reductase; involved in attachment of haem c to cytochrome c552
ompW	31.967	0.483	66.193	1.044	0.926	1.127	outer membrane protein W; colicin S4 receptor; putative transporter
orfX	1.966	0.369	5.325	1.270	0.788	1.611	putative cytoplasmic protein
orgA	9.223	1.194	7.725	13.633	10.311	1.322	putative flagellar biosynthesis/type III secretory pathway protein
pdhR	3.116	0.437	7.125	1.031	0.362	2.844	transcriptional repressor for pyruvate dehydrogenase complex (GntR family)
pepD	9.322	1.798	5.183	2.724	1.163	2.342	aminoacyl-histidine dipeptidase (peptidase D)
pepT	2.345	0.671	3.496	0.700	0.676	1.035	putative peptidase T(aminotripeptidase)
pflB	37.967	1.579	24.045	8.841	3.843	2.301	pyruvate formate lyase I, induced anaerobically
phoP	10.586	2.808	3.770	11.778	7.424	1.587	response regulator in two-component regulatory system with PhoQ, transcribes genes expressed under low Mg+ concentration (OmpR family)
phsA	3.962	0.363	10.900	0.336	0.137	2.455	Hydrogen sulfide production: membrane anchoring protein
phsB	3.156	0.497	6.355	0.401	0.197	2.030	Hydrogen sulfide production: iron- sulfur subunit; electron transfer
phsC	2.261	0.751	3.012	0.458	0.406	1.129	Hydrogen sulfide production: membrane anchoring protein
pmgI	3.195	0.586	5.454	0.687	0.340	2.023	phosphoglyceromutase
prgH	8.401	0.296	28.427	4.325	1.910	2.264	cell invasion protein
prgK	29.425	1.352	21.771	27.172	9.844	2.760	cell invasion protein; lipoprotein, may link inner and outer membranes
proS	4.276	1.301	3.288	1.694	0.793	2.136	proline tRNA synthetase
ptsH	14.637	2.670	5.482	5.157	1.963	2.628	PTS family, Hpr protein, phosphohistidinoprotein-hexose phosphotransferase
pykF	4.144	1.274	3.254	3.176	1.870	1.698	pyruvate kinase I (formerly F), fructose stimulated
rplB	70.832	22.009	3.218	18.979	11.563	1.641	50S ribosomal subunit protein L2
rplE	58.105	15.292	3.800	16.066	15.246	1.054	50S ribosomal subunit protein L5
rplF	50.203	15.869	3.164	22.615	17.833	1.268	50S ribosomal subunit protein L6
rplI	18.553	5.920	3.134	4.715	4.160	1.133	50S ribosomal subunit protein L9
rplR	64.233	12.407	5.177	15.500	9.360	1.656	50S ribosomal subunit protein L18
rpoA	68.896	14.694	4.689	14.900	6.370	2.339	RNA polymerase, alpha subunit
rpsD	63.666	15.324	4.155	13.046	7.750	1.683	30S ribosomal subunit protein S4
rpsE	58.561	12.001	4.880	14.066	7.947	1.770	30S ribosomal subunit protein S5
rpsH	50.002	14.287	3.500	18.755	14.814	1.266	30S ribosomal subunit protein S8, and regulator
rpsN	67.823	14.352	4.726	20.317	15.618	1.301	30S ribosomal subunit protein S14
rpsR	17.789	5.835	3.049	4.970	4.180	1.189	30S ribosomal subunit protein S18
rseA	47.772	12.452	3.837	12.983	7.594	1.710	anti sigma E (sigma 24) factor, negative regulator
rtsA	7.320	0.747	9.798	1.274	0.779	1.635	putative AraC-type DNA-binding domain-containing protein
rtsB	4.220	0.698	6.046	0.937	0.900	1.040	putative bacterial regulatory proteins, luxR family
sdhA	57.242	17.160	3.336	14.776	8.744	1.690	succinate dehydrogenase, flavoprotein subunit
sdhC	32.955	10.084	3.268	5.571	3.940	1.414	succinate dehydrogenase, cytochrome b556
spaP	3.125	0.501	6.231	7.869	6.268	1.256	surface presentation of antigens; secretory proteins
spaQ	2.205	0.722	3.055	6.740	7.822	0.862	surface presentation of antigens; secretory proteins
spaR	1.559	0.318	4.908	4.603	3.600	1.279	surface presentation of antigens; secretory proteins
spaS	1.099	0.233	4.719	2.276	1.570	1.450	surface presentation of antigens; secretory proteins
speF	14.578	0.249	58.660	0.291	0.283	1.028	ornithine decarboxylase isozyme, inducible
sprB	9.709	0.642	15.118	15.081	7.763	1.943	transcriptional regulator
srfA	7.113	0.826	8.609	0.220	0.124	1.776	ssrAB activated gene.
srfB	7.542	1.321	5.708	0.447	0.344	1.297	ssrAB activated gene.
srfC	6.391	0.837	7.635	0.355	0.284	1.251	ssrAB activated gene: predicted coiled-coil structure.
STM0699	4.733	0.431	10.992	0.306	0.296	1.035	putative cytoplasmic protein
STM0972	1.501	0.377	3.981	7.341	9.787	0.750	homologous to secreted protein sopD
STM1255	2.940	0.885	3.323	0.627	0.671	0.935	putative ABC transporter periplasmic binding protein
STM1300	4.332	1.074	4.032	0.385	0.339	1.136	putative periplasmic protein
STM1328	3.319	0.639	5.196	5.797	4.801	1.207	putative outer membrane protein
STM1498	1.130	0.160	7.075	0.147	0.191	0.767	putative dimethyl sulphoxide reductase
STM1499	1.033	0.247	4.178	0.192	0.152	1.262	putative dimethyl sulphoxide reductase, chain A1

STM1731	2.099	0.262	8.012	15.771	13.756	1.146	putative catalase
STM1967	1.553	0.491	3.164	1.312	1.626	0.807	putative 50S ribosomal protein
STM2248	5.490	0.437	12.561	0.682	0.736	0.926	
STM2250	10.256	0.708	14.486	1.171	1.093	1.071	
STM2252	7.641	0.704	10.849	0.915	1.090	0.839	
STM2340	8.842	1.178	7.505	0.901	0.537	1.676	putative transketolase
STM2342	5.943	1.401	4.241	0.569	0.350	1.628	putative inner membrane protein
STM2343	4.213	1.237	3.405	0.520	0.402	1.292	putative cytoplasmic protein
STM2868	8.182	0.821	9.962	10.246	6.631	1.545	putative cytoplasmic protein
STM2914	1.463	0.289	5.060	0.228	0.163	1.403	putative nucleoside-diphosphate-sugar epimerase
STM3137	2.997	0.891	3.362	0.577	0.370	1.560	putative uronate isomerase
STM3138	8.742	0.485	18.042	1.813	2.462	0.736	putative methyl-accepting chemotaxis protein
STM3216	21.944	1.056	20.784	0.355	0.248	1.430	putative methyl-accepting chemotaxis protein
STM3262	3.145	1.046	3.006	0.623	0.353	1.764	transcriptional regulator of sugar metabolism
STM3820	2.745	0.253	10.851	0.527	0.427	1.233	putative cytochrome c peroxidase
STM4305	0.865	0.195	4.429	0.399	0.189	2.115	putative anaerobic dimethyl sulfoxide reductase, subunit A
STM4306	0.957	0.224	4.270	0.378	0.162	2.329	putative anaerobic dimethyl sulfoxide reductase, subunit B
STM4312	1.755	0.483	3.636	0.505	1.287	0.392	putative phage protein
STM4313	2.390	0.502	4.764	0.530	1.002	0.530	putative cytoplasmic protein
STM4496	1.674	0.500	3.346	0.804	0.406	1.981	putative ATPase involved in DNA repair
tdcB	3.745	0.401	9.332	2.254	1.476	1.527	threonine dehydratase, catabolic
tdcC	3.697	0.315	11.721	2.231	1.166	1.914	HAAAP family, L-threonine/ L-serine permease, anaerobically inducible
tdcD	3.036	0.249	12.184	1.200	1.042	1.151	propionate kinase/acetate kinase II, anaerobic
tdcE	2.890	0.356	8.122	1.358	1.391	0.976	pyruvate formate-lyase 4/ 2-ketobutyrate formate-lyase
tktA	26.347	4.252	6.196	5.139	1.849	2.780	transketolase 1 isozyme
treC	3.271	0.899	3.637	0.383	0.222	1.724	trehalose- 6-P hydrolase, alternative inducer of maltose system, cytoplasmic
trg	5.879	1.349	4.358	0.243	0.201	1.210	methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor
yaeT	11.769	3.257	3.613	3.373	3.016	1.118	putative outer membrane antigen
ybgE	6.766	1.218	5.556	1.056	1.181	0.894	putative inner membrane lipoprotein
ybgT	28.247	1.421	19.874	2.445	1.973	1.239	putative outer membrane lipoprotein
ycfJ	0.999	0.308	3.242	0.692	0.443	1.563	putative outer membrane lipoprotein
ycfQ	1.955	0.450	4.347	0.802	0.334	2.400	putative transcriptional repressor (TetR/AcrR family)
ydfZ	4.552	0.485	9.392	0.530	0.406	1.304	putative cytoplasmic protein
yfiD	13.108	0.462	28.356	0.501	0.332	1.508	putative formate acetyltransferase
ygbJ	4.859	0.450	10.789	0.274	0.223	1.230	3-hydroxyisobutyrate dehydrogenase
ygbK	5.377	0.430	12.504	0.336	0.151	2.227	paral putative tRNA synthase
ygbL	2.977	0.276	10.785	0.246	0.153	1.608	putative fuculose phosphate aldolase
ygbM	3.422	0.395	8.669	0.257	0.152	1.696	putative endonuclease
yjdL	1.788	0.578	3.093	0.401	0.304	1.321	putative POT family, di-/tripeptide transport protein
yjjI	2.067	0.322	6.430	0.453	0.165	2.737	putative cytoplasmic protein
ymdA	2.988	0.948	3.151	0.465	0.447	1.040	putative periplasmic protein

Table S2d. Genes showing a ≥3-fold higher expression at 25°C than 37°C in LT2a but no significant change in expression in JH4000

Genes showing less than a 1-fold difference between expression ratios of LT2a and JH4000 were excluded

Gene	LT2a 37°C	LT2a 25°C	Ratio 25/37°C	JH4000 37°C	JH4000 25°C	Ratio 25/37°C	Function
ansP	0.259	1.430	5.515	0.333	0.657	1.975	APC family, L-asparagine transport protein
astA	0.475	2.809	5.909	0.502	0.732	1.460	arginine succinyltransferase
astB	0.179	0.872	4.870	0.391	0.591	1.510	succinylarginine dihydrolase
astC	0.956	5.585	5.844	0.869	0.997	1.147	succinylornithine transaminase, also has acetylornitine transaminase activity
astD	0.321	1.613	5.029	0.555	0.833	1.500	succinylglutamic semialdehyde dehydrogenase
astE	0.173	0.573	3.314	0.528	0.822	1.559	succinylglutamate desuccinylase
atpI	6.185	24.399	3.945	4.799	9.707	2.023	membrane-bound ATP synthase subunit, F1-F0-type proton-ATPase
avtA	0.397	1.629	4.098	0.686	0.596	0.868	valine-pyruvate aminotransferase
bioH	0.848	2.986	3.519	1.077	0.995	0.924	putative hydrolase, biotin biosynthesis; reaction prior to pimeloyl CoA
brnQ	0.872	3.058	3.509	1.215	1.632	1.343	LIVCS family, branched chain amino acid transporter system II (LIV-II)
cybC	1.546	6.759	4.371	4.244	5.899	1.390	cytochrome b(562)
cyoC	10.988	36.743	3.344	23.168	24.591	1.061	cytochrome o ubiquinol oxidase subunit III
cyoD	5.522	33.136	6.001	22.223	18.888	0.850	cytochrome o ubiquinol oxidase subunit IV
cyoE	2.570	30.652	11.926	15.141	14.628	0.966	protohaeme IX farnesyltransferase (haeme O biosynthesis)
dadX	3.105	11.473	3.695	2.364	2.067	0.874	alanine racemase 2, catabolic
ddlA	1.697	6.499	3.830	1.299	2.161	1.663	D-alanine-D-alanine ligase A
dgoT	0.119	0.355	2.983	0.220	0.130	0.590	MFS family, D-galactonate transport protein
dlhH	1.212	5.350	4.413	2.613	3.419	1.309	putative dienelactone hydrolase family
dppB	0.216	0.861	3.979	0.351	0.211	0.601	ABC superfamily (membrane), dipeptide transport protein 1
dppC	0.228	0.745	3.274	0.336	0.217	0.646	ABC superfamily (membrane), dipeptide transport protein 2
exbB	0.400	1.660	4.152	0.875	0.662	0.756	uptake of enterochelin; tonB-dependent uptake of B colicins
fabI	3.860	16.533	4.284	5.996	13.179	2.198	enoyl-[acyl-carrier-protein] reductase (NADH)
feoA	0.468	6.831	14.584	0.899	0.854	0.950	ferrous iron transport protein A
fepB	0.170	0.536	3.162	0.289	0.157	0.544	ABC superfamily (peri_perm), ferric enterobactin (enterochelin) tranporter
fepD	0.148	1.005	6.794	0.247	0.165	0.667	ABC superfamily (membrane), ferric enterobactin (enterochelin) transporter
fepG	0.154	0.948	6.168	0.288	0.202	0.702	ABC superfamily (membrane), ferric enterobactin transporter
fhuA	0.126	0.514	4.076	0.274	0.148	0.542	outer membrane protein receptor / transporter for ferrichrome, colicin M, and phages T1, T5, and phi80
fhuB	0.227	0.717	3.164	0.304	0.206	0.678	ABC superfamily (membrane), hydroxamate-dependent iron uptake
fhuC	0.135	0.621	4.587	0.279	0.176	0.629	ABC superfamily (atp_bind), hydroxymate-dependent iron transport
fhuD	0.109	0.634	5.795	0.295	0.192	0.650	ABC superfamily (bind _prot), hydroxamate-dependent iron uptake
gabT	0.200	0.628	3.136	1.570	0.556	0.354	4-aminobutyrate aminotransferase
gcd	0.336	1.286	3.823	1.444	1.244	0.861	glucose dehydrogenase
gltP	1.772	6.390	3.606	1.738	1.395	0.802	DAACS family, glutamate:aspartate symport protein
gltS	1.836	8.494	4.626	1.048	1.518	1.448	GltS family, glutamate transport protein
hcaT	0.758	3.494	4.610	0.821	2.047	2.492	putative MFS family transport protein
hemC	4.433	13.828	3.119	4.430	6.299	1.422	porphobilinogen deaminase (hydroxymethylbilane synthase)
hpt	1.560	10.680	6.847	1.443	3.938	2.730	hypoxanthine phosphoribosyltransferase
ilvG	0.483	1.591	3.294	0.807	1.328	1.644	acetolactate synthase II, large subunit, fragment 1, cryptic
ilvL	1.339	5.728	4.277	2.700	5.579	2.066	ilvGEDA operon leader peptide
ilvM	1.236	4.137	3.347	1.987	4.169	2.098	acetolactate synthase II, small subunit
leuA	0.190	0.579	3.047	0.599	0.536	0.895	2-isopropylmalate synthase
livJ	0.545	1.662	3.047	0.524	0.479	0.912	ABC superfamily (bind_prot), branched-chain amino acid transporter, high-affinity
lysA	0.324	1.040	3.209	0.644	0.718	1.114	diaminopimelate decarboxylase
lysP	0.493	1.660	3.368	0.686	1.406	2.049	APC family, lysine-specific permease
malG	0.271	1.856	6.849	0.525	0.761	1.451	ABC superfamily (membrane), maltose transport protein
metB	0.862	3.286	3.814	0.762	1.197	1.570	cystathionine gamma-synthase
mioC	1.324	8.465	6.394	1.440	3.537	2.455	initiation of chromosome replication
mntH	0.345	1.100	3.190	0.314	0.529	1.682	Nramp family, manganese/divalent cation transport prortein
mscL	1.742	5.685	3.263	3.179	4.594	1.445	mechanosensitive channel
mtr	0.236	0.838	3.543	0.320	0.518	1.617	HAAAP family, tryptophan-specific transport protein
ndk	11.126	50.722	4.559	7.862	14.602	1.857	nucleoside diphosphate kinase
nikR	1.020	3.631	3.560	0.930	1.181	1.270	nickel-responsive transcriptional regulator
ompX	7.036	37.301	5.301	27.205	28.598	1.051	outer membrane protease, receptor for phage OX2
orfB	3.753	12.887	3.433	7.576	10.318	1.362	putative cytoplasmic protein

pgsA	1.368	5.268	3.852	1.470	1.904	1.295	phosphatidylglycerophosphate synthetase (CDP-1,2-diacyl-sn-glycero-3-phosphate phosphatidyl transferase)
pheP	0.377	1.696	4.494	0.640	1.278	1.997	APC family, phenylalanene transporter
phoU	0.914	3.712	4.061	1.246	1.268	1.018	regulatory gene for high affinity phosphate uptake
ppiC	1.446	6.689	4.625	1.643	3.376	2.054	peptidyl-prolyl cis-trans isomerase C (rotamase C)
proP	0.606	2.106	3.478	1.812	2.024	1.117	MFS family, low-affinity proline transporter (proline permease II)
proV	0.913	3.783	4.144	5.302	5.537	1.044	ABC superfamily (atp_bind), glycine/betaine/proline transport protein
proW	1.095	7.507	6.859	12.100	13.180	1.089	ABC superfamily (membrane), glycine/betaine/proline transport protein
PSLT003	0.923	3.203	3.471	1.039	2.128	2.047	
PSLT015	0.262	0.785	3.000	1.062	0.612	0.576	
PSLT064	0.175	0.680	3.890	0.517	0.687	1.328	
PSLT073	0.171	0.638	3.730	2.568	5.497	2.141	
pstB	0.694	2.119	3.055	1.295	1.317	1.017	ABC superfamily (atp_bind), high-affinity phosphate transporter
rarD	1.038	5.062	4.878	1.717	3.240	1.887	chloramphenicol resistance
rbsD	0.373	2.999	8.047	0.702	0.238	0.339	D-ribose high-affinity transport system; membrane-associated protein
rfaI	0.951	3.716	3.909	2.612	5.138	1.967	UDP-D-galactose:(glucosyl)lipopolysaccharide- alpha-1,3-D-galactosyltransferase
rfaJ	0.741	3.321	4.484	1.832	4.162	2.271	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase
rfaY	0.675	2.952	4.374	1.321	2.981	2.257	lipopolysaccharide core biosynthesis; modification of heptose region of the core
rfbN	1.634	6.634	4.059	3.342	9.462	2.831	LPS side chain defect: rhamnosyl transferase
rfbX	0.968	4.196	4.333	2.922	7.172	2.455	LPS side chain defect: putative O-antigen transferase
rfc	0.686	2.091	3.050	0.867	1.779	2.052	O-antigen polymerase
rfe	1.458	7.496	5.141	2.099	5.530	2.635	undecaprenyl-phosphate N-acetylglucosaminyltransferase
rhtC	0.660	3.430	5.196	1.053	2.528	2.400	RhtB family, threonine efflux protein
ribB	0.989	4.543	4.591	3.339	3.204	0.959	3,4 dihydroxy-2-butanone-4-phosphate synthase
sdiA	1.128	3.497	3.099	1.001	0.538	0.538	transcriptional regulator of ftsQAZ gene cluster (LuxR/UhpA family)
sfbB	0.243	0.752	3.094	0.303	0.204	0.675	putative ABC-type transport system ATPase component/cell division protein
sitA	0.245	0.794	3.236	0.511	0.374	0.731	Salmonella iron transporter: fur regulated
sodA	1.394	23.912	17.150	6.619	7.190	1.086	superoxide dismutase, manganese
speB	2.413	9.612	3.984	3.701	8.054	2.176	agmatinase
stfC	0.100	0.349	3.486	0.243	0.282	1.161	putative fimbrial outer membrane usher
stfG	0.113	0.386	3.409	0.226	0.308	1.365	putative minor fimbrial subunit; putative adhesin
STM0327	4.146	16.648	4.015	0.575	1.213	2.111	putative cytoplasmic protein
STM0334	0.115	0.361	3.136	0.313	0.617	1.972	putative cytoplasmic protein
STM0381	0.227	0.696	3.069	0.417	0.423	1.016	putative inner membrane protein
STM0559	0.138	0.872	6.307	0.242	0.685	2.833	
STM0764	0.152	0.882	5.816	0.526	1.237	2.352	transcriptional regulator, lysR family
STM1012	0.542	1.929	3.561	0.443	0.647	1.462	Gifsy-2 prophage; probable regulatory protein
STM1129	11.130	50.027	4.495	1.143	0.385	0.337	putative inner membrane protein
STM1267	0.630	2.354	3.734	5.878	10.898	1.854	putative cytoplasmic protein
STM1554	0.349	1.288	3.688	0.702	1.000	1.425	putative coiled-coil protein
STM1586	0.303	2.004	6.612	0.481	0.481	1.000	putative periplasmic protein
STM1623	0.703	3.178	4.521	1.187	1.538	1.296	putative carboxylesterase
STM1624	0.550	2.303	4.185	0.711	1.098	1.546	putative cytoplasmic protein
STM2179	0.135	0.429	3.178	0.229	0.194	0.845	putative sugar transporter
STM2400	0.373	1.187	3.186	0.549	1.112	2.024	putative inner membrane protein
STM2722	0.099	0.367	3.711	0.156	0.232	1.491	Fels-2 prophage: similar to gpP, ATP charging, in phage P2
STM2762	0.112	0.375	3.345	0.377	0.834	2.208	putative inner membrane protein
STM2767	1.698	6.765	3.985	3.055	5.970	1.954	putative Superfamily I DNA and RNA helicase
STM3021	0.999	0.316	3.162	0.912	0.584	1.563	putative inner membrane protein
STM3022	0.338	1.329	3.937	0.565	1.348	2.385	putative transport protein
STM3026	0.094	0.361	3.829	0.501	0.478	0.953	putative outer membrane protein
STM3124	0.941	4.293	4.563	0.627	0.510	0.814	putative response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain
STM3253	0.221	1.926	8.714	0.223	0.184	0.825	putative fructose/tagatose biphosphate aldolase
STM3254	0.196	1.319	6.738	0.273	0.203	0.743	putative fructose-1-phosphate kinase
STM3255	0.121	1.118	9.243	0.494	0.511	1.035	putative phosphotransferase system fructose-specific component IIB
STM3256	0.119	0.704	5.934	0.325	0.289	0.887	putative phosphotransferase system mannitol/fructose-specific IIA domain
STM3333	0.477	1.533	3.214	0.376	0.408	1.085	putative purine-cytosine permease
STM3516	0.805	2.879	3.574	0.698	0.944	1.351	putative cytoplasmic protein
STM3745	1.185	6.518	5.500	0.718	0.906	1.262	putative cytoplasmic protein

STM3844	0.353	1.093	3.091	0.266	0.375	1.412	
STM3907	1.419	7.904	5.572	2.885	5.187	1.798	putative cytoplasmic protein
STM3927	1.371	4.466	3.257	2.467	4.373	1.772	putative inner membrane protein
STM3944	0.920	3.244	3.525	1.422	3.258	2.291	putative inner membrane protein
STM4041	0.171	1.058	6.197	0.538	0.428	0.797	putative inner membrane protein
STM4042	0.467	2.362	5.059	0.836	0.788	0.943	putative branched-chain amino acid permease
STM4054	0.145	0.481	3.309	0.321	0.210	0.656	putative dicarboxylate-binding periplasmic protein
STM4272	0.203	0.774	3.809	0.369	0.324	0.879	putative inner membrane protein
STM4427	0.260	0.786	3.022	0.712	0.537	0.754	putative endonuclease
STM4562	0.674	3.215	4.771	3.557	9.499	2.671	putative inner membrane protein
tldD	1.686	7.990	4.738	1.999	3.458	1.730	suppresses inhibitory activity of CsrA
tyrB	1.303	8.289	6.364	1.187	2.143	1.806	tyrosine aminotransferase, tyrosine repressible
wecF	0.830	2.850	3.433	2.141	2.537	1.185	TDP-Fuc4NAc:lipidII transferase
wecG	0.987	5.548	5.624	1.937	4.422	2.282	putative UDP-N-acetyl-D-mannosaminuronic acid transferase
wzxE	1.346	5.982	4.444	2.189	5.411	2.472	O-antigen translocase in LPS biosyntesis
wzzE	2.067	9.710	4.699	3.559	6.084	1.709	modulator of enterobacterial common antigen (ECA) polysaccharide chain length
xerC	1.508	5.326	3.532	1.684	4.173	2.478	putative integrase/recombinase, site-specific
yacC	0.683	3.814	5.588	0.639	1.480	2.314	putative periplasmic protein
yadR	1.084	7.781	7.176	2.878	4.888	1.698	putative HesB-like domain
yafV	0.864	2.769	3.204	1.409	1.621	1.151	putative amidohydrolase
yaiZ	1.382	10.395	7.524	0.801	1.398	1.745	putative inner membrane protein
ybaN	0.358	1.430	3.999	0.688	0.838	1.219	putative phage gene 58
ybaO	1.009	0.323	3.122	1.037	0.601	1.726	putative transcriptional regulator (AsnC familiy)
ybaY	1.884	5.842	3.100	11.020	14.026	1.273	glycoprotein/polysaccharide metabolism
ybdA	0.116	0.713	6.137	0.223	0.140	0.627	putative POT family transport protein
ybdJ	0.496	1.718	3.464	0.458	0.834	1.820	putative inner membrane protein
ybhE	1.249	3.709	2.969	2.359	2.001	0.848	putative 3-carboxymuconate cyclase
ybjO	0.374	1.203	3.215	0.487	0.864	1.774	putative inner membrane protein
yceA	0.326	1.212	3.720	0.804	1.764	2.193	putative enzyme related to sulfurtransferases
ycgO	0.658	2.895	4.401	0.777	1.216	1.565	putative CPA1 family, Na:H transport protein
yciM	0.987	0.311	3.177	0.953	0.526	1.811	putative N-acetylglucosaminyl transferase
ydcZ	0.951	3.461	3.637	0.690	0.812	1.177	putative inner membrane protein
ydgC	1.026	0.333	3.084	1.021	0.661	1.544	putative inner membrane protein
ydgR	3.037	14.321	4.716	2.827	2.899	1.025	putative POT family, peptide transport protein
ydhF	1.388	4.645	3.347	0.596	1.116	1.874	putative aldo/keto reductase
ydhL	0.307	0.942	3.066	0.239	0.432	1.809	putative oxidoreductase
ydiE	0.221	0.916	4.150	0.394	0.653	1.657	putative cytoplasmic protein
ydiQ	0.136	0.431	3.176	0.272	0.251	0.922	putative electron transfer flavoprotein
ydiU	0.419	3.073	7.336	0.806	2.020	2.508	putative cytoplasmic protein
yeaN	0.317	1.283	4.045	0.539	0.762	1.413	putative MFS family transport protein (amino acid/amine transport)
yeaS	1.034	4.819	4.662	3.299	7.040	2.134	paral putative transport protein
yedA	0.238	0.860	3.614	0.318	0.469	1.474	putative permease
yegB	0.177	0.651	3.690	0.409	0.644	1.576	putative MFS family transport protein
yehY	0.352	1.318	3.740	1.392	1.791	1.287	putative ABC-type proline/glycine betaine transport systems, permease component
yehZ	0.571	1.824	3.198	1.969	2.072	1.052	putative ABC superfamily (bind_prot) transport protein (possibly glycine betaine choline transport for osmoprotection)
yejL	0.973	0.264	3.689	0.975	0.395	2.469	putative cytoplasmic protein
yejM	0.846	3.351	3.962	0.996	2.104	2.113	putative hydrolase of alkaline phosphatase superfamily
yfaO	0.863	3.588	4.157	0.871	1.420	1.630	putative NTP pyrophosphohydrolases including oxidative damage repair enzymes
yfaZ	1.031	3.483	3.378	1.267	3.157	2.491	putative inner membrane protein
yfcL	0.929	2.988	3.217	0.810	1.137	1.404	putative cytoplasmic protein
yfdH	0.133	0.529	3.984	0.235	0.471	2.007	putative glycosyltransferase
yfdZ	1.916	7.251	3.784	1.583	2.822	1.783	putative aminotransferase
yfhP	1.272	4.232	3.327	5.873	4.429	0.754	believed to be involved in assembly of Fe-S clusters
ygfY	2.123	7.592	3.576	1.453	2.280	1.569	putative cytoplasmic protein
ygiE	0.539	1.958	3.629	0.740	0.857	1.158	putative divalent heavy-metal cations transporter
yheR	0.806	2.657	3.295	1.936	1.803	0.931	putative NAD(P)H oxidoreductase
yhgG	0.371	1.333	3.599	1.005	1.787	1.778	putative cytoplasmic protein
yhgI	1.723	6.073	3.524	2.866	4.706	1.642	putative Thioredoxin-like proteins and domain

yhhK	0.748	2.619	3.503	0.888	1.247	1.403	putative acetyltransferase
yiaK	0.189	0.630	3.338	0.275	0.209	0.758	putative malate dehydrogenase
yibK	1.691	4.825	2.853	0.751	0.808	1.076	putative tRNA/rRNA methyltransferase
yicM	0.164	0.691	4.212	0.321	0.435	1.354	putative MFS family tranport protein (1st mdule)
yicN	0.572	3.516	6.148	0.640	1.163	1.816	putative inner membrane protein
yieG	0.618	2.035	3.295	0.629	0.670	1.065	putative xanthine/uracil permeases family
yieH	0.850	4.020	4.729	1.118	0.885	0.792	putative phosphatase/phosphohexomutase
yigA	3.021	11.317	3.746	3.346	6.154	1.839	putative cytoplasmic protein
yigB	1.301	5.204	3.999	1.676	4.445	2.652	putative hydrolase of the HAD superfamily
yigI	2.182	11.078	5.077	2.376	5.794	2.438	putative protein PaaI, possibly involved in aromatic compounds catabolism
yigM	0.545	3.303	6.058	0.858	2.283	2.661	paral putative transport protein
yiiG	0.125	0.953	7.631	0.288	0.574	1.998	putative cytoplasmic protein
yijC	4.468	15.433	3.454	2.605	3.740	1.436	putative transcriptional repressor (TetR/AcrR family)
yjaD	1.414	4.683	3.312	1.890	3.212	1.700	putative NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding
yjcD	0.384	1.818	4.728	0.499	1.002	2.008	putative xanthine/uracil permease family
yjcG	0.389	1.616	4.151	0.521	0.351	0.674	putative SSS family transport protein
yjdC	1.422	4.941	3.475	1.906	3.133	1.644	putative bacterial regulatory protein, merR family
yjiJ	0.681	3.271	4.800	0.742	0.376	0.506	putative sugar transporter
yjjU	1.020	3.426	3.360	1.384	2.091	1.511	putative phosphoesterase
yjjY	8.916	29.804	3.343	11.194	16.484	1.472	putative inner membrane protein
yliA	0.901	3.231	3.586	1.023	0.958	0.937	putative ATPase components of ABC-type transport system, contain duplicated ATPase domain
yncA	1.250	5.026	4.020	1.208	1.110	0.918	putative acyltransferase
yniB	0.998	0.320	3.123	0.924	0.558	1.657	putative regulator
yoaB	1.484	5.799	3.908	0.812	1.933	2.380	putative translation initiation inhibitor
yohD	0.230	0.904	3.935	0.496	0.609	1.227	putative DedA family, membrane protein
yojI	0.251	0.923	3.675	0.313	0.406	1.297	putative ABC-type multidrug/protein/lipid transport system, ATPase component
yqeF	4.029	12.283	3.049	1.463	1.330	0.909	putative acetyl-CoA acetyltransferase
yqgA	0.214	0.860	4.027	0.384	0.637	1.658	putative inner membrane protein