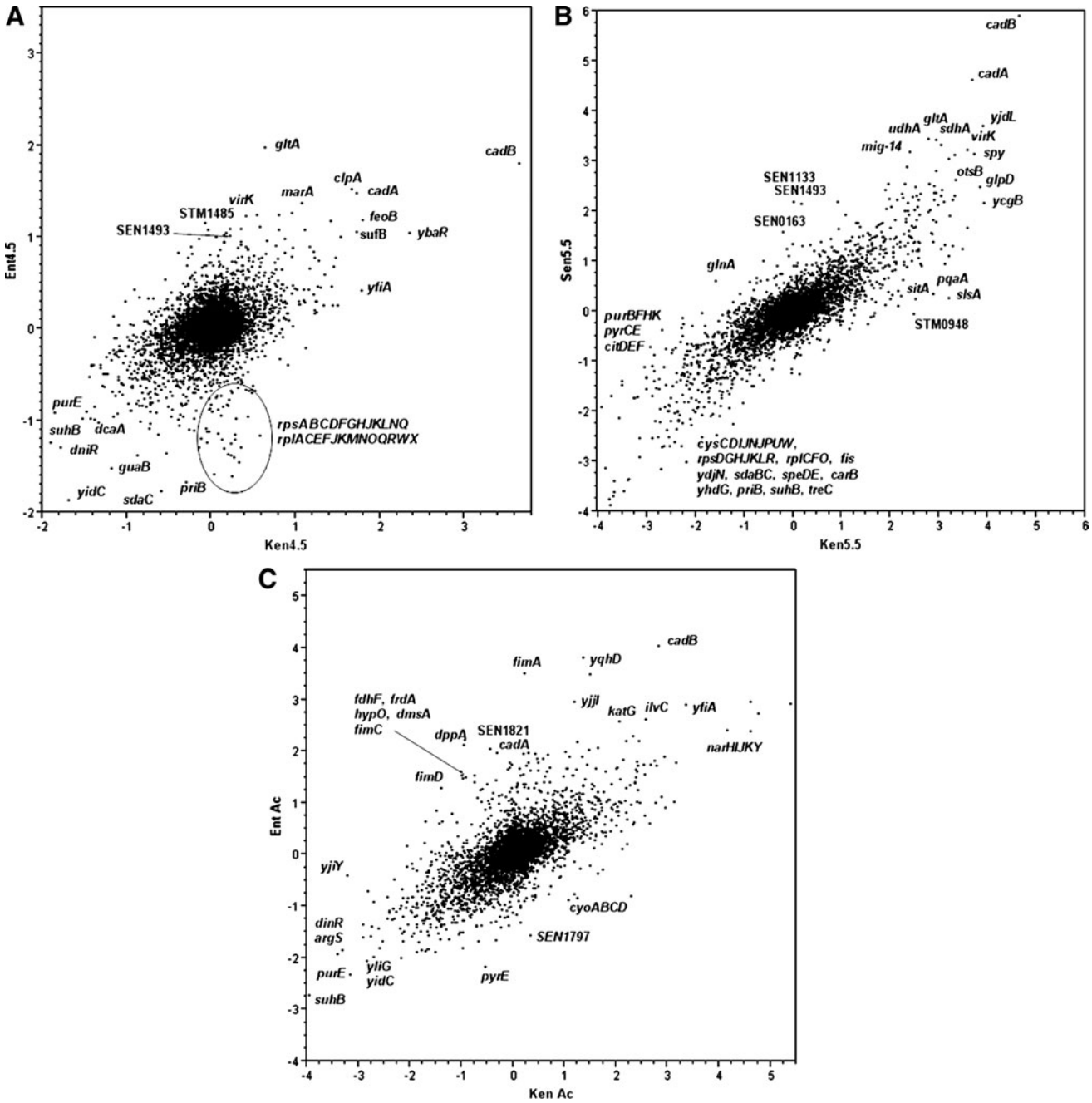
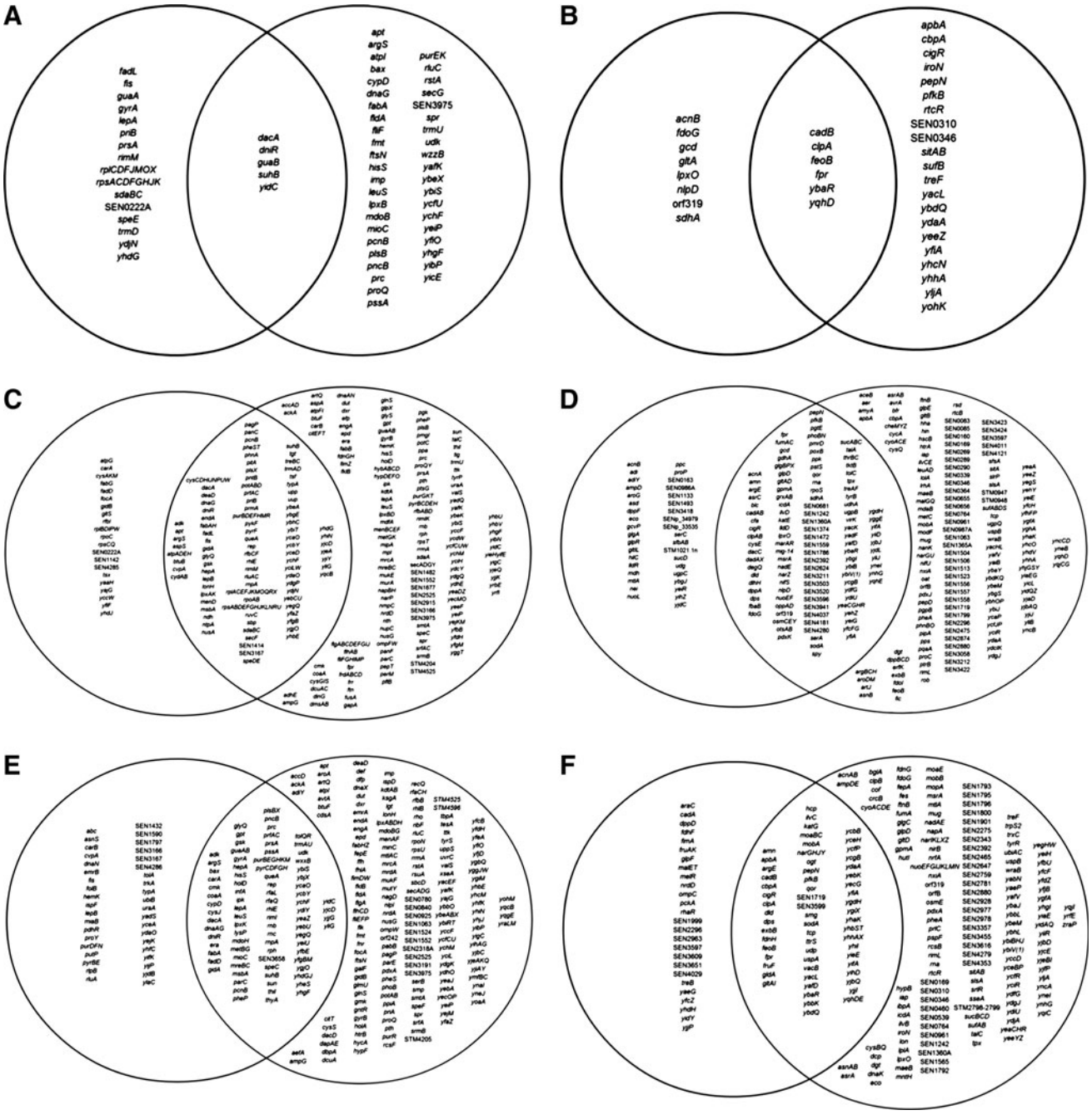
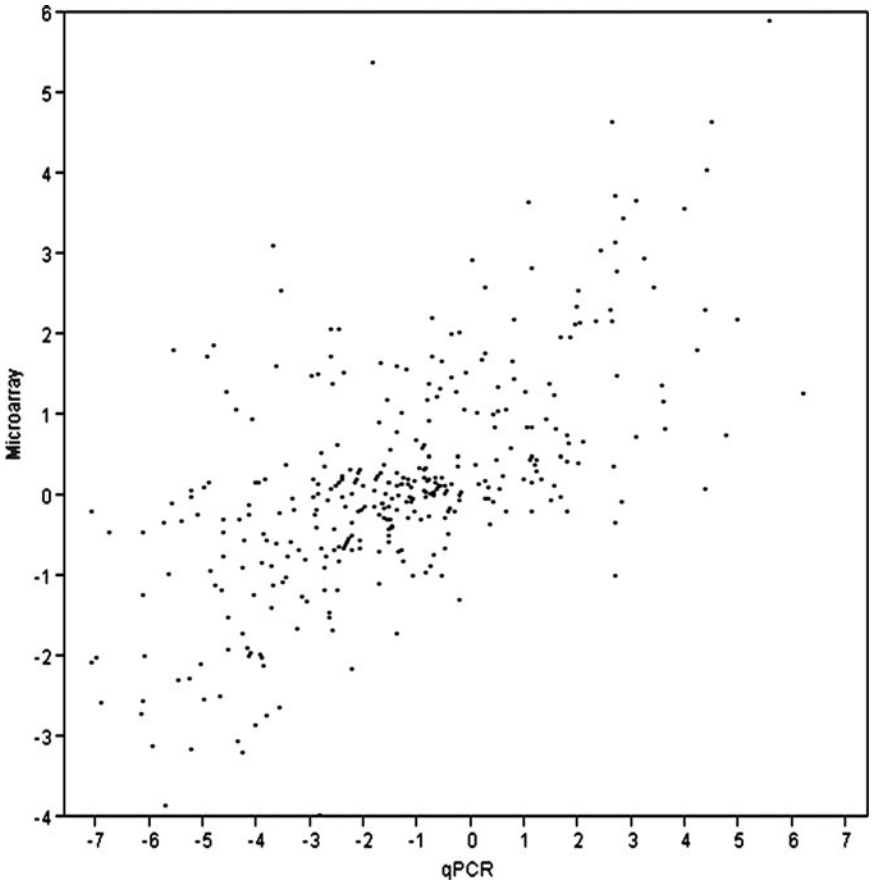
Supplementary Data



SUPPLEMENTARY FIG. 1. Comparison of changes in expression levels for *Salmonella enterica* Enteritidis Nal^R and Kentucky 3795 upon a 10-min exposure to tryptic soy broth (TSB) medium adjusted to pH 4.5 with HCl **(A);** to pH 5.5 with HCl **(B);** and pH 5.5 with acetic acid **(C).** The *x*-axis and *y*-axis scales indicate $\log_2$-fold up- or down-regulation for strains Kentucky 3795 (Ken) and Enteritidis Nal^R (Ent), respectively.



SUPPLEMENTARY FIG. 2. Venn diagrams for genes/loci exhibiting significant changes in expression in *Salmonella enterica* Enteritidis Nal^{R} (right circles) and *Salmonella enterica* Kentucky 3795 (left circles). **(A)** Genes and loci down-regulated upon shift from neutral pH to HCl-induced pH 4.5. **(B)** Genes and loci up-regulated upon shift from neutral pH to HCl-induced pH 4.5. **(C)** Genes and loci down-regulated upon shift from neutral pH to HCl-induced pH 5.5. **(D)** Genes and loci up-regulated in upon shift from neutral pH to HCl-induced pH 5.5. **(E)** Genes and loci down-regulated upon shift from neutral pH to acetic acid-induced pH 5.5. **(F)** Genes and loci up-regulated upon shift from neutral pH to acetic acid-induced pH 5.5.



SUPPLEMENTARY FIG. 3. Comparison of $\log_2$ changes in expression of genes/loci listed in Suppl. Table 3 as measured by quantitative polymerase chain reaction (qPCR; *x*-axis) with corresponding $\log_2$ changes in expression as determined by microarray analysis (*y*-axis).

Supplementary Table 1. Primers Used for Quantitative Polymerase Chain Reaction (qPCR) Analysis

Gene or locus	*Forward primer (5′->3′)*	*Reverse primer (5′->3′)*
adhE	gtggtctggatgcggtaact	cgccatggagtgacatacac
adiA	aacagtccgcaggtgggtta	aatttccgtgccttcggttt
aspA	ctgaaacgtctggcagtgaa	tcgtaacggtggtgtcgtta
cadA	gaaccacatgggcgtctact	cagcggcatatactcgttca
cadB	cggcaggtattgcctgtatt	taacaatggcgtgagagtcg
citD	cgctcgatacgcaggatatt	cagtccagagcgcctttatc
citF	ctgatcgtgcaaatcgaaga	cagggagaaaccttcgttga
clpB	cgtactgaacctttgcgaca	cttgatcgttcacgctttca
cyoA	ttgcaggcactgcattactc	gtgtgaccagttcgggctat
dcuA	ctggtgatgtccttcctggt	ggtgttcatcagcggtttct
dmsA	gcgggaacatgtcttacgtt	tgacgcatccactcttcttg
fdhF	gtggtcgataacggcaaaat	ctcaaacgttcagcgacgta
fimC	tattatctacgccgggcaac	acacgggaaaatttcagcaa
fimD	cacaatctccgctacagcaa	acttatgccttgccatccac
flgD	attggacatggcgttatggt	ccatcccaggtaaaggtgtg
fliG	ggcggaaattatcaacctga	ggacatattgcgcaggaact
glmU	acctgaaacgctggttgtct	cctgttcggcctggtaaata
gltA	ttcggtcaccgtgtttacaa	ctcgatgaagtacgggtcgt
guaB	cagatcaccgctgtttctga	tgtaagaacggccctggtag
hypB	gatctgggcgaaaagcataa	tcaatctccgggttcacttc
hypO	aaactccgcgttcagagaaa	tattctccccgtgagtcagc
katG	gaaaccgaccgacgaatcta	cggtccaggttcatcacttt
malT	cacccgttgtttggtagctt	ggcagcgcttttaatgactc
narG	gccagcttctcgaaacaaac	gtttgctgtgtttcccaggt
oppD	ttattgccgatgagcctacc	ggatgaacgggctgataaaa
osmC	gatttacgccgacatccatt	atttccgcattcagaacctg
pitA	actgaattccactgccatcc	ccaggcaatttcacgacttt
priB	cgaaaggtcagtccatcagg	tgcagaaccattttgctcag
rplC	agctaaccgtgtcaccaagc	ttaacggtaccagcgaaacc
rpoN	gcgacagtattccccgttta	gccagtaccatcggtttcat
rpoS	gcgactcagctttaccttgg	gggtcaaacttctcgactgc
rpsC	ggaactggctaaagcgtctg	ccagctgagaagtgatgctg
secY	tggggatcatgccgtatatt	aagcctggattcatcaccag
sipA	aagatggaaaggtggtcacg	ttcacaatctctgccgtctg
sipB	gtgggcaaaaatacggaaga	cccgatacatcccataatgc
sitA	actcctgattgccggtattg	ccctgcgctcgtttaatatc
sopB	taacgtcaatggcaaaccaa	tgccagggctggttattaag
spy	gcgcaaattacgaaaatgga	gcagcaggcattttaccttc
suhB	tcaaacgtctgccacacttc	gtcgcgtattgtttggcttt
thrA	gacgatctttccggtatgga	cccacatagcgcaatacctt
treB	ttctcgcccacacctttatc	atcgatagcgagcgttgtct
uvrC	ttttgtccggtaaggacgac	caccttaccctggcgaataa
SEN1493	atgagctgccaggagtttgt	tcactctgcgggtttttctt
SEN0629	tgcgcagaatttgtttatgc	tcggttgtttttcgttaccc
SEN1821	tacagagcagtggcgatacg	gctttacgcgcactatcaca
SEN1800	ggatcagacgcactggattt	cgcctttggtttgctttcta
SEN1796	taaccggctggtttttgtct	atcgttgccgacaggataac
SEN1795	catcttgtgttgccggtatg	acagagtgctggggtaatcg
SEN1793	aaccggctggacagacatac	gctgtaccatctgcgtctca
STM1485 -Ent	gtctctcttccgcagcattc	agttggttttgacggggttt
STM1485 -Ken	gtctctcttccgcagcattc	gtagatttggctggggcttt
SEN1242	gtcaccggtaagcctatcca	gtcgcggtatgatcctgaat
SEN2343	gttatcgaaatcggcaggaa	cgcttgctgcattgatgtat
SEN2624	tgggtgtcgtgtcgaattta	gatttgctccggtaaggaca
SEN2977	ctgtcccgtagctcgcttag	tttcagtccgatgacatcca
SEN3609	attttcgtcaacgccaactc	tgcgtgataaaccgtttcaa
SEN3651	gaaatggaaagccagatgga	cgcttaaaggcatggatgat
SEN3847	gatgattcccgatgctgaac	taaagcggttatcggcaaac
SEN3894	gtctctcctcgctgtggttc	gattaacggcgacaccttgt
SEN4029	gcacccgttctttaagcaat	gcaagcaatgcgagttcttt

Supplemental Table 2. Average log_2-fold changes in gene expression in *S. enterica* Enteritidis Nal^R (Ent) and Kentucky 3795 (Ken) upon exposure to TSB adjusted to pH 4.5 (Ent 4.5, Ken 4.5), to pH 5.5 with HCl (Ent 5.5, Ken 5.5), and to pH 5.5 with acetic acid (Ent Ac, Ken Ac)

S. enterica Enteritidis locus[1]	*S. enterica* Typhimurium locus[1]	Gene designation[1]	Function	Average log2-fold changes in expression and p-values																	
				Ent 4.5			Ken 4.5			Ent 5.5			Ken 5.5			Ent Ac			Ken Ac		
				Microarray		qPCR	Microarray		qPCR	Microarray		qPCR	Microarray		qPCR	Microarray		qPCR	Microarray		qPCR
A. pH homeostasis/acid tolerance				Avg.[2]	p-val.	Avg.[3]	Avg.	p-val.	Avg.	Avg.	p-val.	Avg.	Avg.	p-val.	Avg.	Avg.	p-val.	Avg.	Avg.	p-val.	Avg.
SEN4067	STM4296	*adi*	arginine decarboxylase, catabolic; inducible by acid	1.02	0.026	-1.32	0.15	0.138	-2.49	1.65	0.000	0.77	0.93	0.006	-0.81	0.14	0.384	-1.32	0.38	0.017	-1.64
SEN4066	STM4295	*adiY*	transcriptional activator of adiA (AraC/XylS family)	0.73	0.004		0.25	0.075		1.15	0.001		0.54	0.222		0.79	0.011		-1.19	0.000	
SEN1564A	STM1485	*asr*	acid shock protein	1.15	0.001	3.57	-0.07	0.817	2.79	0.11	0.702	1.54	0.44	0.137	0.45	0.14	0.549	0.14	-0.03	0.907	0.24
SEN2539	STM2559	*cadA*	lysine decarboxylase 1	1.47	0.001	-0.37	1.72	0.005	-2.62	4.63	0.000	4.49	3.67	0.000	3.07	1.96	0.000	1.67	-0.31	0.493	-0.96
SEN2538	STM2558	*cadB*	APC family, lysine/cadaverine transport protein	1.80	0.000	4.20	3.65	0.000	1.06	5.90	0.000	5.55	4.64	0.000	2.63	4.04	0.000	4.40	2.82	0.000	1.11
SEN2537	STM2557	*cadC*	transcriptional activator of cad operon (OmpR family)	0.05	0.641		-0.18	0.120		0.19	0.457		-0.51	0.019		-0.05	0.621		-0.65	0.000	
SEN1493	STM1562	*hdeB-like*	putative periplasmic transport protein	1.01	0.008	0.40	0.22	0.275	-0.69	2.14	0.000	2.02	0.17	0.309	-0.69	0.85	0.003	0.43	0.03	0.808	-0.49
SEN2193	STM2200	*lysP*	APC family, lysine-specific permease	-0.36	0.007		-0.61	0.000		-0.68	0.001		-0.44	0.024		-1.09	0.000		-1.56	0.000	
SEN4065	STM4294	*yjdE*	putative APC family, putrescine/ornithine transport protein	0.00	0.983		0.08	0.531		0.23	0.088		0.16	0.310		0.28	0.134		0.42	0.002	
B. protein fate																					
SEN0853	STM0945	*clpA*	ATP-binding subunit of serine protease	1.52	0.000		1.66	0.000		1.79	0.000		2.31	0.000		1.83	0.000		2.13	0.000	
SEN2583	STM2660	*clpB*	ATP-dependent protease, Hsp 100,	0.72	0.001	3.06	0.59	0.005	0.74	1.05	0.000	0.48	1.33	0.000	-0.60	0.83	0.010	1.58	2.01	0.000	-0.37
SEN0430	STM0448	*clpP*	proteolytic subunit of clpA-clpP ATP-dependent serine protease	0.31	0.060		0.31	0.002		0.27	0.048		0.30	0.149		0.52	0.004		0.65	0.000	
C. central intermediary metabolism																					
SEN3874	STM4084	*fpr*	ferredoxin-NADP reductase	1.00	0.000		1.53	0.000		1.24	0.000		1.80	0.000		1.65	0.000		2.39	0.000	
D. Unknown function																					
SEN0262	STM0260	*dniR*	unknown	-1.30	0.000		-1.79	0.000		-2.22	0.000		-2.73	0.000		-1.92	0.000		-3.41	0.000	
SEN2526	STM2546	*suhB*	inositol monophosphatase	-1.24	0.000	-6.13	-1.91	0.001	-4.56	-2.55	0.000	-6.15	-3.15	0.000	-5.25	-2.72	0.000	-6.17	-3.97	0.000	-2.85
SEN1133				0.10	0.373		-0.20	0.182		2.19	0.000		0.01	0.974		0.29	0.180		0.03	0.860	
SEN1735	STM1308	*spy*	periplasmic protein related to spheroblast formation	0.74	0.003	1.79	0.44	0.003	1.21	3.14	0.000	2.67	3.72	0.000	2.69	0.18	0.387	0.24	0.85	0.000	1.11
SEN1792	STM1259		putative ATPase component of ABC-type transport system	-0.29	0.117		-0.04	0.579		-0.03	0.845		-0.06	0.691		0.64	0.002		1.36	0.000	
SEN1793	STM1258		putative ATPase component of ABC-type transport system	-0.45	0.080	-6.15	-0.11	0.481	-4.16	-0.10	0.555	-5.59	-0.24	0.098	-5.12	1.05	0.009	-4.39	1.87	0.000	-4.81
SEN1795	STM1256		putative ABC transporter	-0.59	0.022	-3.37	0.10	0.275	-5.00	-0.31	0.019	-5.42	-0.19	0.194	-7.11	1.60	0.002	-3.64	1.79	0.000	-5.58
SEN1796	STM1255		putative ABC transporter periplasmic binding protein	-0.57	0.059	-4.26	0.19	0.205	-2.96	-0.46	0.065	-6.78	0.16	0.302	-3.97	1.73	0.003	-4.93	2.53	0.000	-3.57
SEN1800	STM1251		putative molecular chaperone (small heat shock protein)	0.37	0.004	1.17	0.66	0.003	2.09	-0.05	0.728	0.32	0.45	0.132	1.08	0.10	0.491	0.32	2.12	0.000	1.92
SEN4327	STM4566	*yjjI*	putative cytoplasmic protein	-0.26	0.197		0.26	0.106		-1.00	0.037		-1.16	0.004		2.95	0.001		1.18	0.000	
	STM0948		putative cytoplasmic protein	0.00	0.979		-0.06	0.530		-0.06	0.767		2.48	0.000		-0.06	0.709		0.16	0.116	
E. cell envelope/membrane																					
SEN0606	STM0637	*dacA*	D-alanyl-D-alanine carboxypeptidase, penicillin-binding protein 5	-1.03	0.000		-1.34	0.000		-1.01	0.000		-1.32	0.000		-1.43	0.000		-2.19	0.000	
SEN0524	STM0543	*fimA*	major type 1 subunit fimbrin (pilin)	-0.05	0.517		0.35	0.010		-0.27	0.093		-0.24	0.083		3.50	0.001		0.22	0.017	
SEN0527	STM0546	*fimD*	outer membrane usher protein	-0.22	0.060	-3.59	-0.23	0.099	-4.15	-0.31	0.055	-1.57	-0.66	0.008	-2.40	1.28	0.030	-4.59	-1.39	0.000	-3.75
SEN0533	STM0552	*fimW*	putative fimbrial protein	-0.28	0.033		-0.37	0.113		-0.01	0.919		-0.98	0.000		0.59	0.027		-1.43	0.000	
SEN0530	STM0549	*fimZ*	fimbrial protein Z, putative transcriptional regulator	-0.10	0.385		0.05	0.637		-0.19	0.633		-1.03	0.000		1.78	0.002		-0.06	0.621	
SEN0235	STM0228	*lpxA*	UDP-N-acetylglucosamine acetyltransferase	-0.70	0.000		-0.82	0.000		-1.04	0.000		-1.24	0.000		-0.46	0.026		-1.54	0.000	
SEN0236	STM0229	*lpxB*	tetraacyldisaccharide-1-P	-0.50	0.000		-1.26	0.000		-0.50	0.001		-1.09	0.000		-0.71	0.002		-1.85	0.000	
SEN0233	STM0226	*lpxD*	UDP-3-O-(3-hydroxymyristoyl)-glucosamine n-acyltransferase	-0.37	0.021		-0.71	0.000		-0.74	0.000		-1.13	0.000		-0.43	0.004		-1.10	0.000	
SEN0516	STM0535	*lpxH*	UDP-2,3-diacylglucosamine hydrolase	-0.25	0.093		-0.64	0.002		-0.07	0.700		-0.71	0.001		-0.62	0.004		-1.48	0.000	
SEN0889	STM0985	*lpxK*	tetraacyldisaccharide 4' kinase (lipid A 4'kinase)	-0.46	0.000		-0.42	0.009		-1.34	0.000		-1.36	0.000		-1.12	0.000		-1.07	0.000	
SEN4057	STM4286	*lpxO*	putative dioxygenase for synthesis of lipid	1.24	0.000		0.54	0.000		2.81	0.000		2.94	0.000		0.13	0.729		1.56	0.000	
SEN2832	STM2988	*mltA*	membrane-bound lytic murein transglycosylase A	-0.23	0.042		-0.63	0.000		0.02	0.835		-0.62	0.003		-0.64	0.004		-1.07	0.000	
SEN2955	STM3112	*mltC*	membrane-bound lytic murein transglycosylase C	-0.04	0.709		-0.55	0.003		0.23	0.058		-0.09	0.552		-0.50	0.003		-1.33	0.000	
SEN3207	STM3374	*mreB*	HSP70 class molecular chaperones	-0.38	0.002		-0.74	0.001		-0.80	0.001		-1.51	0.000		-1.11	0.000		-1.59	0.000	
SEN3206	STM3373	*mreC*	rod shape-determining protein	-0.39	0.005		-0.89	0.000		-0.84	0.000		-1.62	0.000		-1.25	0.000		-1.63	0.000	
SEN1492	STM1563	*osmC*	putative resistance protein, osmotically inducible	0.21	0.055	0.98	0.13	0.200	-0.49	1.36	0.000	3.56	2.59	0.000	3.40	-0.01	0.944	1.66	0.22	0.039	-0.57
SEN1732	STM1311	*osmE*	transcriptional activator of ntrL gene	0.67	0.000		0.48	0.001		1.93	0.000		2.59	0.000		0.62	0.000		1.32	0.000	
SEN4323	STM4561	*osmY*	hyperosmotically inducible periplasmic protein	0.56	0.016		0.45	0.007		1.71	0.000		2.44	0.000		0.21	0.216		0.44	0.026	
SEN4004	STM4235	*plsB*	glycerolphosphate acyltransferase activity	-0.72	0.000		-1.05	0.000		-0.76	0.001		-1.33	0.000		-1.13	0.000		-1.69	0.000	
SEN1857	STM1192	*plsX*	putative fatty acid/phospholipid synthesis protein	-0.77	0.000		-0.79	0.000		-1.10	0.000		-1.27	0.000		-1.00	0.000		-1.66	0.000	
SEN3534	STM3712	*rfaC*	heptosyl transferase I	-0.10	0.337		-0.38	0.009		-0.23	0.069		-0.73	0.002		-0.56	0.002		-1.22	0.000	
SEN3772	STM3977	*rfaH*	transcriptional activator, biosynthesis of lipopolysaccharide core	0.03	0.796		-0.45	0.034		-0.49	0.028		-0.60	0.002		-0.55	0.005		-1.13	0.000	
SEN3535	STM3713	*rfaL*	O-antigen ligase	-0.61	0.000		-0.41	0.002		-0.74	0.001		-0.99	0.000		-1.53	0.000		-1.46	0.000	
SEN3545	STM3723	*rfaQ*	lipopolysaccharide core biosynthesis	-0.39	0.002		-0.44	0.002		-0.70	0.000		-0.57	0.001		-1.09	0.000		-1.47	0.000	
SEN2091	STM2095	*rfbA*	dTDP-glucose pyrophosphorylase	-0.43	0.000		0.35	0.018		-0.70	0.002		-1.20	0.000		-0.71	0.000		-0.10	0.388	

SEN2093	STM2097	*rfbB*	dTDP-glucose 4,6 dehydratase	-0.83	0.000		-0.31	0.022		-0.57	0.000		-1.02	0.000		-0.95	0.000		-1.07	0.000		
SEN2090	STM2094	*rfbC*	dTDP-4,deoxyrhamnose 3,5 epimerase	-0.50	0.000		0.24	0.154		-1.05	0.000		-1.30	0.000		-0.45	0.017		-0.15	0.257		
SEN2092	STM2096	*rfbD*	TDP-rhamnose synthetase	-0.50	0.000		0.03	0.847		-0.98	0.000		-1.34	0.000		-0.96	0.000		-0.55	0.000		
SEN2088	STM2092	*rfbF*	glucose-1-phosphate cytidylyltransferase	-0.32	0.008		0.24	0.038		-1.20	0.000		-1.39	0.000		0.02	0.894		0.08	0.400		
SEN2089	STM2093	*rfbI*	CDP-6-deoxy-delta3,4-glucoseen reductase	-0.38	0.005		0.31	0.006		-1.08	0.000		-0.99	0.004		-0.26	0.090		0.00	0.982		
SEN0697	STM0747	*tolA*	tol protein, membrane spanning protein	-0.28	0.014		-0.35	0.003		0.12	0.408		-0.90	0.001		-1.06	0.000		-0.98	0.000		
SEN3029	STM3186	*tolC*	outer membrane channel	1.09	0.004		0.22	0.106		1.21	0.000		1.54	0.000		0.40	0.002		0.47	0.000		
SEN0695	STM0745	*tolQ*	tol protein, membrane-spanning inner membrane proteins	-0.22	0.048		-0.63	0.001		-0.19	0.283		-0.70	0.000		-1.26	0.000		-1.43	0.000		
SEN0696	STM0746	*tolR*	tol protein, role in outer membrane integrity	-0.27	0.004		-0.39	0.002		-0.06	0.714		-0.90	0.000		-1.39	0.000		-1.40	0.000		
SEN0693	STM0743	*ybgE*	putative inner membrane lipoprotein	-0.24	0.042		0.06	0.710		-1.09	0.000		-1.20	0.001		0.01	0.949		-0.68	0.001		
SEN3659	STM3842	*yidC*	putative Preprotein translocase subunit YidC	-1.87	0.000		-1.69	0.000		-1.20	0.001		-2.85	0.000		-2.06	0.000		-2.85	0.000		
SEN1797	STM1254		putative outer membrane lipoprotein	0.16	0.212		0.16	0.210		-0.51	0.020		-0.10	0.574		-1.56	0.000		0.34	0.005		
F. Purines/pyrimidines and derivatives																						
SEN0469	STM0488	*adk*	adenylate kinase	-0.58	0.000		-0.68	0.001		-1.25	0.000		-2.11	0.000		-1.09	0.001		-1.13	0.000		
SEN0066	STM0066	*carA*	carbamoyl-phosphate synthetase, small subunit	-0.48	0.284		-0.81	0.000		-1.70	0.005		-3.73	0.000		-1.89	0.000		-1.52	0.000		
SEN0067	STM0067	*carB*	carbamoyl-phosphate synthase, large subunit	-0.54	0.224		-0.32	0.009		-2.14	0.001		-3.58	0.000		-1.68	0.000		-0.68	0.003		
SEN0884	STM0980	*cmk*	cytidine monophosphate (CMP) kinase	-0.67	0.000		-0.59	0.002		-0.98	0.000		-1.72	0.000		-1.20	0.000		-1.17	0.000		
SEN0300	STM0317	*gpt*	guanine-hypoxanthine phosphoribosyltransferase	-0.17	0.198		-0.90	0.000		-0.43	0.030		-1.53	0.000		-1.25	0.000		-1.37	0.000		
SEN2490	STM2510	*guaA*	GMP synthetase	-1.38	0.000		-0.88	0.000		-1.40	0.008		-2.85	0.000		-1.33	0.000		-1.18	0.000		
SEN2491	STM2511	*guaB*	IMP dehydrogenase	-1.52	0.000	-2.67	-1.19	0.000	-2.75	-1.72	0.008	-4.28	-3.20	0.000	-4.28	-2.00	0.000	-4.17	-2.17	0.000	-2.24	
SEN1259	STM1780	*prsA*	phosphoribosylpyrophosphate synthetase	-1.16	0.000		-0.63	0.002		-1.36	0.001		-2.75	0.000		-1.35	0.000		-1.34	0.000		
SEN1817	STM1232	*purB*	adenylosuccinate lyase	-1.04	0.002		-0.73	0.000		-1.47	0.000		-3.51	0.000		-1.56	0.000		-1.64	0.000		
SEN3961	STM4175	*purD*	phosphoribosylglycinamide synthetase (GAR synthetase)	-0.30	0.266		0.20	0.482		-1.55	0.000		-3.02	0.000		-1.38	0.000		-0.71	0.000		
SEN0515	STM0534	*purE*	phosphoribosylaminoimidazole carboxylase	-0.92	0.004		-1.86	0.001		-1.32	0.000		-3.01	0.000		-2.32	0.000		-3.16	0.000		
SEN2344	STM2362	*purF*	amidophosphoribosyltransferase (PRPP amidotransferase)	-0.36	0.206		-0.23	0.073		-1.09	0.001		-2.89	0.000		-1.33	0.000		-0.43	0.000		
SEN2545	STM2565	*purG*	phosphoribosylformylglycinamidine synthetase	-0.62	0.046		-0.63	0.007		-0.78	0.006		-1.49	0.000		-1.51	0.000		-1.04	0.000		
SEN3962	STM4176	*purH*	phosphoribosylaminoimidazolecarboxamide formyltransferase	-0.37	0.263		-0.96	0.001		-1.40	0.000		-3.51	0.000		-1.83	0.000		-1.67	0.000		
SEN0514	STM0533	*purK*	phosphoribosylaminoimidazole carboxylase	-0.40	0.058		-1.40	0.000		-0.78	0.000		-2.47	0.000		-1.86	0.000		-1.77	0.000		
SEN2480	STM2499.S	*purM*	phosphoribosylaminoimidazole synthetase	-0.53	0.068		-0.82	0.002		-1.34	0.000		-3.01	0.000		-1.88	0.000		-1.70	0.000		
SEN2481	STM2500	*purN*	polyphosphate kinase, component of RNA degradosome	-0.07	0.711		-0.63	0.001		-0.60	0.002		-0.72	0.030		-1.10	0.000		-0.77	0.000		
SEN1617	STM1430	*purR*	transcriptional repressor for pur regulon, glyA, glnB, prsA, speA	-0.62	0.004		-0.62	0.002		-1.55	0.000		-2.76	0.000		-0.98	0.000		-1.17	0.000		
SEN1120	STM1883	*purT*	phosphoribosylglycinamide formyltransferase 2	-0.48	0.130		-0.47	0.029		-0.67	0.004		-1.95	0.000		-0.87	0.001		-0.37	0.040		
SEN0987	STM1125	*putP*	SSS family, major sodium/proline symporter	-0.39	0.003		-0.20	0.100		-0.59	0.002		-0.54	0.001		-1.23	0.000		-0.17	0.281		
SEN4211	STM4460	*pyrB*	aspartate carbamoyltransferase, catalytic subunit	-0.01	0.980		0.27	0.016		-0.88	0.146		-2.18	0.000		-1.20	0.000		-0.26	0.009		
SEN1885	STM1163	*pyrC*	dihydro-orotase	-0.45	0.010		-1.00	0.000		-0.61	0.059		-2.32	0.000		-1.53	0.000		-2.16	0.000		
SEN0923	STM1058	*pyrD*	dihydro-orotate oxidase	-0.47	0.018		-0.66	0.002		-1.47	0.005		-2.62	0.000		-1.55	0.000		-1.06	0.000		
SEN3555	STM3733	*pyrE*	orotate phosphoribosyltransferase	-0.34	0.090		-0.27	0.030		-0.37	0.577		-2.69	0.000		-2.17	0.000		-0.54	0.005		
SEN1326	STM1707	*pyrF*	orotidine-5'-phosphate decarboxylase	-0.56	0.006		-0.42	0.001		-1.68	0.000		-2.28	0.000		-1.64	0.000		-1.24	0.000		
SEN2792	STM2953	*pyrG*	CTP synthetase	-0.84	0.000		-0.82	0.001		-0.67	0.022		-0.80	0.000		-1.23	0.000		-1.68	0.000		
SEN0225	STM0218	*pyrH*	uridylate kinase	-0.96	0.000		-0.48	0.003		-1.06	0.004		-2.23	0.000		-1.35	0.000		-1.40	0.000		
SEN2843	STM3001	*thyA*	thymidylate synthetase	-0.27	0.004		-0.90	0.000		-0.26	0.120		-0.95	0.000		-1.29	0.000		-1.75	0.000		
SEN2118	STM2122	*udk*	uridine/cytidine kinase	-0.24	0.024		-1.09	0.000		-0.36	0.019		-0.89	0.000		-1.35	0.000		-2.92	0.000		
SEN3218	STM3384	*yhdG*	putative TIM-barrel enzyme, possibly dehydrogenase	-1.36	0.000		-0.53	0.000		-3.38	0.000		-3.39	0.000		-1.28	0.000		-1.72	0.000		
SEN3167	STM3334		putative cytosine deaminase	-0.49	0.053		-0.07	0.402		-1.08	0.000		-2.10	0.000		-1.31	0.000		-0.33	0.002		
G. Protein synthesis																						
SEN1094	STM1909	*argS*	arginine tRNA synthetase	-0.98	0.000		-1.53	0.000		-1.42	0.000		-2.40	0.000		-1.86	0.000		-3.31	0.000		
SEN1102	STM1901	*aspS*	aspartate tRNA synthetase	-0.54	0.001		-0.14	0.208		-1.19	0.000		-1.71	0.000		-0.65	0.000		-0.45	0.000		
SEN3478	STM3656	*glyQ*	glycine tRNA synthetase, alpha subunit	-0.82	0.000		-0.89	0.001		-1.21	0.000		-2.17	0.000		-1.16	0.000		-1.51	0.000		
SEN2502	STM2522	*hisS*	histidine tRNA synthetase	-0.98	0.000		-1.43	0.000		-0.70	0.000		-1.36	0.000		-1.26	0.000		-2.35	0.000		
SEN0617	STM0648	*leuS*	leucine tRNA synthetase	-0.85	0.000		-1.38	0.000		-0.40	0.012		-1.15	0.000		-1.10	0.000		-2.40	0.000		
SEN2148	STM2155	*metG*	methionine tRNA synthetase	-0.63	0.001		-0.42	0.033		-0.41	0.082		-1.56	0.000		-1.42	0.000		-1.87	0.000		
SEN1707	STM1337	*pheS*	phenylalanine tRNA synthetase, alpha-subunit	-0.85	0.000		-0.77	0.001		-1.38	0.000		-1.66	0.000		-0.97	0.000		-1.02	0.000		
SEN1706	STM1338	*pheT*	phenylalanine tRNA synthetase, beta-subunit	-0.76	0.000		0.05	0.651		-1.55	0.000		-2.14	0.000		-0.75	0.001		-0.27	0.012		
SEN1263	STM1776	*prfA*	peptide chain release factor RF-1	-0.54	0.003		-0.90	0.000		-1.07	0.000		-1.27	0.000		-1.25	0.000		-1.64	0.000		
SEN4322	STM4560	*prfC*	peptide chain release factor RF-3	-0.41	0.065		-0.39	0.008		-1.04	0.000		-2.09	0.000		-1.46	0.000		-1.31	0.000		
SEN0387	STM0404	*queA*	S-adenosylmethionine-tRNA ribosyltransferase-isomerase	-0.35	0.003		-0.75	0.000		-1.06	0.000		-1.54	0.000		-1.36	0.000		-2.04	0.000		
SEN2596	STM2675	*rimM*	16S rRNA processing protein	-1.40	0.000		0.27	0.041		-2.51	0.000		-2.55	0.000		-0.19	0.091		-0.04	0.705		
SEN3268	STM3440	*rplC*	50S ribosomal subunit protein L3	-1.46	0.000	-2.65	0.33	0.117	-2.26	-2.01	0.000	-7.02	-2.02	0.000	-3.92	-0.04	0.631	-3.35	0.02	0.911	-1.61	
SEN3267	STM3439	*rplD*	50S ribosomal subunit protein L4	-1.17	0.000		0.58	0.002		-1.94	0.000		-1.98	0.003		0.53	0.013		0.42	0.021		
SEN3256	STM3428	*rplE*	50S ribosomal subunit protein L5	-0.78	0.000		0.21	0.036		-2.20	0.000		-2.84	0.000		-0.44	0.003		-0.13	0.289		
SEN3253	STM3425	*rplF*	50S ribosomal subunit protein L6	-1.21	0.001		0.28	0.034		-2.19	0.000		-2.52	0.000		0.03	0.811		0.15	0.295		
SEN4160	STM4394	*rplI*	50S ribosomal subunit protein L9	-0.27	0.127		-0.08	0.481		-1.18	0.000		-0.89	0.007		-0.19	0.483		-0.24	0.090		

SEN3935	STM4151	*rplJ*	50S ribosomal subunit protein L10	-1.09	0.000		-0.06	0.526		-1.94	0.000		-1.32	0.001		-0.23	0.060		0.04	0.776	
SEN3933	STM4149	*rplK*	50 S ribosomal subunit protein L11	-0.84	0.001		0.20	0.037		-1.91	0.000		-2.63	0.000		0.09	0.445		0.28	0.004	
SEN3178	STM3345	*rplM*	50S ribosomal subunit protein L13	-1.20	0.000		-0.12	0.309		-1.87	0.000		-2.55	0.000		-0.51	0.000		-0.36	0.155	
SEN3249	STM3421	*rplO*	50S ribosomal subunit protein L15	-1.21	0.000		0.13	0.233		-2.71	0.000		-2.69	0.000		-0.09	0.469		0.22	0.083	
SEN3261	STM3433	*rplP*	50S ribosomal subunit protein L16	-0.59	0.002		0.36	0.016		-1.84	0.000		-1.04	0.080		0.16	0.338		0.51	0.145	
SEN3242	STM3414	*rplQ*	50S ribosomal subunit protein L17	-0.91	0.000		0.01	0.891		-1.29	0.000		-1.30	0.001		0.05	0.771		0.12	0.493	
SEN3252	STM3424	*rplR*	50S ribosomal subunit protein L18	-0.70	0.000		0.48	0.004		-1.46	0.000		-1.50	0.000		-0.17	0.226		0.26	0.081	
SEN3266	STM3438	*rplW*	50S ribosomal subunit protein L23	-0.96	0.000		0.43	0.010		-1.14	0.001		-0.81	0.014		-0.01	0.900		0.34	0.069	
SEN3257	STM3429	*rplX*	50S ribosomal subunit protein L24	-1.25	0.000		0.23	0.093		-1.99	0.000		-2.37	0.000		-0.40	0.001		-0.01	0.917	
SEN0885	STM0981	*rpsA*	30S ribosomal subunit protein S1	-1.30	0.000		-0.14	0.334		-1.47	0.000		-2.19	0.000		-0.53	0.188		-0.50	0.002	
SEN0223	STM0216	*rpsB*	30S ribosomal subunit protein S2	-0.73	0.001		0.11	0.390		-1.78	0.000		-1.99	0.000		-0.18	0.194		0.00	0.988	
SEN3262	STM3434	*rpsC*	30S ribosomal subunit protein S3	-1.30	0.000	-0.24	0.35	0.076	-0.85	-2.09	0.000	-5.06	-1.51	0.008	-4.54	0.17	0.289	-1.56	0.48	0.137	-0.81
SEN3244	STM3416	*rpsD*	30S ribosomal subunit protein S4	-1.59	0.000		0.03	0.797		-2.18	0.000		-2.36	0.000		-0.50	0.000		-0.35	0.012	
SEN3251	STM3423	*rpsE*	30S ribosomal subunit protein S5	-0.67	0.003		0.41	0.006		-1.81	0.000		-2.16	0.000		0.08	0.515		0.21	0.103	
SEN4157	STM4391	*rpsF*	30S ribosomal subunit protein S6	-1.24	0.000		-0.05	0.765		-1.81	0.000		-1.94	0.000		-0.52	0.001		-0.80	0.001	
SEN3275	STM3447	*rpsG*	30S ribosomal subunit protein S7, initiates assembly	-1.31	0.000		0.15	0.081		-2.51	0.000		-2.78	0.000		-0.17	0.145		-0.39	0.004	
SEN3254	STM3426	*rpsH*	30S ribosomal subunit protein S8, and regulator	-1.37	0.000		0.20	0.114		-2.20	0.000		-2.35	0.000		-0.16	0.181		0.03	0.861	
SEN3269	STM3441	*rpsJ*	30S ribosomal subunit protein S10	-1.61	0.000		0.25	0.192		-2.35	0.000		-2.39	0.001		0.11	0.741		0.01	0.980	
SEN3245	STM3417	*rpsK*	30S ribosomal subunit protein S11	-1.38	0.000		0.23	0.025		-2.03	0.000		-2.43	0.000		0.04	0.675		-0.19	0.108	
SEN3276	STM3448	*rpsL*	30S ribosomal subunit protein S12	-0.83	0.000		0.00	0.981		-2.07	0.000		-2.34	0.000		-0.10	0.494		-0.40	0.002	
SEN3255	STM3427.S	*rpsN*	30S ribosomal subunit protein S14	-0.68	0.003		0.45	0.019		-1.29	0.000		-1.78	0.000		-0.54	0.000		0.15	0.312	
SEN3259	STM3431	*rpsQ*	30S ribosomal subunit protein S17	-0.98	0.000		0.29	0.049		-1.50	0.000		-0.85	0.031		0.05	0.727		0.47	0.118	
SEN4159	STM4393	*rpsR*	30S ribosomal subunit protein S18	-0.98	0.000		-0.21	0.056		-2.24	0.000		-2.28	0.000		-0.56	0.001		-0.52	0.020	
SEN0043	STM0043	*rpsT*	30S ribosomal subunit protein S20	-0.30	0.034		-0.46	0.001		-0.99	0.000		-1.20	0.000		-0.54	0.000		-0.46	0.009	
SEN3052	STM3209	*rpsU*	30S ribosomal subunit protein S21	-0.56	0.000		-0.88	0.000		-1.14	0.000		-1.65	0.000		-0.83	0.009		-1.11	0.000	
SEN0388	STM0405	*tgt*	tRNA-guanine transglycosylase	-0.82	0.000		-0.30	0.030		-1.61	0.000		-1.46	0.000		-0.79	0.000		-0.55	0.003	
SEN3923	STM4129	*trmA*	tRNA (uracil-5-)-methyltransferase	-0.28	0.078		-0.84	0.001		-1.06	0.000		-1.35	0.000		-1.02	0.000		-1.34	0.000	
SEN2595	STM2674	*trmD*	tRNA (guanine-7-)-methyltransferase	-1.16	0.000		0.28	0.036		-2.55	0.000		-2.90	0.000		0.16	0.120		0.36	0.002	
SEN1815	STM1234.S	*trmU*	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	-0.56	0.000		-1.10	0.000		-0.74	0.001		-1.57	0.000		-1.43	0.000		-2.61	0.000	
SEN0224	STM0217	*tsf*	protein chain elongation factor EF-Ts	-0.48	0.001		-0.02	0.751		-1.49	0.000		-1.82	0.000		0.10	0.437		0.26	0.050	
SEN1331	STM1701	*yciW*	putative cytoplasmic protein	-0.31	0.148		-0.36	0.028		-1.32	0.000		-1.45	0.001		-0.56	0.004		-0.51	0.064	
SEN1187	STM1850	*yebU*	paral putative rRNA methyltransferase	-0.14	0.514		-0.55	0.007		-1.26	0.000		-1.95	0.000		-1.35	0.000		-1.88	0.000	
SEN2587	STM2665	*yfiA*	ribosome associated factor, stabilizes ribosomes	0.41	0.035		1.78	0.000		1.49	0.000		1.68	0.000		2.90	0.000		3.36	0.000	
SEN3062	STM3220	*ygjO*	paral putative methyltransferase	-0.20	0.137		-0.41	0.018		-1.46	0.000		-1.26	0.000		-1.30	0.000		-1.44	0.000	
H. Cations and iron carrying compounds																					
SEN3331	STM3505	*feoA*	ferrous iron transport protein A	0.30	0.114		0.35	0.079		-0.15	0.437		0.25	0.563		0.15	0.475		0.49	0.064	
SEN3332	STM3506	*feoB*	FeoB family, ferrous iron transport protein B	1.18	0.001		1.79	0.000		0.91	0.003		2.63	0.000		1.12	0.000		2.88	0.000	
SEN0554	STM0585	*fepA*	outer membrane porin, receptor for ferric enterobactin	0.12	0.412		0.86	0.001		0.25	0.045		1.10	0.016		0.58	0.005		1.45	0.000	
SEN0555	STM0586	*fes*	enterochelin esterase	0.25	0.075		1.33	0.008		-0.22	0.268		0.95	0.069		0.96	0.000		1.94	0.000	
SEN1073	STM1932	*ftnB*	ferritin-like protein	0.26	0.085		0.65	0.005		0.21	0.329		1.28	0.000		0.47	0.008		1.03	0.000	
SEN0479	STM0498	*ybaR (copA)*	putative copper-transporting ATPase	1.04	0.000		2.35	0.000		2.42	0.000		3.05	0.000		1.34	0.000		2.27	0.000	
I. cellular processes																					
SEN1725	STM1318	*katE*	catalase; hydroperoxidase HPII(III), RpoS dependent	0.38	0.008		0.20	0.056		1.93	0.000		2.38	0.000		0.05	0.717		0.15	0.123	
SEN3900	STM4106	*katG*	catalase; hydroperoxidase HPI(I)	0.32	0.004	-0.89	0.78	0.003	-1.39	0.33	0.015	-2.10	0.49	0.025	-0.27	2.57	0.000	0.25	2.06	0.000	-2.62
SEN1823	STM1226	*potA*	ABC superfamily (atp_bind), spermidine/putrescine transporter	-0.38	0.002		-0.79	0.000		-1.33	0.000		-1.59	0.000		-0.74	0.001		-1.41	0.000	
SEN1824	STM1225	*potB*	ABC superfamily (membrane), spermidine/putrescine transporter	-0.31	0.003		-0.47	0.003		-1.35	0.000		-1.72	0.000		-0.90	0.002		-1.30	0.000	
SEN1826	STM1223	*potC*	ABC superfamily (membrane), spermidine/putrescine transporter	-0.42	0.040		-0.18	0.096		-0.94	0.000		-1.00	0.001		-0.83	0.000		-0.76	0.000	
SEN1827	STM1222	*potD*	ABC superfamily (peri_perm), spermidine/putrescine transporter	-0.99	0.000		-0.39	0.001		-2.08	0.000		-1.87	0.000		-0.98	0.001		-0.90	0.000	
SEN0823	STM0877	*potF*	ABC superfamily (peri_perm), putrescine transporter	-0.01	0.855		-0.24	0.032		0.27	0.131		0.60	0.010		-0.50	0.033		-0.01	0.969	
SEN0824	STM0878	*potG*	ABC superfamily (atp_bind), putrescine transporter	0.13	0.278		-0.13	0.167		0.07	0.692		0.24	0.152		-0.34	0.037		-0.08	0.494	
SEN0825	STM0879	*potH*	ABC superfamily (membrane), putrescine transporter	-0.10	0.306		-0.10	0.277		-0.27	0.526		0.00	0.988		-0.16	0.248		-0.02	0.885	
SEN0826	STM0880	*potI*	ABC superfamily (membrane), putrescine transporter	-0.07	0.499		-0.09	0.335		-0.12	0.441		-0.16	0.439		-0.02	0.903		-0.08	0.642	
SEN3845	STM4055	*sodA*	superoxide dismutase, manganese	0.36	0.007		0.71	0.000		1.78	0.000		2.93	0.000		1.02	0.000		3.12	0.000	
SEN1616	STM1431	*sodB*	superoxide dismutase, iron	0.21	0.024		0.36	0.034		0.02	0.869		-0.28	0.311		0.14	0.199		0.44	0.000	
SEN1149	STM1044	*sodC*	Gifsy-2 prophage: superoxide dismutase precursor (Cu-Zn)	0.05	0.642		-0.61	0.425		0.28	0.115		0.04	0.899		0.05	0.653		-0.01	0.968	
SEN2958	STM3114	*speC*	ornithine decarboxylase isozyme	-0.15	0.104		-0.59	0.000		-0.44	0.003		-1.07	0.000		-1.19	0.000		-1.08	0.000	
SEN0170	STM0165	*speD*	S-adenosylmethionine decarboxylase, proenzyme	-0.94	0.000		-0.37	0.001		-1.98	0.000		-2.05	0.000		-0.97	0.000		-0.93	0.000	
SEN0171	STM0166	*speE*	spermidine synthase (putrescine aminopropyltransferase)	-1.12	0.000		-0.05	0.588		-2.70	0.000		-2.54	0.000		-0.66	0.000		-0.47	0.002	
SEN0665	STM0701	*speF*	ornithine decarboxylase isozyme, inducible	0.01	0.898		0.08	0.468		0.20	0.194		-0.86	0.032		0.85	0.002		-1.50	0.000	
SEN0173	STM0168	*yacK*	putative multicopper oxidase	0.36	0.032		0.41	0.004		1.33	0.000		1.27	0.000		0.31	0.034		0.44	0.000	
J. Energy metabolism																					
SEN1321	STM1712	*acnA*	aconitate hydratase 1	0.96	0.000		0.66	0.000		3.04	0.000		3.19	0.000		0.38	0.006		1.37	0.000	

SEN0162	STM0158	*acnB*	aconitate hydratase 2	1.24	0.000		0.80	0.005		2.55	0.000		2.29	0.001		0.79	0.000		1.35	0.000	
SEN1287	STM1749	*adhE*	iron-dependent alcohol dehydrogenase	-0.48	0.108	-0.44	0.28	0.062	-2.12	-0.84	0.254	-3.92	-2.49	0.000	-4.70	1.35	0.002	0.49	-0.50	0.008	-2.23
SEN2528	STM2548	*asrA*	anaerobic sulfide reductase	0.25	0.121		0.42	0.030		0.63	0.020		2.26	0.000		0.42	0.006		1.03	0.000	
SEN2529	STM2549	*asrB*	anaerobic sulfide reductase	0.23	0.061		-0.08	0.446		0.32	0.171		2.04	0.000		0.31	0.125		0.15	0.163	
SEN2530	STM2550	*asrC*	anaerobic sulfide reductase	0.26	0.077		0.10	0.420		1.20	0.001		2.54	0.000		0.28	0.079		-0.08	0.476	
SEN3681	STM3867	*atpA*	membrane-bound ATP synthase, F1 sector, alpha-subunit	-0.47	0.000		0.11	0.231		-1.21	0.000		-1.41	0.000		-0.13	0.218		0.03	0.711	
SEN3679	STM3865	*atpD*	membrane-bound ATP synthase, F1 sector, beta-subunit	-0.32	0.010		0.17	0.050		-1.25	0.000		-1.16	0.000		0.35	0.004		0.71	0.000	
SEN3684	STM3870	*atpE*	membrane-bound ATP synthase, F0 sector, subunit c	-0.46	0.011		-0.29	0.008		-1.07	0.000		-1.28	0.000		-0.42	0.007		-0.31	0.036	
SEN3683	STM3869	*atpF*	membrane-bound ATP synthase, F0 sector, subunit b	-0.40	0.067		-0.22	0.054		-0.79	0.003		-1.31	0.000		-0.27	0.326		0.11	0.464	
SEN3680	STM3866	*atpG*	membrane-bound ATP synthase, F1 sector, gamma-subunit	-0.46	0.013		-0.10	0.243		-1.12	0.000		-0.80	0.001		-0.05	0.635		0.46	0.000	
SEN3682	STM3868	*atpH*	membrane-bound ATP synthase, F1 sector, delta-subunit	-0.79	0.000		-0.28	0.004		-1.61	0.000		-1.88	0.000		-0.27	0.027		-0.39	0.001	
SEN3686	STM3872	*atpI*	membrane-bound ATP synthase subunit, F1-F0-type proton-ATPase	-0.61	0.000		-1.04	0.000		-0.94	0.000		-1.41	0.000		-0.56	0.004		-1.56	0.000	
SEN0653	STM0689	*citA*	citrate-proton symporter	0.07	0.499		0.06	0.680		0.63	0.006		0.94	0.000		0.21	0.122		0.07	0.534	
SEN0654	STM0690	*citB*	citrate utilization protein b	0.13	0.120		-0.12	0.385		0.04	0.845		0.25	0.198		0.09	0.659		-0.05	0.731	
SEN0593	STM0624	*citC*	citrate lyase synthetase (citrate (pro-3S)-lyase ligase	-0.10	0.462		0.27	0.099		-0.52	0.044		-1.65	0.001		0.24	0.351		-1.27	0.004	
SEN0592	STM0623	*citD*	citrate lyase acyl carrier protein (gamma chain)	0.20	0.251	-3.86	-0.02	0.850	-5.25	-0.29	0.211	-4.64	-2.07	0.001	-7.11	0.14	0.447	-2.86	-0.97	0.024	
SEN0591	STM0622	*citE*	citrate lyase beta chain (acyl lyase subunit)	0.03	0.638		-0.08	0.476		-0.75	0.065		-2.61	0.000		0.19	0.295		-1.25	0.020	
SEN0590	STM0621	*citF*	bifunctional citrate lyase alpha chain/citrate-ACP transferase	0.15	0.254	-4.92	0.07	0.628	-5.25	-0.33	0.158	-5.75	-2.30	0.000	-5.47	-0.02	0.891	-2.41	-1.18	0.005	
SEN0588	STM0619	*citG*	putative modifier of citrate lyase protein	0.20	0.062		0.02	0.841		-0.02	0.924		-0.14	0.435		-0.08	0.586		-0.20	0.101	
SEN0587	STM0618	*citT*	DASS family, citrate:succinate transport (antiport) protein	-0.07	0.423		-0.05	0.741		-0.20	0.255		-1.54	0.000		0.02	0.915		-1.44	0.000	
SEN0589	STM0620	*citX*	putative cytoplasmic protein	-0.01	0.951		0.00	0.984		-0.53	0.036		-1.46	0.004		0.08	0.624		-1.19	0.001	
SEN0690	STM0740	*cydA*	cytochrome d terminal oxidase, polypeptide subunit I	-0.47	0.000		0.43	0.003		-1.73	0.000		-1.47	0.000		0.48	0.021		0.12	0.239	
SEN0691	STM0741	*cydB*	cytochrome d terminal oxidase polypeptide subunit II	-0.48	0.000		0.11	0.475		-2.27	0.000		-2.10	0.000		0.38	0.030		0.03	0.740	
SEN0425	STM0443	*cyoA*	cytochrome o ubiquinol oxidase subunit II	0.35	0.116	-0.97	0.09	0.542	4.35	1.67	0.012	-0.57	3.57	0.000	3.96	-0.81	0.031	-1.29	2.29	0.000	4.36
SEN0424	STM0442	*cyoB*	cytochrome o ubiquinol oxidase subunit I	0.32	0.046		0.27	0.032		0.98	0.042		2.12	0.002		-0.89	0.000		1.08	0.006	
SEN0423	STM0441	*cyoC*	cytochrome o ubiquinol oxidase subunit III	0.30	0.017		0.35	0.004		0.95	0.018		2.11	0.000		-0.84	0.000		1.24	0.000	
SEN0422	STM0440	*cyoD*	cytochrome o ubiquinol oxidase subunit IV	0.25	0.019		0.49	0.000		0.68	0.042		1.54	0.007		-0.77	0.000		1.18	0.000	
SEN0421	STM0439	*cyoE*	protohaeme IX farnesyltransferase (haeme O biosynthesis)	0.18	0.040		0.30	0.005		1.38	0.002		2.57	0.000		-0.27	0.203		1.30	0.000	
SEN2161	STM2167	*dld*	D-lactate dehydrogenase, NADH independent	0.88	0.001		0.96	0.000		2.36	0.000		2.93	0.000		1.01	0.000		1.82	0.000	
SEN0869	STM0964	*dmsA*	anaerobic dimethyl sulfoxide reductase, subunit A	0.06	0.469	-1.83	-0.02	0.850	-2.96	-1.12	0.007	-4.79	-3.06	0.000	-4.38	1.53	0.030	-0.10	-0.76	0.000	-3.45
SEN0870	STM0965	*dmsB*	anaerobic dimethyl sulfoxide reductase, subunit B	0.13	0.248		-0.02	0.852		-0.75	0.034		-1.99	0.000		0.35	0.242		-0.54	0.001	
SEN1485	STM1570	*fdnG*	putative molybdopterin oxidoreductases	0.10	0.241		-0.08	0.509		-1.23	0.003		-1.74	0.000		1.13	0.004		1.16	0.002	
SEN1485	STM1570	*fdnG*	putative molybdopterin oxidoreductases	-0.33	0.043		0.48	0.000		-0.93	0.008		-0.96	0.003		1.06	0.009		1.30	0.000	
SEN1486	STM1569	*fdnH*	formate dehydrogenase-N, Fe-S beta subunit, nitrate-inducible	-0.37	0.023		-0.02	0.871		-1.13	0.006		-1.84	0.000		1.22	0.000		1.13	0.000	
SEN3826	STM4037	*fdoG*	formate dehydrogenase	1.11	0.000		0.58	0.000		1.48	0.000		2.41	0.000		0.36	0.005		1.80	0.000	
SEN3824	STM4035	*fdoI*	formate dehydrogenase, cytochrome B556 (FDO) subunit	0.35	0.010		0.01	0.920		0.86	0.000		1.05	0.041		0.04	0.719		0.75	0.000	
SEN4113	STM4343	*frdA*	fumarate reductase, anaerobic, flavoprotein subunit	-0.32	0.098		0.01	0.971		-1.91	0.009		-3.94	0.000		1.48	0.021		-0.97	0.000	
SEN4112	STM4342	*frdB*	fumarate reductase, anaerobic, Fe-S protein subunit	-0.06	0.729		0.34	0.077		-1.73	0.013		-3.28	0.000		1.03	0.047		-0.09	0.381	
SEN4111	STM4341	*frdC*	fumarate reductase, anaerobic, membrane anchor polypeptide	-0.24	0.250		0.05	0.726		-0.95	0.028		-2.23	0.000		0.70	0.049		0.08	0.431	
SEN4110	STM4340	*frdD*	fumarate reductase, anaerobic, membrane anchor polypeptide	-0.18	0.205		-0.13	0.272		-0.43	0.064		-1.25	0.000		0.19	0.213		-0.10	0.400	
SEN1581	STM1468	*fumA*	fumarase A (fumarate hydratase class I), aerobic isozyme	0.79	0.000		0.51	0.001		2.35	0.000		2.24	0.000		0.56	0.000		1.21	0.000	
SEN1579	STM1469	*fumC*	fumarase C (fumarate hydratase Class II)	0.62	0.000		0.19	0.028		2.02	0.000		2.50	0.000		0.30	0.033		0.51	0.001	
SEN3351	STM3526	*glpD*	sn-glycerol-3-phosphate dehydrogenase (aerobic)	0.43	0.028		0.38	0.003		2.48	0.000		3.83	0.000		0.68	0.003		1.90	0.000	
SEN0680	STM0730	*gltA*	citrate synthase	1.97	0.000	1.85	0.64	0.022	1.80	3.43	0.000	2.84	2.93	0.000	3.23	1.45	0.000	0.78	1.39	0.000	1.46
SEN2992	STM3149	*hybA*	function unknown	-0.42	0.044		0.01	0.947		-1.37	0.009		-2.32	0.000		1.27	0.001		-0.60	0.000	
SEN2991	STM3148	*hybB*	putative cytochrome Ni/Fe component of hydrogenase-2	-0.22	0.060		0.05	0.592		-1.28	0.005		-2.30	0.000		0.69	0.010		-0.48	0.000	
SEN2990	STM3147	*hybC*	hydrogenase-2, large subunit	-0.04	0.632		0.25	0.110		-0.82	0.020		-1.59	0.000		0.88	0.004		0.01	0.907	
SEN2989	STM3146	*hybD*	putative processing element for hydrogenase-2	0.06	0.673		-0.17	0.161		-0.54	0.110		-1.05	0.001		1.08	0.002		-0.03	0.770	
SEN2697	STM2855	*hypB*	hydrogenase-3 accessory protein, assembly of metallocenter	-0.09	0.495	-1.68	0.61	0.007	-2.50	0.39	0.354	-3.48	-0.55	0.019	-3.82	2.03	0.002	-0.23	1.48	0.000	-2.98
SEN2699	STM2857	*hypD*	putative hydrogenase expression/formation protein	-0.09	0.590		0.23	0.070		-0.50	0.051		-1.38	0.000		1.51	0.001		0.62	0.002	
SEN2700	STM2858	*hypE*	putative hydrogenase expression/formation protein	-0.28	0.053		-0.15	0.283		-0.34	0.171		-1.36	0.000		0.85	0.006		-0.14	0.307	
SEN2683	STM2842	*hypF*	hydrogenase maturation protein	-0.46	0.000		-0.71	0.000		-0.21	0.199		-1.21	0.000		-0.61	0.000		-1.60	0.000	
SEN2993	STM3150	*hypO*	putative Ni/Fe hydrogenases, small subunit	-0.49	0.026	-1.55	0.15	0.219	-4.05	-1.23	0.011	-4.08	-2.28	0.000	-5.26	1.50	0.004	-2.86	-0.93	0.000	-4.87
SEN1811	STM1238	*icdA*	isocitrate dehydrogenase in e14 prophage, specific for NADP+	0.93	0.000		0.15	0.448		2.35	0.000		2.61	0.000		-0.15	0.290		1.19	0.000	
SEN2451	STM2472	*maeB*	paral putative transferase	0.17	0.071		0.36	0.001		0.70	0.000		1.14	0.000		0.68	0.001		1.14	0.000	
SEN2242	STM2259	*napA*	periplasmic nitrate reductase, large subunit, in complex with NapB	-0.27	0.298		0.41	0.051		-0.30	0.175		-0.59	0.004		0.75	0.013		1.01	0.000	
SEN2239	STM2256	*napB*	periplasmic nitrate reductase, small subunit	-0.11	0.402		0.15	0.387		-0.77	0.018		-1.01	0.001		1.34	0.012		1.35	0.003	
SEN2240	STM2257	*napH*	ferredoxin-type protein: electron transfer	-0.41	0.057		0.12	0.483		-1.40	0.021		-1.78	0.000		1.99	0.001		1.01	0.006	
SEN1275	STM1764	*narG*	nitrate reductase 1, alpha subunit	-0.40	0.384	-1.49	0.91	0.014	-1.72	0.95	0.032	-4.11	3.11	0.001	-3.70	2.92	0.001	0.01	5.38	0.000	-1.86
SEN1276	STM1763	*narH*	nitrate reductase 1, FeS (beta) subunit	-0.31	0.399		-0.05	0.596		1.20	0.003		2.57	0.006		2.96	0.001		4.61	0.000	
SEN1278	STM1761	*narI*	nitrate reductase 1, cytochrome b(NR), gamma subunit	-0.29	0.208		-0.52	0.016		0.80	0.011		1.74	0.056		1.78	0.004		3.16	0.000	
SEN1277	STM1762	*narJ*	nitrate reductase 1, delta subunit	-0.23	0.503		-0.09	0.319		1.24	0.008		3.03	0.006		2.72	0.001		4.76	0.000	

SEN1274	STM1765	*narK*	MFS superfamily, nitrite extrusion protein	-0.58	0.152		-0.01	0.967		0.07	0.721		1.27	0.004		2.39	0.001		4.61	0.000		
SEN1272	STM1767	*narL*	response regulator in two-component regulatory system	-0.21	0.142		0.10	0.503		0.00	0.995		1.00	0.001		0.45	0.011		2.09	0.000		
SEN2229	STM2246	*narP*	response regulator in two-component regulatory system	-0.26	0.087		0.17	0.108		-0.67	0.008		-1.08	0.000		-0.46	0.005		-0.16	0.206		
SEN1479	STM1576	*narU*	MFS superfamily, nitrate extrusion protein	-0.04	0.624		0.20	0.106		0.99	0.004		1.02	0.000		0.29	0.031		0.47	0.000		
SEN1273	STM1766	*narX*	sensory histidine kinase in two component regulatory system	-0.23	0.187		-0.01	0.951		0.02	0.915		0.78	0.005		0.59	0.014		2.65	0.000		
SEN1477	STM1578	*narY*	nitrate reductase 2, beta subunit	-0.23	0.180		0.16	0.262		1.04	0.003		1.68	0.002		1.89	0.000		2.94	0.000		
SEN1478	STM1577	*narZ*	nitrate reductase 2, alpha subunit	-0.23	0.312		0.22	0.107		1.76	0.000		1.83	0.000		2.41	0.001		4.16	0.000		
SEN1838	STM1211	*ndh*	respiratory NADH dehydrogenase 2; cupric reductase	-0.11	0.390		0.37	0.011		-1.73	0.000		-1.73	0.000		-0.35	0.006		-0.11	0.250		
SEN3301	STM3474	*nirB*	nitrite reductase, large subunit	-0.67	0.081		0.48	0.016		-0.73	0.013		-0.65	0.005		2.28	0.004		2.33	0.000		
SEN4047	STM4277	*nrfA*	nitrite reductase periplasmic cytochrome c(552)	-0.52	0.107		-0.08	0.552		-0.55	0.017		-0.68	0.003		1.65	0.003		1.22	0.000		
SEN2307	STM2325	*nuoE*	NADH dehydrogenase I chain E	0.54	0.003		0.31	0.009		1.01	0.000		1.26	0.000		0.58	0.000		1.24	0.000		
SEN2306	STM2324	*nuoF*	NADH dehydrogenase I chain F	0.63	0.000		0.38	0.001		1.48	0.000		1.86	0.000		0.50	0.000		1.29	0.000		
SEN2305	STM2323.S	*nuoG*	NADH dehydrogenase I chain G	0.09	0.496		0.32	0.009		0.58	0.001		0.51	0.029		0.31	0.013		1.09	0.000		
SEN2303	STM2321	*nuoI*	NADH dehydrogenase I chain I	0.09	0.426		0.43	0.002		0.83	0.000		0.99	0.000		0.23	0.104		1.36	0.000		
SEN2302	STM2320	*nuoJ*	NADH dehydrogenase I chain J	0.03	0.684		0.50	0.002		0.99	0.000		0.79	0.001		0.38	0.041		1.60	0.000		
SEN2301	STM2319	*nuoK*	NADH dehydrogenase I chain K	-0.05	0.795		0.41	0.031		0.31	0.051		0.52	0.026		0.15	0.395		1.01	0.000		
SEN2300	STM2318	*nuoL*	NADH dehydrogenase I chain L	-0.03	0.799		0.47	0.001		1.01	0.000		0.83	0.000		0.49	0.006		1.12	0.000		
SEN2299	STM2317	*nuoM*	NADH dehydrogenase I chain M	-0.08	0.254		0.03	0.722		0.79	0.001		0.93	0.000		0.20	0.247		1.08	0.000		
SEN2298	STM2316.S	*nuoN*	NADH dehydrogenase I chain N	-0.01	0.911		0.22	0.053		0.29	0.250		0.42	0.014		-0.01	0.952		1.00	0.000		
SEN1717	STM1326	*pfkB*	6-phosphofructokinase II	0.84	0.000		1.21	0.000		2.28	0.000		2.46	0.000		1.29	0.000		2.20	0.000		
SEN1569	STM1480	*pntB*	pyridine nucleotide transhydrogenase (proton pump), beta subunit	-0.19	0.094		0.07	0.463		-1.21	0.000		-1.17	0.000		0.65	0.000		0.68	0.000		
SEN4014	STM4245	*qor*	quinone oxidoreductase, NADPH dependent	0.46	0.005		0.49	0.001		1.32	0.000		1.62	0.000		1.07	0.000		1.67	0.000		
SEN2815	STM2971	*sdaB*	L-serine dehydratase (L-threonine deaminase 2)	-1.12	0.001		-0.03	0.827		-3.40	0.000		-3.68	0.000		0.17	0.348		0.28	0.034		
SEN2814	STM2970	*sdaC*	putative HAAAP family, serine transport protein	-1.77	0.000		-0.59	0.001		-3.76	0.000		-3.77	0.000		0.05	0.839		-0.87	0.000		
SEN0684	STM0734	*sdhA*	succinate dehydrogenase, flavoprotein subunit	1.07	0.000		-0.04	0.762		3.32	0.000		3.03	0.000		0.31	0.217		0.97	0.001		
SEN0686	STM0736	*sucA*	2-oxoglutarate dehydrogenase (decarboxylase component)	0.87	0.000		0.43	0.008		2.89	0.000		2.33	0.000		-0.06	0.604		0.90	0.000		
SEN0687	STM0737	*sucB*	2-oxoglutarate dehydrogenase	0.61	0.000		0.56	0.005		2.23	0.000		2.14	0.000		0.22	0.155		1.33	0.000		
SEN0688	STM0738	*sucC*	succinyl-CoA synthetase, beta subunit	0.57	0.000		0.72	0.006		2.55	0.000		1.96	0.000		0.43	0.008		1.34	0.000		
SEN0689	STM0739	*sucD*	succinyl-CoA synthetase, alpha subunit	0.07	0.530		0.48	0.024		1.13	0.000		1.13	0.001		0.22	0.254		1.05	0.000		
SEN2576	STM2649	*trxC*	thioredoxin 2, redox factor	0.44	0.014		0.50	0.008		0.51	0.009		0.79	0.016		0.82	0.002		2.04	0.000		
SEN4003	STM4234	*ubiA*	p-hydroxybenzoate: octaprenyltransferase	0.17	0.072		0.53	0.009		0.54	0.002		0.81	0.001		0.07	0.562		1.04	0.000		
SEN4002	STM4233	*ubiC*	chorismate pyruvate lyase	0.31	0.045		0.82	0.003		0.16	0.446		0.59	0.017		0.73	0.000		1.79	0.000		
SEN3920	STM4126	*udhA*	soluble pyridine nucleotide transhydrogenase	0.98	0.006		-0.14	0.727		3.45	0.000		2.77	0.000		-0.58	0.038		0.12	0.737		
SEN3007	STM3164	*yqhD*	putative alcohol dehydrogenase	1.08	0.000		1.11	0.000		0.85	0.001		1.27	0.000		3.81	0.000		1.36	0.000		
SEN1516	STM1536		putative hydrogenase maturation protease	0.34	0.049		0.12	0.457		0.20	0.410		1.47	0.007		0.11	0.400		-0.03	0.842		
SEN1514	STM1538		putative hydrogenase-1 large subunit	0.46	0.042		0.18	0.121		0.81	0.016		2.03	0.002		0.05	0.711		-0.26	0.036		
SEN1515	STM1537		putative Ni/Fe-hydrogenase 1 b-type cytochrome subunit	0.39	0.047		0.05	0.715		0.29	0.195		1.08	0.015		0.00	0.996		-0.04	0.774		
SEN1519	STM1533		putative hydrogenase	0.08	0.527		-0.20	0.137		0.52	0.008		1.19	0.004		-0.01	0.930		-0.27	0.069		
SEN1520	STM1532		putative dehydrogenase protein	0.16	0.083		-0.05	0.616		0.48	0.049		1.02	0.020		0.05	0.745		-0.28	0.075		
K. regulatory function																						
SEN3219	STM3385	*fis*	site-specific DNA inversion stimulation factor	-1.06	0.000		-0.38	0.003		-2.91	0.000		-3.16	0.000		-1.17	0.001		-0.81	0.000		
SEN0657	STM0693	fur	transcriptional repressor of iron-responsive genes	0.12	0.348		-0.28	0.045		0.34	0.048		0.19	0.205		-0.02	0.886		-0.06	0.592		
SEN1285	STM1751	*hns*	DNA-binding protein HLP-II (HU, BH2, HD, NS)	0.12	0.317		0.07	0.475		0.35	0.167		0.46	0.046		0.46	0.026		0.64	0.000		
SEN1532	STM1519.S	*marA*	transcriptional activator	1.37	0.004		1.07	0.002		2.51	0.000		2.90	0.000		-0.18	0.238		0.27	0.071		
SEN1531	STM1520	*marR*	transcriptional repressor of marRAB operon	0.90	0.007		0.76	0.001		2.01	0.000		2.36	0.000		-0.43	0.015		-0.19	0.225		
SEN1818	STM1231	*phoP*	response regulator in two-component regulatory system	0.32	0.066		0.16	0.106		0.17	0.199		-0.01	0.938		0.32	0.010		0.37	0.000		
SEN1819	STM1230	*phoQ*	sensory kinase protein in two-component regulatory system	0.02	0.907		-0.53	0.003		0.66	0.000		0.48	0.006		0.23	0.078		-0.36	0.005		
SEN3153	STM3320	*rpoN*	sigma N (sigma 54) factor of RNA polymerase	-0.18	0.033	-3.31	-0.77	0.000	-4.65	0.22	0.173	-0.90	0.03	0.783	-2.23	-0.33	0.010	-2.23	-1.27	0.000	-3.16	
SEN2763	STM2924	*rpoS*	sigma S (sigma 38) factor of RNA polymerase, stationary phase	0.94	0.001	1.39	0.15	0.371	1.13	2.16	0.000	2.61	2.35	0.000	1.95	0.42	0.001	1.78	0.85	0.000	1.02	
SEN1574	STM1475	*rstA*	response regulator in two-component regulatory system	-0.30	0.037		-1.02	0.000		0.31	0.040		-0.29	0.094		-0.28	0.183		-1.94	0.000		
SEN1577	STM1471	*rstB*	sensory histidine kinase in two-component regulatory system	-0.06	0.570		0.00	0.999		-0.22	0.173		-0.50	0.003		-0.39	0.024		-0.47	0.000		
SEN4036	STM4266	*soxR*	redox-sensing transcriptional activator SoxR	0.09	0.512		0.29	0.008		-0.15	0.309		0.05	0.770		0.01	0.921		0.09	0.426		
SEN4035	STM4265	*soxS*	transcriptional activator of superoxide response regulon	0.24	0.017		0.24	0.230		-0.08	0.618		0.06	0.689		0.14	0.588		0.30	0.217		
L. DNA metabolism																						
SEN3655	STM3838	*dnaA*	DNA replication initiator protein	-0.41	0.013		-0.71	0.001		-0.55	0.001		-1.17	0.000		-1.14	0.000		-1.96	0.000		
SEN3053	STM3210	*dnaG*	DNA biosynthesis; DNA primase	-0.99	0.000		-1.38	0.000		-1.67	0.000		-1.48	0.000		-1.60	0.000		-2.92	0.000		
SEN2936	STM3093	*endA*	DNA-specific endonuclease I	-0.44	0.016		-0.43	0.038		-1.15	0.000		-1.58	0.000		-0.98	0.000		-1.34	0.000		
SEN2254	STM2272	*gyrA*	DNA gyrase, subunit A, type II topoisomerase	-1.01	0.000		-0.84	0.001		-0.78	0.001		-1.30	0.006		-1.49	0.000		-1.79	0.000		
SEN3652	STM3835	*gyrB*	DNA gyrase, subunit B (type II topoisomerase)	-0.60	0.000		-0.57	0.000		-0.67	0.000		-1.19	0.000		-0.70	0.001		-1.55	0.000		
SEN4319	STM4557	*holD*	DNA polymerase III, psi subunit	-0.25	0.136		-0.88	0.002		-0.62	0.002		-1.65	0.000		-1.25	0.000		-2.45	0.000		
SEN3017	STM3174	*parC*	DNA topoisomerase IV, subunit A	-0.29	0.043		-0.63	0.002		-0.85	0.000		-1.51	0.000		-1.03	0.000		-1.89	0.000		
SEN3024	STM3181	*parE*	DNA topoisomerase IV, subunit B	-0.29	0.001		-0.57	0.001		0.02	0.896		-0.03	0.862		-0.63	0.008		-1.15	0.000		

SEN4158	STM4392	*priB*	primosomal replication protein N	-1.68	0.000	-2.61	-0.30	0.015	-1.51	-3.13	0.000	-5.96	-3.85	0.000	-5.71	-0.48	0.003	-3.88	-0.66	0.000	-0.50
SEN3718	STM3912	*rep*	rep helicase, a single-stranded DNA dependent ATPase	-0.38	0.001		-0.90	0.000		-1.54	0.000		-1.72	0.000		-1.68	0.000		-2.13	0.000	
SEN1105	STM1898	*ruvC*	Holliday junction nuclease	-0.40	0.000		-0.34	0.001		-1.36	0.000		-1.55	0.000		-0.81	0.000		-0.64	0.000	
M. Amino acid biosynthesis/metabolism																					
SEN3915	STM4120	*argE*	acetylornithine deacetylase	0.64	0.000		0.43	0.005		1.38	0.000		2.20	0.000		1.06	0.000		1.21	0.000	
SEN2422	STM2441	*cysA*	ABC superfamily (atp_bind), sulfate permease A protein	-0.25	0.134		0.38	0.012		-2.64	0.000		-0.76	0.294		0.17	0.434		0.95	0.009	
SEN1320	STM1713	*cysB*	transcriptional regulator for cysteine regulon (LysR familiy)	0.03	0.843		0.34	0.015		-0.45	0.002		0.16	0.501		0.42	0.026		1.74	0.000	
SEN2772	STM2933	*cysC*	adenosine 5'-phosphosulfate kinase	-0.38	0.042		-0.33	0.035		-2.69	0.000		-2.65	0.000		-0.40	0.237		0.10	0.776	
SEN2774	STM2935	*cysD*	ATP-sulfurylase, subunit 1 (ATP:sulfate adenylyltransferase)	-0.85	0.007		-0.51	0.000		-3.61	0.000		-3.67	0.000		-0.97	0.016		-0.49	0.270	
SEN3521	STM3699	*cysE*	serine acetyltransferase	0.51	0.004		0.20	0.033		1.14	0.000		1.21	0.000		0.38	0.023		0.49	0.002	
SEN3304	STM3477	*cysG*	siroheme synthase	-0.44	0.041		-0.27	0.063		-0.79	0.004		-1.15	0.000		0.59	0.071		0.15	0.365	
SEN2785	STM2946	*cysH*	3'-phosphoadenosine 5'-phosphosulfate (PAPS) reductase	-0.36	0.023		-0.15	0.193		-2.47	0.000		-1.58	0.001		-0.50	0.007		-0.09	0.790	
SEN2786	STM2947	*cysI*	sulfite reductase, alpha subunit, NADPH dependent	-0.43	0.026		-0.26	0.060		-0.64	0.000		-1.19	0.000		-0.52	0.017		-0.52	0.043	
SEN2786	STM2947	*cysI*	sulfite reductase, alpha subunit, NADPH dependent	-0.88	0.005		-0.47	0.001		-3.69	0.000		-3.69	0.000		-1.11	0.002		-0.76	0.023	
SEN2787	STM2948	*cysJ*	sulfite reductase, beta (flavoprotein) subunit	-0.90	0.002		-0.96	0.000		-3.35	0.000		-3.37	0.000		-1.42	0.001		-1.60	0.000	
SEN2411	STM2430	*cysK*	subunit of cysteine synthase A and O-acetylserine sulfhydrolase A	-0.36	0.035		-0.07	0.393		-1.50	0.000		-0.82	0.027		0.41	0.095		1.12	0.006	
SEN2421	STM2440	*cysM*	cysteine synthase B (O-acetylserine sulfhydrolase B)	-0.14	0.235		-0.47	0.005		-1.37	0.000		-0.62	0.002		-0.95	0.000		-0.68	0.006	
SEN2773	STM2934	*cysN*	ATP-sulfurylase, subunit 1 (ATP:sulfate adenylyltransferase)	-0.68	0.017		0.23	0.140		-3.16	0.000		-2.71	0.000		0.05	0.863		1.08	0.016	
SEN2425	STM2444	*cysP*	ABC superfamily (bind_prot), thiosulfate transport protein	-0.91	0.013		-0.72	0.000		-3.88	0.000		-3.76	0.000		-0.74	0.031		0.01	0.975	
SEN4172	STM4404	*cysQ*	affects pool of 3'-phosphoadenosine-5'-phosphosulfate	0.27	0.003		0.89	0.000		0.39	0.045		1.04	0.001		0.86	0.000		1.92	0.000	
SEN0518	STM0537	*cysS*	cysteine tRNA synthetase	-0.65	0.000		-0.77	0.000		-0.23	0.079		-1.23	0.000		-0.62	0.004		-1.88	0.000	
SEN2424	STM2443	*cysU*	ABC superfamily (membrane), thiosulfate transport protein	-0.36	0.070		-0.23	0.109		-2.69	0.000		-2.29	0.000		-0.21	0.506		-0.15	0.612	
SEN2423	STM2442	*cysW*	ABC superfamily (membrane), thiosulfate permease W protein	-0.38	0.068		-0.18	0.148		-3.02	0.000		-2.20	0.000		-0.31	0.212		-0.03	0.922	
SEN1744	STM1299	*gdhA*	glutamate dehydrogenase, NADP-specific	0.36	0.023		-0.16	0.203		1.18	0.000		2.05	0.000		0.17	0.071		-0.53	0.001	
SEN3612	STM3796	*ilvB*	acetolactate synthase I, large subunit, valine sensitive	-0.05	0.755		0.81	0.018		-0.35	0.121		0.23	0.147		0.69	0.001		1.14	0.000	
SEN3715	STM3909	*ilvC*	ketol-acid reductoisomerase	0.09	0.440		0.69	0.000		0.94	0.008		2.62	0.000		2.62	0.000		2.57	0.000	
SEN3710	STM3904	*ilvD*	dihydroxyacid dehydratase	0.40	0.000		0.12	0.414		1.14	0.000		1.78	0.000		0.59	0.002		0.55	0.000	
SEN3709	STM3903	*ilvE*	branched-chain amino-acid aminotransferase	0.31	0.032		0.52	0.009		0.88	0.004		1.46	0.000		0.82	0.000		0.76	0.000	
SEN2905	STM3062	*serA*	D-3-phosphoglycerate dehydrogenase	0.65	0.001		0.18	0.139		1.82	0.000		2.10	0.000		0.38	0.007		0.46	0.003	
SEN0002	STM0003	*thrB*	homoserine kinase	0.23	0.031		0.08	0.572		0.87	0.002		1.36	0.000		0.50	0.006		0.58	0.000	
SEN0002	STM0003	*thrB*	homoserine kinase	0.04	0.723		0.04	0.699		1.16	0.000		1.90	0.000		0.47	0.007		0.43	0.002	
SEN0003	STM0004	*thrC*	threonine synthase	0.25	0.037		0.09	0.303		1.45	0.000		1.99	0.000		0.39	0.016		0.65	0.000	
SEN4017	STM4248	*tyrB*	tyrosine aminotransferase, tyrosine repressible	0.32	0.013		-0.37	0.014		1.11	0.000		1.00	0.000		0.30	0.053		-0.64	0.000	
SEN1242	STM1795		putative homologue of glutamic dehyrogenase	0.48	0.033	1.67	0.37	0.013	2.64	2.55	0.000	1.99	2.79	0.000	2.70	-0.21	0.350	1.12	1.49	0.000	2.70
N. Iron-sulfur cluster synthesis																					
SEN2519	STM2539	*hscA*	chaperone, member of Hsp70 protein family	-0.13	0.331		0.23	0.111		0.52	0.043		0.72	0.001		-0.87	0.000		-0.31	0.001	
SEN2520	STM2540	*hscB*	co-chaperone protein Hsc20	0.36	0.070		0.05	0.639		0.84	0.002		1.29	0.000		-0.70	0.001		-0.10	0.331	
SEN2523	STM2543	*nifS*	putative aminotransferase class-V	0.34	0.129		0.30	0.018		1.05	0.001		1.32	0.000		-0.67	0.006		0.07	0.373	
SEN2522	STM2542	*nifU*	NifU homologs involved in Fe-S cluster formation	0.38	0.054		0.52	0.000		0.74	0.003		1.09	0.000		-0.34	0.151		0.31	0.004	
SEN1676	STM1369	*sufA*	putative HesB-like domain	0.44	0.029		0.99	0.000		0.41	0.058		1.42	0.000		0.81	0.000		1.13	0.000	
SEN1675	STM1370	*sufB*	putative ABC transporter	1.05	0.002		1.72	0.000		1.33	0.003		3.12	0.000		0.99	0.001		2.46	0.000	
SEN1673	STM1372	*sufD*	required for stability of iron-sulfur component of FhuF	0.51	0.032		0.68	0.000		0.89	0.006		2.33	0.000		0.24	0.285		0.72	0.011	
SEN1672	STM1373	*sufS*	selenocysteine lyase	0.49	0.095		0.75	0.000		0.64	0.007		1.88	0.000		0.35	0.085		0.40	0.085	
SEN2521	STM2541	*yfhF*	putative regulator	0.23	0.232		0.31	0.006		0.87	0.001		1.35	0.000		-0.76	0.004		0.01	0.955	
SEN2524	STM2544	*yfhP*	believed to be involved in assembly of Fe-S clusters	0.45	0.024		0.16	0.078		0.97	0.000		1.59	0.000		-0.96	0.004		-0.28	0.031	
O. Osmolarity																					
SEN1076	STM1928	*otsA*	trehalose-6-phosphate synthase	0.73	0.000		0.49	0.000		2.36	0.000		2.89	0.000		-0.04	0.739		0.66	0.000	
SEN1075	STM1929	*otsB*	trehalose-6-phosphate phophatase, biosynthetic	0.73	0.002		0.28	0.016		2.63	0.000		3.34	0.000		-0.16	0.221		0.42	0.000	
SEN1241	STM1796	*treA*	trehalase, periplasmic	0.38	0.008		0.20	0.096		1.66	0.000		2.47	0.000		-0.04	0.727		0.13	0.252	
SEN4204A	STM4454	*treB*	pseudogene; frameshift	-0.69	0.045	-1.31	-0.06	0.666	-2.70	-1.89	0.001	-4.19	-2.54	0.000	-5.01	1.53	0.001	-2.39	0.15	0.496	-2.17
SEN4204	STM4453	*treC*	trehalose- 6-P hydrolase, alternative inducer of maltose system	-0.85	0.009		0.14	0.205		-1.99	0.001		-2.55	0.000		0.99	0.008		0.87	0.000	
SEN3426	STM3603	*treF*	cytoplasmic trehalase	1.17	0.001		1.41	0.000		2.03	0.000		2.82	0.000		0.41	0.027		1.51	0.000	
P. Transport and binding proteins																					
SEN1723	STM1320	*ydjN*	part of a kinase, putative domain shared with transporter	-1.11	0.000		-0.21	0.154		-3.59	0.000		-3.47	0.000		-0.91	0.000		-0.54	0.083	
SEN3454	STM3630	*dppA*	ABC superfamily (peri_perm), dipeptide transport protein	0.17	0.381		-0.40	0.026		1.19	0.000		1.53	0.000		2.12	0.003		-0.96	0.000	
SEN3454	STM3630	*dppA*	ABC superfamily (peri_perm), dipeptide transport protein	0.14	0.381		-0.41	0.020		1.08	0.001		1.04	0.000		2.21	0.003		-0.94	0.000	
SEN3453	STM3629	*dppB*	ABC superfamily (membrane), dipeptide transport protein 1	0.04	0.617		0.03	0.798		0.90	0.006		1.10	0.000		0.63	0.064		0.17	0.101	
SEN3452	STM3628	*dppC*	ABC superfamily (membrane), dipeptide transport protein 2	0.01	0.933		0.18	0.110		0.80	0.009		1.12	0.000		0.66	0.005		0.13	0.390	
SEN3451	STM3627	*dppD*	ABC superfamily (atp_bind), dipeptide transport protein	-0.04	0.736		0.25	0.059		1.05	0.002		1.30	0.000		1.94	0.000		0.20	0.106	
SEN3450	STM3626	*dppF*	ABC superfamily (atp_bind), dipeptide transport protein	0.06	0.443		0.20	0.167		1.28	0.000		0.80	0.010		1.62	0.005		0.33	0.024	
SEN1289	STM1746.S	*oppA*	oligopeptide transport protein	0.51	0.005		0.02	0.895		1.16	0.000		2.05	0.000		-0.18	0.568		-0.18	0.327	
SEN1292	STM1743	*oppD*	ABC superfamily (atp-binding), oligopeptide transport protein	0.07	0.515	-0.47	0.21	0.100	-1.78	1.24	0.000	1.53	1.07	0.000	0.65	-0.99	0.025	-0.56	0.15	0.290	-1.54

SEN2540	STM2560	*yjdL*	putative POT family, di-/tripeptide transport protein	0.89	0.003		-0.24	0.224		3.71	0.000		3.89	0.000		0.35	0.090		-0.29	0.138	
SEN1832	STM1217.S	ycfU	integral membrane protein	-0.24	0.094		-1.08	0.000		-0.34	0.092		-1.01	0.000		-0.93	0.000		-1.74	0.000	
SEN1831	STM1218	ycfV	ABC transporter, ATP-binding protein	-0.01	0.930		-0.16	0.104		-0.39	0.008		-0.97	0.000		-0.73	0.000		-0.67	0.001	
SEN1830	STM1219	ycfW	ABC transporter, integral membrane protein	-0.31	0.023		-0.37	0.006		-0.34	0.044		-1.08	0.000		-0.50	0.007		-0.83	0.000	
Q. Motility																					
SEN1875	STM1173	*flgA*	flagellar biosynthesis; assembly of basal-body periplasmic P ring	-0.55	0.021		-0.76	0.000		-0.87	0.001		-1.67	0.000		-0.82	0.001		-1.38	0.000	
SEN1874	STM1174	*flgB*	flagellar biosynthesis, cell-proximal portion of basal-body rod	-0.66	0.011		-0.28	0.010		-0.78	0.023		-1.72	0.000		-0.95	0.001		-0.90	0.000	
SEN1873	STM1175	*flgC*	flagellar biosynthesis, cell-proximal portion of basal-body rod	-0.75	0.005		-0.12	0.201		-0.74	0.046		-2.41	0.000		-0.86	0.002		-0.60	0.000	
SEN1872	STM1176	*flgD*	flagellar biosynthesis, initiation of hook assembly	-0.54	0.036	-2.29	-0.04	0.697	-1.48	-0.79	0.055	-3.12	-2.12	0.000	-3.88	-0.40	0.049	-2.91	-0.23	0.020	-1.72
SEN1871	STM1177	*flgE*	flagellar biosynthesis, hook protein	-0.47	0.011		0.06	0.594		-0.74	0.045		-1.96	0.000		-0.18	0.136		-0.08	0.440	
SEN1870	STM1178	*flgF*	flagellar biosynthesis, cell-proximal portion of basal-body rod	-0.38	0.015		-0.02	0.830		-0.88	0.022		-2.21	0.000		-0.44	0.003		-0.03	0.715	
SEN1869	STM1179	*flgG*	flagellar biosynthesis, cell-distal portion of basal-body rod	-0.22	0.069		0.04	0.718		-0.62	0.069		-1.66	0.001		-0.33	0.019		-0.17	0.183	
SEN1867	STM1181	*flgI*	putative flagella basal body protein	0.02	0.860		-0.18	0.254		-0.42	0.073		-1.53	0.000		-0.55	0.017		-0.52	0.001	
SEN1866	STM1182	*flgJ*	flagellar biosynthesis	-0.33	0.003		-0.29	0.006		-0.68	0.007		-1.90	0.000		-0.75	0.000		-0.76	0.000	
SEN1090	STM1913	*flhA*	flagellar biosynthesis; possible export of flagellar proteins	-0.18	0.143		-0.30	0.017		-0.29	0.042		-1.28	0.000		-0.15	0.519		-0.68	0.000	
SEN1089	STM1914	*flhB*	putative part of export apparatus for flagellar proteins	-0.27	0.038		-0.62	0.003		-0.19	0.148		-1.19	0.000		-0.47	0.044		-0.87	0.000	
SEN1079	STM1924.S	*flhC*	flagellar transcriptional activator	-0.05	0.625		-0.42	0.001		-0.01	0.965		-0.73	0.018		-0.02	0.862		-1.09	0.000	
SEN1078	STM1925	*flhD*	regulator of flagellar biosynthesis, acts on class 2 operons	-0.06	0.470		-0.28	0.013		-0.09	0.633		-0.73	0.005		0.36	0.007		-1.08	0.000	
SEN1041	STM1968	*fliE*	putative Flagellar hook-basal body protein	-0.13	0.725		-0.46	0.001		-0.23	0.072		-1.22	0.001		-0.55	0.022		-1.09	0.000	
SEN1040	STM1969	*fliF*	flagellar biosynthesis; basal-body MS	-0.60	0.003		-1.07	0.000		-0.88	0.001		-1.96	0.000		-0.84	0.000		-2.13	0.000	
SEN1039	STM1970	*fliG*	flagellar biosynthesis, component of motor switching and energizing	-0.63	0.009	-2.47	-0.17	0.050	-2.89	-0.69	0.013	-3.24	-1.98	0.000	-3.94	-0.88	0.001	-3.75	-0.62	0.000	-2.36
SEN1038	STM1971	*fliH*	flagellar biosynthesis; possible export of flagellar proteins	-0.82	0.003		-0.36	0.001		-0.52	0.109		-1.75	0.000		-0.77	0.001		-0.32	0.024	
SEN1037	STM1972	*fliI*	flagellum-specific ATP synthase	-0.14	0.367		-0.20	0.059		-0.67	0.008		-1.99	0.000		-0.71	0.000		-0.66	0.000	
SEN1033	STM1976	*fliM*	flagellar biosynthesis, component of motor switch and energizing	-0.04	0.657		-0.36	0.010		-0.28	0.141		-1.05	0.001		-0.34	0.049		-0.56	0.000	
SEN1030	STM1979	*fliP*	flagellar biosynthesis	0.00	0.969		-0.55	0.033		0.02	0.855		-1.17	0.000		-0.01	0.971		-1.03	0.000	
SEN2353	STM2371	*flk*	Couples flagellar P- and L-ring assembly to flagellar morphogenesis	-0.07	0.490		-0.39	0.018		-0.17	0.236		-0.93	0.003		-0.64	0.003		-1.03	0.000	
R. Protein fate																					
SEN0137	STM0136	*secA*	preprotein translocase; secretion protein of IISP family	-0.63	0.001		-0.84	0.002		-0.15	0.196		-1.14	0.000		-0.43	0.070		-1.16	0.000	
SEN0390	STM0407	*secD*	preprotein translocase, IISP family, part of the channel	-0.82	0.000		-0.98	0.000		-0.76	0.000		-1.41	0.000		-0.97	0.000		-1.88	0.000	
SEN0391	STM0408	*secF*	preprotein translocase, IISP family, membrane subunit	-0.74	0.000		-0.30	0.029		-1.18	0.000		-1.60	0.000		-0.90	0.000		-0.46	0.001	
SEN3126	STM3293	*secG*	preprotein translocase IISP family	-0.63	0.002		-1.29	0.000		-0.32	0.041		-1.16	0.000		-0.71	0.000		-1.57	0.000	
SEN3248	STM3420	*secY*	preprotein translocase of IISP family, membrane subunit	-0.95	0.001	-0.86	0.11	0.197	-0.62	-2.00	0.001	-6.12	-2.57	0.000	-6.92	0.12	0.213	-2.04	0.04	0.777	-0.20
S. Pathogenicity																					
SEN2624	STM2780		homologue of pipB, putative pentapeptide repeats (8 copies)	0.58	0.001	-0.93	0.12	0.306	-1.40	2.30	0.000	2.60	3.04	0.000	2.42	0.15	0.369	-0.39	0.36	0.347	-0.27
SEN2707	STM2865	*avrA*	putative inner membrane protein	0.28	0.047		0.28	0.097		0.82	0.010		2.09	0.000		0.36	0.045		0.50	0.000	
SEN3584	STM3762	*cigR*	putative inner membrane protein	0.77	0.001		1.22	0.000		1.25	0.000		2.57	0.000		1.81	0.000		2.75	0.000	
SEN2718	STM2876	*hilA*	invasion genes transcription activator	0.15	0.326		0.03	0.799		-0.33	0.019		-0.04	0.839		0.42	0.038		-0.23	0.007	
SEN2709	STM2867	*hilC*	bacterial regulatory helix-turn-helix proteins, araC family	0.48	0.005		0.14	0.394		1.33	0.000		0.36	0.031		1.01	0.004		0.00	0.001	
SEN2626	STM2782	*mig-14*	putative transcription activator	0.69	0.041		-0.09	0.670		3.19	0.000		2.40	0.000		-0.02	0.858		-0.17	0.000	
SEN1656	STM1389	*orf319*	putative inner membrane protein	1.09	0.000		0.35	0.002		2.43	0.000		1.90	0.000		0.96	0.001		1.58	0.000	
SEN0951	STM1087	*pipA*	Pathogenicity island encoded protein: SPI3	0.20	0.178		-0.01	0.956		0.32	0.236		1.00	0.000		0.24	0.062		0.48	0.376	
SEN0952	STM1088	*pipB*	Pathogenicity island encoded protein: SPI3	-0.04	0.782		-0.03	0.868		0.07	0.699		-0.04	0.790		-0.24	0.255		0.20	0.125	
SEN2253	STM2271	*rcsC*	sensory histidine kinase in two-component regulatory system	-0.03	0.770		-0.39	0.051		-0.30	0.076		-0.54	0.004		-0.38	0.023		-0.61	0.001	
SEN2723	STM2882	*sipA*	cell invasion protein	0.02	0.852	-0.77	0.23	0.031	-2.43	-0.20	0.135	-1.07	-0.17	0.328	-1.64	1.55	0.001	-1.21	0.20	0.133	-2.43
SEN2726	STM2885	*sipB*	cell invasion protein	0.07	0.471	0.51	0.23	0.075	-1.74	-0.20	0.317	-0.43	-0.14	0.304	-1.55	1.67	0.001	0.16	0.13	0.219	-1.31
SEN2725	STM2884	*sipC*	cell invasion protein	-0.01	0.895		0.10	0.512		-0.20	0.094		-0.33	0.038		1.28	0.019		0.40	0.007	
SEN2724	STM2883	*sipD*	cell invasion protein	-0.06	0.562		0.11	0.318		-0.05	0.784		-0.04	0.800		1.68	0.002		-0.07	0.499	
SEN2703	STM2861	*sitA*	Salmonella iron transporter: fur regulated	0.74	0.025	4.76	1.27	0.000	6.20	0.41	0.020	2.00	2.15	0.001	2.32	0.81	0.008	3.61	2.19	0.980	4.95
SEN2704	STM2862	*sitB*	Salmonella iron transporter: fur regulated	0.42	0.020		1.09	0.000		0.44	0.007		1.42	0.007		0.28	0.191		1.18	0.026	
SEN2705	STM2863	*sitC*	Salmonella iron transporter: fur regulated	0.07	0.384		0.21	0.106		0.05	0.684		0.77	0.017		0.19	0.262		0.32	0.000	
SEN2706	STM2864	*sitD*	Salmonella iron transporter: fur regulated	0.09	0.382		0.01	0.934		0.10	0.578		0.63	0.020		0.39	0.039		0.15	0.000	
SEN3583	STM3761	*slsA*	putative inner membrane protein	0.41	0.039		0.68	0.015		0.26	0.214		3.20	0.000		0.70	0.001		1.32	0.000	
SEN0848	STM0940	*somA (ybjX)*	homologue of virK	-0.92	0.000		-0.65	0.001		-0.63	0.000		-0.76	0.066		-1.25	0.000		-1.70	0.006	
SEN2625	STM2781	*virK*	virulence gene; homologous sequence to virK in Shigella	1.23	0.022		0.41	0.362		3.22	0.000		3.58	0.000		0.22	0.046		0.59	0.257	
T. Cofactor biosynthesis																					
SEN0748	STM0802	moaA	molybdopterin biosynthesis, protein A	-0.37	0.044		-0.35	0.071		-0.74	0.004		-0.93	0.000		1.20	0.001		0.08	0.768	
SEN0749	STM0803	moaB	molybdopterin biosynthesis, protein B	0.07	0.644		0.64	0.000		-0.48	0.031		0.15	0.476		1.72	0.000		2.42	0.000	
SEN0750	STM0804	moaC	molybdopterin biosynthesis, protein C	0.00	0.978		0.18	0.201		-0.53	0.062		-0.46	0.026		1.36	0.001		1.90	0.000	
SEN0752	STM0806	moaE	molybdopterin converting factor, subunit 2	-0.21	0.105		-0.07	0.563		-0.56	0.015		-0.04	0.813		1.03	0.002		1.68	0.000	
SEN0751	STM0805	moaD	molybdopterin biosynthesis protein	-0.25	0.062		0.04	0.724		-0.54	0.008		-0.30	0.073		0.60	0.057		1.17	0.001	
SEN3782	STM3993	mobB	molybdopterin-guanine dinucleotide biosynthesis protein B	0.46	0.016		0.66	0.001		0.70	0.001		0.94	0.001		0.91	0.000		1.20	0.000	
SEN3783	STM3994	mobA	putative molybdopterin-guanine dinucleotide biosynthesis protein	0.13	0.324		0.57	0.004		0.60	0.004		1.18	0.000		1.03	0.000		1.46	0.000	

U. Transcription

SEN3243	STM3415	*rpoA*	RNA polymerase, alpha subunit	-0.89	0.001	-0.03	0.749	-1.57	0.000	-1.96	0.000	-0.26	0.071	-0.12	0.397
SEN3937	STM4153	*rpoB*	RNA polymerase, beta subunit	-0.68	0.000	0.00	0.983	-1.43	0.000	-1.58	0.000	-0.58	0.000	-0.28	0.001
SEN3938	STM4154	*rpoC*	RNA polymerase, beta prime subunit	0.00	0.967	0.42	0.001	-1.27	0.000	-0.69	0.003	0.15	0.143	0.24	0.043

[1] Empty cells indicate that no locus is present or that no gene designation has been assigned

[2] Framed numbers are significant (2-fold up- or down-regulated; p<0.001)

[3] Framed numbers are significant (2-fold up- or down-regulated;....)

Supplementary Table 3. Relative mRNA Levels Determined by Quantitative Polymerase Chain Reaction (qPCR)[1]

Gene or locus	*Ent 7*[2]	*Ent 4.5*	*Ent 5.5*	*Ent Ac*	*Ken 7*	*Ken 4.5*	*Ken 5.5*	*Ken Ac*
adhE	5903^{bc}	4359^{bc}	389^{c}	8264^{ab}	13667^{a}	3153^{bc}	525^{c}	2910^{bc}
adiA	10^{bc}	4^{c}	17^{b}	4^{b}	28^{a}	5^{b}	16^{b}	9^{b}
aspA	1384^{b}	751^{b}	78^{b}	1268^{b}	4923^{a}	1529^{b}	301^{b}	826^{b}
cadA	259^{c}	201^{c}	5835^{b}	827^{c}	927^{c}	151^{c}	7807^{a}	478^{c}
cadB	119^{c}	2185^{b}	5578^{a}	2520^{b}	755^{bc}	1571^{bc}	4666^{a}	1629^{bc}
citD	174^{b}	12^{b}	7^{b}	24^{b}	3728^{a}	98^{b}	27^{b}	74^{b}
citF	484^{b}	16^{b}	9^{b}	91^{b}	2390^{a}	63^{b}	54^{b}	94^{b}
clpB	341^{b}	2848^{a}	474^{b}	1016^{ab}	570^{b}	950^{ab}	376^{b}	440^{b}
cyoA	954^{a}	486^{a}	643^{a}	389^{a}	35^{a}	712^{a}	543^{a}	720^{a}
dcuA	575^{b}	316^{b}	44^{b}	311^{b}	2016^{a}	328^{b}	168^{b}	174^{b}
dmsA	499^{ab}	140^{b}	18^{b}	467^{b}	1085^{a}	139^{b}	52^{b}	99^{b}
fdhF	105^{ab}	48^{b}	15^{b}	40^{b}	231^{a}	33^{b}	24^{b}	21^{b}
fimC	291^{b}	67^{d}	120^{cd}	48^{d}	511^{a}	67^{d}	175^{c}	78^{cd}
fimD	145^{b}	12^{c}	49^{c}	6^{c}	337^{a}	19^{c}	64^{bc}	25^{c}
flgD	2090^{b}	426^{b}	240^{b}	278^{b}	5785^{a}	2070^{b}	394^{b}	1755^{b}
fliG	739^{b}	133^{b}	78^{b}	55^{b}	2061^{a}	279^{b}	134^{b}	401^{b}
glum	1161^{a}	348^{b}	510^{b}	263^{b}	1111^{a}	195^{b}	428^{b}	418^{b}
gltA	95^{c}	342^{b}	681^{a}	163^{bc}	61^{c}	213^{bc}	572^{a}	168^{bc}
guaB	1671^{b}	262^{c}	86^{c}	93^{c}	5035^{a}	748^{bc}	259^{c}	1063^{bc}
hypB	2689^{ab}	840^{b}	241^{b}	2288^{ab}	5116^{a}	902^{b}	361^{b}	649^{b}
hypO	590^{b}	201^{c}	35^{c}	81^{c}	1987^{a}	120^{c}	52^{c}	68^{c}
katG	184^{ab}	99^{ab}	43^{b}	219^{a}	222^{a}	85^{ab}	184^{ab}	36^{b}
malT	0.1^{a}	0.2^{a}	0.03^{a}	0.06^{a}	2^{a}	0.3^{a}	0.3^{a}	3^{a}
narG	13456^{a}	4778^{a}	780^{a}	13540^{a}	14301^{a}	4351^{a}	1104^{a}	3937^{a}
oppD	303^{b}	219^{bc}	872^{a}	205^{bc}	96^{cd}	28^{d}	151^{cd}	33^{d}
osmC	46^{b}	91^{b}	541^{a}	145^{b}	49^{b}	35^{b}	519^{a}	33^{b}
pitA	367^{ab}	87^{c}	21^{c}	19^{c}	455^{a}	97^{c}	32^{c}	213^{bc}
priB	39426^{a}	6471^{bc}	632^{c}	2672^{bc}	41909^{a}	14715^{abc}	801^{bc}	29586^{ab}
rplC	117453^{a}	18760^{b}	907^{b}	11495^{b}	74449^{ab}	15563^{b}	4915^{b}	24311^{b}
rpoN	754^{b}	76^{b}	404^{b}	161^{b}	1989^{a}	79^{b}	425^{b}	223^{b}
rpoS	2094^{b}	5488^{b}	12800^{a}	7204^{ab}	1945^{b}	4252^{b}	7510^{ab}	3949^{b}
rpsC	21608^{ab}	18327^{b}	647^{d}	7348^{cd}	29636^{a}	16418^{bc}	1275^{d}	16899^{bc}
secY	9597^{a}	5270^{b}	138^{d}	2328^{c}	363^{d}	237^{d}	3^{d}	316^{d}
SEN1493	183^{b}	241^{b}	741^{a}	246^{b}	21^{b}	13^{b}	13^{b}	15^{b}
sipA	337^{a}	198^{b}	160^{b}	146^{bc}	81^{cd}	15^{d}	26^{d}	15^{d}
sipB	434^{bc}	620^{a}	322^{c}	494^{ab}	47^{d}	14^{d}	16^{d}	19^{d}
sitA	19^{c}	516^{a}	76^{c}	232^{bc}	6^{c}	442^{ab}	30^{c}	186^{c}
sopB	658^{a}	419^{b}	313^{c}	201^{d}	16^{e}	21^{e}	7^{e}	5^{e}
spy	11^{b}	38^{b}	70^{ab}	13^{b}	25^{b}	58^{b}	161^{a}	54^{b}
SEN0629	55^{bc}	38^{bc}	13^{c}	21^{c}	329^{a}	101^{b}	20^{c}	47^{bc}
SEN1821	84^{b}	27^{b}	14^{b}	15^{b}	224^{a}	11^{b}	18^{b}	9^{b}
SEN1800	8^{b}	18^{b}	10^{b}	10^{b}	44^{b}	187^{a}	93^{ab}	166^{a}
SEN1796	5929^{a}	309^{a}	54^{a}	194^{a}	1688^{a}	217^{a}	108^{a}	142^{a}
SEN1795	299^{b}	29^{b}	7^{b}	24^{b}	1247^{a}	39^{b}	9^{b}	26^{b}
SEN1793	1779^{b}	25^{b}	37^{b}	85^{b}	590^{a}	33^{b}	17^{b}	21^{b}
STM1485[3]	10^{c}	119^{b}	29^{c}	11^{c}	22^{c}	152^{a}	30^{c}	26^{c}
SEN1242	72^{c}	229^{c}	286^{bc}	157^{c}	87^{c}	543^{ab}	567^{a}	564^{a}
SEN2343	92^{ab}	142^{ab}	23^{b}	159^{ab}	255^{a}	267^{a}	44^{b}	154^{ab}
SEN2624	21^{b}	11^{b}	127^{a}	16^{b}	29^{b}	11^{b}	155^{a}	24^{b}
SEN2977	16^{ab}	45^{a}	6^{b}	32^{ab}	13^{b}	32^{ab}	11^{b}	14^{b}
SEN3609	25^{ab}	19^{ab}	6^{b}	16^{b}	40^{a}	23^{ab}	17^{ab}	14^{b}
SEN3651	159^{b}	203^{b}	97^{b}	131^{b}	568^{a}	251^{b}	101^{b}	216^{b}
SEN3847	34^{bc}	29^{bc}	21^{c}	19^{c}	60^{a}	34^{bc}	48^{ab}	29^{bc}
SEN3894	9^{ab}	5^{b}	4^{b}	3^{b}	14^{a}	4^{b}	10^{ab}	5^{b}
SEN4029	76^{a}	50^{ab}	26^{bcd}	44^{bc}	13^{cd}	5^{d}	8^{d}	6^{d}
suhB	5757^{a}	82^{c}	81^{c}	80^{c}	3543^{b}	150^{c}	93^{c}	493^{c}
treB	586^{b}	237^{b}	32^{b}	112^{b}	4409^{a}	677^{b}	137^{b}	983^{b}
uvrC	51^{a}	10^{bc}	24^{bc}	7^{c}	51^{a}	12^{bc}	29^{b}	6^{c}

[1]The mRNA levels are relative to those of *thrA*, which were arbitrarily set at 100. Values are averages of three measurements. Superscripts that are different in each row indicate that the values are different (95% confidence level).

[2]Ent, Enteritidis Nal^{R}; Ken, Kentucky 3795. 7 indicates the pH of the TSB medium. 4.5 and 5.5 indicate the pH of the TSB medium after addition of HCl. Ac indicates the addition of acetic acid to achieve a pH of 5.5.

[3]While for all other genes, the assumption was made that amplification efficiency was the same for Enteritidis Nal^{R} and Kentucky 3795, and therefore statistical differences were determined across the treatments of both isolates, this assumption could not be made for locus STM1485 since different primers had to be used for qPCR of this locus. Thus, the superscript designations only apply to the columns for Enteritidis Nal^{R} and Kentucky 3795, respectively.