

## SUPPLEMENTARY MATERIAL

### Deep sequencing analysis of small noncoding RNA and mRNA targets of the global post-transcriptional regulator, Hfq

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## SUPPLEMENTARY MATERIALS AND METHODS

### *Analysis and visualization of pyrosequencing results*

After 5' end linker and polyA-tail clipping from the initial pyrosequencing results, all inserts  $\geq 18$  nt of the Hfq coIP and control coIP libraries were separately mapped to the *Salmonella* LT2 genome (NC\_003197.fna) using WU-BLAST (<http://blast.wustl.edu/>). From the resulting blast positions one graph for each strand of the *Salmonella* chromosome was calculated, where the number of cDNA hits for each nucleotide position was plotted. To compare the graphs of the Hfq coIP and control coIP, the graphs were normalized to number of blastable reads. Following upload of the *Salmonella* genome sequence and annotation (NC\_003197.fna and NC\_003197.gff), the two graphs for each library were loaded into the Integrated Genome Browser (IGB) of Affymetrix ([http://www.affymetrix.com/support/developer/tools/download\\_igb.aff](http://www.affymetrix.com/support/developer/tools/download_igb.aff), version IGB-4.56). Different panels show the annotations for the "+" and "-" strand (blue), the graphs for the "+" and "-" strand of the Hfq coIP (red) and the control coIP (black), and the genome coordinates in the center. A specific genomic region can be selected for further analysis (e.g. SPI-1, Fig. 4).

SPI-1 represents an example of an entire genomic region highly enriched in the Hfq coIP library. In contrast, very few cDNA sequences mapping to SPI-1 are contained in the control coIP library. The flanking genes of *invR* (i.e. the border of SPI-1) nicely give an example of the specificity of the method (Fig. 4). While cDNAs mapping to the *InvR* sRNA gene represent the most abundant cluster in the Hfq coIP library, the genes in the closest proximity are barely represented in this library. In addition, the example of *InvR* underlines the reliability of the method to identify Hfq-dependent sRNAs.

The numbers of cDNA clones that overlap *Salmonella* sRNA genes or annotated ORFs are listed in Table S3 (sRNAs) and S4 (mRNAs). Comparing the numbers of cDNAs obtained for the Hfq coIP *vs.* control coIP, false positive sequences in the list of cDNAs of Hfq-bound RNAs were easily detected (see CsrB and CsrC, Table S3), based on the number of sequences received from the control

coIP. In those cases the number of sequences was almost identical in the Hfq coIP and the control coIP libraries (note that the numbers are not normalized to the number of blastable reads.) While Table S3 and S4 only present absolute numbers of sequences, which map along an entire RNA transcript, it is necessary to analyze a gene of interest in detail. The ratio of hits per nucleotide of the Hfq coIP to hits from the control coIP provides a measure of enrichment, which can be visualized for every single nucleotide in a stepstair diagram. In the case of *ompD*, the number of cDNAs obtained in the Hfq coIP library (246) compared to those of control coIP library (76) lead to an overall enrichment factor of 3.3. Analysis of the single cDNA sequences over the entire transcript length reveals single “hot spots” in the transcript bound by Hfq, leading to enrichment factors up to 30 (for the region spanning the ATG start codon; Fig. 7A). However, the number of *ompA* cDNA sequences received in Hfq coIP (102) vs. control coIP (77) only lead to an overall enrichment factor of 1.3. At first glance, this would lead one to assume that *ompA* is not an Hfq-bound mRNA. However, closer inspection of the clone distribution along the entire mRNA, and of the enrichment of certain parts of the mRNA, reveals that the 5' region (around ATG start codon) and a central region are highly enriched in the Hfq coIP (up to 12-fold; Fig. 7B)). Such detailed inspection offers the advantage of being able to analyze the 5'/3' UTRs of mRNAs, which are not included in Table S4, but are known to be often bound by Hfq.

#### *Quantitative RT-PCR*

The wild-type strain SL1344 and JVS-0255 ( $\Delta hfq$ ) were grown in liquid culture from single colonies to an OD<sub>600</sub> of 2 or for 12 hours under SPI-1 inducing conditions, respectively. Experiments were carried out as described previously [1]. Briefly, RNA was isolated using the SV40 Total RNA Isolation kit (Promega) according to manufacturer's instructions. Expression of *rpoE*, *degP*, and *rpoS* mRNA was quantitatively assessed by qRT-PCR in a 7900HT (Applied Biosystems), with the *rfaH* gene as reference. For each reaction (25 $\mu$ L final vol.) 1 $\mu$ L of RNA sample (100 ng/reaction) were mixed with 0.25 $\mu$ L of primer pairs (0.5  $\mu$ M final) and 12.5  $\mu$ L of SYBR Green mix (Qiagen). For coupled cDNA synthesis and target gene amplification

0.25µl of Quantitect RT mix was added. Each sample was assayed in triplicate for each run. Control RNA from wild-type cells was used to construct a standard curve for all inspected genes. Reaction conditions were: 30 min 50°C, 15 min 95°C, and 45 cycles at 94°C for 20 sec, 60°C for 40 sec, and 72°C for 40 sec. Oligodeoxynucleotides used in this experiment (JVO-1234/1235 (*degP*), JVO-1117/1118 (*rfaH*), JVO-1236/1237 (*rpoE*), JVO-1342/1343 (*rpoS*)) are listed in Table S6.

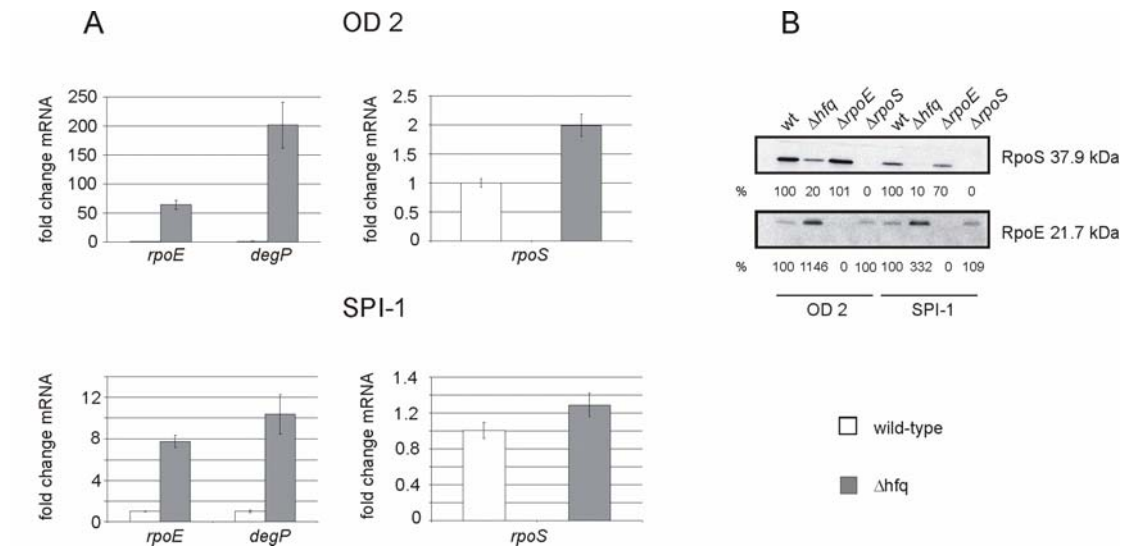
#### *Western blot*

Cultures were inoculated into fresh medium 1/100 from o/n cultures. Incubation was carried out under standard conditions to early stationary phase (OD<sub>600</sub> of 2) or for 12 hours under SPI-1 inducing condition, respectively. Whole cell proteins were resolved by 12 % SDS PAGE and transferred to a PVDF membrane. Sigma proteins were detected using monoclonal antibodies against RpoE or RpoS, respectively (Neoclone).

#### *Northern analysis*

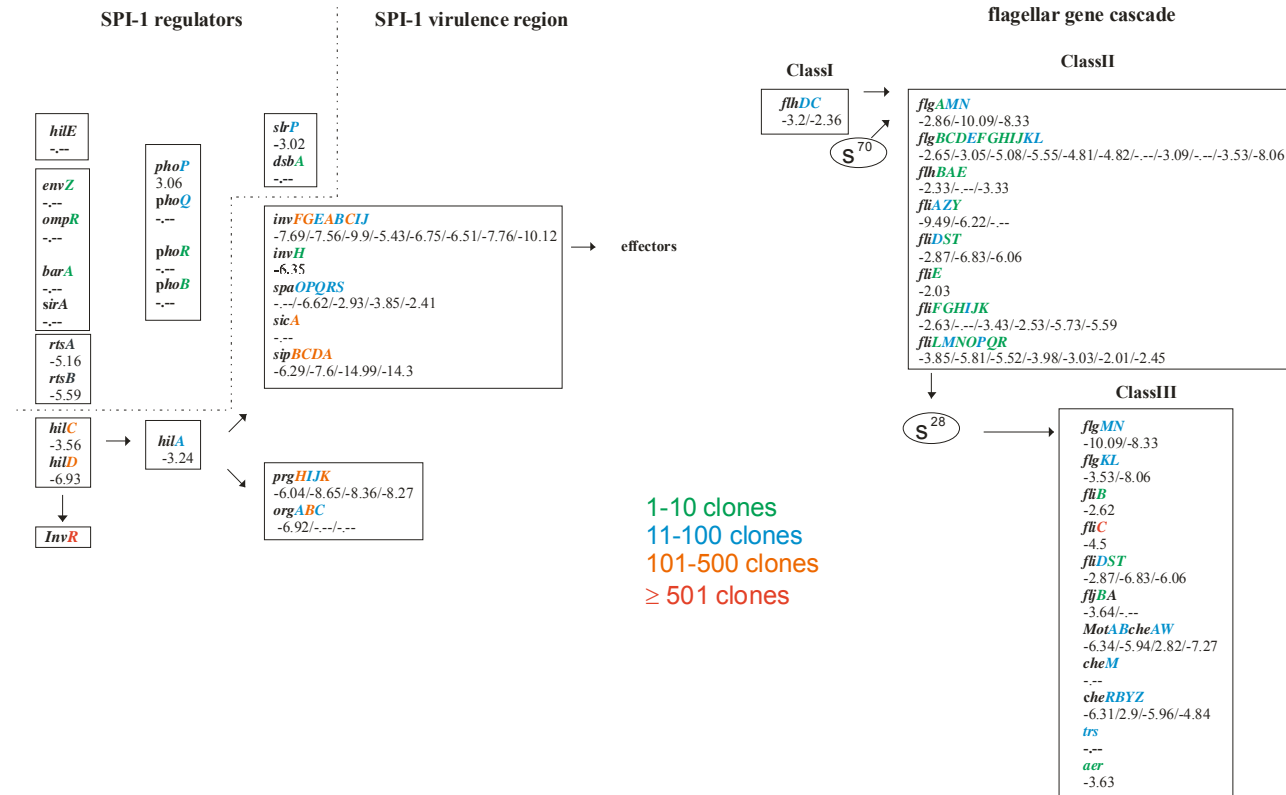
Cultures were inoculated into fresh medium 1/100 from o/n cultures. Incubation was carried out under standard conditions to logarithmic phase. RNA was extracted using TRIzol Reagent. For detailed protocol see [2].

**Figure S1**



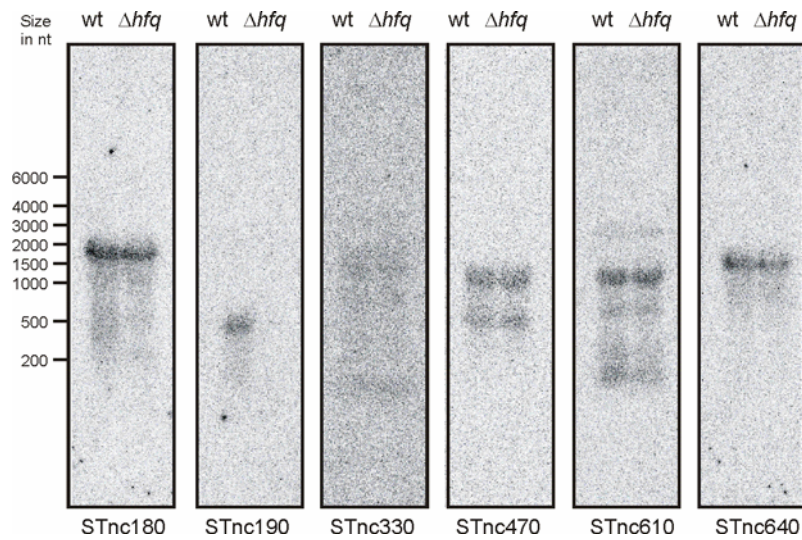
**Expression levels of RpoE and RpoS in wild-type and  $\Delta hfq$  cells.** Samples were taken from wild-type and  $\Delta hfq$  strains grown under standard conditions to early stationary phase (OD<sub>600</sub> of 2) or for 12 hours under SPI-1 inducing condition, respectively. (A) Analysis of mRNA level by real time PCR for *rpoE*, *degP*, and *rpoS* mRNA. (B) Whole cell proteins were separated by 12% SDS PAGE and sigma factors detected via Western blot. Expression levels of each protein were determined by densitometry and are given as a percentage of the wild-type level of expression below each gel.

Figure S2



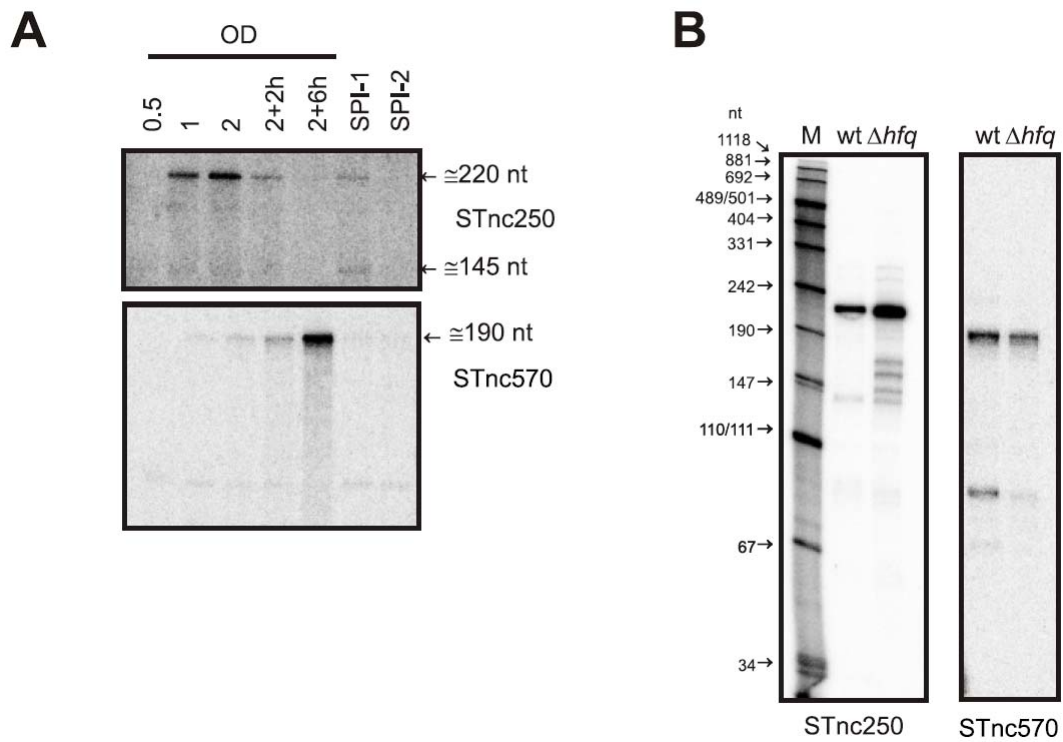
**Hfq binds significantly to a few but not all mRNAs of the SPI-1 and the flagellar regulon.** Shown are all genes belonging to the SPI-1 and the flagellar regulon. The level of Hfq-dependent gene regulation is shown as fold change below each gene (taken from the transcriptomic dataset; Table S1). Representation of cDNAs in pyrosequencing is indicated by different colours (green: 1-10 clones, turquoise: 11-100 clones, orange: 101-500 clones, magenta: ≥501 clones).

**Figure S3**



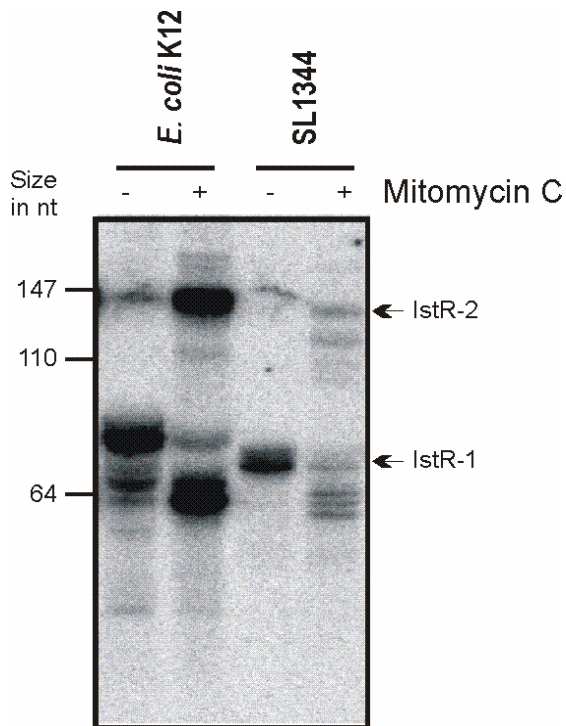
**Northern detection of Hfq bound mRNAs** Total RNA was isolated from *Salmonella* at  $OD_{600}$  of 2. Northern blots based on agarose gel for detection of long transcripts showing the detection of six mRNAs.

**Figure S4**



**Expression levels of small peptide encoding mRNAs in *Salmonella*.** RNA samples were either taken from wild-type or *hfq* mutant *Salmonella* at different growth stages (as in Fig. 6 in the main manuscript), and probed for STnc250 and STnc570 over growth (**A**) or at early stationary phase (**B**).

**Figure S5**



**Expression of *IstR-1* and *IstR-2* in *Salmonella*.** Northern analysis of *istR* transcripts. Total RNA was extracted from of *E. coli* K12 and *Salmonella* Typhimurium SL1344 cells grown to an OD600 of 2, exposed to Mitomycin C (0.5  $\mu\text{g/ml}$ ) for 30 min as described by [2]. Length is indicated according to marker sizes in nt. Full-length *IstR-1* and *IstR-2* are indicated by arrows.

**Table S1: Deregulated genes in *Δhfq* at ESP**

Gene name <sup>a</sup>	Fold change	Product <sup>b</sup>	2D-analysis <sup>c</sup>	HGT <sup>d</sup>	coIP on ChIP	cDNA coverage
ybfM	231,48	putative outer membrane protein	X		X	X
ybfN	179,86	putative lipoprotein				X
napC	48,08	periplasmic nitrate reductase, cytochrome c-type protein				
htrA	41,15	periplasmic serine protease Do, heat shock protein	X			
napG	39,68	ferredoxin-type protein: electron transfer				
napH	35,84	ferredoxin-type protein: electron transfer				
napF	29,5	ferredoxin-type protein: electron transfer				X
rseA	27,32	anti sigma E (sigma 24) factor, negative regulator				
yraP	24,75	paral putative periplasmic protein	X			
napB	19,12	periplasmic nitrate reductase, small subunit, cytochrome C550, in complex with NapA				
aphA	18,55	non-specific acid phosphatase/phosphotransferase, class B	X		X	X
narP	18,42	response regulator in two-component regulatory system with NarQ (or NarX)			X	X
yfaZ	17,7	putative inner membrane protein			X	
yhjW	17,18	putative membrane-associated, metal-dependent hydrolase			X	
napD	17,04	periplasmic nitrate reductase				
cysA	15,48	ABC superfamily (atp_bind), sulfate permease A protein; chromate resistance				
STM1253	15,41	putative inner membrane protein		X		
ycbK	14,22	putative outer membrane protein				
nrfA	13,64	nitrite reductase periplasmic cytochrome c(552)				
rpoE	12,76	sigma E (sigma 24 ) factor of RNA polymerase, response to periplasmic stress				X
tpx	12,41	thiol peroxidase	X			X
ygiM	11,93	putative SH3 domain protein				
yraO	11,78	putative phosphoheptose isomerase				
nrfD	11,55	putative nitrate reductase, formate dependent				
yfiO	10,88	putative lipoprotein				
cysD	10,65	ATP-sulfurylase, subunit 1 (ATP:sulfate adenyllyltransferase)				
yiaD	10,55	putative outer membrane lipoprotein	X			
glnH	10,27	ABC superfamily (bind_prot), glutamine high-affinity transporter	X		X	
rseB	9,9	anti sigma E (sigma 24) factor, negative regulator				X
nrfB	9,26	formate-dependent nitrite reductase; a penta-haeme cytochrome c				
phnA	8,93	putative alkylphosphonate uptake protein in phosphonate metabolism			X	
yggN	8,93	putative periplasmic protein			X	X
cysW	8	ABC superfamily (membrane), thiosulfate permease W protein				
citA	7,87	citrate-proton symporter				
cysP	7,69	ABC superfamily (bind_prot), thiosulfate transport protein	X			
ydjN	7,63	part of a kinase, putative domain shared with transporter				
ccmG	7,58	heme lyase disulfide oxidoreductase, cytochrome c-type biogenesis		X		
ygiU	7,58	putative dicarboxylate permease			X	X
yaeT	7,25	putative outer membrane antigen	X			X
ansB	7,09	periplasmic L-asparaginase II			X	X
rfaK	7,04	putative hexose transferase, lipopolysaccharide core biosynthesis		X	X	
dctA	6,76	DAACS family, C4-dicarboxylic acids transport protein				X
dppA	6,49	ABC superfamily (peri_perm), dipeptide transport protein	X		X	X
oppA	6,45	ABC superfamily (periplasm), oligopeptide transport protein with chaperone properties	X		X	X
STM2447	6,37	putative outer membrane lipoprotein				
lrfA	6,33	NADH dehydrogenase transcriptional repressor (LysR family)			X	X
ccmF	6,21	cytochrome c-type biogenesis protein		X		
cysI	6,21	sulfite reductase, alpha subunit, NADPH dependent				
gcvH	6,06	glycine cleavage complex protein H, carrier of aminomethyl moiety via covalently bound lipoyl cofactor				X
ycbL	5,85	putative Metallo-beta-lactamase				
yhjG	5,81	putative inner membrane protein				
stdA	5,78	putative fimbrial-like protein		X	X	
STM1539	5,75	putative hydrogenase-1 small subunit				
rplD	5,68	50S ribosomal subunit protein L4, regulates expression of S10 operon				X
sdaC	5,65	putative HAAAP family, serine transport protein			X	
nlpB	5,59	lipoprotein-34	X			
hlpA	5,52	histone-like protein, located in outer membrane				
STM1255	5,38	putative ABC transporter periplasmic binding protein				
rpsG	5,35	30S ribosomal subunit protein S7, initiates assembly				
yhjJ	5,35	putative Zn-dependent peptidase				
rplW	5,05	50S ribosomal subunit protein L23				
STM4351	5,05	putative arginine-binding periplasmic protein				
nrfC	5	putative nitrite reductase; formate-dependent, Fe-S centers				
rplB	4,83	50S ribosomal subunit protein L2				
STM4466	4,76	putative carbamate kinase				

cysK	4,69	subunit of cysteine synthase A and O-acetylserine sulfhydrylase A				
yfgD	4,61	putative arsenate reductase				
mgIB	4,52	ABC superfamily (peri_perm), galactose transport protein	X			X
nrfE	4,52	formate-dependent nitrite reductase; involved in attachment of haem c to cytochrome c552				
STM4195	4,52	putative Na <sup>+</sup> -dependent transporter				
ushA	4,52	UDP-sugar hydrolase 5'-nucleotidase			X	X
yijD	4,41	putative inner membrane protein				
rseC	4,39	regulator of sigma E (sigma 24) factor				
STM4465	4,31	putative ornithine carbamoyltransferase				
cspD	4,27	similar to CspA but not cold shock induced	X			X
cutC	4,24	copper homeostasis protein			X	X
STM0509	4,24	putative outer membrane protein				
STM0719	4,18	putative UDP-galactopyranose mutase		X		
rbsB	4,17	ABC superfamily (peri_perm), D-ribose transport protein	X		X	X
gdhA	4,1	glutamate dehydrogenase, NADP-specific				
yabJ	4,07	putative ABC-transport protein			X	
gcvT	4,03	glycine cleavage complex protein T, aminomethyltransferase, tetrahydrofolate-dependent				X
cysN	4	ATP-sulfurylase, subunit 1 (ATP:sulfate adenyltransferase)				
hflK	3,94	with HflC, part of modulator for protease specific for FtsH phage lambda cII repressor				
STM1747	3,94	putative inner membrane protein			X	
cycA	3,89	APC family, D-alanine/D-serine/glycine transport protein				
pal	3,88	tol protein required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA to cytoplasm	X			X
ybhQ	3,77	putative inner membrane protein				X
glpT	3,76	MFS family, sn-glycerol-3-phosphate transport protein				X
purC	3,75	phosphoribosylaminoimidazole-succinocarboxamide synthetase (SAICAR synthetase)				
STM1538	3,73	putative hydrogenase-1 large subunit				
rpsC	3,72	30S ribosomal subunit protein S3				X
rplV	3,7	50S ribosomal subunit protein L22				
STM4276	3,65	putative cytoplasmic protein				
ddg	3,64	cold shock-induced palmitoleoyl transferase				
glpQ	3,64	glycerophosphodiester phosphodiesterase, periplasmic	X			X
livK	3,62	ABC superfamily (bind_prot), branched-chain amino acid transporter, high-affinity				
tsx	3,62	nucleoside channel; receptor of phage T6 and colicin K				
rplC	3,6	50S ribosomal subunit protein L3	X			X
ndk	3,58	nucleoside diphosphate kinase				X
PSLT103	3,58					
gcvP	3,57	glycine cleavage complex protein P, glycine decarboxylase				X
hflC	3,55	with HflK, part of modulator for protease specific for FtsH phage lambda cII repressor				
STM2494	3,55	putative inner membrane or exported	X			X
rplP	3,52	50S ribosomal subunit protein L16				
STM3169	3,5	putative dicarboxylate-binding periplasmic protein				
tig	3,5	peptidyl-prolyl cis/trans isomerase, trigger factor; a molecular chaperone involved in cell division				
cysC	3,48	adenosine 5'-phosphosulfate kinase				
cpxP	3,45	periplasmic repressor of cpx regulon by interaction with CpxA, rescue from transitory stresses			X	X
cca	3,42	tRNA nucleotidyl transferase				
yglL	3,4	putative serine/threonine protein kinase				X
rpsS	3,39	30S ribosomal subunit protein S19				X
STM2238	3,39	putative phage protein			X	
rfbP	3,36	LPS side chain defect: bifunctional enzyme: undecaprenol-phosphate galactosephosphotransferase, and O-antigen transfer		X	X	X
ibpB	3,33	small heat shock protein				X
ptr	3,32	protease III	X			
ytfJ	3,32	putative transcriptional regulator			X	
PSLT066	3,31					
ompF	3,29	outer membrane protein 1a (ia;b;f), porin	X			X
STM3170	3,28	putative inner membrane protein				
STM4467	3,26	putative arginine deiminase				
ycfS	3,26	putative periplasmic protein				
mreB	3,23	rod shape-determining protein; HSP70 class molecular chaperones involved in cell morphogenesis				
mod	3,18	DNA methylase; restriction system				
mgTA	3,16	P-type ATPase, Mg <sup>2+</sup> ATPase transporter				
mgIA	3,15	ABC superfamily (atp_bind), galactose (methyl-galactoside) transport protein			X	X
slp	3,14	putative outer membrane protein				
rplN	3,12	50S ribosomal subunit protein L14				X
oppB	3,05	ABC superfamily (membrane), oligopeptide transport protein				X
sixA	3,04	phosphohistidine phosphatase				
fadD	2,94	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)			X	
pyrI	2,94	aspartate carbamoyltransferase, regulatory subunit (allosteric regulation)				
ycfR	2,94	putative outer membrane protein				
lrp	2,92	regulator for lrp regulon and high-affinity branched-chain amino acid			X	X

		transport system; mediator of of leucine response (AsnC family)			
rplF	2,87	50S ribosomal subunit protein L6			
STM2747	2,87	putative cytoplasmic protein	X	X	
mgIC	2,86	ABC superfamily (membrane), methyl-galactoside transport protein		X	
ydgH	2,86	putative periplasmic protein			
STM2746	2,85	putative Excinuclease ATPase subunit	X	X	
rplX	2,83	50S ribosomal subunit protein L24			
cysM	2,82	cysteine synthase B (O-acetylserine sulfhydrylase B)			
rpmC	2,82	50S ribosomal subunit protein L29			
STM0906	2,82	Fels-1 prophage	X		
glpF	2,81	MIP channel, glycerol diffusion		X	X
STM4305	2,79	putative anaerobic dimethyl sulfoxide reductase, subunit A			X
STM1368	2,78	putative Na <sup>+</sup> -dicarboxylate symporter			
yfgM	2,76	putative inner membrane protein			
agp	2,69	glucose-1-phosphatase			
priB	2,69	primosomal replication protein N			X
pyrB	2,68	aspartate carbamoyltransferase, catalytic subunit			
yaeL	2,67	putative membrane-associated Zn-dependent protease			
STM1256	2,65	putative ABC transporter			
hflX	2,64	putative GTP-ase, together with HflCK possibly involved in phage lambda cII repressor stability		X	X
STM1250	2,64	putative cytoplasmic protein	X		
fabI	2,62	enoyl-[acyl-carrier-protein] reductase (NADH)			
stdB	2,62	putative outer membrane usher protein			
ytgA	2,62	putative inner membrane protein		X	
rplE	2,61	50S ribosomal subunit protein L5			X
rpsA	2,6	30S ribosomal subunit protein S1			
ybhC	2,6	putative pectinesterase			
greA	2,59	transcription elongation factor, cleaves 3' nucleotide of paused mRNA	X		
nhaB	2,59	NhaB family of transport protein, Na <sup>+</sup> /H <sup>+</sup> antiporter, regulator of intracellular pH			
lpxD	2,58	UDP-3-O-(3-hydroxymyristoyl)-glucosamine n-acyltransferase			X
potD	2,56	ABC superfamily (peri_perm), spermidine/putrescine transporter			
tktA	2,54	transketolase 1 isozyme			
fumA	2,53	fumarase A (fumarate hydratase class I), aerobic isozyme			X
serA	2,52	D-3-phosphoglycerate dehydrogenase			
mdoH	2,51	membrane glycosyltransferase; synthesis of membrane-derived oligosaccharide (MDO)/synthesis of OPGs (osmoregulated periplasmic glucans)			
hmpA	2,48	dihydropteridine reductase 2 and nitric oxide dioxygenase activity			
tsf	2,48	protein chain elongation factor EF-Ts	X		X
serC	2,46	3-phosphoserine aminotransferase / phosphohydroxythreonine transaminase			X
tolB	2,46	tol protein required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA to cytoplasm, may be part of multiprotein peptidoglycan recycling complex (Two domains)			X
rpmG	2,44	50S ribosomal subunit protein L33			
sbp	2,44	ABC superfamily (bind_prot), sulfate transport protein			
STM3127	2,44	putative cytoplasmic protein			
surA	2,44	peptidyl-prolyl cis-trans isomerase, survival protein	X		
hemN	2,43	O2-independent coproporphyrinogen III oxidase			
rpsB	2,43	30S ribosomal subunit protein S2			X
rpsH	2,43	30S ribosomal subunit protein S8, and regulator			X
yfcB	2,43	putative methylase			
STM4423	2,42	putative AraC-type DNA-binding domain-containing protein			
STM4424	2,42	putative endonuclease			
bacA	2,4	bacitracin resistance; possibly phosphorylates undecaprenol			
fabB	2,4	3-oxoacyl-[acyl-carrier-protein] synthase I			X
oppD	2,4	ABC superfamily (atp-binding), oligopeptide transport protein			X
ybhR	2,4	putative ABC superfamily (membrane) transport protein			
btuB	2,39	outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23			
kdgK	2,39	ketodeoxygluconokinase			
rpsN	2,39	30S ribosomal subunit protein S14			
htpX	2,38	heat shock protein, integral membrane protein			
PSLT102	2,38			X	
plsB	2,37	glycerolphosphate acyltransferase activity			
fusA	2,36	protein chain elongation factor EF-G, GTP-binding			X
engA	2,35	putative GTP-binding protein			
pyrL	2,34	pyrBI operon leader peptide			
rpoH	2,33	sigma H (sigma 32) factor of RNA polymerase; transcription of heat shock proteins induced by cytoplasmic stress			X
rpsL	2,33	30S ribosomal subunit protein S12			
rpsD	2,31	30S ribosomal subunit protein S4	X		X
sbmA	2,31	putative ABC superfamily transporter		X	X
tkk	2,3	putative transcriptional regulator (TetR/ArcR family)		X	
fepE	2,29	ferric enterobactin (enterochelin) transporter		X	
STM2706	2,28	Fels-2 prophage: similar to tail fiber protein in phage P2			
oafA	2,26	O-antigen five: acetylation of the O-antigen (LPS)		X	
rpsQ	2,26	30S ribosomal subunit protein S17			
sdaB	2,26	L-serine dehydratase (L-threonine deaminase 2)			

rfbK	2,25	LPS side chain defect: phosphomannomutase		X	X	X
yjC	2,25	putative transcriptional repressor (TetR/AcrR family)				X
glyQ	2,24	glycine tRNA synthetase, alpha subunit				
prsA	2,24	phosphoribosylpyrophosphate synthetase	X			
psd	2,24	phosphatidylserine decarboxylase				
dinI	2,23	DNA damage-inducible protein I, inhibits UmuD processing				
rplR	2,23	50S ribosomal subunit protein L18				
STM0908	2,23	Fels-1 prophage				
tgt	2,23	tRNA-guanine transglycosylase				
trmA	2,23	tRNA (uracil-5-)-methyltransferase				
yiiD	2,23	putative acetyltransferase				
ydgR	2,22	putative POT family, peptide transport protein				
res	2,21	DNA restriction (DNA helicase)				
tolQ	2,21	tol protein, membrane-spanning inner membrane proteins, required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA to cytoplasm				
PSLT068	2,2					
STM2705	2,2	Fels-2 prophage			X	
rpsE	2,19	30S ribosomal subunit protein S5				X
STM1131	2,19	putative outer membrane protein	X			
yceH	2,19	putative cytoplasmic protein				
yhgG	2,19	putative cytoplasmic protein				
STM1530	2,18	putative outer membrane protein			X	
ushB	2,17	CDP-diacylglycerol phosphatidylhydrolase				
glyA	2,16	serine hydroxymethyltransferase				
glyS	2,16	glycine tRNA synthetase, beta subunit				
mopB	2,16	chaperone Hsp10, affects cell division				
rpmD	2,16	50S ribosomal subunit protein L30				
trmD	2,16	tRNA (guanine-7-)-methyltransferase				X
STM4306	2,15	putative anaerobic dimethyl sulfoxide reductase, subunit B				
feoB	2,14	FeoB family, ferrous iron transport protein B				
pyrE	2,14	orotate phosphoribosyltransferase				
yidC	2,14	putative Preprotein translocase subunit YidC				
hybC	2,13	hydrogenase-2, large subunit				X
STM1607	2,13	putative outer membrane lipoprotein				
cadB	2,12	APC family, lysine/cadaverine transport protein				
gnd	2,12	gluconate-6-phosphate dehydrogenase, decarboxylating			X	X
rfbU	2,12	LPS side chain defect: mannosyl transferase	X	X	X	X
STM4307	2,12	putative anaerobic dimethyl sulfoxide reductase, subunit C				
nirC	2,11	FNT family, nitrite transport protein				
yggT	2,11	putative integral membran resistance protein				
yhcB	2,11	putative periplasmic protein				X
PSLT069	2,1					
STM1252	2,1	putative cytoplasmic protein	X			
STM2237	2,1	putative inner membrane protein				
STM2754	2,1	putative hexulose 6 phosphate synthase			X	
ycdG	2,1	paral putative periplasmic glucans biosynthesis protein				
rplO	2,09	50S ribosomal subunit protein L15				X
yaiW	2,09	putative outer membrane lipoprotein				
aroP	2,08	APC family, aromatic amino acid transporter				
STM3604	2,08	putative inner membrane protein				X
STM4464	2,07	putative arginine repressor				
yhcG	2,07	putative cytoplasmic protein				
prpC	2,06	putative citrate synthase				
rpmF	2,06	50S ribosomal subunit protein L32				
yheO	2,06	putative regulator				
asd	2,05	aspartate-semialdehyde dehydrogenase				
kbl	2,05	2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)	X			
STM0149	2,05	putative permease of the Na <sup>+</sup> :galactoside symporter family				
STM3259	2,05	PTS family galactitol-specific enzyme IIB				
STM4418	2,05	sugar (and other) transporter				
agsA	2,04	Molecular chaperone (small heat shock protein) Tomoyasu, T (2003) J. Bact. 185: 6331-9		X		
PSLT003	2,04					
STM1485	2,04	acid shock protein				
STM1540	2,04	putative hydrolase				
STM2236	2,04	putative phage protein				
STM2636	2,04	Gifsy-1 prophage: similar to integrase in phage				
STM2767	2,04	putative Superfamily I DNA and RNA helicase		X	X	X
uraA	2,04	NCS2 family, uracil transport protein				
sfbA	2,03	putative ABC-type transport system ATPase component/cell division protein			X	
crp	2,02	catabolite activator protein (CAP), cyclic AMP receptor protein (CRP family)			X	X
maeB	2,02	paral putative transferase	X			X
ompD	2,02	new outer membrane protein; predicted bacterial porin				X
nirD	2,01	nitrite reductase, small subunit			X	
mpl	2	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl- meso-diaminopimelate ligase				X
STM3633	2	putative bacterial regulatory proteins, lacl family				
rfaD	-2	ADP-L-glycero-D-mannoheptose-6-epimerase				X

STM1324	-2	putative cytoplasmic protein				X
STM2905	-2	putative acetyltransferase		X		
fhlA	-2,01	formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons (EBP family)				
fliQ	-2,01	flagellar biosynthesis				
gcd	-2,01	glucose dehydrogenase				
proW	-2,01	ABC superfamily (membrane), glycine/betaine/proline transport protein				
ptsG	-2,02	Sugar Specific PTS family, glucose-specific IIBCcomponent			X	X
fliE	-2,03	putative Flagellar hook-basal body protein				
STM0856	-2,03	putative electron transfer flavoprotein alpha subunit		X		
yneC	-2,03	putative inner membrane protein		X		
yijV	-2,04	putative hydrolase				
PSLT023	-2,05					
yhjD	-2,05	putative tRNA-processing ribonuclease				
yncD	-2,05	paral putative outer membrane receptor				
celA	-2,06	PTS family, sugar specific enzyme IIB for cellobiose, arbutin, and salicin		X	X	X
ybhL	-2,06	putative permease				X
celD	-2,07	transcriptional repressor of cel operon (AraC/XylS family)				
ddlB	-2,07	D-alanine-D-alanine ligase B, affects cell division				X
pagD	-2,08	PhoP regulated		X		
rfaF	-2,08	ADP-heptose; LPS heptosyltransferase 1				X
STM1630	-2,08	putative inner membrane protein		X		
STM2614	-2,08	Gifsy-1 prophage				
ynbE	-2,08	putative outer membrane lipoprotein				
ynfD	-2,08	putative outer membrane protein				
ldhA	-2,09	fermentative D-lactate dehydrogenase, NAD-dependent				
ydfZ	-2,09	putative cytoplasmic protein				
yjiU	-2,09	putative phosphoesterase				X
ynhG	-2,09	putative LysM domain				
qor	-2,1	quinone oxidoreductase, NADPH dependent				
csgA	-2,11	curlin major subunit, coiled surface structures; cryptic		X		
STM1859	-2,11	putative cytoplasmic protein				
STM1939	-2,11	putative glucose-6-phosphate dehydrogenase		X	X	X
ugpC	-2,11	ABC superfamily (atp_bind), sn-glycerol 3-phosphate transport protein				
ycfH	-2,11	putative metal-dependent hydrolase				
yegH	-2,11	putative inner membrane protein				
ygdP	-2,11	putative invasion protein; NTP pyrophosphohydrolase				X
deoC	-2,13	2-deoxyribose-5-phosphate aldolase				
STM0081	-2,13	putative secreted protein				
pfkB	-2,14	6-phosphofructokinase II				
soxR	-2,14	redox-sensing transcriptional activator SoxR, contains iron-sulfur center for redox-sensing (MerR family)				
ugpA	-2,14	ABC superfamily (membrane), sn-glycerol 3-phosphate transport protein				
STM1123	-2,15	putative periplasmic protein				
STM1809	-2,15	putative cytoplasmic protein				
rhaS	-2,16	positive regulator for rhaBAD operon (AraC/XylS family)			X	
dmsA	-2,17	anaerobic dimethyl sulfoxide reductase, subunit A				X
mscL	-2,17	mechanosensitive channel				X
pgpB	-2,18	phosphatidylglycerophosphate phosphatase B				X
ssaV	-2,19	Secretion system apparatus: homology with the LcrD family of proteins		X		
fidL	-2,2	putative inner membrane protein		X		X
ybeL	-2,2	putative cytoplasmic protein				X
yohl	-2,2	putative nitrogen regulation protein				
ssaT	-2,21	Secretion system apparatus: homology with YscT of the secretion system of Yersinia		X	X	
STM2208	-2,21	putative inner membrane protein				
yohD	-2,21	putative DedA family, membrane protein				
modB	-2,22	ABC superfamily (membrane), molybdate transporter				
STM1562	-2,22	putative periplasmic transport protein		X		
yhjQ	-2,22	putative ATPase involved in chromosome partitioning				
erfK	-2,23	putative periplasmic protein				
modC	-2,23	ABC superfamily (atp_bind), molybdate transporter				
STM1672	-2,23	putative cytoplasmic protein		X		
pfkA	-2,24	6-phosphofructokinase I				X
ssaS	-2,24	Secretion system apparatus: homology with YscS of the secretion system of Yersinia		X	X	
ycgR	-2,24	putative inner membrane protein				
bcfA	-2,25	fimbrial subunit				
STM2126	-2,25	putative HlyD family secretion protein				
caiF	-2,27	transcriptional regulator of cai and fix operon				X
STM1858	-2,27	putative cytoplasmic protein		X		
hopD	-2,28	leader peptidase HopD				
STM1633	-2,28	putative periplasmic binding protein		X		
STM1988	-2,28	putative cytoplasmic protein				
STM4310	-2,28	putative inner membrane protein		X	X	
glgX	-2,29	glycosyl hydrolase				X
STM1624	-2,29	putative cytoplasmic protein				

ynhA	-2,29	putative SufE protein probably involved in Fe-S center assembly				
glgB	-2,3	1,4-alpha-glucan branching enzyme		X		X
STM1054	-2,31	Gifsy-2 prophage				
ygiW	-2,31	putative outer membrane protein				
marT	-2,32	putative transcriptional regulatory protein				
pgtE	-2,32	Phosphoglycerate transport: outer membrane protein E				
yehV	-2,32	putative transcriptional repressor (MerR family)				
ymgE	-2,32	putative transglycosylase-associated protein				
flhB	-2,33	putative part of export apparatus for flagellar proteins				
yadI	-2,33	putative PTS enzyme				
astE	-2,35	succinylglutamate desuccinylase				
STM0810	-2,35	putative inner membrane protein				
flhC	-2,36	regulator of flagellar biosynthesis, acts on class 2 operons		X		X
yhjL	-2,36	putative TPR-repeat-containing protein				X
ymdC	-2,36	putative phospholipase				X
STM0381	-2,37	putative inner membrane protein				
STM4206	-2,37	putative phage glucose translocase				
glgC	-2,38	glucose-1-phosphate adenyltransferase				X
phnB	-2,38	putative cytoplasmic protein				
ycdC	-2,38	putative transcriptional repressor (TetR/AcrR family)				
acrR	-2,39	acrAB operon repressor (TetR/AcrR family)		X		
STM0053	-2,39	putative transcription regulator, histidine kinase for citrate		X		
yaiA	-2,39	putative cytoplasmic protein				
pflA	-2,4	pyruvate formate lyase activating enzyme 1				
srfA	-2,4	ssrAB activated gene				
STM0033	-2,4	putative 5'-nucleotidase		X		
STM4257	-2,4	putative inner membrane or exported		X	X	X
gppA	-2,41	guanosine pentaphosphatase and exopolyphosphatase				
spaS	-2,41	surface presentation of antigens; secretory proteins		X		X
STM2245	-2,42	putative outer membrane protein				
tdcC	-2,43	HAAAP family, L-threonine/ L-serine permease, anaerobically inducible				
STM3681	-2,44	putative transcriptional regulator				
STM4071	-2,44	putative Mannose-6-phosphate isomerase				
fliR	-2,45	putative flagellar biosynthetic protein				
pykF	-2,45	pyruvate kinase I (formerly F), fructose stimulated				
ssaQ	-2,46	Secretion system apparatus		X	X	
STM2803	-2,46	putative regulatory protein, gntR family				
PSLT040	-2,47					
yeeY	-2,47	putative transcriptional regulator, LysR family				
ssaP	-2,5	Secretion system apparatus		X		
STM1055	-2,51	Gifsy-2 prophage				
STM1147	-2,51	putative ACR related to the C-terminal domain of histone macroH2A1				X
STM2585A	-2,51	Gifsy-1 prophage: Homolog of pagK				
sseF	-2,52	Secretion system effector				
yehM	-2,52	putative SulP family transport protein				
fliI	-2,53	flagellum-specific ATP synthase				X
STM2137	-2,54	putative cytoplasmic protein				
yhjO	-2,54	glycosyltransferase, probably involved in cell wall biogenesis				
ydeV	-2,56	putative sugar kinase				
STM0082	-2,57	putative secreted protein			X	
STM1491	-2,57	ABC-type proline/glycine betaine transport systems, ATPase component				
STM2904	-2,57	putative ABC-type transport system		X		
glgA	-2,58	glycogen synthase				
otsB	-2,59	trehalose-6-phosphate phosphatase, biosynthetic				
uspB	-2,61	universal stress protein B, involved in stationary-phase resistance to ethanol				X
fliB	-2,62	N-methylation of lysine residues in flagellin				
fliF	-2,63	flagellar biosynthesis; basal-body MS(membrane and supramembrane)-ring and collar protein				
sscB	-2,63	Secretion system chaparone		X		
ycdX	-2,63	putative inner membrane protein				
ydiU	-2,63	putative cytoplasmic protein				X
sanA	-2,64	vancomycin sensitivity			X	X
sinR	-2,64	transcriptional regulator			X	
yeeZ	-2,64	putative dehydratase				
flgB	-2,65	flagellar biosynthesis, cell-proximal portion of basal-body rod				
yneB	-2,65	putative fructose-1,6-bisphosphate aldolase				X
yjcC	-2,67	putative diguanylate cyclase/phosphodiesterase				
STM4575	-2,68	putative outer membrane protein				
adiY	-2,7	transcriptional activator of adia (AraC/XylS family)			X	
mtlR	-2,7	repressor for mtl				
STM0860	-2,7	putative inner membrane protein		X		
mug	-2,72	DNA glycosylase, G/U mismatch specific				
suhB	-2,72	inositol monophosphatase				
yjfO	-2,72	putative lipoprotein				X
ftnB	-2,73	ferritin-like protein				X
STM1484	-2,73	putative protease				
STM2475	-2,73	putative cytoplasmic protein				

yqjG	-2,73	putative glutathione S-transferase				X
malT	-2,74	transcriptional activator of the mal genes, binds inducer (maltotriose) and ATP (LysR family)				X
orf319	-2,75	putative inner membrane protein				X
STM3152	-2,75	putative methyl-accepting chemotaxis protein				
mnc	-2,76	RNase III, ds RNA				
ssaD	-2,78	Secretion system apparatus		X		
yhbP	-2,78	putative cytoplasmic protein				
zur	-2,78	transcriptional repressor of znuABC operon (Fur family)				X
STM4219	-2,79	putative cytoplasmic protein				
yneA	-2,79	putative ABC superfamily (peri_perm), sugar transport protein				
pagK	-2,8	PhoPQ-activated gene		X		X
ybeQ	-2,8	putative TPR repeat protein				
yhhT	-2,8	putative PerM family permease				
aidB	-2,81	putative acyl-CoA dehydrogenase; adaptive response (transcription activated by Ada)				
exbD	-2,81	uptake of enterochelin; tonB-dependent uptake of B colicins				
cheA	-2,82	sensory histidine protein kinase, transduces signal between chemo-signal receptors and CheB and CheY				X
pagC	-2,82	PhoP regulated: reduced macrophage survival	X	X		X
proP	-2,83	MFS family, low-affinity proline transporter (proline permease II)			X	X
yajO	-2,83	putative oxidoreductase / K + channel protein				
soxS	-2,84	transcriptional activator of superoxide response regulon (AraC/XylS family)				
ydcW	-2,84	putative aldehyde dehydrogenase				
bcsC	-2,85	endo-1,4-D-glucanase				
flgA	-2,86	flagellar biosynthesis; assembly of basal-body periplasmic P ring				
PSLT039	-2,86					
dbpA	-2,87	ATP-dependent RNA helicase, stimulated by 23S rRNA				
fliD	-2,87	flagellar biosynthesis; filament capping protein; enables filament assembly				X
sifB	-2,87	Salmonella translocated effector: translocated by SPI-2		X		X
gabT	-2,88	4-aminobutyrate aminotransferase				
yehX	-2,88	putative ABC-type proline/glycine betaine transport system, ATPase component				
modA	-2,89	ABC superfamily (peri_perm), molybdate transporter				X
STM1987	-2,89	putative inner membrane protein				
ybaJ	-2,89	putative cytoplasmic protein		X		X
yhjR	-2,89	putative cytoplasmic protein				
cheB	-2,9	methyl esterase, response regulator for chemotaxis (cheA sensor)				X
srfC	-2,9	ssrAB activated gene: predicted coiled-coil structure				
ssaO	-2,9	Secretion system apparatus		X		
fruA	-2,91	Sugar Specific PTS system, fructose-specific transport protein				
phsA	-2,91	Hydrogen sulfide production: membrane anchoring protein				X
yhjN	-2,91	putative cellulose synthase				
STM1330	-2,92	putative DNA/RNA non-specific endonuclease				
astB	-2,93	succinylarginine dihydrolase				
spaQ	-2,93	surface presentation of antigens; secretory proteins		X		
galP	-2,96	MFS family, galactose:proton symporter				
STM0948	-2,96	putative cytoplasmic protein				
cfa	-3	cyclopropane fatty acyl phospholipid synthase				
cigR	-3,02	putative inner membrane protein				
slrP	-3,02	leucine-rich repeat protein			X	X
STM1698	-3,02	putative inner membrane protein				
STM3155	-3,02	putative cytoplasmic protein			X	
yjcB	-3,02	putative inner membrane protein			X	
fliP	-3,03	flagellar biosynthesis				X
ycgB	-3,03	putative cytoplasmic protein				X
yhjS	-3,03	putative cytoplasmic protein				
yjgB	-3,03	putative alcohol dehydrogenase				
STM1934	-3,04	putative outer membrane lipoprotein				
flgC	-3,05	flagellar biosynthesis, cell-proximal portion of basal-body rod				
sufS	-3,05	selenocysteine lyase				
ssaC	-3,06	Secretion system apparatus		X		
STM2715	-3,07	Fels-2 prophage: probable prophage lysozyme		X		
ychH	-3,08	putative inner membrane protein				X
flgI	-3,09	putative flagella basal body protein				
yhjT	-3,09	putative inner membrane protein				
phsB	-3,12	Hydrogen sulfide production: iron- sulfur subunit; electron transfer				
ssaN	-3,12	Secretion system apparatus: homology with the YscN family of proteins				X
fic	-3,14	putative cell filamentation protein, stationary phase induced gene, affects cell division				
ssaB	-3,14	Secretion system apparatus		X		
STM1056	-3,15	Gifsy-2 prophage; Homolog of msgA				
yohC	-3,16	paral putative transport protein				
manY	-3,19	Sugar Specific PTS family, mannose-specific enzyme IIC				X
STM1026	-3,19	Gifsy-2 prophage				
flhD	-3,2	regulator of flagellar biosynthesis, acts on class 2 operons			X	X
ybhK	-3,21	putative cytoplasmic protein				
yjfN	-3,22	putative inner membrane protein				X
hilA	-3,24	invasion genes transcription activator		X	X	X

ompA	-3,27	putative hydrogenase, membrane component				X
STM4258	-3,28	putative methyl-accepting chemotaxis protein	X	X		X
manX	-3,31	Sugar Specific PTS family, mannose-specific enzyme IIAB				X
STM4316	-3,31	putative cytoplasmic protein	X	X		
grxB	-3,32	glutaredoxin 2				X
flhE	-3,33	flagellar protein				
blc	-3,34	outer membrane lipoprotein (lipocalin)				
pipB2	-3,34	Pathogenicity island encoded protein: SPI3	X			X
yqhE	-3,37	2,5-diketo-D-gluconate reductase A				
ratA	-3,41	putative outer membrane protein				
trg	-3,42	methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor				X
ydeJ	-3,42	putative Competence-damaged protein				
fliH	-3,43	flagellar biosynthesis; possible export of flagellar proteins				
sseJ	-3,44	Salmonella translocated effector: regulated by SPI-2	X			
yhcN	-3,44	putative outer membrane protein				
ycfQ	-3,45	putative transcriptional repressor (TetR/AcrR family)				
yebW	-3,46	putative inner membrane lipoprotein				
sseG	-3,47	Secretion system effector	X			
ugpQ	-3,47	glycerophosphodiester phosphodiesterase, cytosolic				
csgC	-3,49	putative curli production protein	X			
narY	-3,49	nitrate reductase 2, beta subunit				
yobG	-3,5	putative inner membrane protein				X
ssrA	-3,52	Secretion system regulator:Sensor component	X			
flgK	-3,53	flagellar biosynthesis, hook-filament junction protein 1				X
otsA	-3,54	trehalose-6-phosphate synthase				
STM1561	-3,54	putative outer membrane or secreted lipoprotein				
celG	-3,55	putative glucosidase		X		X
sscA	-3,55	Secretion system chaparone				X
ybil	-3,55	putative DnaK suppressor protein				
hilC	-3,56	bacterial regulatory helix-turn-helix proteins, araC family	X	X		X
STM1851	-3,57	putative cytoplasmic protein				
talA	-3,58	transaldolase A				
acnA	-3,61	aconitate hydratase 1				X
STM1398	-3,61		X			
sptP	-3,62	protein tyrosine phosphate	X	X		X
ssaR	-3,62	Secretion system apparatus: homology with YscR of the secretion system of Yersinia	X			
ugpB	-3,62	ABC superfamily (peri_perm), sn-glycerol 3-phosphate transport protein				
aer	-3,63	aerotaxis sensor receptor, senses cellular redox state or proton motive force				
STM1967	-3,63	putative 50S ribosomal protein				
fliB	-3,64	Flagellar synthesis: phase 2 flagellin (filament structural protein)	X			
yedP	-3,65	putative hydrolase of the HAD superfamily				
STM4574	-3,67	putative outer membrane protein				
ybhO	-3,67	cardiolipin (CL) synthase				
STM2405	-3,69	putative thiamine pyrophosphate enzymes				
yibF	-3,69	putative glutathione S-transferase				
STM1261	-3,7	putative cytoplasmic protein				
tsr	-3,71	methyl-accepting chemotaxis protein I, serine sensor receptor				X
osmC	-3,74	putative resistance protein, osmotically inducible				
STM0972	-3,74	homologous to secreted protein sopD				
yhfG	-3,74	putative cytoplasmic protein				
sufC	-3,75	putative ABC superfamily (atp_bind) transport protein				
ydiY	-3,76	putative salt-induced outer membrane protein				
narW	-3,8	nitrate reductase 2, delta subunit, assembly function				
fliL	-3,85	flagellar biosynthesis				
spaR	-3,85	surface presentation of antigens; secretory proteins	X			X
STM3154	-3,86	putative ATP-dependent RNA helicase-like protein				X
STM1329	-3,89	putative inner membrane protein				
sufD	-3,89	required for stability of iron-sulfur component of FhuF				
manZ	-3,91	Sugar Specific PTS family, mannose-specific enzyme IID				X
sugE	-3,93	putative DMT superfamily transport protein				
rpsV	-3,95	30S ribosomal subunit protein S22				
yebF	-3,95	putative periplasmic protein				X
STM1239	-3,96	putative cytoplasmic protein	X	X		X
fliO	-3,98	flagellar biosynthesis	X			
yncB	-3,98	putative NADP-dependent oxidoreductase				X
yceK	-4,02	putative outer membrane lipoprotein				
yqjK	-4,04	putative inner membrane protein				
STM3774	-4,05	putative inner membrane protein				
yehY	-4,11	putative ABC-type proline/glycine betaine transport systems, permease component				X
yhjE	-4,12	putative MFS family transport protein				
sitD	-4,15	Salmonella iron transporter: fur regulated				
yahO	-4,16	putative periplasmic protein				X
aldB	-4,25	aldehyde dehydrogenase B (lactaldehyde dehydrogenase)				X
STM4259	-4,25	putative ABC exporter outer membrane component homolog	X			X
yjhH	-4,27	putative Diguanylate cyclase/phosphodiesterase domain 3				X
sicP	-4,29	chaperone, related to virulence	X	X		X

chaB	-4,31	cation transport regulator				
sseD	-4,35	Secretion system effector	X			
yfdC	-4,35	putative transport				
sufA	-4,41	putative HesB-like domain				
ggT	-4,49	gamma-glutamyl/transpeptidase				
ssaK	-4,49	Secretion system apparatus	X			
fliC	-4,5	flagellar biosynthesis; flagellin, filament structural protein	X			X
sseE	-4,5	Secretion system effector		X		
phsC	-4,52	Hydrogen sulfide production: membrane anchoring protein				
STM1267	-4,62	putative cytoplasmic protein		X		
STM3156	-4,67	putative cytoplasmic protein				
yhhA	-4,69	putative outer membrane protein				
STM4262	-4,7	putative ABC-type bacteriocin/antibiotic exporter, contain an N-terminal double-glycine peptidase domain		X		X
yeaH	-4,72	putative cytoplasmic protein				X
tktB	-4,75	transketolase 2, isozyme				
sufB	-4,79	putative ABC transporter				
flgF	-4,81	flagellar biosynthesis, cell-proximal portion of basal-body rod				X
flgG	-4,82	flagellar biosynthesis, cell-distal portion of basal-body rod				
cheZ	-4,84	chemotactic response; CheY protein phosphatase				X
STM3362	-4,92	putative periplasmic protein			X	X
STM1731	-5,03	putative catalase				X
STM3688	-5,05	putative cytoplasmic protein				
flgD	-5,08	flagellar biosynthesis, initiation of hook assembly				X
yohF	-5,09	putative oxidoreductase				
sopB	-5,11	Salmonella outer protein: homologous to ipgD of Shigella		X		X
rtsA	-5,16	putative AraC-type DNA-binding domain-containing protein	X		X	
iagB	-5,2	cell invasion protein	X			X
ssrB	-5,24	Secretion system regulator: transcriptional activator, homologous with degU/uvrY/bvgA		X		X
STM0080	-5,25	putative outer membrane lipoprotein				
STM1397	-5,26		X			
bfr	-5,29	bacterioferrin, an iron storage homoprotein	X			
STM4312	-5,31	putative phage protein	X		X	
ugtL	-5,34	putative membrane protein: homology with chitinase from Schizosaccharomyces				X
yegS	-5,36	putative diacylglycerol kinase catalytic domain				
STM1558	-5,37	putative glycosyl hydrolase				X
STM4313	-5,42	putative cytoplasmic protein	X		X	
invA	-5,43	invasion protein	X		X	X
adhE	-5,44	iron-dependent alcohol dehydrogenase of the multifunctional alcohol dehydrogenase AdhE				X
yfbK	-5,46	putative von Willebrand factor, vWF type A domain				
STM4260	-5,47	membrane permease, predicted cation efflux pump	X		X	X
STM1301	-5,5	putative mutator MutT protein				
fliN	-5,52	flagellar biosynthesis, component of motor switch and energizing				
flgE	-5,55	flagellar biosynthesis, hook protein				X
fliK	-5,59	flagellar hook-length control protein				
rtsB	-5,59	putative bacterial regulatory proteins, luxR family	X			
sseC	-5,66	Secretion system effector	X			X
sdiA	-5,69	transcriptional regulator of ftsQAZ gene cluster (LuxR/UhpA family)				X
STM3132	-5,72	putative xylanase/chitin deacetylase				X
treA	-5,72	trehalase, periplasmic				X
fliJ	-5,73	flagellar fliJ protein				
fliM	-5,81	flagellar biosynthesis, component of motor switch and energizing				X
spy	-5,85	periplasmic protein related to spheroblast formation				
ssaL	-5,89	Secretion system apparatus	X			
yodD	-5,9	putative cytoplasmic protein				
motB	-5,94	enables flagellar motor rotation, linking torque machinery to cell wall				X
cheY	-5,96	chemotaxis regulator, transmits chemoreceptor signals to flagellar motor components				X
prgH	-6,04	cell invasion protein	X			X
STM2780	-6,04	Homolog of pipB, putative pentapeptide repeats (8 copies)	X			
yehZ	-6,05	putative ABC superfamily (bind_prot) transport protein (possibly glycine betaine choline transport for osmoprotection)				X
fliT	-6,06	flagellar biosynthesis; possible export chaperone for FliD				
STM0362	-6,13	putative cytoplasmic protein				
psiF	-6,14	induced by phosphate starvation				
STM2404	-6,14	putative chloride channel permease				
sprB	-6,2	transcriptional regulator	X			X
ygaE	-6,2	putative transcriptional repressor (GntR family)				
fliZ	-6,22	putative regulator of FliA				X
avrA	-6,28	putative inner membrane protein	X		X	X
sipB	-6,29	cell invasion protein				X
cheR	-6,31	glutamate methyltransferase, response regulator for chemotaxis				X
motA	-6,34	proton conductor component of motor, torque generator				X
invH	-6,35	invasion protein	X		X	
ssaI	-6,36	Secretion system apparatus	X			
STM1328	-6,4	putative outer membrane protein	X		X	X
poxB	-6,42	pyruvate dehydrogenase/oxidase FAD and thiamine PPI cofactors, cytoplasmic in absence of cofactors				

invC	-6,51	surface presentation of antigens; secretory proteins			X	X
STM3133	-6,52	putative amidohydrolase				X
yhbO	-6,54	putative intracellular proteinase				
invB	-6,57	surface presentation of antigens; secretory proteins		X		X
osmE	-6,58	transcriptional activator of ntrL gene				X
yccJ	-6,6	putative cytoplasmic protein				
spaP	-6,62	surface presentation of antigens; secretory proteins		X	X	X
ssaG	-6,73	Secretion system apparatus		X		
fliS	-6,83	flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)				X
ssaH	-6,86	Secretion system apparatus		X		
STM1089	-6,91	putative inner membrane protein		X		
orgA	-6,92	putative flagellar biosynthesis/type III secretory pathway protein		X	X	X
hilD	-6,93	regulatory helix-turn-helix proteins, araC family		X	X	X
ecnR	-7,26	putative bacterial regulatory protein, luxR family				
cheW	-7,27	purine-binding chemotaxis protein; regulation				X
msyB	-7,28	acidic protein suppresses mutants lacking function of protein export				
ssaJ	-7,28	Secretion system apparatus: homology with the yscJ/mxiJ/prgK family of lipoproteins		X		X
yeaQ	-7,43	putative inner membrane protein		X		X
invG	-7,56	invasion protein; outer membrane		X	X	X
sipC	-7,6	cell invasion protein	X	X		X
yqjE	-7,62	putative inner membrane protein				
invF	-7,69	invasion protein		X	X	X
STM2870	-7,75	putative inner membrane protein		X	X	
invI	-7,76	surface presentation of antigens; secretory proteins		X		
tcp	-7,91	methyl-accepting transmembrane citrate/phenol chemoreceptor				X
sopA	-7,93	Secreted effector protein of Salmonella dublin				X
iacP	-7,94	putative acyl carrier protein		X	X	X
flgL	-8,06	flagellar biosynthesis; hook-filament junction protein			X	X
prgK	-8,27	cell invasion protein; lipoprotein, may link inner and outer membranes		X		X
sodC	-8,3	copper/zinc superoxide dismutase				
flgN	-8,33	flagellar biosynthesis: believed to be export chaperone for FlgK and FlgL				X
prgJ	-8,36	cell invasion protein; cytoplasmic		X		X
sopE2	-8,64	TypeIII-secreted protein effector: invasion-associated protein		X	X	X
prgI	-8,65	cell invasion protein; cytoplasmic		X		
adhP	-8,66	alcohol dehydrogenase, propanol preferring				
STM4261	-8,67	putative inner membrane protein		X	X	X
STM4519	-8,71	putative NAD-dependent aldehyde dehydrogenase				
wraB	-8,77	trp-repressor binding protein				X
STM1300	-8,79	putative periplasmic protein				X
STM2585	-8,91	Gifsy-1 prophage: similar to transposase				
STM2139	-9,13	putative inner membrane protein		X		
osmB	-9,36	osmotically inducible lipoprotein				
fliA	-9,49	sigma F (sigma 28) factor of RNA polymerase, transcription of late flagellar genes (class 3a and 3b operons)				X
STM1560	-9,54	putative alpha amylase				
invE	-9,9	invasion protein		X		X
flgM	-10,09	anti-FlhA (anti-sigma) factor; also known as RflB protein				X
invJ	-10,12	surface presentation of antigens; secretory proteins		X		X
viaG	-10,17	putative transcriptional regulator			X	
yqjC	-10,17	putative periplasmic protein				X
STM0359	-10,31	putative cytoplasmic protein				
ybaY	-10,35	glycoprotein/polysaccharide metabolism				X
STM2868	-10,64	putative cytoplasmic protein		X	X	
sopD	-10,73	secreted protein in the Sop family; transferred to eukaryotic cells				X
cheM	-10,78	methyl accepting chemotaxis protein II, aspartate sensor-receptor				X
dps	-10,99	stress response DNA-binding protein; starvation induced resistance to H2O2	X			X
STM1629	-11,31	putative dipicolinate reductase		X	X	
phoH	-11,78	PhoB-dependent, ATP-binding pho regulon component				
yeaG	-11,81	putative Ser protein kinase				X
ecnB	-12,19	putative entericidin B precursor				X
ygaU	-12,72	putative LysM domain				
fbaB	-13,2	3-oxoacyl-[acyl-carrier-protein] synthase I				
STM1841	-13,44	putative outer membrane or exported			X	X
ampH	-14,03	penicillin- binding protein				
sipA	-14,3	cell invasion protein	X	X		X
elaB	-14,43	putative inner membrane protein				
sipD	-14,99	cell invasion protein		X	X	X
ydeI	-15,37	putative periplasmic protein				
ygdI	-16,14	putative lipoprotein				X
pipC	-16,34	Pathogenicity island encoded protein: homologous to ipgE of Shigella		X		X
yciE	-16,68	putative cytoplasmic protein				
katE	-16,7	catalase; hydroperoxidase HPiII(III), RpoS dependent				X
ygaM	-17,53	putative inner membrane protein				
ybgS	-17,94	putative homeobox protein				
STM1513	-18,8	putative cytoplasmic protein				

ymdF	-20,76	putative cytoplasmic protein				
hfq	-21,66	host factor I for bacteriophage Q beta replication, a growth-related protein			X	X
yghA	-24,47	putative oxidoreductase				X
yciF	-24,49	putative cytoplasmic protein				
yjbJ	-28,92	putative cytoplasmic protein				X
yciG	-33,88	putative cytoplasmic protein				
osmY	-34,13	hyperosmotically inducible periplasmic protein, RpoS-dependent stationary phase gene	X			X

<sup>a</sup>Gene names according to ColiBase [3]

<sup>b</sup> Product according to KEGG (<http://www.genome.jp/kegg/>; [4]).

<sup>c</sup> Assignment according to [5]

<sup>d</sup> Assignment according to HGT-GB (<http://www.tinet.org/~debb/HGT/>; [6])

**Table S2: Deregulated genes in *Δhfq* after 12 hrs SPI-inducing conditions**

Gene name <sup>a</sup>	Fold change	Product <sup>b</sup>	2D-analysis <sup>c</sup>	HGT <sup>d</sup>
ybfM	62,11	putative outer membrane protein	X	
pagC	45,66	PhoP regulated: reduced macrophage survival	X	X
ybfN	34,36	putative lipoprotein		
virK	16,31	virulence gene; homologous sequence to virK in Shigella		
yggN	8,70	putative periplasmic protein		
ugtL	8,70	putative membrane protein: homology with chitinase from Schizosaccharomyces		X
rseA	8,20	anti sigma E (sigma 24) factor, negative regulator		
ddg	7,04	cold shock-induced palmitoleoyl transferase		
ygiM	6,85	putative SH3 domain protein		
STM1044	6,45			
STM1253	6,33	putative inner membrane protein		X
STM1583	6,21	putative cytoplasmic protein		
rseB	6,17	anti sigma E (sigma 24) factor, negative regulator		
STM2585A	6,10	Gifsy-1 prophage: Homolog of pagK		
yhjW	6,06	putative membrane-associated, metal-dependent hydrolase		
STM4257	5,68	putative inner membrane or exported		X
STM4260	5,21	membrane permease, predicted cation efflux pump		X
STM1698	5,18	putative inner membrane protein		
STM4259	5,18	putative ABC exporter outer membrane component homolog		X
yraP	4,85	paral putative periplasmic protein	X	
phoN	4,78	non-specific acid phosphatase		
sscB	4,69	Secretion system chaperone		X
sixA	4,65	phosphohistidine phosphatase		
pmrD	4,55	polymyxin resistance protein B		
mig-14	4,46	putative transcription activator		
ssel	4,46	Gifsy-2 prophage; putative type III secreted protein		
yobG	4,44	putative inner membrane protein		
STM1330	4,44	putative DNA/RNA non-specific endonuclease		
sseJ	4,39	Salmonella translocated effector: regulated by SPI-2		X
yraO	4,29	putative phosphoheptose isomerase		
gcvH	4,26	glycine cleavage complex protein H, carrier of aminomethyl moiety via covalently bound lipoyl cofactor		
rpoE	4,18	sigma E (sigma 24 ) factor of RNA polymerase, response to periplasmic stress		
gcvP	4,17	glycine cleavage complex protein P, glycine decarboxylase		
STM1854	3,94	putative inner membrane protein		
ompC	3,91	outer membrane protein 1b (lb;c), porin		
htrA	3,91	periplasmic serine protease Do, heat shock protein	X	
pagK	3,91	PhoPQ-activated gene		X
ybhQ	3,88	putative inner membrane protein		
rna	3,82	RNase I, cleaves phosphodiester bond between any two nucleotides		
hflK	3,77	with HflC, part of modulator for protease specific for FtsH phage lambda cII repressor		
pgtE	3,65	Phosphoglycerate transport: outer membrane protein E		
ydgR	3,64	putative POT family, peptide transport protein		

cutC	3,57	copper homeostasis protein		
rseC	3,56	regulator of sigma E (sigma 24) factor		
STM2303	3,56	putative inner membrane protein		
pdgL	3,38	Periplasmic dipeptidase for D-ala-D-ala digestion in peptidoglycan		
hflC	3,36	with HflK, part of modulator for protease specific for FtsH phage lambda cII repressor		
sseD	3,24	Secretion system effector		X
pagD	3,23	PhoP regulated		X
STM4504	3,13	putative cytoplasmic protein		
yaeT	3,13	putative outer membrane antigen	X	
hflX	3,11	putative GTP-ase, together with HflCK possibly involved in phage lambda cII repressor stability		
yhjJ	3,08	putative Zn-dependent peptidase		
phoP	3,06	response regulator in two-component regulatory system with PhoQ, transcribes genes expressed under low Mg <sup>+</sup> concentration (OmpR family)		
STM1052	3,06			
ycbK	3,03	putative outer membrane protein		
STM1697	2,99	putative Diguanylate cyclase/phosphodiesterase domain 2		
sspH2	2,96	Leucine-rich repeat protein, induced by the SPI-2 regulator ssrA/B		
hlpA	2,91	histone-like protein, located in outer membrane		
gst	2,89	glutathionine S-transferase		
STM1839	2,88	putative periplasmic or exported protein		
STM2447	2,83	putative outer membrane lipoprotein		
gcvT	2,82	glycine cleavage complex protein T, aminomethyltransferase, tetrahydrofolate-dependent		
STM3036	2,72	putative inner membrane protein		
yfcN	2,67	putative Smr domain		
cca	2,62	tRNA nucleotidyl transferase		
surA	2,62	peptidyl-prolyl cis-trans isomerase, survival protein	X	
mreB	2,57	rod shape-determining protein; HSP70 class molecular chaperones involved in cell morphogenesis		
ycbL	2,56	putative Metallo-beta-lactamase		
citA	2,55	citrate-proton symporter		
STM0081	2,53	putative secreted protein		
ybhR	2,50	putative ABC superfamily (membrane) transport protein		
lpxD	2,49	UDP-3-O-(3-hydroxymyristoyl)-glucosamine n-acyltransferase		
STM2585	2,49	Gifsy-1 prophage: similar to transposase		
STM4261	2,46	putative inner membrane protein		X
ydiV	2,44	putative Diguanylate cyclase/phosphodiesterase domain 1		
kdgK	2,44	ketodeoxygluconokinase		
yraR	2,43	putative nucleoside-diphosphate-sugar epimerase		
pdxA	2,38	NAD-dependent dehydrogenase/carboxylase; pyridoxine phosphate biosynthetic protein PdxJ-PdxA subunit		
yfiD	2,33	putative formate acetyltransferase		
STM0082	2,22	putative secreted protein		
yfeK	2,21	putative periplasmic protein		
ydiY	2,19	putative MFS family transport protein (1st mdule)		
STM1940	2,16	putative cell wall-associated hydrolase		
bacA	2,15	bacitracin resistance; possibly phosphorylates undecaprenol		
yiiD	2,14	putative acetyltransferase		
aphA	2,13	non-specific acid phosphatase/phosphotransferase, class B	X	
yjiD	2,07	putative inner membrane protein		
ygcA	2,05	putative RNA methyltransferase		
thrC	2,03	threonine synthase		

yheO	2,02	putative regulator		
yciE	-2,04	putative cytoplasmic protein		
yjhH	-2,05	putative Diguanylate cyclase/phosphodiesterase domain 3		
wraB	-2,07	trp-repressor binding protein		
ygaM	-2,10	putative inner membrane protein		
nrdA	-2,13	ribonucleoside diphosphate reductase 1, alpha subunit		
STM3362	-2,16	putative periplasmic protein		
glmS	-2,18	L-glutamine:D-fructose-6-phosphate aminotransferase		
mtlR	-2,23	repressor for mtl		
ybgS	-2,23	putative homeobox protein		
cheZ	-2,27	chemotactic response; CheY protein phosphatase		
yjfN	-2,29	putative inner membrane protein		
ecnR	-2,29	putative bacterial regulatory protein, luxR family		
fbaB	-2,30	3-oxoacyl-[acyl-carrier-protein] synthase I		
flgK	-2,33	flagellar biosynthesis, hook-filament junction protein 1		
fimD	-2,35	outer membrane usher protein		
ydeZ	-2,38	putative ABC superfamily (membrane), sugar transport protein		
STM3156	-2,39	putative cytoplasmic protein		
osmB	-2,43	osmotically inducible lipoprotein		
katE	-2,46	catalase; hydroperoxidase HPII(III), RpoS dependent		
potE	-2,46	APC family, putrescine/ornithine antiporter		
yciF	-2,50	putative cytoplasmic protein		
cheB	-2,52	methyl esterase, response regulator for chemotaxis (cheA sensor)		
STM0699	-2,52	putative cytoplasmic protein		
gapA	-2,60	glyceraldehyde-3-phosphate dehydrogenase A		
STM3155	-2,60	putative cytoplasmic protein		
cfa	-2,63	cyclopropane fatty acyl phospholipid synthase		
STM2281	-2,64	putative transcriptional regulator, LysR family		
STM3154	-2,65	putative ATP-dependent RNA helicase-like protein		
cyoC	-2,67	cytochrome o ubiquinol oxidase subunit III		
hha	-2,74	hemolysin expression modulating protein (involved in environmental regulation of virulence factors)		
cyoD	-2,74	cytochrome o ubiquinol oxidase subunit IV		
fliT	-2,82	flagellar biosynthesis; possible export chaperone for FliD		
fliZ	-2,82	putative regulator of FliA		
nuoA	-2,83	NADH dehydrogenase I chain A		
cheW	-2,88	purine-binding chemotaxis protein; regulation		
yccJ	-2,97	putative cytoplasmic protein		
ybaJ	-2,98	putative cytoplasmic protein		X
agsA	-2,99	Molecular chaperone (small heat shock protein)		X
flgL	-2,99	Flagellar biosynthesis; hook-filament junction protein		
STM1093	-3,07	putative cytoplasmic protein		
fimC	-3,08	periplasmic chaperone, required for type 1 fimbriae		X
ygaU	-3,16	putative LysM domain		
cyoB	-3,17	cytochrome o ubiquinol oxidase subunit I		
sodC	-3,19	copper/zinc superoxide dismutase		
osmE	-3,20	transcriptional activator of ntrL gene		
yqjC	-3,25	putative periplasmic protein		
STM0731	-3,29	putative inner membrane protein		
tcp	-3,39	methyl-accepting transmembrane citrate/phenol chemoreceptor		X

cheR	-3,44	glutamate methyltransferase, response regulator for chemotaxis		
flgN	-3,56	flagellar biosynthesis: believed to be export chaperone for FlgK and FlgL		
yeaG	-3,60	putative Ser protein kinase		
mopA	-3,65	chaperone Hsp60 with peptide-dependent ATPase activity, affects cell division		
cheY	-3,88	chemotaxis regulator, transmits chemoreceptor signals to flagellar motor components		
fliS	-3,94	flagellar biosynthesis; repressor of class 3a and 3b operons (RfIA activity)		
cyoA	-4,09	cytochrome o ubiquinol oxidase subunit II	X	
cheM	-4,29	methyl accepting chemotaxis protein II, aspartate sensor-receptor		
motB	-4,31	enables flagellar motor rotation, linking torque machinery to cell wall		
speF	-4,40	ornithine decarboxylase isozyme, inducible		
motA	-4,44	proton conductor component of motor, torque generator		
mopB	-4,63	chaperone Hsp10, affects cell division		
ygdI	-4,69	putative lipoprotein		
fimA	-4,76	major type 1 subunit fimbrin (pilin)		
ecnB	-6,04	putative entericidin B precursor		
orfX	-6,20	putative cytoplasmic protein		
osmY	-6,39	hyperosmotically inducible periplasmic protein, RpoS-dependent stationary phase gene	X	X
dps	-6,62	stress response DNA-binding protein; starvation induced resistance to H <sub>2</sub> O <sub>2</sub>	X	
STM1851	-6,68	putative cytoplasmic protein		
yciG	-7,37	putative cytoplasmic protein		
flgM	-10,31	anti-FlIA (anti-sigma) factor; also known as RfIB protein		
STM1513	-15,52	putative cytoplasmic protein		
fliC	-15,65	flagellar biosynthesis; flagellin, filament structural protein	X	
ymdF	-19,63	putative cytoplasmic protein		
hfq	-32,55	host factor I for bacteriophage Q beta replication, a growth-related protein		

<sup>a</sup>Gene names according to ColiBase [3]

<sup>b</sup> Product according to KEGG (<http://www.genome.jp/kegg/>; [4]).

<sup>c</sup> Assignment according to [5]

<sup>d</sup> Assignment according to HGT-GB (<http://www.tinet.org/~debb/HGT/>; [6])

**Table S3: Coverage of known and candidate *Salmonella* sRNA loci in pyrosequencing data**

sRNA <sup>a</sup>	Alternative IDs <sup>b</sup>	Identification <sup>c</sup>	Adjacent genes <sup>d</sup>	Orientation <sup>e</sup>	5' end <sup>f</sup>	3' end <sup>f</sup>	454 control colP <sup>g</sup>	454 Hfq colP <sup>h</sup>	Enrichment <sup>i</sup>	Northern <sup>j</sup>
STnc10	-	V	STM0038/ <i>nhaA</i>	→ ↑ →	46114	46050	0	0		np
STnc20	-	V	STM0042/ <i>rpsT</i>	← → ←	51926	52260	1	2	2.0	np
STnc30	-	V	<i>lytB</i> /STM005	→ → →	58792	58923	1	0		np
STnc470	-	IV	STM0081/STM0082	→ ← ←	94548	94770	0	70	≥70.0	~1250nt
<i>sgrS</i>	<i>ryaA</i>	I	<i>yabN/leuD</i>	← → ←	128574	128812	3	61	20.3	
STnc40	-	V	<i>secA/mutT</i>	→ → →	161464	161537	0	0		np
STnc50	-	V	<i>lpdA</i> /STM0155	→ ← →	182539	182458	0	0		np
STnc60	-	V	<i>fhuB/stfA</i>	→ ↑ →	230277	230063	0	0		np
<i>isrA</i>	-	II	STM0294.In/STM0295	→ → →	339338	339760	0	0		
<i>sroB</i>	<i>rybC</i>	I	<i>ybaK/ybaP</i>	← → ←	556005	556085	27	1530	56.7	
STnc480	-	IV	<i>glxK/ylbA</i>	→ ← ←	587848	587926	4	74	18.5	nd
STnc70	-	V	<i>dsbG/ahpC</i>	← → →	670157	670305	5	7	1.4	np
<i>sroC</i>	-	I	<i>gltJ/gltI</i>	← ← ←	728913	728761	26	898	34.5	
<i>rybB</i>	p25	III	STM0869/STM0870	→ ← ←	942632	942554	3	103	34.3	
STnc80	-	V	STM0897/STM0898	← → ←	967580	967900	0	0		np
STnc90	-	V	STM0903/STM0904	→ → ←	974284	974363	0	0		np
STnc100	-	V	STM0904/STM0905	← → →	975011	975224	0	0		np
STnc110	-	V	STM0905/STM0906	→ → →	976578	976765	0	0		np
STnc120	-	V	STM0929/ <i>orfB</i>	← → →	1004777	1004432	0	0		np
STnc490 <sup>k</sup>	-	IV	<i>clpA/tnpA_1</i>	→ → →	1024975	1025165	75	385	5.1	~85nt
STnc130	-	V	<i>serS/dmsA</i>	→ → →	1045232	1045098	0	0		nd
<i>isrB-1</i>	-	II	<i>sbcA</i> /STM1010	← → ←	1104179	1104266	2	4	2.0	
STnc140	-	V	STM1025/STM1026	← → ←	1113681	1113750	0	0		np
STnc500	-	IV	STM1127/STM1128	← ← ←	1216157	1216440	7	84	12.0	~65nt
<i>sraB</i>	<i>pke2</i>	I	<i>yceF/yceD</i>	← → →	1275071	1275236	0	0		
STnc640	-	IV	<i>icdA</i> /STM1239	→ → →	1325636	1326082	0	10	≥10.0	~1500nt
STnc150	-	V	<i>icdA</i> /STM1239	→ → →	1325914	1325649	0	1	≥1.0	~90nt
<i>isrC</i>	-	II	<i>envF/msgA</i>	← → ←	1329145	1329432	0	1	≥1.0	
STnc510	-	IV	STM1245/ <i>pagC</i>	→ → →	1331440	1332250	4	28	7.0	nd
STnc520	-	IV	STM1248/STM1249	→ → ←	1332809	1334044	12	100	8.3	~80nt
STnc160	-	V	STM1262/STM1263	→ → →	1345782	1345732	0	0		np
<i>isrD</i>	-	II	STM1261/STM1263	→ → →	1345788	1345738	0	0		
<i>ryhB-2</i>	<i>isrE</i>	II	STM1273/ <i>yeaQ</i>	→ → →	1352987	1352875	0	0		
STnc530	-	IV	<i>yeaJ/yeaH</i>	→ → →	1359779	1360418	2	15	7.5	nd
STnc540	-	IV	<i>himA/btuC</i>	→ → →	1419369	1419570	7	23	3.3	~85nt
<i>rprA</i>	IS083	I	<i>ydiK/ydiI</i>	← ← ←	1444938	1444832	37	286	7.7	
<i>rydB</i>	tpe7, IS082	I	<i>ydiH</i> /STM1368	→ → ←	1450415	1450519	4	10	2.5	
STnc550	-	IV	<i>purR/sodB</i>	← → ←	1508946	1509412	6	10	1.7	nd
<i>STnc570<sup>l</sup></i>	<i>yneM</i> , small ORF	IV	<i>ydeI/ydeE</i>	→ ← ←	1593723	1594413	2	21	10.5	~190nt
STnc560	<i>hbrC</i>	IV	<i>ydeI/ydeE</i>	→ → ←	1593723	1594413	10	290	29.0	~90nt
STnc170	-	V	STM1528/STM1530	← → →	1606116	1605784	0	0		np
<i>isrF</i>	-	II	STM1552/STM1554	→ → ←	1630160	1629871	1	0		
<i>rydC</i>	IS067	I	STM1638/ <i>cybB</i>	→ → ←	1729673	1729738	5	245	49.0	
<i>micC</i>	IS063, tke8	III	<i>nifJ/ynaF</i>	→ → →	1745786	1745678	0	15	≥15.0	
STnc580	-	IV	<i>dbpA</i> /STM1656	← ← ←	1749662	1750147	11	311	28.3	~100nt
STnc180	-	V	<i>acnA/cysB</i>	← → ←	1807776	1807565	1	5	5.0	~200nt
STnc190	-	V	STM1841/ <i>kdgR</i>	→ → →	1937518	1937652	1	12	12.0	~500nt
<i>ryeB</i>	tpke79	I	STM1871/STM1872	→ → ←	1968155	1968053	24	653	27.2	
STnc200	-	V	<i>edd/zwf</i>	← → ←	1979598	1979550	0	3	≥3.0	nd
STnc210	-	V	<i>yecA</i> /STM1939	← → ←	2032404	2032580	0	0		np
<i>dsrA</i>	-	I	<i>yodD/yedP</i>	→ → →	2068736	2068649	6	149	24.8	
<i>rseX</i>	-	I	STM1994/ <i>ompS</i>	← → →	2077175	2077269	0	3	≥3.0	
STnc220	-	V	<i>ompS/cspB</i>	→ → ←	2079068	2078990	0	8	≥8.0	nd
STnc230	-	V	<i>pocR/pduF</i>	← → →	2115370	2115452	0	0		np
STnc240	-	V	<i>yeeF/yeeY</i>	← → ←	2147409	2147333	0	1	≥1.0	np
<i>ryeC</i>	tp11	I	<i>yegD</i> /STM2126	→ → →	2213871	2214016	42	72	1.7	
<i>cyaR</i>	<i>ryeE</i>	III	<i>yegQ</i> /STM2137	→ → →	2231130	2231216	31	659	21.3	
<i>isrG</i>	-	II	STM2243/STM2244	← → →	2344732	2345013	0	0		
<i>micF</i>	-	III	<i>ompC/yojN</i>	← → →	2366913	2367005	0	11	≥11.0	
<i>isrH-2</i>	-	II	<i>glpC</i> /STM2287	→ → →	2394582	2394303	0	0		
<i>isrH-1</i>	-	II	<i>glpC</i> /STM2287	→ → →	2394753	2394303	0	0		
STnc250 <sup>l</sup>	<i>ypfM</i> , small ORF	V	<i>acrD/yfjB</i>	→ → →	2596882	2596789	6	24	4.0	~220nt
<i>ryfA</i>	tp1	I	STM2534/ <i>sseB</i>	→ → ←	2674934	2675228	3	6	2.0	
<i>glmY</i>	tke1, <i>sroF</i>	I	<i>yfhK/purG</i>	← → ←	2707847	2707664	20	92	4.6	
<i>isrI</i>	-	II	STM2614/STM2616	→ → ←	2761576	2761329	0	2	≥2.0	
<i>isrJ</i>	-	II	STM2614/STM2616	→ → ←	2762031	2761957	1	0		
<i>isrK</i>	-	II	STM2616/STM2617	← → ←	2762867	2762791	0	0		
<i>isrB-2</i>	-	II	STM2631/ <i>sbcA</i>	→ → →	2770965	2770872	0	0		
<i>isrL</i>	-	II	<i>smpB</i> /STM2690	→ → →	2839399	2839055	0	0		

<i>isrM</i>	-	II	STM2762/STM2763	← → →	2905050	2905378	0	0		
<i>isrN</i>	-	II	STM2764/STM2765	← → ←	2906925	2907067	0	0		
<b>STnc260</b>	-	V	STM2816/ <i>luxS</i>	← → ←	2966073	2966247	0	0		np
<i>micA</i>	<i>sraD</i>	I	<i>luxS/gshA</i>	← → ←	2966853	2966926	1	128	128.0	
<b>STnc590</b>	-	IV	<i>avrA/sprB</i>	← ← ←	3010807	3010966	3	27	9.0	nd
<b>STnc600</b>	-	IV	<i>hilD/hilA</i>	→ → →	3018766	3019855	3	68	22.7	nd
<i>invR</i>	STnc270	III	<i>invH/STM 2901</i>	→ → →	3044924	3045014	113	3236	28.6	
<i>csrB</i>	-	III	<i>yqcC/syd</i>	← ← ←	3117059	3116697	69	67		
<i>gcvB</i>	IS145	III	<i>gcvA/ygdI</i>	← → ←	3135317	3135522	12	402	33.5	
<i>omrA</i>	<i>rygB</i>	III	<i>aas/galR</i>	← ← →	3170208	3170122	0	51	≥51.0	
<i>omrB</i>	<i>t59, rygA, sraE</i>	III	<i>aas/galR</i>	← ← →	3170408	3170322	1	52	52.0	
<b>STnc280</b>	-	V	<i>kduL/yqeF</i>	← → ←	3179540	3179622	0	1	≥1.0	np
<b>STnc290</b>	-	V	<i>tnpA_4/STM3033</i>	← ← ←	3194996	3194914	2	72	36.0	~85nt
<i>isrO</i>	-	II	STM3038/STM3039	← → →	3198380	3198580	0	0		
<i>ssrS</i>	-	I	<i>ygfE/ygfA</i>	→ → →	3222098	3222280	836	451		
<i>rygC</i>	t27	I	<i>ygfA/serA</i>	→ → ←	3222913	3223065	14	17	1.2	
<b>STnc300</b>	-	V	STM3123/STM3124	← ← →	3283965	3283807	0	0		np
<i>rygD</i>	tp8, C0730	I	<i>yqiK/rfaE</i>	→ ← ←	3362474	3362327	17	104	6.1	
<i>sraF</i>	tpk1, IS160	I	<i>yqiR/yqiT</i>	→ → →	3392069	3392261	0	25	≥25.0	
<b>STnc310</b>	-	V	<i>yqiT/yqiU</i>	→ ← →	3393327	3393267	0	0		np
<b>STnc320</b>	-	V	<i>yhaO/tdcG</i>	← → ←	3404895	3404949	0	1	≥1.0	np
<b>STnc610</b>	-	IV	<i>yhbC/metY</i>	← ← ←	3458296	3458578	1	19	19.0	~1250nt
<b>STnc330</b>	-	V	<i>greA/dacB</i>	← ← →	3468553	3468497	1	12	12.0	~1500nt
<i>sraH</i>	<i>ryhA</i>	I	<i>yhbL/arcB</i>	← → ←	3490383	3490500	55	2292	41.7	
<b>STnc340</b>	-	V	<i>tnpA_5/yhfL</i>	← ← →	3635884	3635756	0	0		nd
<i>ryhB-1</i>	<i>sraI, IS176</i>	I	<i>yhhX/yhhY</i>	← ← →	3715495	3715401	0	2	≥2.0	
<b>STnc350</b>	-	V	<i>uspA/yhiP</i>	→ ← →	3761440	3761373	0	0		nd
<b>STnc360</b>	-	V	<i>yhjB/yhjC</i>	← → →	3780254	3780402	0	0		np
<b>STnc370</b>	-	V	STM3654/ <i>glyS</i>	← → ←	3839688	3839758	0	0		np
<b>STnc380</b>	-	V	STM3691/ <i>lldP</i>	→ ← →	3885736	3885629	0	0		np
<b>STnc390</b>	-	V	<i>yibD/tdh</i>	← ← ←	3902653	3902594	0	0		nd
<i>istR-1</i>	-	VI	<i>ilvB/emrD</i>	← ← →	3998147	3998018	0	0		~75nt
<i>istR-2</i>	-	VI	<i>ilvB/emrD</i>	← ← →	3998147	3998018	0	0		~140nt
<b>STnc400</b>	-	V	STM3844/STM3845	→ → →	4051145	4051340	112	42		~55nt
<b>STnc410</b>	-	V	<i>glmU/STM3863</i>	← → ←	4072507	4072730	0	0		np
<i>glmZ</i>	k19, <i>ryiA, sraJ</i>	I	<i>yifK/hemY</i>	→ → ←	4141650	4141854	20	196	9.8	
<i>spf</i>	-	I	<i>polA/yihA</i>	→ → ←	4209066	4209175	2	33	16.5	
<i>csrC</i>	<i>sraK, ryiB, tpk2</i>	III	<i>yihA/yihI</i>	← → →	4210157	4210400	63	64		
<b>STnc420</b>	-	V	<i>yiiG/STM4041</i>	→ ← ←	4251539	4251480	0	0		np
<i>isrP</i>	-	II	STM4097/STM4098	← → ←	4306719	4306866	0	2	≥2.0	
<i>oxyS</i>	-		<i>argH/oxyR</i>	→ ← →	4342986	4342866	0	10	10.0	
<b>STnc430</b>	-	V	<i>pgi/yjbe</i>	→ ← →	4442059	4441898	0	0		np
<b>STnc620</b>	-	IV	<i>ssb/STM4257</i>	→ → →	4476817	4477856	4	41	10.3	nd
<i>sraL</i>	<i>ryjA</i>	III	<i>soxR/STM4267</i>	→ ← →	4505010	4504870	0	0		
<b>STnc630</b>	-	IV	<i>proP/basS</i>	→ → ←	4532473	4532638	1	27	27.0	nd
<b>STnc440</b>	-	V	STM4310/ <i>tnpA_6</i>	→ → →	4559193	4559277	9	456	50.7	~85nt
<b>STnc450</b>	-	V	<i>ytfL/msrA</i>	← ← ←	4645134	4645079	0	0		np
<b>STnc460</b>	-	V	STM4503/STM4504	→ ← →	4758332	4758187	0	0		np
<i>isrQ</i>	-	II	STM4508/STM4509	← → →	4762997	4763158	0	0		

<sup>a</sup> Gene names of *Salmonella* sRNAs considered experimentally as a result of this and previous studies. Method of identification is given in the third column. sRNA names follow *Salmonella* and/or *E. coli* nomenclature referenced in [7,8,9].

<sup>b</sup> Alternative sRNA IDs. References in [7,8,9], except STnc490, 500, 520, 540, 560, 570, 580, which have been newly predicted in this study (see Supplementary Table S ?).

<sup>c</sup> Evidence for sRNAs in *Salmonella*.

(I) Conserved sRNA found in *Salmonella* cDNA libraries, and previously shown to be expressed in *E. coli* (relevant ref. in [7]; Table 1).

(II) sRNA previously predicted and validated on northern blots in *Salmonella* by [9].

(III) sRNA previously validated on northern blots in *Salmonella* [1,7,10,11,12,13,14,15].

(IV) sRNA predicted through cDNA sequencing and validated by northern blot analysis in this study.

(V) sRNA previously predicted by [11].

(VI) IstR sRNAs [2] were not recovered in cDNA sequences but their expression in *Salmonella* validated by northern blot analysis in this study (Fig. S5).

- <sup>d</sup> Flanking genes of the intergenic region in which the sRNA candidate is located.
- <sup>e</sup> Orientation of sRNA candidate (middle) and flanking genes (→ and ← denote location of a gene on the clockwise or the counterclockwise strand of the *Salmonella* chromosome).
- <sup>f</sup> Genomic location of sRNA candidate gene according to the *Salmonella typhimurium* LT2 genome. For STnc470 through STnc640 start and end of the entire intergenic region are given.
- <sup>g</sup> Out of 145,873 sequences in total.
- <sup>h</sup> Out of 122,326 sequences in total.
- <sup>i</sup> Enrichment factor calculated by the number of blastable reads from Hfq coIP over control coIP.
- <sup>j</sup> Denotes verification on Northern blot in this study for new RNA transcripts; the estimated size is given in nucleotides (np = not probed; nd = no detectable transcript).
- <sup>k</sup> The cDNA reads map antisense internally of the IS200 element. Based on sequence identity they map to all IS200 elements (*tnpA\_1* to *tnpA\_6*).
- <sup>l</sup> STnc250 and STnc570 contain small ORFs annotated as *ypfM* or *yneM*, respectively, in *E. coli* [16].

**Table S4: mRNAs in Hfq CoIP identified by  $\geq 10$  of 170,000 inserts in pyrosequencing data**

STM number	Gene name <sup>a</sup>	Number of inserts in control coIP <sup>b</sup>	Number of inserts in Hfq coIP <sup>c</sup>	Product <sup>d</sup>
STM4261		254	1042	putative inner membrane protein
STM2665	yfiA	72	648	ribosome stabilization factor
STM1377	lpp	168	608	murein lipoprotein
STM4087	glpF	40	570	glycerol diffusion
STM1959	fliC	248	547	flagellar biosynthesis protein
STM2874	prgH	73	415	needle complex inner membrane protein
STM2267	ompC	63	385	outer membrane protein C precursor
STM2882	sipA	36	354	secreted effector protein
STM2885	sipB	126	335	translocation machinery component
STM4326	aspA	79	328	aspartate ammonia-lyase
STM2925	nlpD	30	300	lipoprotein
STM4086	glpK	115	278	glycerol kinase
STM2883	sipD	34	269	translocation machinery component
STM0739	sucD	14	261	succinyl-CoA synthetase alpha subunit
STM1572	ompD	76	246	putative outer membrane porin precursor
STM2898	invG	16	226	outer membrane secretin precursor
STM2879	sicP	6	224	secretion chaperone
STM2283	glpT	30	221	sn-glycerol-3-phosphate transport protein
STM1091	sopB	23	216	secreted effector protein
STM1732	ompW	28	206	outer membrane protein W precursor
STM0451	hupB	14	198	DNA-binding protein HU-beta
STM2871	prgK	46	198	needle complex inner membrane lipoprotein
STM2884	sipC	96	192	translocation machinery component
STM4406.S	ytfK	6	191	putative cytoplasmic protein
STM2867	hilC	3	187	invasion regulatory protein
STM2869	orgB	8	182	needle complex export protein
STM2878	sptP	20	177	protein tyrosine phosphatase/GTPase activating protein
STM2894	invC	14	175	type III secretion system ATPase
STM2875	hilD	23	174	invasion protein regulatory protein
STM2284	glpA	57	149	sn-glycerol-3-phosphate dehydrogenase large subunit
STM3526	glpD	39	147	sn-glycerol-3-phosphate dehydrogenase
STM2886	sicA	23	146	secretion chaperone
STM3138		19	143	putative methyl-accepting chemotaxis protein
STM2896	invA	19	142	needle complex export protein
STM0833	ompX	6	137	outer membrane protein X
STM2899	invF	18	129	invasion regulatory protein
STM2924	rpoS	19	129	RNA polymerase sigma factor
STM0629	cspE	9	125	cold shock protein E
STM2285	glpB	33	119	anaerobic glycerol-3-phosphate dehydrogenase subunit B
STM0736	sucA	42	110	2-oxoglutarate dehydrogenase
STM2445	ucpA	5	105	short chain dehydrogenase
STM1070	ompA	77	102	putative hydrogenase membrane component precursor
STM2282	glpQ	31	98	periplasmic glycerophosphodiester phosphodiesterase
STM3500	pckA	33	96	phosphoenolpyruvate carboxykinase
STM3649	cspA	7	94	major cold shock protein
STM0748	tolB	7	90	translocation protein TolB precursor
STM1782	yehH	10	90	putative inner membrane protein

STM3420	secY	30	87	preprotein translocase SecY
STM1171	flgN	8	80	putative FlgK/FlgL export chaperone
STM0737	sucB	12	79	dihydrolipoamide acetyltransferase
STM2891	spaO	8	77	type III secretion protein
STM2892	invJ	10	75	needle length control protein
STM3281	nlpI	19	75	lipoprotein
STM1887	yebK	0	74	putative transcriptional regulator
STM4360	miaA	5	74	tRNA delta(2)-isopentenylpyrophosphate transferase
STM4260		16	71	predicted cation efflux pump
STM0738	sucC	19	70	succinyl-CoA synthetase subunit beta
STM1919	cheM	12	70	methyl accepting chemotaxis protein II
STM0740	cydA	21	69	cytochrome d terminal oxidase polypeptide subunit I
STM2870	orgA	16	69	needle complex assembly protein
STM3150	hypO	2	68	putative Ni/Fe hydrogenase small subunit
STM3630	dppA	6	68	dipeptide transport protein
STM2328	nuoA	3	66	NADH dehydrogenase alpha subunit
STM0945	clpA	13	65	ATP-binding subunit of serine protease
STM1923	motA	9	65	flagellar motor protein
STM2897	invE	14	65	invasion protein
STM1921	cheA	16	62	chemotaxis sensory histidine protein kinase
STM2314		20	61	putative chemotaxis signal transduction protein
STM2895	invB	11	60	secretion chaperone
STM1230	phoQ	8	58	sensor kinase protein
STM4262		8	58	putative ABC-type bacteriocin/lantibiotic exporter
STM1751	hns	13	57	DNA-binding protein HLP-II
STM4336	ecnB	3	57	putative entericidin B precursor
STM1090	pipC	10	55	pathogenicity island-encoded protein C
STM2957	rumA	4	55	23S rRNA (uracil-5-)-methyltransferase
STM1922	motB	10	54	flagellar motor protein
STM2868	orgC	7	54	putative cytoplasmic protein
STM2872	prgJ	8	54	needle complex minor subunit
STM4232	malM	7	54	periplasmic protein precursor
STM1184	flgL	8	53	flagellar hook-associated protein
STM4258		10	53	putative methyl-accepting chemotaxis protein
STM4362	hflX	7	53	putative GTP-ase
STM1066	rmf	4	52	ribosome modulation factor
STM1431	sodB	21	52	superoxide dismutase
STM3604		8	52	putative inner membrane protein
STM1765	narK	11	50	nitrite extrusion protein
STM2261	napF	13	50	electron transfer protein
STM3053	gcvP	30	50	glycine dehydrogenase
STM3466	crp	4	50	catabolite activator protein
STM0600	cstA	19	49	carbon starvation protein
STM1285	yeaG	16	49	putative serine protein kinase
STM1311	osmE	11	49	transcriptional activator
STM3515	malT	14	49	transcriptional regulator MalT
STM0960	ftsK	8	47	cell division protein
STM1203	ptsG	8	47	glucose-specific IIBC component
STM3711	rfaF	3	47	ADP-heptose-LPS heptosyltransferase 1
STM4361	hfq	5	47	RNA-binding protein Hfq
STM0943	cspD	5	46	stress response protein
STM1183	flgK	5	46	flagellar hook-associated protein

STM2065	phsA	3	46	thiosulfate reductase precursor
STM2088	rfbX	1	46	putative O-antigen transferase
STM2873	prgI	15	46	needle complex major subunit
STM4151	rplJ	6	46	50S ribosomal protein L10
STM4325	dcuA	19	45	anaerobic C4-dicarboxylate transporter
STM0617	rna	3	44	RNase I
STM1231	phoP	3	44	response regulator
STM2889	spaQ	2	44	needle complex export protein
STM3803	yidF	5	44	putative cytoplasmic protein
STM4152	rplL	2	44	50S ribosomal protein L7/L12
STM0439	cyoE	16	43	protoheme IX farnesyltransferase
STM2001	yeel	6	43	putative inner membrane protein
STM2893	invI	10	43	needle complex assembly protein
STM2876	hilA	4	42	invasion protein transcriptional activator
STM2881	iacP	6	42	acyl carrier protein
STM3197	glgS	2	42	glycogen synthesis protein GlgS
STM0158	acnB	21	41	aconitate hydratase
STM0741	cydB	20	41	cytochrome d terminal oxidase polypeptide subunit II
STM2286	glpC	27	41	sn-glycerol-3-phosphate dehydrogenase K-small subunit
STM0039	nhaA	2	40	Na <sup>+</sup> /H antiporter
STM1336	rplT	10	40	50S ribosomal protein L20
STM1917	cheB	16	40	chemotaxis-specific methyltransferase
STM2081	gnd	3	40	6-phosphogluconate dehydrogenase
STM2082	rfbP	3	40	undecaprenol-phosphate galactosephosphotransferase/O-antigen transferase
STM2326	nuoC	7	40	NADH dehydrogenase I chain C/D
STM2827	alaS	3	40	alanyl-tRNA synthetase
STM3106	ansB	3	40	periplasmic L-asparaginase II
STM3807	yidE	1	40	hypothetical protein
STM0457	cof	2	39	putative hydrolase
STM1960	fliD	14	39	flagellar hook-associated protein
STM3404	smg	9	39	hypothetical protein
STM4060	cpxP	1	39	periplasmic repressor
STM0831	dps	9	38	DNA protection during starvation conditions
STM1057	pepN	5	37	aminopeptidase N
STM1838	yobF	7	37	putative cytoplasmic protein
STM3359	mdh	14	37	malate dehydrogenase
STM4315		0	37	putative DNA-binding protein
STM0994	mukB	4	36	condesin subunit B
STM1746.S	oppA	5	36	oligopeptide transport protein
STM1841		0	36	hypothetical protein
STM2660	clpB	46	36	ATP-dependent protease
STM3884	rbsB	6	36	D-ribose transport protein
STM4305.S		3	36	putative anaerobic dimethylsulfoxide reductase subunit A
STM0129	murC	4	35	UDP-N-acetylmuramate-L-alanine ligase
STM1165	grxB	5	35	glutaredoxin 2
STM1386	ttrS	6	35	sensory histidine kinase
STM1742	oppF	3	35	oligopeptide transport protein
STM1855	sopE2	4	35	type III-secreted effector protein
STM3162	yghB	2	35	hypothetical protein
STM1238	icdA	17	34	isocitrate dehydrogenase
STM1333	thrS	10	34	threonyl-tRNA synthetase
STM1918	cheR	8	34	glutamate methyltransferase

STM2323.S	nuoG	15	34	NADH dehydrogenase gamma subunit
STM3419	rpmJ	9	34	50S ribosomal protein L36
STM3430	rplN	10	34	50S ribosomal protein L14
STM3445	tuf	37	34	elongation factor Tu
STM4259		7	34	putative ABC exporter outer membrane component
STM0013	dnaJ	2	33	heat shock protein
STM1925	flhD	1	33	transcriptional activator FlhD
STM1956	fliA	11	33	flagellar biosynthesis sigma factor FliA
STM2956	relA	5	33	(p)ppGpp synthetase I
STM3700	gpsA	1	33	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
STM4154	rpoC	37	33	DNA-directed RNA polymerase beta' subunit
STM4237	lexA	6	33	LexA repressor
STM0964	dmsA	7	32	anaerobic dimethyl sulfoxide reductase subunit A
STM1085	yccA	4	32	putative transport protein
STM1164	yceB	3	32	putative outer membrane lipoprotein
STM3592	yhiP	4	32	putative peptide transport protein
STM4562		3	32	putative inner membrane protein
STM0614	ybdQ	9	31	putative universal stress protein
STM1837	cspC	11	31	cold shock protein
STM3183	icc	4	31	cyclic 3',5'-adenosine monophosphate phosphodiesterase
STM3577	tcp	11	31	methyl-accepting transmembrane citrate/phenol chemoreceptor
STM0749	pal	7	30	peptidoglycan-associated lipoprotein precursor
STM1583		1	30	putative cytoplasmic protein
STM1955	fliZ	3	30	putative FliA-regulator
STM2432	ptsI	7	30	PEP-protein phosphotransferase
STM3006	ygdQ	3	30	putative transport protein
STM4582	slt	0	30	soluble lytic murein transglycosylase
STM0093	imp	2	29	organic solvent tolerance protein precursor
STM0224	yaeT	5	29	putative outer membrane protein precursor
STM0687	ybfM	2	29	putative outer membrane protein
STM0688	ybfN	1	29	putative lipoprotein
STM1888	pykA	6	29	pyruvate kinase
STM3705	yibP	2	29	hypothetical protein
STM0120	mraW	4	28	S-adenosyl-methyltransferase
STM1172	flgM	10	28	anti-FliA factor
STM1334.c	infC	11	28	translation initiation factor IF-3
STM1996	cspB	0	28	putative cold-shock protein
STM3918	rfe	2	28	undecaprenyl-phosphate N-acetylglucosaminyltransferase
STM4153	rpoB	11	28	DNA-directed RNA polymerase beta subunit
STM0472	maa	4	27	maltose O-acetyltransferase
STM0800	slrP	9	27	leucine-rich repeat protein
STM2301	pqaB	4	27	putative melittin resistance protein
STM2532		3	27	putative inner membrane lipoprotein
STM3004	ygdP	3	27	dinucleoside polyphosphate hydrolase
STM3055	gcvT	7	27	aminomethyltransferase
STM3865	atpD	17	27	ATP synthase subunit B
STM4243	yjbN	1	27	hypothetical protein
STM4561	osmY	7	27	hyperosmotically-inducible periplasmic protein
STM0130	ddl	6	26	D-alanylalanine synthetase
STM0226	lpxD	3	26	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
STM0366	yahO	5	26	putative periplasmic protein
STM0734	sdhA	25	26	succinate dehydrogenase catalytic subunit

STM1290	gapA	11	26	glyceraldehyde-3-phosphate dehydrogenase
STM1924.S	flhC	3	26	flagellar transcriptional activator
STM2368	truA	0	26	tRNA pseudouridine synthase A
STM3070	epd	3	26	D-erythrose 4-phosphate dehydrogenase
STM3216		6	26	putative methyl-accepting chemotaxis protein
STM4037	fdoG	26	26	formate dehydrogenase alpha subunit
STM4076	ydeZ	6	26	putative sugar transport protein
STM0122	ftsI	7	25	division specific transpeptidase
STM0125	mraY	1	25	phospho-N-acetylmuramoyl-pentapeptide-transferase
STM1196	acpP	10	25	acyl carrier protein
STM1317	celG	0	25	hypothetical protein
STM1318	katE	4	25	hydroperoxidase HP11
STM1324		5	25	putative cytoplasmic protein
STM1338	pheT	13	25	phenylalanyl-tRNA synthetase beta subunit
STM1661	ydaA	18	25	putative universal stress protein
STM1801	ycgO	2	25	cell volume regulation protein CvrA
STM1938	yecA	7	25	putative metal-binding protein
STM1947	uvrY	2	25	response regulator
STM2318	nuoL	6	25	NADH dehydrogenase subunit L
STM2983	ygdl	6	25	putative lipoprotein
STM3003	ptsP	8	25	transcriptional regulator
STM3403	yrdD	4	25	putative DNA topoisomerase
STM3616	yhlL	5	25	tetratricopeptide repeat protein
STM3701	secB	5	25	export protein SecB
STM3968	udp	8	25	uridine phosphorylase
STM4343	frdA	15	25	fumarate reductase
STM1349	pps	9	24	phosphoenolpyruvate synthase
STM1601	ugtL	1	24	hypothetical protein
STM2530		3	24	putative anaerobic dimethylsulfoxide reductase
STM2888	spaR	2	24	needle complex export protein
STM4170	hupA	12	24	DNA-binding protein HU-alpha
STM4368	vacB	4	24	putative exoribonuclease
STM0735	sdhB	8	23	succinate dehydrogenase catalytic subunit
STM0863	dacC	2	23	D-alanyl-D-alanine carboxypeptidase
STM1000	asnS	3	23	asparaginyln-tRNA synthetase
STM1749	adhE	9	23	iron-dependent alcohol dehydrogenase
STM1920	cheW	6	23	chemotaxis docking protein
STM2083	rfbK	1	23	phosphomannomutase
STM2327	nuoB	3	23	NADH dehydrogenase beta subunit
STM2526	ndk	2	23	nucleoside diphosphate kinase
STM2651	yfiQ	11	23	putative acetyl-CoA synthetase
STM3591	uspA	14	23	universal stress protein A
STM3702	grxC	2	23	glutaredoxin 3
STM3808.S	ibpB	1	23	small heat shock protein
STM3972	aarF	8	23	putative ubiquinone biosynthesis protein UbiB
STM4257		5	23	hypothetical protein
STM0186	dksA	12	22	dnaK suppressor protein
STM0452	cypD	3	22	peptidyl-prolyl isomerase
STM0730	glfA	16	22	citrate synthase
STM1094	pipD	2	22	pathogenicity island-encoded protein D
STM1249		5	22	utative periplasmic protein
STM2091	rfbG	3	22	CDP glucose 4,6-dehydratase

STM2296	ais	0	22	aluminum-inducible protein
STM2780	pipB2	3	22	secreted effector protein
STM2890	spaP	2	22	needle complex export protein
STM4410	ytfN	6	22	putative periplasmic protein
STM1161.S	yceP	1	21	putative cytoplasmic protein
STM1190	yceD	9	21	putative metal-binding protein
STM1283	yeaJ	2	21	putative methyl-accepting chemotaxis protein
STM1286	mipA	6	21	MitA-interacting protein A
STM1291	yeaA	1	21	methionine sulfoxide reductase B
STM1683	tyrR	1	21	transcriptional regulator
STM1795		9	21	putative glutamic dehydrogenase-like protein
STM1916	cheY	3	21	chemotaxis regulator
STM1941		0	21	putative inner membrane protein
STM1945	pgsA	2	21	phosphatidylglycerophosphate synthetase
STM2391	fadL	1	21	outer membrane-bound fatty acid transporter
STM3147	hybC	3	21	hydrogenase-2 large subunit
STM3282	pnp	4	21	polynucleotide phosphorylase
STM3415	rpoA	11	21	DNA-directed RNA polymerase alpha subunit
STM3417	rpsK	8	21	30S ribosomal protein S11
STM4240	yjbJ	13	21	putative cytoplasmic protein
STM4330	groEL	43	21	chaperonin GroEL
STM0653	ybeL	3	20	putative cytoplasmic protein
STM0732	sdhC	4	20	succinate dehydrogenase cytochrome b556 large membrane subunit
STM1713	cysB	3	20	transcriptional regulator for cysteine regulon
STM2035	cbiA	4	20	cobyrinic acid a,c-diamide synthase
STM2322	nuoH	6	20	NADH dehydrogenase subunit H
STM2533	sseA	4	20	putative sulfurtransferase
STM3187	ygiB	0	20	putative inner membrane protein
STM3538	glgB	10	20	glycogen branching enzyme
STM3708	tdh	5	20	L-threonine 3-dehydrogenase
STM3710	rfaD	9	20	ADP-L-glycero-D-mannoheptose-6-epimerase
STM3900	ilvL	2	20	ilvGEDA operon leader peptide
STM3996	yihE	1	20	putative type II homoserine kinase
STM0088	apaH	2	19	diadenosinetetraphosphatase
STM0124	murF	6	19	D-alanine-D-alanine ligase
STM0128	murG	4	19	N-acetylglucosaminyl transferase
STM0133	ftsZ	7	19	cell division protein FtsZ
STM0449	clpX	10	19	ATP-dependent protease ATP-binding subunit
STM1398	sseB	2	19	translocation machinery component
STM1660.S	fnr	4	19	transcriptional regulator
STM1754	yhcK	0	19	putative phosphoesterase
STM1796	treA	6	19	trehalase
STM1875	yobA	0	19	putative copper resistance protein
STM2059	yeeX	1	19	hypothetical protein
STM2184	sanA	3	19	vancomycin sensitivity
STM2270	rscB	0	19	response regulator
STM2280		1	19	putative permease
STM2433	crr	7	19	glucose-specific PTS system enzyme IIA component
STM2681	grpE	1	19	heat shock protein
STM2782	mig-14	1	19	putative transcriptional activator
STM3113	nupG	2	19	nucleoside transport
STM3426	rpsH	6	19	30S ribosomal protein S8

STM3986	trkH	3	19	potassium transport protein
STM4331	yjel	6	19	putative outer membrane lipoprotein
STM4391	rpsF	1	19	30S ribosomal protein S6
STM0132	ftsA	6	18	cell division protein
STM0474	ybaJ	4	18	putative cytoplasmic protein
STM0508	ybbP	2	18	putative inner membrane protein
STM0750	ybgF	4	18	putative periplasmic protein
STM0959	lrp	1	18	leucine-responsive regulatory protein
STM1148.S	ymdC	6	18	putative phospholipase
STM1335	rpmI	5	18	50S ribosomal protein L35
STM1602	sifB	0	18	secreted effector protein
STM1745	oppB	1	18	oligopeptide permease ABC transporter membrane component
STM1804.S	ycgB	4	18	putative cytoplasmic protein
STM1840	yobG	2	18	putative inner membrane protein
STM1867	pagK	0	18	PagK
STM1950	sdiA	3	18	transcriptional regulator
STM2214	spr	2	18	putative lipoprotein
STM2333	yfbS	1	18	putative response regulator
STM2486		1	18	putative inner membrane protein
STM2640	rpoE	2	18	RNA polymerase sigma-70 factor
STM2675	rimM	3	18	16S rRNA-processing protein
STM2945	sopD	3	18	secreted effector protein
STM3186	tolC	10	18	outer membrane channel precursor protein
STM3229	ycjD	3	18	putative inner membrane protein
STM3272	yhbS	4	18	putative transport protein
STM3286	infB	4	18	translation initiation factor IF-2
STM3373	mreC	0	18	rod shape-determining protein
STM3434	rpsC	20	18	30S ribosomal protein S3
STM3611	yhjH	1	18	hypothetical protein
STM3680	aldB	3	18	aldehyde dehydrogenase B
STM3867	atpA	27	18	ATP synthase subunit A
STM4078	yneB	9	18	hypothetical protein
STM0134	lpxC	15	17	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
STM0160	yacL	1	17	hypothetical protein
STM0211	yaeH	13	17	putative cytoplasmic protein
STM0311	yafJ	0	17	putative glutamine amidotransferase
STM0327		6	17	putative cytoplasmic protein
STM0440	cyoD	6	17	cytochrome o ubiquinol oxidase subunit IV
STM0465	ybaY	11	17	hypothetical protein
STM0733	sdhD	6	17	succinate dehydrogenase cytochrome b556 small membrane subunit
STM0772	gpmA	12	17	phosphoglyceromutase
STM0962	ycaJ	3	17	hypothetical protein
STM0971		0	17	putative cytoplasmic protein
STM1177	figE	13	17	flagellar hook protein
STM1444	slyA	2	17	transcriptional regulator SlyA
STM1626	trg	1	17	methyl-accepting chemotaxis protein III
STM1638		1	17	putative SAM-dependent methyltransferase
STM1830	manX	12	17	mannose-specific enzyme IIAB
STM1972	fliI	3	17	flagellum-specific ATP synthase
STM2061	sbmC	8	17	DNA gyrase inhibitor
STM2767		1	17	putative DNA/RNA helicase
STM2796	yqaE	0	17	putative transport protein

STM2800		1	17	putative inner membrane protein
STM2865	avrA	2	17	secreted effector protein
STM3056	visC	3	17	hypothetical protein
STM3069	pgk	17	17	phosphoglycerate kinase
STM3154		0	17	putative ATP-dependent RNA helicase-like protein
STM3184	yqiB	3	17	putative cytoplasmic protein
STM3188	ygiC	6	17	putative glutathionylspermidine synthase
STM3228	yqjC	5	17	putative periplasmic protein
STM3407	fmt	3	17	methionyl-tRNA formyltransferase
STM3436	rpsS	8	17	30S ribosomal protein S19
STM3440	rplC	3	17	50S ribosomal protein L3
STM3715	rfaZ	0	17	lipopolysaccharide core biosynthetic protein
STM3879	yieN	0	17	putative regulatory protein
STM3885	rbsK	1	17	ribokinase
STM4411	ytfP	2	17	putative cytoplasmic protein
STM0068	caiF	0	16	of cai/fix operon transcriptional regulator
STM0222	cdsA	4	16	CDP-diglyceride synthase
STM0228	lpxA	1	16	UDP-N-acetylglucosamine acyltransferase
STM0446	bolA	1	16	putative regulatory protein
STM0448	clpP	2	16	ATP-dependent Clp protease proteolytic subunit
STM1227	pepT	4	16	peptidase T
STM1313	celB	0	16	sugar-specific enzyme II
STM1328		2	16	putative outer membrane protein
STM1389	orf319	4	16	putative inner membrane protein
STM1682	tpx	1	16	thiol peroxidase
STM1839		1	16	hypothetical protein
STM1915	cheZ	2	16	chemotactic response protein
STM2060	yeeA	1	16	putative inner membrane protein
STM2259	napA	23	16	periplasmic nitrate reductase
STM2299	yfbG	9	16	hypothetical protein
STM2300		3	16	putative cytoplasmic protein
STM2316.S	nuoN	2	16	NADH dehydrogenase subunit N
STM2325	nuoE	5	16	ATP synthase subunit E
STM2337	ackA	5	16	acetate/propionate kinase
STM2390	yfcZ	4	16	putative cytoplasmic protein
STM2652	pssA	2	16	phosphatidylserine synthase
STM3068	fba	9	16	fructose-bisphosphate aldolase
STM3320	rpoN	9	16	DNA-directed RNA polymerase subunit N
STM3321	yhbH	7	16	putative sigma N modulation factor
STM3728	rpmB	1	16	50S ribosomal protein L28
STM3917	rho	2	16	transcription termination factor Rho
STM4495		5	16	putative type II restriction enzyme methylase subunit
STM4512	iadA	1	16	isoaspartyl dipeptidase
STM4541	mdoB	3	16	phosphoglycerol transferase I
STM0012	dnaK	8	15	molecular chaperone DnaK
STM0126	murD	4	15	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
STM0127	ftsW	3	15	essential cell division gene
STM0666	Int	4	15	apolipoprotein N-acyltransferase
STM0667	ybeX	3	15	putative transport protein
STM1071	sulA	3	15	cell division inhibitor
STM1400	sseC	2	15	translocation machinery component
STM1445	slyB	6	15	putative outer membrane lipoprotein

STM1463	add	2	15	adenosine deaminase
STM1480	pntB	1	15	pyridine nucleotide transhydrogenase
STM1533		1	15	putative hydrogenase
STM1641	hrpA	3	15	ATP-dependent helicase
STM1651	nifJ	3	15	putative pyruvate-flavodoxin oxidoreductase
STM1805	fadR	1	15	fatty acid metabolism regulator
STM2084	rfbM	1	15	mannose-1-phosphate guanylyltransferase
STM2089	rfbJ	1	15	CDP-abequose synthase
STM2309	menD	4	15	2-oxoglutarate decarboxylase
STM2346		0	15	putative NTP pyrophosphohydrolase
STM2472	maeB	5	15	phosphate acetyltransferase
STM2646	yfiD	9	15	putative formate acetyltransferase
STM2952	eno	5	15	phosphopyruvate hydratase
STM3002	lgt	0	15	prolipoprotein diacylglycerol transferase
STM3054	gcvH	3	15	glycine cleavage system protein H
STM3209	rpsU	2	15	30S ribosomal protein S21
STM3402	yrdC	1	15	putative dsRNA-binding protein
STM3416	rpsD	7	15	30S ribosomal protein S4
STM3418	rpsM	4	15	30S ribosomal protein S13
STM3446	fusA	19	15	elongation factor EF-2
STM3537	glgX	3	15	glycogen debranching enzyme
STM3586.S	yhiH	5	15	putative ABC-type multidrug transport system ATPase component
STM3864	atpC	13	15	ATP synthase subunit epsilon
STM3958	recQ	0	15	ATP-dependent DNA helicase
STM3999	polA	4	15	DNA polymerase I
STM4073	ydeW	1	15	putative transcriptional repressor
STM4241	zur	0	15	transcriptional repressor
STM4290	proP	2	15	low-affinity proline transporter
STM4297	melR	1	15	melibiose operon regulator
STM4359	mutL	4	15	DNA mismatch repair protein
STM0064	dapB	1	14	dihydrodipicolinate reductase
STM0365	yahN	0	14	putative transport protein
STM0417	ribH	0	14	riboflavin synthase subunit beta
STM0665	gltI	5	14	glutamate/aspartate transporter
STM0694	fldA	0	14	flavodoxin
STM0743	ybgE	3	14	putative inner membrane lipoprotein
STM0963	serS	5	14	seryl-tRNA synthetase
STM1234.S	trmU	4	14	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
STM1239		1	14	putative cytoplasmic protein
STM1284	yeaH	4	14	hypothetical protein
STM1409	ssaJ	0	14	needle complex inner membrane lipoprotein
STM1589	yncB	9	14	putative NADP-dependent oxidoreductase
STM1712	acnA	8	14	aconitate hydratase
STM1731		3	14	putative catalase
STM1845	prc	2	14	carboxy-terminal protease
STM1846	proQ	0	14	putative solute/DNA competence effector
STM2033	cbiC	1	14	precorrin-8X methylmutase
STM2090	rfbH	6	14	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase
STM2297	yfbE	2	14	4-amino-4-deoxy-L-arabinose lipopolysaccharide-modifying enzyme
STM2298	pmrF	3	14	putative glycosyl transferase
STM2320	nuoJ	3	14	NADH dehydrogenase subunit J
STM2489	dapA	2	14	dihydrodipicolinate synthase

STM2674	trmD	3	14	tRNA (guanine-N(1)-)-methyltransferase
STM2829	recA	3	14	recombinase A
STM2866	sprB	2	14	transcriptional regulator
STM2877	iagB	4	14	invasion protein precursor
STM3058	pepP	4	14	proline aminopeptidase P II
STM3061	ygfA	0	14	putative ligase
STM3149	hybA	0	14	putative hydrogenase-2 component
STM3223	ygiR	4	14	putative dehydrogenase
STM3225	ygiU	3	14	putative dicarboxylate permease
STM3342	sspA	2	14	stringent starvation protein A
STM3369	yhdP	2	14	putative protease
STM3534	glgP	4	14	glycogen phosphorylase
STM3919	wzzE	0	14	enterobacterial common antigen chain length regulator
STM3939	cyaA	3	14	adenylate cyclase
STM3947	dapF	2	14	diaminopimelate epimerase
STM4089	menG	5	14	ribonuclease activity regulator protein RraA
STM4409	ytfM	2	14	putative outer membrane protein
STM4517	yjiO	0	14	putative transport protein
STM4586	rob	1	14	transcriptional regulator
STM0123	murE	5	13	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
STM0212		1	13	putative inner membrane protein
STM0537	cysS	2	13	cysteinyI-tRNA synthetase
STM0543	fimA	1	13	fimbrin
STM0791	hutH	7	13	histidine ammonia-lyase
STM0865	ybjG	1	13	putative permease
STM0940	ybjX	1	13	VirK-like protein
STM0944	clpS	2	13	ATP-dependent Clp protease adaptor protein ClpS
STM0961	lolA	4	13	outer-membrane lipoprotein carrier protein precursor
STM1112	cbpA	0	13	DNA-binding protein
STM1221	cobB	1	13	NAD-dependent deacetylase
STM1488	mlc	4	13	pts operon transcriptional repressor
STM1679	mppA	4	13	periplasmic murein tripeptide transport protein
STM1777	hemA	3	13	glutamyl-tRNA reductase
STM1848	yebS	1	13	putative inner membrane protein
STM1881	yebF	4	13	putative periplasmic protein
STM1886	zwf	3	13	glucose-6-phosphate 1-dehydrogenase
STM1935	ftn	3	13	cytoplasmic ferritin
STM1946	uvrC	5	13	excinuclease ABC subunit C
STM1979	fljP	3	13	flagellar biosynthesis protein
STM2080	udg	1	13	UDP-glucose/GDP-mannose dehydrogenase
STM2086	rfbU	2	13	mannosyl transferase
STM2093	rfbI	6	13	CDP-6-deoxy-delta-3,4-glucoseen reductase
STM2215	rtn	1	13	hypothetical protein
STM2226	yejK	0	13	nucleoid-associated protein NdpA
STM2317	nuoM	5	13	NADH dehydrogenase subunit M
STM2321	nuoI	3	13	NADH dehydrogenase subunit I
STM2324	nuoF	8	13	NADH dehydrogenase I chain F
STM2336		0	13	hypothetical protein
STM2638	rseB	0	13	periplasmic negative regulator of sigmaE
STM2662	rluD	3	13	ribosomal large subunit pseudouridine synthase D
STM2677	ffh	5	13	4.5S-RNP protein
STM2887	spaS	2	13	type III secretion protein

STM3157	yghA	6	13	oxidoreductase
STM3226	yqjA	1	13	hypothetical protein
STM3296	hflB	9	13	ATP-dependent zinc-metallo protease
STM3368	tldD	4	13	microcin B17-processing protein
STM3410	mscL	4	13	large-conductance mechanosensitive channel
STM3536	glgC	7	13	glucose-1-phosphate adenylyltransferase
STM3569	ftsX	2	13	putative cell division protein
STM3704	pmgI	5	13	phosphoglyceromutase
STM3719	rfaB	0	13	lipopolysaccharide-1,6-D-galactosyltransferase
STM3871	atpB	6	13	ATP synthase subunit A
STM3973	tatA	2	13	twin arginine translocase protein A
STM4275	acs	1	13	acetyl-coenzyme A synthetase
STM4367	yjeB	3	13	putative negative regulator
STM4404	cysQ	2	13	sulfite biosynthetic protein
STM4580.S	nadR	0	13	nicotinamide-nucleotide adenylyltransferase
STM0131	ftsQ	2	12	cell division protein
STM0216	rpsB	5	12	30S ribosomal protein S2
STM0217	tsf	6	12	elongation factor Ts
STM0408	secF	1	12	protein export protein SecF
STM0442	cyoB	11	12	cytochrome o ubiquinol oxidase subunit I
STM0450	lon	5	12	ATP-dependent protease Lon
STM0542	folD	0	12	5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase
STM0669	phoL	3	12	putative phosphate starvation-inducible protein
STM0683	nagA	5	12	N-acetylglucosamine-6-phosphate deacetylase
STM0802	moaA	2	12	molybdenum cofactor biosynthesis protein A
STM0807	ybhL	3	12	putative permease
STM0888	artM	0	12	arginine transport system component
STM0934	ltaA	1	12	L-allo-threonine aldolase
STM1119	wraB	8	12	TrpR binding protein WraB
STM1246	pagC	14	12	virulence membrane protein PAGC precursor
STM1486	ynfM	0	12	putative transport protein
STM1511	ydfG	0	12	putative oxidoreductase
STM1558		2	12	putative glycosyl hydrolase
STM1582	nhoA	0	12	putative arylamine N-acetyltransferase
STM1710	pgpB	0	12	phosphatidylglycerophosphate phosphatase B
STM1743	oppD	3	12	oligopeptide transporter ATP-binding component
STM1752	galU	1	12	glucose-1-phosphate uridylyltransferase
STM1807	dsbB	0	12	disulfide bond formation protein B
STM1976	fliM	9	12	flagellar motor switch protein
STM2067	sbcB	2	12	exonuclease I
STM2217	yjeB	1	12	putative ABC-type dipeptide/oligopeptide/nickel transport system permease
STM2246	narP	0	12	response regulator
STM2378	fabB	10	12	3-oxoacyl-(acyl carrier protein) synthase
STM2388	yfcX	1	12	putative dehydrogenase
STM2520	yfgL	3	12	putative serine/threonine protein kinase
STM2688	smpB	1	12	SsrA-binding protein
STM2781	virK	1	12	virulence protein
STM2814	emrA	0	12	multidrug resistance secretion protein
STM2950		2	12	putative metal-dependent hydrolase
STM3040	lysS	5	12	lysyl-tRNA synthetase
STM3107	yggN	1	12	putative periplasmic protein
STM3153	yqhA	3	12	hypothetical protein

STM3189	ygiD	0	12	putative cytoplasmic protein
STM3201	glnE	2	12	adenyl transferase for glutamine synthetase
STM3297	ftsJ	2	12	23S rRNA methyltransferase
STM3441	rpsJ	2	12	30S ribosomal protein S10
STM3453	fkpA	3	12	FKBP-type peptidyl-prolyl cis-trans isomerase
STM3589	pitA	0	12	low-affinity phosphate transporter
STM3602		1	12	putative regulatory protein
STM3758	fidL	0	12	putative inner membrane protein
STM3872	atpI	2	12	ATP synthase subunit I
STM3970	ubiE	0	12	ubiquinone/menaquinone biosynthesis methyltransferase
STM4127	yijC	1	12	putative transcriptional repressor
STM4249	aphA	3	12	non-specific acid phosphatase/phosphotransferase
STM4390		1	12	putative cytoplasmic protein
STM4392	priB	1	12	primosomal replication protein N
STM0046	ileS	4	11	isoleucyl-tRNA synthetase
STM0047	lspA	3	11	signal peptidase II
STM0121	ftsL	0	11	cell division protein
STM0221	uppS	0	11	undecaprenyl pyrophosphate synthetase
STM0475	acrB	12	11	acridine efflux pump
STM0476	acrA	2	11	acridine efflux pump
STM0484	dnaX	2	11	DNA polymerase III subunits gamma and tau
STM0648	leuS	7	11	leucyl-tRNA synthetase
STM0685	nagE	2	11	N-acetylglucosamine-specific enzyme IIABC
STM0781	modA	4	11	molybdate transporter
STM0814	ybhQ	5	11	putative inner membrane protein
STM0819	ybiH	1	11	putative transcriptional repressor
STM0870		0	11	hypothetical protein
STM0941	ybjY	1	11	hypothetical protein
STM0977	serC	3	11	phosphoserine aminotransferase
STM1147		0	11	hypothetical protein
STM1167	rimJ	0	11	acetylase
STM1185	rne	0	11	RNase E
STM1195	fabG	4	11	3-ketoacyl-(acyl-carrier-protein) reductase
STM1300		1	11	putative periplasmic protein
STM1415	ssaN	0	11	type III secretion system ATPase
STM1468	fumA	5	11	fumarase A
STM1594	srfB	5	11	putative virulence protein
STM1744	oppC	3	11	oligopeptide transport protein
STM1847	yebR	0	11	putative nucleotide-binding protein
STM1900	ntpA	0	11	dATP pyrophosphohydrolase
STM1939		0	11	putative glucose-6-phosphate dehydrogenase
STM2028	cbiG	2	11	cobalamin biosynthesis protein CbiG
STM2066	sopA	0	11	secreted effector protein
STM2165	yehZ	0	11	putative transport protein
STM2186		4	11	putative NADPH-dependent glutamate synthase beta chain
STM2362	purF	6	11	amidophosphoribosyltransferase
STM2446		0	11	putative iron-dependent peroxidase
STM2494		3	11	hypothetical protein
STM2536	pepB	1	11	aminopeptidase B
STM2819	yqaA	0	11	putative inner membrane protein
STM3132		4	11	putative xylanase/chitin deacetylase
STM3133		2	11	putative amidohydrolase

STM3144	hypA	0	11	hydrogenase nickel incorporation protein
STM3207	ygiH	2	11	hypothetical protein
STM3230	yqjE	6	11	putative inner membrane protein
STM3362		0	11	putative periplasmic protein
STM3421	rplO	11	11	50S ribosomal protein L15
STM3428	rplE	4	11	50S ribosomal protein L5
STM3465	yhfA	3	11	putative inner membrane protein
STM3467	yhfK	1	11	putative inner membrane protein
STM3481	trpS	3	11	tryptophanyl-tRNA synthetase
STM3568	rpoH	7	11	RNA polymerase sigma factor
STM3590	uspB	0	11	universal stress protein UspB
STM3614	dctA	0	11	C4-dicarboxylate transport protein
STM3617		1	11	endo-1,4-D-glucanase
STM3718	rfal	4	11	lipopolysaccharide-alpha-1,3-D-galactosyltransferase
STM3773		2	11	putative transcriptional regulator
STM3797	ivbL	3	11	ivb operon leader peptide
STM3915	trxA	5	11	thioredoxin
STM3938	hemC	4	11	porphobilinogen deaminase
STM3961	pdB	2	11	lysophospholipase L2
STM3975	tatC	0	11	Sec-independent protein secretion pathway component
STM3978	yigC	1	11	putative oxidoreductase
STM4062	pfkA	4	11	6-phosphofructokinase
STM4221	pgi	3	11	glucose-6-phosphate isomerase
STM4239		5	11	putative cytoplasmic protein
STM4334	efp	1	11	elongation factor P
STM4378	yjfN	8	11	putative inner membrane protein
STM4379	yjfO	14	11	putative lipoprotein
STM4416	mpl	0	11	UDP-N-acetylmuramate/L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
STM4470	yjgD	1	11	putative cytoplasmic protein
STM4514.S	yjih	0	11	putative inner membrane protein
STM4533	tsr	3	11	methyl-accepting chemotaxis protein I
STM4563	yjU	0	11	putative phosphoesterase
STM0003	thrB	2	10	homoserine kinase
STM0159		1	10	putative restriction endonuclease
STM0318	yafA	3	10	hypothetical protein
STM0376	sbmA	0	10	putative ABC transporter membrane protein
STM0407	secD	1	10	protein export protein SecD
STM0494	ushA	3	10	UDP-sugar hydrolase/5'-nucleotidase
STM0652		6	10	putative sigma-54 dependent transcriptional regulator
STM0872	grxA	0	10	glutaredoxin 1
STM0890	artI	1	10	arginine transport system
STM0999	ompF	3	10	outer membrane protein F precursor
STM1018		0	10	hypothetical protein
STM1176	flgD	6	10	flagellar basal body rod modification protein
STM1178	flgF	4	10	cell-proximal portion of basal-body rod
STM1269		0	10	chorismate mutase
STM1270	yeaS	0	10	putative transport protein
STM1274	yeaQ	1	10	putative inner membrane protein
STM1297	selD	1	10	selenophosphate synthetase
STM1312	celA	0	10	sugar-specific enzyme IIB
STM1345	ydiU	2	10	hypothetical protein
STM1391	ssrB	3	10	transcriptional activator

STM1399	sscA	0	10	secretion system chaparone
STM1410		0	10	putative cytoplasmic protein
STM1433	ydhD	3	10	putative glutaredoxin protein
STM1536		0	10	putative hydrogenase maturation protease
STM1685	ycjX	0	10	putative ATPase
STM1714	topA	2	10	DNA topoisomerase I
STM1815	minD	5	10	cell division inhibitor protein
STM1831	manY	8	10	mannose-specific enzyme IIC
STM1832	manZ	5	10	mannose-specific enzyme IID
STM1907	cutC	0	10	copper homeostasis protein
STM1961	fliS	5	10	flagellar protein FliS
STM2026	cbiJ	2	10	precorrin-6x reductase
STM2032	cbiD	3	10	cobalt-precorrin-6A synthase
STM2034	cobD	1	10	cobalamin biosynthesis protein
STM2036	pocR	2	10	transcriptional regulator
STM2039	pudB	7	10	polyhedral body protein
STM2087	rfbV	1	10	abequosyltransferase
STM2154	mrp	0	10	putative ATP-binding protein
STM2164	yehY	2	10	putative ABC-type proline/glycine betaine transport system permease component
STM2189	mgIA	0	10	methyl-galactoside transport protein
STM2190	mgIB	1	10	galactose transport protein
STM2201	yeiE	1	10	putative transcriptional regulator
STM2306	menC	1	10	O-succinylbenzoate synthase
STM2330	lrhA	0	10	NADH dehydrogenase transcriptional repressor
STM2361		3	10	putative regulatory protein
STM2483	dapE	2	10	succinyl-diaminopimelate desuccinylase
STM2523	gcpE	1	10	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
STM2524	yfgA	9	10	hypothetical protein
STM2557	cadC	0	10	transcriptional activator
STM2679	yfjD	1	10	hypothetical protein
STM2858	hypE	2	10	putative hydrogenase formation protein
STM3043	dsbC	0	10	protein disulfide isomerase II
STM3122		1	10	putative arylsulfatase
STM3195	ribB	3	10	3,4-dihydroxy-2-butanone 4-phosphate synthase
STM3266	yraO	1	10	putative phosphoheptose isomerase
STM3338	nanT	0	10	putative sialic acid transporter
STM3341	sspB	1	10	stringent starvation protein B
STM3347	yhcB	0	10	putative periplasmic protein
STM3363	yhcO	1	10	putative cytoplasmic protein
STM3423	rpsE	6	10	30S ribosomal protein S5
STM3439	rplD	1	10	50S ribosomal protein L4
STM3570	ftsE	0	10	putative cell division ATPase
STM3594	prlC	2	10	oligopeptidase A
STM3624	yhjU	4	10	putative inner membrane protein
STM3703	yibN	3	10	putative rhodanese-like sulfurtransferase
STM3845		0	10	putative inner membrane protein
STM3926	wzxE	0	10	O-antigen translocase
STM4091	hslU	2	10	ATP-dependent protease ATP-binding subunit
STM4093	ftsN	0	10	essential cell division protein
STM4147	secE	0	10	translocase
STM4314		0	10	putative regulatory protein
STM4403	cpdB	1	10	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase bifunctional periplasmic precursor protein

STM4438	pmbA	0	10	putative antibiotic maturation protein
STM4503		3	10	putative inner membrane protein
STM4513	yjiG	0	10	putative permease
STM4524	hsdS	0	10	type I restriction enzyme specificity protein

<sup>a</sup>Gene names according to ColiBase [3]

<sup>b</sup>Based on 145,873 sequences

<sup>c</sup>Based on 122,326 sequences

<sup>d</sup>Product according to KEGG (<http://www.genome.jp/kegg/>; [4]).

**Table S5: Statistically significant enriched spots in coIP on Chip and occurrence in 454 sequencing**

Gene name <sup>a</sup>	Enrichment over wt <sup>b</sup>	454
STM2506	21.12	
ybfM	19.29	X
STM1747	17.10	
aphA	15.51	X
ytfK	14.23	X
cpxP	11.67	X
cof	10.15	X
yqjA	10.15	X
STM1841	8.92	X
oppA	8.66	X
STM2880	8.53	
STM1939	8.40	X
ygdQ	8.22	X
cutC	8.09	X
glpF	7.95	X
yceB	7.87	X
cspE	7.50	X
sicP	7.47	X
yihO	7.42	
dppA	7.42	X
STM0159	7.37	X
STM2281	7.35	
hfg	7.31	X
yceP	7.30	X
truA	7.05	X
gltI	7.03	X
rfbP	7.03	X
yejG	7.02	
yafJ	7.01	X
orgA	6.89	X
miaA	6.89	X
yidF	6.86	X
zwf	6.72	X
acrR	6.71	
rfbX	6.62	X
nuoA	6.57	X
STM1128	6.51	
rfbU	6.41	X
yehK	6.38	X
lrhA	6.26	X
yeaJ	6.21	X
STM2507	6.16	
rfaB	6.11	X
yabl	6.08	
pykA	6.07	X
hilA	6.04	X
ssaS	6.00	
ssaT	6.00	
ytfL	5.92	
STM3845	5.87	X
pepN	5.85	X
fnt	5.83	X
ucpA	5.83	X
yqiB	5.79	X
pitA	5.71	X
icc	5.68	X
rpoS	5.64	X
STM0082	5.62	
ybaP	5.62	
hilC	5.62	X
hsdS	5.59	X
ddlA	5.56	
STM0571	5.49	
ycbW	5.46	
celA	5.43	X
pocR	5.39	X
rfbJ	5.37	X
STM1530	5.35	
maa	5.33	X
sucD	5.31	X
yafK	5.27	
ygiJ	5.24	X
STM1093	5.22	

STM4312	5.19	
yeel	5.13	X
STM2901	5.09	
STM4313	5.07	
marA	5.07	
STM2870	5.06	
narP	5.06	X
STM2742	5.06	
sptP	5.00	X
yrdC	4.96	X
dedA	4.95	
STM2747	4.95	
yibN	4.94	X
STM2690	4.94	
nlpC	4.92	
yibA	4.90	
STM2705	4.87	
STM3461	4.82	
marR	4.80	
ycgA	4.80	
invH	4.80	
rfaZ	4.79	X
solA	4.79	
yebK	4.78	X
sanA	4.76	X
sdhC	4.75	X
glmS	4.74	
imp	4.72	X
iacP	4.72	X
STM2986	4.71	
argR	4.70	
ytfJ	4.70	
nirD	4.70	
relA	4.70	X
STM4257	4.69	X
mglA	4.68	X
phnA	4.66	
mltC	4.65	
rfal	4.63	X
rfaC	4.63	
STM3846	4.62	
yidG	4.60	
rtsA	4.58	
ycfJ	4.57	
STM0497	4.56	
glnH	4.55	
rbsB	4.54	X
cspA	4.49	X
rfaJ	4.49	
yecA	4.47	X
mglC	4.45	
STM4493	4.42	
STM4497	4.41	
yhjW	4.41	
thyA	4.39	
hilD	4.39	X
ompX	4.39	X
STM1018	4.38	X
hha	4.36	
ptsG	4.33	X
ytfM	4.32	X
STM1839	4.32	X
ais	4.30	X
STM4316	4.30	
oppF	4.29	X
celG	4.27	X
ydeD	4.26	
yiaG	4.25	
flgL	4.25	X
yejK	4.24	X
STM3528	4.24	
STM2280	4.22	X
rfbV	4.20	X
STM2238	4.19	
STM4261	4.19	X
ydiV	4.18	
STM1554	4.17	
ychJ	4.16	
STM1023	4.12	
STM4260	4.11	X
STM4310	4.10	

STM2530	4.10	X
ubiB	4.08	
STM2746	4.07	
foxA	4.06	
nlpD	4.06	X
adiY	4.06	
STM1629	4.05	
STM1656	4.02	
STM2767	4.02	X
polA	4.02	X
kdpE	4.01	
aefA	4.01	
STM2868	4.00	
nirB	3.99	
def	3.97	
STM2610	3.97	
flhD	3.94	X
malM	3.94	X
rfaK	3.94	
slt	3.93	X
STM3251	3.93	
oafA	3.92	
STM4258	3.92	X
hybG	3.91	
baeR	3.90	
yidQ	3.90	
yeiU	3.88	
glpK	3.88	X
araC	3.88	
cobB	3.87	X
sdhD	3.87	X
STM2314	3.86	X
gnd	3.86	X
STM3773	3.86	X
Int	3.85	X
acrD	3.84	
STM1874	3.82	
uvrY	3.81	X
ssaQ	3.79	
ytgA	3.78	
crp	3.77	X
STM2135	3.76	
STM1785	3.76	
yihG	3.76	
STM2329	3.74	
tdh	3.73	X
rfaQ	3.72	
STM1239	3.72	X
spaO	3.72	X
rbsK	3.70	X
marB	3.70	
invG	3.69	X
sdaC	3.69	
aroE	3.67	
sucC	3.66	X
rfc	3.66	
rfl	3.65	X
avrA	3.64	X
ymbA	3.63	
STM4534	3.62	
STM2225	3.62	
dsbB	3.61	X
STM3362	3.61	X
ybeX	3.61	X
STM4495	3.61	X
alkB	3.61	
STM1328	3.59	X
STM1014	3.59	
lgt	3.57	X
nuoB	3.57	X
smpB	3.54	X
STM1130	3.54	
apaG	3.53	
apaH	3.53	X
ybjE	3.53	
dihH	3.53	
ttk	3.52	
stdA	3.51	
invF	3.51	X
STM0053	3.50	
yahN	3.50	X

STM2950	3.50	X
STM0341	3.50	
sbmA	3.50	X
clpB	3.49	X
STM3155	3.49	
rfbM	3.48	X
yibR	3.48	
hnr	3.48	
STM4494	3.47	
STM1254	3.46	
yfeA	3.46	
STM2186	3.45	X
STM3651	3.44	
invC	3.44	X
STM3533	3.44	
hpaR	3.43	
ydeZ	3.43	X
STM0307	3.43	
ygaC	3.42	
yfaZ	3.42	
orf245	3.42	
STM2754	3.42	
rfaL	3.41	
ftn	3.40	X
pldB	3.39	X
hupB	3.38	X
yajD	3.38	
STM3291	3.38	
dacC	3.38	X
STM4597	3.38	
yobA	3.37	X
yffH	3.36	
ybjT	3.36	
lpxO	3.35	
invA	3.35	X
glfJ	3.34	
mdoC	3.34	
STM1673	3.34	
fepE	3.34	
STM2766	3.34	
sfbA	3.34	
STM4420	3.34	
mukB	3.33	X
STM2449	3.33	
yfeZ	3.33	
yhfK	3.32	X
glfB	3.32	
msbB	3.31	
yecH	3.31	
STM3084	3.31	
STM4308	3.31	
ubiX	3.30	
flk	3.30	
dfp	3.30	
hflX	3.30	X
glnA	3.29	
ydiJ	3.29	
ygiH	3.29	X
lasT	3.29	
STM1041	3.28	
STM0344	3.27	
yigG	3.27	
STM3906	3.26	
STM3907	3.26	
lrp	3.26	X
yciT	3.25	
yeaL	3.25	
fadD	3.24	
ydeW	3.23	X
STM3698	3.23	
proP	3.23	X
yigZ	3.22	
yicL	3.22	
STM2011	3.22	
ybfE	3.22	
rfbK	3.21	X
hemF	3.21	
fihC	3.20	X
STM1532	3.19	
perM	3.19	
yfgB	3.19	

rfbC	3.19	
ytfN	3.18	X
orfX	3.18	
aroM	3.17	
yabJ	3.17	
yggN	3.17	X
proQ	3.15	X
STM3516	3.15	
yadQ	3.14	
glgB	3.14	X
sopE2	3.12	X
STM3138	3.12	X
pagP	3.12	
STM1697	3.11	
sipD	3.11	X
pqiA	3.11	
sinR	3.11	
STM0672	3.11	
yeaS	3.11	X
dapB	3.10	X
STM3785	3.09	
rpIL	3.09	X
STM0870	3.09	X
STM1550	3.08	
nhaA	3.08	X
STM0652	3.07	X
ushA	3.07	X
STM3517	3.07	
ydgT	3.06	
hscA	3.06	
hscB	3.06	
spaP	3.06	X
yjcB	3.06	
STM2377	3.05	
yeaA	3.05	X
STM0835	3.05	
yfeL	3.05	
araJ	3.05	
cysS	3.04	X
yfiL	3.04	
yfcH	3.04	
ytfP	3.04	X
leuZ	3.04	
allC	3.03	
tatB	3.03	
tatC	3.03	X
ssaU	3.02	
ansB	3.01	X
asnS	3.00	X

<sup>a</sup>Gene names according to ColiBase [3]

<sup>b</sup>When several oligonucleotides displaying significant enrichment corresponded to a single gene, the average enrichment over those oligonucleotides is shown.

**Table S6: Oligodeoxynucleotides used in this study.**

Name	Sequence
JVO-0686	GGCCATGGAAAATGTAACCTTTGTAAG
JVO-0687	GTTTTGAATTCATGGTTCGCCATTTTATGA
JVO-1034	GTTTTTTTAATACGACTCACTATAGGATGAGGGGCATTTATG
JVO-1035	TTGCTGCAACGGTCAT
JVO-1117	TCAGCCATTTTGTGCGCTT
JVO-1118	TTCAGGATCGACAACGCCTT
JVO-1234	AGGTTTGGCATTGTGCGCT
JVO-1235	CTTTTTCGAGCATCGGTGC
JVO-1236	ACTATTGAGTCCCTCCCGGAAG
JVO-1237	ACCGGACAATCCATGATAGCC
JVO-1342	TCGCTTGCCGATTACATT
JVO-1343	CAATTTCTTCCGCACTCGGT
JVO-2152	GTTTTCCATGGGAACAATGCATAC
JVO-2153	GTTTTCTCGAGAACAGCCTGTTGATC
JVO-2284	GTTTTTAATACGACTCACTATAGGTTCCCGGCGACATCA
JVO-2285	ATGTGTTTTAGCAACTCGGATG
JVO-2286	GTTTTTAATACGACTCACTATAGGTCTATACGCCTGACTTTCCT
JVO-2287	TTACAGTTACTGCAACCTTTG
JVO-2405	CCTATGGGAGCGCGGTG
JVO-2406	GTCAGAATACGACATTTTGGTACTC
JVO-2446	GATAACCTGAGACCCCTG
JVO-2447	AATACCCCAAAGCATTTCG
JVO-2448	ATATAAACGCGCCAGTCCAT
JVO-2471	GTTTTTAATACGACTCACTATAGGATAAGCAAGGCTGGCAG
JVO-2472	GCCTTGTAGAGAGTGGGG
JVO-3140	CGGGTGGGATGAAATCGTAA
JVO-3141	TTAGTGTCTGGCGAAACGCT
JVO-3142	GTTGCTGCGGTGTAATAAGACA
JVO-3143	TACGTTTGAGCTCAGGGTCG
JVO-3249	AGAGAGTCAGCGCCGGG
JVO-3250	AATTAACACCCCGCCG
JVO-3251	CAGGCTACCAACCACCTCC
JVO-3252	TATGGAGCGCAACGCC
JVO-3253	GCGGTCTGGTGTACCTTCC
JVO-3254	CGGGTCATCTTTCAGGCTG
JVO-3255	TGCTTATACGCTACCGGGC
JVO-3256	CTGCCTAACATCTCGTTTCTCC
JVO-3257	GCCACGGTTCTCACCG
JVO-3258	CAGCACACTACACAGGGTCCG
JVO-3259	ACCTTGCTGGCGCTCTC
JVO-3260	CATCTTGCGGTCTGGCA
JVO-3261	CATCGCCTTGCCAACTT
JVO-3262	AAGACCCTGGCGCGGTT
JVO-3263	CTTAGCAGCCTTGTAGAAGAGC
JVO-3264	AAACTTGACACCGTTTCGGC
JVO-3265	GTGCCTCCGAACGGAAG
JVO-3266	GCGACAATCACGCCAG

**Table S7: Oligodeoxynucleotides used for Northern detection.**

Name	Sequence	target region
JVO-2405	CCTATGGGAGCGCGGTG	STnc250
JVO-2406	GTCAGAATACGACATTTGGTACTC	STnc290
JVO-2407	TTATTTGGACTACCTGGATG	STnc340
JVO-2408	TATGAGGAGGACAATTACCG	STnc440
JVO-2445	TACCGGACAATAATCCCTAC	STnc130
JVO-2446	GATAACCTGAGACCCCCCTG	STnc150
JVO-2448	ATATAAACGCGCCAGTCCAT	STnc180
JVO-2466	TCTGGCGGAACCTGCC	STnc220
JVO-2468	CACACCTGTCGGGCGTT	STnc310
JVO-2469	CGCAGTCCCAGGTCAGC	STnc330
JVO-2498	CTTATGTGGGCGTTTTGTTT	STnc350
JVO-2499	AATGACACCAACCTTTTACG	STnc390
JVO-2500	CTAGAGGAGGCGCTAGAAAG	STnc400
JVO-3140	CGGGTGGGATGAAATCGTAA	STnc190
JVO-3141	TTAGTGTCTGGCGAAACGCT	STnc400
JVO-3142	GTTGCTGCGGTGTAATAAGACA	STnc180
JVO-3143	TACGTTTGAGCTCAGGGTCG	STnc180
JVO-3144	TCATGTTACCGGTAATAACACC	STnc200
JVO-3249	AGAGAGTCAGCGCCGGG	STnc600
JVO-3250	AATTAACCAACCCGCGG	STnc620
JVO-3251	CAGGCTACCAACCACCTCC	STnc590
JVO-3252	TATGGAGCGCAACGCC	STnc580
JVO-3253	GCGGTCTGGTGTACCTTCC	STnc610
JVO-3254	CGGGTCATCTTTCAGGCTG	STnc540
JVO-3255	TGCTTATACGCTACCGGGC	STnc560
JVO-3256	CTGCCTAACATCTCGTTTCTCC	STnc570
JVO-3257	GCCACGGTTCTCACCG	STnc480
JVO-3258	CAGCACACTACACAGGGTCG	STnc630
JVO-3259	ACCTTGCTGGCGCTCTC	STnc470
JVO-3260	CATCTTGCGGTCTGGCA	STnc490
JVO-3261	CATCGCGTTGCCAATT	STnc500
JVO-3262	AAGACCCTGGCGCGGTT	STnc520
JVO-3263	CTTAGCAGCCTTGTAGAAGAGC	STnc640
JVO-3264	AAACTTGACACCGTTTCGGC	STnc510
JVO-3265	GTGCCTCCGAACGGAAG	STnc530
JVO-3266	GCGACAATCACGCCAG	STnc550

## References

1. Papenfort K, Pfeiffer V, Mika F, Lucchini S, Hinton JC, et al. (2006) sigma(E)-dependent small RNAs of Salmonella respond to membrane stress by accelerating global omp mRNA decay. *Mol Microbiol* 62: 1674-1688.
2. Vogel J, Argaman L, Wagner EG, Altuvia S (2004) The small RNA IstR inhibits synthesis of an SOS-induced toxic peptide. *Curr Biol* 14: 2271-2276.
3. Chaudhuri RR, Khan AM, Pallen MJ (2004) coliBASE: an online database for Escherichia coli, Shigella and Salmonella comparative genomics. *Nucleic Acids Res* 32: D296-299.
4. Goto S, Bono H, Ogata H, Fujibuchi W, Nishioka T, et al. (1997) Organizing and computing metabolic pathway data in terms of binary relations. *Pac Symp Biocomput*: 175-186.
5. Sittka A, Pfeiffer V, Tedin K, Vogel J (2007) The RNA chaperone Hfq is essential for the virulence of Salmonella typhimurium. *Mol Microbiol* 63: 193-217.
6. Garcia-Vallve S, Guzman E, Montero MA, Romeu A (2003) HGT-DB: a database of putative horizontally transferred genes in prokaryotic complete genomes. *Nucleic Acids Res* 31: 187-189.
7. Papenfort K, Pfeiffer V, Lucchini S, Sonawane A, Hinton JC, et al. (2008) Systematic deletion of Salmonella small RNA genes identifies CyaR, a conserved CRP-dependent riboregulator of OmpX synthesis. *Mol Microbiol* in press.
8. Hershberg R, Altuvia S, Margalit H (2003) A survey of small RNA-encoding genes in Escherichia coli. *Nucleic Acids Res* 31: 1813-1820.
9. Padalon-Brauch G, Hershberg R, Elgrably-Weiss M, Baruch K, Rosenshine I, et al. (2008) Small RNAs encoded within genetic islands of Salmonella typhimurium show host-induced expression and role in virulence. *Nucleic Acids Res*.
10. Sharma CM, Darfeuille F, Plantinga TH, Vogel J (2007) A small RNA regulates multiple ABC transporter mRNAs by targeting C/A-rich elements inside and upstream of ribosome-binding sites. *Genes Dev* 21: 2804-2817.
11. Pfeiffer V, Sittka A, Tomer R, Tedin K, Brinkmann V, et al. (2007) A small non-coding RNA of the invasion gene island (SPI-1) represses outer membrane protein synthesis from the Salmonella core genome. *Mol Microbiol* 66: 1174-1191.
12. Figueroa-Bossi N, Lemire S, Maloriol D, Balbontin R, Casades J, et al. (2006) Loss of Hfq activates the sigma-dependent envelope stress response in Salmonella enterica. *Mol Microbiol* 62: 838-852.
13. Fortune DR, Suyemoto M, Altier C (2006) Identification of CsrC and characterization of its role in epithelial cell invasion in Salmonella enterica serovar Typhimurium. *Infect Immun* 74: 331-339.
14. Viegas SC, Pfeiffer V, Sittka A, Silva IJ, Vogel J, et al. (2007) Characterization of the role of ribonucleases in Salmonella small RNA decay. *Nucleic Acids Res* 35: 7651-7664.
15. Altier C, Suyemoto M, Ruiz AI, Burnham KD, Maurer R (2000) Characterization of two novel regulatory genes affecting Salmonella invasion gene expression. *Mol Microbiol* 35: 635-646.
16. Wassarman KM, Repoila F, Rosenow C, Storz G, Gottesman S (2001) Identification of novel small RNAs using comparative genomics and microarrays. *Genes Dev* 15: 1637-1651.