Supporting Information

Yeom et al. 10.1073/pnas.1722246115

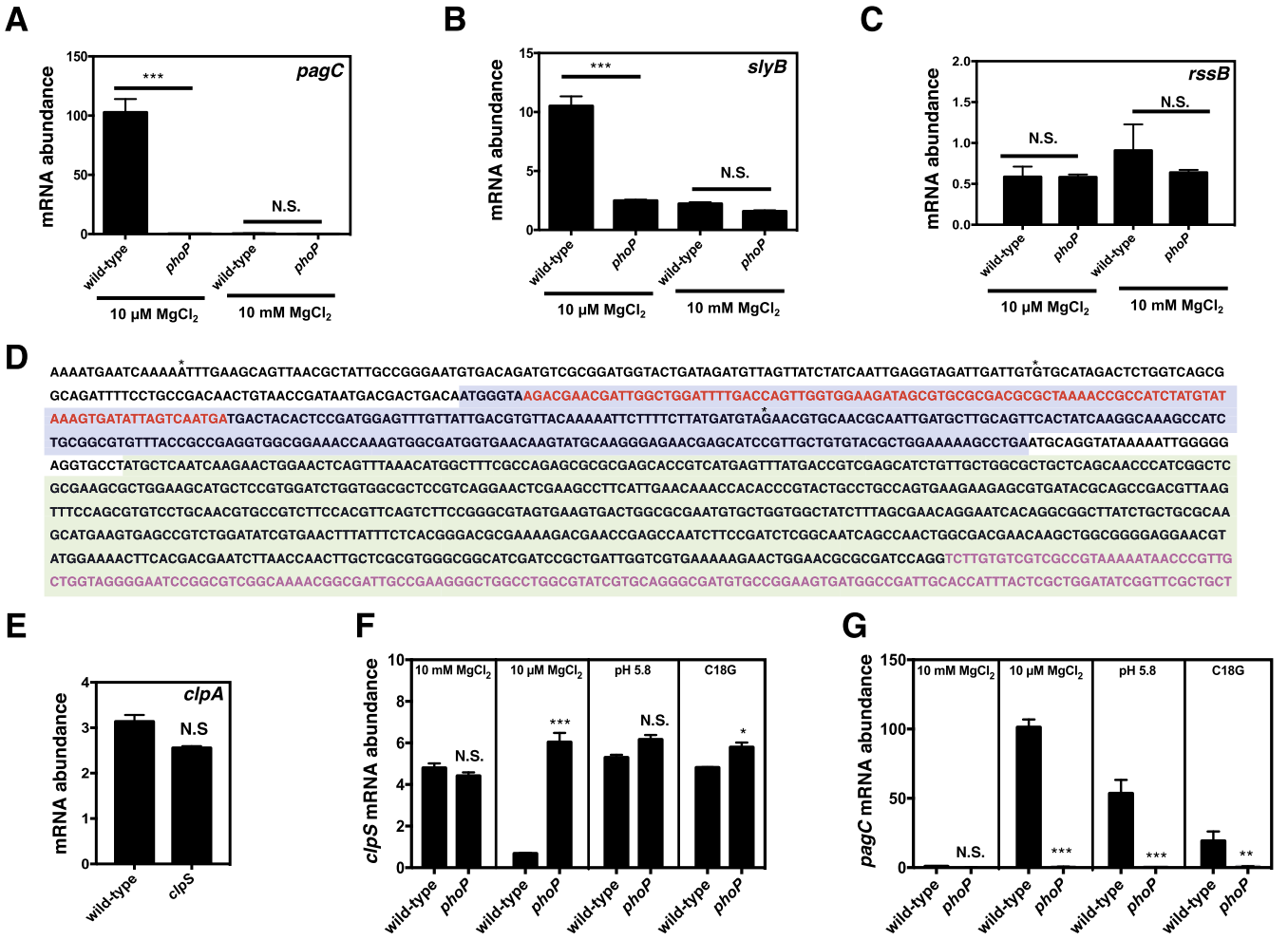

Fig. S1. The PhoP protein represses transcription of the *clpS* gene when *Salmonella* experiences low cytoplasmic Mg^{2+}. (*A*–*C*) mRNA abundance of the *pagC* (*A*), *slyB* (*B*), and *rssB* (*C*) genes produced by wild-type (14028s) and *phoP* (MS7953s) *Salmonella* following growth in in N-minimal medium (pH 7.7) containing 10 μM or 10 mM $MgCl_2$ at 37 °C for 5.5 h. (*D*) Nucleotide sequence of the *clpS* (blue) and *clpA* (green) coding regions from wild-type *S. enterica* serovar Typhimurium (14028s). The locations of qRT-PCR primers for the *clpS* and *clpA* genes are indicated by red and pink font, respectively. Intergenic regions are in white background. The asterisks indicate transcription start sites for the *clpS* and the *clpA* genes according to the *Salmonella* gene-expression database (bioinf.gen.tcd.ie/cgi-bin/salcom.pl?_HL). (*E*) mRNA abundance of the *clpA* gene produced by wild-type (14028s) and *clpS* (JY651) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for 5.5 h. (*F* and *G*) mRNA abundance of the *clpS* (*F*) and *pagC* (*G*) genes produced by wild-type (14028s) and *phoP* (MS7953s) *Salmonella* following growth in N-minimal medium containing 10 mM or 10 μM $MgCl_2$ at pH 7.7 or 10 mM $MgCl_2$ at pH 5.8 or 10 mM $MgCl_2$ at pH 7.7 with C18G (7 μg/mL) at 37 °C for 5.5 h. For *A*–*C* and *E*–*G*, mRNA abundance was normalized to that of the *ompA* gene. Primers used in qRT-PCR are listed in Table S2. Data shown are the mean and SD from three independent experiments. N.S., not significant. $^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, two-tailed *t* test with each sample vs. wild-type.

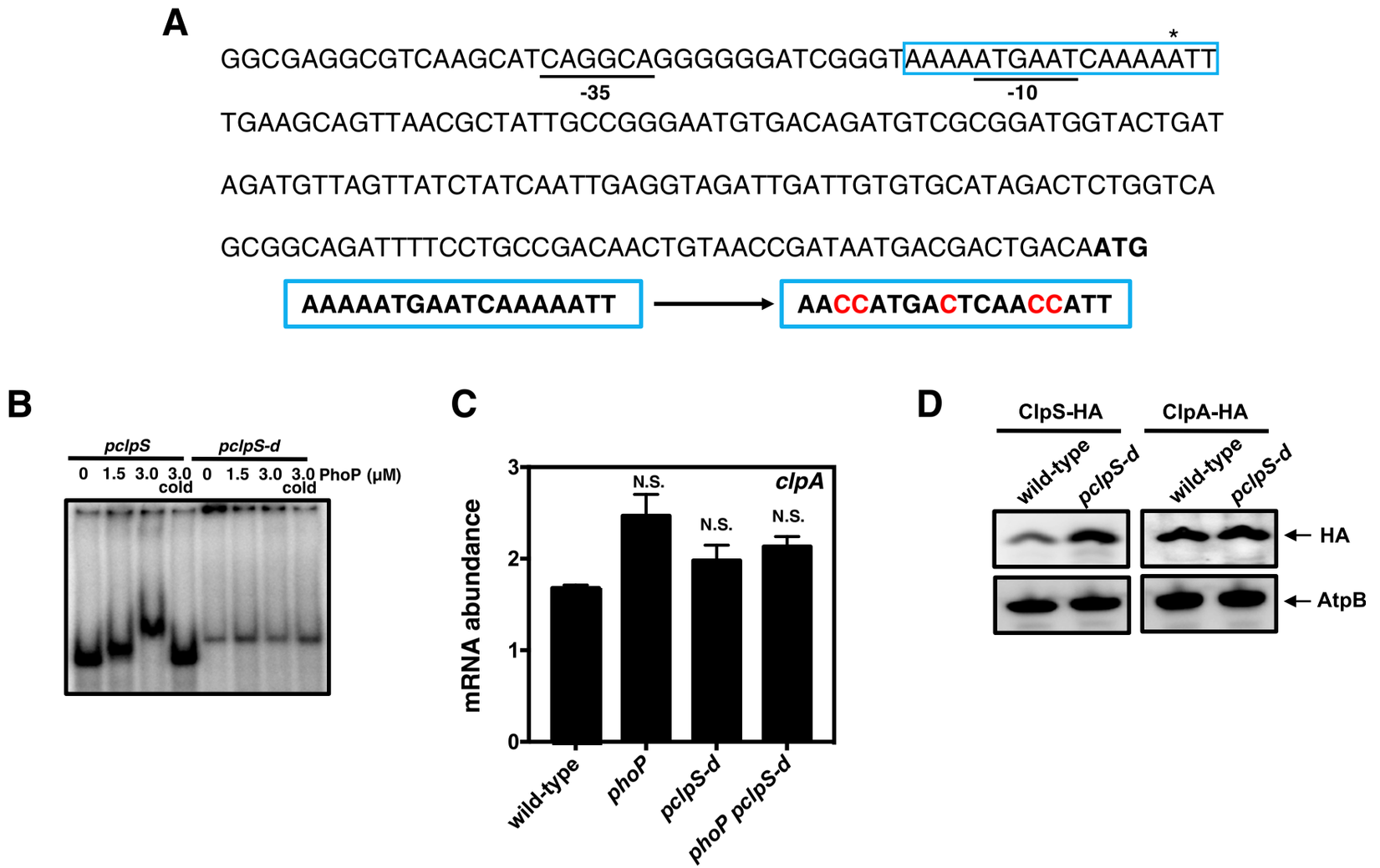

Fig. S2. Nucleotide substitutions in the putative PhoP box in the *clpS* promoter region abolish PhoP binding in vitro but do not affect *clpA* expression in vivo. (*A*, *Upper*) Nucleotide sequence of the *clpS* promoter region from wild-type *S. enterica* serovar Typhimurium (14028s). The putative PhoP box is in blue. The predicted −35 and −10 promoter elements are indicated by black bars. The asterisk indicates the transcription start site near the putative PhoP binding box according to the *Salmonella* gene-expression database (bioinf.gen.tcd.ie/cgi-bin/salcom.pl?_HL). (*Lower*) Sequences of the PhoP box (*Left*) and of the mutated version (*Right*) with mutated nucleotides in red. (*B*) EMSA of DNA fragments corresponding to wild-type and PhoP box mutant *clpS* promoters with purified PhoP protein. The gel is representative of three independent experiments. Samples were incubated at room temperature for 20 min and then were electrophoresed on 6% Tris/borate/EDTA gels at 100 V for 90 min. (*C*) mRNA abundance of the *clpA* gene produced by wild-type (14028s), *phoP* (MS7953s), *pclpS-d* (JY665), and *phoP pclpS-d* double mutant (JY939) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for 5.5 h. mRNA abundance was normalized to that of the *ompA* gene. Primers used in qRT-PCR are listed in Table S2. Data shown are the mean and SD from three independent experiments. (*D*) Western blot analysis of crude extracts prepared from *clpS-HA* (JY691), *clpS-HA pclpS-d* (JY937), *clpA-HA* (JY694), and *clpA-HA pclpS-d* (JY935) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for 6 h. Samples were analyzed using antibodies directed to the HA tag or the AtpB protein. Data are representative of three independent experiments, which gave similar results. N.S., not significant.

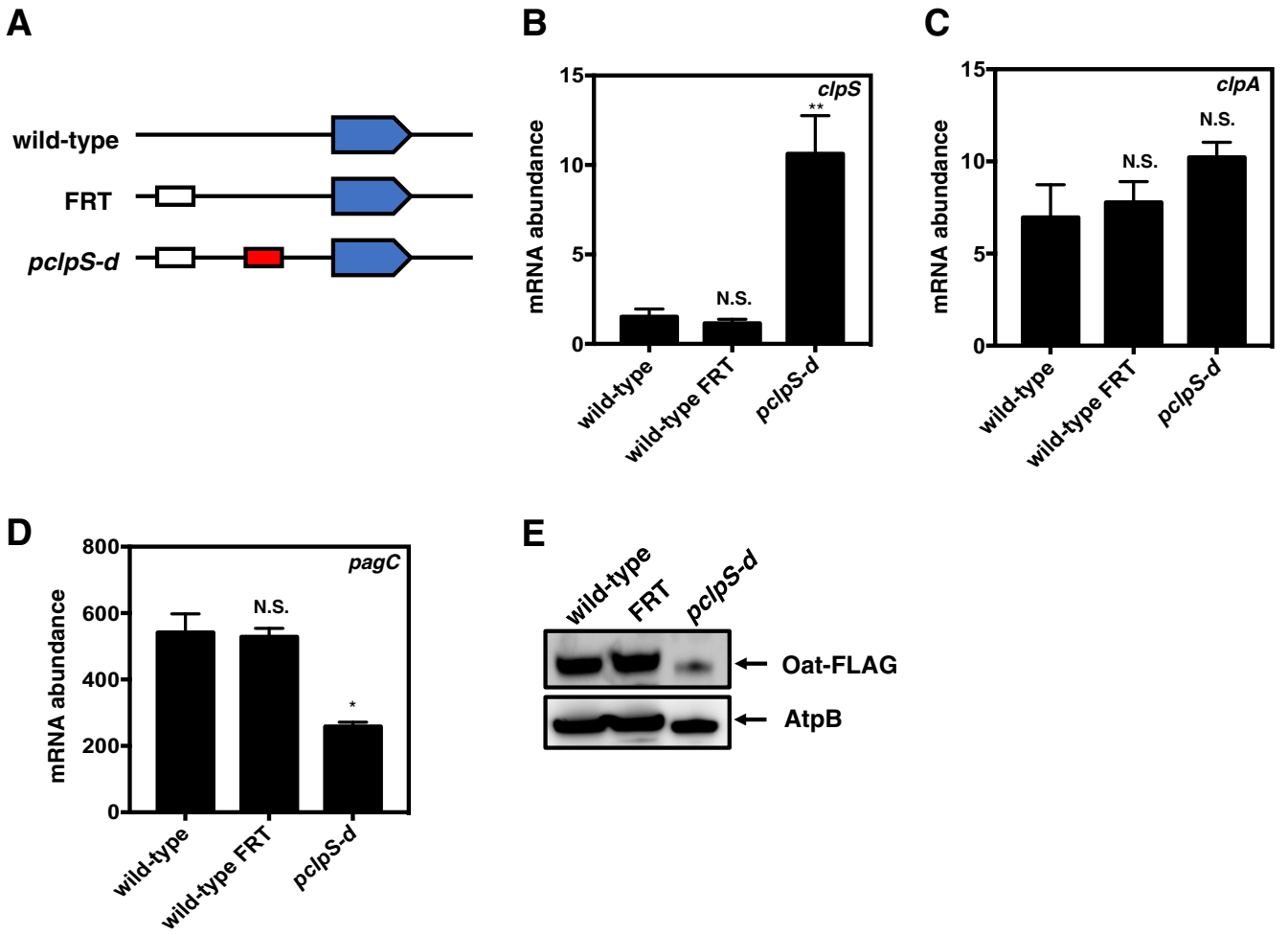

Fig. S3. The 83-nt-long FRT sequence upstream of the *clpS* promoter does not alter *clpS* expression. (*A*) Diagram of the *clpS* promoter chromosomal region in wild-type *Salmonella*, a strain with the 83-nt-long FRT sequence upstream of the *clpS* promoter (white box), and a strain with the 83-nt-long FRT sequence upstream of the mutant *clpS* promoter (red box). (*B–D*) mRNA abundance of the *clpS* (*B*), *clpA* (*C*), and *pagC* (*D*) genes produced by wild-type (14028s), wild-type FRT (JY937), and *pclpS-d* (JY665) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for 5.5 h. mRNA abundance was normalized to that of the *ompA* gene. Primers used in qRT-PCR are listed in Table S2. Data shown are the mean and SD from three independent experiments. (*E*) Western blot analysis of crude extracts prepared from *oat-FLAG* (JY655), *oat-FLAG* FRT (JY938), and *oat-FLAG pclpS-d* (JY684) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for 6 h. Samples were analyzed using antibodies directed to the FLAG tag or the AtpB protein. N.S., not significant. $*P < 0.05$, $**P < 0.01$, two-tailed *t* test with each sample *vs.* wild-type.

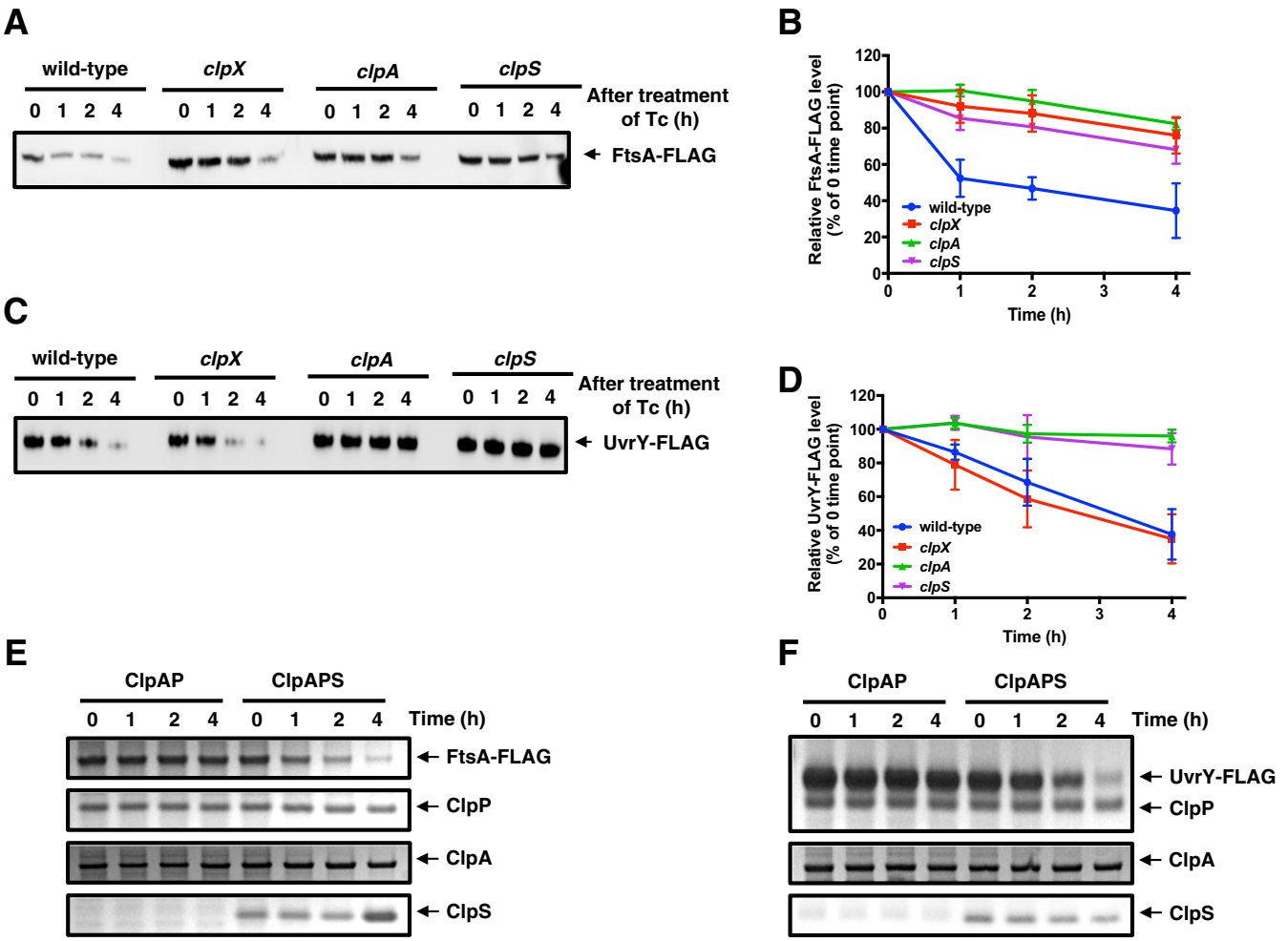

Fig. S4. The FtsA-FLAG and UvrY-FLAG proteins are substrates of the ClpSAP protease. (*A* and *C*) FtsA-FLAG (*A*) stability determined in *ftsA-FLAG* (JY905), *ftsA-FLAG clpX* (JY909), *ftsA-FLAG clpA* (JY910), and *ftsA-FLAG clpS* (JY907) *Salmonella*. UvrY-FLAG (*C*) stability determined in *uvrY-FLAG* (JY911), *uvrY-FLAG clpX* (JY915), *uvrY-FLAG clpA* (JY916), and *uvrY-FLAG clpS* (JY913) *Salmonella*. Bacteria were grown in 10 mL N-minimal medium containing 10 μM $MgCl_2$ for 5 h. Samples were harvested at the indicated times following the addition of the protein synthesis inhibitor tetracycline (Tc) (50 μg/mL) and were analyzed by Western blotting with antibodies directed to the FLAG tag. (*B* and *D*) Relative FtsA-FLAG (*B*) and UvrY-FLAG (*D*) abundance was calculated from three independent experiments. (*E* and *F*) SDS/PAGE analysis for the time course of in vitro degradation of purified FtsA-FLAG (*E*) and UvrY-FLAG (*F*) proteins. FtsA-FLAG (0.2 μM) or UvrY-FLAG (0.5 μM) was mixed with ClpA (0.2 μM) or ClpP (0.2 μM) in the absence or presence of ClpS (0.2 μM). All reactions were carried out at 30 °C for the indicated times in the presence of an ATP regeneration system and were started by the addition of substrates. After incubation, protein amounts were determined by a Coomassie-stained band following separation on a 4–12% SDS/PAGE gel. Data are representative of three independent experiments, which gave similar results.

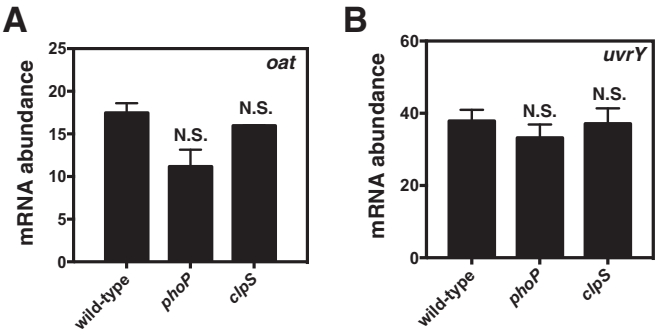

Fig. S5. *phoP* and *clpS* mutants exhibit wild-type mRNA abundance of the *oat* and *uvrY* genes. mRNA abundance of the *oat* (*A*) and *uvrY* (*B*) genes produced by wild-type (14028s), *phoP* (MS7953s), and *clpS* (JY651) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for 5.5 h. mRNA abundance was normalized to that of the *ompA* gene. Primers used in qRT-PCR are listed in Table S2. Data shown are the mean and SD from three independent experiments. N.S., not significant.

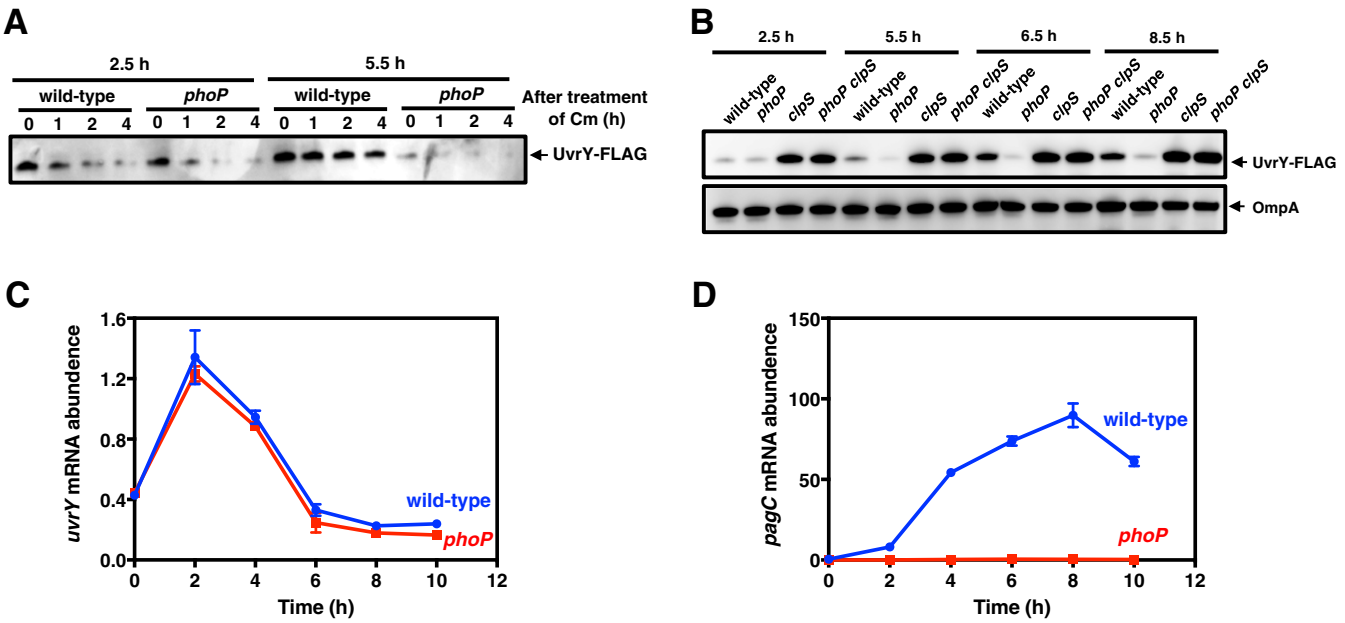

Fig. S6. Stability of the UvrY-FLAG protein increases following *Salmonella* growth in low Mg^{2+} medium for 5.5 h when the abundance of *uvrY* mRNA is low. (*A*) UvrY-FLAG stability determined in *uvrY-FLAG* (JY911) and *uvrY-FLAG phoP* (JY912) *Salmonella*. Bacteria were grown in 10 mL N-minimal medium containing 10 μM $MgCl_2$ for 2.5 or 5.5 h. Samples were harvested at the times indicated in the figure following the addition of the protein synthesis inhibitor chloramphenicol (Cm) (1 mg/mL) and were analyzed by Western blotting with antibodies directed to the FLAG epitope. Data are representative of two independent experiments, which gave similar results. (*B*) Western blot analysis of crude extracts prepared from *uvrY-FLAG* (JY911), *uvrY-FLAG phoP* (JY912), *uvrY-FLAG clpS* (JY913), and *uvrY-FLAG clpS phoP* double mutant (JY983) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for the indicated times. Samples were analyzed using antibodies directed to the FLAG tag or the OmpA protein. Data are representative of two independent experiments, which gave similar results. (*C* and *D*) mRNA abundance of the *uvrR* (*C*) and *pagC* (*D*) genes produced by wild-type (14028s) and *phoP* (MS7953s) *Salmonella* following growth in N-minimal medium (pH 7.7) containing 10 μM $MgCl_2$ at 37 °C for the indicated times. mRNA abundance was normalized to that of the *ompA* gene. Primers used in qRT-PCR are listed in Table S2. Data shown are the mean and SD from three independent experiments.

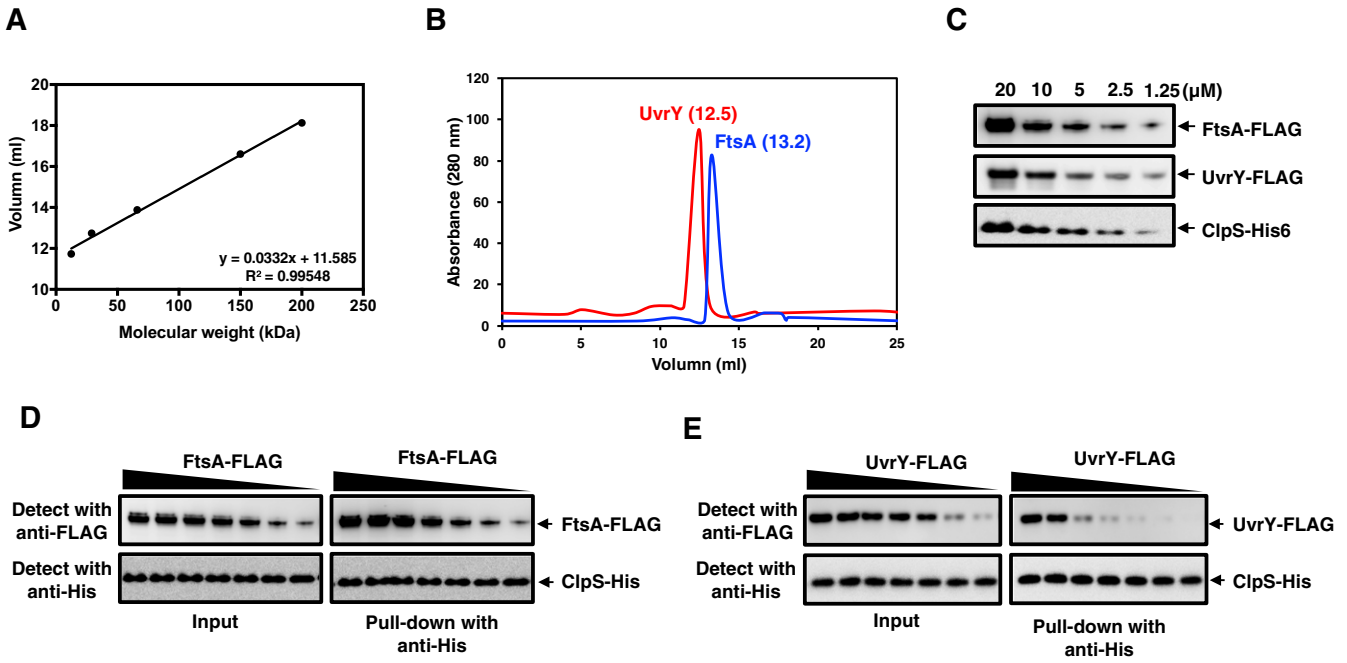

Fig. S7. The FtsA-FLAG and UvrY-FLAG proteins are monomeric and have different affinities toward ClpS. (*A* and *B*) Molecular weight of the FtsA-FLAG and UvrY-FLAG proteins calculated based on purified standard proteins. (*A*) Cytochrome *c*, carbonic anhydrase, albumin, alcohol dehydrogenase, and β-amylase were used as the standard proteins for molecular weight calculation. (*B*) Purified FtsA-FLAG and UvrY-FLAG protein were run in size-exclusion chromatography. FtsA-FLAG and UvrY-FLAG have peaks at 13.2 and 12.5 mL, respectively. (*C*) Calculated concentrations of the FtsA-FLAG, UvrY-FLAG, and ClpS-His proteins based on known amounts of purified proteins. The indicated amounts of purified proteins were loaded onto the same gel and detected using antibodies directed to the FLAG or His tags. (*D* and *E*) In vitro protein–protein interactions determined by coimmunoprecipitation of purified ClpS-His, FtsA-FLAG, and UvrY-FLAG proteins followed by Western blot analysis using antibodies directed against the FLAG or His tags. (*D*) Affinity between ClpS-His and FtsA-FLAG measured at different amounts of FtsA-FLAG and a constant amount of ClpS-His by Western blot analysis using the antibodies described in *C*. (*E*) Affinity between ClpS-His and UvrY-FLAG measured using different amounts of UvrY-FLAG and a constant amount of ClpS-His by Western blot analysis using the antibodies described in *C*.

Table S1. Bacterial strains and plasmids used in this study

Strains	Relevant characteristics	Source or reference
E. coli		
BL21 (DE3)	*F- ompT hsdS gal [lon] [dcat] (lts857 ind1 Sam7 nin5 lacUV5-T7 gene 1)*	(62)
DH5a	Host strain used for generation and propagation of plasmid constructs	Life Technologies
EG12976	*phoP::km*	(63)
JY670	*patA-FLAG::cat*	This study
JY671	*patA-FLAG::cat phoP::km*	This study
JY680	*clpS::km*	This study
JY681	*patA-FLAG::cat clpS::km*	This study
MG1655	*F- lambda- rph-1*	(64)
S. enterica serovar Typhimurium		
14028s	wild-type	(59)
EG13918	*phoP-HA*	(65)
EG16735	Δ*mgtA*	(27)
EG17133	Δ*iraP*	(37)
EG18499	*clpX::cat*	(37)
EL1	*mgtC::km*	(60)
EL4	Δ*mgtC*	(20)
JY199	*clpA::cat*	(7)
JY570	*clpS::cat*	(7)
JY619	Δ*clpS phoP::*Tn*10*	(7)
JY649	Δ*clpX*	(7)
JY650	Δ*clpA*	(7)
JY651	Δ*clpS*	(7)
JY655	*oat-FLAG*	(7)
JY656	*oat-FLAG phoP::*Tn*10*	This study
JY657	*oat-FLAG clpS*	(7)
JY658	*oat-FLAG phoP::*Tn*10/clpS*	This study
JY664	*pclpS-d::cat*	This study
JY665	Δ*pclpS-d*	This study
JY684	*oat-FLAG pclpS-d*	This study
JY691	*clpS-HA*	This study
JY694	*clpA-HA*	This study
JY854	*clpS-HA phoP::Tn10*	This study
JY879	*phoP-HA mgtC*	This study
JY881	*phoP-HA clpS*	This study
JY903	*oat::cat*	This study
JY905	*ftsA-FLAG::km*	This study
JY906	*ftsA-FLAG::km phoP::*Tn*10*	This study
JY907	*ftsA-FLAG::km clpS::cat*	This study
JY908	*ftsA-FLAG::km pclpS-d*	This study
JY909	*ftsA-FLAG::km clpX::cat*	This study
JY910	*ftsA-FLAG::km clpA::cat*	This study
JY911	*uvrY-FLAG::km*	This study
JY912	*uvrY-FLAG::km phoP::*Tn*10*	This study
JY913	*uvrY-FLAG::km clpS::cat*	This study
JY914	*uvrY-FLAG::km pclpS-d*	This study
JY915	*uvrY-FLAG::km clpX::cat*	This study
JY916	*uvrY-FLAG::km clpA::cat*	This study
JY917	*uvrY::cat*	This study
JY933	*phoP-HA pclpS-d*	This study
JY934	*clpS-HA pclpS-d*	This study
JY935	*clpA-HA pclpS-d*	This study
JY936	Δ*iraP pclpS-d*	This study
JY937	*pclpS::FRT*	This study
JY938	*oat-FLAG pclpS::FRT*	This study
JY939	*phoP::*Tn*10/pclpS-d*	This study
JY981	*oat::cat pclpS-d*	This study
MS7953s	*phoP::*Tn*10*	(59)
Plasmids		
pCP20	$rep_{pSC101}{}^{ts}$ I cI857 FLP Amp^R Cat^R	(58)
pKD3	rep_{R6Kg} Amp^R FRT Cat^R FRT	(58)

Table S1. Cont.

Strains	Relevant characteristics	Source or reference
pKD4	rep_{R6Kg} Amp^R FRT Km^R FRT	(58)
pKD46	$rep_{pSC101}{}^{ts}$ Amp^R P_{araBAD}-gbexo	(58)
pET28+a	pBR332 *lacI* KmR pT7	Novagen
pET28+a-*clpS*	pBR332 *lacI* KmR pT7- *clpS*	This study
pET28+a-*clpA*	pBR332 *lacI* KmR pT7- *clpA*	This study
pET28+a-*clpP*	pBR332 *lacI* KmR pT7- *clpP*	This study
pUHE-21-2-*lacI*^{q}	rep_{pMB1} *lacI*^{q} Amp^R	(61)
pUHE-*clpS*	rep_{pMB1} *lacI*^{q} Amp^R P_{lac}-*clpS*	(7)
pUHE-*ftsA-FLAG*	rep_{pMB1} *lacI*^{q} Amp^R P_{lac}-*ftsA-FLAG*	This study
pUHE-*uvrY-FLAG*	rep_{pMB1} *lacI*^{q} Amp^R P_{lac}-*uvrY-FLAG*	This study

Table S2. Primers used for strain or plasmid constructions or qRT-PCR

Primer number	Purpose	Sequence (5′–3′)
16494	*oat* inactivation in *Salmonella*	CCCCGCTAATCCCTGCAATACTTAATTCAGTATCATGTGTAGGCTGGAGCTGCTTC
16495	*oat* inactivation in *Salmonella*	AAACAGGCCGGATAAGCACAGCGCCATCCGGCATCGTTTTATGAATATCCTCCTTAGT
15945	*aat* inactivation in *Salmonella*	CCGACTTGCGTACTGGAGTTTCGCCGTCATGTGTAGGCTGGAGCTGCTTC
15946	*aat* inactivation in *Salmonella*	TTAAGTACCTGACAATCAATAAGTTTATATGAATATCCTCCTTAGT
16500	*uvrY* inactivation in *Salmonella*	TAAAGTTGTCGGTGAAGCGTGCTGCGGAGAGGATGCGGTAGTGTAGGCTGGAGCTGCTTC
16501	*uvrY* inactivation in *Salmonella*	GATAGCGATAGCTGTTCACCGTTTTAGGACTGAGATTCAGTATGAATATCCTCCTTAGT
16502	Insertion of sequence for FLAG tag at C terminus of f*tsA* gene in *Salmonella*	GATCAAGCGACTTAATAGCTGGCTGCGAAAAGAGTTTGACTACAAGGA-CGACGATGACAAGTAAGTGTAGGCTGGAGCTGCTTC
16503	Insertion of sequence for FLAG tag at C terminus of *ftsA* gene in *Salmonella*	TGCCTGTCGCCTGAGGCCGTAATATCTGGCGGCCTCATAATATGAATATCCTCCTTAGT
16504	Insertion of sequence for FLAG tag at C terminus of uvrY gene in *Salmonella*	CCGCCATGGCCTGTGTAATGCGGAGACGTTAACAAGCCAGGACTACAAGGACGACGATGAC-AAGTGAGTGTAGGCTGGAGCTGCTTC
16505	Insertion of sequence for FLAG tag at C terminus of *uvrY* gene in *Salmonella*	CGGTTTTCAAAAACGCCTTTGCGTCAAATATTTCAGACACACCCTTGAATATGAATATCCTCCTTAGT
16048	Insertion of sequence for HA tag at C terminus of *clpS* gene in *Salmonella*	GGAGAACGAGCATCCGTTGCTGTGTACGCTGGAAAAAGCCTACCCATACGATGTTCCAGATTACGCT-TGAGTGTAGGCTGGAGCTGCTTC
16049	Insertion of sequence for HA tag at C terminus of *clpS* gene in *Salmonella*	TTCTTGATTGAGCATAGGCACCTCCCCCAATTTTTATACCTGTATGAATATCCTCCTTAGT
16050	Insertion of sequence for HA tag at C terminus of *clpA* gene in *Salmonella*	GAGTGCGCAAAAGCACAAGCCGGAAGCCGCGCACTACCCATACGATGTTCCAGATTACGCTTAAGTG-TAGGCTGGAGCTGCTTC
16051	Insertion of sequence for HA tag at C terminus of *clpA* gene in *Salmonella*	AGGCCCGGTTTGTACGACAGTGAAACGAAGTATGAATATCCTCCTTAGT
15964	Insertion of sequence for FLAG tag at C terminus of *patA* gene in *E. coli*	GGCGCTGGCGGCCATGCGAGTAAGTGTCGAAGAAGCGGACTACAAGGACGACGATGACAAGTAAGTG-TAGGCTGGAGCTGCTTC
15965	Insertion of sequence for FLAG tag at C terminus of *patA* gene in *E. coli*	GATCGGATGGCGACGTCGTATCGCCATCCGATTTGTATGAATATCCTCCTTAGT
16009	*clpS* inactivation in *E. coli*	CCGATAACCGTAACCGAAGATGATAACTGACAGTGTAGGCTGGAGCTGCTTC
16010	*clpS* inactivation in *E. coli*	ATATCACTTTATACATAGATGGCGGTTTTAGCTATGAATATCCTCCTTAGT
15937	Amplification of *cigR* promoter region in *Salmonella*	TTTTTTATCAGGTTGTCCTGATAGCAATCATCC
15938	Amplification of *cigR* promoter region in *Salmonella*	GCCCTTCTGATGTGGGATACCATGAAAATAGCGCCCCGC
15939	Amplification of *mgtC* promoter region in *Salmonella*	GAACCCATTTTTTCCTCGTCATGTT
15940	Amplification of *mgtC* promoter region in *Salmonella*	TACGTTCCTCCATTTTTTCTGGAAG
15933	Amplification of *clpS* promoter region in *Salmonella*	ATTGTTGAACCACTTTACAGTACCCGTTTC
15936	Amplification of *clpS* promoter region in *Salmonella*	TTACCCATTGTCAGTCGTCATTATCGGTTACAG
16437	Amplification of *clpS* gene from *Salmonella* for protein purification	TAACTTTAAGAAGGAGATATACCATGGGTAAGACGAACGATTGGCTG
16437	Amplification of *clpS* gene from *Salmonella* for protein purification	CAGTGGTGGTGGTGGTGGTGCTCGAGGGCTTTTTCCAGCGTACA
16441	Amplification of *clpA*gene from *Salmonella* for protein purification	TAACTTTAAGAAGGAGATATACCATGCTCAATCAAGAACTGGAACTCAGT
16442	Amplification of *clpA*gene from *Salmonella* for protein purification	CAGTGGTGGTGGTGGTGGTGCTCGAGTTAGTGCGCGGCTTCCGG

Table S2. Cont.

Primer number	Purpose	Sequence (5′–3′)
16439	Amplification of *clpP* gene from *Salmonella* for protein purification	TAACTTTAAGAAGGAGATATACCATGTCATACAGCGGAGAACGAGATAAT
16440	Amplification of *clpP* gene from *Salmonella* for protein purification	CAGTGGTGGTGGTGGTGGTGCTCGAGATTACGATGGGTCAAAATTGAGTCAACCAA
16618	Amplification of *ftsA-flag* gene from *Salmonella* for protein purification	GCGGGATCCAATGATCAAGGCGACGGACAGAAAACTGGTAGTAGGACTGG
16619	Amplification of *ftsA-flag* gene from *Salmonella* for protein purification	GCGAAGCTTTTACTTGTCATCGTCGTCCTTGTAGTCAAACTCTTTTCGCAGCCAGCT
16620	Amplification of uvrY-*flag* gene from *Salmonella* for protein purification	GCGGGATCCAATGATCAACGTTCTTCTTGTTGATGACCACGAACTGGTGCGC
16621	Amplification of uvrY-*flag* gene from *Salmonella* for protein purification	GCGAAGCTTTCACTTGTCATCGTCGTCCTTGTAGTCCTGGCTTGTTAACGTCTCCGCA
16627	FRT insertion of *clpS* promoter in *Salmonella*	ATTGTTGAACCACTTTACAGTACCCGTTTCCATGTGTAGGCTGGAGCTGCTTC
16628	FRT insertion of *clpS* promoter in *Salmonella*	CCACTCCGTCACCGGTTCATTCCATCTTACTTATATAAGATTTACGAAGGATGTCGAAGTATGAATA-TCCTCCTTAGT
15962	PhoP-binding site inactivation of *clpS* promoter in *Salmonella*	TTTAGAGAAATCAGGCGAGGCGTCAAGGTGTAGGCTGGAGCTGCTTC
15963	PhoP-binding site inactivation of *clpS* promoter in *Salmonella*	ATGGTTGAGTCATGGTTACCCGATCCCCCCTGCCTGATGCTTGACGCCTATGAATATCCTCCTTAGT
15927	qRT-PCR of *clpS* gene in *Salmonella*	AGACGAACGATTGGCTGGATTTTGACC
15928	qRT-PCR of *clpS* gene in *Salmonella*	TCATTGACTAATATCACTTTATAC
15929	qRT-PCR of *clpA* gene in *Salmonella*	TCTTGTGTCGTCGCCGTAAA
15930	qRT-PCR of *clpA* gene in *Salmonella*	AGCAGCGAACCGATATCCAG
15931	qRT-PCR of *rssB* gene in *Salmonella*	TCCTCTTTGGGAGCGACAAC
15932	qRT-PCR of *rssB* gene in *Salmonella*	GAGACCGTTCATTCTCGGCA
6492	qRT-PCR of *pagC* gene in *Salmonella*	CGGGTCTGTTGAGCCTGAAG
6493	qRT-PCR of *pagC* gene in *Salmonella*	TAGGCTGGCCCAACCATTAA
4493	qRT-PCR of *slyB* gene in *Salmonella*	CAAGTTCAGAATGTAACGTACGGTACT
4494	qRT-PCR of *slyB* gene in *Salmonella*	GAATCATCACCGCCCTGAAT
16506	qRT-PCR of *uvrY* gene in *Salmonella*	CCAGTTTGTCTGAACGCGAG
16507	qRT-PCR of *uvrY* gene in *Salmonella*	AGCGATAGCTGTTCACCGTT
16512	qRT-PCR of *cspA* gene in *Salmonella*	CAACGCTGATAAAGGCTTCGG
16513	qRT-PCR of *cspA* gene in *Salmonella*	CGCTTTCGATGGTGAAGGAA
16508	qRT-PCR of *csrB* gene in *Salmonella*	GACACGCCAGGATGGTGTTA
16509	qRT-PCR of *csrB* gene in *Salmonella*	CTGATCGGCTCTCGTTCTCC
15054	qRT-PCR of *ompA* gene in *Salmonella*	GGGCTGGTCTCAGTACCATGA
15055	qRT-PCR of *ompA* gene in *Salmonella*	TCATGAGTCGGGCCATCA

Table S2. Cont.

Primer number	Purpose	Sequence (5′–3′)
3023	qRT-PCR of *rrs* gene in *Salmonella*	CCAGCAGCCGCGGTAAT
3024	qRT-PCR of *rrs* gene in *Salmonella*	TTTACGCCCAGTAATTCCGATT
15790	qRT-PCR of *clpA* gene in *E. coli*	GAAATCGAGAAAGCGCACCC
15791	qRT-PCR of *clpA* gene in *E. coli*	CCACGTTACGGAAGTCTGCT
15792	qRT-PCR of *clpS* gene in *E. coli*	AAGACGAACGATTGGCTGGA
15793	qRT-PCR of *clpS* gene in *E. coli*	ACATAGATGGCGGTTTTAGCG
16496	qRT-PCR of *ompA* gene in *E. coli*	CCCGACCCATGAAAACCAAC
16497	qRT-PCR of *ompA* gene in *E. coli*	TGAACGCCCTGAGCTTTGTA