Supplementary Information

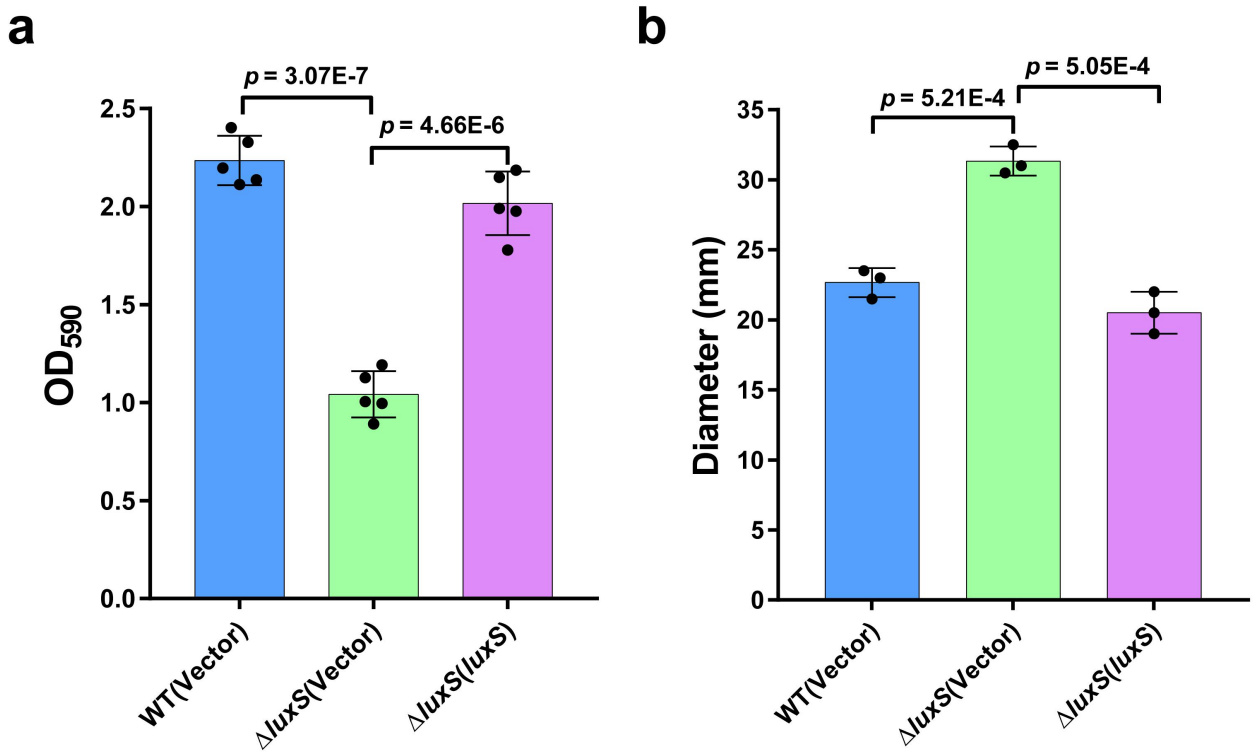
Autoinducer-2 and bile salts induce c-di-GMP synthesis to repress the T3SS via the CesD/SycD/LcrH family of chaperones

This PDF file includes:

Supplementary Figures 1-27

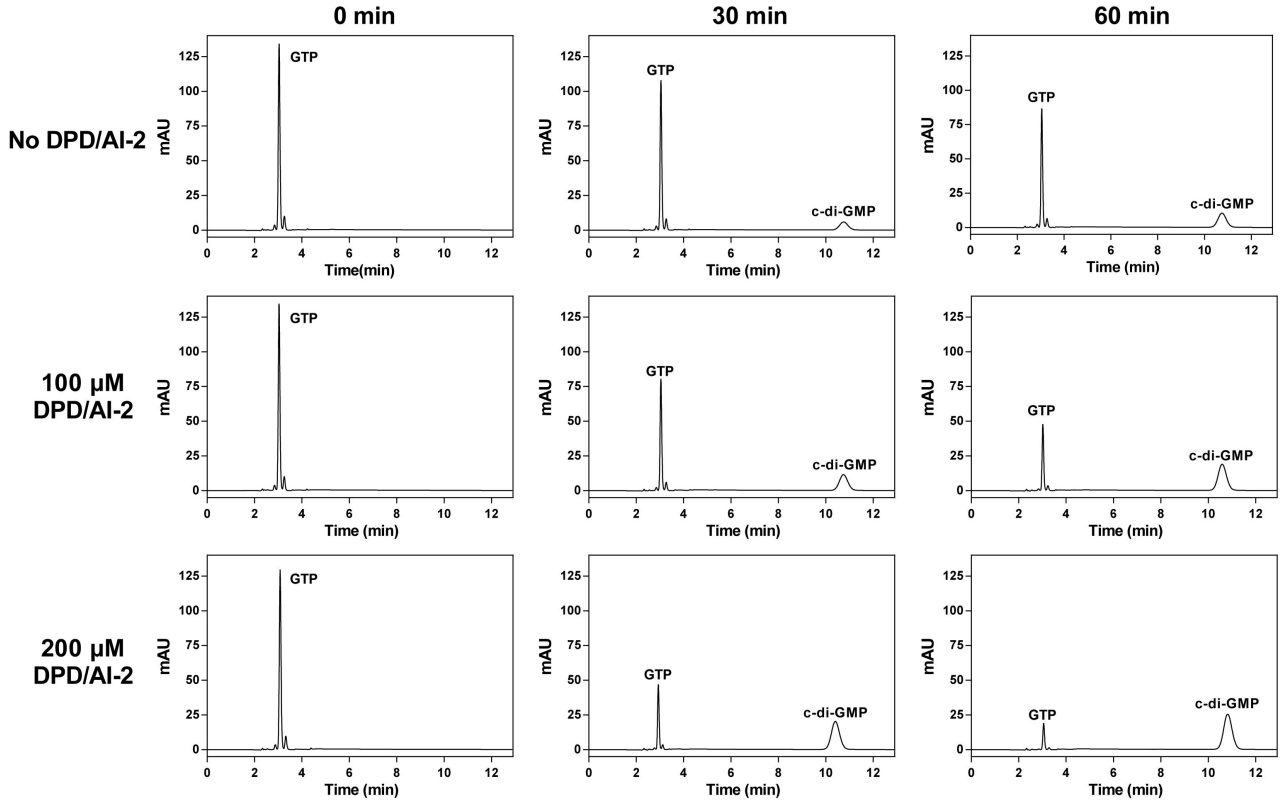
Supplementary Tables 1-2

Supplementary References



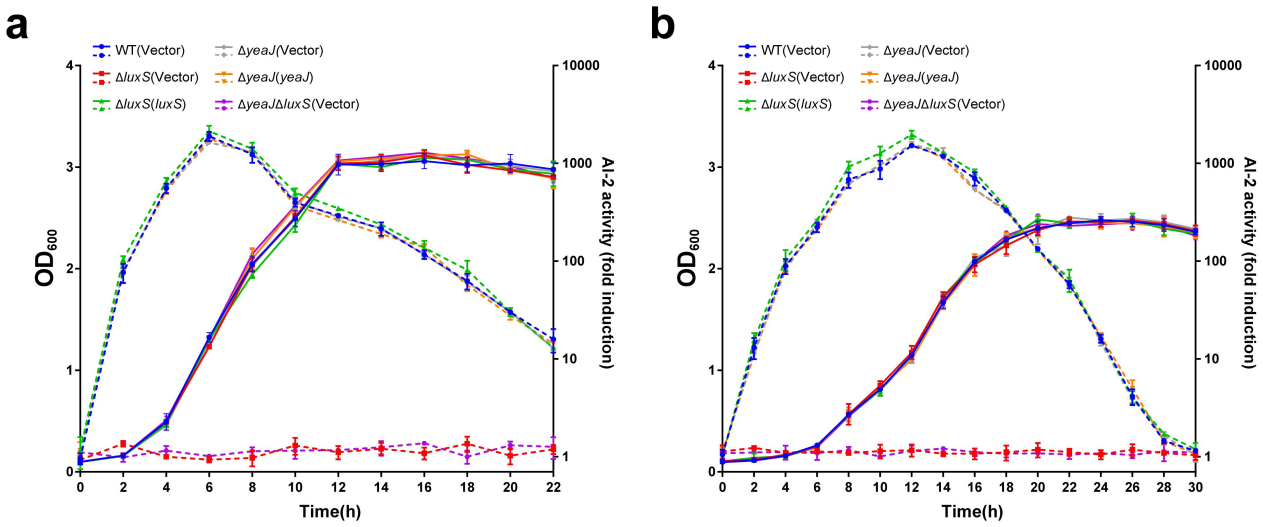
Supplementary Fig. 1 AI-2 regulates biofilm formation and swimming motility in *S.* Typhimurium

a 200 µl aliquots of *S.* Typhimurium strains with an OD_{600} of 0.05 in LB medium were placed into the wells of a 96-well plate. After incubation at 37 °C for 24 h, biofilms were stained with crystal violet and quantified using optical density measurement. Data are mean ± s.e.m. of five independent experiments. **b** 2 µl aliquots of *S.* Typhimurium strains with an OD_{600} of 0.5 in LB medium were spotted onto 0.3% tryptone agar. After incubation at 37 °C for 12 h, motility halos were measured. Data are mean ± s.e.m. of three independent experiments. **a, b** Statistical significance was determined using two-tailed unpaired Student's *t*-test and $p < 0.05$ was considered statistically significant.



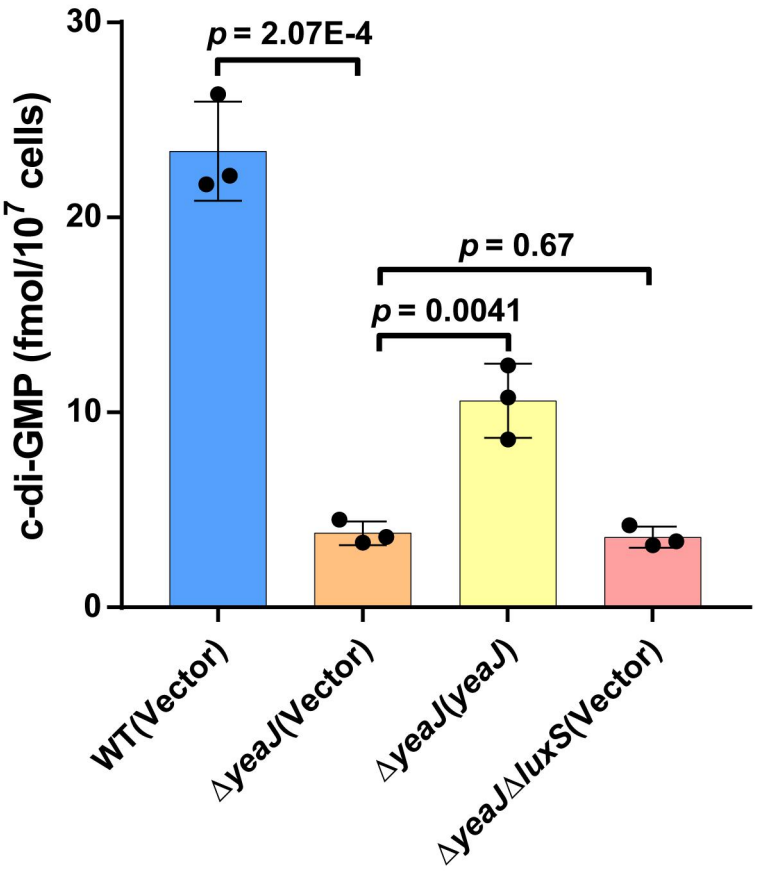
Supplementary Fig. 2 AI-2 induces the DGC activity of YeaJ in c-di-GMP synthesis

Membrane fractions containing full-length YeaJ were incubated with GTP in the presence or absence of DPD/AI-2 at 30°C for 0, 30 and 60 min and the products were analyzed by HPLC. HPLC spectra shown are representatives of three independent experiments with similar results.



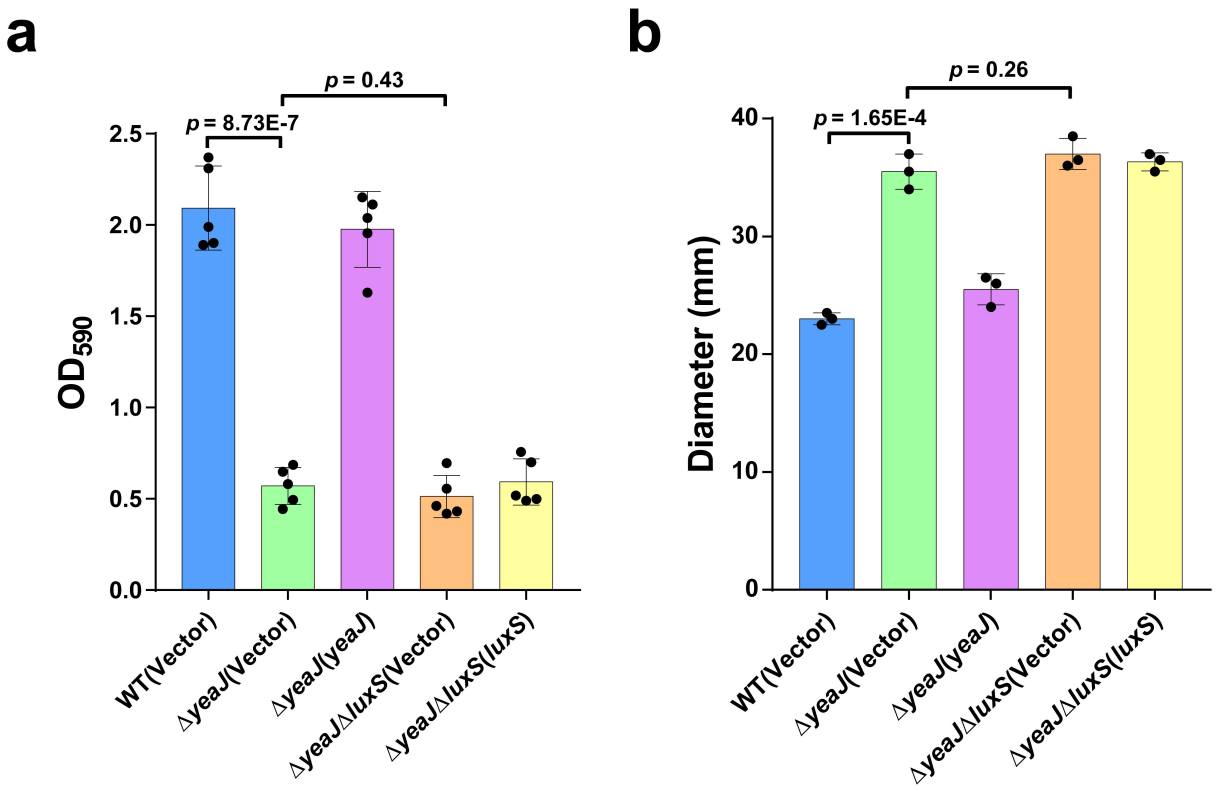
Supplementary Fig. 3 Growth curves and extracellular AI-2 activities of *S*. Typhimurium strains

S. Typhimurium strains were grown at 37 °C in LB medium with shaking (**a**) or in modified LB medium containing 0.3 M NaCl without agitation (**b**). At each time point during growth, cell density was recorded by measuring the optical density at 600 nm (solid line) and cell supernatants were collected, filtered, and measured for AI-2 activity by using the *V. harveyi* MM32 reporter assay (dashed line). Data are mean ± s.d. of three biological replicates.



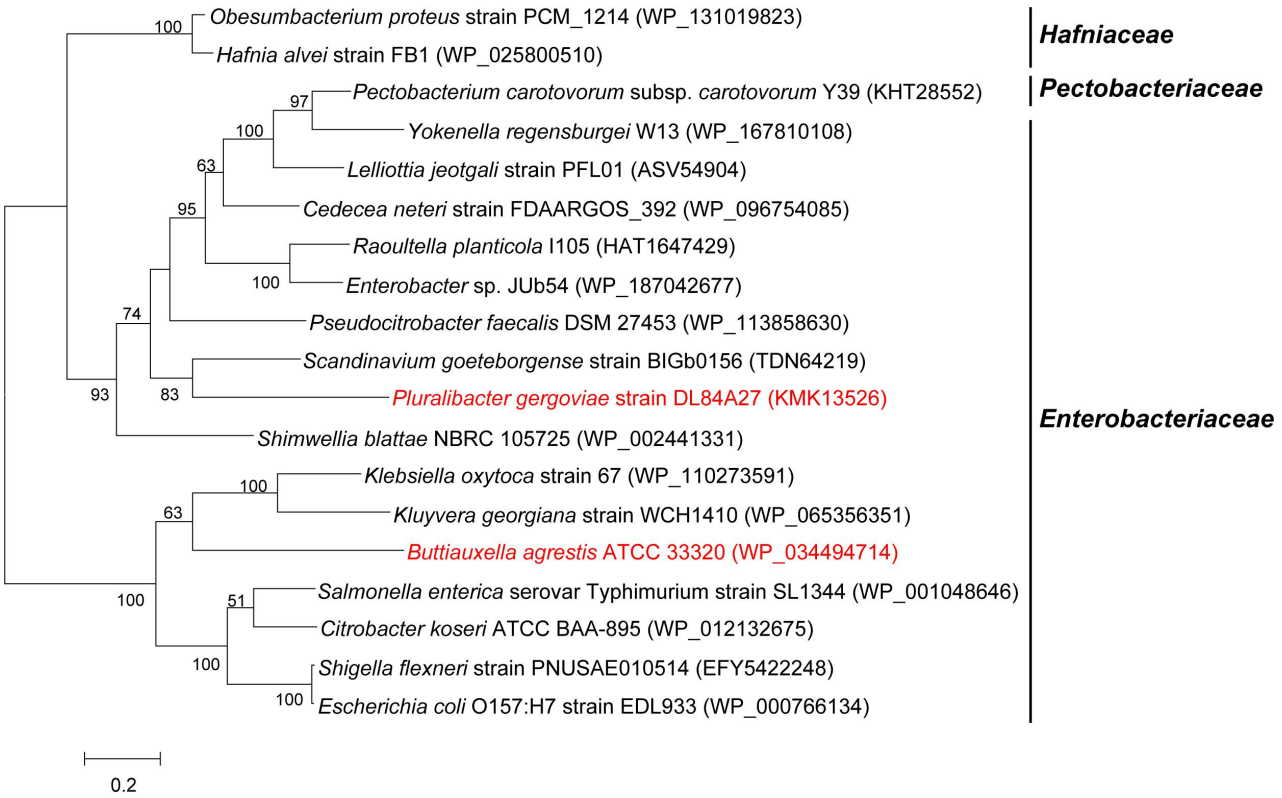
Supplementary Fig. 4 Deletion of *luxS* did not alter intracellular levels of c-di-GMP in a Δ*yeaJ* background

LC-MS/MS measurements of cellular levels of c-di-GMP in *S.* Typhimurium strains. All strains were grown in LB broth at 37 °C with shaking to an OD_{600} of 1.3 (Supplementary Fig. 3a), and then 15 ml aliquots of the bacterial cultures were subjected to nucleotide extractions. Cellular levels of c-di-GMP were quantified by LC-MS/MS analysis. Data are mean ± s.d. of three biological replicates. Statistical significance was evaluated using the two-tailed unpaired Student's *t*-test. *P* values < 0.05 indicate significant differences.



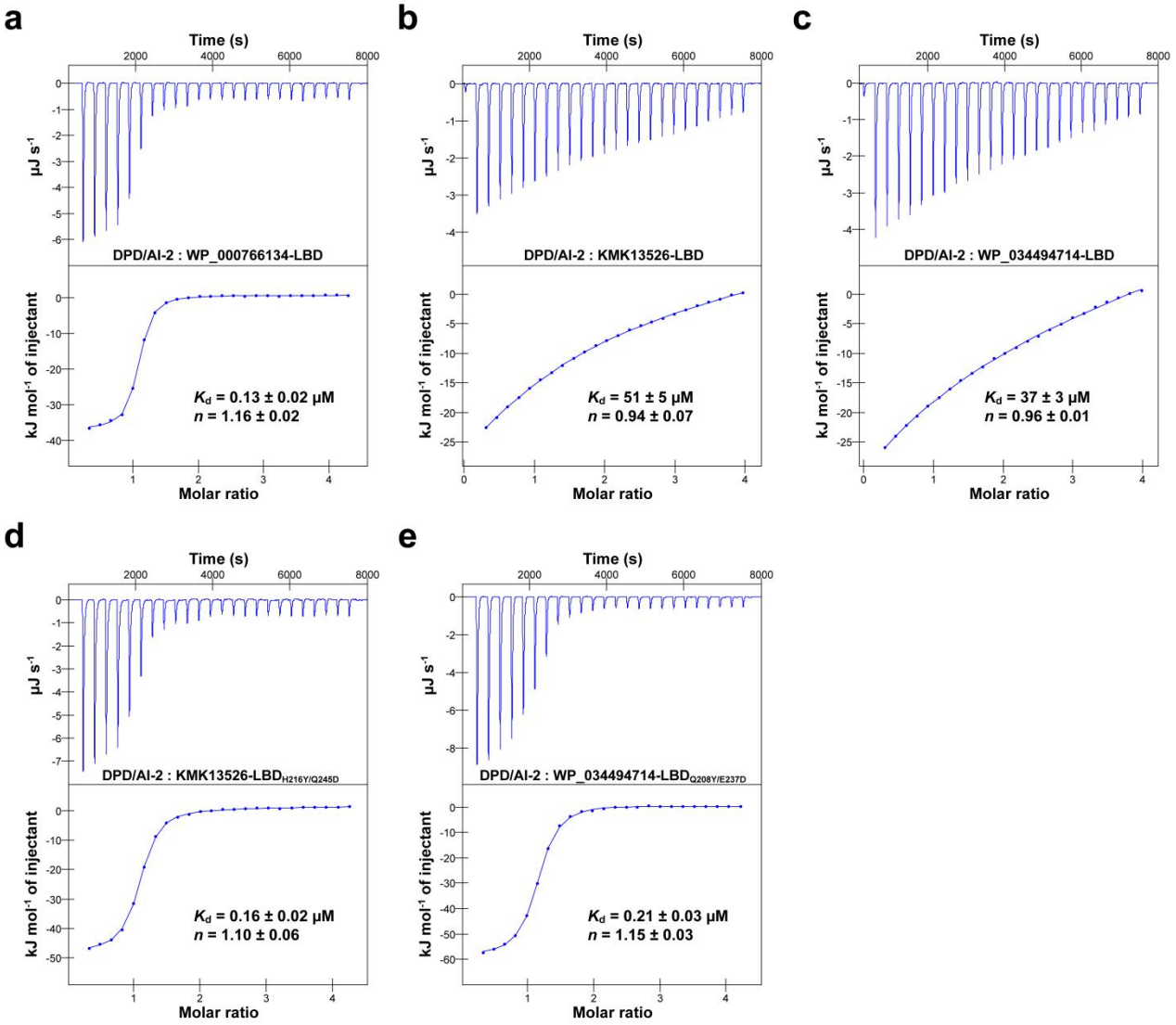
Supplementary Fig. 5 AI-2-mediated regulation of biofilm formation and motility in *S.* Typhimurium is dependent on the DGC YeaJ

a Biofilm formation by *S.* Typhimurium strains was measured using a crystal violet staining method as described in Supplementary Fig. 1a. Data are mean ± s.e.m. of five independent experiments. **b** *S.* Typhimurium strains were measured for swimming motility as described in Supplementary Fig. 1b. Data are mean ± s.e.m. of three independent experiments. **a, b** Statistical significance was determined by the two-tailed unpaired Student's *t*-test and $p < 0.05$ was considered to be statistically significant.



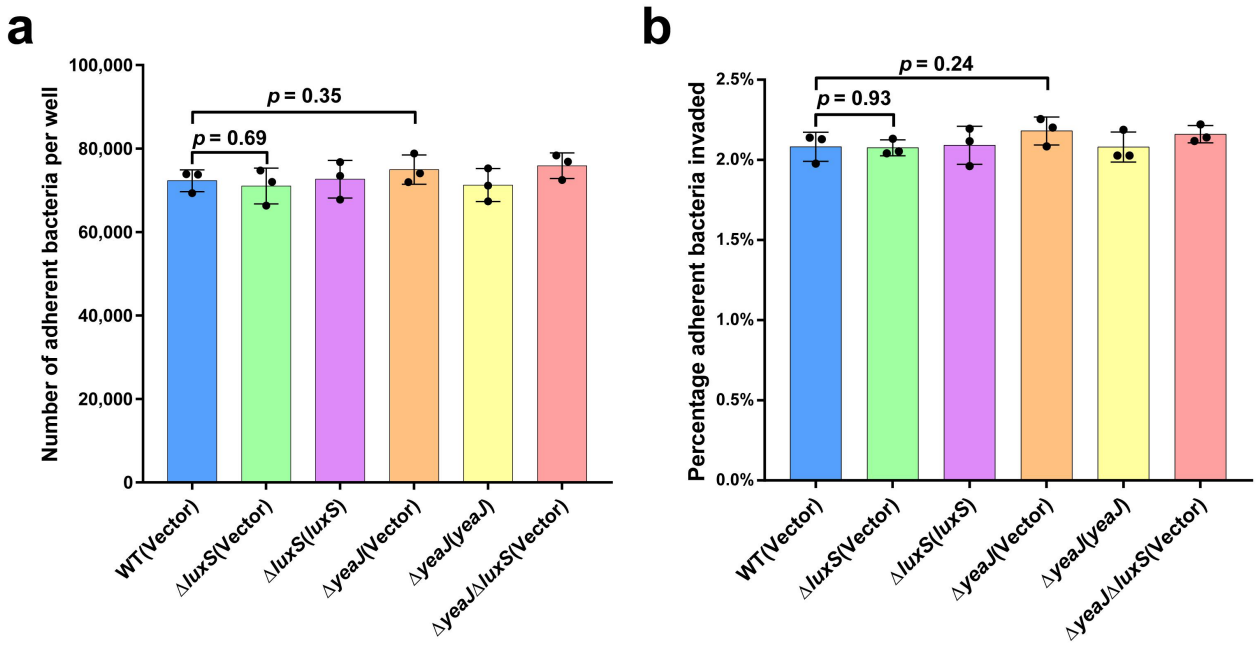
Supplementary Fig. 6 Maximum-likelihood phylogenetic tree showing the relationship of the GAPES1 domain-containing diguanylate cyclase YeaJ from *S.* Typhimurium and 18 high-confidence YeaJ orthologs from other genera

High-confidence YeaJ homologs were searched by BLASTP and further identified using InterProScan 5 against the Pfam 34.0 database (Supplementary Data 1). One representative sequence for each genus was randomly selected and multiple sequence alignments were performed with clustalX version 1.81. The phylogenetic tree was reconstructed by using the maximum-likelihood method based on the Jones-Taylor-Thornton (JTT) model embedded in the MEGA7 software. The bacterial species to which YeaJ homologs belong are provided and the NCBI accession number for each YeaJ homolog is given in parentheses. The YeaJ homologs whose GAPES1 domains showed no detectable AI-2 binding activity are indicated in red. Phyletic distribution of the 19 GAPES1-containing proteins at the family level is shown. Bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown on the branch. Scale bar indicates evolutionary distance of 0.2 amino acid substitutions per position.



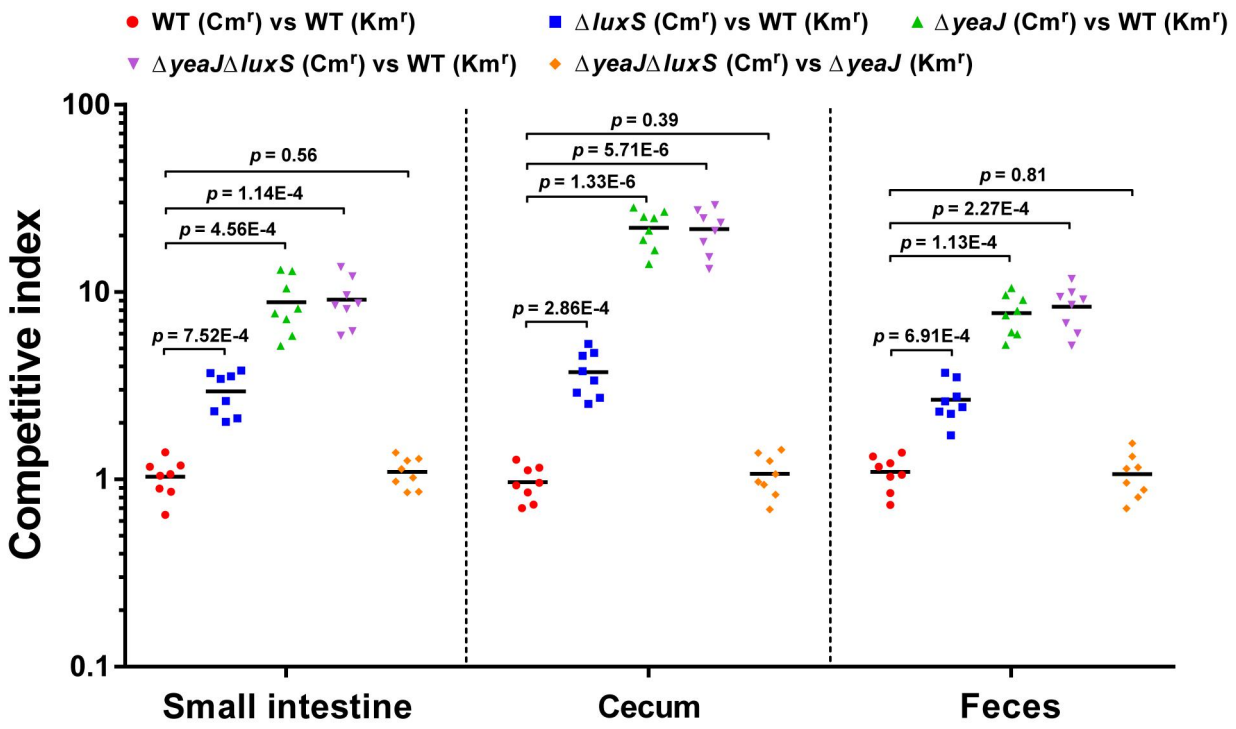
Supplementary Fig. 7 Isotherms representing binding of the wild type or mutant GAPES1 domains of YeaJ homologs with DPD/AI-2 as measured by ITC

ITC data and plots of injected heat for injections of 700 µM DPD/AI-2 into the sample cell containing 70 µM WP_000766134-LBD (**a**), KMK13526-LBD (**b**), WP_034494714 (**c**), KMK13526-LBD$_{H216Y/Q245D}$ (**d**) or WP_034494714$_{Q208Y/E237D}$ (**e**) are shown in the upper and lower plots, respectively. The heats of ligand dilution were subtracted from the heats of injection and the corrected data were fit to a one-site binding model to determine the K_d values and binding stoichiometry (n) by the NanoAnalyze software. Isotherms shown are one representative of three independent experiments with similar results, and the K_d and n values are presented as mean ± s.d. of the three independent experiments.



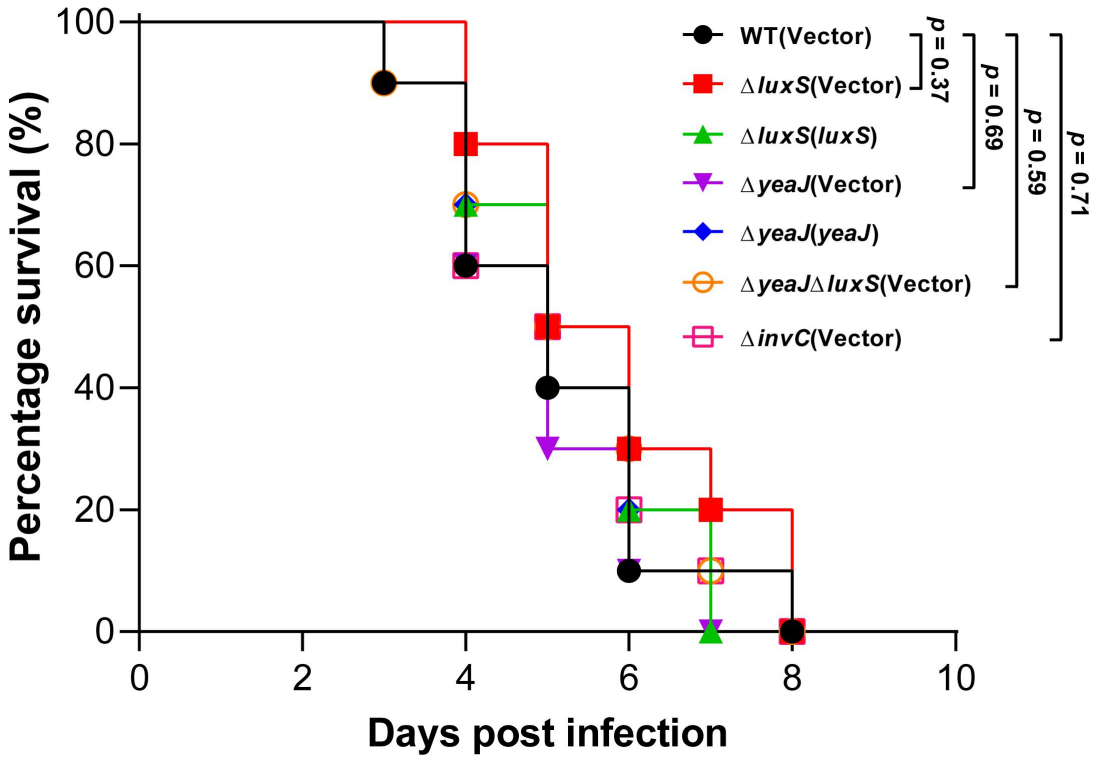
Supplementary Fig. 8 Adherence to and invasion of Caco-2 cells by S. Typhimurium cultures grown in LB broth with agitation until log phase when the AI-2 concentration in wild-type culture supernatant is maximal

S. Typhimurium strains were grown to an OD_{600} of 1.3 (Supplementary Fig. 3a), and then bacterial cells were collected, washed and resuspended in PBS. Monolayer cultures of Caco-2 cells at a density of 1 × 10^5 cells per well were infected with bacterial cultures at a multiplicity of infection (MOI) of 50. Bacterial adherence (**a**) was measured by CFU counting and presented as the total number of cell-associated bacteria per well, and bacterial invasion (**b**) was expressed as a percentage of intracellular bacterial counts relative to the total adherent bacteria. Data are mean ± s.e.m. of three independent experiments. Statistical significance was determined by two-tailed Student's *t*-test. $P < 0.05$ indicates a statistically significant difference.



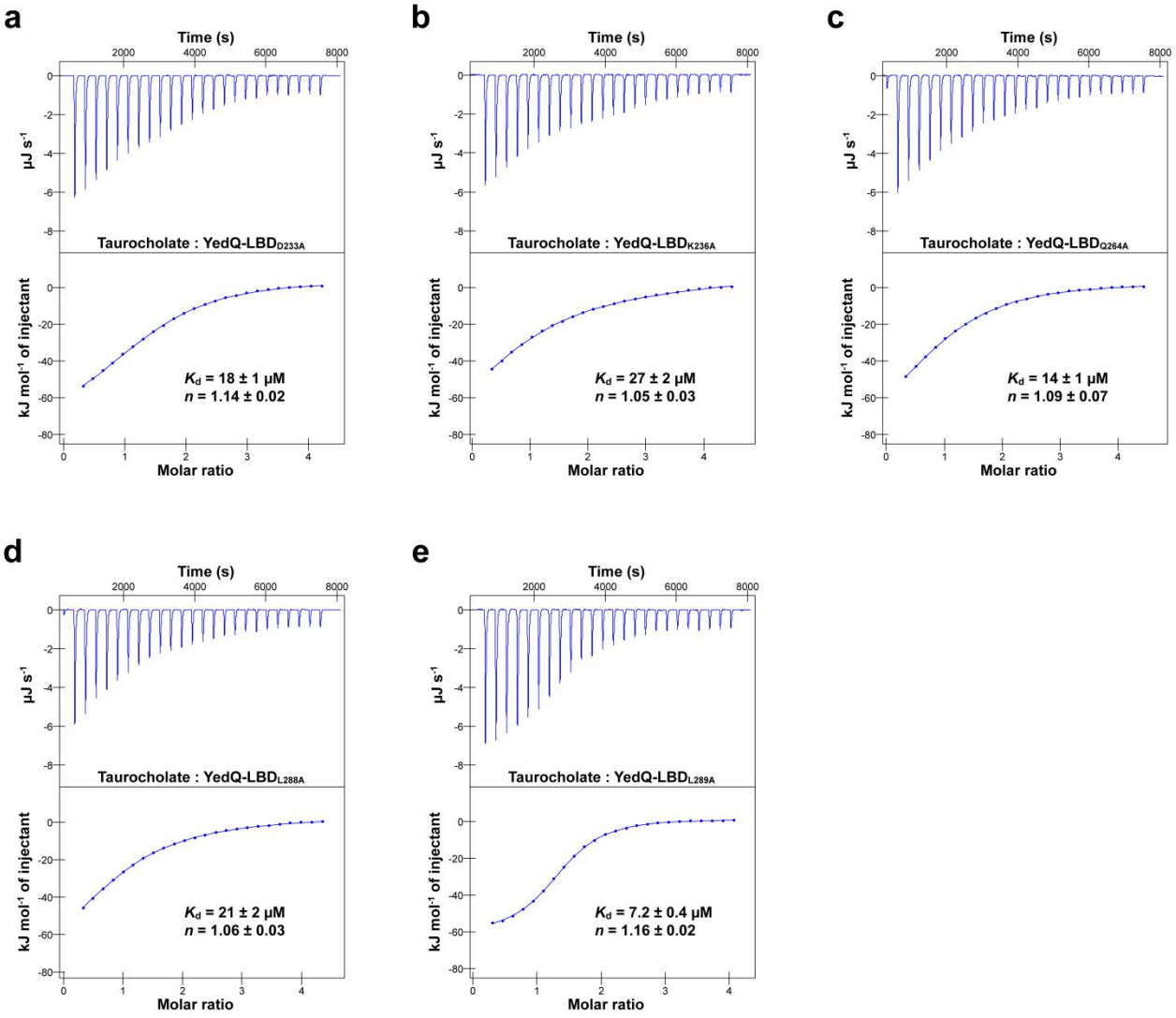
Supplementary Fig. 9 Competition assays in mice between *S.* Typhimurium strains

S. Typhimurium cultures grown in modified LB medium containing 0.3 M NaCl at 37 °C without agitation to an OD_{600} of 1.1 were collected, washed and resuspended in PBS. BALB/c mice pre-treated with streptomycin were orally gavaged with a 1:1 mixture of two *S.* Typhimurium strains (5×10^8 CFU for each) carrying chloramphenicol-resistant (Cm^r) pBBR1MCS1 and kanamycin-resistant (Km^r) pKT100, respectively. Feces, cecum and small intestine tissues harvested at day 2 post infection were homogenized, serially diluted and plated on antibiotic selective LB agar plates for CFU enumeration. CI values were calculated as the ratios of the test strains carrying pBBR1MCS1 versus (vs) the control strains carrying pKT100 recovered from mice. Horizontal lines represent the geometric mean CI value for each group (n = 8 mice per group). Statistical significance was determined with a two-tailed Mann–Whitney *U* test. A *p* value less than 0.05 was considered to be statistically significant.



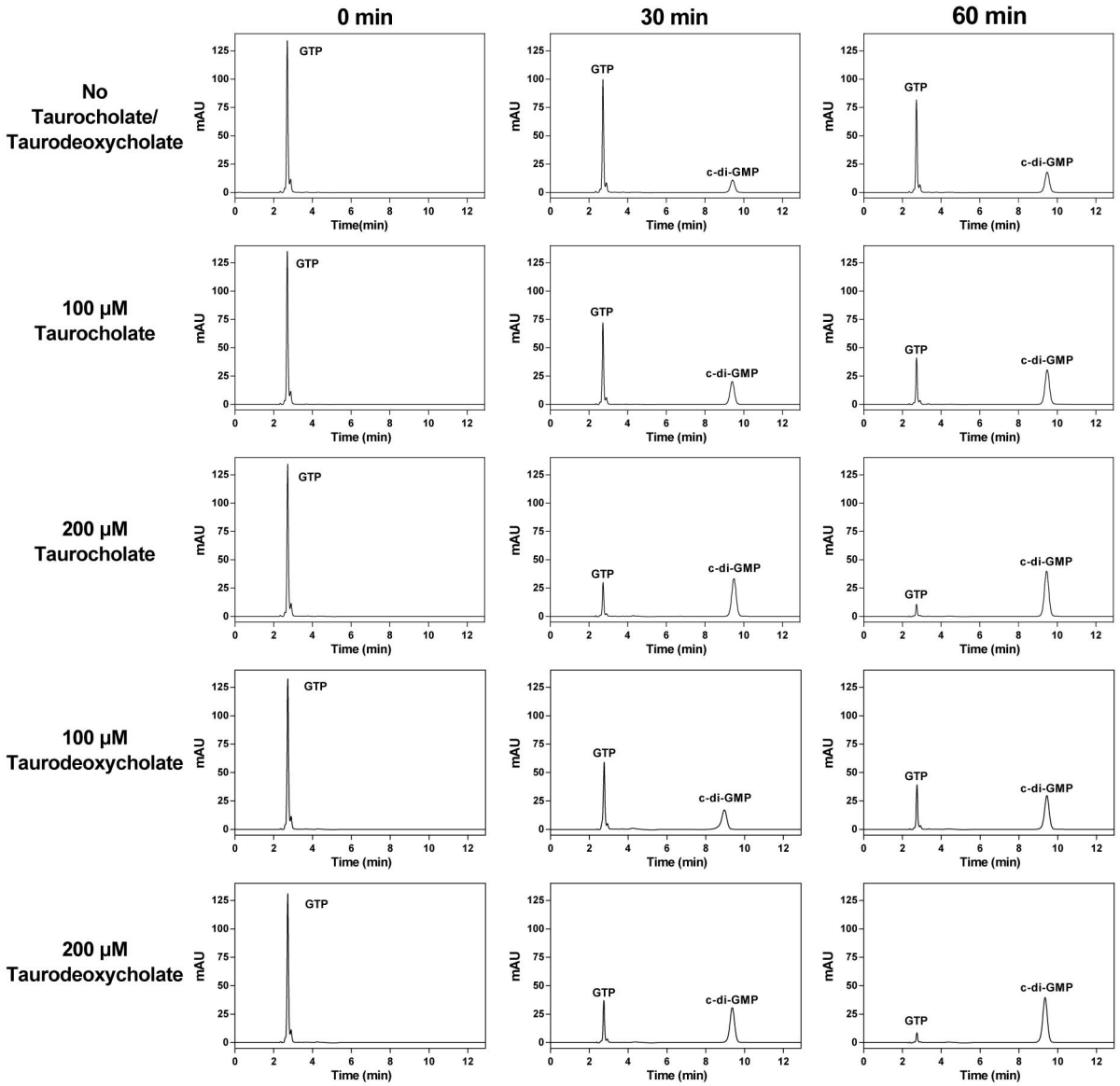
Supplementary Fig. 10 Survival curves of mice infected intraperitoneally with *S.* Typhimurium strains

S. Typhimurium strains were grown in modified LB medium containing 0.3 M NaCl at 37 °C under static conditions to an OD_{600} of 1.1, and then bacterial cells were collected, washed and resuspended in PBS. BALB/c mice were injected intraperitoneally with 10^4 CFU of each *S.* Typhimurium strain in 100 µl of PBS and the mortality of infected mice was recorded daily. Data are illustrated as percentage of mice survival (n = 10 mice per group). Statistical significance was determined using Log-rank (Mantel–Cox) test. Differences were considered statistically significant at $p < 0.05$.



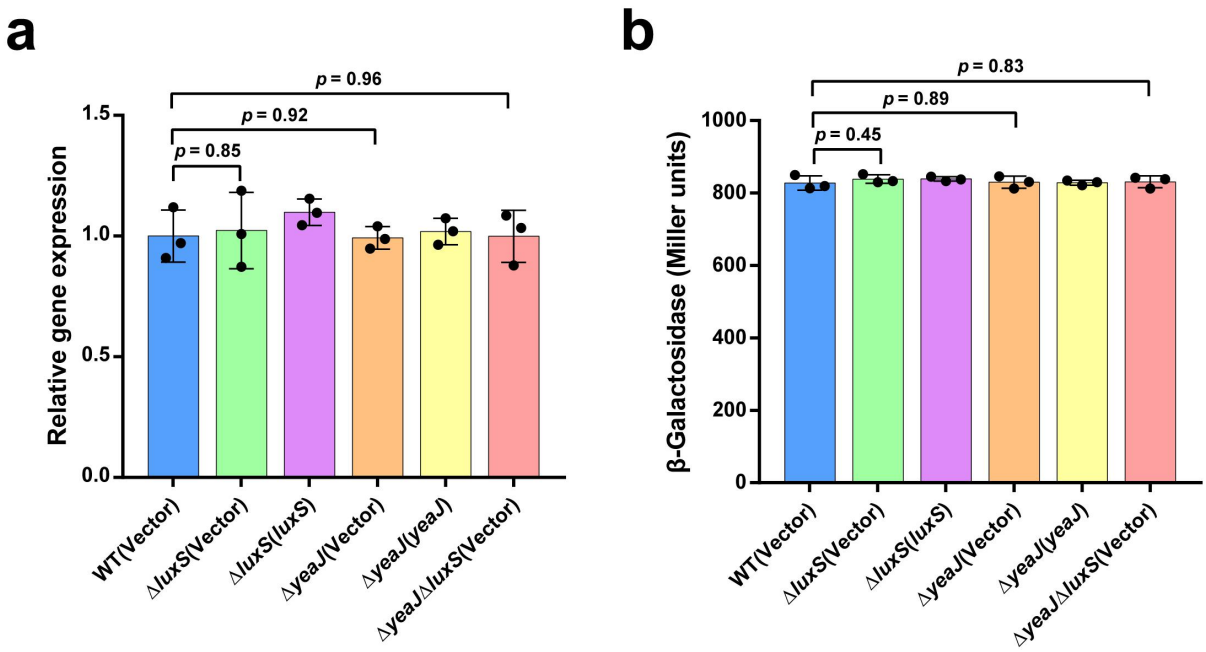
Supplementary Fig. 11 Five mutants of YedQ-LBD show lower binding affinity to taurocholate compared with the wild type

The binding affinity was evaluated using ITC analysis. ITC data and plots of injected heat for injections of 100 µM taurocholate into the sample cell containing 10 µM D233A (**a**), K236A (**b**), Q264A (**c**), L288A (**d**) or L289A (**e**) mutants of YedQ-LBD are shown in the upper and lower plots, respectively. The binding curves were corrected for the dilution effects in the final analysis. Data shown are one representative of three independent experiments with similar results. The K_d and binding stoichiometry (n) values were presented as mean ± s.d. of three independent experiments.



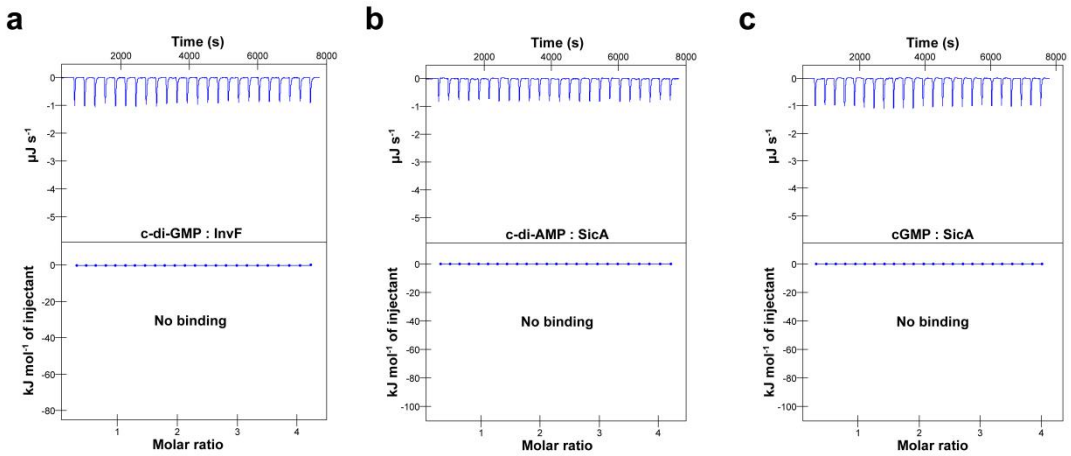
Supplementary Fig. 12 Taurocholate and taurodeoxycholate induce the DGC activity of YedQ in c-di-GMP synthesis

Membrane fractions containing full-length YedQ were incubated with GTP in the presence and absence of the bile components taurocholate or taurodeoxycholate at 30°C for 0, 30 and 60 min and then the reaction products were analyzed by HPLC. The shown spectra are representatives of three independent experiments with similar results.



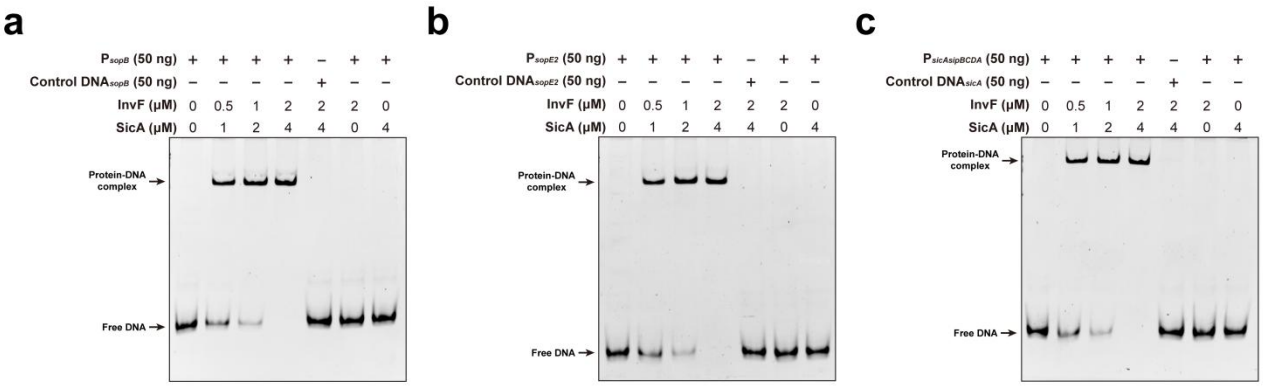
Supplementary Fig. 13 Deletion of *luxS* or *yeaJ* does not affect mRNA levels of *invF* and its promoter activity

Cultures were grown in modified LB medium containing 0.3 M NaCl at 37 °C without agitation to an OD_{600} of 1.1, and then harvested for qRT-PCR analyses (**a**) and promoter activity assays (**b**). The level of *invF* gene expression was normalized to 16S rRNA and reported as fold change relative to that of the wild type. Promoter activity of *invF* was determined by quantifying β-galactosidase activity. Data are mean ± s.e.m. of three independent experiments. Statistical significance was determined by two-tailed Student's *t*-test. $P < 0.05$ indicates that the difference is statistically significant.



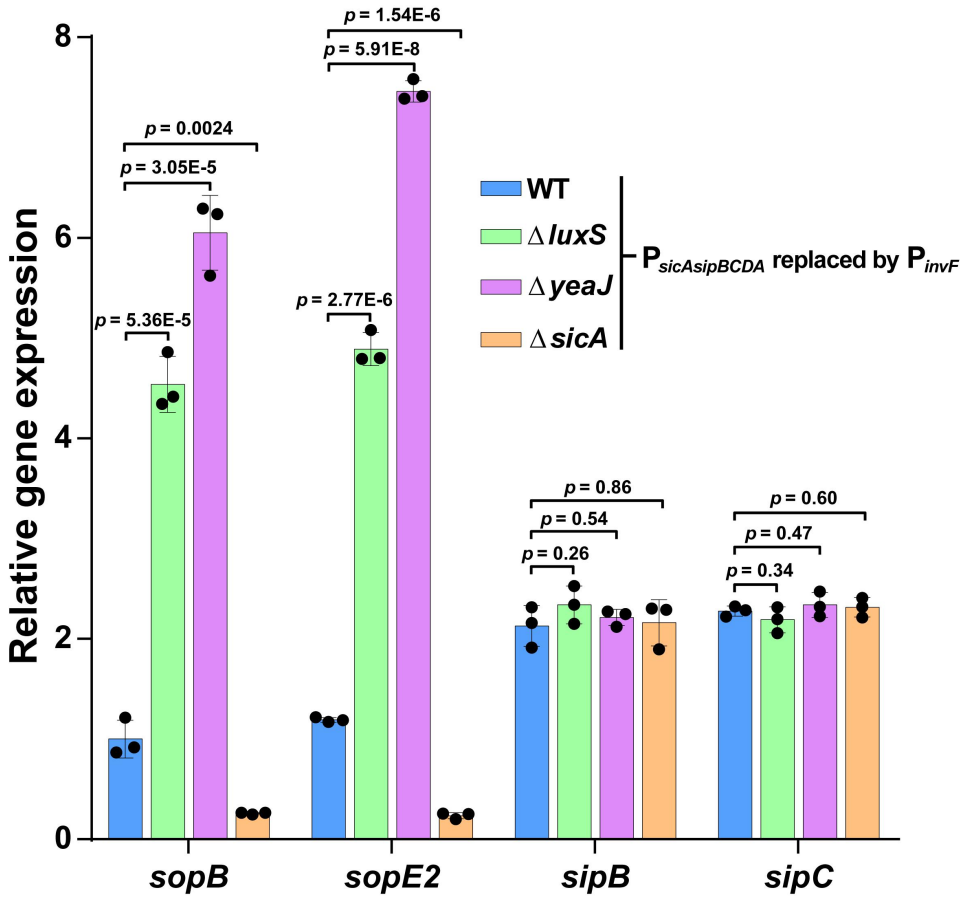
Supplementary Fig. 14 Isotherms representing binding of InvF with c-di-GMP and SicA with c-di-AMP and cGMP, measured by ITC

ITC data and plots of injected heat for injections of 100 µM c-di-GMP (**a**), c-di-AMP (**b**) or cGMP (**c**) into the sample cell containing 10 µM InvF (**a**) or SicA (**b**, **c**) are shown in the upper and lower plots, respectively. The heats of ligand dilution were subtracted from the heats of injection and the corrected data were fit to a one-site binding model. Data shown are one representative of three independent experiments with similar results.



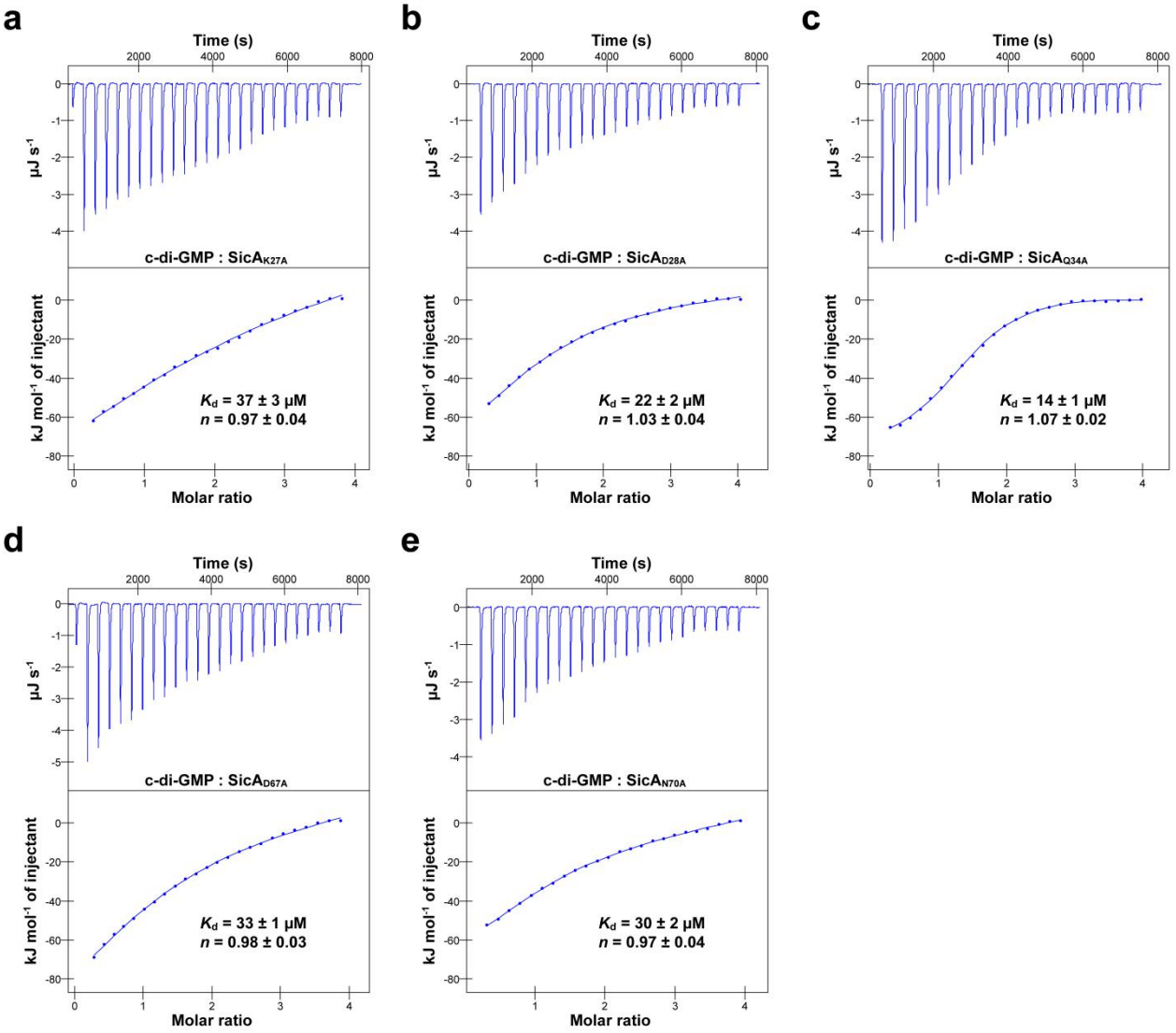
Supplementary Fig. 15 EMSAs demonstrating specificity of InvF/SicA binding to promoters of *sopB*, *sopE2* and the *sicAsipBCDA* operon

50 ng of P_{sopB} (**a**), P_{sopE2} (**b**) or $P_{sicAsipBCDA}$ (**c**) DNA was incubated with InvF and SicA (the concentrations are noted in the panel) in a 20-μl reaction system. DNA fragments amplified from the coding regions of the *sopB* (**a**), *sopE2* (**b**) and *sicA* (**c**) genes were used as controls. Data shown are one representative of three independent experiments with similar results. Uncropped images of EMSA gels are shown in Supplementary Fig. 27.



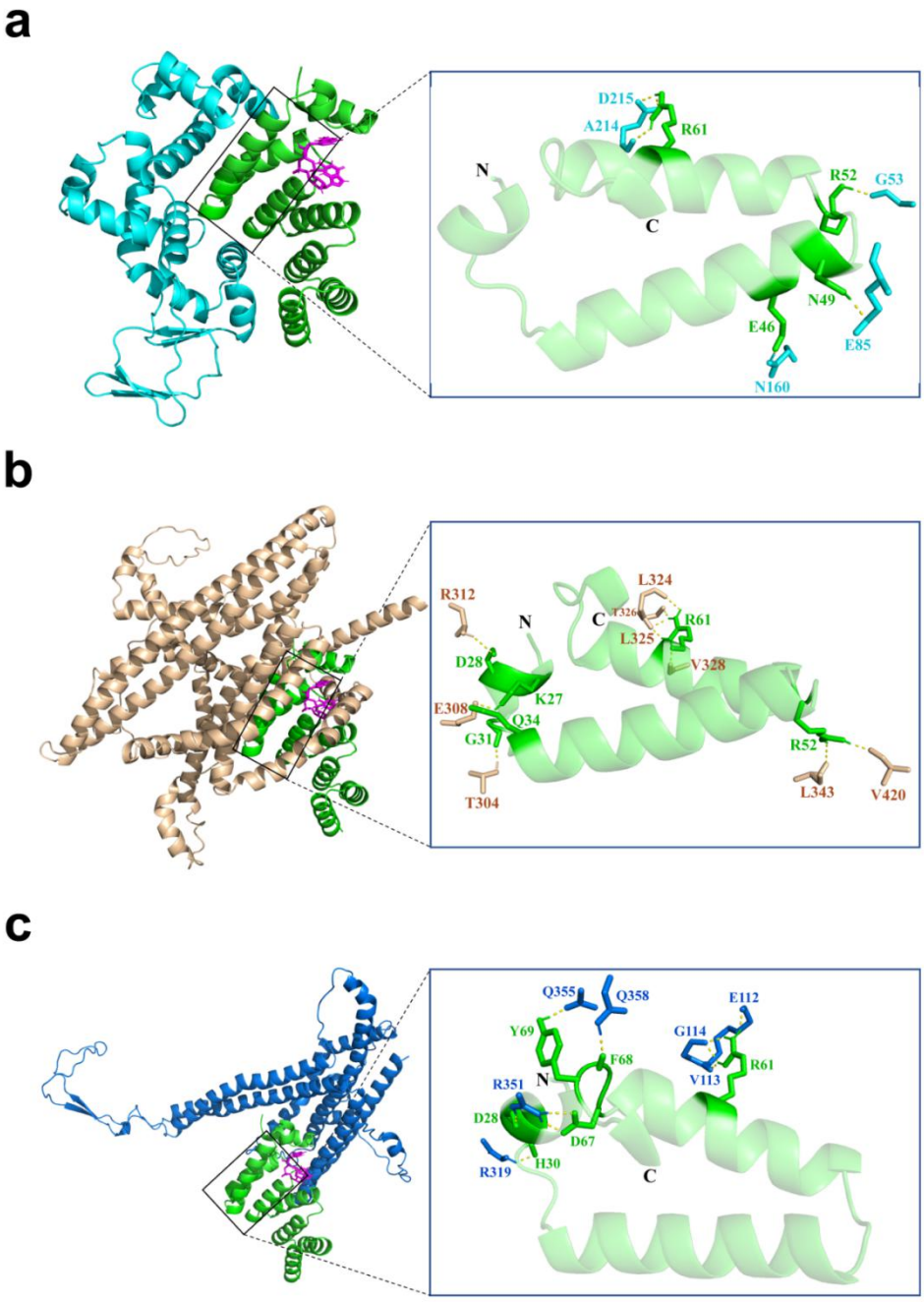
Supplementary Fig. 16 Replacement of the *sicAsipBCDA* promoter with the *invF* promoter in *S.* Typhimurium strains abolishes the response of *sipB* and *sipC* gene expression to the deletion of *luxS*, *yeaJ* or *sicA*

Cultures grown in modified LB medium containing 0.3 M NaCl at 37 °C without agitation to an OD_{600} of 1.1 were harvested for total RNA extraction and qRT-PCR analyses. Gene expression levels were normalized to 16S rRNA and presented as values relative to that of the *sopB* gene of the wild-type (WT) strain with $P_{sicAsipBCDA}$ replaced by P_{invF}. Data are mean ± s.e.m. of three independent experiments. Statistical significance was determined by two-tailed Student's *t*-test. Differences were considered to be statistically significant when *p* values were less than 0.05.



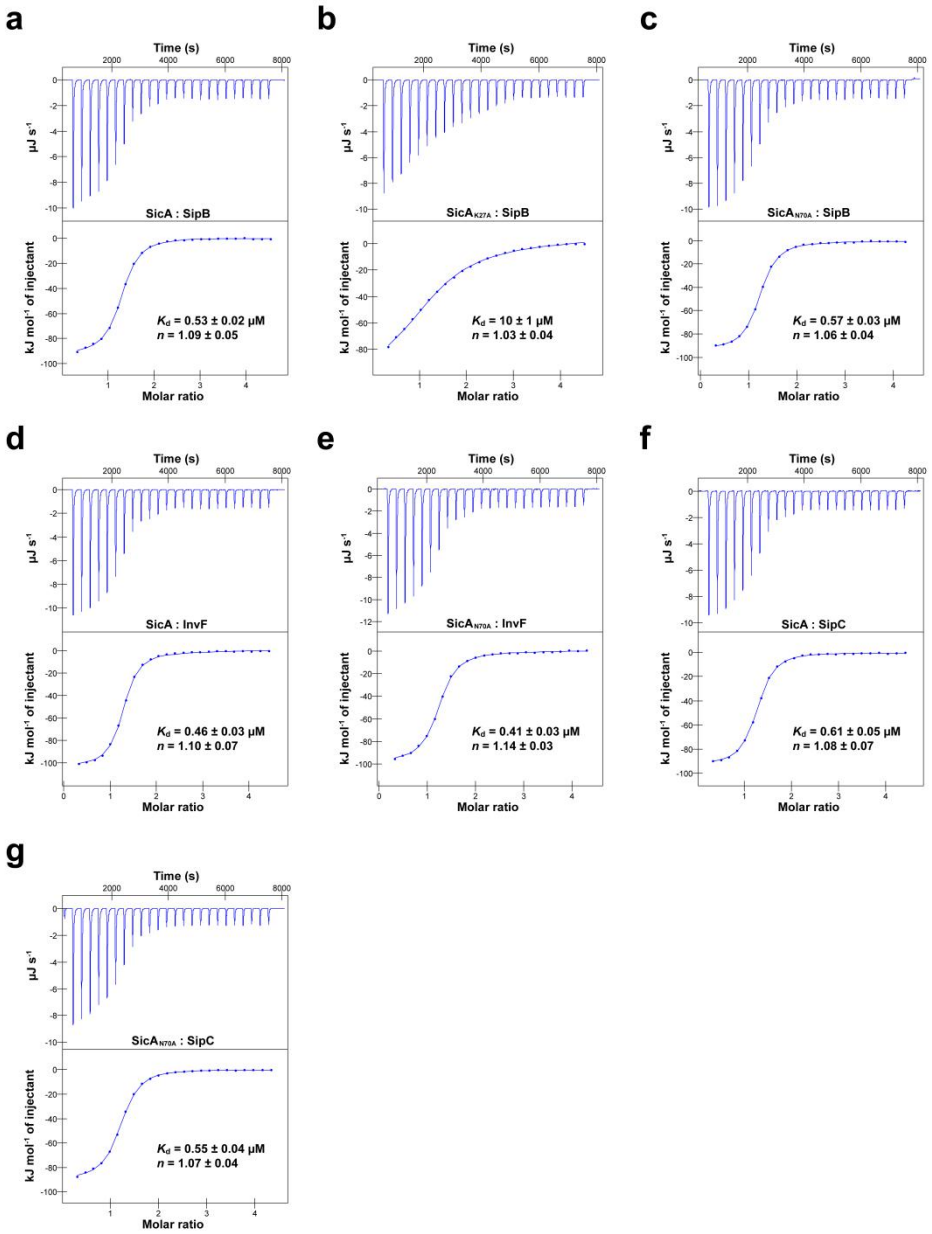
Supplementary Fig. 17 Five mutants of SicA show lower binding affinity to c-di-GMP compared with the wild type

The binding affinity was measured by ITC. ITC data and plots of injected heat for 25 automatic injections of 100 µM c-di-GMP into the sample cell containing 10 µM SicA mutants K27A (**a**), D28A (**b**), Q34A (**c**), D67A (**d**) or N70A (**e**) are shown in the upper and lower plots, respectively. The binding curves were corrected for the dilution effects in the final analysis. Isotherms shown are one representative of three independent experiments and the K_d and binding stoichiometry (n) values were presented as mean ± s.d. of the three independent experiments.



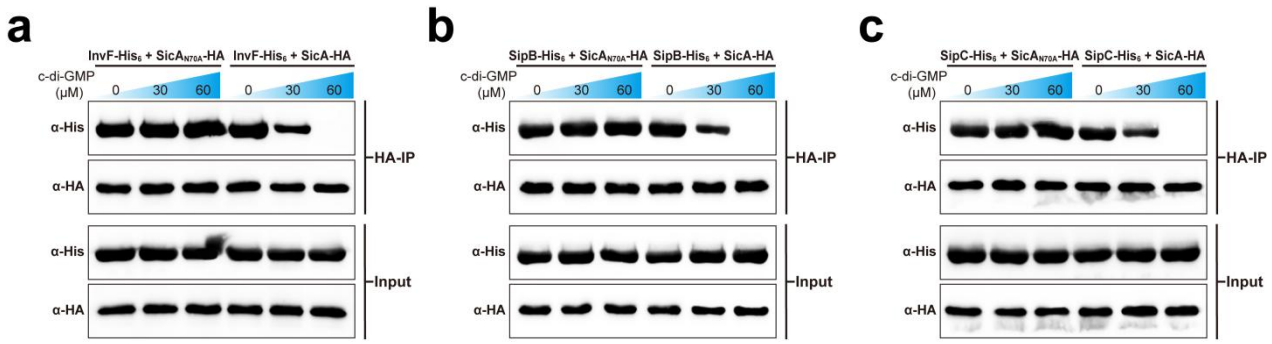
Supplementary Fig. 18 Docking analysis of SicA with InvF, SipB and SipC

A homology model of SicA was constructed via the Phyre2 server based on the crystal structure of IpgC from *S. flexneri* (PDB ID: 3GYZ). The 3D structures of InvF, SipB and SipC were predicted by AlphaFold2. Docking simulation of SicA with InvF (**a**), SipB (**b**) and SipC (**c**) was performed using the Cluspro 2.0 web server (https://cluspro.org). In left panels, cartoon representations of the SicA (green) in complex with InvF (cyan), SipB (gold) and SipC (blue) are shown. Right panels depict interactions of SicA (residues 25-72) with InvF, SipB and SipC, and residues important for binding are shown in sticks with hydrogen bonds indicated by dashed lines. C-di-GMP is also shown as pink sticks in the predicted c-di-GMP binding site of SicA as indicated in Fig. 5i.



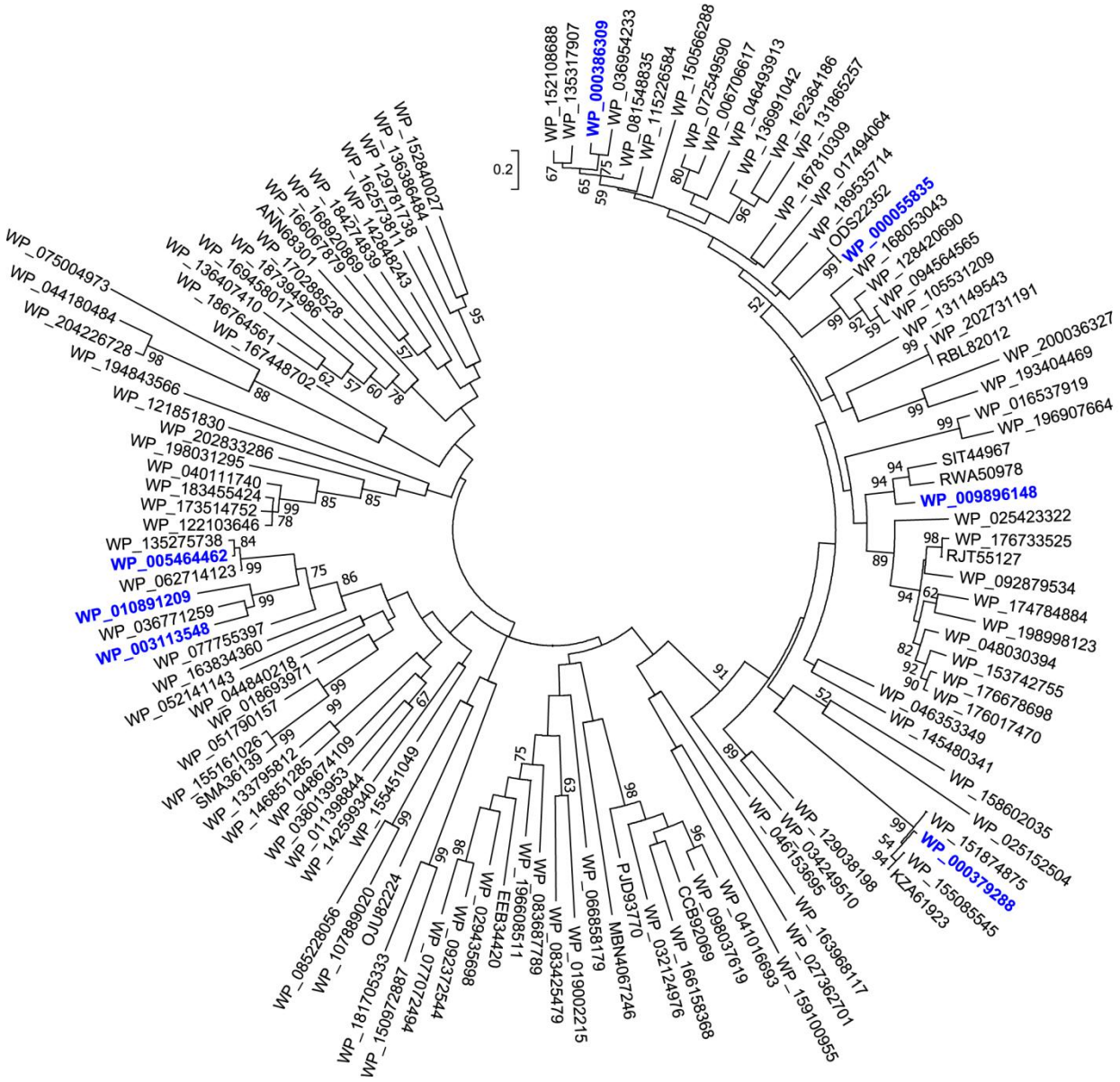
Supplementary Fig. 19 Isotherms representing binding of SicA and its variants with InvF, SipB and SipC as measured by ITC

ITC data and plots of injected heat for 25 automatic injections of 100 μM SicA (**a, d, f**), SicA$_{K27A}$ (**b**) or SicA$_{N70A}$ (**c, e, g**) into the sample cell containing 10 μM SipB (**a-c**), InvF (**d, e**), or SipC (**f, g**) are shown in the upper and lower plots, respectively. The binding curves were corrected for the dilution effects and fit to a one-site binding model. Isotherms shown are one representative of three independent experiments with similar results. The K_d and binding stoichiometry (n) values are shown as mean ± s.d. of three independent experiments.



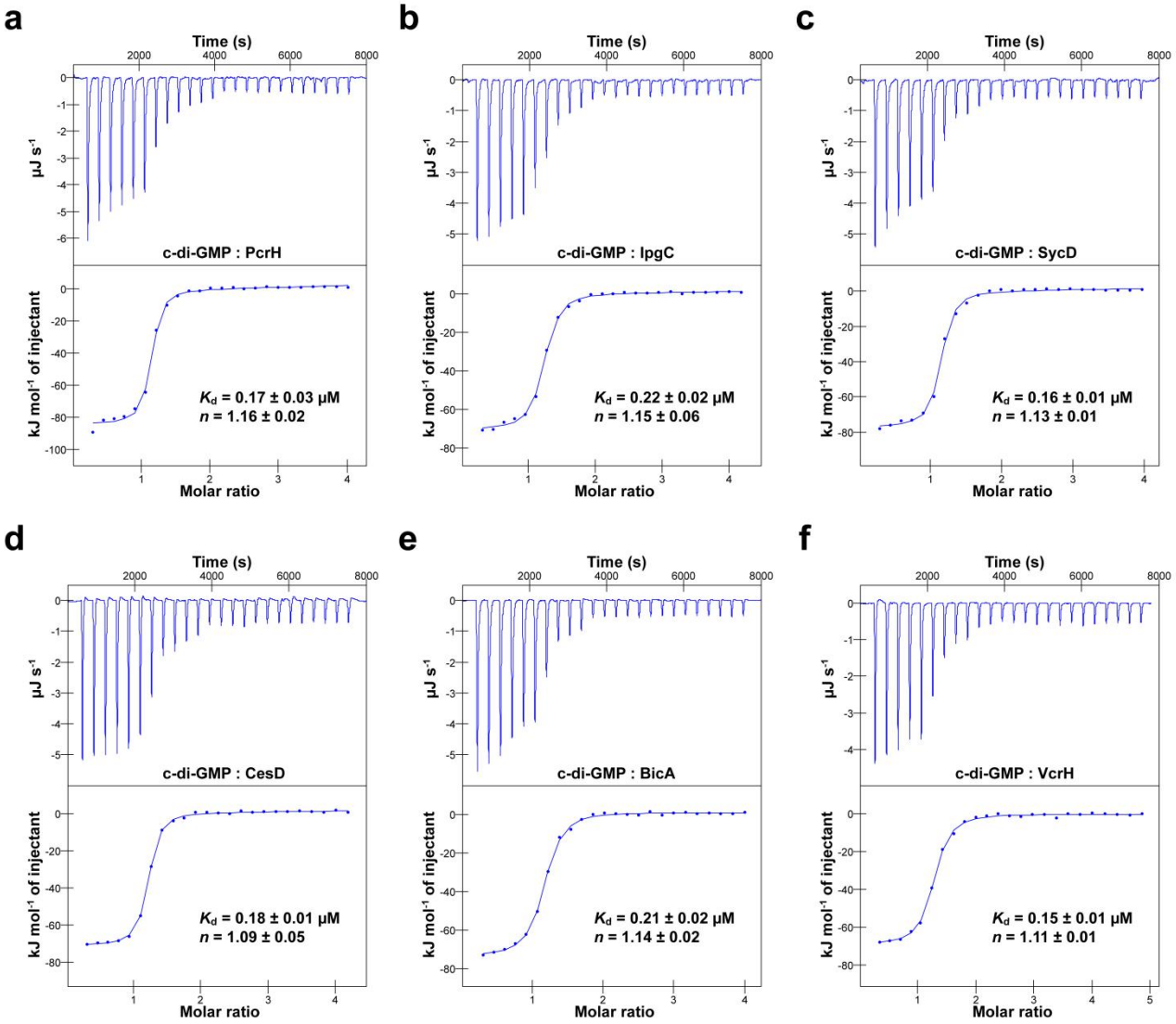
Supplementary Fig. 20 C-di-GMP does not impair co-IP of InvF-His_6, SipB-His_6 and SipC-His_6 with $SicA_{N70A}$-HA

S. Typhimurium strain SL1344 producing both HA-tagged and His_6-tagged proteins were grown at 37 °C in LB medium to an OD_{600} of 2.0, and then bacterial cells were collected, lysed and immunoprecipitated using beads coupled to anti-HA antibodies in the presence and absence of c-di-GMP (0, 30 or 60 μM). The immunoprecipitated proteins (HA-IP) and the total cell lysates used for co-IP (Input) were assessed by western blot with anti-HA or anti-His antibodies. Uncropped images of blots are shown in Supplementary Fig. 27.



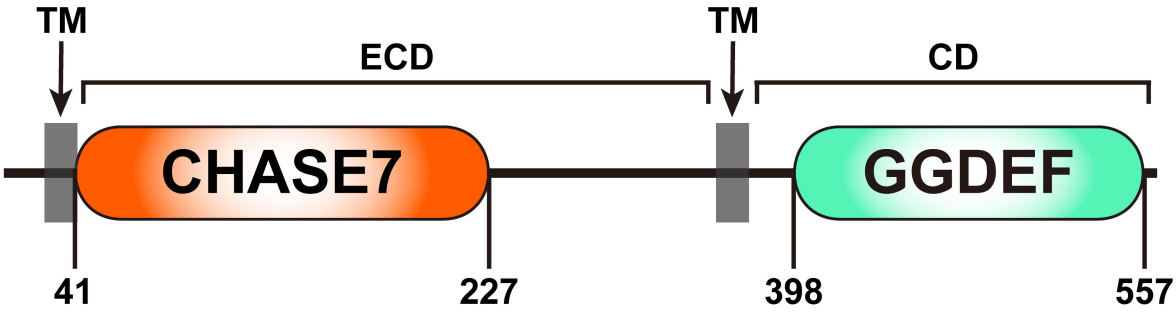
Supplementary Fig. 21 Maximum-likelihood phylogenetic tree showing the relationship of the T3SS-1 chaperone SicA from *S.* Typhimurium and its homologs from other genera

SicA homologs were searched by BLASTP against the NCBI non-redundant protein database with a cutoff E-value of 1E-03 and a coverage threshold of 60% (Supplementary Data 2). One representative sequence for each genus was randomly selected and multiple sequence alignments were performed with clustalX version 1.81. A maximum-likelihood phylogenetic tree was constructed based on the Jones-Taylor-Thornton (JTT) model with bootstrap values determined by 1,000 replicates in the MEGA7 software. The NCBI accession numbers for SicA homologs are shown and their taxonomy affiliations are provided in Supplementary Data 2. SicA (WP_000386309) and its homologs from the phylum *Proteobacteria* that have been found to bind c-di-GMP are indicated in blue. Bootstrap values greater than 50% are shown on the branch. Scale bar indicates evolutionary distance of 0.2 amino acid substitutions per position.



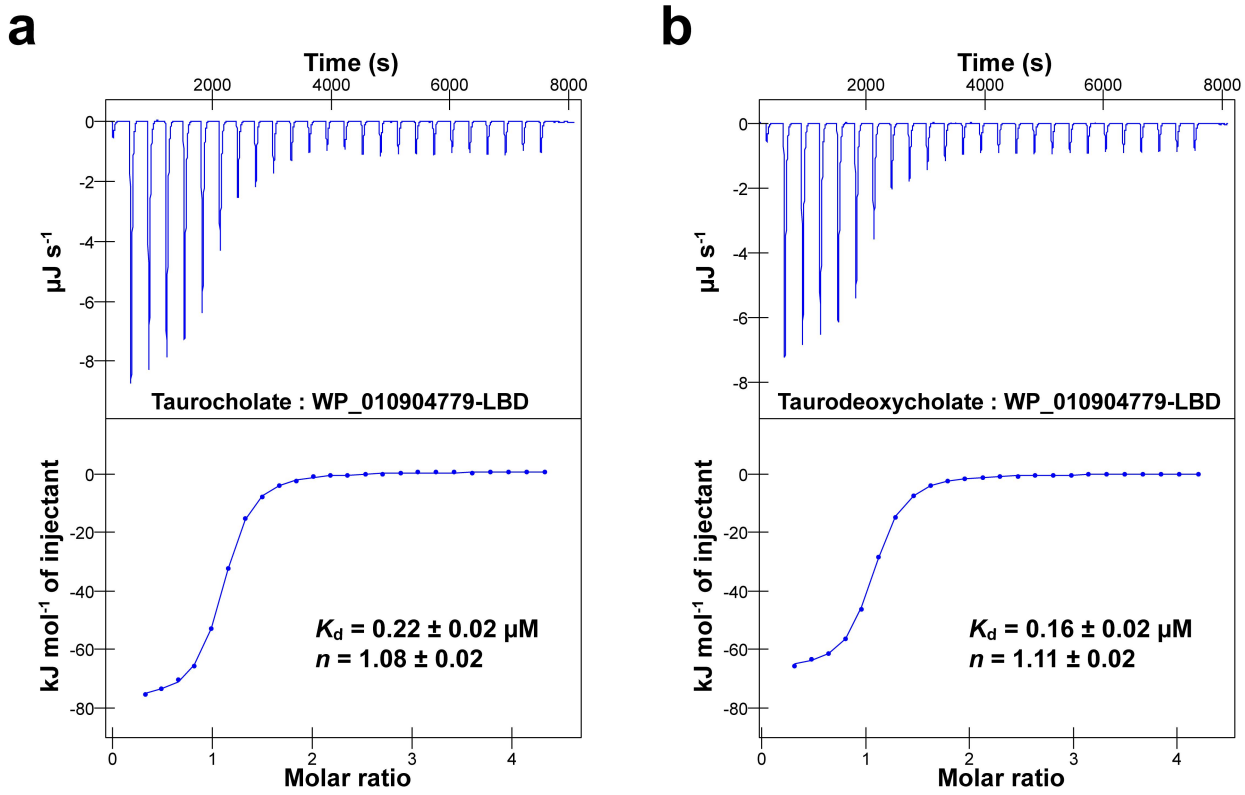
Supplementary Fig. 22 SicA homologs from six pathogenic bacteria belonging to the phylum *Proteobacteria* show high binding affinity to c-di-GMP

The binding affinity was measured by ITC. ITC data and plots of injected heat for 25 automatic injections of 100 µM c-di-GMP into the sample cell containing 10 µM PcrH (NCBI accession number WP_003113548) of *P. aeruginosa* (**a**), IpgC (WP_000055835) of *S. flexneri* serotype 2a (**b**), SycD (WP_010891209) of *Y. enterocolitica* (**c**), CesD (WP_000379288) of EHEC O157:H7 (**d**), BicA (WP_009896148) of *B. thailandensis* (**e**) or VcrH (WP_005464462) of *V. parahaemolyticus* (**f**) are shown in the upper and lower plots, respectively. The binding curves were corrected for the dilution effects in the final analysis. Isotherms shown are one representative of three independent experiments with similar results. K_d and binding stoichiometry (n) shown are mean ± s.d. of three independent experiments.



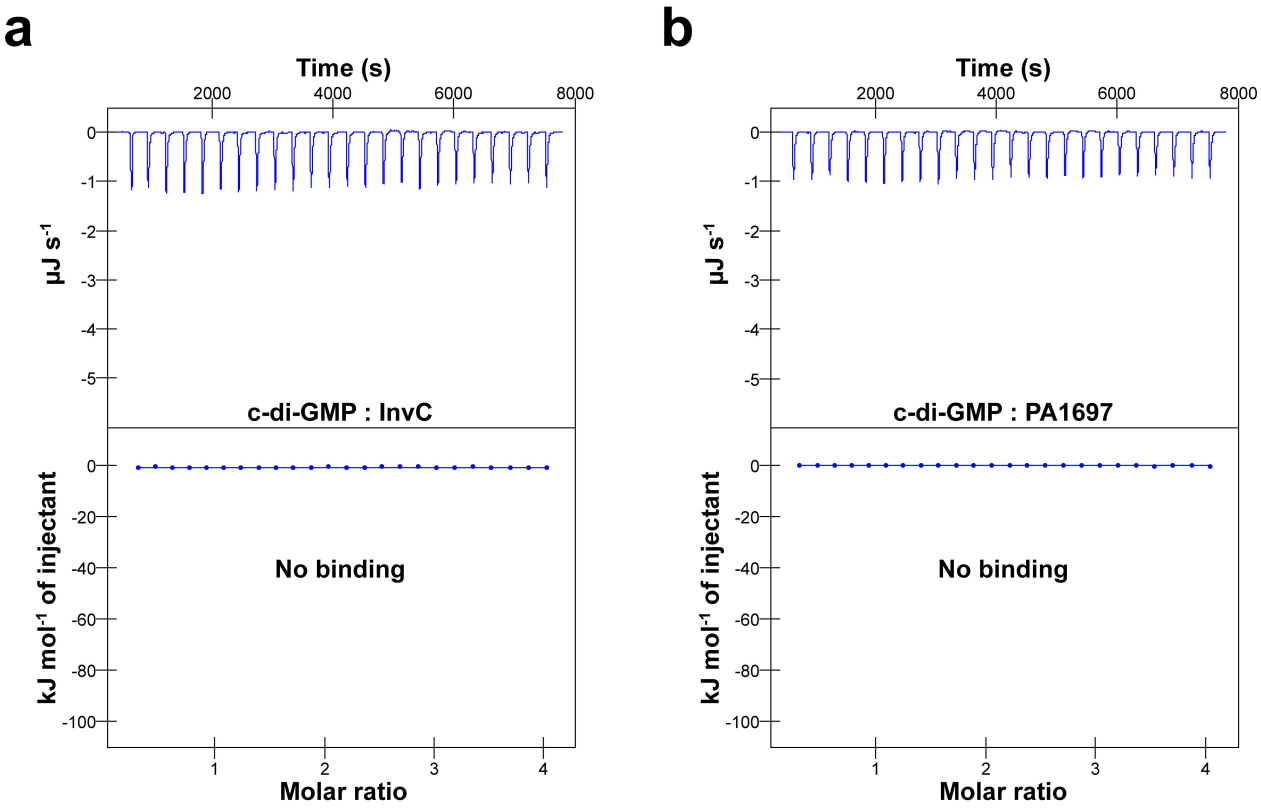
Supplementary Fig. 23 Schematic illustrating the predicted domain organization of YedQ

Domain architecture for YedQ from *S*. Typhimurium strain SL1344 was predicted using hmmscan against the Pfam 34.0 database. The gathering threshold is used to determine hit significance. TM, transmembrane domain; ECD, extracytoplasmic domain; CD, cytoplasmic domain.



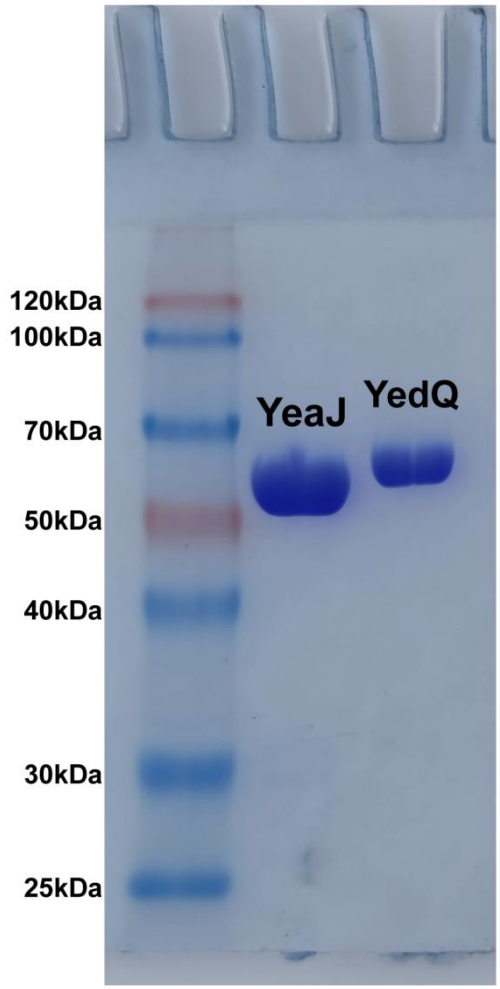
Supplementary Fig. 24 The LBD of the YedQ homolog from EHEC O157:H7 shows high binding affinity to taurocholate and taurodeoxycholate

The binding affinity was evaluated by ITC analysis. ITC data and plots of injected heat for automatic injections of 100 µM taurocholate (**a**) or taurodeoxycholate (**b**) into the sample cell containing 10 µM WP_010904779-LBD are shown in the upper and lower plots, respectively. The binding curves were corrected for the dilution effects in the final analysis. Results shown are one representative of three experiments with similar results. K_d and binding stoichiometry (n) are presented as mean ± s.d. of three independent experiments.



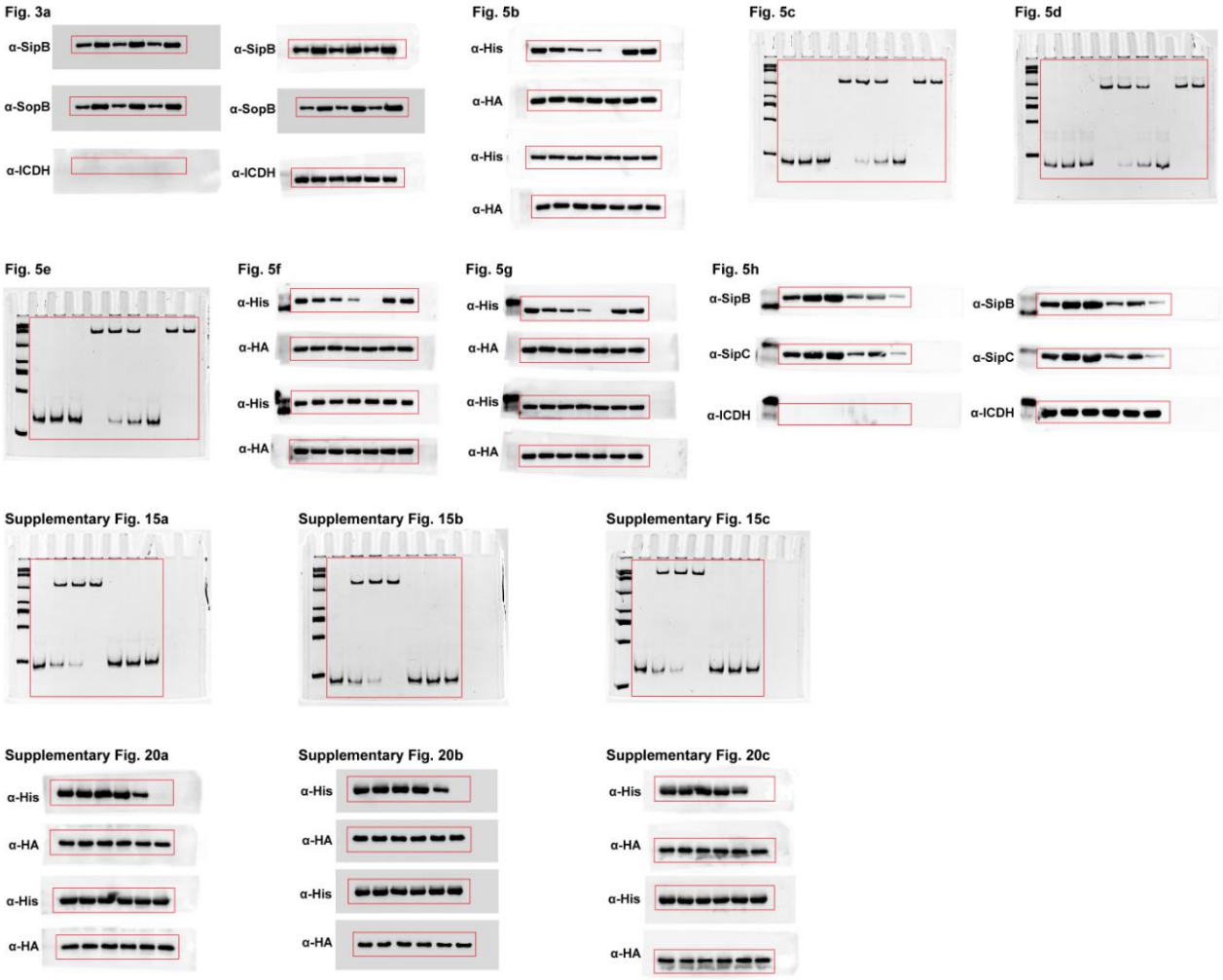
Supplementary Fig. 25 Neither the T3SS ATPase InvC (STM2894) from *S.* Typhimurium nor the T3SS ATPase PA1697 from *P. aeruginosa* interacts with c-di-GMP

The binding affinity was evaluated by ITC analysis. ITC data and plots of injected heat for automatic injections of 100 µM c-di-GMP into the sample cell containing 10 µM InvC (**a**) or PA1697 (**b**) are shown in the upper and lower plots, respectively. The binding curves were corrected for the dilution effects in the final analysis. Results shown are one representative of three experiments with similar results.



Supplementary Fig. 26 SDS-PAGE gels of purified full-length YeaJ and YedQ from *S.* Typhimurium

After inverted membrane extraction and further purification by Ni^{2+}-NTA affinity chromatography, membrane fractions containing full-length YeaJ and YedQ were subjected to SDS-PAGE analysis to examine the purity. Similar results were obtained in three independent experiments.



Supplementary Fig. 27 Uncropped blots and gels.

Supplementary Table 1. Bacterial strains and plasmids used in this study.

Strains and plasmids	Relevant characteristics*	Source
Strains		
***S.* Typhimurium**		
SL1344	Wild-type	Laboratory stock
Δ*luxS*	*luxS* deletion mutant in SL1344	This study
Δ*lsrB*	*lsrB* deletion mutant in SL1344	This study
Δ*yeaJ*	*yeaJ* deletion mutant in SL1344	This study
Δ*sicA*	*sicA* deletion mutant in SL1344	This study
sicA(N70A)	SL1344 Wild-type strain with the N70A mutation *of SicA*	This study
sicA(N70A)Δ*luxS*	Δ*luxS* strain with the N70A mutation *of SicA*	This study
sicA(N70A)Δ*yeaJ*	Δ*yeaJ* strain with the N70A mutation *of SicA*	This study
Δ*luxS*Δ*yeaJ*	*luxS*/*yeaJ* double deletion mutant in SL1344	This study
Δ*lsrB*Δ*luxS*	*lsrB*/*luxS* double deletion mutant in SL1344	This study
Δ*invC*	*invC* deletion mutant in SL1344	This study
Δ*invC*Δ*luxS*	*invC*/*luxS* double deletion mutant in SL1344	This study
Δ*invC*Δ*yeaJ*	*invC*/*yeaJ* double deletion mutant in SL1344	This study
Δ*STM0343*	*STM0343* deletion mutant in SL1344	This study
Δ*adrA*	*adrA* deletion mutant in SL1344	This study
Δ*STM0468*	*STM0468* deletion mutant in SL1344	This study
Δ*STM1703*	*STM1703* deletion mutant in SL1344	This study
Δ*STM1827*	*STM1827* deletion mutant in SL1344	This study
Δ*yedQ*	*yedQ* deletion mutant in SL1344	This study
Δ*STM2123*	*STM2123* deletion mutant in SL1344	This study
Δ*STM2215*	*STM2215* deletion mutant in SL1344	This study
Δ*STM2410*	*STM2410* deletion mutant in SL1344	This study
Δ*STM2503*	*STM2503* deletion mutant in SL1344	This study
Δ*STM2672*	*STM2672* deletion mutant in SL1344	This study
Δ*STM3388*	*STM3388* deletion mutant in SL1344	This study
Δ*STM3611*	*STM3611* deletion mutant in SL1344	This study
Δ*STM3615*	*STM3615* deletion mutant in SL1344	This study
Δ*STM4264*	*STM4264* deletion mutant in SL1344	This study
Δ*STM4551*	*STM4551* deletion mutant in SL1344	This study
SL1344::P_{invF}	SL1344 Wild-type strain with the promoter of the *sicAsipBCDA* operon replaced by the *invF* promoter	This study
Δ*luxS*::P_{invF}	Δ*luxS* strain with the promoter of the *sicAsipBCDA* operon replaced by the *invF* promoter	This study
Δ*yeaJ*::P_{invF}	Δ*yeaJ* strain with the promoter of the *sicAsipBCDA* operon replaced by the *invF* promoter	This study
Δ*sicA*::P_{invF}	Δ*yeaJ* strain with the promoter of the *sicAsipBCDA* operon replaced by the *invF* promoter	This study

E. coli		
BL21(DE3)	Host for expression vector pET-28a	Novagen
LuxS$^-$ BL21(DE3)	Δ*luxS* deletion mutant in *E. coli* BL21(DE3)	This study
TG1	Host for cloning	Stratagene
S17-1λpir	λ-pir lysogen of S17-1, F$^-$ *thi pro hsdR* [RP4-2 Tc::Mu Km::Tn7 (Tp Sm)]	1
EHEC O157:H7 strain EDL933	Multilocus Sequence Type (MLST): ST-32	Laboratory stock
V. harveyi		
V. harveyi MM32	*luxN*::*cat luxS*::Tn*5kan*	2
V. parahaemolyticus		
V. parahaemolyticus RIMD 2210633	Wild-type	Laboratory stock
Plasmids		
pCas	Crispr-Cas9 system plasmid used for in-frame deletion, Km^r	3
pTargetF1	pTargetF with the spectinomycin resistance gene replaced by a chloramphenicol resistance gene, Cm^r	4
pTargetF1-Δ*luxS*	pTargetF1 derivative for *luxS* deletion in SL1344	This study
pTargetF1-Δ*lsrB*	pTargetF1 derivative for *lsrB* deletion in SL1344	This study
pTargetF1-Δ*yeaJ*	pTargetF1 derivative for *yeaJ* deletion in SL1344	This study
pTargetF1-Δ*sicA*	pTargetF1 derivative for *sicA* deletion in SL1344	This study
pTargetF1-Δ*invC*	pTargetF1 derivative for *invC* deletion in SL1344	This study
pTargetF1-Δ*STM0343*	pTargetF1 derivative for *STM0343* deletion in SL1344	This study
pTargetF1-Δ*adrA*	pTargetF1 derivative for *adrA* deletion in SL1344	This study
pTargetF1-Δ*STM0468*	pTargetF1 derivative for *STM0468* deletion in SL1344	This study
pTargetF1-Δ*STM1703*	pTargetF1 derivative for *STM1703* deletion in SL1344	This study
pTargetF1-Δ*STM1827*	pTargetF1 derivative for *STM1827* deletion in SL1344	This study
pTargetF1-Δ*yedQ*	pTargetF1 derivative for *yedQ* deletion in SL1344	This study
pTargetF1-Δ*STM2123*	pTargetF1 derivative for *STM2123* deletion in SL1344	This study
pTargetF1-Δ*STM2215*	pTargetF1 derivative for *STM2215* deletion in SL1344	This study
pTargetF1-Δ*STM2410*	pTargetF1 derivative for *STM2410* deletion in SL1344	This study
pTargetF1-Δ*STM2503*	pTargetF1 derivative for *STM2503* deletion in SL1344	This study
pTargetF1-Δ*STM2672*	pTargetF1 derivative for *STM2672* deletion in SL1344	This study
pTargetF1-Δ*STM3388*	pTargetF1 derivative for *STM3388* deletion in SL1344	This study
pTargetF1-Δ*STM3611*	pTargetF1 derivative for *STM3611* deletion in SL1344	This study
pTargetF1-Δ*STM3615*	pTargetF1 derivative for *STM3615* deletion in SL1344	This study
pTargetF1-Δ*STM4264*	pTargetF1 derivative for *STM4264* deletion in SL1344	This study
pTargetF1-Δ*STM4551*	pTargetF1 derivative for *STM4551* deletion in SL1344	This study
pTargetF1-P$_{invF}$	pTargetF1 derivative for promoter replacement in SL1344 Wild-type, Δ*luxS,* Δ*yeaJ* strain	This study
pTargetF1-Δ*sicA*::P$_{invF}$	pTargetF1 derivative for promoter replacement in Δ*sicA* strain	This study
pTargetF1-*sicA*(N70A)	pTargetF1 derivative for the N70A mutation *of SicA* in SL1344 Wild-type, Δ*luxS,* and Δ*yeaJ* strain	This study

pKT100	Cloning vector, p15A replicon, Km^r	5
pKT100-*luxS*	*luxS* cloned into pKT100 for complementation	This study
pKT100-*yeaJ*	*yeaJ* cloned into pKT100 for complementation	This study
pKT100-*yedQ*	*yedQ* cloned into pKT100 for complementation	This study
pKT100-*sicA*	*sicA* cloned into pKT100 for complementation	This study
pKT100-*sicA-HA*	pKT100 expressing *sicA* with a C-terminal HA tag	This study
pKT100-*sicA*(N70A)-*HA*	pKT100 expressing *sicA*(N70A) with a C-terminal HA tag	This study
pET-28a	Expression vector with N-terminal hexahistidine affinity tag, Km^r	Novagen
pET28a-*dpiB-LBD*	pET-28a expressing *dpiB-LBD*	This study
pET28a-*yeaJ-LBD*	pET-28a expressing *yeaJ-LBD*	This study
pET28a-*yedQ-LBD*	pET-28a expressing *yedQ-LBD*	This study
pET28a-*dcuS-LBD*	pET-28a expressing *dcuS-LBD*	This study
pET28a-*creC-LBD*	pET-28a expressing *creC-LBD*	This study
pET28a-*lsrB*	pET-28a expressing *lsrB*	This study
pET28a-*WP_000766134-LBD*	pET-28a expressing *WP_000766134-LBD*	This study
pET28a-*WP_110273591-LBD*	pET-28a expressing *WP_110273591-LBD*	This study
pET28a-*EFY5422248-LBD*	pET-28a expressing *EFY5422248-LBD*	This study
pET28a-*WP_096754085-LBD*	pET-28a expressing *WP_096754085-LBD*	This study
pET28a-*WP_065356351-LBD*	pET-28a expressing *WP_065356351-LBD*	This study
pET28a-*WP_002441331-LBD*	pET-28a expressing *WP_002441331-LBD*	This study
pET28a-*WP_167810108-LBD*	pET-28a expressing *WP_167810108-LBD*	This study
pET28a-*WP_113858630-LBD*	pET-28a expressing *WP_113858630-LBD*	This study
pET28a-*WP_012132675-LBD*	pET-28a expressing *WP_012132675-LBD*	This study
pET28a-*ASV54904-LBD*	pET-28a expressing *ASV54904-LBD*	This study
pET28a-*TDN64219-LBD*	pET-28a expressing *TDN64219-LBD*	This study
pET28a-*HAT1647429-LBD*	pET-28a expressing *HAT1647429-LBD*	This study
pET28a-*KHT28552-LBD*	pET-28a expressing *KHT28552-LBD*	This study
pET28a-*WP_187042677-LBD*	pET-28a expressing *WP_187042677-LBD*	This study
pET28a-*KMK13526-LBD*	pET-28a expressing *KMK13526-LBD*	This study
pET28a-*WP_034494714-LBD*	pET-28a expressing *WP_034494714-LBD*	This study
pET28a-*WP_131019823-LBD*	pET-28a expressing *WP_131019823-LBD*	This study
pET28a-*WP_025800510-LBD*	pET-28a expressing *WP_025800510-LBD*	This study
pET28a-*yeaJ-LBD*^{Y210A}	pET-28a expressing *yeaJ-LBD*^{Y210A}	This study
pET28a-*yeaJ-LBD*^{D239A}	pET-28a expressing *yeaJ-LBD*^{D239A}	This study
pET28a-*KMK13526-LBD*$^{H126Y/Q245D}$	pET-28a expressing *KMK13526-LBD*$^{H126Y/Q245D}$	This study
pET28a-*WP_034494714-LBD*$^{Q208A/E237D}$	pET-28a expressing *WP_034494714-LBD* $^{Q208A/E237D}$	This study
pET28a-*sipB*	pET-28a expressing *sipB*	This study
pET28a-*sopB*	pET-28a expressing *sopB*	This study
pET28a-*invF*	pET-28a expressing *invF*	This study

pET28a-*sicA*	pET-28a expressing *sicA*	This study
pET28a-*sicA*^{K27A}	pET-28a expressing *sicA*^{K27A}	This study
pET28a-*sicA*^{D28A}	pET-28a expressing *sicA*^{D28A}	This study
pET28a-*sicA*^{Q34A}	pET-28a expressing *sicA*^{Q34A}	This study
pET28a-*sicA*^{D67A}	pET-28a expressing *sicA*^{D67A}	This study
pET28a-*sicA*^{N70A}	pET-28a expressing *sicA*^{N70A}	This study
pET28a-*yedQ-LBD*^{D233A}	pET-28a expressing *yedQ-LBD*^{D233A}	This study
pET28a-*yedQ-LBD*^{K236A}	pET-28a expressing *yedQ-LBD*^{K236A}	This study
pET28a-*yedQ-LBD*^{Q264A}	pET-28a expressing *yedQ-LBD*^{Q264A}	This study
pET28a-*yedQ-LBD*^{L288A}	pET-28a expressing *yedQ-LBD*^{L288A}	This study
pET28a-*yedQ-LBD*^{L289A}	pET-28a expressing *yedQ-LBD*^{L289A}	This study
pET28a-*sipC*	pET-28a expressing *sipC*	This study
pET28a-*pcrH*	pET-28a expressing *pcrH*	This study
pET28a-*ipgC*	pET-28a expressing *ipgC*	This study
pET28a-*sycD*	pET-28a expressing *sycD*	This study
pET28a-*cesD*	pET-28a expressing *cesD*	This study
pET28a-*bicA*	pET-28a expressing *bicA*	This study
pET28a-*vcrH*	pET-28a expressing *vcrH*	This study
pET28a-*invC*	pET-28a expressing *invC*	This study
pET28a-*PA1697*	pET-28a expressing *PA1697*	This study
pDM4	Suicide vector, *mob*RK2, *ori*R6K, *pir*, *sacB*, Cm^r	6
pDM4-P$_{sicAsipBCDA}$::lacZ	pDM4 derivative for *sicAsipBCDA* promoter fusion	This study
pDM4-P$_{sopB}$::lacZ	pDM4 derivative for *sopB* promoter fusion	This study
pDM4-P$_{sopE2}$::lacZ	pDM4 derivative for *sopE2* promoter fusion	This study
pDM4-P$_{invF}$::lacZ	pDM4 derivative for *invF* promoter fusion	This study
pBBR1MCS1	Cloning vector containing REP, Cm^r	7
pBBR1MCS1-*invF-his$_6$*	pBBR1MCS1 expressing *invF* with a C-terminal His$_6$ tag	This study
pBBR1MCS1-*sipB-his$_6$*	pBBR1MCS1 expressing *sipB* with a C-terminal His$_6$ tag	This study
pBBR1MCS1-*sipC-his$_6$*	pBBR1MCS1 expressing *sipC* with a C-terminal His$_6$ tag	This study
pHSe5	the *E. coli* expression plasmid pHSe5, Ap^r	8
pHSe5-*yeaJ-His$_6$*	pHSe5 expressing *yeaJ* with a C-terminal His$_6$ tag	This study
pHSe5-*yedQ-His$_6$*	pHSe5 expressing *yedQ* with a C-terminal His$_6$ tag	This study

***Km^r, Cm^r and Ap^r represent resistance to kanamycin, chloramphenicol and ampicillin, respectively.**

Supplementary Table 2. Primers used in this study.

Primiers	5'-3' sequence*	
Δ*luxS*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTACGCTTGAGCATCTGTTTGCGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*luxS*
Δ*luxS*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*luxS*-up-F	CCGAGTCGGTGCTTTTTTTGAAAAAGGTGTGTGACGAGTTGG	
Δ*luxS*-up-R	GCACATCACGCTCCAGAATCTGCGAAGCTATCTAATAATGG	
Δ*luxS*-down-F	CCATTATTAGATAGCTTCGCAGATTCTGGAGCGTGATGTGC	
Δ*luxS*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACATGAGAAAAGCAAGCACCG	
Δ*lsrB*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTTGAAGCGGGCAATGCAAAGGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*lsrB*
Δ*lsrB*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*lsrB*-up-F	CCGAGTCGGTGCTTTTTTTGAAATTACTGGTTTCTTACTTTGGCTC	
Δ*lsrB*-up-R	CACCGACATTCATTGGCATAGACCAAACGCAGTGAGTAAGG	
Δ*lsrB*-down-F	CCTTACTCACTGCGTTTGGTCTATGCCAATGAATGTCGGTG	
Δ*lsrB*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACAAGACATCAGCATATTCAAAGAGC	
Δ*yeaJ*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTTATACCCAGGACCGTCCGCGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*yeaJ*
Δ*yeaJ*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*yeaJ*-up-F	CCGAGTCGGTGCTTTTTTTGAAATCCCACGGACTATCACTACC	
Δ*yeaJ*-up-R	GCAGGTTACGAATAATACGCTATGACGCTTGCCGAGATAA	
Δ*yeaJ*-down-F	TTATCTCGGCAAGCGTCATAGCGTATTATTCGTAACCTGC	
Δ*yeaJ*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACAGAGAGGTCGGCTTGCTG	
Δ*sicA*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTCCCGATTACACCATGGGACGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*sicA*
Δ*sicA*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*sicA*-up-F	CCGAGTCGGTGCTTTTTTTGAATTGAAAACTCACGCCTGATTGT	
Δ*sicA*-up-R	AGATAGACCAACGCTTTTGCCCATTACTTACTCCTGTTATCTGTCACC	
Δ*sicA*-down-F	GGTGACAGATAACAGGAGTAAGTAATGGGCAAAAGCGTTGGTCTATCT	

Δ*sicA*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACTCAATCAT CGCCTGCCATAC	
Δ*STM0343*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTCGCTGCGA AGTTGCGCGGTAGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM0343*
Δ*STM0343*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM0343*-up-F	CCGAGTCGGTGCTTTTTTTGAAAGTTGTAGCCAATAAT CCCTGT	
Δ*STM0343*-up-R	ACAGTTCTTTCAGCGTGTCAG	
Δ*STM0343*-down-F	CTGACACGCTGAAAGAACTGTAGGATTCGTTCAGGGA TTTC	
Δ*STM0343*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACAGGGCGA GTCACAACAGAC	
Δ*adrA*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTGTATCCG CTTCTGTTCGCCGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*adrA*
Δ*adrA*-sg20-R	GCCAAAAAGTAAAGTCACCAGTTCAAAAAAAGCACCGA CTCGG	
Δ*adrA*-up-F	CCGAGTCGGTGCTTTTTTTGAACTGGTGACTTTACTTT TTGGC	
Δ*adrA*-up-R	TATCCGCAGACTTTAGCCATCGCCTGTTCAACCGCT	
Δ*adrA*-down-F	AGCGGTTGAACAGGCGATGGCTAAAGTCTGCGGATA	
Δ*adrA*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACAAGTGATT GCTGAGCCGAT	
Δ*STM0468*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTCGTAACGG GTCTGCTGGCCGGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM0468*
Δ*STM0468*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM0468*-up-F	CCGAGTCGGTGCTTTTTTTGAATTCATTTGCGCTGGTG TC	
Δ*STM0468*-up-R	ATCCAGCTCTTCATTAAACCTC	
Δ*STM0468*-down-F	GAGGTTTAATGAAGAGCTGGATTAAGATGGTCGCAGA AGGC	
Δ*STM0468*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACGACATCG CCGTAGGTCGT	
Δ*STM1703*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTCACGAATC CTTACCCGTCTGGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM1703*
Δ*STM1703*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM1703*-up-F	CCGAGTCGGTGCTTTTTTTGAACTTCTTCTCCCTTCCG TCAT	
Δ*STM1703*-up-R	AGCGGTAACCTGTTTTTCTATC	
Δ*STM1703*-down-F	GATAGAAAAACAGGTTACCGCTAGTGATTGCCGAAGG TGTAG	
Δ*STM1703*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACCCGTCTTT AACCTGATCTAACAG	
Δ*STM1827*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTACAGACCA ATCGTTACTCAAGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*yeaJ*

Δ*STM1827*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM1827*-up-F	CCGAGTCGGTGCTTTTTTTGAAACACCCGCTACTTCCTGG	
Δ*STM1827*-up-R	CGGATGCTCAGCGTAAGA	
Δ*STM1827*-down-F	TCTTACGCTGAGCATCCGATTGAACTGGTGGCGGA	
Δ*STM1827*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACGGGCTGGATAGTGAAGGG	
Δ*yedQ*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTAACCATCTCCGTTTGTTGAGTTTTAGAGCTAGAAATAGC	
Δ*yedQ*-sg20-R	AAAGACCATACCTGCCTCCTTTCAAAAAAAGCACCGACTCGG	
Δ*yedQ*-up-F	CCGAGTCGGTGCTTTTTTTGAAAGGAGGCAGGTATGGTCTTT	To generate pTargetF1-Δ*yedQ*
Δ*yedQ*-up-R	CTATTTCTTTTCCCGCTCCTTAAACCAGCCTTGATTGTCTAA	
Δ*yedQ*-down-F	TTAGACAATCAAGGCTGGTTTAAGGAGCGGGAAAAGAAATAG	
Δ*yedQ*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACCAGTCTGCCCTAACCCGT	
Δ*STM2123*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTAGGATATTTATCGCGCCGACGTTTTAGAGCTAGAAATAGC	
Δ*STM2123*-sg20-R	CAGTCTCATCAGTGCGTCATTTTCAAAAAAAGCACCGACTCGG	
Δ*STM2123*-up-F	CCGAGTCGGTGCTTTTTTTGAAAATGACGCACTGATGAGACTG	To generate pTargetF1-Δ*STM2123*
Δ*STM2123*-up-R	GAGGTCAGCATTTCATCCATTAACTGACCAGACGCAATAGC	
Δ*STM2123*-down-F	GCTATTGCGTCTGGTCAGTTAATGGATGAAATGCTGACCTC	
Δ*STM2123*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACTCTTTTTGCCCGATGATTAC	
Δ*STM2215*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTTCGCGTCTACTGACCGTCGGTTTTAGAGCTAGAAATAGC	
Δ*STM2215*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM2215*-up-F	CCGAGTCGGTGCTTTTTTTGAAAGCGGCGTCATTATCTCC	To generate pTargetF1-Δ*STM2215*
Δ*STM2215*-up-R	CCGTTTATGCCACGACAG	
Δ*STM2215*-down-F	CTGTCGTGGCATAAACGGCGATCACGGTGTTAATTACTTG	
Δ*STM2215*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACGCAGCGAATAGCGATTGA	
Δ*STM2410*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTGCGCGTGCATTGCGAACGCGGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM2410*
Δ*STM2410*-sg20-R	TTCAAAAAAAGCACCGACTCGG	

Δ*STM2410*-up-F	CCGAGTCGGTGCTTTTTTTGAACCACCAACATTCAAACCCT	
Δ*STM2410*-up-R	AGTCAACATCATTCCGCCTA	
Δ*STM2410*-down-F	TAGGCGGAATGATGTTGACTCGAAAGCGAAATCGTTGA	
Δ*STM2410*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACAAGTATCATGGCGACCAAAC	
Δ*STM2503*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTGCGTAGTGAGTGGTCGCGCAGTTTTAGAGCTAGAAATAGC	
Δ*STM2503*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM2503*-up-F	CCGAGTCGGTGCTTTTTTTGAAAACAAGCCTGCGTTCACTC	To generate pTargetF1-Δ*STM2503*
Δ*STM2503*-up-R	CCCTGTCTGCGGGTATCT	
Δ*STM2503*-down-F	AGATACCCGCAGACAGGGCAGATTGTGGCTTCTATTTGTC	
Δ*STM2503*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACTGCCGTTAATTCAGCTACTTC	
Δ*STM2672*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTCAATAGCCTTCTGGATGAGAGTTTTAGAGCTAGAAATAGC	
Δ*STM2672*-sg20-R	CAGTCAGCCTCTTCGCTAAGTTCAAAAAAAGCACCGACTCGG	
Δ*STM2672*-up-F	CCGAGTCGGTGCTTTTTTTGAACTTAGCGAAGAGGCTGACTG	To generate pTargetF1-Δ*STM2672*
Δ*STM2672*-up-R	TCATCGTTATTCGCTGGCCGCCGTAGTGTGCGTTTA	
Δ*STM2672*-down-F	TAAACGCACACTACGGCGGCCAGCGAATAACGATGA	
Δ*STM2672*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACTGGTAAAGCGGCTCGTATC	
Δ*STM3388*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTACAATAGATCCGTACGAACGTTTTAGAGCTAGAAATAGC	
Δ*STM3388*-sg20-R	CATCGTCAAATCCTGTGTATTCTTCAAAAAAAGCACCGACTCGG	
Δ*STM3388*-up-F	CCGAGTCGGTGCTTTTTTTGAAGAATACACAGGATTTGACGATG	To generate pTargetF1-Δ*STM3388*
Δ*STM3388*-up-R	GGCATCCTAACTGGGTCAAAATAGCGACAGCAAATGAAAC	
Δ*STM3388*-down-F	GTTTCATTTGCTGTCGCTATTTTGACCCAGTTAGGATGCC	
Δ*STM3388*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACGGTTTCCATCATCAGTCGC	
Δ*STM3611*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTTCGCCATCACTTATTGGCATGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM3611*
Δ*STM3611*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM3611*-up-F	CCGAGTCGGTGCTTTTTTTGAAGAGCGGCAGAATCGACC	

Δ*STM3611*-up-R	CGGCTGGTAAGTATAGGCAC	
Δ*STM3611*-down-F	GTGCCTATACTTACCAGCCGCGCTCGAAGAGGTGATTCT	
Δ*STM3611*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACATGCACCATCGTGACTTCC	
Δ*STM3615*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTGTGCGAAACGTTGCGTGACAGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM3615*
Δ*STM3615*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM3615*-up-F	CCGAGTCGGTGCTTTTTTTGAACGATATTCAGCAGGCGAA	
Δ*STM3615*-up-R	TTCGGCAATACCACATCG	
Δ*STM3615*-down-F	CGATGTGGTATTGCCGAAGGTGACGGCGATTATCCT	
Δ*STM3615*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACACCGCTTTCATGCTTTCC	
Δ*STM4264*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTCCGATCATTGATATCCGAAAGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM4264*
Δ*STM4264*-sg20-R	TTCAAAAAAAGCACCGACTCGG	
Δ*STM4264*-up-F	CCGAGTCGGTGCTTTTTTTGAACGCCAGATCGGCAATGTAT	
Δ*STM4264*-up-R	TTCCGAGAAATCTCAACACCTT	
Δ*STM4264*-down-F	AAGGTGTTGAGATTTCTCGGAAAGTATTGTCAGGGATGGCACTT	
Δ*STM4264*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACGTCGCATCAGCAGATAATTCAG	
Δ*STM4551*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTACAGCTCATGTTTAAGCTGCGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*STM4551*
Δ*STM4551*-sg20-R	TCGTTGGACTGGCGTTTATTTCAAAAAAAGCACCGACTCGG	
Δ*STM4551*-up-F	CCGAGTCGGTGCTTTTTTTGAAATAAACGCCAGTCCAACGA	
Δ*STM4551*-up-R	AGCGTCTCCGATATTGCGGCGTTGAGAAACAAGAAAAGAC	
Δ*STM4551*-down-F	GTCTTTTCTTGTTTCTCAACGCCGCAATATCGGAGACGCT	
Δ*STM4551*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACCACTGGGCAAGAGTCATCG	
Δ*invC*-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTATCGGTCTTATCGGTGAACGGTTTTAGAGCTAGAAATAGC	To generate pTargetF1-Δ*invC*
Δ*invC*-sg20-R	ATCGCAACCACTTACTTCCATTCAAAAAAAGCACCGACTCGG	
Δ*invC*-up-F	CCGAGTCGGTGCTTTTTTTGAATGGAAGTAAGTGGTTGCGAT	
Δ*invC*-up-R	AACCAGGCTTTCAGGCTATCCGGTTATTTTTTGTGGGTAGG	

Δ*invC*-down-F	CCTACCCACAAAAAATAACCGGATAGCCTGAAAGCCTGGTT	
Δ*invC*-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACTGATAGTTCCCTTCTTTGCG	
sicA(N70A)-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTCAAAGTCGGTGACAGATAACGTTTTAGAGCTAGAAATAGC	
sicA(N70A)-sg20-R	CGCCAACCTTCTCCGCATAGTTCAAAAAAAGCACCGACTCGG	
sicA(N70A)-up-F	CCGAGTCGGTGCTTTTTTTGAACTATGCGGAGAAGGTTGGCG	To generate pTargetF1-*sicA*(N70A)
sicA(N70A)-up-R	CAGTCCCATGGTGTAATCGGGAGCGTAAAAATCATAAATGCATAAGAAA	
sicA(N70A)-down-F	TTTCTTATGCATTTATGATTTTTACGCTCCCGATTACACCATGGGACTG	
sicA(N70A)-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACGCTACGGCTAATGCTACTTGCG	
P_{invF}-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTGTACGGCATTGAGCCGCGTAGTTTTAGAGCTAGAAATAGC	
P_{invF}-sg20-R	AAGTTCACGCCAAATGACGGTTCAAAAAAAGCACCGACTCGG	
P_{invF}-up-F	CCGAGTCGGTGCTTTTTTTGAACCGTCATTTGGCGTGAACTT	
P_{invF}-up-R	GAAACGCATTCGCCCCCATCATAACGGCGATGGGTTTT	To generate pTargetF1-P_{invF}
P_{invF}-middle-F	AAAACCCATCGCCGTTATGATGGGGGCGAATGCGTTTC	
P_{invF}-middle-R	TCGCTGACATTATTTTGATAATCCATATGCAGCTTTTGCGCGG	
P_{invF}-down-F	CCGCGCAAAAGCTGCATATGGATTATCAAAATAATGTCAGCGA	
P_{invF}-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACTCTTGTTCACTGTGCTGCTCTGTC	
Δ*sicA*::P_{invF}-sg20-F	AGCTAGCTCAGTCCTAGGTATAATACTAGTGTACGGCATTGAGCCGCGTAGTTTTAGAGCTAGAAATAGC	
Δ*sicA*::P_{invF}-sg20-R	AAGTTCACGCCAAATGACGGTTCAAAAAAAGCACCGACTCGG	
Δ*sicA*::P_{invF}-up-F	CCGAGTCGGTGCTTTTTTTGAACCGTCATTTGGCGTGAACTT	
Δ*sicA*::P_{invF}-up-R	GAAACGCATTCGCCCCCATCATAACGGCGATGGGTTTT	To generate pTargetF1-Δ*sicA*::P_{invF}
Δ*sicA*::P_{invF}-middle-F	AAAACCCATCGCCGTTATGATGGGGGCGAATGCGTTTC	
Δ*sicA*::P_{invF}-middle-R	AGACCAACGCTTTTGCCCATATGCAGCTTTTGCGCGG	
Δ*sicA*::P_{invF}-down-F	CCGCGCAAAAGCTGCATATGGGCAAAAGCGTTGGTCT	
Δ*sicA*::P_{invF}-down-R	GGTAATAGATCTAAGCTTCTGCAGGTCGACCGATACCT	

	GAATCCCCATCTCTT	
C*luxS*-F	GACGACAAGCTTACTAGTCTGCAGGGATCCATGCCAT TATTAGATAGCTTCG	To generate pKT100-*luxS*
C*luxS*-R	ATCTTAGTTACTTAGGTACCCGGGGTCGACCTAAATAT GCAGTTCCTGCAGT	
C*yeaJ*-F	GACGACAAGCTTACTAGTCTGCAGGGATCCATGAATTT GCATCATAAAGCG	To generate pKT100-*yeaJ*
C*yeaJ*-R	ATCTTAGTTACTTAGGTACCCGGGGTCGACCTATGATG AACGATGTTGTTTTTG	
C*yedQ*-F	GACGACAAGCTTACTAGTCTGCAGGGATCCGTGCCGC ACGAAACACTGT	To generate pKT100-*yedQ*
C*yedQ*-R	ATCTTAGTTACTTAGGTACCCGGGGTCGACCTATTTCT TTTCCCGCTCCTGA	
sicA-F	GACGACAAGCTTACTAGTCTGCAGGGATCCATGGATT ATCAAAATAATGTCAGC	To generate pKT100-*sicA*, pKT100-*sicA-HA* and pKT100-*sicA*(N70A)-*HA*
sicA-R	ATCTTAGTTACTTAGGTACCCGGGGTCGACTTATTCCT TTTCTTGTTCACTGTG	
sicA-HA-R	ATCTTAGTTACTTAGGTACCCGGGGTCGACTTAAGCGT AGTCTGGGACGTCGTATGGGTATTCCTTTTCTTGTTCA CTGTG	
dpiB-LBD-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCGCCAGTT TCGAAGATTAT	To generate pET28a-*dpiB-LBD*
dpiB-LBD-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAGAAG TCCAGCCGCC	
yeaJ-LBD-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCGCCAGC GACAGGGCAAT	To generate pET28a-*yeaJ-LBD*
yeaJ-LBD-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTAATCA AGGGACAACGAAACGC	
yedQ-LBD-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCAGGGAA GTGATGATACTGAAAGAC	To generate pET28a-*yedQ-LBD*
yedQ-LBD-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAGCTG CCAAAATTCCCTTG	
dcuS-LBD-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCCAAATCA GCAGCATGACGC	To generate pET28a-*dcuS-LBD*
dcuS-LBD-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAACTG CCGCGGCTATTGTT	
creC-LBD-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCTTGGCGA AGGCATTCGCC	To generate pET28a-*creC-LBD*
creC-LBD-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAGCG CCGTTCGCTGCG	
lsrB-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGGCAA GACACAGCATTAAA	To generate pET28a-*lsrB*
lsrB-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAGAAA TCATATTTGTCGATATTG	
000766134-LBD-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGAGCG	To generate

000766134-LBD-R	ACAGAGCAATGAGTG GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAATCA ATGGATAACGAGACACG	pET28a-*WP_000766134-LBD*
yeaJ-LBD^{Y210A}-up-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCGCCAGC GACAGGGCAAT	To generate pET28a-*yeaJ-LBD*^{Y210A}
yeaJ-LBD^{Y210A}-up-R	CGTTTTCCTGAGTAATATCATCCATGGCGATACTTGAA ATAACCGTAC	
yeaJ-LBD^{Y210A}-down-F	ATGGATGATATTACTCAGGAAAACG	
yeaJ-LBD^{Y210A}- down-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTAATCA AGGGACAACGAAACGC	
yeaJ-LBD^{D239A}-up-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCGCCAGC GACAGGGCAAT	To generate pET28a-*yeaJ-LBD*^{D239A}
yeaJ-LBD^{D239A}-up-R	TATTTTTTAAATTATCCTGGTTAACAGCCACCATCACGA TGCCT	
yeaJ-LBD^{D239A}-down-F	GTTAACCAGGATAATTTAAAAAATA	
yeaJ-LBD^{D239A}-down-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTAATCA AGGGACAACGAAACGC	
KMK13526-LBD^{H126Y} -up-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCGCTCTCC AAAGCTATATGGC	To generate pET28a-*KMK13526 -LBD*$^{H126Y/Q245D}$
KMK13526-LBD^{H126Y} -up-R	GCCGAGGATCTGATCGATATAAATGTGCGAAGTTATAC TGTTG	
KMK13526-LBD^{H126Y} -down-F	CAACAGTATAACTTCGCACATTTATATCGATCAGATCCT CGGC	
KMK13526-LBD^{H126Y} -down-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTCTAATCG ACGGAAATGTGCAG	
KMK13526-LBD^{Q245D} -up-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCGCTCTCC AAAGCTATATGGC	
KMK13526-LBD^{Q245D} -up-R	GGATAAATCATCGGCATTAATATCGGTAACTATCATTC CCTTAA	
KMK13526-LBD^{Q245D} -down-F	TTAAGGGAATGATAGTTACCGATATTAATGCCGATGAT TTATCC	
KMK13526-LBD^{Q245D} -down-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTCTAATCG ACGGAAATGTGCAG	
WP_034494714-LBD^{Q208A} -up-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCTACCGCT CAATGAATGCC	To generate pET28a-*WP_034494714 -LBD*$^{Q208A/E237D}$
WP_034494714-LBD^{Q208A} -up-R	TGTTTTTATTATTGAAGGTATCATGGTAAATCTCAGATG TGGTTTTTTT	
WP_034494714-LBD^{Q208A} -down-F	AAAAAAACCACATCTGAGATTTACCATGATACCTTCAAT AATAAAAACA	
WP_034494714-LBD^{Q208A} -down-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTCTAATCG AGGGAAAGCAGAATT	
WP_034494714-LBD^{E237D} -up-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCTACCGCT CAATGAATGCCT	
WP_034494714-LBD^{E237D} -up-R	TATCTTTTAGATTGCTAAGGGTGTAATCAGTTACGACA ATCCCTTTTA	

WP_034494714-LBD^{E237D}-down-F	TAAAAGGGATTGTCGTAACTGATTACACCCTTAGCAATCTAAAAGATA	
WP_034494714-LBD^{E237D}-down-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTCTAATCGAGGGAAAGCAGAATTT	
sipB-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGGTAAATGACGCAAGTAGC	To generate pET28a-*sipB*
sipB-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTATGCGCGACTCTGGC	
sopB-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGCAAATACAGAGCTTCTATC	To generate pET28a-*sopB*
sopB-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAAGATGTGATTAATGAAGAAA	
invF-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGTCATTTTCTGAAAGCCGA	To generate pET28a-*invF*
invF-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCATTTGTCTGCCAATTGAATAA	
sicA-pET28a-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGGATTATCAAAATAATGTCAGC	To generate pET28a-*sicA*
sicA-pET28a-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTATTCCTTTTCTTGTTCACTGTG	
sicA^{K27A}-up-F	AATGAAGGAGCAGGAAGGGAAC	To generate pET28a-*sicA*^{K27A}
sicA^{K27A}-up-R	TGAGGGATCCCATGAACGTCTGCTAGCGTGGCGCCTT	
sicA^{K27A}-down-F	AAGGCGCCACGCTAGCAGACGTTCATGGGATCCCTCA	
sicA^{K27A}-down-R	TCTTGTTCACTGTGCTGCTCTGT	
sicA^{D28A}-up-F	GCAGTCTTTTCAAAACCCATC	To generate pET28a-*sicA*^{D28A}
sicA^{D28A}-up-R	TCTTGAGGGATCCCATGAACAGCTTTTAGCGTGGCGC	
sicA^{D28A}-down-F	GCGCCACGCTAAAAGCTGTTCATGGGATCCCTCAAGA	
sicA^{D28A}-down-R	TTATTCCTTTTCTTGTTCACTGTG	
sicA^{Q34A}-up-F	TATGCGGAGAAGGTTGGCG	To generate pET28a-*sicA*^{Q34A}
sicA^{Q34A}-up-R	GAGCATATAAACCGTCCATCATATCTGCAGGGATCCCATGAACG	
sicA^{Q34A}-down-F	CGTTCATGGGATCCCTGCAGATATGATGGACGGTTTATATGCTC	
sicA^{Q34A}-down-R	ATCCGCTACGGCTAATGCTACTT	
sicA^{D67A}-up-F	TATGCGGAGAAGGTTGGCG	To generate pET28a-*sicA*^{D67A}
sicA^{D67A}-up-R	CATGGTGTAATCGGGATTGTAAAATGCATAAATGCATAAGAAACGAAAG	
sicA^{D67A}-down-F	CTTTCGTTTCTTATGCATTTATGCATTTTACAATCCCGATTACACCATG	
sicA^{D67A}-down-R	TGCCCTTCGCTGGAGAGTT	
sicA^{N70A}-up-F	ATGGATTATCAAAATAATGTCAGC	To generate pET28a-*sicA*^{N70A}
sicA^{N70A}-up-R	TCCCATGGTGTAATCGGGAGCGTAAAAATCATAAATGCATA	
sicA^{N70A}-down-F	TATGCATTTATGATTTTTACGCTCCCGATTACACCATGG	

	GA	
sicA^{N70A}-down-R	TTATTCCTTTTCTTGTTCACTGTG	
yedQ-LBD^{D233A}-up-F	GAAACACTGTTAGACAATCAAGGCT	
yedQ-LBD^{D233A}-up-R	TGGCTGTCACTTTTTTCTGCTCGGCAGTAACATAGGGC TGTGC	To generate pET28a-*yedQ-LBD*^{D233A}
yedQ-LBD^{D233A}-down-F	GCACAGCCCTATGTTACTGCCGAGCAGAAAAAAGTGA CAGCCA	
yedQ-LBD^{D233A}-down-R	ACAGCATCGCCGTAAAAAGC	
yedQ-LBD^{K236A}-up-F	AGGGAAGTGATGATACTGAAAGA	
yedQ-LBD^{K236A}-up-R	CGGTAGACTGGCTGTCACTTTTGCCTGCTCGTCAGTAA CA	To generate pET28a-*yedQ-LBD*^{K236A}
yedQ-LBD^{K236A}-down-F	TGTTACTGACGAGCAGGCAAAAGTGACAGCCAGTCTA CCG	
yedQ-LBD^{K236A}-down-R	GCCTGATGACCAAAGCGA	
yedQ-LBD^{Q264A}-up-F	TTACCTGGAGGGAAGTGATGATAC	
yedQ-LBD^{Q264A}-up-R	CATCGCGCAGGAACCGCGCTAATGACGCGACGG	To generate
yedQ-LBD^{Q264A}-down-F	CCGTCGCGTCATTAGCGCGGTTCCTGCGCGATG	pET28a-*yedQ-LBD*^{Q264A}
yedQ-LBD^{Q264A}-down-R	CGCCTGCCTGATGACCAA	
yedQ-LBD^{L288A}-up-F	CCTGGAGGGAAGTGATGAT	
yedQ-LBD^{L288A}-up-R	CGCGGAGTCCGTCAACGCACGGAGATGGTTATC	To generate
yedQ-LBD^{L288A}-down-F	GATAACCATCTCCGTGCGTTGACGGACTCCGCG	pET28a-*yedQ-LBD*^{L288A}
yedQ-LBD^{L288A}-down-R	GCAGCACGATACAAAACTCT	
yedQ-LBD^{L289A}-up-F	TTACCTGGAGGGAAGTGATGATAC	
yedQ-LBD^{L289A}-up-R	CGGCGCGGAGTCCGTCGCCAAACGGAGATGGTTAT	To generate
yedQ-LBD^{L289A}-down-F	ATAACCATCTCCGTTTGGCGACGGACTCCGCGCCG	pET28a-*yedQ-LBD*^{L289A}
yedQ-LBD^{L289A}-down-R	TACAAAACTCTTCGCCCCCTAC	
sipC-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGTTAA TTAGTAATGTGGGAAT	To generate
sipC-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTAAGCG CGAATATTGC	pET28a-*sipC*
pcrH-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGAACC AGCCGACCCCTT	To generate
pcrH-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCAAGC GTTATCGGATTCATATGC	pET28a-*pcrH*
cesD-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGGACA CAGAAACAATTGAA	To generate
cesD-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTAGCCA TTATCTTCTGAATTATC	pET28a-*cesD*
bicA-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGACGC AACGCGACGTGAAC	To generate
bicA-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTCTAGTG GTCGTTCTCGACGGATGC	pET28a-*bicA*
vcrH-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGACTA	To generate

	AAACAAACGCGACC	pET28a-*vcrH*
vcrH-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTCTAATTA CTCCTTTTGTTTCTCACC	
invC-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGAAAA CACCTCGTTTACTGCA	To generate pET28a-*invC*
invC-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTTAATTC TGGTCAGCGAATGC	
PA1697-F	ACTGGTGGACAGCAAATGGGTCGCGGATCCATGCCCG CGCCTCTCTCT	To generate pET28a-*PA1697*
PA1697-R	GTGGTGGTGCTCGAGTGCGGCCGCAAGCTTTCATGCG CAGAGGCTCCG	
$P_{sicAsipBCDA}$::lacZ-F	ACGCGTCGACGAAGGAGCAGGAAGGGAA	To generate pDM4-$P_{sicAsipBCDA}$::lacZ
$P_{sicAsipBCDA}$::lacZ-R	CTAGTCTAGATTGATAATCCATTACTTACTCCTGT	
P_{sopB}::lacZ-F	ACGCGTCGACTACATAACTTTTCCCGACAGG	To generate pDM4-P_{sopB}::lacZ
P_{sopB}::lacZ-R	CTAGTCTAGACTGTATTTGCATAGCGTTTTTAA	
P_{sopE2}::lacZ-F	ACGCGTCGACATCCATTTCATTTGTAGTTTTTCT	To generate pDM4-P_{sopE2}::lacZ
P_{sopE2}::lacZ-R	CTAGTCTAGATATGTTAGTCACGGTAGTTCTCCT	
P_{invF}::lacZ-F	ACGCGTCGACAAGAGACTGACACTCATCAATACTAT	To generate pDM4-P_{invF}::lacZ
P_{invF}::lacZ-R	CTAGTCTAGAAGAAAATGACATATGCAGCTTT	
invF-pBBR1-F	GAGCTCCACCGCGGTGGCGGCCGCTCTAGAATGTCAT TTTCTGAAAGCCG	To generate pBBR1MCS1-*invF-his*$_6$
invF-pBBR1-*his*$_6$-R	CAAAAGCTGGGTACCGGGCCCCCCCTCGAGTCAATGG TGATGGTGATGATGTTTGTCTGCCAATTGAAT	
sipB-pBBR1-F	GAGCTCCACCGCGGTGGCGGCCGCTCTAGAATGGTA AATGACGCAAGTAGC	To generate pBBR1MCS1-*sipB-his*$_6$
sipB-pBBR1-*his*$_6$-R	CAAAAGCTGGGTACCGGGCCCCCCCTCGAGTTAATGG TGATGGTGATGATGTGCGCGACTCTGGC	
sipC-pBBR1-F	GAGCTCCACCGCGGTGGCGGCCGCTCTAGAATGTTAA TTAGTAATGTGGGAAT	To generate pBBR1MCS1-*sipC-his*$_6$
sipC-pBBR1-*his*$_6$-R	CAAAAGCTGGGTACCGGGCCCCCCCTCGAGTTAATGG TGATGGTGATGATGAGCGCGAATATTGC	
yeaJ-F	CGCGGATCCATGAATTTGCATCATAAAGCG	To generate pHSe5-*yeaJ-His*$_6$
yeaJ-His$_6$-R	CCCAAGCTTCTAATGGTGATGGTGATGATGTGATGAAC GATGTTGTTTTTGT	
yedQ-F	CGCGGATCCGTGCCGCACGAAACACTG	To generate pHSe5-*yedQ-His*$_6$
yedQ-His$_6$-R	CCCAAGCTTCTAATGGTGATGGTGATGATGTTTCTTTT CCCGCTCCTGA	
16S-F	GAAGGTGTTGTGGTTAATA	qRT-PCR
16S-R	AGTAATTCCGATTAACGCTT	
sipB-RT-F	GACCCTACTGGGCGATGT	qRT-PCR
sipB-RT-R	GTCGCAGCGTCATAAACAC	
sopB-RT-F	AGAAGGCGTCTAACCACTCG	qRT-PCR
sopB-RT-R	GTGCTGCAATAAGTTCGATAAGA	

sopE2-RT-F	CATAACACTATCCACCCAGC	qRT-PCR
sopE2-RT-R	TACCGCCCTACCCTCAG	
invF-RT-F	CAGGATTAGTGGACACGACAT	qRT-PCR
invF-RT-R	ACTGAGCGAGTAAATAGCCAA	
sipC-RT-F	GCTCTGGCAAATAATGTCAC	qRT-PCR
sipC-RT-R	CAACGCATTCATCCCTTC	
$P_{sicAsipBCDA}$-EMSA-F	CTGGTGAGTCTGGAAGAAAT	EMSA
$P_{sicAsipBCDA}$-EMSA-R	ATAATCCATTACTTACTCCTGTTAT	
$P_{sicAsipBCDA}$-EMSA-CK-F	TAACCAGGGACGACTGGAT	To generate fragment of
$P_{sicAsipBCDA}$-EMSA-CK-R	TACGTTCATTGACAAGTTCAAA	negative control for EMSA
P_{sopB}-EMSA-F	CCCATGATCGCCACTACG	EMSA
P_{sopB}-EMSA-R	GCTCTGTATTTGCATAGCGTTT	
P_{sopB}-EMSA-CK-F	GAGTTGCTTAACAAAGCCTTAG	To generate fragment of
P_{sopB}-EMSA-CK-R	TGTAGATCGCCATCTTTATTG	negative control for EMSA
P_{sopE2}-EMSA-F	AAAAGTCGATCACCTTGCG	EMSA
P_{sopE2}-EMSA-R	TATGTTAGTCACGGTAGTTCTCCT	
P_{sopE2}-EMSA-CK-F	GCCGTGTACAGTAATAATAAAGATC	To generate fragment of
P_{sopE2}-EMSA-CK-R	ACTCGCGGAAGCAATGAG	negative control for EMSA

***Underlined sites indicate restriction enzyme cutting sites added for cloning.**

Supplementary References

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