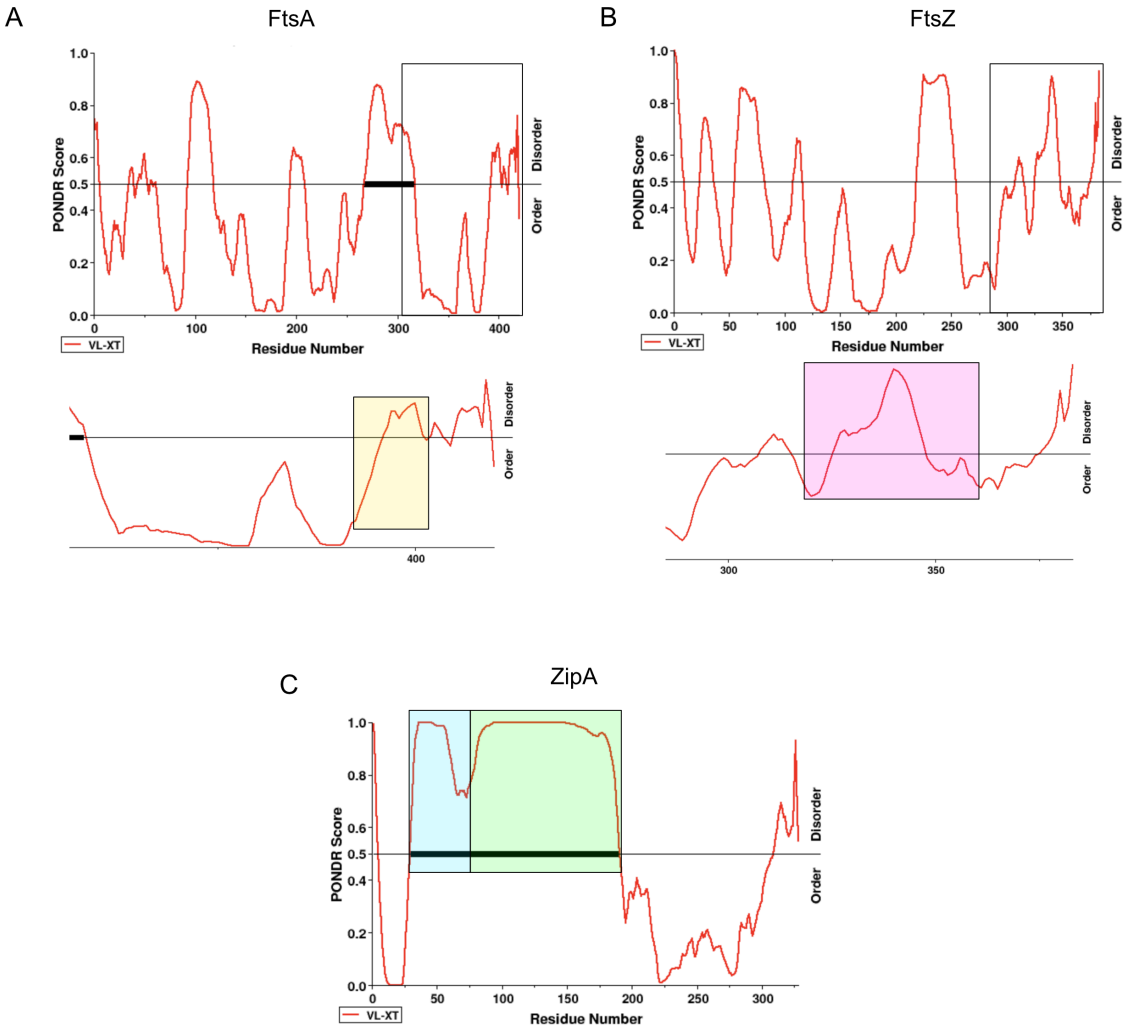

Fig. S1. The FtsA, FtsZ and ZipA linkers all contain disordered regions. (A) PONDR VL-XT (pondr.com) prediction for FtsA. The inset region is indicated in the black box. The linker region is indicated in the shaded yellow box on the inset. (B) PONDR VL-XT prediction for FtsZ. The inset region is indicated in the black box, and the linker region is indicated in the shaded pink box on the inset. (C) PONDR VL-XT prediction for ZipA. The blue and green boxes correspond to the charged and P/Q-rich domains of the linker, respectively. Residues with a score higher than 0.5 are predicted to be intrinsically disordered.

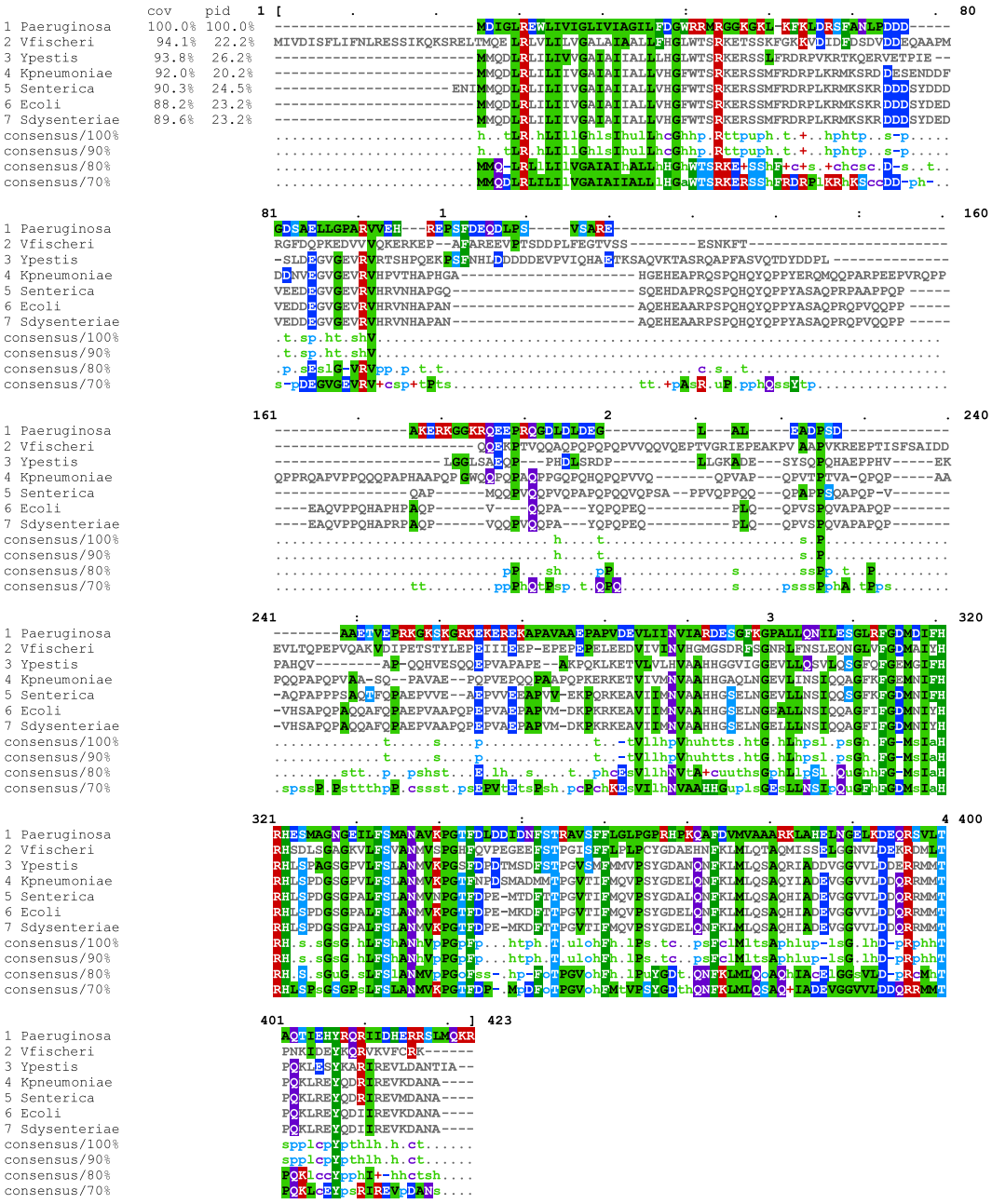

Fig. S2. Multiple sequence alignment for ZipA proteins from different species. The Clustal Omega Multiple Sequence Alignment tool from the European Molecular Biology Laboratory- European Bioinformatics Institute (https://www.ebi.ac.uk/Tools/msa/clustalo/; see reference) was used to align the primary sequences of ZipA proteins from several different species, and MView (https://www.ebi.ac.uk/Tools/msa/mview/) was used to visualize the alignment. Sequences were collected from the NCBI Gene database. Sequences were collected from *Pseudomonas aeruginosa, Vibrio fischeri, Yersinia pestis, Klebsiella pneumoniae, Salmonella enterica, Escherichia coli,* and *Shigella dysenteriae.* Residues are colored by identity. Consensus sequences are shown below the species alignment.

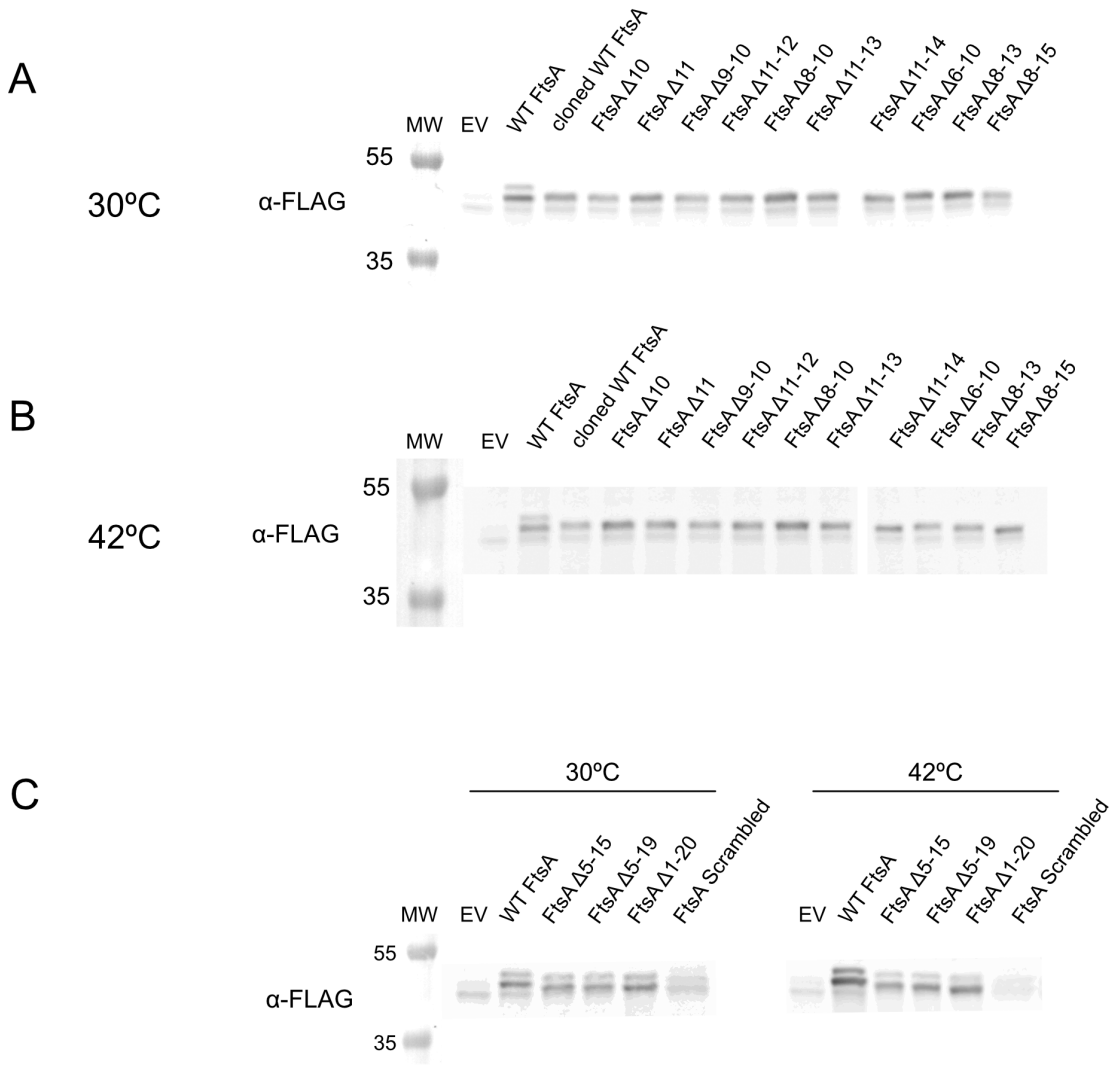

Fig. S3. Immunoblots of plasmid-expressed FtsA linker mutant derivatives. (A) Extracts of WM1074 cells producing various FLAG-FtsA derivatives from pDSW210F after induction with 50 μM IPTG at 30˚C were normalized for protein levels, subjected to SDS-PAGE, and Western blots were probed with anti-FLAG to show relative protein levels.. B) Same as (A), except cells were grown at 42˚C. In both (A) and (B), samples were all run on one gel, but the last 4 lanes on the right are separated from the others to exclude a lane that had no sample run on the gel. (C) Same as (A) and (B), from additional FtsA derivatives grown at the indicated temperatures. The samples were all run on one gel, but the images are separated to exclude a blank lane.

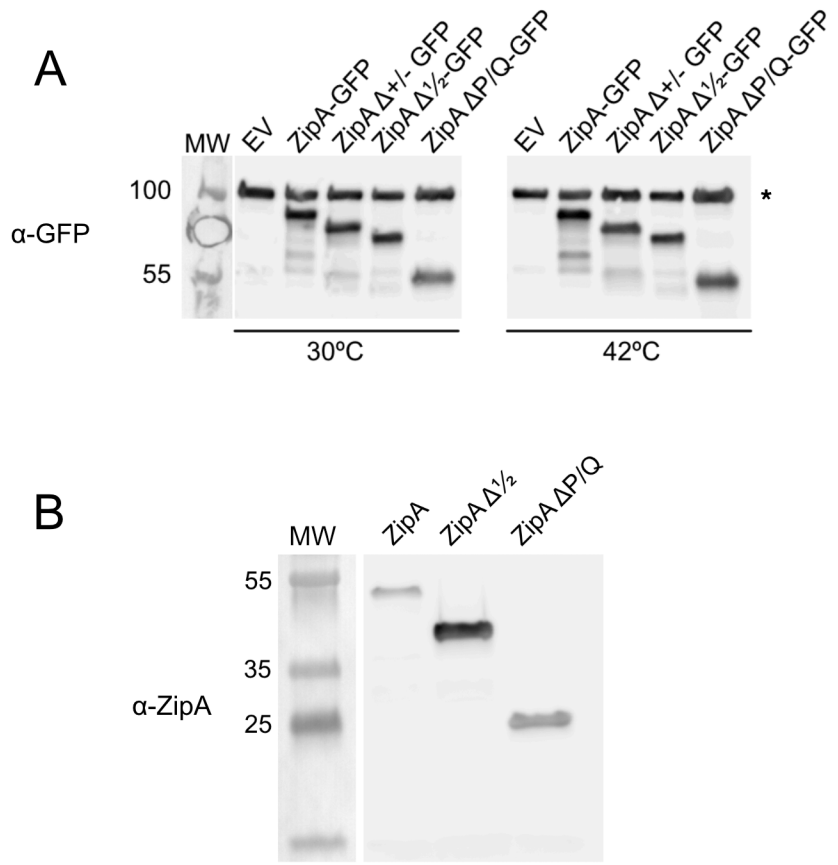

Fig. S4. Immunoblots of ZipA linker derivatives. (A) Extracts of WM1074 cells producing various ZipA-GFP derivatives from pDSW210 after induction with 50 μM IPTG were normalized for protein levels, subjected to SDS-PAGE, and probed with anti-GFP on Western blots to show relative protein levels and sizes. As also shown in Fig. 3B, ZipAΔP/Q-GFP migrates at the expected size, while all other ZipA derivatives migrate aberrantly slowly, between ~95 and 70 kDa. The asterisk denotes a nonspecific band at 100 kDa present in all the lanes. (B) Same as (A), except extracts were from cells with ZipA linker deletions replacing the native chromosomally-encoded *zipA*, and the blot was probed with anti-ZipA. As in (A), only ZipAΔP/Q runs at the expected size.

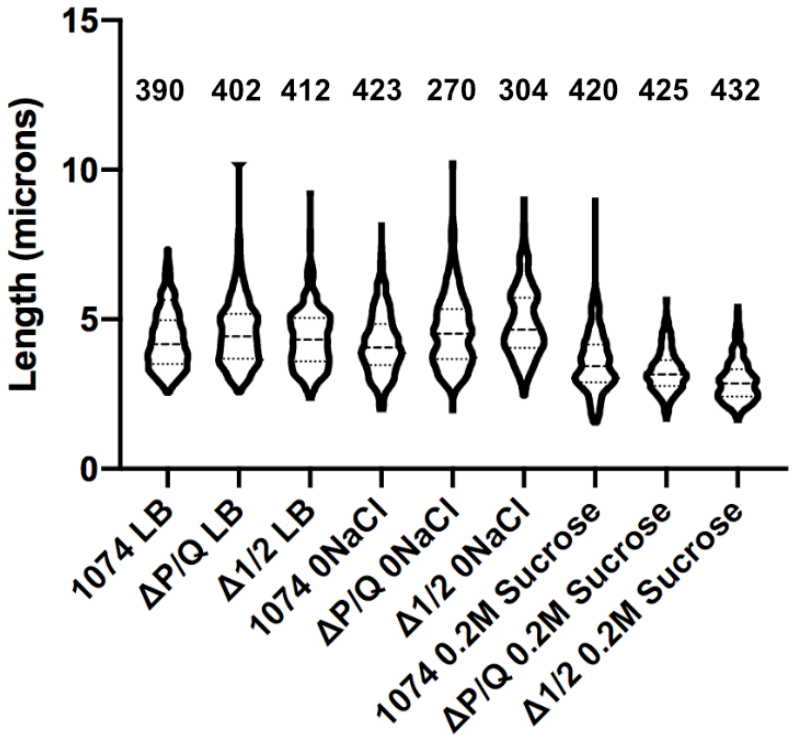

Fig. S5. Cell length measurements of chromosomal ZipA linker mutants in various growth media. Cell lengths were measured in ImageJ from phase contrast images of cells grown to an OD between 0.3-0.4. A violin plot was assembled in Prism8 by GraphPad. Numbers above each violin correspond to the number of cells measured for each strain in each condition. The thick dashed line in each represents the average measured cell length, with the thinner dashed lines representing the 1st and 3rd quartiles.

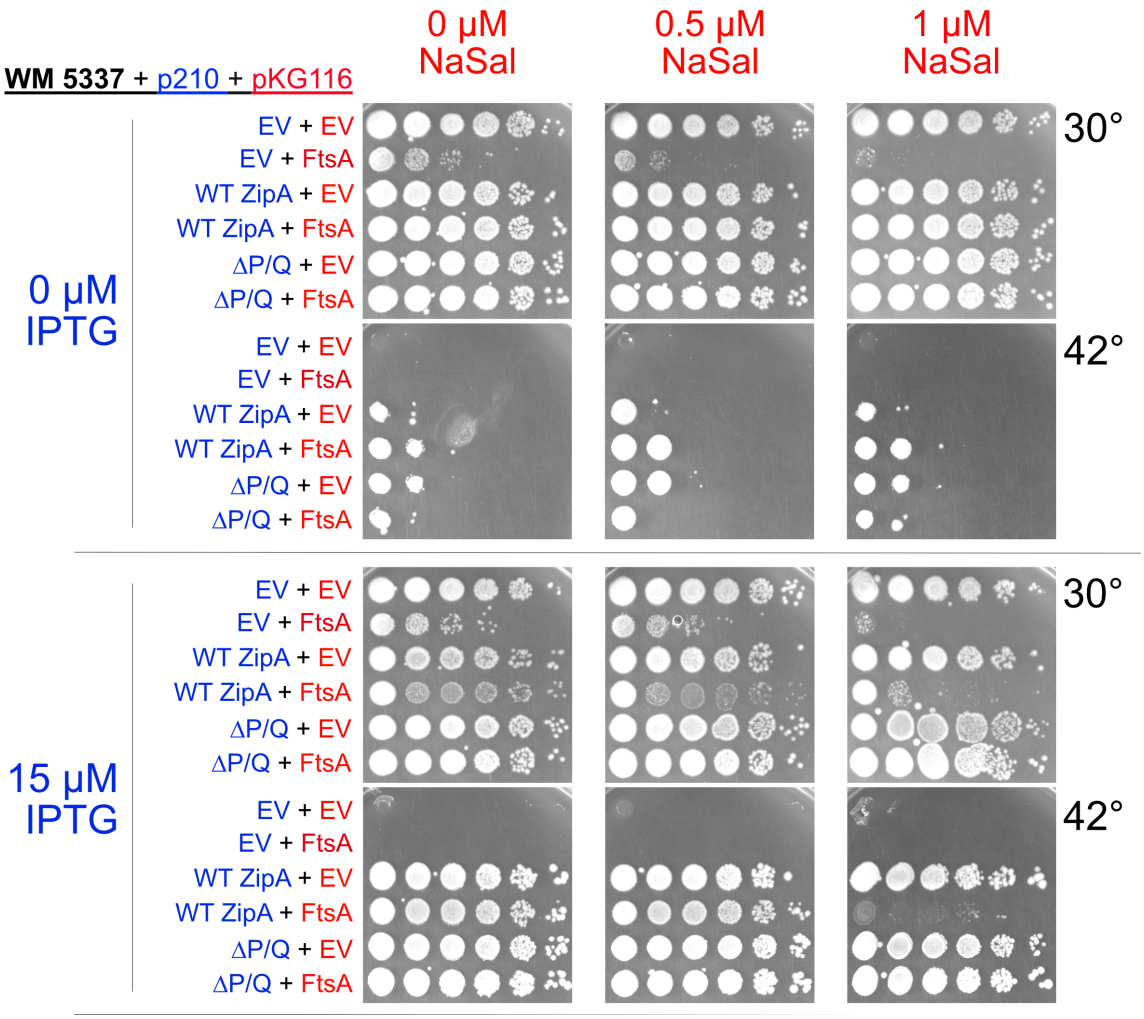

Fig. S6. Overexpression of FtsA is less toxic in cells also overproducing ZipAΔP/Q, but not WT ZipA. WM 5337 (*zipA1*) cells cotransformed with pDSW210 derivatives expressing WT ZipA or ZipAΔP/Q (labeled in blue) and either empty pKG116 vector or pKG116-FtsA (labeled in red) were serially-diluted 10-fold and spotted on LB plates with the indicated concentrations of IPTG (labeled in blue as it induces pDSW210 derivatives) and/or sodium salicylate (NaSal; labeled in red as it induces pKG116 derivatives) and incubated at 30°C or 42°C overnight. The asterisks indicate the rows with cells overexpressing both ZipAΔP/Q and FtsA.

Table S1. Oligonucleotide primers used in this study.

Primer #	Sequence	Description
2280	TCATGCCCCGGCTAACGCTCAGGAGCATGAGGCTGCTCGTTTATATTCCCCAGAACATCA	ZipA ΔP/Q *ccdB*:*kan* forward
2281	CGTTCATGATAATCACCGCTTCTTTGCGCTTCGGTTTATCATAGGAACTTCAAGATCCCCTTATTA	ZipA ΔP/Q *ccdB*:*kan* reverse
2196	TCAGTTGGCTCGTGGATC	FtsA Δ5-19 forward
2197	CTCTTTCCCATAGTGAAGC	FtsA Δ5-19 reverse
2188	GCATCAGTTGGCTCGTGG	FtsA Δ5-15 forward
2189	ATGTGACTCTTTCCCATAGTG	FtsA Δ5-15 reverse
2190	GATAAACCGAAGCGCAAAGAAG	ZipA ΔPQ forward
2191	ACGAGCAGCCTCATGCTC	ZipA ΔPQ reverse
2192	CCGTCGCCGCAACACCAG	ZipA Δ+/- forward
2193	GCTGGTCCAGAAACCATGTACC	ZipA Δ+/- reverse
2194	CAGCCGTTGCAGCAGCCA	ZipA Δ½ forward
2195	GACATCCTCGTCATAAGAATCGTCGTC	ZipA Δ½ reverse
2163	GGCCATACCAAAAGCGAAGTGGCGGAAGAAGGCTCGTGGATCAAGCGA	FtsA scrambled linker insertion forward
2164	GCGGCTTTCGTTTTTGCCCACCAGCACCGCATAGTGAAGCAATCCCACCG	FtsA scrambled linker insertion reverse
2159	GGCTCGTGGATCAAGCGA	FtsA Δ1-20 forward
2160	ATAGTGAAGCAATCCCACCG	FtsA Δ1-20 reverse
265	TGCAGGATTTGCGTCTGATA	Internal ZipA forward
2364	CAGGAAAATTCTGCGTATTTTAC	Forward primer for sequencing ZipA in chromosome
2365	CGCGCAGTTCGCGCATCAG	Reverse primer for sequencing ZipA in chromosome
2366	TATATATCTAGATCAGGCGTTGGCGTCTTTGAC	Internal ZipA reverse
1157	CCGACATCATAACGGTTCTGGCA	pDSW210 vector forward primer
1158	GCCATCTAATTCAACAAGAACTG	pDSW210 vector reverse primer for ZipA-GFP fusions
1225	TGCCGCCAGGCAAATTCTGTTTTATCAGAC	pDSW210 vector reverse primer for FtsA linker mutants