

Supporting Information.

Roles for both FtsA and the FtsBLQ subcomplex in FtsN-stimulated cell constriction in *Escherichia coli*.

Bing Liu, Logan Persons, Lynda Lee, and Piet A. J. de Boer

Department of Molecular Biology & Microbiology, School of Medicine, Case Western Reserve University, Cleveland, Ohio 44106-4960

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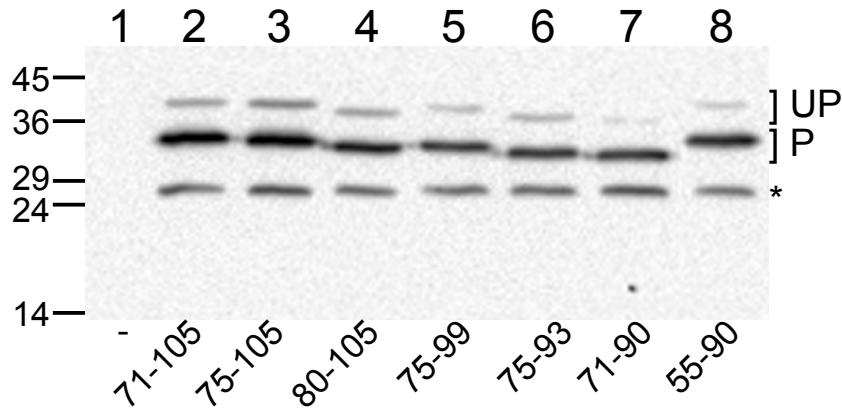


Figure S1. Immunoblot of periplasmic ^{TT}GFP fusions to various FtsN peptides.

Lanes contained whole cell extracts of strain TB28 [*wf*] harboring pMLB1113ΔH3 [vector] (1), pMG14 [*P_{lac}::torA¹⁻⁴³-gfp-ftsN⁷¹⁻¹⁰⁵*] (2), pLP168 [*P_{lac}::torA¹⁻⁴³-gfp-ftsN⁷⁵⁻¹⁰⁵*] (3), pLP169 [*P_{lac}::torA¹⁻⁴³-gfp-ftsN⁸⁰⁻¹⁰⁵*] (4), pLP219 [*P_{lac}::torA¹⁻⁴³-gfp-ftsN⁷⁵⁻⁹⁹*] (5), pLP218 [*P_{lac}::torA¹⁻⁴³-gfp-ftsN⁷⁵⁻⁹³*] (6), pMG50 [*P_{lac}::torA¹⁻⁴³-gfp-ftsN⁷¹⁻⁹⁰*] (7), or pLP221 [*P_{lac}::torA¹⁻⁴³-gfp-ftsN⁵⁵⁻⁹⁰*] (8). Overnight cultures were diluted 100-fold in M9-maltose medium with 50 μg/ml ampicillin and 100 μM IPTG and incubated at 30°C to OD₆₀₀≈0.5. Fusion proteins were detected using α-GFP polyclonal antibodies. Migration of molecular weight standards (kD) is indicated on the left. Unprocessed (UP) and processed (P, lacking the TorA signal sequence) forms of the fusions are indicated on the right. A degradation product is indicated with an asterisk (*). FtsN residues present in the various fusions are indicated at the bottom.

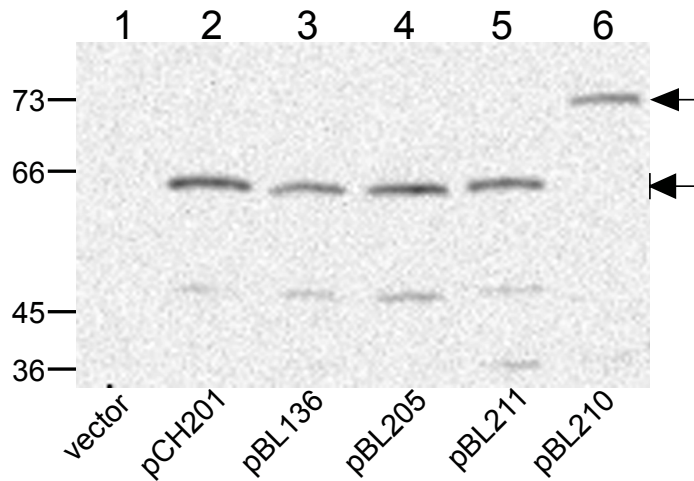


Figure S2. Immunoblot of GFP fusions to various FtsN deletion-substitution variants.

Lanes contained whole cell extracts of strain TB28 [*wt*] harboring pMLB1113 Δ H3 [vector] (1), pCH201 [$P_{lac}::gfp-ftsN$] (2), pBL136 [$P_{lac}::gfp-ftsN^{\Delta(64-101)<>22}$] (3), pBL205 [$P_{lac}::gfp-ftsN^{\Delta(59-73)<>5}$] (4), pBL211 [$P_{lac}::gfp-ftsN^{\Delta(59-73)<>15}$] (5), or pBL210 [$P_{lac}::gfp-ftsN^{\Delta(59-73)<>95}$] (6). Overnight cultures were diluted 100-fold in LB medium with 50 μ g/ml ampicillin and 5 μ M IPTG and incubated at 30°C to $OD_{600} \approx 0.5$. Fusion proteins were detected using α -GFP polyclonal antibodies, and are marked by arrows on the right. Molecular weight standards (kD) are indicated on the left.

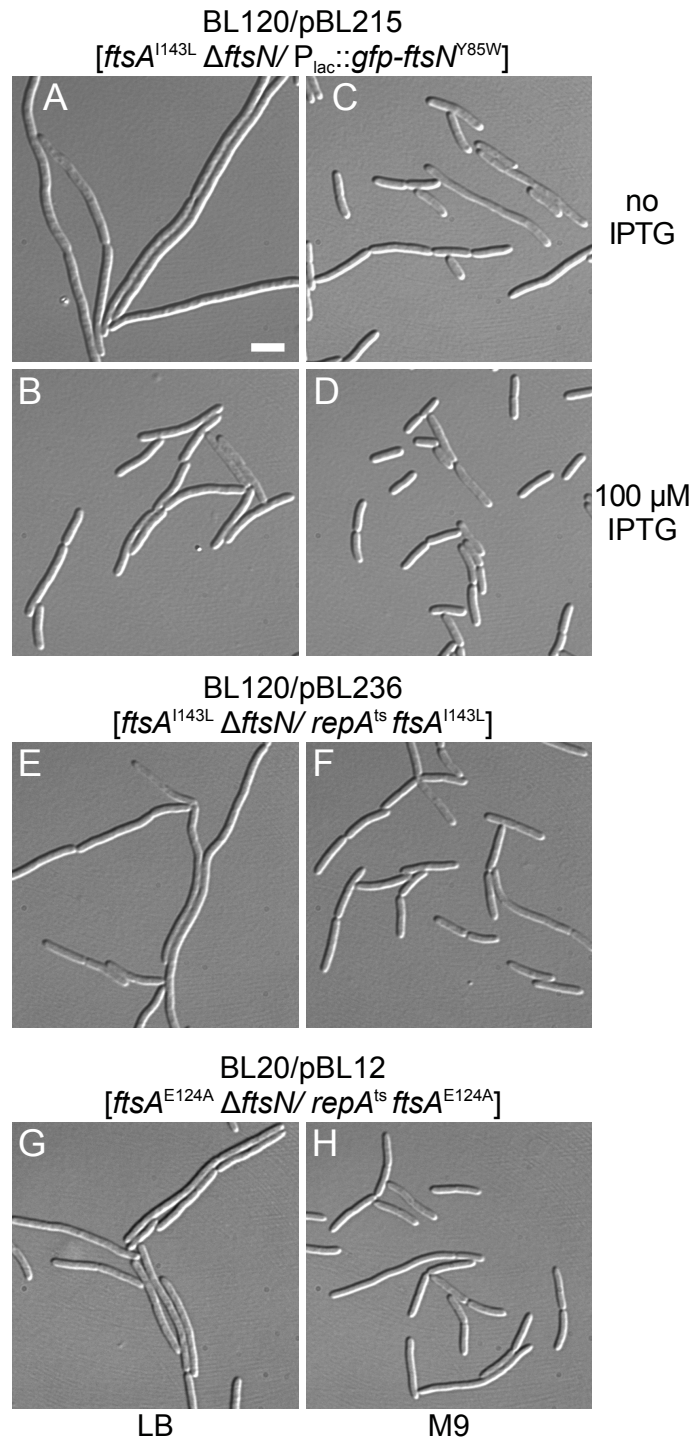


Figure S3. Cell fission in the absence of (functional) FtsN by (over)production of FtsA^{I143L} or FtsA^{E124A}.

Differential interference contrast images of live BL120 [*ftsA*^{I143L} Δ *ftsN*] cells carrying pBL215 [P_{lac}::*gfp-ftsN*^{Y85W}] (A-D) or pBL236 [*repA*^{ts} *ftsA*^{I143L}] (E and F), and of BL20 [*ftsA*^{E124A} Δ *ftsN*] cells carrying pBL12 [*repA*^{ts} *ftsA*^{E124A}] (G and H). Cells were grown to OD₆₀₀~0.5 in LB (E, G), LB supplemented with 0.2% glucose (A) or 100 μ M IPTG (B), M9-glucose (C, F, H), or M9-glucose with 100 μ M IPTG (D). Bar equals 4 μ m.

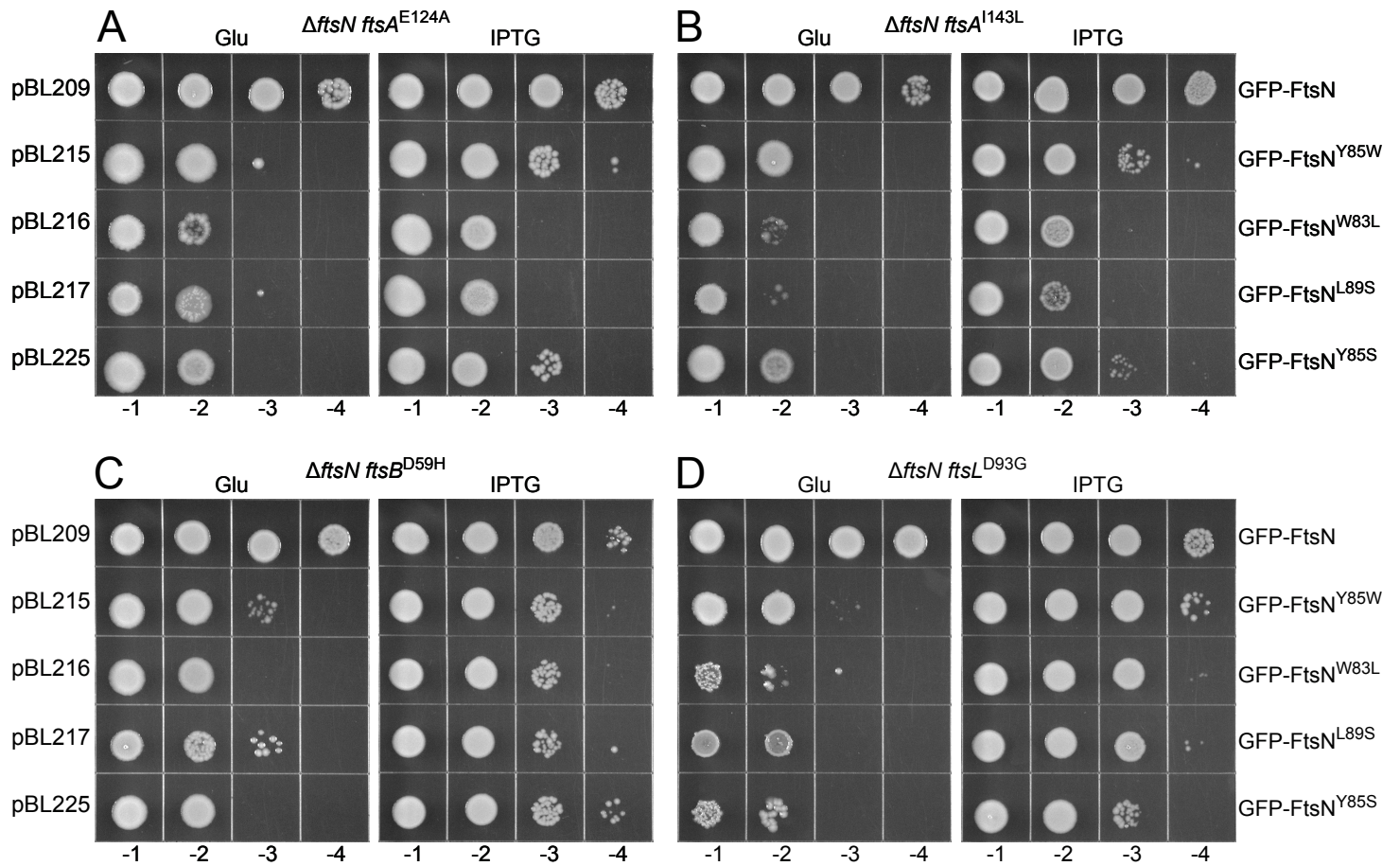


Figure S4. Little allele-specificity of ^EFtsN*-suppressing mutations in *ftsA*, *ftsB*, or *ftsL*.

Spot titer analyses of strains BL20 [*ftsA*^{E124A} $\Delta ftsN$] (A), BL120 [*ftsA*^{I143L} $\Delta ftsN$] (B), BL141 [*ftsB*^{D59H} $\Delta ftsN$] (C), and BL157 [*ftsL*^{D93G} $\Delta ftsN$] (D), carrying mini-F plasmids encoding WT or mutant variants of GFP-FtsN under control of the *lac* regulatory region as indicated on the sides of each row. Cells were grown overnight at 30°C in LB with 100 μ M IPTG, serially diluted to $OD_{600}=4 \times 10^X$, and 5 μ l of each dilution was spotted on M9-maltose agar supplemented with 0.2% glucose or 100 μ M IPTG, as indicated. Plates were incubated at 30°C for 42 hr.

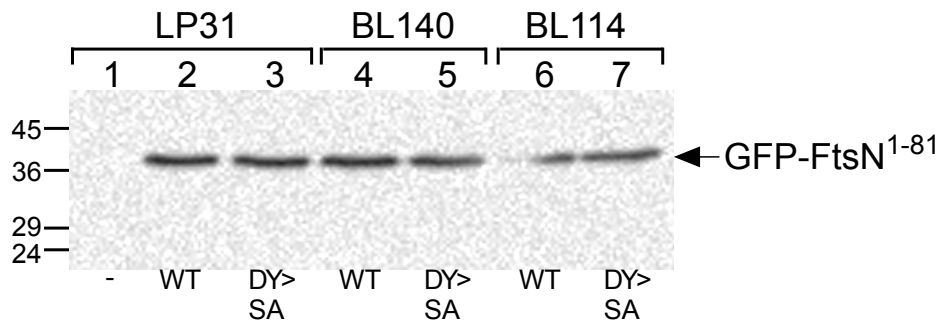


Figure S5. Immunoblot of GFP-FtsN¹⁻⁸¹ and GFP-FtsN^{1-81, DY>SA} fusions.

Lanes contained whole cell extracts of strain LP31 [*recA*] harboring pMLB1113ΔH [vector] (1), pMG13 [*P_{lac}::gfp-ftsN¹⁻⁸¹*] (2), or pBL335 [*P_{lac}::gfp-ftsN^{1-81, DY>SA}*] (3), strain BL140 [*ftsB^{D59H}*] harboring pMG13 (4), or pBL335 (5), and strain BL114 [*ftsA^{I143L}*] harboring pMG13 (6), or pBL335 (7). Overnight cultures were diluted 100-fold in M9-maltose medium with 50 μg/ml ampicillin and 100 μM IPTG and incubated at 30°C to OD₆₀₀≈~0.5. Fusion proteins were detected using α-GFP polyclonal antibodies. Molecular weight standards (kD) are indicated on the left.

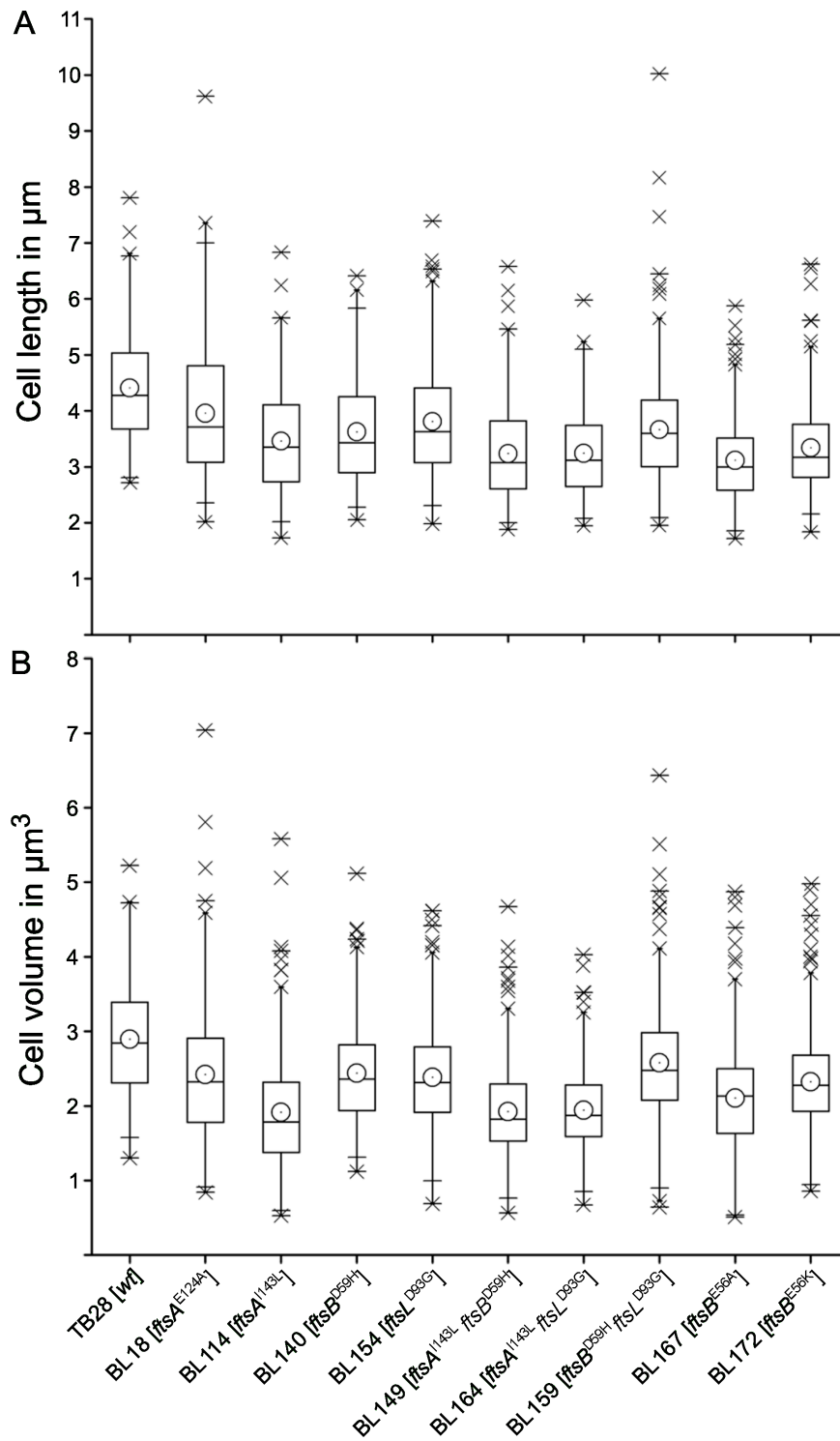


Figure S6. Cell size distributions of FtsN⁺ strains harboring ^EFtsN⁻-suppressing mutations.

Box plots showing cell length (A) and volume (B) distributions of the LB-grown strains listed in Table 5. In each plot, values within the 25th-50th and 50th-75th percentile ranges (boxed), minimum, maximum, 1st and 99th percentile values (horizontal cross-hatches), and average (⊙) and outlier (X) values are indicated. Values below $Q1-1.5 \times IQR$ or above $Q3+1.5 \times IQR$ (with $Q1$ =first quartile, $Q3$ =third quartile, and IQR =interquartile range) were considered outliers.

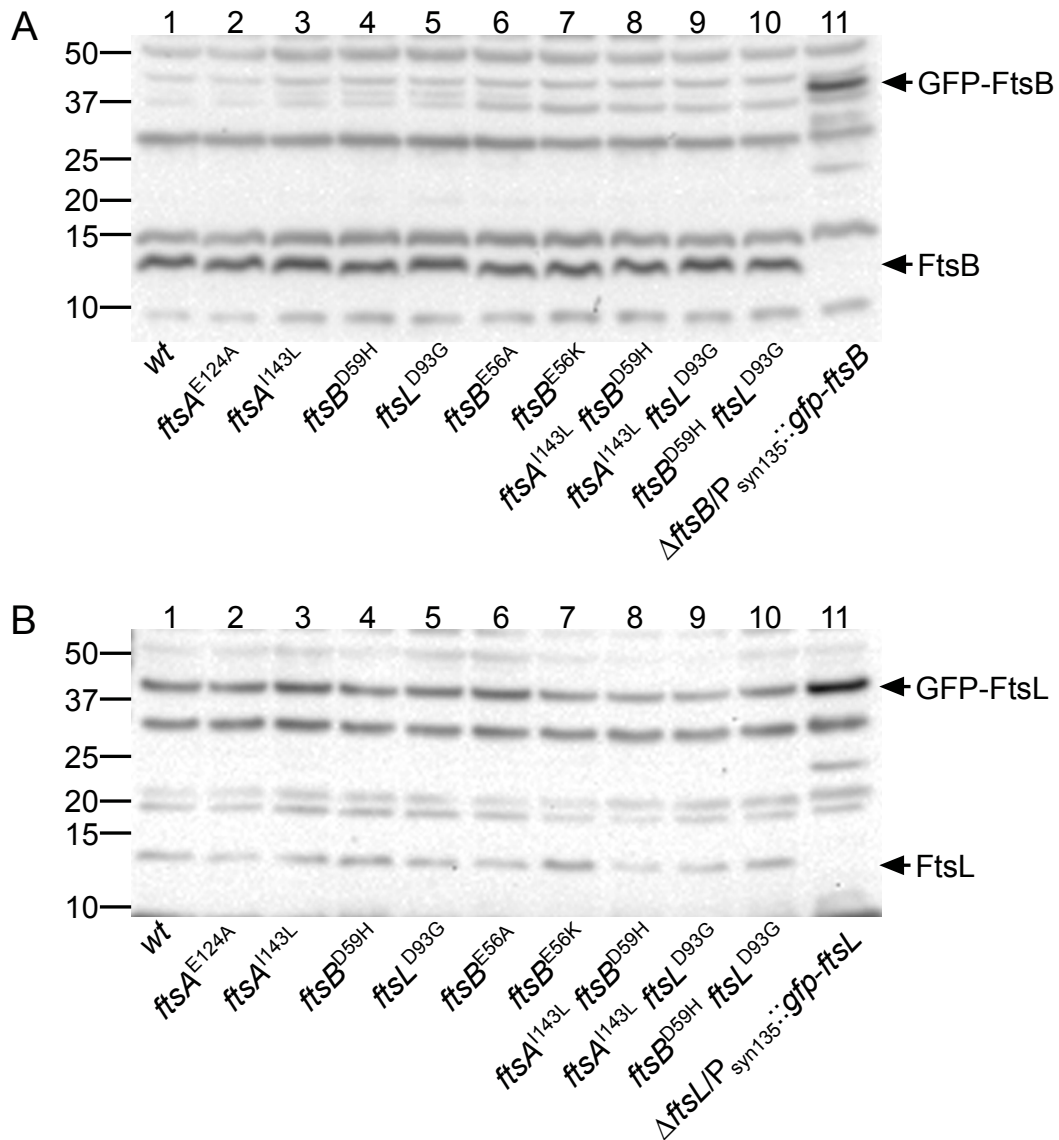


Figure S7. Immunoblot of FtsB, FtsL, and mutant variants.

(A, B) Lanes contained whole cell extracts of strain TB28 [*wt*] (1), BL18 [*ftsA*^{E124A}] (2), BL114 [*ftsA*^{I143L}] (3), BL140 [*ftsB*^{D59H}] (4), BL154 [*ftsL*^{D93G}] (5), BL167 [*ftsB*^{E56A}] (6), BL172 [*ftsB*^{E56K}] (7), BL149 [*ftsA*^{I143L} *ftsB*^{D59H}] (8), BL164 [*ftsA*^{I143L} *ftsL*^{D93G}] (9), BL159 [*ftsB*^{D59H} *ftsL*^{D93G}] (10), and BL155/pBL194 [Δ *ftsB* / *P*_{syn135}::*gfp-ftsB*] (11, panel A only), or BL156/pBL195 [Δ *ftsL* / *P*_{syn135}::*gfp-ftsL*] (11, panel B only). Cells were grown to OD₆₀₀=0.5-0.6 at 30°C in LB, whole cell extracts were prepared, and 40 μ g of total protein was loaded in each lane of a 10-20% Tricine gradient gel (Invitrogen). Proteins were detected using α -FtsB (A) or α -FtsL (B) polyclonal antibodies. The positions of FtsB (A, lanes 1-10), GFP-FtsB (A, lane 11), FtsL (B, lanes 1-10), and GFP-FtsL (B, lane 11) are indicated. Most other bands represent non-specific cross-reactive species. Molecular weight standards (kD) are indicated on the left.

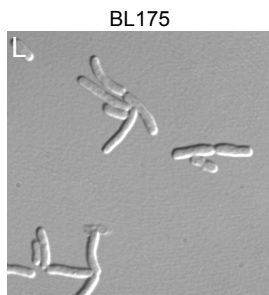
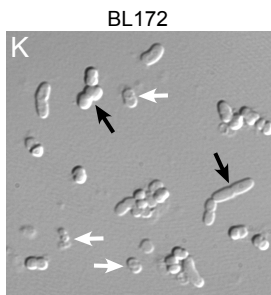
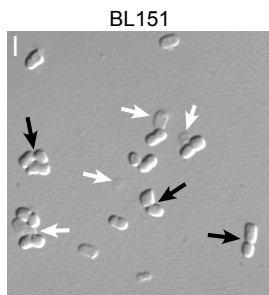
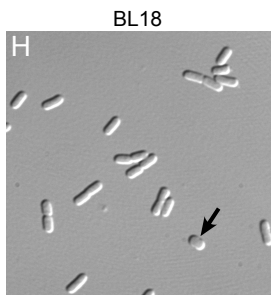
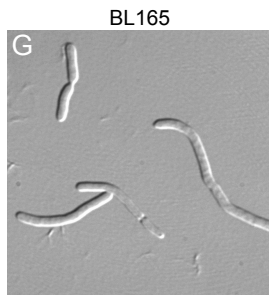
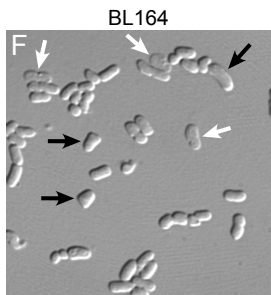
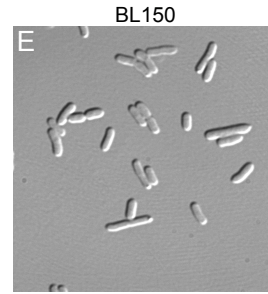
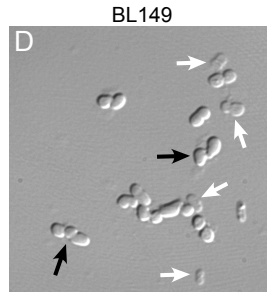
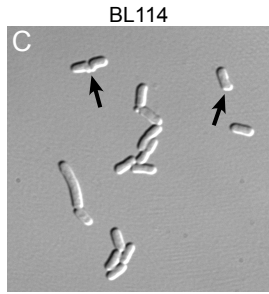
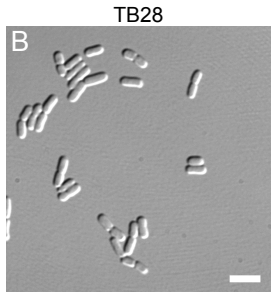
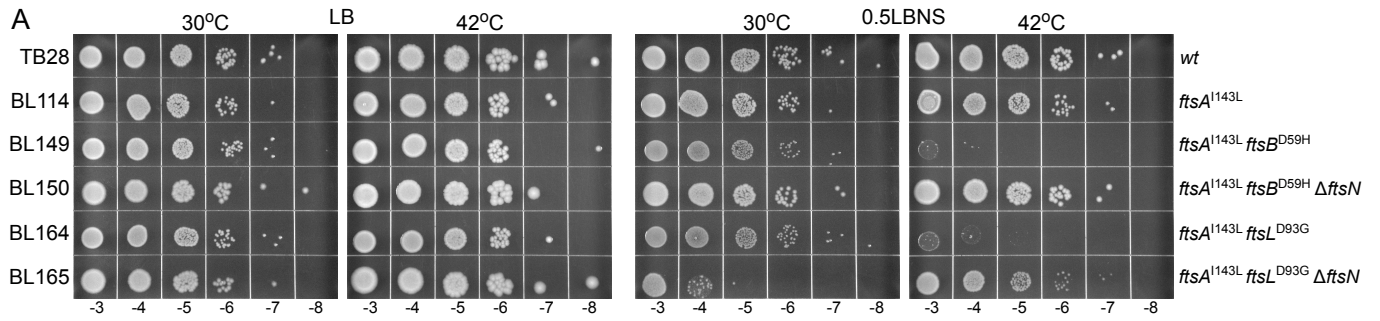


Figure S8. Conditional lethality of E FtsN*-suppressing mutations in FtsN⁺ cells.

(A) Cells of the indicated strains were grown overnight in LB at 30°C. Cultures were serially diluted in LB to $OD_{600}=4 \times 10^X$ as indicated, and 5 μ l of each dilution was spotted on LB or 0.5LBNS agar. Plates were incubated for 16 hr at 42°C or 20 hr at 30°C. Growth phenotypes of the *ftsA*^{E124A} strains BL18, BL151, and BL152 (not shown) were similar to those of the *ftsA*^{I143L} strains BL114, BL149, and BL150, respectively.

(B-L) Cells of the indicated strains were grown overnight in LB at 30°C, diluted 400-fold in 0.5LBNS, grown for 3.5 hr at 42°C, and imaged live. Arrows point at examples of cells with shape defects (black) or of cell ghosts/debris (white).

Table S1. Single residue substitutions in the essential domain of FtsN obtained by site-directed and scanning mutagenesis.

| Plasmid name | wt residue | wt codon | new codon | new residue | d/s ^a | > 1 ^b | CH31 rescue ^c | | |
|---------------|------------|----------|-----------|-------------|------------------|------------------|--------------------------|---|---|
| pBL321 | L75 | CTA | GCT | A | d | | + | | |
| pBL322 | P76 | CCA | GCA | A | d | | + | | |
| pBL323 | P77 | CCA | GCA | A | d | | + | | |
| pBL324 | K78 | AAA | GCA | A | d | | + | | |
| pBL325 | P79 | CCA | GCA | A | d | | + | | |
| pBL326 | E80 | GAA | GCA | A | d | | + | | |
| pBL116(E81A) | E81 | GAA | GCG | A | s | | + | | |
| pBL93 | | | AAG | K | d | | + | | |
| pBL116(R82T) | R82 | CGC | ACG | T | s | | + | | |
| pBL116(W83A) | W83 | TGG | GCG | A | s | | - | | |
| pBL163 | | | TTT | F | d | | + | | |
| pBL116(W83G) | | | GGT | G | s | | - | | |
| pBL116(W83L) | | | CTG | L | s | | - | | |
| pBL116(W83M) | | | ATG | M | s | | - | | |
| pBL116(W83Q) | | | CAG | Q | s | | - | | |
| pBL180 | | | ACC | T | d | | - | | |
| pBL116(W83T) | | | ACG | T | s | | - | | |
| pBL327 | | | R84 | CGC | GCC | A | d | | + |
| pBL116(R84R) | | | | | CGT | R | s | | + |
| pBL116(Y85A) | | | Y85 | TAC | GCA | A | s | 2 | - |
| pBL116(Y85A2) | | | | | GCC | A | s | | - |
| pBL116(Y85C) | TGT | C | | | s | | - | | |
| pBL116(Y85E) | GAA | E | | | s | 3 | - | | |
| pBL165 | TTC | F | | | d | | + | | |
| pBL116(Y85G) | GGG | G | | | s | | + | | |
| pBL116(Y85G2) | GGT | G | | | s | | + | | |
| pBL116(Y85I) | ATT | I | | | s | 2 | - | | |
| pBL116(Y85K) | AAA | K | | | s | 4 | - | | |
| pBL116(Y85K2) | | | | | AAG | K | s | 2 | - |

| | | | | | | | |
|---------------|-----|-----|-----|---|---|---|---|
| pBL116(Y85L) | | | CTC | L | s | | - |
| pBL116(Y85L2) | | | CTG | L | s | 2 | - |
| pBL116(Y85P) | | | CCA | P | s | 3 | - |
| pBL116(Y85P2) | | | CCC | P | s | 2 | - |
| pBL116(Y85Q) | | | CAA | Q | s | | - |
| pBL116(Y85R) | | | AGA | R | s | | - |
| pBL116(Y85R2) | | | AGG | R | s | | - |
| pBL116(Y85R3) | | | CGA | R | s | | - |
| pBL94 | | | CGC | R | d | | - |
| pBL116(Y85R4) | | | CGC | R | s | | - |
| pBL116(Y85R5) | | | CGG | R | s | 2 | - |
| pBL160 | | | AGC | S | d | | - |
| pBL116(Y85S) | | | AGC | S | s | | - |
| pBL116(Y85T) | | | ACT | T | s | 4 | - |
| pBL116(Y85V) | | | GTA | V | s | | - |
| pBL116(Y85W) | | | TGG | W | s | | - |
| pBL116(Y85Y) | | | TAT | Y | s | | + |
| pBL116(Y85*) | | | TAG | * | s | | - |
| pBL116(I86R) | I86 | ATT | CGC | R | s | | + |
| pBL100 | K87 | AAA | GAA | E | d | | + |
| pBL116(K87I) | | | ATT | I | s | | + |
| pBL116(E88V) | E88 | GAG | GTG | V | s | | + |
| pBL116(L89A) | L89 | CTG | GCA | A | s | 2 | - |
| pBL116(L89A2) | | | GCC | A | s | 2 | - |
| pBL328 | | | GCG | A | d | | - |
| pBL116(L89A3) | | | GCG | A | s | | - |
| pBL116(L89C) | | | TGC | C | s | | - |
| pBL116(L89E) | | | GAA | E | s | | - |
| pBL116(L89F) | | | TTC | F | s | 2 | + |
| pBL116(L89F2) | | | TTT | F | s | | + |
| pBL116(L89G) | | | GGG | G | s | | - |
| pBL116(L89H) | | | CAC | H | s | | - |
| pBL116(L89H2) | | | CAT | H | s | 2 | - |
| pBL116(L89I) | | | ATC | I | s | | + |

| | | | | | | | |
|---------------|-----|-----|-----|---|---|---|---|
| pBL116(L89K) | | | AAA | K | s | | - |
| pBL116(L89L) | | | CTA | L | s | | + |
| pBL116(L89L2) | | | TTA | L | s | | + |
| pBL116(L89M) | | | ATG | M | s | | + |
| pBL116(L89N) | | | AAC | N | s | | - |
| pBL116(L89P) | | | CCA | P | s | 2 | - |
| pBL116(L89P2) | | | CCG | P | s | | - |
| pBL116(L89P3) | | | CCT | P | s | 3 | - |
| pBL116(L89Q) | | | CAA | Q | s | 2 | - |
| pBL116(L89R) | | | CGA | R | s | | - |
| pBL116(L89S) | | | TCA | S | s | 2 | - |
| pBL116(L89S2) | | | TCG | S | s | | - |
| pBL116(L89T) | | | ACA | T | s | | - |
| pBL116(L89T2) | | | ACC | T | s | | - |
| pBL116(L89Y) | | | TAC | Y | s | 3 | + |
| pBL116(L89Y2) | | | TAT | Y | s | 2 | + |
| pBL116(L89*) | | | TAA | * | s | | - |
| pBL329 | E90 | GAA | GCA | A | d | | + |
| pBL116(E90*) | | | TAG | * | s | | - |
| pBL116(S91H) | S91 | AGT | CAC | H | s | | + |
| pBL116(R92L) | R92 | CGC | TTA | L | s | | + |
| pBL116(Q93H) | Q93 | CAG | CAC | H | s | | + |
| pBL116(Q93K) | | | AAA | K | s | | + |

^a Obtained by site-directed (d) or site-scanning (s) mutagenesis.

^b Multiples of independent clones of an allele that were isolated and analyzed.

^c Cells of strain CH31 [$P_{BAD}::ftsM$] harboring mutant derivatives of pCH201 [$bla\ lacI^R P_{lac}::gfp-ftsN$] (d) or of pBL116 [$bla\ lacI^R P_{lac}::gfp-ftsN^{T64G, S67G, +A102}$] (s) were colony purified on LB agar containing ampicillin and either no or 0.5% arabinose. +, good growth; -, no or very poor growth. Note that CH31 cells harboring unmutated pCH201 or pBL116 produce sufficient GFP-FtsN to allow normal growth, even in the absence of IPTG inducer.

Table S2. Isolation of plasmid-borne ^EFtsN*-suppressors in *ftsB* and *ftsL*.

| Residue substitutions in FtsB | | | | ^a Originating screen(s) | | | |
|-------------------------------|----------|-----------|-------------|------------------------------------|--|-----------------|-------------------------|
| wt residue | wt codon | new codon | new residue | mini-F plasmid | Protein under P _{lac} control | Selection temp. | ^b No. clones |
| A55 | GCC | ACC | T | pBL215 | GFP-FtsN ^{Y85W} | 37°C | 1 |
| E56 | GAA | GCA | A | pBL215 | GFP-FtsN ^{Y85W} | 37°C | 1 |
| E56 | GAA | GGA | G | pBL215 | GFP-FtsN ^{Y85W} | 42°C | 1 |
| | | | | pJH10 | GFP-MalF ²⁻³⁹ -FtsN ^{55-320, Y85W} | 37°C | 2 |
| | | | | pJH11 | GFP-MalF ²⁻³⁹ -FtsN ^{55-320, W83L} | 37°C | 1 |
| E56 | GAA | AAA | K | pBL216 | GFP-FtsN ^{W83L} | 37°C | 1 |
| | | | | pJH11 | GFP-MalF ²⁻³⁹ -FtsN ^{55-320, W83L} | 37°C | 2 |
| E56 | GAA | GTA | V | pBL215 | GFP-FtsN ^{Y85W} | 37°C | 1 |
| | | | | pBL215 | GFP-FtsN ^{Y85W} | 42°C | 2 |
| | | | | pBL216 | GFP-FtsN ^{W83L} | 42°C | 2 |
| D59 | GAT | GTT | V | pJH10 | GFP-MalF ²⁻³⁹ -FtsN ^{55-320, Y85W} | 37°C | 1* |
| No survivors | | | | pBL217 | GFP-FtsN ^{Y85W} | 37°C | NA |
| | | | | pBL217 | GFP-FtsN ^{Y85W} | 42°C | NA |
| Residue substitutions in FtsL | | | | | | | |
| E88 | GAG | AAG | K | pBL215 | GFP-FtsN ^{Y85W} | 42°C | 1 |
| | | | | pJH11 | GFP-MalF ²⁻³⁹ -FtsN ^{55-320, W83L} | 37°C | 1* |
| E88 | GAG | GTG | V | pBL215 | GFP-FtsN ^{Y85W} | 37°C | 2 |
| | | | | pBL216 | GFP-FtsN ^{W83L} | 42°C | 1 |
| N89 | AAT | AGT | S | pBL215 | GFP-FtsN ^{Y85W} | 37°C | 1 |
| | | | | pBL215 | GFP-FtsN ^{Y85W} | 42°C | 3 |
| | | | | pBL225 | GFP-FtsN ^{Y85S} | 37°C | 1 |
| D93 | GAC | GGC | G | pBL215 | GFP-FtsN ^{Y85W} | 42°C | 2 |
| H94 | CAT | TAT | Y | pBL215 | GFP-FtsN ^{Y85W} | 37°C | 1 |
| No survivors | | | | pBL217 | GFP-FtsN ^{Y85W} | 37°C | NA |
| | | | | pBL217 | GFP-FtsN ^{Y85W} | 42°C | NA |
| | | | | pJH10 | GFP-MalF ²⁻³⁹ -FtsN ^{55-320, Y85W} | 37°C | NA |

^a Strain JH1/pBL200 [Δ *ftsN*<>*aph* Δ *recA*/*aadA repA*^{ts} P_{syn135}::*ftsN* *I-SceI* *cI857* P_R::*i-sceI*] harboring the indicated mini-F plasmid (*bla*) was transformed with a library of plasmid pBL336 [*tetA* P_{syn135}::*ftsB**] containing randomly mutated *ftsB* (upper rows), or with a library of plasmid pJH2 [*tetA*

$P_{syn135}::ftsL^*$] containing randomly mutated *ftsL* (lower rows). Cells were plated on LB agar with Kan, Amp, Tet, and 200 μ M IPTG at 37°C or 42°C. Survivor colonies were purified, the absence of pBL200 was verified (Spec^S), and the plasmid-borne *ftsB* or *ftsL* allele was sequenced. pBL336 or pJH2 derivatives with multiple silent and/or missense mutations in *ftsB* or *ftsL*, respectively, were used for subcloning to unambiguously identify the ^EFtsN*-suppressing mutation as summarized in Table 4 and Figure 3.

^b Number of independent clones isolated. Asterisk (*) indicates poor growth. NA, not applicable. Parallel transformation of JH1/pBL200 bearing pBL209 [$P_{lac}::gfp-ftsN$] with either mutant library under similar conditions yielded 700-1400 transformants per screen.

Table S3. FtsB^{E56A} promotes early sPG synthesis and cell fission.

| Strain [genotype] | TB28 [<i>wt</i>] | BL167 [<i>ftsB</i> ^{E56A}] | |
|--|--------------------|---------------------------------------|------|
| Number of cells measured | 308 | 318 | % WT |
| Average cell length in μ m (SD) | 4.35 (0.98) | 3.36 (0.77) | 77 |
| Average cell volume in μ m ³ (SD) | 3.96 (1.25) | 3.06 (0.99) | 77 |
| % cells with 'HADA ring' | 51 | 56 | 110 |
| % cells with visible constriction | 40 | 35 | 88 |
| % 'HADA rings' without obvious constriction | 23 | 40 | 174 |
| % constrictions without obvious 'HADA ring' | 2 | 2 | 100 |
| Mass doubling time (min) | 43 | 43 | 100 |

^a Overnight cultures in LB were diluted to OD₆₀₀=0.02 in LB, and growth was continued at 30°C to OD₆₀₀=0.5-0.6. Cells were pulse-labeled with HADA for 1 min and immediately fixed in ethanol. SD, standard deviation of the mean. Average cell length and volume of BL167 was significantly smaller than those of TB28 by two-sample t-test ($p < 0.005$). See also Fig.6.

Table S4. *E. coli* strains used in this study.

| Strain | Relevant genotype | Source or Reference |
|------------|--|--------------------------------|
| BL17 | TB28, <i>leu</i> ::Tn10 | This work |
| BL18 | TB28, <i>ftsA</i> ^{E124A} | (Gerding <i>et al.</i> , 2009) |
| BL19 | TB28, <i>ftsA</i> ^{E124A} <i>leu</i> ::Tn10 | This work |
| BL20* | TB28, <i>ftsA</i> ^{E124A} <i>ftsN</i> <> <i>aph</i> | (Gerding <i>et al.</i> , 2009) |
| BL23 | TB10, <i>ponB</i> <> <i>cat</i> | This work |
| BL24 | TB28, <i>ponB</i> <> <i>cat</i> | This work |
| BL71* | TB10, <i>ftsN</i> <> <i>cat</i> | This work |
| BL79 | TB28, <i>ponA</i> <> <i>aph</i> | This work |
| BL84* | TB28, <i>ponB</i> <> <i>cat ftsN</i> ^{slm117} [=ftsN::EZTnKan-2] | This work |
| BL85* | TB28, <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph</i> | This work |
| BL86* | TB28, <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph recA</i> :: <i>cat</i> | This work |
| BL86-AK1* | TB28, <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph recA</i> :: <i>cat ftsL</i> ^{D93G} | This work |
| BL86-AK11* | TB28, <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph recA</i> :: <i>cat ftsB</i> ^{D59H} | This work |
| BL86-AK12* | TB28, <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph recA</i> :: <i>cat ftsB</i> ^{D59H} | This work |
| BL86-KK1* | TB28, <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph recA</i> :: <i>cat ftsA</i> ^{I143L} | This work |
| BL105 | TB28, <i>ponA</i> <> <i>frit ftsN</i> ^{slm117} [=ftsN::EZTnKan-2] | This work |
| BL114 | TB28, <i>ftsA</i> ^{I143L} | This work |
| BL120* | TB28, <i>ftsA</i> ^{I143L} <i>ftsN</i> <> <i>aph</i> | This work |
| BL140 | TB28, <i>ftsB</i> ^{D59H} | This work |
| BL141* | TB28, <i>ftsB</i> ^{D59H} <i>ftsN</i> <> <i>aph</i> | This work |
| BL148 | TB28, <i>ftsA</i> ^{I143L} <i>leu</i> ::Tn10 | This work |
| BL149 | TB28, <i>ftsB</i> ^{D59H} <i>ftsA</i> ^{I143L} <i>leu</i> ::Tn10 | This work |
| BL150 | TB28, <i>ftsB</i> ^{D59H} <i>ftsA</i> ^{I143L} <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph</i> | This work |
| BL151 | TB28, <i>ftsB</i> ^{D59H} <i>ftsA</i> ^{E124A} <i>leu</i> ::Tn10 | This work |
| BL152 | TB28, <i>ftsB</i> ^{D59H} <i>ftsA</i> ^{E124A} <i>leu</i> ::Tn10 <i>ftsN</i> <> <i>aph</i> | This work |
| BL153* | TB28, <i>leu</i> ::Tn10 <i>ftsL</i> ^{D93G} <i>ftsN</i> <> <i>aph</i> | This work |
| BL154 | TB28, <i>leu</i> ::Tn10 <i>ftsL</i> ^{D93G} | This work |
| BL155* | TB28, <i>ftsB</i> <> <i>aph</i> | This work |
| BL156* | TB28, <i>ftsL</i> <> <i>aph</i> | This work |
| BL157* | TB28, <i>leu</i> ::Tn10 <i>ftsL</i> ^{D93G} <i>ftsN</i> <> <i>aph</i> | This work |
| BL159 | TB28, <i>leu</i> ::Tn10 <i>ftsL</i> ^{D93G} <i>ftsB</i> ^{D59H} | This work |
| BL163 | TB28, <i>leu</i> ::Tn10 <i>ftsL</i> ^{D93G} <i>ftsB</i> ^{D59H} <i>ftsN</i> <> <i>aph</i> | This work |
| BL164 | TB28, <i>leu</i> ::Tn10 <i>ftsL</i> ^{D93G} <i>ftsA</i> ^{I143L} | This work |

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|---|--|-----------------------------|
| BL165 | TB28, <i>leu::Tn10 ftsL^{D93G} ftsA^{I143L} ftsN<>aph</i> | This work |
| BL167 | TB28, <i>ftsB^{E56A}</i> | This work |
| BL172 | TB28, <i>ftsB^{E56K}</i> | This work |
| BL173 | TB28, <i>ftsB^{E56A} ftsN<>aph</i> | This work |
| BL175 | TB28, <i>ftsB^{E56K} ftsN<>aph</i> | This work |
| BTH101 | <i>cya-99 araD139 galE15 galK16 rpsL1 hsdR2 mcrA1 mcrB1</i> | Karimova & Ladant |
| BW10724 (λ <i>recA</i> ⁺) | <i>recA::cat lac169 pho-510 thi</i> | (Wanner & Boline, 1990) |
| BW25113 | Δ (<i>araD-araB</i>)567 Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>) λ^- <i>rph-1</i> Δ (<i>rhaD-rhaB</i>)568 <i>hsdR514</i> | (Datsenko & Wanner, 2000) |
| CH31* | TB28, <i>aph araC P_{BAD}::ftsN</i> | (Gerding et al., 2009) |
| CH34* | TB28, <i>ftsN<>aph</i> | (Gerding et al., 2009) |
| CH82 | TB28, <i>ponA<>frt</i> | This work |
| DH5 α | <i>hsdR17 deoR recA1 endA1 phoA supE44 thi-1 gyrA96 relA1 Δ(<i>lacZYA-argF</i>)U169 ϕ80<i>dlacZ</i>ΔM15</i> | Gibco BRL |
| JH1* | TB28, <i>ftsN<>aph recA::cat</i> | This work |
| JW2669 | BW25113, <i>recA<>aph</i> | (Baba et al., 2006) |
| JW3359 | BW25113, <i>ponA<>aph</i> | (Baba et al., 2006) |
| LP31 | TB28, <i>recA<>aph</i> | This work |
| MDG277 | Δ (<i>argF-lac</i>)U169 e14 ⁻ <i>flhD5301 Δ(fruK-yeiR)725 relA1 rpsL150 rbsR22 Δ(fimB-fimE)632 deoC1 spoT1 ftsL<>aph Δ(λ<i>attL-lom</i>)::<i>bla araC P_{BAD}::ftsL</i></i> | (Gonzalez & Beckwith, 2009) |
| MG1655 | <i>ilvG rfb50 rph1</i> | (Guyer et al., 1981) |
| NB946 | Δ (<i>argF-lac</i>)U169 e14 ⁻ <i>flhD5301 Δ(fruK-yeiR)725 relA1 rpsL150 rbsR22 Δ(fimB-fimE)632 deoC1 spoT1 ftsB<>aph Δ(λ<i>attL-lom</i>)::<i>bla araC P_{BAD}::ftsB</i></i> | (Buddelmeijer et al., 2002) |
| SG13109 | <i>his rpsL sulA366 leu::Tn10</i> | (Gottesman et al., 1981) |
| TB10 | MG1655, <i>nadA::Tn10 gal490 λcI857 Δ(cro-bioA)</i> | (Johnson et al., 2004) |
| TB28 | MG1655, <i>lacIZYA<>frt</i> | (Bernhardt & de Boer, 2003) |
| TB77 | TB28, <i>ftsN^{slm117} [=ftsN::EZTnKan-2]</i> | (Gerding et al., 2009) |

Note that strains marked with * required an appropriate plasmid, phage, and/or inducer for survival. The symbol <> denotes DNA replacement by recombineering, and *frt* a scar

sequence remaining after eviction of an *aph* or *cat* cassette by FLP recombinase (Datsenko & Wanner, 2000, Yu *et al.*, 2000).

Table S5. Plasmids used in this study.

| Plasmid | Relevant genotype ^a | ori | Source or Reference |
|------------------|---|----------------------|--------------------------------|
| pAB12 | <i>bla lacI^q P_{T7}::ftsL</i> | ColE1 | This work |
| pACBSCE | <i>Scel cat araC P_{BAD}::i-scel γ β exo</i> | pACYC | (Lee <i>et al.</i> , 2009) |
| pAH162 | <i>attφ80 tetA</i> | R6K | (Haldimann & Wanner, 2001) |
| pBAD33 | <i>cat araC P_{BAD}::</i> | pACYC | (Guzman <i>et al.</i> , 1995) |
| pBL3 | <i>attHK022 bla lacI^q P_{lac}::zapC-le</i> | R6K | (Hale <i>et al.</i> , 2011) |
| pBL12 | <i>cat repA^{ts} ftsA^{E124A}</i> | pSC101 ^{ts} | (Gerding <i>et al.</i> , 2009) |
| pBL93 | <i>bla lacI^q P_{lac}::gfp-ftsN^{E81K}</i> | ColE1 | This work |
| pBL94 | <i>bla lacI^q P_{lac}::gfp-ftsN^{Y85R}</i> | ColE1 | This work |
| pBL100 | <i>bla lacI^q P_{lac}::gfp-ftsN^{K87E}</i> | ColE1 | This work |
| pBL114 | <i>bla lacI^q P_{T7}::gfp-ftsN^{+A102}</i> | ColE1 | This work |
| pBL115 | <i>bla lacI^q P_{T7}::gfp-ftsN^{T64G, S67G, +A102}</i> | ColE1 | This work |
| pBL116 | <i>bla lacI^q P_{lac}::gfp-ftsN^{T64G, S67G, +A102}</i> | ColE1 | This work |
| pBL116 (Y85W) | <i>bla lacI^q P_{lac}::gfp-ftsN^{T64G, S67G, Y85W, +A102}</i> | ColE1 | This work |
| pBL116 (W83L) | <i>bla lacI^q P_{lac}::gfp-ftsN^{T64G, S67G, W83L, +A102}</i> | ColE1 | This work |
| pBL116 (L89S) | <i>bla lacI^q P_{lac}::gfp-ftsN^{T64G, S67G, L89S, +A102}</i> | ColE1 | This work |
| pBL116 (W83M) | <i>bla lacI^q P_{lac}::gfp-ftsN^{T64G, S67G, W83M, +A102}</i> | ColE1 | This work |
| pBL116 (L89H) | <i>bla lacI^q P_{lac}::gfp-ftsN^{T64G, S67G, L89H, +A102}</i> | ColE1 | This work |
| pBL120 | <i>bla lacI^q P_{lac}::gfp-ftsI</i> | ColE1 | This work |
| pBL136 | <i>bla lacI^q P_{lac}::gfp-ftsN^{Δ(64-101)<>22}</i> | ColE1 | This work |
| pBL138 | <i>cat araC P_{BAD}::rfp-malF²⁻³⁹-ftsN⁵⁵⁻¹²³</i> | pACYC | This work |
| pBL141 | <i>cat araC P_{BAD}::rfp-ftsN¹⁻¹⁰⁵-le</i> | pACYC | This work |

| | | | |
|--------|--|----------------------|-----------|
| pBL142 | <i>cat araC</i> P _{BAD} :: <i>rfp-ftsN</i> ¹⁻⁹⁰ | pACYC | This work |
| pBL143 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{Δ(64-101)<>(SphI_XhoI-stuffer)} | ColE1 | This work |
| pBL145 | <i>aadA cl857</i> P _R :: <i>ftsN</i> ¹⁻⁹⁰ | pSC101 | This work |
| pBL147 | <i>attHK022 bla lacI</i> ^q P _{lac} :: <i>gfp-ftsI</i> | R6K | This work |
| pBL153 | <i>aadA</i> P _{syn135} :: <i>ftsN</i> | pSC101 | This work |
| pBL154 | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>ftsN</i> | pSC101 ^{ts} | This work |
| pBL160 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{Y85S} | ColE1 | This work |
| pBL161 | <i>attHK022 bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{Y85S} | R6K | This work |
| pBL163 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{W83F} | ColE1 | This work |
| pBL165 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{Y85F} | ColE1 | This work |
| pBL180 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{W83T} | ColE1 | This work |
| pBL181 | <i>attHK022 bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{W83T} | R6K | This work |
| pBL190 | <i>aadA Scel cl857</i> P _R :: <i>ftsN</i> ¹⁻⁹⁰ | pSC101 | This work |
| pBL191 | <i>aadA Scel cl857</i> P _R :: <i>scel</i> | pSC101 | This work |
| pBL193 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsB</i> | ColE1 | This work |
| pBL194 | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>gfp-ftsB</i> | pSC101 ^{ts} | This work |
| pBL195 | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>gfp-ftsL</i> | pSC101 ^{ts} | This work |
| pBL200 | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>ftsN Scel</i> <i>cl857</i> P _R :: <i>i-scel</i> | pSC101 ^{ts} | This work |
| pBL203 | <i>bla lacI</i> ^q P _{T7} :: <i>gfp-ftsN</i> ^{Δ(59-73)<>6} | ColE1 | This work |
| pBL205 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{Δ(59-73)<>6} | ColE1 | This work |
| pBL206 | <i>tetA repA</i> ^{ts} <i>ftsA</i> ^{E124A} | pSC101 ^{ts} | This work |
| pBL209 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> :: ^G <i>lacZYA</i> | F | This work |
| pBL210 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{Δ(59-73)<>95} | ColE1 | This work |
| pBL211 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{Δ(59-73)<>15} | ColE1 | This work |
| pBL215 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{T64G, S67G, Y85W, +A102} :: ^G <i>lacZYA</i> | F | This work |
| pBL216 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{T64G, S67G, W83L, +A102} :: ^G <i>lacZYA</i> | F | This work |
| pBL217 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{T64G, S67G, L89S, +A102} :: ^G <i>lacZYA</i> | F | This work |
| pBL218 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{T64G, S67G, W83M, +A102} :: ^G <i>lacZYA</i> | F | This work |
| pBL219 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{T64G, S67G, L89H, +A102} :: ^G <i>lacZYA</i> | F | This work |

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| pBL222 | <i>cat araC</i> P _{BAD} :: <i>ftsL</i> | pACYC | This work |
| pBL225 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{Y85S..G} <i>lacZYA</i> | F | This work |
| pBL226 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{W83T..G} <i>lacZYA</i> | F | This work |
| pBL236 | <i>cat repA</i> ^{ts} <i>ftsA</i> ^{L143L} | pSC101 ^{ts} | This work |
| pBL289 | <i>bla lacI^q</i> P _{T7} :: <i>ftsB</i> | ColE1 | This work |
| pBL294 | <i>bla lacI^q</i> P _{lac} :: <i>ftsB</i> | ColE1 | This work |
| pBL295 | <i>bla lacI^q</i> P _{lac} :: <i>ftsL</i> | ColE1 | This work |
| pBL300 | <i>attHK022 bla lacI^q</i> P _{lac} :: <i>ftsB</i> ^{D59H} | R6K | This work |
| pBL301 | <i>bla lacI^q</i> P _{lac} :: <i>ftsL</i> ^{D93G} | ColE1 | This work |
| pBL303 | <i>aadA</i> P _{syn135} :: <i>ftsL</i> ^{D93G} | pSC101 | This work |
| pBL304 | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>ftsB</i> ^{D59H} | pSC101 ^{ts} | This work |
| pBL305 | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>ftsL</i> ^{D93G} | pSC101 ^{ts} | This work |
| pBL306 (E56A) | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>ftsB</i> ^{E56A} <i>ispD</i> ¹⁻⁴⁸ | pSC101 ^{ts} | This work |
| pBL306 (E56K) | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>ftsB</i> ^{E56K} <i>ispD</i> ¹⁻⁴⁸ | pSC101 ^{ts} | This work |
| pBL306 (D59H) | <i>aadA repA</i> ^{ts} P _{syn135} :: <i>ftsB</i> ^{D59H} <i>ispD</i> ¹⁻⁴⁸ | pSC101 ^{ts} | This work |
| pBL309 | <i>aadA</i> P _{syn135} :: <i>ftsL</i> | pSC101 | This work |
| pBL312 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-malF</i> ²⁻¹⁴ - <i>ftsN</i> ²⁷⁻⁸¹ - <i>le</i> | ColE1 | This work |
| pBL313 | <i>cat araC</i> P _{BAD} :: <i>rfp-malF</i> ²⁻³⁹ - <i>ftsN</i> ⁵⁵⁻¹⁰⁵ - <i>le</i> | pACYC | This work |
| pBL315 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-malF</i> ²⁻³⁹ - <i>ftsN</i> ⁵⁵⁻⁸¹ - <i>le</i> | ColE1 | This work |
| pBL321 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{L75A} | ColE1 | This work |
| pBL322 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{P76A} | ColE1 | This work |
| pBL323 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{P77A} | ColE1 | This work |
| pBL324 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{K78A} | ColE1 | This work |
| pBL325 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{P79A} | ColE1 | This work |
| pBL326 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{E80A} | ColE1 | This work |
| pBL327 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{R84A} | ColE1 | This work |
| pBL328 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{L89A} | ColE1 | This work |
| pBL329 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{E90A} | ColE1 | This work |
| pBL330 | <i>bla lacI^q</i> P _{lac} :: <i>gfp-ftsN</i> ^{D5S,Y6A} | ColE1 | This work |
| pBL331 | <i>tetA</i> P _{syn135} :: <i>ftsL</i> ^{H94Y} | pSC101 | This work |
| pBL332 | <i>tetA</i> P _{syn135} :: <i>ftsL</i> ^{E88V} | pSC101 | This work |
| pBL333 | <i>tetA</i> P _{syn135} :: <i>ftsL</i> ^{E88K} | pSC101 | This work |

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| pBL334 | <i>tetA</i> P _{syn135} :: <i>ftsL</i> ^{N89S} | pSC101 | This work |
| pBL335 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ^{1-81; D5S,Y6A} - <i>le</i> | ColE1 | This work |
| pBL336 | <i>tetA</i> P _{syn135} :: <i>ftsB</i> | pSC101 | This work |
| pBL338 | <i>tetA</i> P _{syn135} :: <i>ftsB</i> ^{E56V} | pSC101 | This work |
| pBL339 | <i>tetA</i> P _{syn135} :: <i>ftsB</i> ^{E56A} | pSC101 | This work |
| pBL340 | <i>tetA</i> P _{syn135} :: <i>ftsB</i> ^{A55T} | pSC101 | This work |
| pBL341 | <i>tetA</i> P _{syn135} :: <i>ftsB</i> ^{E56K} | pSC101 | This work |
| pBL342 | <i>tetA</i> P _{syn135} :: <i>ftsB</i> ^{E56G} | pSC101 | This work |
| pBL343 | <i>tetA</i> P _{syn135} :: <i>ftsB</i> ^{D59V} | pSC101 | This work |
| pBL356 | <i>bla Scel</i> P _{syn135} :: <i>ftsB</i> ^{E56K} <i>ispD</i> ¹⁻⁴⁸ <i>Scel sacB</i> | ColE1 | This work |
| pBT3-N | <i>aph leu2</i> P _{CYC1} :: <i>lexA-vp16-cub-</i> | ColE1, CEN | Dualsystems Biotech |
| pCH38 | <i>bla lacI</i> ^q P _{T7} :: <i>zipA-h</i> | ColE1 | (Hale <i>et al.</i> , 2000) |
| pCH181 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-minD minE-le</i> | ColE1 | (Bendezu & de Boer, 2008) |
| pCH195 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsL</i> | ColE1 | (Hale & de Boer, 2002) |
| pCH198 | <i>bla lacI</i> ^q P _{T7} :: <i>gfp-ftsN</i> | ColE1 | (Hale & de Boer, 2002) |
| pCH201 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> | ColE1 | (Hale & de Boer, 2002) |
| pCH276 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ¹⁻¹²³ | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pCH277 | <i>bla lacI</i> ^q P _{lac} :: <i>amiC</i> ¹⁻³¹ - <i>ftsN</i> ⁵²⁻¹²³ - <i>gfp</i> | ColE1 | This work |
| pCH282 | <i>bla lacI</i> ^q P _{lac} :: ^{ss} <i>torA-gfp-ftsN</i> ⁵⁵⁻³¹⁹ | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pCH286 | <i>bla lacI</i> ^q P _{lac} :: <i>amiC</i> ¹⁻³¹ - <i>ftsN</i> ⁵²⁻¹²³ | ColE1 | This work |
| pCH287 | <i>aadA cl857</i> P _R :: <i>amiC</i> ¹⁻³¹ - <i>ftsN</i> ⁵²⁻¹²³ | pSC101 | This work |
| pCH288 | <i>bla lacI</i> ^q P _{lac} :: ^{ss} <i>torA-gfp-ftsN</i> ⁵⁵⁻¹²³ | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pCH309 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-malF</i> ²⁻³⁹ - <i>mreC</i> ³⁸⁻³⁶⁷ - <i>le</i> | ColE1 | This work |
| pCH310 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-malF</i> ²⁻³⁹ - <i>ftsN</i> ⁵⁵⁻¹²³ | ColE1 | This work |
| pCH327 | <i>aph leu2</i> P _{CYC1} :: <i>lexA-vp16-cub-ftsN</i> ¹⁻¹⁰⁵ | ColE1, CEN | This work |
| pCH354 | <i>bla lacI</i> ^q P _{lac} :: <i>gfp-ftsN</i> ¹⁻²⁴³ - <i>le</i> | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pCH358 | <i>aph</i> P _{lac} :: <i>t25-rodZ</i> | pACYC | (Bendezu <i>et al.</i> , 2009) |
| pCH362 | <i>aadA</i> P _{syn135} :: <i>gfp-zapA</i> | pSC101 | (Bendezu <i>et al.</i> , |

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| pCH371 | <i>bla lacI^q P_{lac}::t18-rodZ</i> | ColE1 | 2009) (Bendezu et al., 2009) |
| pCH391 | <i>aph P_{lac}::t25-ftsN¹⁻¹⁰⁵</i> | pACYC | This work |
| pCH391 (DY>SA) | <i>aph P_{lac}::t25-ftsN¹⁻¹⁰⁵; D5S,Y6A</i> | pACYC | This work |
| pCH392 | <i>bla lacI^q P_{lac}::t18-ftsN¹⁻¹⁰⁵</i> | ColE1 | This work |
| pCH392 (DY>SA) | <i>bla lacI^q P_{lac}::t18-ftsN¹⁻¹⁰⁵; D5S,Y6A</i> | ColE1 | This work |
| pCH399 | <i>bla lacI^q P_{lac}::t18-ftsA</i> | ColE1 | This work |
| pCH400 | <i>bla lacI^q P_{lac}::t18-ftsQ</i> | ColE1 | This work |
| pCH425 | <i>bla lacI^q P_{lac}::t18-ftsB</i> | ColE1 | This work |
| pCH433 | <i>aph P_{lac}::t25-ftsI</i> | pACYC | This work |
| pCP20 | <i>bla cat repA^{ts} cl857 P_R::flp</i> | pSC101 ^{ts} | (Cherepanov & Wackernagel, 1995) |
| pDB326 | <i>aadA repA^{ts}</i> | pSC101 ^{ts} | (Hale & de Boer, 1997) |
| pDB344 | <i>aadA cl857 P_R::</i> | pSC101 | (Raskin & de Boer, 1997) |
| pDB357 | <i>bla lacI^q P_{T7}::ftsN</i> | ColE1 | This work |
| pDOC-C | <i>bla <u>Scel</u> <u>Scel</u> sacB</i> | ColE1 | (Lee et al., 2009) |
| pET21A | <i>bla lacI^q P_{T7}::</i> | ColE1 | Novagen |
| pFB243 | <i>bla lacI^q P_{lac}::malF¹⁻³⁹-mreC³⁸⁻³⁶⁷</i> | ColE1 | (Bendezu et al., 2009) |
| pFB261 | <i>bla lacI^q P_{lac}::gfp-malF²⁻¹⁴-rodZ¹¹¹⁻³¹⁹</i> | ColE1 | (Bendezu et al., 2009) |
| pJH1 | <i>tetA repA^{ts} P_{syn135}::ftsL</i> | pSC101 ^{ts} | This work |
| pJH2 | <i>tetA P_{syn135}::ftsL</i> | pSC101 | This work |
| pJH3 | <i>tetA P_{syn135}::ftsL^{D93G}</i> | pSC101 | This work |
| pJH5 | <i>bla lacI^q P_{lac}::gfp-malF²⁻³⁹- ftsN⁵⁵⁻³²⁰; T64G, S67G, Y85W, +A102</i> | ColE1 | This work |
| pJH6 | <i>bla lacI^q P_{lac}::gfp-malF²⁻³⁹- ftsN⁵⁵⁻³²⁰; T64G, S67G, W83L, +A102</i> | ColE1 | This work |
| pJH10 | <i>bla lacI^q P_{lac}::gfp-malF²⁻³⁹- ftsN⁵⁵⁻³²⁰; T64G, S67G, Y85W, +A102..G</i> <i>::lacZYA</i> | F | This work |

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| pJH11 | <i>bla lacI^q P_{lac}::gfp-malF²⁻³⁹-ftsN^{55-320; T64G, S67G, W83L, +A102,..G}lacZYA</i> | F | This work |
| pKD3 | <i>bla frt-cat-frt</i> | R6K | (Datsenko & Wanner, 2000) |
| pKD46 | <i>bla repA^{ts} araC P_{BAD}::γ β exo</i> | pSC101 ^{ts} | (Datsenko & Wanner, 2000) |
| pKNT25 | <i>aph P_{lac}::lacZ'-t25</i> | pACYC | (Karimova <i>et al.</i> , 2005) |
| pLP7 | <i>bla lacI^q P_{lac}::t18-ponA</i> | ColE1 | (van den Ent <i>et al.</i> , 2010) |
| pLP10 | <i>aph P_{lac}::t25-ponA</i> | pACYC | This work |
| pLP13 | <i>bla lacI^q P_{lac}::gfp-</i> | ColE1 | (van den Ent <i>et al.</i> , 2010) |
| pLP160 | <i>cat araC P_{BAD}::rfp-malF²⁻³⁹-ftsN⁵⁵⁻⁹⁰</i> | pACYC | This work |
| pLP163 | <i>bla lacI^q P_{lac}::gfp-ftsN</i> | ColE1 | This work |
| pLP164 | <i>bla lacI^q P_{lac}::gfp-ftsN⁷⁵⁻¹⁰⁵-le</i> | ColE1 | This work |
| pLP165 | <i>bla lacI^q P_{lac}::gfp-ftsN⁸⁰⁻¹⁰⁵-le</i> | ColE1 | This work |
| pLP168 | <i>bla lacI^q P_{lac}::^{ss}torA-gfp-ftsN⁷⁵⁻¹⁰⁵-le</i> | ColE1 | This work |
| pLP169 | <i>bla lacI^q P_{lac}::^{ss}torA-gfp-ftsN⁸⁰⁻¹⁰⁵-le</i> | ColE1 | This work |
| pLP170 | <i>bla lacI^q P_{lac}::gfp-ftsN¹⁻³¹-malF¹⁷⁻³⁹-ftsN⁵⁵⁻⁸¹-le</i> | ColE1 | This work |
| pLP171 | <i>bla lacI^q P_{lac}::gfp-ftsN¹⁻⁷¹-le</i> | ColE1 | This work |
| pLP218 | <i>bla lacI^q P_{lac}::^{ss}torA-gfp-ftsN⁷⁵⁻⁹³-le</i> | ColE1 | This work |
| pLP219 | <i>bla lacI^q P_{lac}::^{ss}torA-gfp-ftsN⁷⁵⁻⁹⁹-le</i> | ColE1 | This work |
| pLP221 | <i>bla lacI^q P_{lac}::^{ss}torA-gfp-ftsN⁵⁵⁻⁹⁰</i> | ColE1 | This work |
| pMLB1113 | <i>bla lacI^q P_{lac}::lacZ</i> | ColE1 | (de Boer <i>et al.</i> , 1989) |
| pMLB1113ΔH | <i>bla lacI^q P_{lac}::</i> | ColE1 | (Gerding <i>et al.</i> , 2007) |
| pMLB1115 | <i>bla lacI^q P_{lac}::lacZ</i> | ColE1 | (de Boer <i>et al.</i> , 1989) |
| pMG12 | <i>bla lacI^q P_{lac}::gfp-ftsN¹⁻¹⁰⁵-le</i> | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pMG13 | <i>bla lacI^q P_{lac}::gfp-ftsN¹⁻⁸¹-le</i> | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pMG14 | <i>bla lacI^q P_{lac}::^{ss}torA-gfp-ftsN⁷¹⁻¹⁰⁵-le</i> | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pMG21 | <i>bla lacI^q P_{lac}::ftsN</i> | ColE1 | This work |
| pMG47 | <i>bla lacI^q P_{lac}::gfp-ftsN¹⁻⁹⁰</i> | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pMG50 | <i>bla lacI^q P_{lac}::^{ss}torA-gfp-ftsN⁷¹⁻⁹⁰</i> | ColE1 | (Gerding <i>et al.</i> , 2009) |
| pMG59 | <i>attHK022 bla lacI^q P_{lac}::gfp-ftsN</i> | R6K | (Gerding <i>et al.</i> , 2009) |
| pMG62 | <i>attHK022 bla lacI^q P_{lac}::gfp-ftsN¹⁻¹²³</i> | R6K | This work |

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| pRC7 | <i>bla lacI^f P_{lac}::galk¹⁻⁵⁴-lacZ¹⁰⁻¹⁰²⁴ lacY lacA</i> [~P _{lac} :: ^G <i>lacZYA</i>] | F | (de Boer et al., 1989) |
| pTB8 | <i>bla lacI^f P_{lac}::minCDE::^GlacZYA</i> | F | (Bernhardt & de Boer, 2004) |
| pTB37 | <i>bla lacI^f P_{lac}::amiC¹⁻³¹-gfp</i> | ColE1 | (Bernhardt & de Boer, 2003) |
| pTB51 | <i>cat repA^{ts} araC P_{BAD}::γ β exo</i> | pSC101 ^{ts} | This work |
| pTB222 | <i>attHK022 bla lacI^f P_{lac}::zipA-gfp</i> | R6K | (Bendezu et al., 2009) |
| pZAQ | <i>tetA ftsQ ftsA ftsZ</i> | ColE1 | (Ward & Lutkenhaus, 1985) |
| pZC100 | <i>aadA</i> | pSC101 | (Wang et al., 1991) |

Genotypes indicate when constructs encode in-frame Gfpmut2 (*gfp*), mCherry (*rfp*), hexahistidine (*h*), Leu-Glu dipeptide (*le*), CyaA T18-domain (*t18*), CyaA T25-domain (*t25*), or the signal peptide of TorA (^{ss}*torA*). Scel indicates the presence of a substrate site for the I-SceI homing endonuclease. ^G*lacZ* refers to a *galk¹⁻⁵⁴-lacZ¹⁰⁻¹⁰²⁴* fusion in which the first 10 residues of LacZ are replaced with the first 54 residues of GalK (Koop et al., 1987).

Strain construction:

Construction of strains involved P1-mediated transduction (transduction for short) (Miller, 1992), λRed-mediated recombineering (Datsenko & Wanner, 2000, Yu et al., 2000), Gene doctoring (Lee et al., 2009), Flp-mediated eviction of antibiotic cassettes (Cherepanov & Wackernagel, 1995), replacement of chromosomal genes using plasmids that are temperature sensitive for replication (Hamilton et al., 1989), and other methods specified below or elsewhere in the text.

BL17 [*leu*::Tn10] was obtained by transduction of *leu*::Tn10 from SG13109 to TB28.

BL19 [*ftsA*^{E124A} *leu*::Tn10] was obtained by transduction of *leu*::Tn10 from SG13109 to BL18. Retention of *ftsA*^{E124A} was verified by the presence of a diagnostic FspI site on a fragment that was amplified from BL19 chromosomal DNA using primers 5'-CCGCTCTTCCGGTATGATCAAGGCGACGGACAG-3' and 5'-_CCTCACTCGAGTTAAACTCTTTTCGCAGC-3'.

For BL23 and BL24 [*ponB*<>*cat*], the *cat* cassette of pKD3 was amplified with primers 5'-AAATCGGGCTTTTGC GCCTGAATATTGCGGAGAAAAAGCCCATATGAATATCCTCCTTAG-3' and 5'-ATGGCAACTCGCCATCCGGTATTTACGCTTAGATGTTAGTGTAGGCTGGAGCTGCTTCG-3', yielding a 1093 bp fragment with end sequences homologous to the chromosomal *ponB* locus (underlined). Recombination with the chromosome of TB10 yielded BL23 [*ponB*<>*cat*], in which 2538 bp of the *ponB* gene (from bp +1 to bp +2538) is replaced with *cat* and transcription of the latter is in the same direction as the replaced gene. Transduction of *ponB*<>*cat* from BL23 to TB28 resulted in BL24.

For BL71/pCH288 [*ftsN*<>*cat*/P_{lac}::^{ss}*torA-gfp-ftsN*⁵⁵⁻¹²³], the *cat* cassette of pKD3 was amplified with primers 5'-CGGTTTCTCCCGCTATGGTCGCTATTGCTGCCGCCGTTCTTGTGCCATATGAATATCCTCCTTAG-3' and 5'-TCCAGCCATTGTTGGTGGTGATTTTCGAGTCAAAGCCTTCGTGTAGGCTGGAGCTGCTTCG-3', yielding a 1099 bp fragment with end sequences homologous to the chromosomal *ftsN* locus (underlined). Recombination with the chromosome of TB10/pCH288 in the presence of 250 μM IPTG yielded BL71/pCH288, in which 673 bp of the *ftsN* gene (from bp +136 to bp +809) is replaced with *cat* and transcription of the latter is in the same direction as the replaced gene.

BL79 [*ponA*<>*aph*] was obtained by transduction of *ponA*<>*aph* from JW3359 to TB28.

BL84(iMG62) [Δ *ponB ftsN*^{slm117}(P_{lac}::*gfp-ftsN*¹⁻¹²³)] was obtained by transduction of *ponB*<>*cat* from BL23 to TB77(iMG62) in the presence of 500 μM IPTG.

BL85/pBL200 [*leu*::Tn10 *ftsN*<>*aph* / *aadA repA*^{ts} P_{syn135}::*ftsN* Scel *cl857* P_R::*i-sceI*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL17/pBL200 at 30°C.

BL86/pBL200 [*leu*::Tn10 *ftsN*<>*aph* *recA*::*cat* / *aadA repA*^{ts} P_{syn135}::*ftsN* Scel *cl857* P_R::*i-sceI*] was obtained by transduction of *recA*::*cat* from BW10724 to BL85/pBL200 at 30°C.

BL86-AK1, BL86-AK11, BL86-AK12, and BL86-KK1 were obtained as described in the text.

BL105 [*ponA*<>*frt ftsN*^{slm117}] was obtained by transduction of *ftsN*::EZTnKan-2 [= *ftsN*^{slm117}] from TB77 to CH82.

For BL114 [*ftsA*^{I143L}], TB28 chromosomal *ftsA* was exchanged with the *ftsA*^{I143L} allele on pBL236 [*repA*^{ts} *ftsA*^{I143L}] by the method of Hamilton et al (Hamilton et al., 1989). To verify the presence and integrity of *ftsA*^{I143L} in BL114, chromosomal DNA was amplified using primers 5'-CCGCTCTTCCGGTATGATCAAGGCGACGGACAG-3' and 5'-CCTCACTCGAGTTAAAACCTTTTTTCGCAGC-3', and the *ftsA*^{I143L} gene present on the resulting fragment was sequenced.

BL120/pX [*ftsA*^{I143L} *ftsN*<>*aph* /] strains were obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL114/pX in the presence of inducer if so required.

For BL140 [*ftsB*^{D59H}], TB28 chromosomal *ftsB* was exchanged with the *ftsB*^{D59H} allele on pBL306(D59H) [*repA*^{ts} P_{syn135}::*ftsB*^{D59H} *ispD*¹⁻⁴⁸] by the method of Hamilton et al (Hamilton et al., 1989). To verify the presence and integrity of *ftsB*^{D59H} in BL140, chromosomal DNA was amplified using primers 5'-CGCATATGGGTAAACTAACGCTGCTGTTGC-3' and 5'-GCGTCGACTTAATGCGCCAGCAGCGCATGCACCG-3', and the *ftsB*^{D59H} gene present on the resulting fragment was sequenced.

BL141/pX [*ftsB*^{D59H} *ftsN*<>*aph* /] strains were obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL140/pX in the presence of inducer if so required.

BL148 [*ftsA*^{I143L} *leu*::Tn10] was obtained by transduction of *leu*::Tn10 from SG13109 to BL114. Retention of *ftsA*^{I143L} was verified by the presence of a diagnostic SmlI site on a fragment that was amplified from BL148 chromosomal DNA using primers 5'-CCGCTCTTCCGGTATGATCAAGGCGACGGACAG-3' and 5'-CCTCACTCGAGTTAAAACCTTTTTTCGCAGC-3'.

BL149 [*ftsB*^{D59H} *ftsA*^{I143L} *leu*::Tn10] was obtained by co-transduction of *leu*::Tn10 and *ftsA*^{I143L} from BL148 to BL140. The presence of *ftsA*^{I143L} was verified as for BL148.

BL150 [*ftsB*^{D59H} *ftsA*^{I143L} *leu*::Tn10 *ftsN*<>*aph*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL149.

BL151 [*ftsB*^{D59H} *ftsA*^{E124A} *leu*::Tn10] was obtained by co-transduction of *leu*::Tn10 and *ftsA*^{E124A} from BL19 to BL140. The presence of *ftsA*^{E124A} was verified as for BL19.

BL152 [*ftsB*^{D59H} *ftsA*^{E124A} *leu*::Tn10 *ftsN*<>*aph*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL151.

For BL153/pBL215 [*leu*::Tn10 *ftsL*^{D93G} *ftsN*<>*aph* / *bla lacI*^q P_{lac}::*gfp-ftsN*^{Y85W}], a portion of pBL305 [P_{syn135}::*ftsL*^{D93G}] was amplified with primers 5'- CCGAATTCCATATGATCAGCAGAGTGACAG-3' and 5'- CGTGTGCGACTTATTTTTGCACTACGAT-3', yielding a 386 bp *ftsL*^{D93G} fragment largely homologous to native chromosomal *ftsL* (underlined). Recombination with the chromosome of BL85/pBL200/pBL215/pTB51 and growth at 37°C, to cure both pBL200 [*aadA repA*^{ts} P_{syn135}::*ftsN* *Scel* *cI857* P_R::*i-sceI*] and pTB51 [*repA*^{ts} *cat araC* P_{BAD}::*γ β exo*], in the presence of ampicillin and 100 μM IPTG yielded BL153/pBL215.

BL154 [*leu*::Tn10 *ftsL*^{D93G}] was obtained by co-transduction of *leu*::Tn10 and *ftsL*^{D93G} from BL153/pBL215 to TB28. To verify the presence and integrity of *ftsL*^{D93G} in BL154, chromosomal DNA was amplified using primers 5'- GATCGGCCATTACGGCCATGATCAGCAGAGTGACAGAAGC-3' and 5'- GCGTCGACTTAAACTTGTAACCACGCTACGCGTCC-3', and the *ftsL*^{D93G} gene present on the resulting fragment was sequenced.

BL155/pX [*ftsB*<>*aph* /] strains were obtained by transduction of *ftsB*<>*aph* from NB946 to TB28/pX in the presence of inducer if so required.

BL156/pX [*ftsL*<>*aph* /] strains were obtained by transduction of *ftsL*<>*aph* from MDG277 to TB28/pX in the presence of inducer if so required.

BL157/pX [*leu*::Tn10 *ftsL*^{D93G} *ftsN*<>*aph* /] strains were obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL154/pX in the presence of inducer if so required.

BL159 [*leu*::Tn10 *ftsL*^{D93G} *ftsB*^{D59H}] was obtained by co-transduction of *leu*::Tn10 and *ftsL*^{D93G} from BL154 to BL140. The presence of *ftsL*^{D93G} was verified by the presence of a diagnostic *Hae*III site on a fragment that was amplified from BL159 chromosomal DNA using primers 5'- GATCGGCCATTACGGCCATGATCAGCAGAGTGACAGAAGC-3' and 5'- GCGTCGACTTAAACTTGTAACCACGCTACGCGTCC-3'.

BL163 [*leu*::Tn10 *ftsL*^{D93G} *ftsB*^{D59H} *ftsN*<>*aph*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL159. The presence and integrity of native *ftsA* in this strain was verified by amplification of a 2153 bp fragment of BL163 chromosomal DNA using primers 5'-

GTAGTACGAATTCTGGAAGTGGCGGAC-3' and 5'- ACTCGTCGACATCATCGTCGGCCTC-3', followed by nucleotide sequencing of the entire *ftsA* gene on the fragment.

BL164 [*leu*::Tn10 *ftsL*^{D93G} *ftsA*^{I143L}] was obtained by co-transduction of *leu*::Tn10 and *ftsL*^{D93G} from BL154 to BL114. The presence of both *ftsL*^{D93G} and *ftsA*^{I143L} was verified as for BL159 and BL148, respectively.

BL165 [*leu*::Tn10 *ftsL*^{D93G} *ftsA*^{I143L} *ftsN*<>*aph*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL164.

For BL167 [*ftsB*^{E56A}], TB28 chromosomal *ftsB* was exchanged with the *ftsB*^{E56A} allele on pBL306(E56A) [*repA*^{ts} P_{syn135}::*ftsB*^{E56A} *ispD*¹⁻⁴⁸] by the method of Hamilton et al (Hamilton et al., 1989). The presence and integrity of *ftsB*^{E56A} in BL167 was verified by sequencing, as described for BL140.

For BL172 [*ftsB*^{E56K}], the *ftsB*^{E56K} allele of pBL356 [*bla* Scel P_{syn135}::*ftsB*^{E56K} *ispD*¹⁻⁴⁸ Scel *sacB*] was amplified with primers 5'-
GTCGTCTTCGGATGCATGGGATGATGATGCCGTTTTTCAGGGGGCAGGATGGGTAAACTAACGCTGCTGTTGC -3' and 5'- GCGTCGACTTAATGCGCCAGCAGCGCATGCACCG-3', yielding a 533 bp *ftsB*^{E56K} fragment largely homologous to native chromosomal *ftsB* (underlined). This fragment was recombined with the chromosomal *ftsB*<>*aph* allele of BL155/pBL356/pACBSCE [*ftsB*<>*aph* / *bla* Scel P_{syn135}::*ftsB*^{E56K} *ispD*¹⁻⁴⁸ Scel *sacB* / Scel *cat* *araC* P_{BAD}::*i-scel* γ β *exo*] with selection for growth on LB containing 5% sucrose, to counterselect for pBL356, and for sensitivity to kanamycin, chloramphenicol and ampicillin. The presence and integrity of *ftsB*^{E56K} in BL172 was verified by sequencing, as described for BL140.

BL173 [*ftsB*^{E56A} *ftsN*<>*aph*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL167. The integrity of native *ftsA* in this strain was verified by nucleotide sequencing as described for BL163. The integrity of native *ftsL* was verified by amplification of a 601 bp fragment of BL173 chromosomal DNA using primers 5'-
GGTCTAGAGGTGGCTGAGAACCCTCGTGCC-3' and 5'-
GCGTCGACTTAACTTGTAACCACGCTACGCGTCC-3', followed by nucleotide sequencing of the *ftsL* gene on the fragment.

BL175 [*ftsB*^{E56K} *ftsN*<>*aph*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to BL172. The integrity of native *ftsA* and *ftsL* in this strain was verified by nucleotide sequencing as described for BL163 and BL173, respectively.

CH34/pBL200 [*ftsN*<>*aph* / *aadA repA*^{ts} P_{syn135}::*ftsN* Scel *cI857* P_R::*i-sceI*] was obtained by transduction of *ftsN*<>*aph* from CH34/pCH201 to TB28/pBL200.

CH82 [*ponA*<>*frt*] was obtained by eviction of *aph* from BL79, using pCP20.

JH1/pBL200 [*ftsN*<>*aph* *recA*::*cat* / *aadA repA*^{ts} P_{syn135}::*ftsN* Scel *cI857* P_R::*i-sceI*] was obtained by transduction of *recA*<>*cat* from BW10724 to CH34/pBL200.

LP31 [*recA*<>*aph*] was obtained by transduction of *recA*<>*aph* from JW2669 to TB28.

Plasmid construction:

Unless indicated otherwise, MG1655 or TB28 chromosomal DNA was used as template in amplification reactions. Sites of interest (e.g. relevant restriction sites, those allowing for targeted recombination, or site-directed mutations) are underlined in primer sequences. When plasmids construction involved PCR amplification and/or mutagenesis, the nucleotide sequence of plasmid inserts was verified.

For pAB12 [P_{T7}::*ftsL*], *ftsL* was amplified with primers 5'-CCGAATTCCATATGATCAGCAGAGTGACAG-3' and 5'-CGTGTCGACTTATTTTTGCACTACGAT-3', and the 368 bp *NdeI-SalI* fragment of the product was used to replace the 57 bp *NdeI-SalI* fragment of pET21A [P_{T7}:::].

For pBL93 [P_{lac}::*gfp-ftsN*^{E81K}], pMG59 [P_{lac}::*gfp-ftsN*] was mutagenized using 5'-GGACTACCACCAAACCAGAAAGCGCTGGCGCTACATTAAAGAG-3' and its reverse complement. The 973 bp *BamHI-HindIII* fragment of pMG59(E81K) was next used to replace the equivalent fragment of pCH201 [P_{lac}::*gfp-ftsN*].

For pBL94 [P_{lac}::*gfp-ftsN*^{Y85R}], pMG59 [P_{lac}::*gfp-ftsN*] was mutagenized using 5'-CCAGAAGAACGCTGGCGCATTAAGAGCTGGAAAG-3' and its reverse complement. The 973 bp

*Bam*HI-*Hind*III fragment of pMG59(Y85R) was next used to replace the equivalent fragment of pCH201 [P_{lac}::*gfp-ftsN*].

For pBL100 [P_{lac}::*gfp-ftsN*^{K87E}], pMG59 [P_{lac}::*gfp-ftsN*] was mutagenized using 5'-GAACGCTGGCGCTACATTGAAGAGCTGGAAAGTCGCC-3' and its reverse complement. The 973 bp *Bam*HI-*Hind*III fragment of pMG59(K87E) was next used to replace the equivalent fragment of pCH201 [P_{lac}::*gfp-ftsN*].

For pBL114 [P_{T7}::*gfp-ftsN*^{+A102}], one portion of pCH201 [P_{lac}::*gfp-ftsN*] was amplified with primers 5'-CAGCGAATTCCATATGGCACAACGAGATTATG-3' and 5'-CAGGCCGAAGGGCCCTCTGTGGGCGCACGCACTCCCGG-3' and digested with *Eco*RI and *Sfi*I, yielding a 318 bp fragment. A second portion was amplified with 5'-GTGAGGCCCTTCGGCCGGTGGTGAAGTGAAAACGCCG-3' and 5'-TGAGAAGCTTAACCCCGCGGCGAG-3' and digested with *Sfi*I and *Hind*III, yielding a 652 bp fragment. The two fragments were then used in a three-way ligation with the 6119 bp *Eco*RI-*Hind*III fragment of pCH198 [P_{T7}::*gfp-ftsN*]. pBL114 encodes a fully functional version of GFP-FtsN in which an alanine residue is inserted between residues 101 and 102.

For pBL115 [P_{T7}::*gfp-ftsN*^{T64G, S67G, +A102}], one portion of pCH201 [P_{lac}::*gfp-ftsN*] was amplified with primers 5'-CAGCGAATTCCATATGGCACAACGAGATTATG-3' and 5'-CTGGCCTTGCAGGCCCTCGGACTCTTCTTTCTTGTGATG-3' and digested with *Eco*RI and *Sfi*I, yielding a 205 bp fragment. A second portion was amplified with 5'-GTGGCCTGCAAGGCCAGAAAGTGACCGGAAACGG-3' and 5'-CAGGCCGAAGGGCCCTCTGTGGGCGCACGCACTCCCGG-3' and digested with *Sfi*I, yielding a 113 bp fragment. The two fragments were then used in a three-way ligation with the 6771 bp *Eco*RI-*Sfi*I fragment of pBL114 [P_{T7}::*gfp-ftsN*^{+A102}]. pBL115 encodes a fully functional version of GFP-FtsN in which an alanine residue is inserted between residues 101 and 102, and residues 64-67 (TLQS) have been replaced with GLQG. In addition, pBL115 contains two unique *Sfi*I sites flanking codons 68-101.

For pBL116 [P_{lac}::*gfp-ftsN*^{T64G, S67G, +A102}], the 976 bp *Bam*HI-*Hind*III fragment of pBL115 [P_{T7}::*gfp-ftsN*^{T64G, S67G, +A102}] was used to replace the 973 bp *Bam*HI-*Hind*III fragment of pCH201 [P_{lac}::*gfp-ftsN*]. pBL116 encodes a fully functional version of GFP-FtsN in which an alanine residue is inserted between residues 101 and 102, and residues 64-67 (TLQS) have been replaced with GLQG. In addition, pBL116 contains two unique *Sfi*I sites flanking codons 68-101.

Mutant derivatives of pBL116 were obtained by screening pBL116-based site-scanning libraries for derivatives that fail to rescue growth of strain CH31 [$P_{BAD}::ftsN$] in the absence of arabinose, as detailed in the Experimental Procedures.

For pBL120 [$P_{lac}::gfp-ftsI$], the 1780 bp *SfiI* fragment of pCH433 [$P_{lac}::t25-ftsI$] was used to replace the 16 bp *SfiI* fragment of pLP13 [$P_{lac}::gfp-$].

The construction of pBL131 [$P_{BAD}::rfp-dedD^{1-118}-le$] will be detailed elsewhere.

For pBL136 [$P_{lac}::gfp-ftsN^{\Delta(64-101)<>22}$], oligo 5'-
CGAGGGCCTGCAAGGCCAGAAAGTGACCGGAAACGGACTCGAGCCGGGAGTGCGTGCGCCACAGAGGCC
CTTCGGCCGGTG-3' and its reverse complement were annealed and the 62 bp *SfiI* fragment of the product was used to replace the 113 bp *SfiI* fragment of pBL116 [$P_{lac}::gfp-ftsN^{T64G, S67G, +A102}$]. In pBL136, *ftsN* codons 64-101 (TLQSQKVTGNGLPPKPEERWRYIKELESRQPGVRAPTE) are replaced by a *SfiI* fragment containing a unique *XhoI* site, and encoding an in-frame arbitrary peptide of 22 residues (GLQGQKVTGNGLPEPGVRAPTEA).

For pBL138 [$P_{BAD}::rfp-malF^{2-39}-ftsN^{55-123}$], a portion of pCH310 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-123}$] was amplified with primers 5'- GAGCTGTACAAAGCTAGCATGACTGGTG-3' and 5'- CTGGTTCGACAAAACGACGGCCAGTGCCAAGC-3', and the 377 bp *BsrGI-SalI* fragment was used to replace the 410 bp *BsrGI-SalI* fragment of pBL131 [$P_{BAD}::rfp-dedD^{1-118}-le$].

For pBL141 [$P_{BAD}::ecrfp-ftsN^{1-105}-le$], a portion of pMG12 [$P_{lac}::gfp-ftsN^{1-105}-le$] was amplified with primers 5'- GAGCTGTACAAAGCTAGCATGACTGGTG-3' and 5'- CTGGTTCGACAAAACGACGGCCAGTGCCAAGC-3', and the 371 bp *BsrGI-XhoI* fragment was used to replace the 401 bp *BsrGI-XhoI* fragment of pBL131 [$P_{BAD}::rfp-dedD^{1-118}-le$].

For pBL142 [$P_{BAD}::rfp-ftsN^{1-90}$], a portion of pMG47 [$P_{lac}::gfp-ftsN^{1-90}$] was amplified with primers 5'- GAGCTGTACAAAGCTAGCATGACTGGTG-3' and 5'- CTGGTTCGACAAAACGACGGCCAGTGCCAAGC-3', and the 320 bp *BsrGI-XhoI* fragment was used to replace the 401 bp *BsrGI-XhoI* fragment of pBL131 [$P_{BAD}::rfp-dedD^{1-118}-le$].

For pBL143 [$P_{lac}::gfp-ftsN^{\Delta(64-101)<>(SphI_XhoI-stuffer)}$], a portion of pCH201 [$P_{lac}::gfp-ftsN$] was amplified with primers 5'- CGAGGGCCTGCAAGGCCAGGCATGCAAAGTGACCGGAAACGGACTAC-3' and

5'- CACCGGCCGAAGGGGCTCGAGTGTGGGCGCACGCACTCCCGGC-3', and the 122 bp *SfiI* fragment of the 143 bp product was used to replace the 113 bp *SfiI* fragment of pBL116 [$P_{lac}::gfp-ftsN^{T64G, S67G, +A102}$]. In pBL143, *ftsN* codons 64-101 are replaced by a non-coding *SfiI* fragment containing unique *SphI* and *XhoI* sites. The plasmid was used to facilitate directional cloning of 113 bp *SfiI* mutant site scanning library fragments to generate pBL116 derivatives encoding GFP-FtsN variants with single amino acid substitutions within the FtsN⁸⁰⁻⁹³ interval.

For pBL145 [$cI857 P_{iR}::ftsN^{1-90}$], a portion of pDB357 [$P_{T7}::ftsN$] was amplified with primers 5'- GATCCCGCGAAATTAATACGACTCACTATAGGGG-3' and 5'- ATTTCTCGAGCTCTTTAATGTAGCGCCAGCGTTCTTCTGG-3', and the 306 bp *XbaI-XhoI* fragment was used to replace the 326 bp *XbaI-XhoI* fragment of pCH287 [$cI857 P_{iR}::amiC^{1-31}-ftsN^{52-123}$].

For pBL147 [$P_{lac}::gfp-ftsI$], the 605 bp *XbaI-HindIII* fragment of pBL3 [$P_{lac}::zapC-le$] was replaced with the 2578 bp *XbaI-HindIII* fragment of pBL120 [$P_{lac}::gfp-ftsI$].

For pBL153 [$P_{syn135}::ftsN$], the 1127 bp *XbaI-HindIII* fragment of pCH362 [$P_{syn135}::gfp-zapA$] was replaced with the 1000 bp *XbaI-HindIII* fragment of pDB357 [$P_{T7}::ftsN$].

To construct pBL154 [$repA^{ts} P_{syn135}::ftsN$], the 2128 bp *NarI-SphI* fragment of pBL153 [$P_{syn135}::ftsN$] was replaced with the 2128 bp *NarI-SphI* fragment of pDB326 [$repA^{ts}$].

pBL160 and pBL161 [$P_{lac}::gfp-ftsN^{Y85S}$] were obtained by site directed mutagenesis of pMG59 [$P_{lac}::gfp-ftsN$], using mutagenic primer 5'- CCAGAAGAACGCTGGCGCAGCATTAAGAGCTGGAAAG-3' and its reverse complement. The 581 *BamHI-AgeI* fragment of pMG59(Y85S) was next used to replace that of pCH201 [$P_{lac}::gfp-ftsN$], yielding pBL160, or that of pMG59, yielding pBL161.

pBL163 [$P_{lac}::gfp-ftsN^{W83F}$] was obtained by site directed mutagenesis of pMG59 [$P_{lac}::gfp-ftsN$], using mutagenic primer 5'- CCAAACCAGAAGAACGCTTTCGCTACATTAAGAGCTGG-3' and its reverse complement. The 581 *BamHI-AgeI* fragment of pMG59(W83F) was next used to replace that of pCH201 [$P_{lac}::gfp-ftsN$].

pBL165 [$P_{lac}::gfp-ftsN^{Y85F}$] was obtained by site directed mutagenesis of pMG59 [$P_{lac}::gfp-ftsN$], using mutagenic primer 5'- ACCAGAAGAACGCTGGCGCTTCATTAAGAGCTGGAAAGTC-3' and its reverse

complement. The 581 *Bam*HI-AgeI fragment of pMG59(Y85F) was next used to replace that of pCH201 [$P_{lac}::gfp-ftsN$].

pBL180 and pBL181 [$P_{lac}::gfp-ftsN^{W83T}$] were obtained by site directed mutagenesis of pMG59 [$P_{lac}::gfp-ftsN$], using mutagenic primer 5'-CCACCAAACCAGAAAGAACGCACCCGCTACATTAAAGAGCTGGAA-3' and its reverse complement. The 581 *Bam*HI-AgeI fragment of pMG59(W83T) was next used to replace that of pCH201 [$P_{lac}::gfp-ftsN$], yielding pBL180, or with that of pMG59, yielding pBL181.

For pBL190 [Scel *cI857* $P_{iR}::ftsN^{1-90}$], oligos 5'-AATTAGTTACGCTAGGGATAACAGGGTAATATA-3' and 5'-GATCTATATTACCCTGTTATCCCTAGCGTAACT-3' were annealed and the resulting fragment, with a unique I-Scel site (Scel, underlined) and with *Eco*RI and *Bam*HI compatible overhangs, was used to replace the 21 bp *Eco*RI-*Bam*HI fragment of pBL145 [*cI857* $P_{iR}::ftsN^{1-90}$].

For pBL191 [Scel *cI857* $P_{iR}::l-sceI$], primers 5'-GCTCTAGACAGGAGGGTACCTATATGCATATG-3' and 5'-CAGGTCGACGCATGCGAATTCGACGTCGGGCCCTTATTTTCAGGAAAGTTTCGGAGG-3' were used to amplify a portion of pACBSCE [$P_{BAD}::l-sceI$], and the 759 bp *Xba*I-*Sal*I fragment was used to replace the 315 bp *Xba*I-*Sal*I fragment of pBL190.

For pBL193 [$P_{lac}::gfp-ftsB$], the 1780 bp *Sfi*I fragment of pBL120 [$P_{lac}::gfp-ftsI$] was replaced with the 325 bp *Sfi*I fragment of pCH425 [$P_{lac}::t18-ftsB$].

For pBL194 [$repA^{ts}$ $P_{syn135}::gfp-ftsB$], the 1000 bp *Xba*I-*Hind*III fragment of pBL154 [$repA^{ts}$ $P_{syn135}::ftsN$] was replaced with the 1123 bp *Xba*I-*Hind*III fragment of pBL193 [$P_{lac}::gfp-ftsB$].

For pBL195 [$repA^{ts}$ $P_{syn135}::gfp-ftsL$], the 1000 bp *Xba*I-*Hind*III fragment of pBL154 [$repA^{ts}$ $P_{syn135}::ftsN$] was replaced with the 1142 bp *Xba*I-*Hind*III fragment of pCH195 [$P_{lac}::gfp-ftsL$].

For pBL200 [$repA^{ts}$ $P_{syn135}::ftsN$ Scel *cI857* $P_{iR}::l-sceI$], the 685 bp *Spe*I-*Eco*RI fragment of pBL154 [$repA^{ts}$ $P_{syn135}::ftsN$] was replaced with the 2880 bp *Spe*I-*Eco*RI fragment of pBL191 [Scel *cI857* $P_{iR}::l-sceI$].

For pBL203 [$P_{T7}::gfp-ftsN^{\Delta(59-73)<6}$], one portion of pCH201 [$P_{lac}::gfp-ftsN$] was amplified with primers 5'-CAGCGAATTCCATATGGCACAACGAGATTATG-3' and 5'-GCTAGGCCGGCCTCTTCTGCGGCCGCTTGTGATGCGTAATGAAGTACAG-3' and digested with *Eco*RI

and *FseI*, yielding a 202 bp fragment. A second portion was amplified with 5'-
GCGGCCGGCCTACCACCAAACCAGAAGAACGC-3' and 5'- TGAGAAGCTTAACCCCCGGCGGCGAG-3'
and digested with *FseI* and *HindIII*, yielding a 738 bp fragment. The two fragments were then
used in a three-way ligation with the 6119 bp *EcoRI-HindIII* fragment of pCH198 [$P_{T7}::gfp-ftsN$].
pBL203 encodes a version of GFP-FtsN in which FtsN residues 59-73 (KEESETLQSQKVTGN)
are replaced with the peptide RPQEEA.

For pBL205 [$P_{lac}::gfp-ftsN^{\Delta(59-73)<>6}$], the 946 bp *BamHI-HindIII* fragment of pBL203 [$P_{T7}::gfp-ftsN^{\Delta(59-73)<>6}$] was used to replace the 973 bp *BamHI-HindIII* fragment of pCH201 [$P_{lac}::gfp-ftsN$]. pBL205 encodes a version of GFP-FtsN in which FtsN residues 59-73 (KEESETLQSQKVTGN) are replaced with the peptide RPQEEA.

For pBL206 [$tetA repA^{ts} ftsA^{E124A}$], the 133 bp *EagI-ClaI* fragment of pBL12 [$cat repA^{ts} ftsA^{E124A}$] was replaced with the 1325 bp *EagI-ClaI* fragment of pAH162 [$tetA$], yielding pBL204 [$tetA cat repA^{ts} ftsA^{E124A}$]. Deletion of the 952 bp *BstBI* fragment of pBL204 then resulted in pBL206.

For pBL209 [$P_{lac}::gfp-ftsN$], the 2480 bp *Apal-HindIII* fragment of pCH201 [$P_{lac}::gfp-ftsN$] was used to replace the 2503 bp *Apal-HindIII* fragment of pTB8 [$P_{lac}::minCDE$].

For pBL210 [$P_{lac}::gfp-ftsN^{\Delta(59-73)<>95}$], primers 5'- GTCAGCGGCCGCAACACCAGTACCAACCGCC-3' and 5'- GTCAGGCCGGCCTCCGCTACAGGCTCAGGCTGTGG-3' were used to amplify a portion of pCH38 [$P_{T7}::zipA-h$], and the 286 bp *NotI-FseI* fragment was used to replace the 19 bp *NotI-FseI* fragment of pBL205 [$P_{lac}::gfp-ftsN^{\Delta(59-73)<>6}$]. pBL210 encodes a version of GFP-FtsN in which FtsN residues 59-73 (KEESETLQSQKVTGN) are replaced with a 95 residue P/Q-rich linker derived from ZipA⁸⁸⁻¹⁸⁰ (RPQHQQPPYASAQPRQPVQQPPEAQVPPQHAPHPAQPVQQPAYQPQPEQPLQQPVSPQV APAPQPVHSAPQPAQQAQFQPAEPVAAPQPEPVAEA).

For pBL211 [$gfp-ftsN^{\Delta(59-73)<>15}$], oligos 5'-
GGCCGTCGCCGCAACACCAGTACCAACCGCCTTATGCGTCTGCCGG-3' and 5'-
CAGACGCATAAGCGGTTGGTACTGGTGTTCGGCGAC-3' were annealed and the fragment with compatible overhangs was used to replace the 19 bp *NotI-FseI* fragment of pBL205 [$P_{lac}::gfp-ftsN^{\Delta(59-73)<>6}$]. pBL211 encodes a version of GFP-FtsN in which FtsN residues 59-73

(KEESETLQSQKVTGN) are replaced with a 15 residue P/Q-rich linker derived from ZipA⁸⁵⁻⁹⁹ (RPSPQHGYQPPYASA).

Plasmids pBL215 [Y85W], pBL216 [W83L], pBL217 [L89S], pBL218 [W83M], and pBL219 [L89H] encode mutant versions of GFP-FtsN in which a single FtsN residue has been replaced, as indicated in brackets. They were obtained by replacing the 2503 bp *Apal-HindIII* fragment of pTB8 [P_{lac}::*minCDE*] with the 2483 bp *Apal-HindIII* fragment of mutant pBL116 derivatives carrying the corresponding allele.

For pBL222 [P_{BAD}::*ftsL*], the 24 bp *XbaI-HindIII* fragment of pBAD33 [P_{BAD}::] was replaced with the 414 bp *XbaI-HindIII* fragment of pAB12 [P_{T7}::*ftsL*].

For pBL225 [P_{lac}::*gfp-ftsN*^{Y85S}], the 2480 bp *Apal-HindIII* fragment of pBL161 [P_{lac}::*gfp-ftsN*^{Y85S}] was used to replace the 2503 bp *Apal-HindIII* fragment of pTB8 [P_{lac}::*minCDE*].

For pBL226 [P_{lac}::*gfp-ftsN*^{W83T}], the 2480 bp *Apal-HindIII* fragment of pBL181 [P_{lac}::*gfp-ftsN*^{W83T}] was used to replace the 2503 bp *Apal-HindIII* fragment of pTB8 [P_{lac}::*minCDE*].

For pBL236 [*ftsA*^{I143L}], primers 5'- GTAGTACGAATTCTGGAAGCTGGCGGAC-3' and 5'- GAGGCCGTAATCATCGTCGGCCTC-3' were used to amplify a chromosomal *ftsQA* fragment of strain BL86-KK1/pBL215 [*ftsA*^{I143L} Δ *ftsN* / P_{lac}::*gfp-ftsN*^{Y85W}]. The 852 bp *BglII-AscI* fragment of the product was then used to replace that of pBL12 [*ftsA*^{E124A}].

For pBL289 [P_{T7}::*ftsB*], primers 5'- CGCATATGGGTAAACTAACGCTGCTGTTGC-3' and 5'- AAAGGGGGATGTGCTGCAAG-3' were used to amplify a portion of pBL193 [P_{lac}::*gfp-ftsB*], and the 334 bp *NdeI-HindIII* fragment of the product was used to replace the 63 bp *NdeI-HindIII* fragment of pET21A [P_{T7}::].

For pBL294 [P_{lac}::*ftsB*], the 1000 bp *XbaI-HindIII* fragment of pMG21 [P_{lac}::*ftsN*] was replaced with the 374 bp *XbaI-HindIII* fragment of pBL289 [P_{T7}::*ftsB*].

For pBL295 [P_{lac}::*ftsL*], the 1000 bp *XbaI-HindIII* fragment of pMG21 [P_{lac}::*ftsN*] was replaced with the 414 bp *XbaI-HindIII* fragment of pBL222 [P_{BAD}::*ftsL*].

For pBL300 [$P_{lac}::ftsB^{D59H}$], primers 5'-CGCATATGGGTAAACTAACGCTGCTGTTGC-3' and 5'-GTCAGGCCGAGGCGGCCTTATCGATTGTTTTGCCCGC-3' were used to amplify chromosomal $ftsB^{D59H}$ from strain BL86-AK11/pBL216 [$ftsB^{D59H} \Delta ftsN / P_{lac}::gfp-ftsN^{W83L}$], and the 321 bp *NdeI-SfiI* fragment was ligated to the 3521 *NdeI-SfiI* fragment of pBL147 [$P_{lac}::gfp-ftsI$].

For pBL301 [$P_{lac}::ftsL^{D93G}$], primers 5'- CCGAATTCCATATGATCAGCAGAGTGACAG-3' and 5'-CGTGTCGACTTATTTTTGCACTACGAT-3' were used to amplify chromosomal $ftsL^{D93G}$ from strain BL86-AK1/pBL215 [$ftsL^{D93G} \Delta ftsN / P_{lac}::gfp-ftsN^{Y85W}$], and the 298 bp *NsiI-SalI* fragment was used to replace that of pBL295 [$P_{lac}::ftsL$].

For pBL303 [$P_{syn135}::ftsL^{D93G}$], the 1000 bp *XbaI-HindIII* fragment of pBL153 [$P_{syn135}::ftsN$] was replaced with the 414 bp *XbaI-HindIII* fragment of pBL301 [$P_{lac}::ftsL^{D93G}$].

For pBL304 [$repA^{ts} P_{syn135}::ftsB^{D59H}$], the 1000 bp *XbaI-HindIII* fragment of pBL154 [$repA^{ts} P_{syn135}::ftsN$] was replaced with the 358 bp *XbaI-HindIII* fragment of pBL300 [$P_{lac}::ftsB^{D59H}$].

For pBL305 [$repA^{ts} P_{syn135}::ftsL^{D93G}$], the 1000 bp *XbaI-HindIII* fragment of pBL154 [$repA^{ts} P_{syn135}::ftsN$] was replaced with the 414 bp *XbaI-HindIII* fragment of pBL301 [$P_{lac}::ftsL^{D93G}$].

For pBL306(D59H) [$repA^{ts} P_{syn135}::ftsB^{D59H} ispD^{1-48}$], primers 5'-CGCATATGGGTAAACTAACGCTGCTGTTGC-3' and 5'-GCGTCGACTTAATGCGCCAGCAGCGCATGCACCG-3' were used to amplify chromosomal $ftsB^{D59H}$ and a portion of *ispD* from strain BL86-AK11/pBL216 [$ftsB^{D59H} \Delta ftsN / P_{lac}::gfp-ftsN^{W83L}$], and the 209 bp *MluI-SalI* fragment was used to replace the 58 bp *MluI-SalI* fragment of pBL304 [$repA^{ts} P_{syn135}::ftsB^{D59H}$].

For pBL306(E56A) [$repA^{ts} P_{syn135}::ftsB^{E56A} ispD^{1-48}$], the 331 bp *XbaI-ClaI* fragment of pBL306(D59H) [$repA^{ts} P_{syn135}::ftsB^{D59H} ispD^{1-48}$] was replaced with the 347 bp *XbaI-ClaI* fragment of pBL339 [$P_{syn135}::ftsB^{E56A}$].

For pBL306(E56K) [$repA^{ts} P_{syn135}::ftsB^{E56K} ispD^{1-48}$], the 331 bp *XbaI-ClaI* fragment of pBL306(D59H) [$repA^{ts} P_{syn135}::ftsB^{D59H} ispD^{1-48}$] was replaced with the 347 bp *XbaI-ClaI* fragment of pBL341 [$P_{syn135}::ftsB^{E56K}$].

For pBL309 [$P_{\text{syn135}}::ftsL$], the 1000 bp *XbaI-HindIII* fragment of pBL153 [$P_{\text{syn135}}::ftsN$] was replaced with the 414 bp *XbaI-HindIII* fragment of pBL295 [$P_{\text{lac}}::ftsL$].

For pBL312 [$P_{\text{lac}}::gfp-malF^{2-14}-ftsN^{27-81}-le$], primers 5'-
GTCGGCCGAAATGTGCCTGCGGTTTCTCCC-3' and 5'-
AGCGCTCGAGTTCTTCTGGTTTTGGTGGTAGTCCGTTTCC-3' were used to amplify a portion of pMG13 [$P_{\text{lac}}::gfp-ftsN^{1-81}$], and the 169 bp *EagI-XhoI* fragment was used to replace the 691 bp *EagI-XhoI* fragment of pFB261 [$P_{\text{lac}}::gfp-malF^{2-14}-rodZ^{111-319}$].

For pBL313 [$P_{\text{BAD}}::rfp-malF^{2-39}-ftsN^{55-105}-le$], the 972 bp *XbaI-XcmI* fragment of pBL138 [$P_{\text{BAD}}::rfp-malF^{2-39}-ftsN^{55-123}$] was used to replace the 1023 bp *XbaI-XcmI* fragment of pBL141 [$P_{\text{BAD}}::rfp-ftsN^{1-105}-le$].

For pBL315 [$P_{\text{lac}}::gfp-malF^{2-39}-ftsN^{55-81}-le$], primers 5'-
CTGTACGGATCCACGCATCACAAGAAAGAAGAGTCC-3' and 5'-
AGCGCTCGAGTTCTTCTGGTTTTGGTGGTAGTCCGTTTCC-3' were used to amplify a portion of pCH201 [$P_{\text{lac}}::gfp-ftsN$], and the 87 bp *BamHI-XhoI* fragment was used to replace the 207 bp *BamHI-XhoI* fragment of pCH310 [$P_{\text{lac}}::gfp-malF^{2-39}-ftsN^{55-123}$].

For pBL321 [$P_{\text{lac}}::gfp-ftsN^{L75A}$], pMG59 [$P_{\text{lac}}::gfp-ftsN$] was mutagenized using 5'-
GAAAGTGACCGAAACGGAGCTCCACCAAACCAGAAGAAC-3' and its reverse complement. The 581 bp *BamHI-AgeI* fragment of pMG59(L75A) was next ligated to the 8804 bp *BamHI-AgeI* fragment of pBL210 [$P_{\text{lac}}::gfp-ftsN^{\Delta(59-73)<>95}$].

For pBL322 [$P_{\text{lac}}::gfp-ftsN^{P76A}$], a mutagenized 732 bp fragment of pMG59 was obtained by asymmetric amplification and overlap extension (AAOE) according to Xiao and Pei (Xiao & Pei, 2011) using primer pairs 5'- GCTGCTGGGATTACACATGGC-3' with 5'-
GTGACCGGAAACGGACTAGCACCAAAACCAGAAGAACGC-3', and 5'-
GCGTTCTTCTGGTTTTGGTGCTAGTCCGTTTCCGGTCAC-3' with 5'- CGCAGGAGTTTGCAGCAGATC-3'. The 581 bp *BamHI-AgeI* fragment encoding the P76A substitution was next ligated to the 8804 bp *BamHI-AgeI* fragment of pBL210 [$P_{\text{lac}}::gfp-ftsN^{\Delta(59-73)<>95}$].

For pBL323 [$P_{\text{lac}}::gfp-ftsN^{P77A}$], pMG59 was mutagenized using 5'-
CCGGAACGGACTACCAGCAAACCAGAAGAACGCTGG-3' and its reverse complement. The 581 bp

*Bam*HI-AgeI fragment of pMG59(P77A) was next ligated to the 8804 bp *Bam*HI-AgeI fragment of pBL210 [*P*_{lac}::*gfp-ftsN*^{Δ(59-73)<>95}].

For pBL324 [*P*_{lac}::*gfp-ftsN*^{K78A}], pMG59 was mutagenized using 5'-GGAAACGGACTACCACCAGCACCAGAAGAACGCTGGCGC-3' and its reverse complement. The 581 bp *Bam*HI-AgeI fragment of pMG59(K78A) was next ligated to the 8804 bp *Bam*HI-AgeI fragment of pBL210 [*P*_{lac}::*gfp-ftsN*^{Δ(59-73)<>95}].

For pBL325 [*P*_{lac}::*gfp-ftsN*^{P79A}], a mutagenized 732 bp fragment of pMG59 was obtained by asymmetric amplification and overlap extension using primer pairs 5'-GCTGCTGGGATTACACATGGC-3' with 5'-GGAAACGGACTACCACAAAAGCAGAAGAACGCTGGCGCTAC-3', and 5'-GTAGCGCCAGCGTTCTTCTGCTTTTGGTGGTAGTCCGTTTCC-3' with 5'-CGCAGGAGTTTGCAGCAGATC-3'. The 581 bp *Bam*HI-AgeI fragment encoding the P79A substitution was next ligated to the 8804 bp *Bam*HI-AgeI fragment of pBL210 [*P*_{lac}::*gfp-ftsN*^{Δ(59-73)<>95}].

For pBL326 [*P*_{lac}::*gfp-ftsN*^{E80A}], a mutagenized 732 bp fragment of pMG59 was obtained by asymmetric amplification and overlap extension using primer pairs 5'-GCTGCTGGGATTACACATGGC-3' with 5'-CTACCACAAAACCAGCAGAACGCTGGCGCTAC-3', and 5'-GTAGCGCCAGCGTTCTGCTGGTTTTGGTGGTAG-3' with 5'-CGCAGGAGTTTGCAGCAGATC-3'. The 581 bp *Bam*HI-AgeI fragment encoding the E80A substitution was next ligated to the 8804 bp *Bam*HI-AgeI fragment of pBL210 [*P*_{lac}::*gfp-ftsN*^{Δ(59-73)<>95}].

For pBL327 [*P*_{lac}::*gfp-ftsN*^{R84A}], a mutagenized 732 bp fragment of pMG59 was obtained by asymmetric amplification and overlap extension using primer pairs 5'-GCTGCTGGGATTACACATGGC-3' with 5'-CCAGAAGAACGCTGGGCCTACATTAAGAGCTGGAAAG-3', and 5'-CTTTCCAGCTCTTTAATGTAGGCCAGCGTTCTTCTGG-3' with 5'-CGCAGGAGTTTGCAGCAGATC-3'. The 581 bp *Bam*HI-AgeI fragment encoding the R84A substitution was next ligated to the 8804 bp *Bam*HI-AgeI fragment of pBL210 [*P*_{lac}::*gfp-ftsN*^{Δ(59-73)<>95}].

For pBL328 [*P*_{lac}::*gfp-ftsN*^{L89A}], pMG59 was mutagenized using 5'-GGCGCTACATTAAGAGGCGGAAAGTCGCCAGCCGGG-3' and its reverse complement. The 581 bp *Bam*HI-AgeI fragment of pMG59(L89A) was next ligated to the 8804 bp *Bam*HI-AgeI fragment of pBL210 [*P*_{lac}::*gfp-ftsN*^{Δ(59-73)<>95}].

For pBL329 [$P_{lac}::gfp-ftsN^{E90A}$], pMG59 was mutagenized using 5'-CGCTACATTAAAGAGCTGGCAAGTCGCCAGCCGGGAGTG-3' and its reverse complement. The 581 bp *BamHI*-*AgeI* fragment of pMG59(E90A) was next ligated to the 8804 bp *BamHI*-*AgeI* fragment of pBL210 [$P_{lac}::gfp-ftsN^{(1-58)-P/Q95-(74-319)}$].

For pBL330 [$P_{lac}::gfp-ftsN^{D5S,Y6A}$], a mutagenized 732 bp fragment of pMG59 [$P_{lac}::gfp-ftsN$] was obtained by asymmetric amplification and overlap extension using primer pairs 5'-GCTGCTGGGATTACACATGGC-3' with 5'-CCGAATTCCATATGGCACAACGATCTGCTGTACGCCGACGCCAACC GG C-3', and 5'-GCCGGTTGGCTGCGGCGTACAGCAGATCGTTGTGCCATATGGAATTCGG-3' with 5'-CGCAGGAGTTTGCAGCAGATC-3'. The 581 bp *BamHI*-*AgeI* fragment encoding the D5S and Y6A substitutions was next ligated to the 8804 bp *BamHI*-*AgeI* fragment of pBL210 [$P_{lac}::gfp-ftsN^{\Delta(59-73)\rightarrow 95}$].

For pBL331 [$P_{syn135}::ftsL^{H94Y}$], the 138 bp *Bpml-HindIII* fragment of pJH2 [$P_{syn135}::ftsL$] was replaced with that of a mutant derivative [pJH2(L9V, V27A, H94Y)-pBL215-L6], selected from a library of mutant *ftsL* alleles that allow growth of strain JH1/pBL200/pBL215 at 37°C.

For pBL332 [$P_{syn135}::ftsL^{E88V}$], the 138 bp *Bpml-HindIII* fragment of pJH2 [$P_{syn135}::ftsL$] was replaced with that of a mutant derivative [pJH2(L77I, E88V)-pBL215-L7], selected from a library of mutant *ftsL* alleles that allow growth of strain JH1/pBL200/pBL215 at 37°C.

Plasmid pBL333 [$P_{syn135}::ftsL^{E88k}$], was selected from a library of mutant *ftsL* alleles that allow growth of strain JH1/pBL200/pBL215 at 42°C.

For pBL334 [$P_{syn135}::ftsL^{N89S}$], the 138 bp *Bpml-HindIII* fragment of pJH2 [$P_{syn135}::ftsL$] was replaced with that of a mutant derivative [pJH2(K37R, N89S)-pBL215-L7], selected from a library of mutant *ftsL* alleles that allow growth of strain JH1/pBL200/pBL215 at 42°C.

For pBL335 [$P_{lac}::gfp-ftsN^{1-81:D5S,Y6A}-le$], primers 5'-GCTGCTGGGATTACACATGGC-3' and 5'-AGCGCTCGAGTTCTTCTGGTTTTGGTGGTAGTCCGTTCC-3' were used to amplify a portion of pBL330 [$P_{lac}::gfp-ftsN^{D5S,Y6A}$], and the 291 bp *NheI-XhoI* fragment was used to replace the 777 bp *NheI-XhoI* fragment of pCH354 [$P_{lac}::gfp-ftsN^{1-243}-le$].

For pBL336 [$P_{\text{syn135}}::ftsB$], the 414 bp *XbaI-HindIII* fragment of pJH2 [$P_{\text{syn135}}::ftsL$] was replaced with the 374 bp *XbaI-HindIII* fragment of pBL294 [$P_{\text{lac}}::ftsB$].

Plasmid pBL338 [$P_{\text{syn135}}::ftsB^{E56V}$], was selected from a library of mutant *ftsB* alleles that allow growth of strain JH1/pBL200/pBL215 at 42°C.

For pBL339 [$P_{\text{syn135}}::ftsB^{E56A}$], the 121 bp *BstZ17I-SapI* fragment of pBL336 [$P_{\text{syn135}}::ftsB$] was replaced with that of a mutant derivative [pBL336(K3R, E56A, S92L)-pBL215-B2], selected from a library of mutant *ftsB* alleles that allow growth of strain JH1/pBL200/pBL215 at 37°C.

For pBL340 [$P_{\text{syn135}}::ftsB^{A55T}$], the 238 bp *XbaI-SapI* fragment of pBL336 [$P_{\text{syn135}}::ftsB$] was replaced with that of a mutant derivative [pBL336(A55T, T83S)-pBL215-B3], selected from a library of mutant *ftsB* alleles that allow growth of strain JH1/pBL200/pBL215 at 37°C.

Plasmid pBL341 [$P_{\text{syn135}}::ftsB^{E56K}$], was selected from a library of mutant *ftsB* alleles that allow growth of strain JH1/pBL200/pBL215 at 37°C.

Plasmid pBL342 [$P_{\text{syn135}}::ftsB^{E56G}$], was selected from a library of mutant *ftsB* alleles that allow growth of strain JH1/pBL200/pBL215 at 37°C.

Plasmid pBL343 [$P_{\text{syn135}}::ftsB^{D59V}$], was selected from a library of mutant *ftsB* alleles that allow growth of strain JH1/pBL200/pJH10 at 37°C.

For pBL356 [Scel $P_{\text{syn135}}::ftsB^{E56K}$ *ispD*¹⁻⁴⁸ Scel *sacB*], the 58 bp *EcoRI-SalI* fragment of pDOC-C [Scel Scel *sacB*] was replaced with the 573 bp *EcoRI-SalI* fragment of pBL306(E56K) [$P_{\text{syn135}}::ftsB^{E56K}$ *ispD*¹⁻⁴⁸].

For pCH277 [$P_{\text{lac}}::amiC^{1-31}$ -*ftsN*⁵²⁻¹²³-*gfp*], primers 5'-GTCTCTGCTAGCTTACTTCATTACGCATCACAAGAAAGAAG-3' and 5'-CGAACTCGAGAAGCTGACGTTGTTCTGGTGTTCAG-3' were used to amplify a portion of pCH276 [$P_{\text{lac}}::gfp$ -*ftsN*¹⁻¹²³], and the 217 bp *NheI-XhoI* fragment was used to replace the 19 bp *NheI-XhoI* fragment of pTB37 [$P_{\text{lac}}::amiC^{1-31}$ -*gfp*].

For pCH286 [$P_{lac}::amiC^{1-31}-ftsN^{52-123}$], the 1859 bp *XbaI-XhoI* fragment of pCH181 [$P_{lac}::gfp-minD minE-le$] was replaced with the 326 bp *XbaI-XhoI* fragment of pCH277 [$P_{lac}::amiC^{1-31}-ftsN^{52-123}-gfp$].

For pCH287 [$cl857 P_{R}::amiC^{1-31}-ftsN^{52-123}$], the 6 bp *XbaI-SalI* fragment of pDB344 [$cl857 P_{R}::$] was replaced with the 335 bp *XbaI-SalI* fragment of pCH286 [$P_{lac}::amiC^{1-31}-ftsN^{52-123}$].

For pCH309 [$P_{lac}::gfp-malF^{2-39}-mreC^{38-367}-le$], primers 5'-GCAGAGATCTGATGTCATTA AAAAGAAACATTGGTGGC-3' and 5'-CGTTCTCGAGTTGCCCTCCCGGCGCACGCGCAGGC-3' were used to amplify a portion of pFB243 [$P_{lac}::malF^{1-39}-mreC^{38-367}$], and the 1116 bp *BglII-XhoI* fragment was used to replace the 330 bp *BamHI-XhoI* fragment of pMG12 [$P_{lac}::gfp-ftsN^{1-105}-le$].

For pCH310 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-123}$], the 1562 bp *Apal-BamHI* fragment of pCH288 [$P_{lac}::ss torA-gfp-ftsN^{55-123}$] was replaced with the 1627 bp *Apal-BamHI* fragment of pCH309 [$P_{lac}::gfp-malF^{2-39}-mreC^{38-367}-le$].

For pCH327 [$P_{CYC1}::lexA-vp16-cub-ftsN^{1-105}$], a portion of pMG12 [$P_{lac}::gfp-ftsN^{1-105}-le$] was amplified with primers 5'-CTGAGGCCATTACGGCCGTGGCACAACGAGATTATGTACG-3' and 5'-ATCGGGCCGAGGCGGCCTTAACCGGCAGAAGGTTCTGTGGG-3', and the 331 bp *SfiI* fragment was used to replace the 27 bp *SfiI* fragment of pBT3-N [$P_{CYC1}::lexA-vp16-cub$].

For pCH391 [$P_{lac}::t25-ftsN^{1-105}$], the 1027 bp *SfiI* fragment of pCH358 [$P_{lac}::t25-rodZ$] was replaced with the 331 bp *SfiI* fragment of pCH327 [$P_{CYC1}::lexA-vp16-cub-ftsN^{1-105}$].

For pCH391(DY>SA) [$P_{lac}::t25-ftsN^{1-105; D5S, Y6A}$], the 2565 bp *SfiI* fragment of pLP10 [$P_{lac}::t25-ponA$] was replaced with the 331 bp *SfiI* fragment of pCH392(DY>SA) [$P_{lac}::t18-ftsN^{1-105; D5S, Y6A}$].

For pCH392 [$P_{lac}::t18-ftsN^{1-105}$], the 1027 bp *SfiI* fragment of pCH371 [$P_{lac}::t18-rodZ$] was replaced with the 331 bp *SfiI* fragment of pCH327 [$P_{CYC1}::lexA-vp16-cub-ftsN^{1-105}$].

For pCH392(DY>SA) [$P_{lac}::t18-ftsN^{1-105; D5S, Y6A}$], a portion of pBL330 [$P_{lac}::gfp-ftsN^{D5S, Y6A}$] was amplified with primers 5'-AAAAGGCCATTACGGCCGTGGCACAACGATCTGCTGTACGC-3' and 5'-ATCGGGCCGAGGCGGCCTTAACCGGCAGAAGGTTCTGTGGG-3', and the 331 bp *SfiI* fragment was used to replace the 2565 bp *SfiI* fragment of pLP7 [$P_{lac}::t18-ponA$].

For pCH399 [$P_{lac}::t18-ftsA$], a portion of pZAQ [$ftsQAZ$] was amplified with primers 5'-GGCCATTACGGCCATGATCAAGGCGACGGACAG-3' and 5'-GGCCGAGGCGGCCTTAAACTCTTTTCGCAGCC-3', and the 1276 bp *SfiI* fragment was used to replace the 1027 bp *SfiI* fragment of pCH371 [$P_{lac}::t18-rodZ$].

For pCH400 [$P_{lac}::t18-ftsQ$], a portion of pZAQ [$ftsQAZ$] was amplified with primers 5'-GGCCATTACGGCCATGTCGCAGGCTGCTCTG-3' and 5'-GGCCGAGGCGGCCTCATTTGTTGTTCTGCCTGTGCC-3', and the 844 bp *SfiI* fragment was used to replace the 1027 bp *SfiI* fragment of pCH371 [$P_{lac}::t18-rodZ$].

For pCH425 [$P_{lac}::t18-ftsB$], *ftsB* was amplified with primers 5'-GATCGGCCATTACGGCCATGGGTAAACTAACGCTGCTG-3' and 5'-GTCAGGCCGAGGCGGCCTTATCGATTGTTTTGCCCGC-3', and the 325 bp *SfiI* fragment was used to replace the 1027 bp *SfiI* fragment of pCH371 [$P_{lac}::t18-rodZ$].

For pCH433 [$P_{lac}::t25-ftsI$], *ftsI* was amplified with primers 5'-GATCGGCCATTACGGCCATGAAAGCAGCGGCGAAAAC-3' and 5'-GATCGGCCGAGGCGGCCTTACGATCTGCCACCTGTC-3'. The product was digested with *SfiI*, and the 1780 bp fragment was used to replace the 1027 bp *SfiI* fragment of pCH358 [$P_{lac}::t25-rodZ$].

For pDB357 [$P_{T7}::ftsN$], *ftsN* was amplified with primers 5'-CAGCGAATTCCATATGGCACAACGAGATTATG-3' and 5'-TGAGAAGCTTAACCCCCGGCGGCGAG-3', and the 960 bp *NdeI-HindIII* fragment was used to replace the 63 bp *NdeI-HindIII* fragment of pET21A [$P_{T7}::$].

For pJH1 [$tetA repA^{ts} P_{syn135}::ftsL$], the 468 bp *EcoRI-HindIII* fragment of pBL309 [$P_{syn135}::ftsL$] was ligated to the 5779 bp *EcoRI-HindIII* fragment of pBL206 [$tetA repA^{ts} ftsA^{E124A}$].

For pJH2 [$tetA P_{syn135}::ftsL$], the 2674 bp *AflII-ApaLI* fragment of pJH1 [$tetA repA^{ts} P_{syn135}::ftsL$] was replaced with the 2127 bp *AflII-ApaLI* fragment of pBL153 [$P_{syn135}::ftsN$].

For pJH3 [$tetA P_{syn135}::ftsL^{D93G}$], the 414 bp *XbaI-HindIII* fragment of pJH2 [$tetA P_{syn135}::ftsL$] was replaced with that of pBL303 [$aadA P_{syn135}::ftsL^{D93G}$].

For pJH5 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-320; T64G, S67G, Y85W, +A102}$], a portion of pBL215 [$P_{lac}::gfp-ftsN^{T64G, S67G, Y85W, +A102}::lacZYA$] was amplified with primers 5'-CTGTACGGATCCACGCATCACAAGAAAGAAGAGTCC-3', and 5'-TGAGAAGCTTAACCCCCGGCGGCGAG-3', and the 794 bp *Bam*HI-*Hind*III fragment was used to replace the 230 bp *Bam*HI-*Hind*III fragment of pCH310 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-123}$].

For pJH6 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-320; T64G, S67G, W83L, +A102}$], a portion of pBL216 [$P_{lac}::gfp-ftsN^{T64G, S67G, W83L, +A102}::lacZYA$] was amplified with primers 5'-CTGTACGGATCCACGCATCACAAGAAAGAAGAGTCC-3', and 5'-TGAGAAGCTTAACCCCCGGCGGCGAG-3', and the 794 bp *Bam*HI-*Hind*III fragment was used to replace the 230 bp *Bam*HI-*Hind*III fragment of pCH310 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-123}$].

For pJH10 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-320; T64G, S67G, Y85W, +A102}$], the 30 bp *Eco*RI-*Hind*III fragment of pRC7 [$P_{lac}::$] was replaced with the 1774 bp *Eco*RI-*Hind*III fragment of pJH5.

For pJH11 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-320; T64G, S67G, W83L, +A102}$], the 30 bp *Eco*RI-*Hind*III fragment of pRC7 [$P_{lac}::$] was replaced with the 1774 bp *Eco*RI-*Hind*III fragment of pJH6.

For pLP10 [$P_{lac}::t25-ponA$], the 2566 bp *Sfi*I fragment of pLP7 [$P_{lac}::t18-ponA$] was used to replace the 1027 bp *Sfi*I fragment of pCH358 [$P_{lac}::t25-rodZ$].

For pLP160 [$P_{BAD}::rfp-malF^{2-39}-ftsN^{55-90}$], the 2232 bp *Xcm*I-*Nco*I fragment of pBL313 [$P_{BAD}::ecrfp-malF^{2-39}-ftsN^{55-105}-le$] was replaced with the 2181 bp *Xcm*I-*Nco*I fragment of pBL142 [$P_{BAD}::ecrfp-ftsN^{1-90}$].

For pLP163 [$P_{lac}::gfp-ftsN$], a portion of pCH201 [$P_{lac}::gfp-ftsN$] was amplified with primers 5'-GGTGAGATCTGTGGCACAAACGAGATTATGTACGC-3' and 5'-TGAGAAGCTTAACCCCCGGCGGCGAG-3', and the 964 bp *Bgl*II-*Hind*III fragment was used to replace the 973 bp *Bam*HI-*Hind*III fragment of pCH201. pLP163 is similar to pCH201, but 3 codons in the linker between *gfp* and *ftsN*, as well as three restriction sites (*Bam*HI, *Eco*RI, and *Nde*I), have been eliminated.

For pLP164 [$P_{lac}::gfp-ftsN^{75-105}-le$], a portion of pMG14 [$P_{lac}::^{ss}torA-gfp-ftsN^{71-105}-le$] was amplified with primers 5'-CATCGGATCCCTACCACCAAACCAGAAGAACGC-3' and 5'-GCGATCGGCATAACCACCACGCTC-3', and the 955 bp *Bam*HI-*Cla*I fragment of the product was used to replace the 1129 bp *Bam*HI-*Cla*I fragment of pMG47 [$P_{lac}::gfp-ftsN^{1-90}$].

For pLP165 [$P_{lac}::gfp-ftsN^{80-105}-le$], a portion of pMG14 [$P_{lac}::^{ss}torA-gfp-ftsN^{71-105}-le$] was amplified with primers 5'- GAAGGGATCCGAAGAACGCTGGCGCTACATTAAGAG-3' and 5'- GCGATCGGCATAACCACCACGCTC-3', and the 940 bp *BamHI-ClaI* fragment of the product was used to replace the 1129 bp *BamHI-ClaI* fragment of pMG47 [$P_{lac}::gfp-ftsN^{1-90}$].

For pLP168 [$P_{lac}::^{ss}torA-gfp-ftsN^{75-105}-le$], the 1629 bp *BamHI-ClaI* fragment of pCH282 [$P_{lac}::^{ss}torA-gfp-ftsN^{55-319}$] was replaced with the 955 bp *BamHI-ClaI* fragment of pLP164 [$P_{lac}::gfp-ftsN^{75-105}-le$].

For pLP169 [$P_{lac}::^{ss}torA-gfp-ftsN^{80-105}-le$], the 1629 bp *BamHI-ClaI* fragment of pCH282 [$P_{lac}::^{ss}torA-gfp-ftsN^{55-319}$] was replaced with the 940 bp *BamHI-ClaI* fragment of pLP165 [$P_{lac}::gfp-ftsN^{75-105}-le$].

For pLP170 [$P_{lac}::gfp-ftsN^{1-31}-malF^{17-39}-ftsN^{55-81}-le$], a portion of pLP163 [$P_{lac}::gfp-ftsN$] was amplified with primers 5'- ATGACCATGATTACGAATTCCTCG-3' and 5'- CCATCGGCCCGCAGGCAGATTTTCGTTGCTTTTTTCCG-3', and the 871 bp *XbaI-EagI* fragment of the product was used to replace the 817 bp *XbaI-EagI* fragment of pBL315 [$P_{lac}::gfp-malF^{2-39}-ftsN^{55-81}-le$].

For pLP171 [$P_{lac}::gfp-ftsN^{1-71}-le$], a portion of pCH201 [$P_{lac}::gfp-ftsN$] was amplified with primers 5'- GCTGCTGGGATTACACATGGC-3' and 5'- TAGGCTCGAGGGTCACTTTCTGGCTTTGCAG-3', and the 261 bp *NheI-XhoI* fragment was used to replace the 777 bp *NheI-XhoI* fragment of pCH354 [$P_{lac}::gfp-ftsN^{1-243}-le$].

For pLP218 [$P_{lac}::^{ss}torA-gfp-ftsN^{75-93}-le$], a portion of pLP168 [$P_{lac}::^{ss}torA-gfp-ftsN^{75-105}-le$] was amplified with primers 5'- GCTGCTGGGATTACACATGGC-3' and 5'- GGTCCTCGAGCTGGCGACTTTCCAGCTCTTTAATG-3', and the 96 bp *NheI-XhoI* fragment of the product was used to replace the 132 bp *NheI-XhoI* fragment of pLP168.

For pLP219 [$P_{lac}::^{ss}torA-gfp-ftsN^{75-99}-le$], a portion of pLP168 [$P_{lac}::^{ss}torA-gfp-ftsN^{75-105}-le$] was amplified with primers 5'- GCTGCTGGGATTACACATGGC-3' and 5'- GTGTCTCGAGGGGCGCACGCACTCCCGGCTG-3', and the 114 bp *NheI-XhoI* fragment of the product was used to replace the 132 bp *NheI-XhoI* fragment of pLP168.

For pLP221 [$P_{lac}::^{ss}torA-gfp-ftsN^{55-90}$], the 72 bp *Bam*HI-*Sal*I fragment of pLP218 [$P_{lac}::^{ss}torA-gfp-ftsN^{75-93}-le$] was replaced with the 117 bp *Bam*HI-*Sal*I fragment of pLP160 [$P_{BAD}::ecrfp-malF^{2-39}-ftsN^{55-90}$].

For pMG21 [$P_{lac}::ftsN$], the 1746 bp *Xba*I-*Hind*III fragment of pCH201 [$P_{lac}::gfp-ftsN$] was replaced with the 1000 bp *Xba*I-*Hind*III fragment of pDB357 [$P_{T7}::ftsN$].

For pMG62 [$P_{lac}::gfp-ftsN^{1-123}$], the 1779 bp *Xba*I-*Hind*III fragment of pTB222 [$P_{lac}::zipA-gfp$] was replaced with the 1174 bp *Xba*I-*Hind*III fragment of pCH276 [$P_{lac}::gfp-ftsN^{1-123}$].

For pTB51 [$cat\ repA^{ts}\ araC\ P_{BAD}::\gamma\ \beta\ exo$], the *cat* cassette of pKD3 was amplified with primers 5'- ATGAGACAATAACCCCTGATAAATGCTTCAATAATATTGAAATGAATATCCTCCTTAGTTCC-3' and 5'- TTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGGTGTAGGCTGGAGCTGCTTCG-3', yielding a 1091 bp fragment with end sequences homologous to those flanking the *bla* gene on pKD46 [$bla\ repA^{ts}\ araC\ P_{BAD}::\gamma\ \beta\ exo$] (underlined). Recombination of the fragment with the plasmid in strain TB28/pKD46, followed by selection for chloramphenicol resistance and ampicillin sensitivity, yielded TB28/pTB51. Plasmid pTB51 is similar to pKD46, except that an 888 bp *bla* fragment has been replaced with an 1010 bp *cat* fragment, which is transcribed in the same direction as the replaced gene.

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