SUPPLEMENTARY DATA

	1	2	3	4	5	6	7	8	9	10	11	12
A	EEKA	EEKA	EEKA		BW	BW	BW		JW	JW	JW	
B	EEKA amp	EEKA amp	EEKA amp		BW amp	BW amp	BW amp		JW amp	JW amp	JW amp	
C	EEKA kan	EEKA kan	EEKA kan		BW kan	BW kan	BW kan					
D												
E	EEKA neg	EEKA neg	EEKA neg		BW neg	BW neg	BW neg		JW neg	JW neg	JW neg	
F	EEKA amp neg	EEKA amp neg	EEKA amp neg		BW amp neg	BW amp neg	BW amp neg		JW amp neg	JW amp neg	JW amp neg	
G	EEKA kan neg	EEKA kan neg	EEKA kan neg		BW kan neg	BW kan neg	BW kan neg					
H									Blank	Blank	Blank	

Figure S1. Plate set-up of 96-well absorbance-based lysis assay showing *E. coli* strains and type of antibiotic. Rows E-G contain negative controls (no phage) used to construct growth curves. Row A contains the "no antibiotic" control. EEKA = *E. coli* EEKA18-1, BW = *E. coli* BW25113, JW = *E. coli* JW5437, amp = ampicillin, kan = kanamycin, neg = negative control.

A

```
  1 NNNNNNNNNN NNNNCCGATG GCATCGGAC CTTTTATTGT GCACAGAAAA
 51 GGCCAGCCTC GCTTGAGACT GGCCTTTCTG ACAGATGCTT ACTTACTCGC
101 GGAACAGCGC TTCTGTAGGC TGGAGCTGCT TCGAAGTTCC TATACTTTCT
151 AGAGAATAGG AACTTCGAAC TGCAGGTCGA CGGATCCCGA ATCAAATCGT
201 TATCACTGGG TTCCTGTTCT ACTAAGGCCT TTTCGTCAAA AACCTCAACT
251 CCGTTCTCAT CAAATTCCGC ATCTTCATTT AAATCATGAA CTTTCAGCGT
301 ATTCTGACTC ATAAGGTGGC TCCTACCCGT GATCCCTTGA CGGAACATTC
351 AAGCAAAAGC CTGGTTCCGC CGATNNNNNC NTGGCGGCAA A
```

B

```
ALIGNMENTS
>CP009273.1 Escherichia coli BW25113, complete genome
Length=4631469

ALIGNMENT 1:

 Score = 42.1 bits (21),  Expect = 8e-06
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query  1        TTACTCGCGGAACAGCGCTTC  21
                ||||||||||||||||||||
Sbjct  2859918  TTACTCGCGGAACAGCGCTTC  2859938


ALIGNMENT 2:

 Score = 217 bits (117),  Expect = 2e-57
 Identities = 117/117 (100%), Gaps = 0/117 (0%)
 Strand=Plus/Plus

Query  5        CAAATCGTTATCACTGGGTTCCTGTTCTACTAAGGCCTTTTCGTCAAAAACCTCAACTCC  64
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2860791  CAAATCGTTATCACTGGGTTCCTGTTCTACTAAGGCCTTTTCGTCAAAAACCTCAACTCC  2860850

Query  65       GTTCTCATCAAATTCCGCATCTTCATTTAAATCATGAACTTTCAGCGTATTCTGACT  121
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2860851  GTTCTCATCAAATTCCGCATCTTCATTTAAATCATGAACTTTCAGCGTATTCTGACT  2860907
```

Figure S2. Sanger sequencing of the colony #1 amplicon shows the presence of a partial 'scar' sequence after kanamycin resistance cassette removal. The sequence of the purified PCR product was mailed to GeneWiz for Sanger sequencing using the *rpoS* forward primer. Note that *rpoS* lies on the negative strand of the *E. coli* BW25113 genome. (A) Raw sequencing results (5' to 3'). The nucleotide sequence of the stop codon is italicized and bolded. 18 nucleotides that correspond to 6 C-terminal amino acids are italicized. The partial 'scar' sequence is bolded. The 121 unexpected nucleotides are underlined. The sequence corresponding to the start codon is bolded and underlined. (B) BLASTN 2.8.0+ alignment results. Alignment 1 shows the 18 nucleotides present in the 3' region of *rpoS* as well as the stop codon nucleotide sequence aligns with *rpoS*. Alignment 2 shows 117 nucleotides out of the extra 121 nucleotides align with a sequence in the 5' region of *rpoS*.

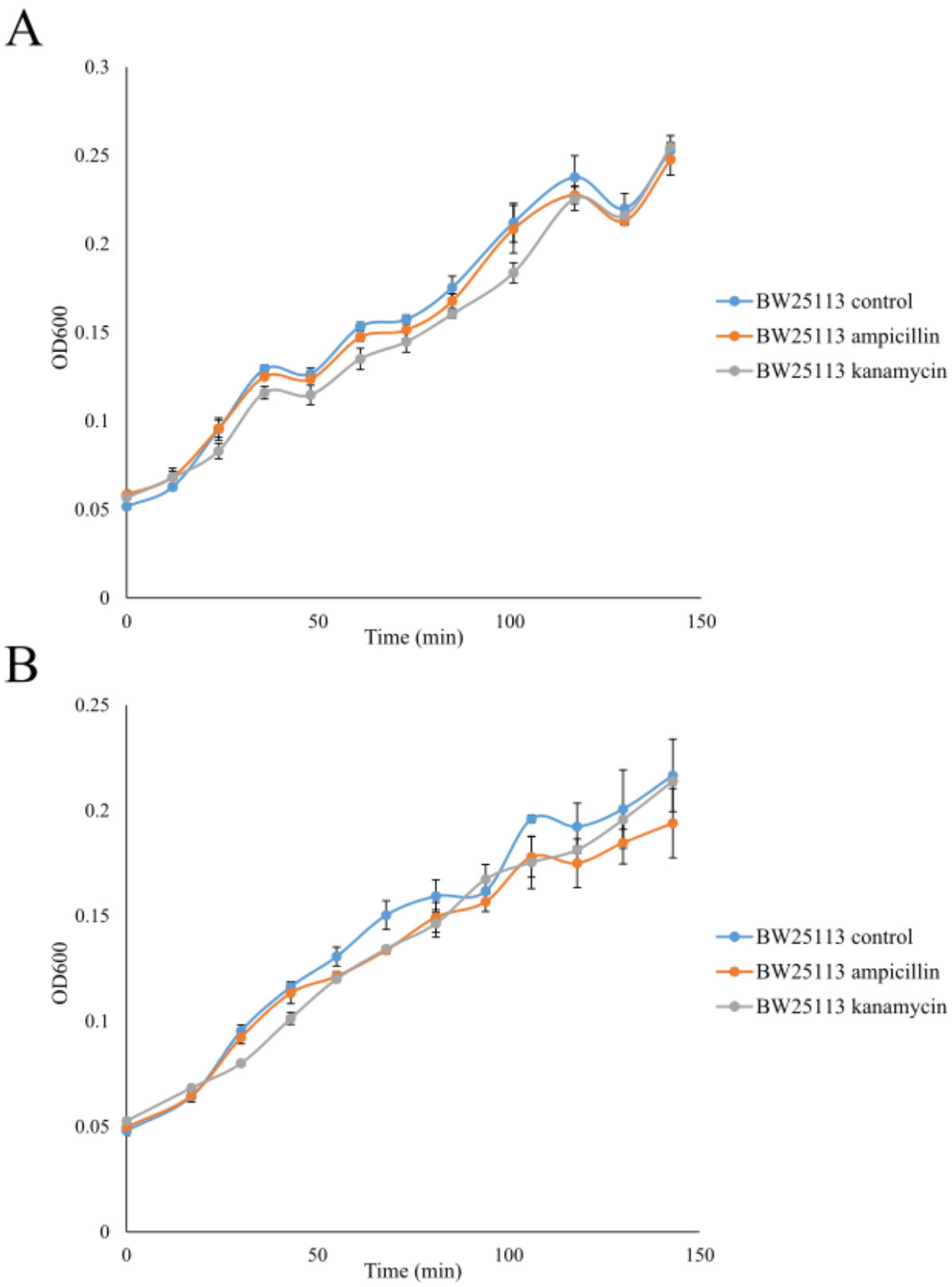


Figure S3. The growth rate of *E. coli* BW25113 pre-treated with sub-lethal concentrations of ampicillin or kanamycin is similar to untreated BW25113. Individual graphs in A and B represent growth curves from two biological replicates. *E. coli* BW25113

was cultured overnight in three media conditions: LB control, LB with sub-lethal concentrations of kanamycin, or LB with sub-lethal concentrations of ampicillin. The cells were subcultured to obtain log-phase cells. The cultures were normalized to an OD_{600} of 0.3, plated in triplicates on a 96-well plate, and incubated at 37°C. OD_{600} measurements were taken in 10-minute intervals using a BioTek Epoch Microplate Spectrophotometer to generate the growth curves. Error bars represent standard deviations.

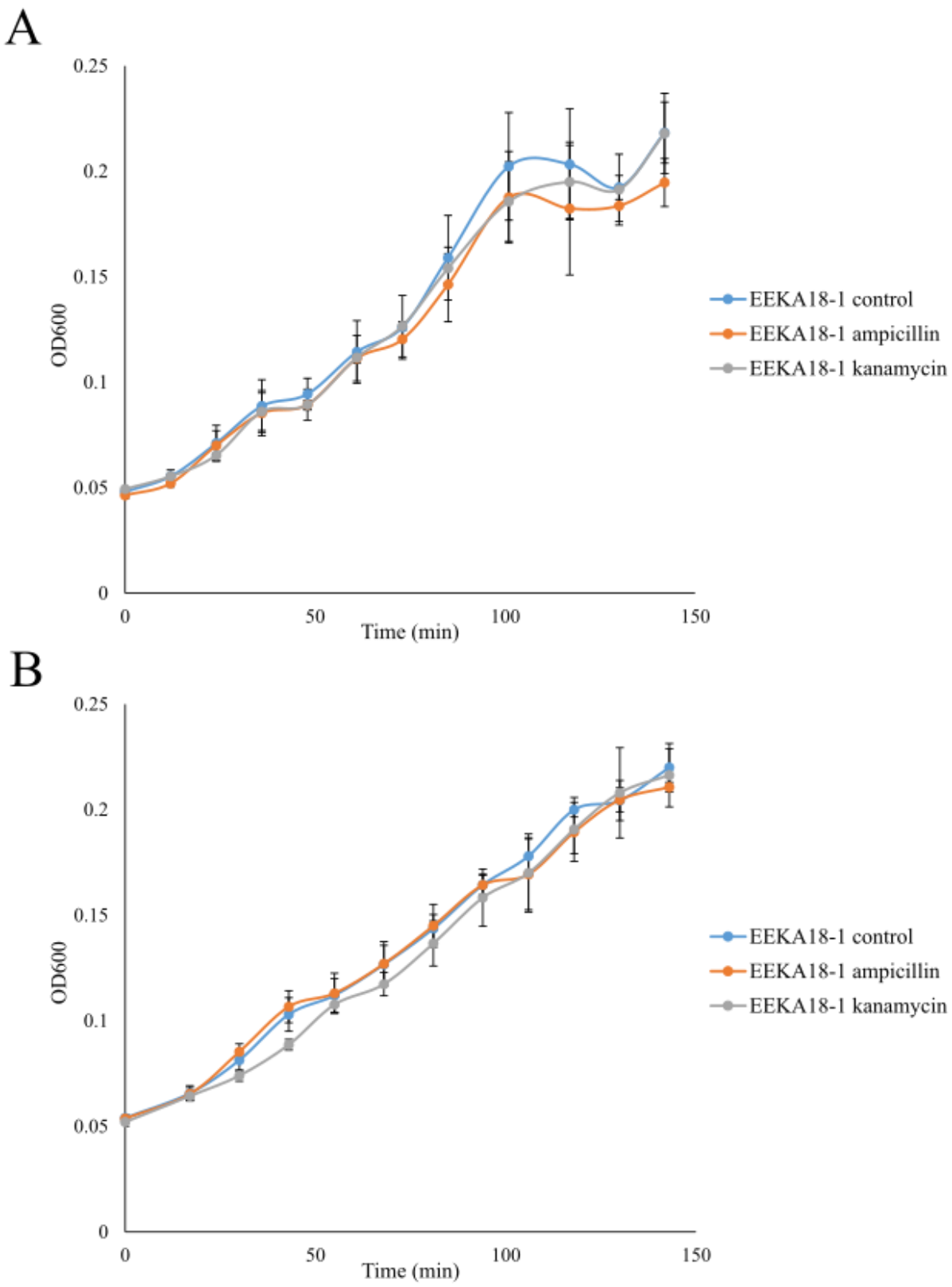
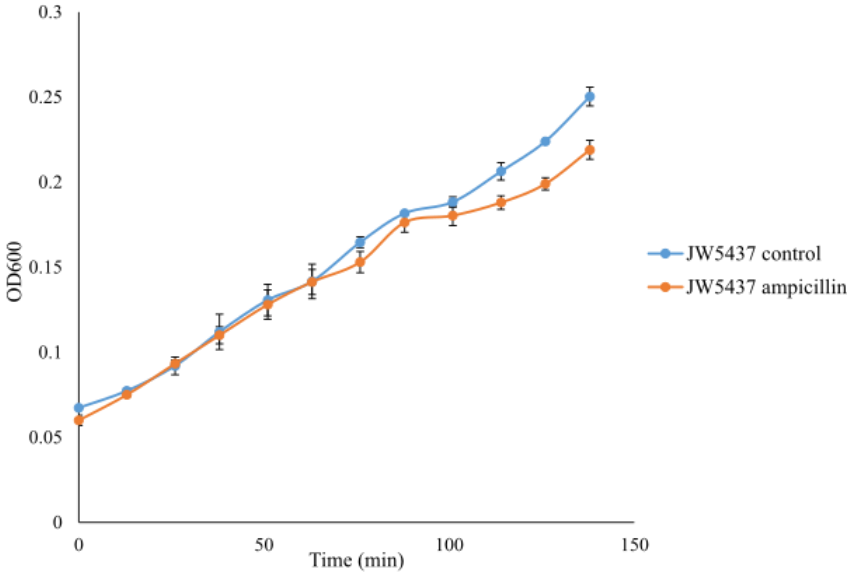


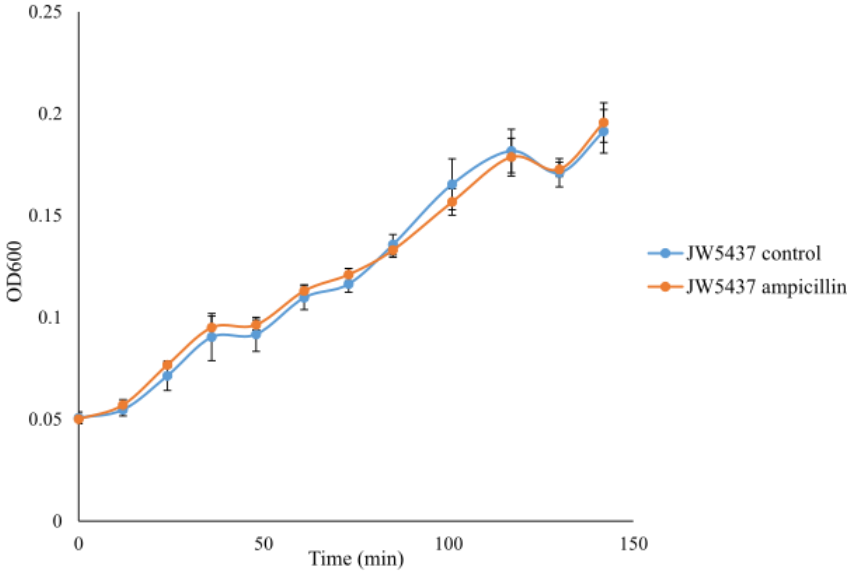
Figure S4. The growth rate of *E. coli* EEKA18-1 pre-treated with sub-lethal concentrations of ampicillin or kanamycin is similar to untreated EEKA18-1. Individual graphs in A and B represent growth curves from two biological replicates. *E. coli* EEKA18-1

was cultured overnight in three media conditions: LB control, LB with sub-lethal concentrations of kanamycin, or LB with sub-lethal concentrations of ampicillin. The cells were subcultured to obtain log-phase cells. The cultures were normalized to an OD_{600} of 0.3, plated in triplicates on a 96-well plate, and incubated at 37°C. OD_{600} measurements were taken in 10 minute intervals using a BioTek Epoch Microplate Spectrophotometer to generate the growth curves. Error bars represent standard deviations.

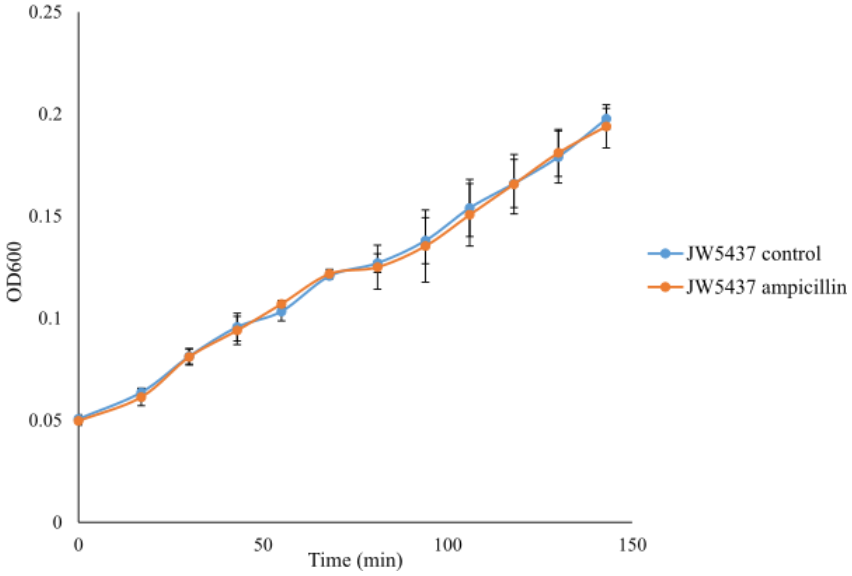
A


0.3
0.25
0.2
0.15
0.1
0.05
0
OD600
0
50
100
150
Time (min)
JW5437 control
JW5437 ampicillin

B


0.25
0.2
0.15
0.1
0.05
0
OD600
0
50
100
150
Time (min)
JW5437 control
JW5437 ampicillin

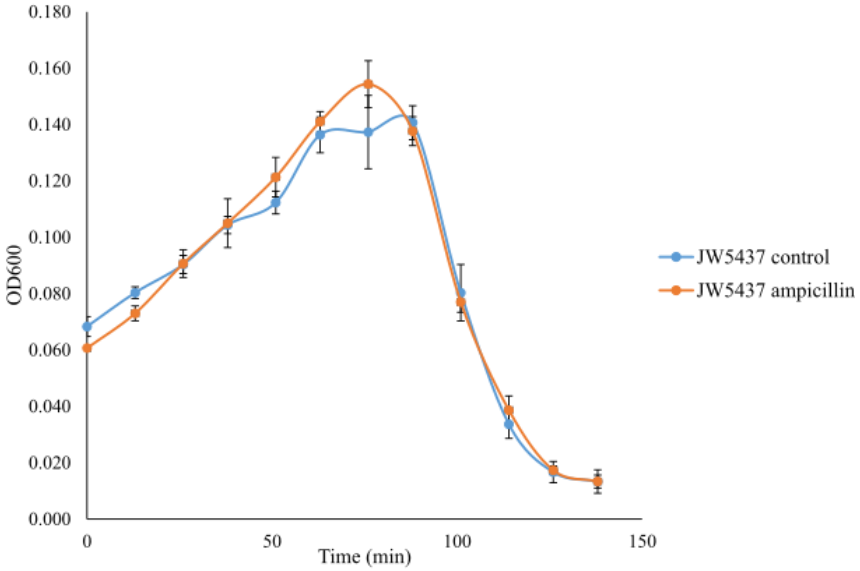
C


0.25
0.2
0.15
0.1
0.05
0
OD600
0
50
100
150
Time (min)
JW5437 control
JW5437 ampicillin

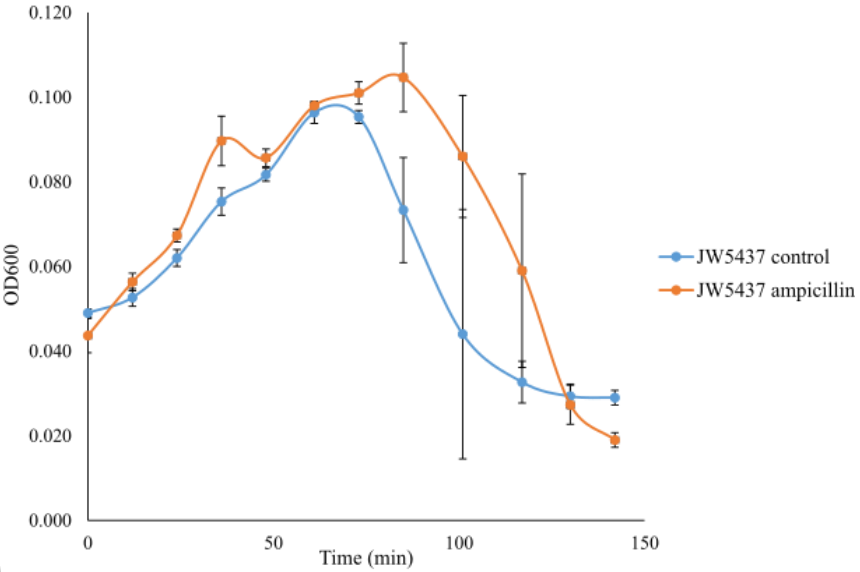
41

Figure S5. The growth rate of *E. coli* JW5437 pre-treated with sub-lethal concentrations of ampicillin is similar to untreated JW5437. Individual graphs in A, B, and C represent growth curves from three biological replicates. *E. coli* BW25113 was cultured overnight in two media conditions: LB control or LB with sub-lethal concentrations of ampicillin. The cells were subcultured to obtain log-phase cells. The cultures were normalized to an OD_{600} of 0.3, plated in triplicates on a 96-well plate, and incubated at 37°C. OD_{600} measurements were taken in 10 minute intervals using a BioTek Epoch Microplate Spectrophotometer to generate the growth curves. Error bars represent standard deviation.

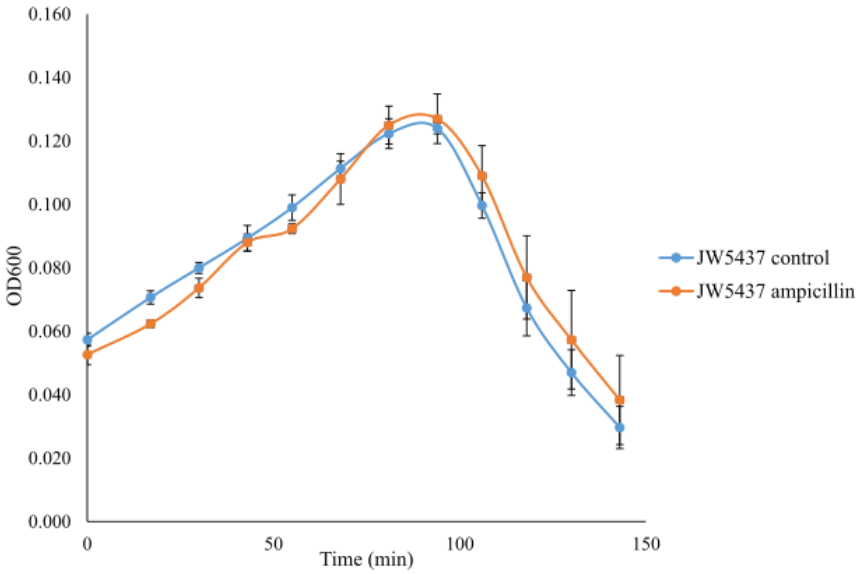
A


0.180
0.160
0.140
0.120
0.100
0.080
0.060
0.040
0.020
0.000
OD600
0
50
100
150
Time (min)
JW5437 control
JW5437 ampicillin

B


0.120
0.100
0.080
0.060
0.040
0.020
0.000
OD600
0
50
100
150
Time (min)
JW5437 control
JW5437 ampicillin

C


0.160
0.140
0.120
0.100
0.080
0.060
0.040
0.020
0.000
OD600
0
50
100
150
Time (min)
JW5437 control
JW5437 ampicillin

50

Figure S6. Pre-treatment of *E. coli* JW5437 with sub-lethal concentrations of ampicillin does not delay bacteriophage T7-mediated cell lysis. Individual graphs in A, B, and C represent lysis curves from three biological replicates. *E. coli* JW5437 was grown overnight in two media conditions: LB broth or LB broth with sub-lethal concentrations of ampicillin. The cells were subcultured the next day and grown to log phase. The cultures were normalized to an OD_{600} of 0.3, and 90 µL of each culture was plated in triplicates in a 96-well plate. A total of 10 µL of diluted T7 bacteriophage was added to the cells to obtain a MOI of 0.05. Negative controls were plated in triplicates using 10 µL of LB broth instead of bacteriophage. The plated cells were incubated at 37°C, and the OD_{600} was read in a plate reader in 10 minute intervals until the OD_{600} dipped below the starting values. Error bars represent standard deviations.