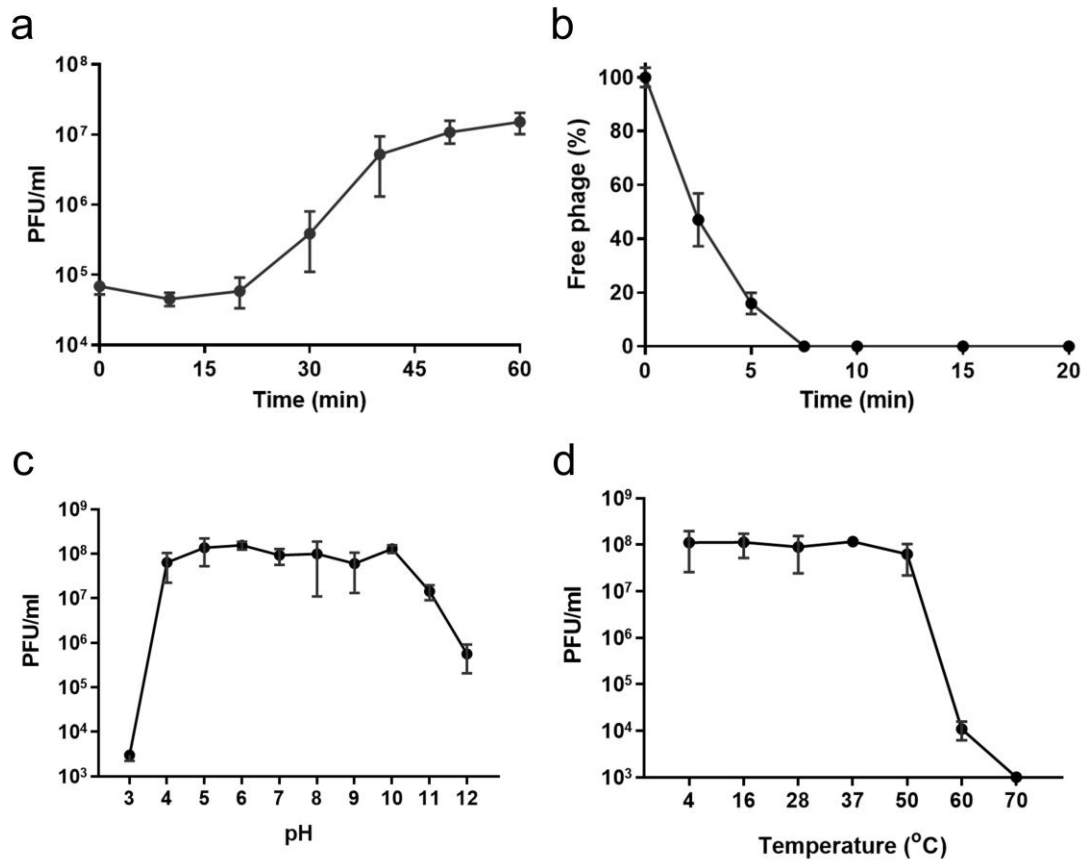


1 **Supplementary Materials**

2 **TABLE S1** The accession numbers of the phages used in this study.

phage strains	accession no.
<i>Enterobacteria</i> phage T4	NC_000866.4
<i>Erwinia</i> phage vB_EamM-M7	HQ728263.1
<i>Escherichia</i> phage SUSP1	NC_028808.2
<i>Klebsiella</i> phage JD18	KT239446.1
<i>Pseudomonas</i> phage phiPMW	NC_041880.1
<i>Pseudomonas</i> phage VCM	NC_029065.1
<i>Rheinheimera</i> phage vB_RspM_Barba5S	NC_048187.1
<i>Shigella</i> phage Sf24	MF327008.1
<i>Pseudomonas</i> phage vB_PpS_SYP	OQ183418.1
<i>Pseudomonas</i> phage PMBT3	MG596799.1
<i>Pseudomonas</i> phage Lana	MK473373.2
<i>Pseudomonas</i> phage PB1	EU716414.1
<i>Pseudomonas</i> phage Epa6	MT108726.1
<i>Pseudomonas</i> phage JJ01	ON324181.1
<i>Pseudomonas</i> phage LMA2	FM201282.1



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6 **FIG S1** (a) One-step growth curve of phage vB_PpS_SYP. (b) Dynamics of phage SYP adsorption
7 to hosts. (c) pH stability of phage SYP treated with different pH for 2 h. (d) Thermal stability of
8 phage SYP treated with different temperature for 2 h. The results are shown as the mean $\pm$ S.D. (n
9 = 3).

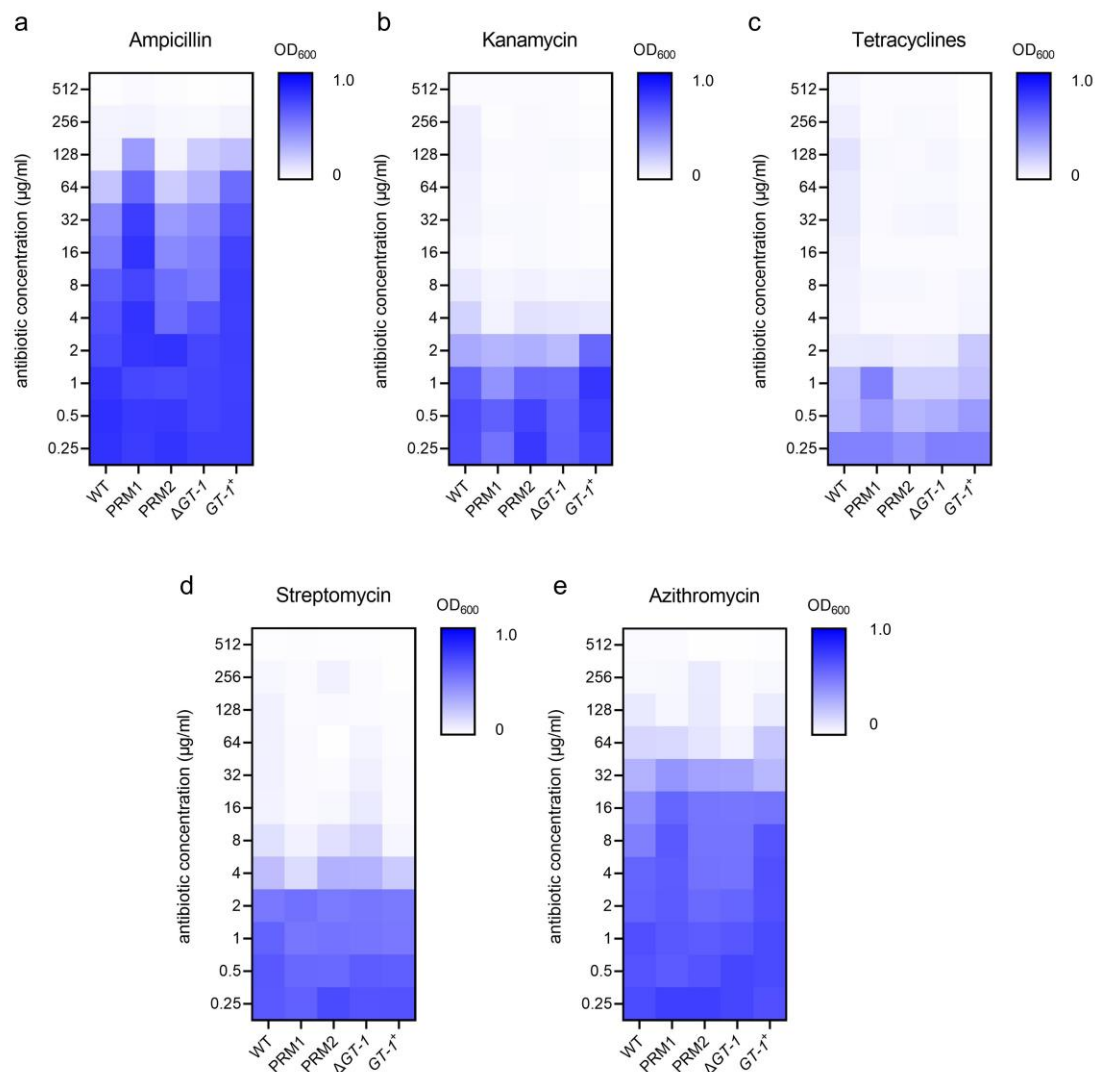
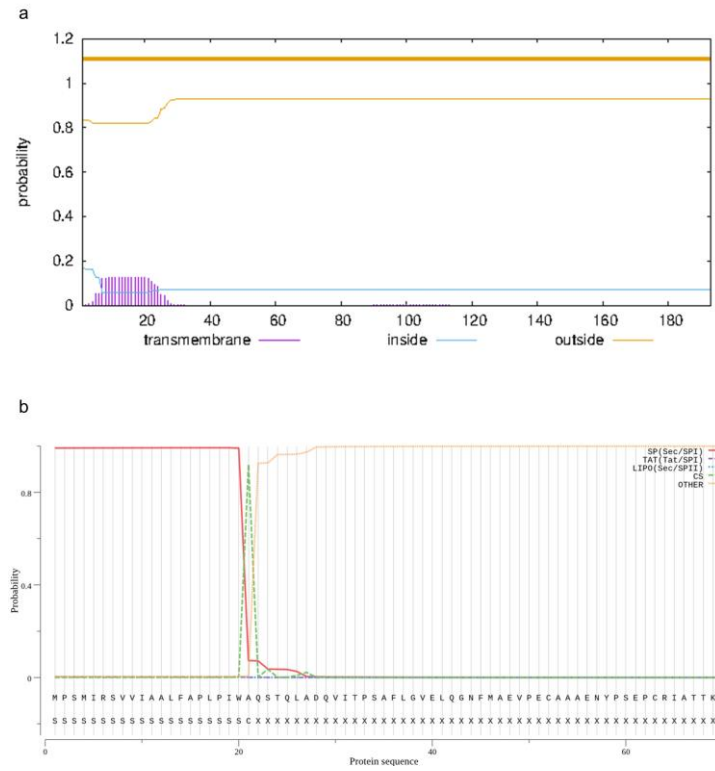


FIG S2 Antibiotic sensitivity of *GT-1* mutants, wild-type strains, and complementary strains. Optical density at 600 nm of mutants grown in TSB medium containing a 2-fold gradient dilution of (a) Ampicillin, (b) Kanamycin, (c) Streptomycin, (d) Tetracycline, or (e) Azithromycin. OD₆₀₀ ranges from 0 (white) to 1.0 (blue) from three biological replicates.



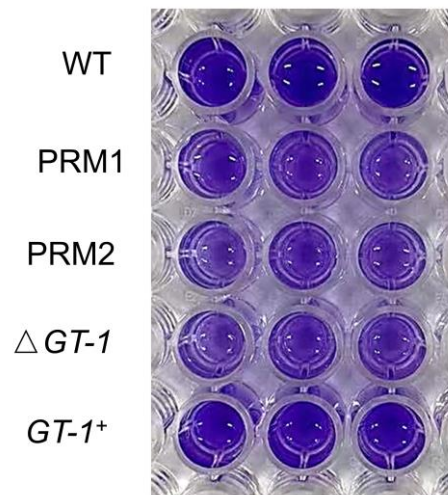
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FIG S3 Prediction of Homp characteristics. (a) Transmembrane helices in proteins. (b) Signal peptide and cleavage sites.



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FIG S4 Biofilm of the GT-1 mutant strain and its crystalline violet staining.

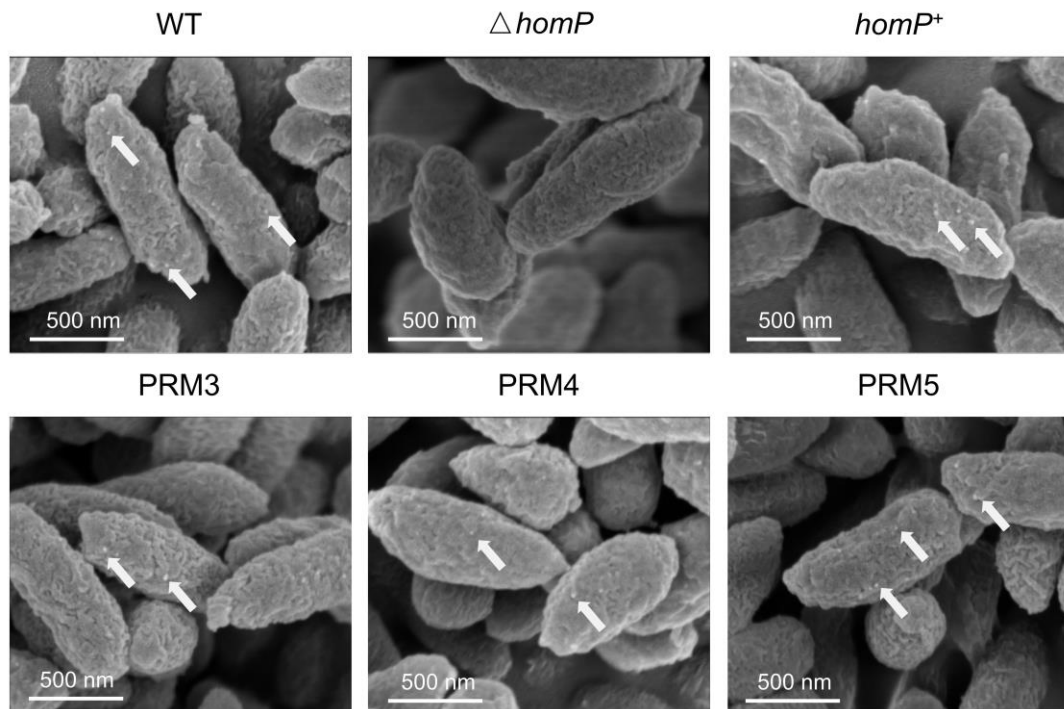


FIG S5 Scanning electron microscope images of the wild-type strain, phage-resistant mutants, deletion mutants, and complementary strains. Arrows point to white dots on the surface of the bacteria. Scale bar, 500 nm.