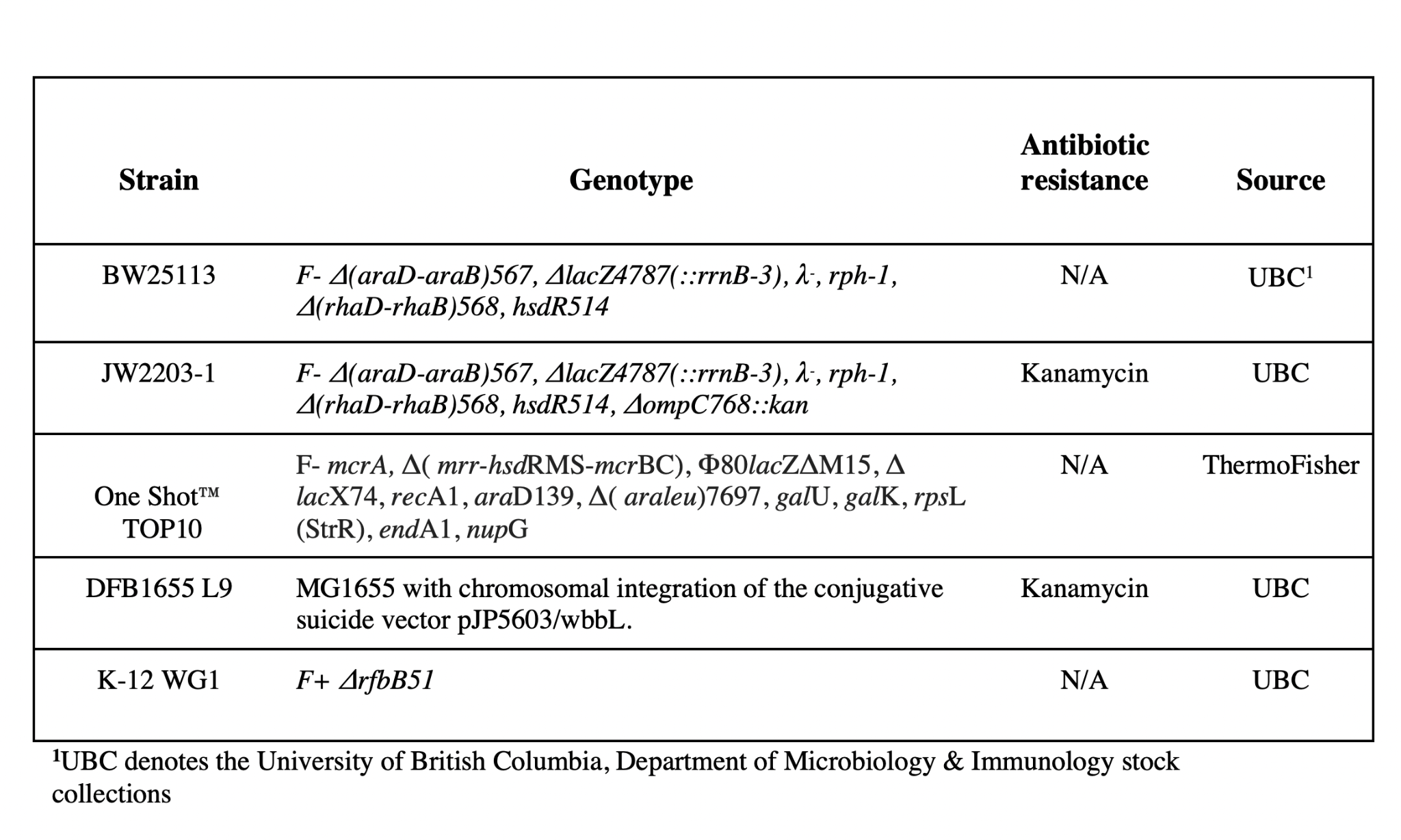
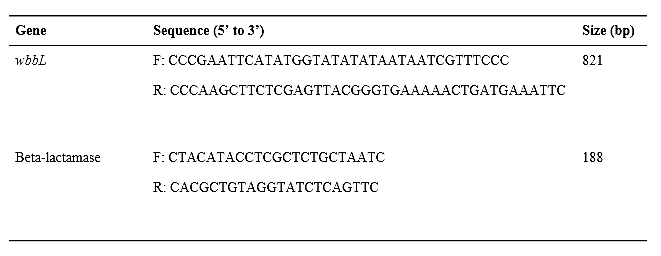
**Exploring the role of OmpC deletion and O-antigen expression in T4 bacteriophage-induced lysis of Escherichia coli K12 cells**

Camila Quintana, Eleanor Chen, Daniel Song

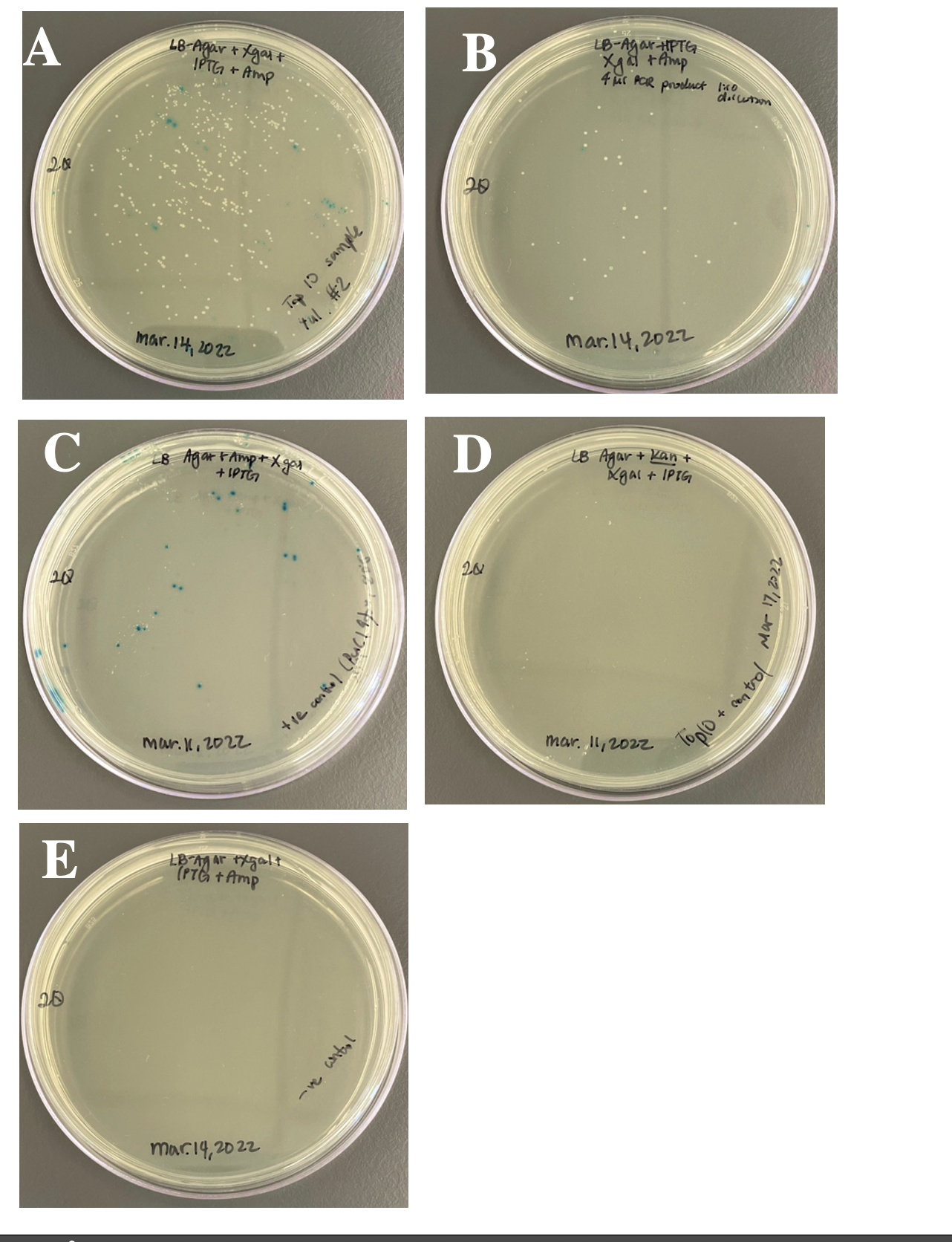
University of British Columbia, Department of Microbiology and Immunology, MICB 401 WT2.

**SUPPLEMENTAL MATERIAL**

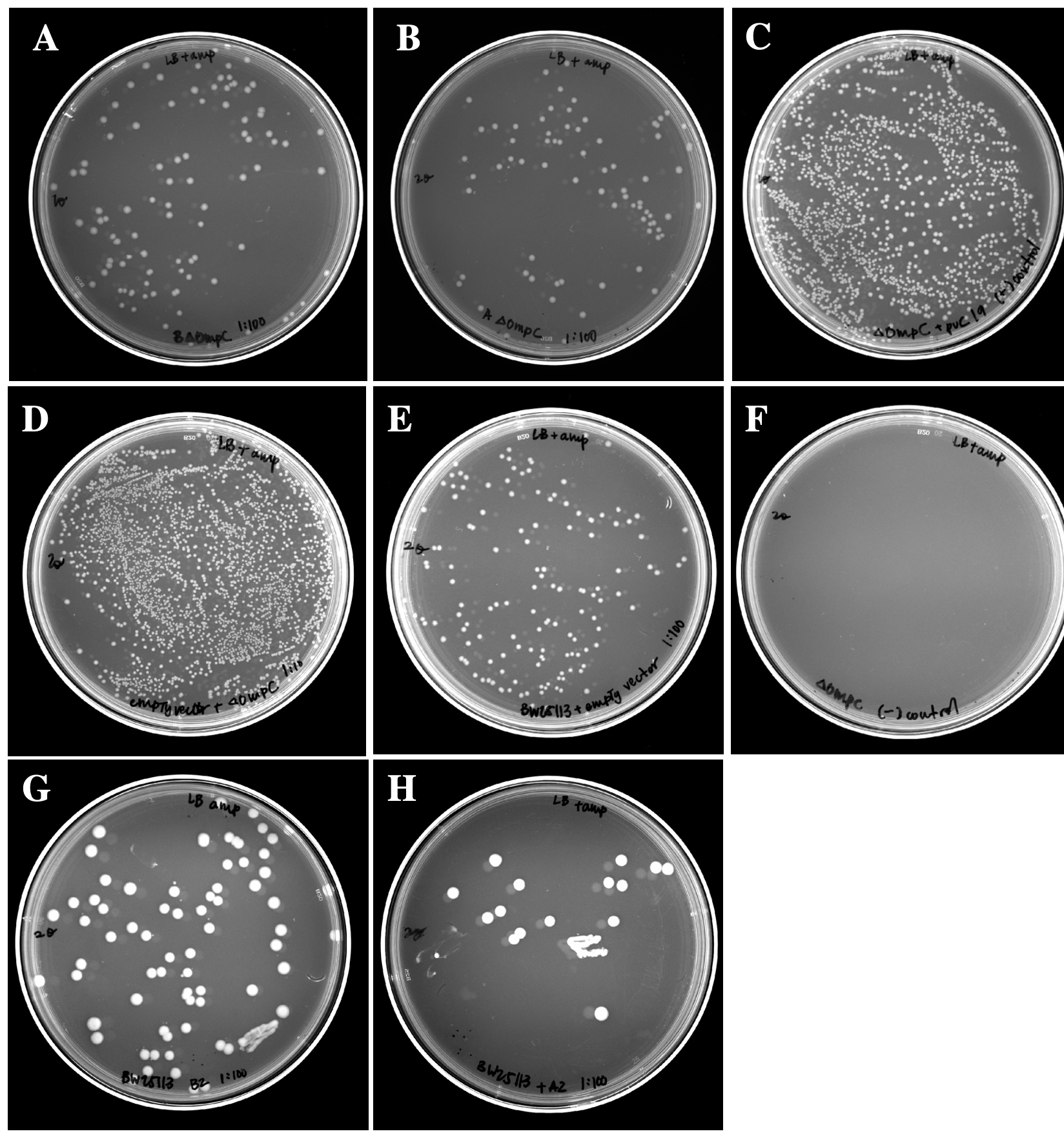
**Table S1. List of Bacterial Strains Used.** 1UBC denotes the University of British Columbia, Department of Microbiology & Immunology stock collections

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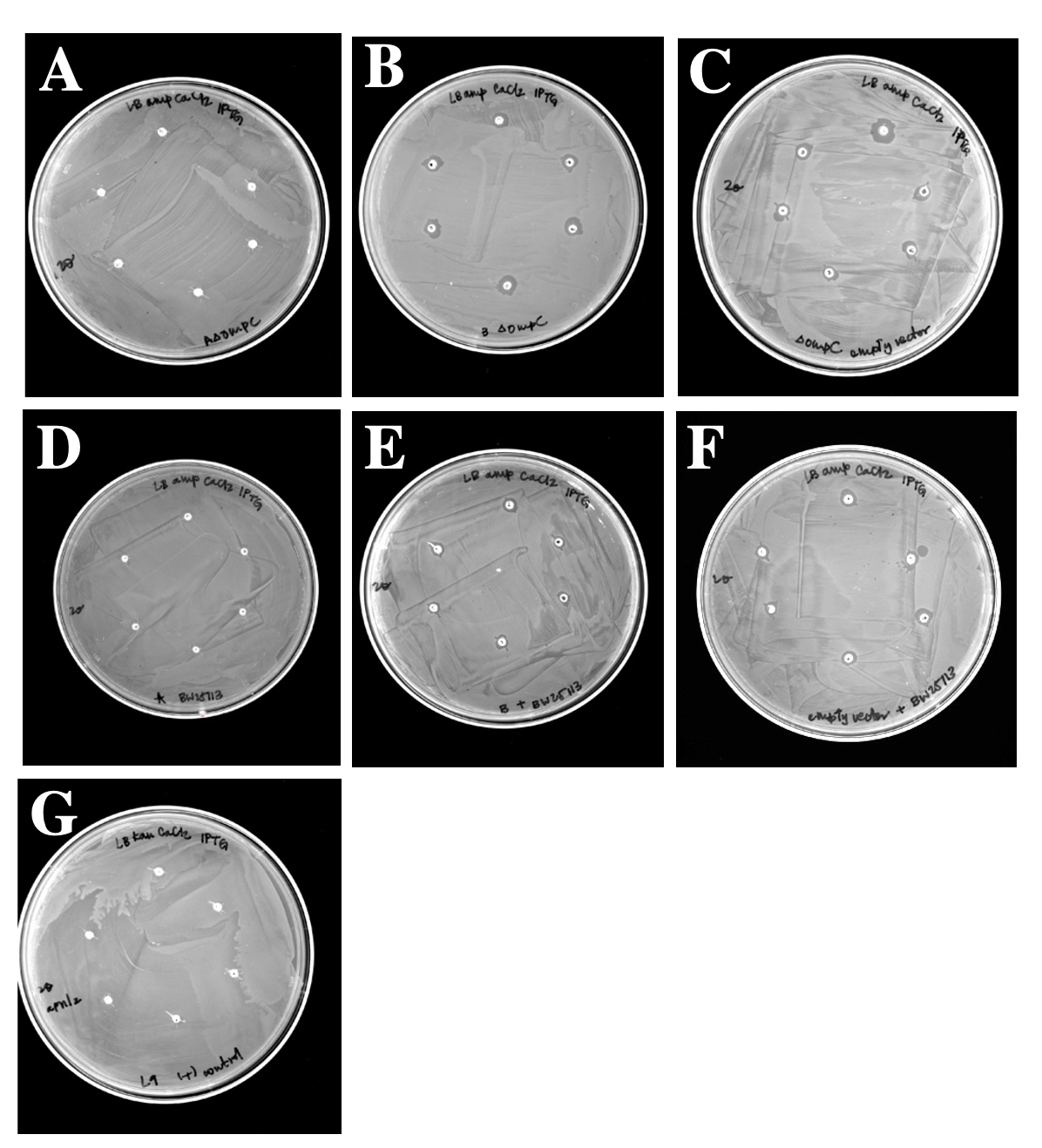
**Table S2. Primer sequences for PCR amplification.** F and R represent forward and reverse primer sequences respectively.



**Figure S1. Blue-white colony screening following transformation of competent TOP10 cells with pCR.21-*wbbL-a.*** Cells were transformed with 4µL of PCR product in undiluted (A), 1:10 dilution (B), positive control (pUC19), TOP10 positive control (D), and a water negative control (E). Blue colonies acquired the empty vector, whereas white colonies acquired the plasmid with an insert.



**Figure S2. Transformation of cells with pCR2.1-*wbbL-a* and pCR2.1-*wbbL-ꞵ* .** Chemically competent BW25113 cells were transformed with pCR2.1-*wbbL-ꞵ* (A), pCR2.1-*wbbL-a* (B), or an empty vector (E). Similarly, JW2203-1 cells were transformed with pCR2.1-*wbbL-ꞵ* (G), pCR2.1-*wbbL-a* (H), or an empty vector (D).1:100 dilutions of the pCR2.1-*wbbL-a* and *ꞵ* transformed cells were plated on LB-agar ampicillin plates and transformation efficiencies were calculated to be 6.1 x 105 CFU/ug (A), 3.8 x 105 CFU/ug (B), 3.3 x 105 CFU/ug (G), and 8.2 x 104 CFU/ug (H). JW2203-1 cells transformed with pUC19 (C) serve as a positive control, while JW2203-1 cells transformed with water (F) serve as a negative control for transformation.

**Figure S3. Stab assay results reveal resistance in cells transformed with pCR2.1-*wbbL-𝛼*.** Transformation was performed in three conditions pCR2.1-*wbbL-𝛼*, pCR2.1-*wbbL-ß*, and empty vector in *∆ompC* JW2203-1 cells (A, B, C) and BW25113 cells (D, E, F), and a positive L9 control (G). 



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| Sample\_A\_F-M13F  NNNNNNNNNNNNNNGGCGANTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCCCAAGCTTCTCGAGTTACGGGTGAAAAACTGATGAAATTCGATCAAAGTTGCGATTTGATAAAATACGTTTTCTGGCTAAATATCTAAAAGTACTTTTTAAGTGCCATCTGAAGGCTTTTGAAAAAAAACTTCGATTGTCATGATGAGCATAATGTATCGCATGAAAAGCGGGAACATAATGAAGTCTGACACCAGCCAGGCTAAGCCTCAAGCACAGGTCAATATCTTCACAGTACATAAAGTAACCTTGATCGAAGCCATTTACACGCACAAAATCTGAAAAACGTACCAGCATAAATGATCCTGCGCACCAATCAACAACCGTATCAGAATAGATACTTTCTTTAGGAATTTTTGTTTTATTAATCCCTAACATAAATGACACAATAAAATCAGAAAGCACAGGAAATTTTCTTACGGAATAATCATGTAAAGATTTCGCTTCATCTCGGAACAGGCATAATGTACTAAAAGCATAACGCTTACTTTCGACATATTTAATATATGTCAGCAAATCATCATGCTTCATGATGATATCGGGATTCAAAAACAAAATGTAATCATCATCTGCGGGTCTATATTTTTCCTTTACATACGCCACCGCAATATTATTATTATGACCAAAGCCGTATACACCTCCACTAATATAGTCCAGGCCTGCATAATGCTGGCATATTTGTTTCAATAATAGAGAGTCTTTGTTGTCGCGTACGATAATCTTGTAGTGCTCATCGTCAGCATTAANATTTTCGAGTAATTTTTTGATGTAGTCTTTCATGTCCGTGGGAAACGATTATTATATATACCATATGAATTTCGGGAAAGGGCGAATTCCAGCNCA |



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| Sample\_A\_R-M13R  GNNNNNNNNNNNCGAGCTCGGATCCNCTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCCCGAATTCATATGGTATATATAATAATCGTTTCCCACGGACATGAAGACTACATCAAAAAATTACTCGAAAATCTTAATGCTGACGATGAGCACTACAAGATTATCGTACGCGACAACAAAGACTCTCTATTATTGAAACAAATATGCCAGCATTATGCAGGCCTGGACTATATTAGTGGAGGTGTATACGGCTTTGGTCATAATAATAATATTGCGGTGGCGTATGTAAAGGAAAAATATAGACCCGCAGATGATGATTACATTTTGTTTTTGAATCCCGATATCATCATGAAGCATGATGATTTGCTGACATATATTAAATATGTCGAAAGTAAGCGTTATGCTTTTAGTACATTATGCCTGTTCCGAGATGAAGCGAAATCTTTACATGATTATTCCGTAAGAAAATTTCCTGTGCTTTCTGATTTTATTGTGTCATTTATGTTAGGGATTAATAAAACAAAAATTCCTAAAGAAAGTATCTATTCTGATACGGTTGTTGATTGGTGCGCAGGATCATTTATGCTGGTACGTTTTTCAGATTTTGTGCGTGTAAATGGCTTCGATCAAGGTTACTTTATGTACTGTGAAGATATTGACCTGTGCTTGAGGCTTAGCCTGGCTGGTGTCAGACTTCATTATGTTCCCGCTTTTCATGCGATACATTATGCTCATCATGACAATCGAAGTTTTTTTTCAAAAGCCTTCAGATGGCACTTAAAAAGTACTTTTAGATATTTAGCCAGAAAACGTATTTTATCAAATCGCAACTTTGATCGAATTTCATCAGTTTTTCACCCGTAACTCGAGAAGCTTGGGAAGGCNAATTCTGCANATATCCATCACACTGGCGGCNGCTCGAGCATGCATCTAGA |

**Figure S4. Sanger sequencing results of pCR2.1-*wbbL*-𝛼.** Sanger sequencing of pCR2.1-*wbbL*-𝛼 was performed by GeneWiz sequencing facility using M13 forward and reverse primers. The forward (A) and reverse (B) reads are displayed above. The average quality score for both reads was 49.



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| Sample\_B\_F-M13F  NNNNNNNNNNNNNNNGGCGATTGGNCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCCCGAATTCATATGGTATATATAATAATCGTTTCCCACGGACATGAAGACTACATCAAAAAATTACTCGAAAATCTTAATGCTGACGATGAGCACTACAAGATTATCGTACGCGACAACAAAGACTCTCTATTATTGAAACAAATATGCCAGCATTATGCAGGCCTGGACTATATTAGTGGAGGTGTATACGGCTTTGGTCATAATAATAATATTGCGGTGGCGTATGTAAAGGAAAAATATAGACCCGCAGATGATGATTACATTTTGTTTTTGAATCCCGATATCATCATGAAGCATGATGATTTGCTGACATATATTAAATATGTCGAAAGTAAGCGTTATGCTTTTAGTACATTATGCCTGTTCCGAGATGAAGCGAAATCTTTACATGATTATTCCGTAAGAAAATTTCCTGTGCTTTCTGATTTTATTGTGTCATTTATGTTAGGGATTGATAAAACAAAAATTCCTAAAGAAAGTATCTATTCTGATACGGTTGTTGATTGGTGCGCAGGATCATTTATGCTGGTACGTTTTTCAGATTTTGTGCGTGTAAATGGCTTCGATCAAGGTTACTTTATGTACTGTGAAGATATTGACCTGTGCTTGAGGCTTAGCCTGGCTGGTGTCAGACTTCATTATGTTCCCGCTTTTCATGCGATACATTATGCTCATCATGACAATCAAAGTTTTTTTTCAAAAGCCTTCAGATGGCACTTAAAAAGTACTTTTAGATATTTAGCCAGAAAACGTATTTTATCAAATCGCAACTTTGATCGAATTTCATCAGTTTTTCACCCGTAACTCGAGAGCCTTGGGAANGGCGAATTCCAGCACACTGGCGGCCGTNACTANTGGATCCGANCTCGGTAC |



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| Sample\_B\_R-M13R  GNNNNNNNNNNNNNNGAGCTCGGATCCNCTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCCCAAGCTTCTCGAGTTACGGGTGAAAAACTGATGAAATTCGATCAAAGTTGCGATTTGATAAAATACGTTTTCTGGCTAAATATCTAAAAGTACTTTTTAAGTGCCATCTGAAGGCTTTTGAAAAAAAACTTTGATTGTCATGATGAGCATAATGTATCGCATGAAAAGCGGGAACATAATGAAGTCTGACACCAGCCAGGCTAAGCCTCAAGCACAGGTCAATATCTTCACAGTACATAAAGTAACCTTGATCGAAGCCATTTACACGCACAAAATCTGAAAAACGTACCAGCATAAATGATCCTGCGCACCAATCAACAACCGTATCAGAATAGATACTTTCTTTAGGAATTTTTGTTTTATCAATCCCTAACATAAATGACACAATAAAATCAGAAAGCACAGGAAATTTTCTTACGGAATAATCATGTAAAGATTTCGCTTCATCTCGGAACAGGCATAATGTACTAAAAGCATAACGCTTACTTTCGACATATTTAATATATGTCAGCAAATCATCATGCTTCATGATGATATCGGGATTCAAAAACAAAATGTAATCATCATCTGCGGGTCTATATTTTTCCTTTACATACGCCACCGCAATATTATTATTATGACCAAAGCCGTATACACCTCCACTAATATAGTCCAGGCCTGCATAATGCTGGCATATTTGTTTCAATAATAGAGAGTCTTTGTTGTCGCGTACGATAATCTTGTAGTGCTCATCG  TCAGCATTAAGATTTTCGAGTAATTTTTTGATGTAGTCTTCATGTCCGTGGGAAACGATTATTATATATACCATATGAATTTCGGGAAGGGCGAATTCTGCAGATATCCATCANACTGGCGGCCGCTCGAGCATGNCATCTAGAGGGNCCANTTCGCCCTATANTGGAGTCGTA |

**Figure S5. Sanger sequencing results pCR2.1-*wbbL-ß*.** Sanger sequencing of pCR2.1-wbbL-*ß* was performed by GeneWiz sequencing facility using M13 forward and reverse primers. The forward (A) and reverse (B) reads are displayed above. The average quality score of the forward read was 49, while the quality score of the forward read was 48.