**Supplementary material**

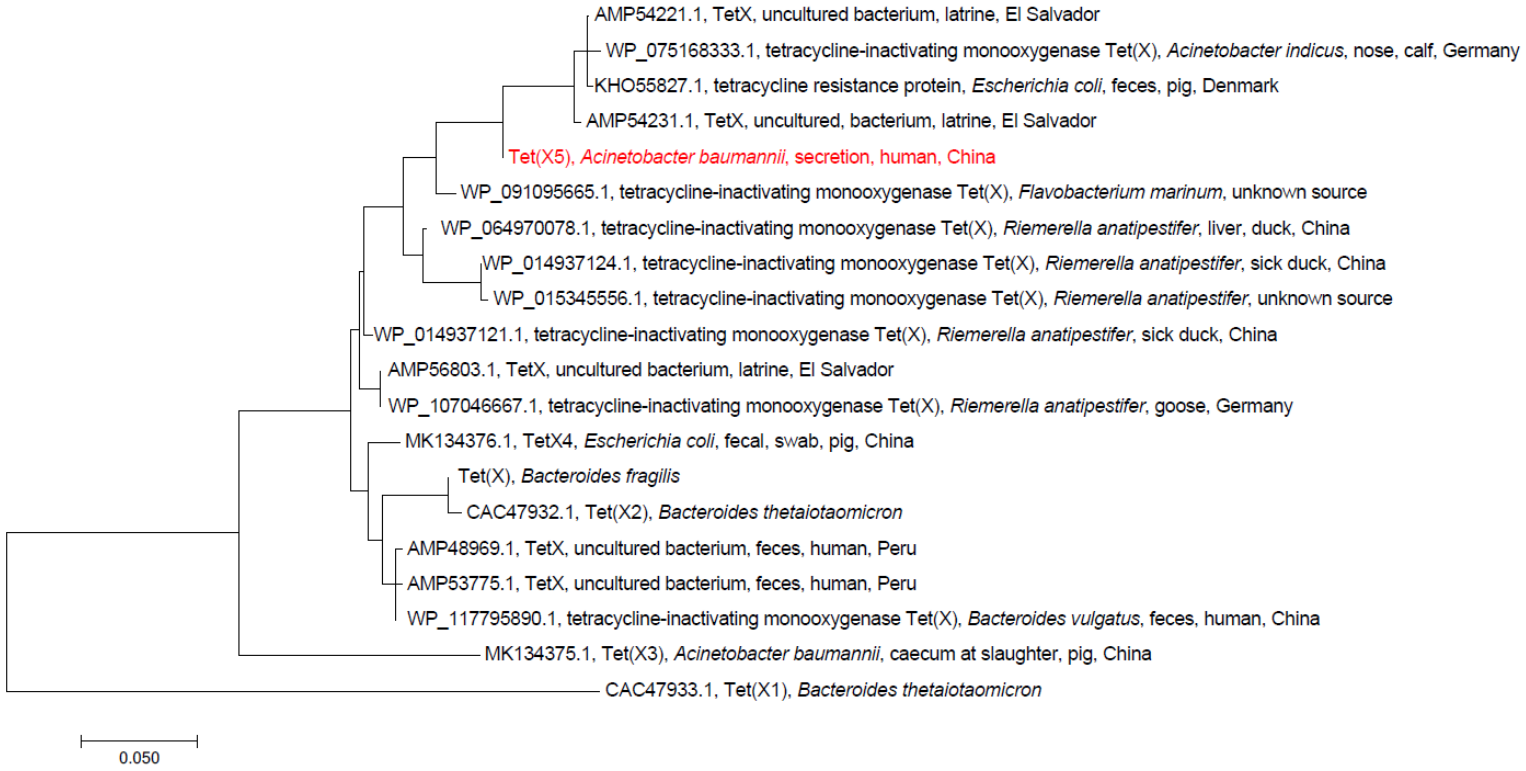


**FIG S1** Phylogenetic analysis of the Tet(X5) protein sequence. Phylogenetic tree of the deduced amino acid sequences of putative phosphoethanolamine transferases from different bacterial species. The tree was generated using MEGA 7 by Maximum likelihood method.

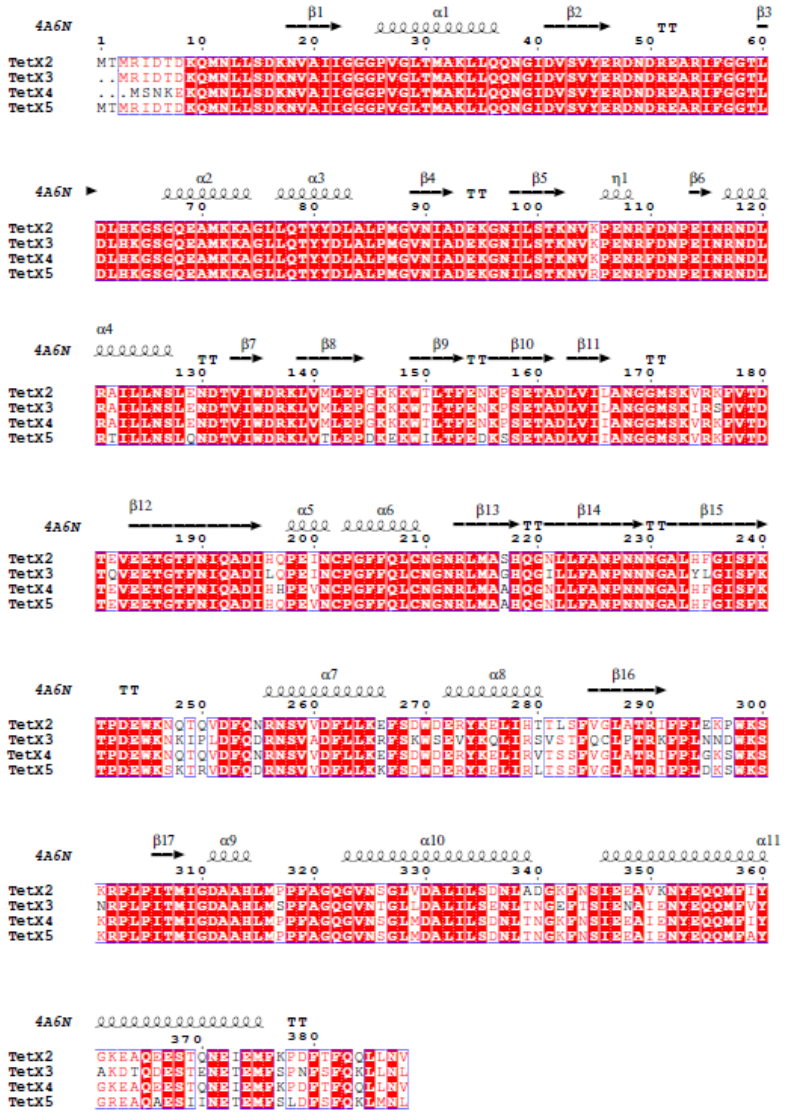


**FIG S2** BLAST alignments of amino acid sequences of four *tet*(X) variants using Clustal 2.1 and ESPript 3.0 (https://www.genome.jp/tools-bin/clustalw and http://espript.ibcp.fr/ESPript/cgi-bin/ESPript.cgi). Original Tet(X2)-tigecycline complex (PDB ID: 4A6N) served as the reference for secondary structure depiction.

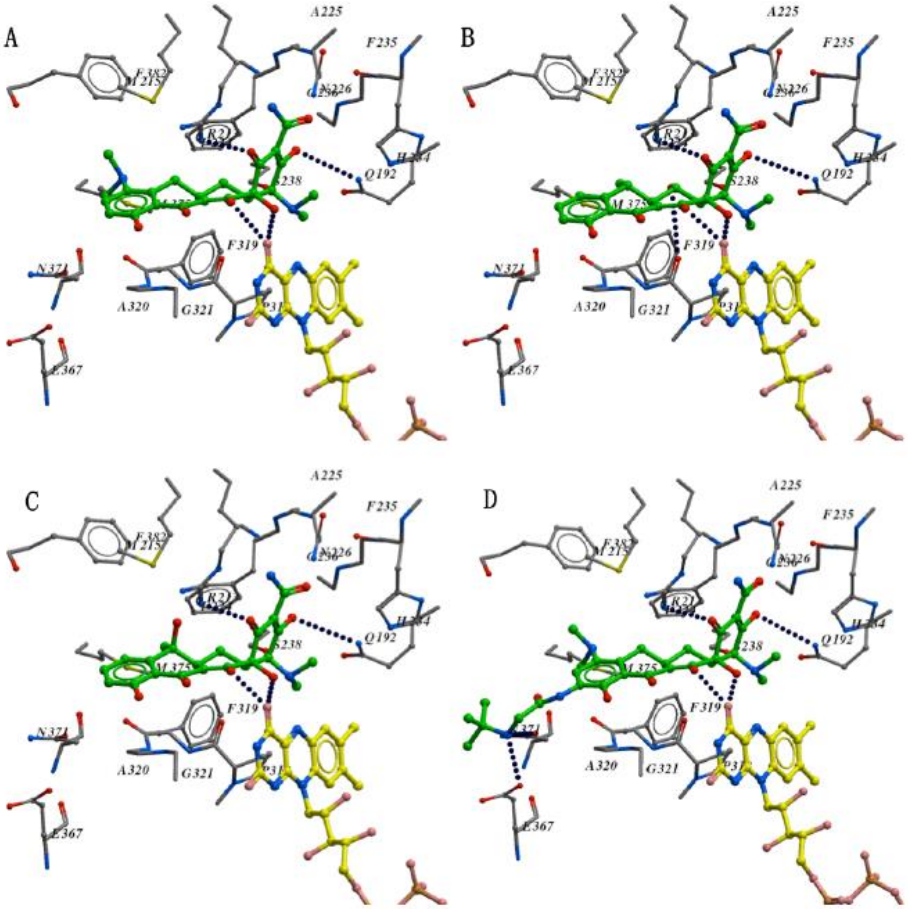


**FIG S3** Predicted binding conformations of minocycline (A), doxycycline (B), tetracycline (C) and tigecycline (D) in the substrate-binding site of the modelled Tet(X5) structure. The binding conformations suggest that the tetracycline core has an essentially identical interaction with Tet(X5). Hydrogen bonds are depicted by blue dotted lines.

**TABLE S1 Minimum inhibitory concentration (MIC) values of various antimicrobial agents against *Acinetobacter baumannii* AB17H194**

| | MIC (mg/L) of various antimicrobials |
|---|---|
| | AB17H194 |
| Tetracycline | 256 |
| Doxycycline | 32 |
| Minocycline | 8 |
| Tigecycline | 32 |
| Eravacycline | 32 |
| Omadacycline | 32 |
| Piperacillin | 64 |
| Ceftazidime | 16 |
| Cefepime | 32 |
| Aztreonam | 0.5 |
| Imipenem | 0.5 |
| Meropenem | 1 |
| Gentamycin | >256 |
| Amikacin | >256 |
| Ciprofloxacin | 64 |
| Levofloxacin | 32 |
| Colistin | 0.6 |

**TABLE S2 Predicted binding affinity of tetracyclines to TetX5.**

| | Doxycycline | Minocycline | Tetracycline | Tigecycline |
|---|---|---|---|---|
| Tet(X5) | -6.9 | -7.3 | -6.5 | -8.7 |