

Supplementary Figures

Figure S1

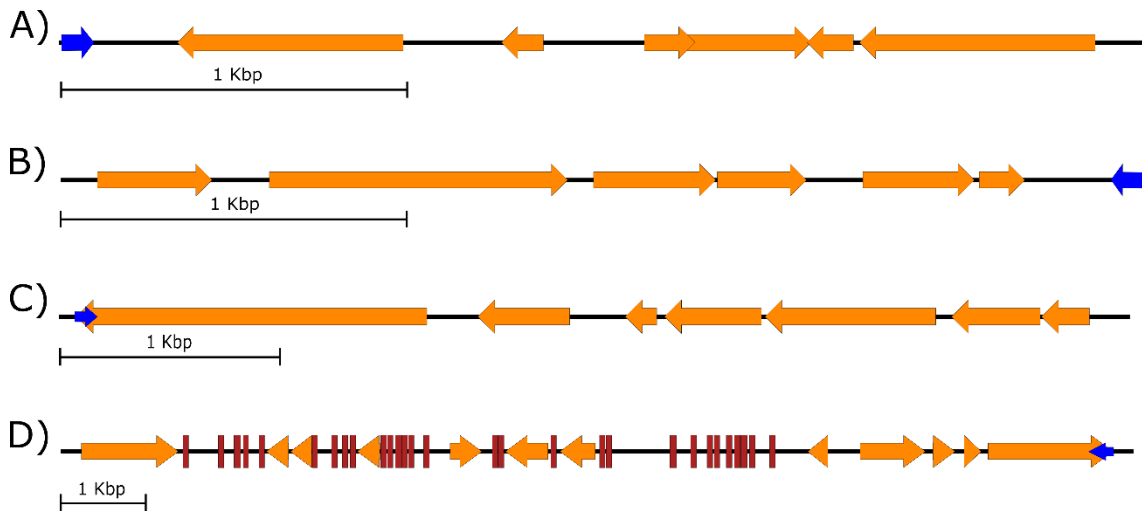


Fig. S1. Inverted repeats of pCBMA213_1. Inverted terminal repeats of pCBMA213_1 on the left side (A) and on right side (B). Inverted repeats flanking the left (C) and right (D) sides of a ~89 kb region (169,352 - 258,453 bp). The blue and orange arrows represent the inverted repeats and protein-coding genes, respectively, while the red blocks represent tRNA genes. The scale is shown below each figure.

Figure S2

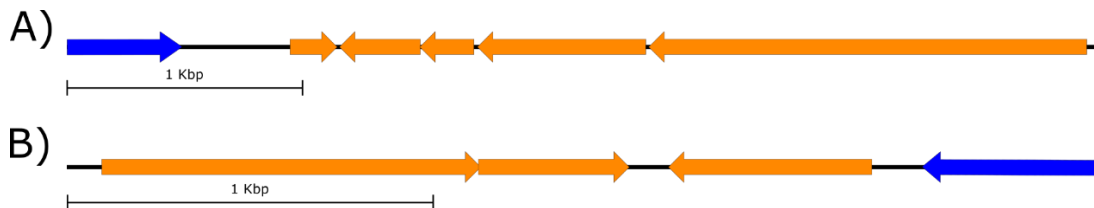


Fig. S2. Inverted terminal repeats of pCBMA213_3 on the left side (A) and on right side (B). The blue and orange arrows represent the inverted terminal repeats and protein-coding genes, respectively. The scale is shown below each figure.

Figure S3

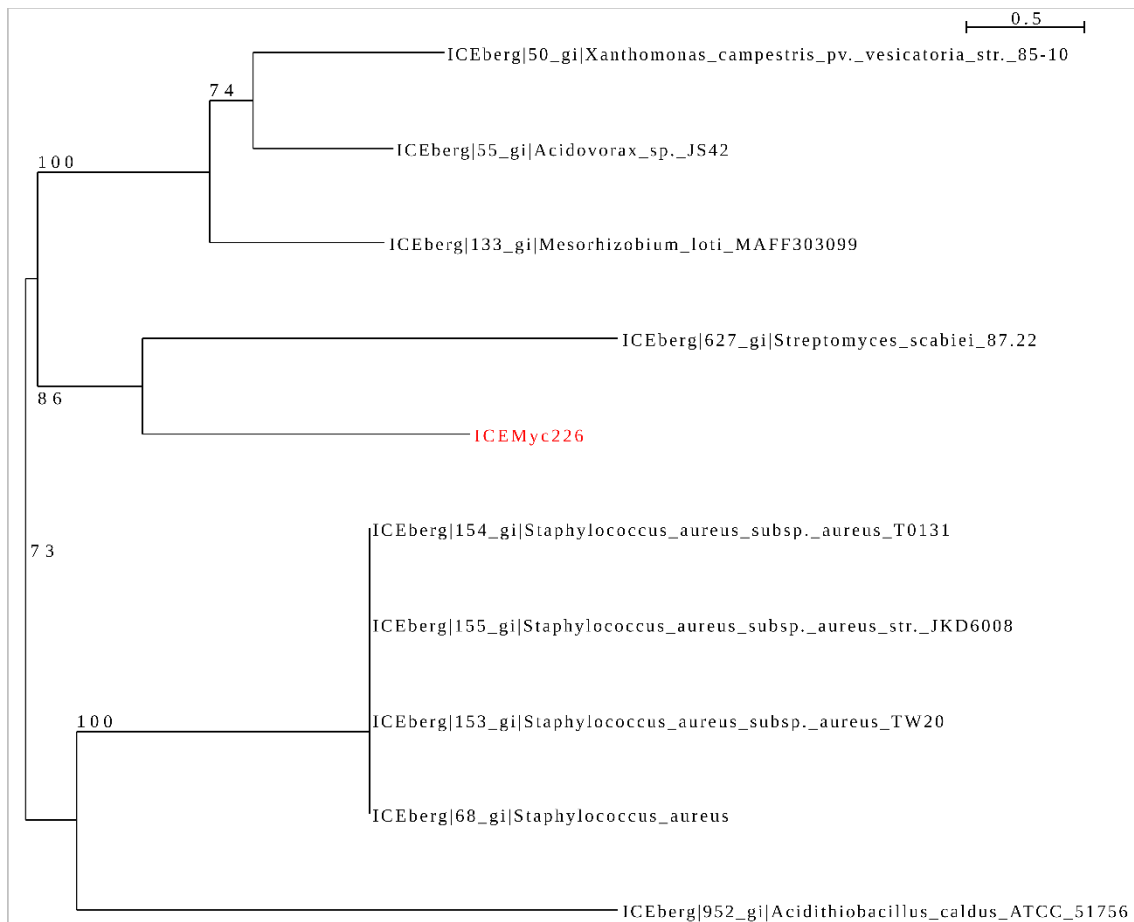


Fig. S3. Maximum likelihood tree (100 bootstrap replicates) of ICEMyc226 DDE-integrase/transposase/recombinase with the most similar integrases and transposases from the ICEberg database.

