



Figure S3. Molecular phylogenetic analysis of the sequences of relaxases of IMEs of the *IME_oriT* family, ICEs of the Tn916 superfamily and Rep-trans proteins encoded by plasmids of Firmicutes.

Amino acid sequences were aligned using ClustalW. Sequences that were identical were included only once (see Table S2 for further details). The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model. The tree with the highest log likelihood is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches only when higher than 50%. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Evolutionary analyses were conducted in MEGA7 [19].