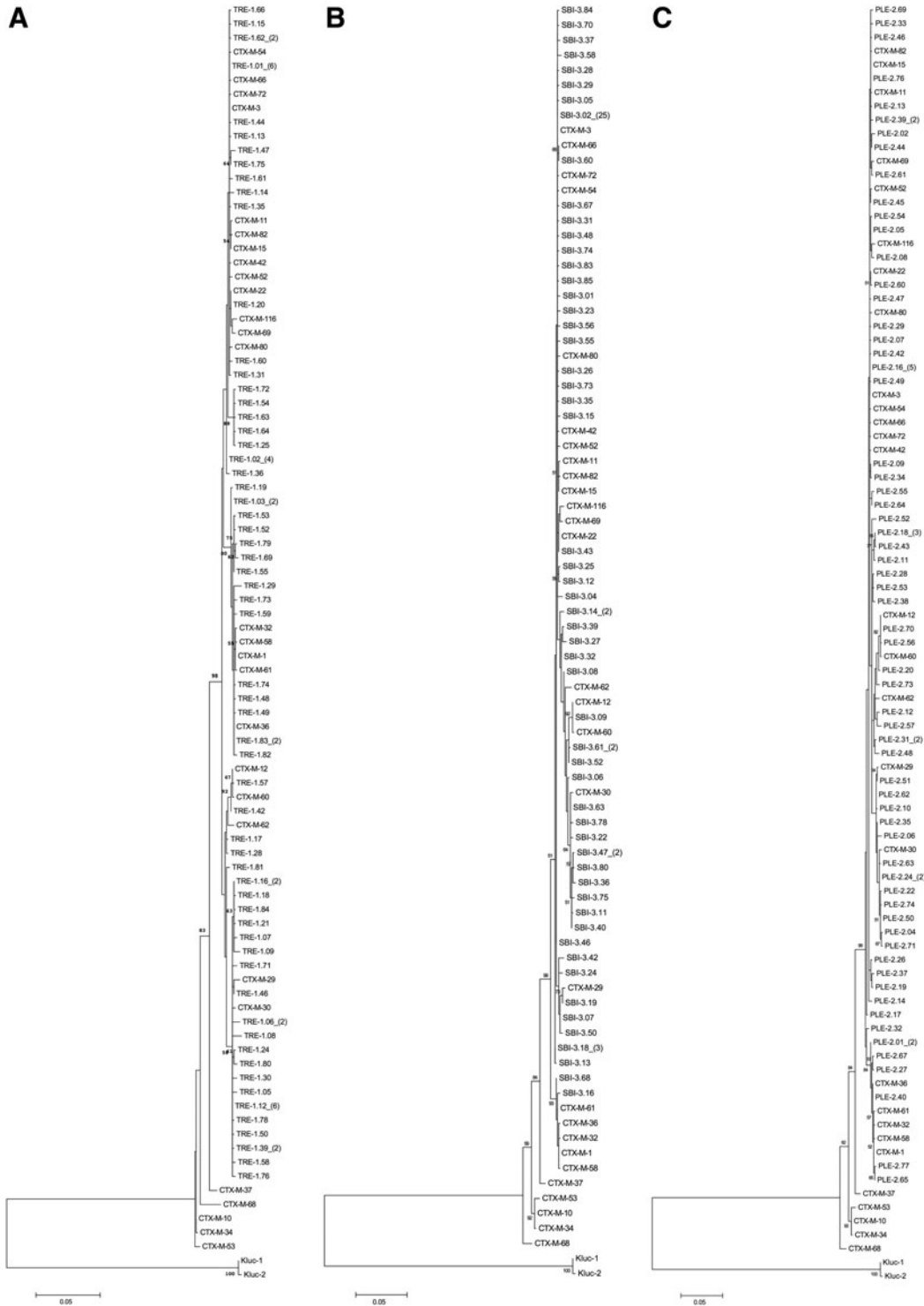


Supplementary Data



SUPPLEMENTARY FIG. S1. Maximum likelihood phylogenetic trees of *bla*_{CTX-M} group 1 clones from (A) the Tijuana River Estuary, (B) the South Bay International Wastewater Treatment Plant, and (C) the Point Loma Wastewater Treatment Plant, including reference sequences. CTX-M-like extended-spectrum β -lactamases (ESBLs), *kluo-1* and *kluo-2*, from *Kluyvera* chromosomes were included as outgroups. Bootstrap values > 50% (1,000 replicates) are shown. Number in parentheses indicates the number of clones represented by the sequence shown. The evolutionary history was inferred using the maximum composite likelihood method³⁸ based on the best-fit evolutionary model: GTR + G (General Time Reversible model with a discrete Gamma distribution used to model evolutionary rate differences among sites). The trees are drawn to scale, with branch lengths measured in the number of substitutions per site. Phylogenetic analysis was performed using MEGA5⁵⁶. Scale bars represent 0.05 substitutions per site.