



Figure S1 Complete phylogenetic tree as shown in Figure 1.

The phylogenetic tree includes all strains in per collapsed node in Figure 1. The nucleotide sequences *gyrB*, *recA*, *rpoD*, *recN* and *topA* were aligned using MUSCLE. MEGAX was used to generate a Maximum Likelihood (ML) tree, with the settings GTR (General Time Reversible) model, Gamma Distributed with Invariant (G+I), and Bootstrap with 1,000 pseudoreplicates. RefSeq assembly accession is shown in parentheses.