

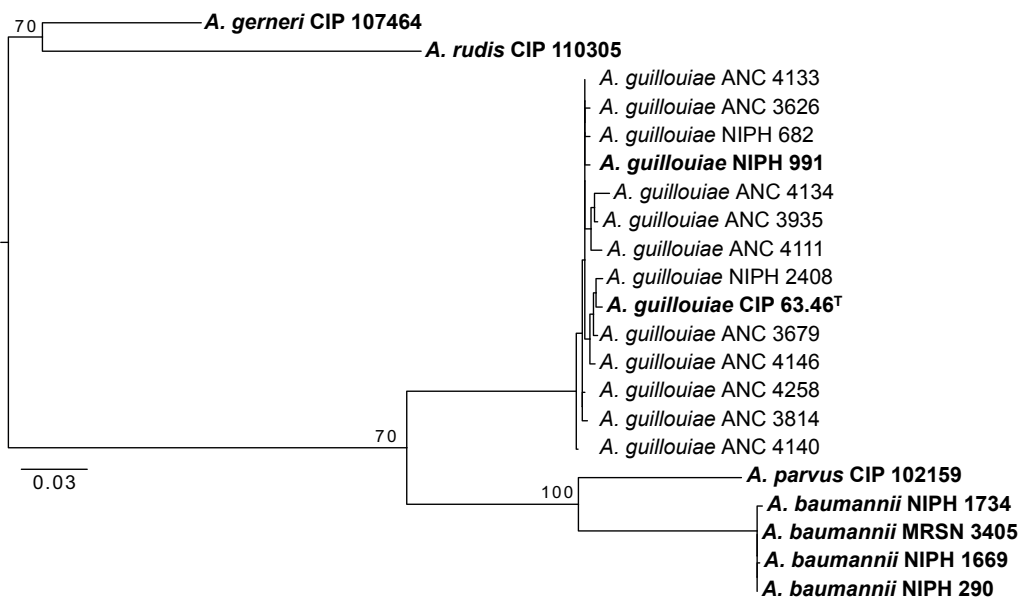
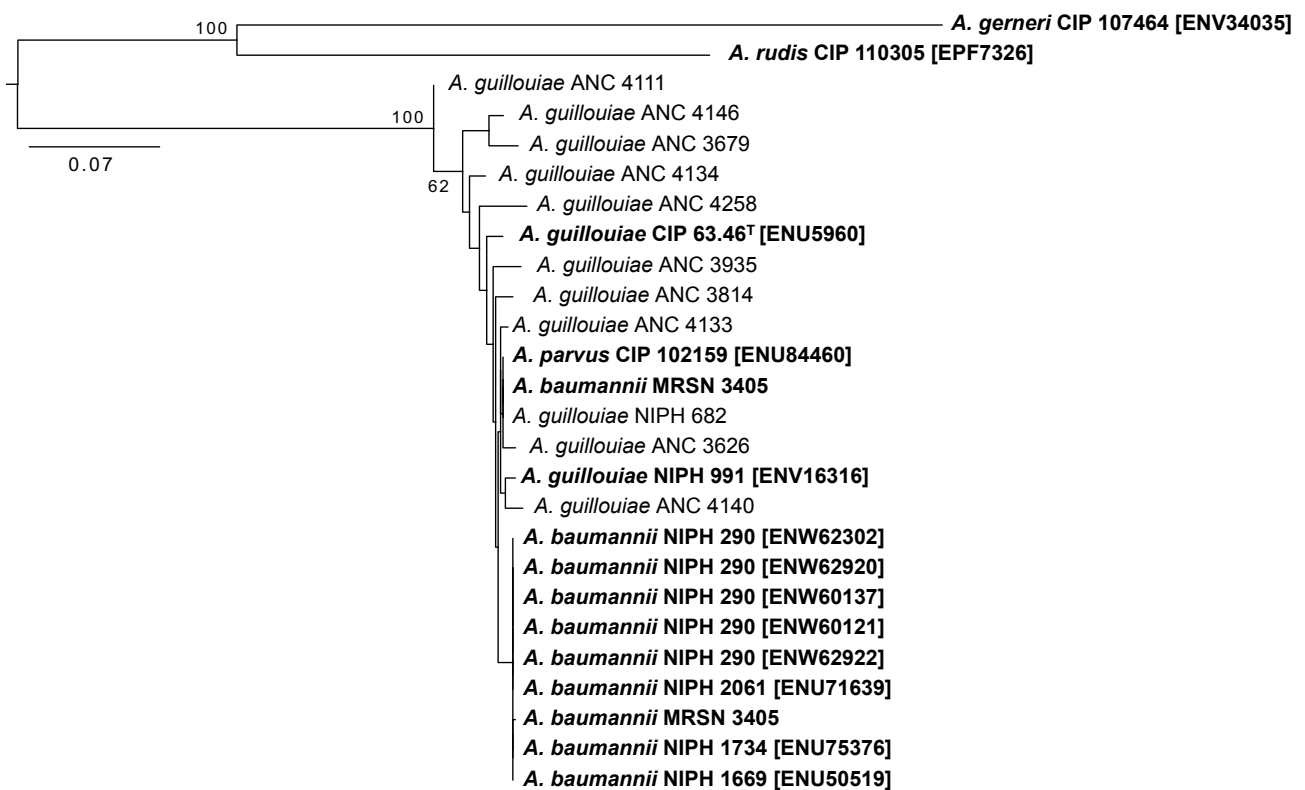
A**B**

FIG S3 Molecular phylogeny of *rpoB* and *aphA6* sequences. Phylogenetic trees of *aphA6* containing *Acinetobacter* were constructed using a partial sequence (861 bp) of *rpoB* (A) or that of the *aphA6* gene (B). Multiple sequence alignments with muscle v3.7 (39) were performed and the phylogenetic trees were reconstructed using the maximum likelihood method implemented in the PhyML program (v3.0 aLRT) with the GTR matrix (40). GenBank accession ID of each protein is indicated in brackets. The trees were rooted using *A. gernerii* and *A. rudis* as outgroups. We performed 100 bootstrap experiments on the sequences to assess the robustness of the topology. Bold, whole genome sequenced strains.