

Fig. S1. Maximum-likelihood (A) and maximum-parsimony (B) trees showing the phylogenetic relationships among strains Mo2-6 , S9, KG4-3 , and 50Mo3-2, and their closely related type strains, based on 16S rRNA gene sequences. Numbers at the nodes represent bootstrap percentages from 1,000 replicates; only values greater than 70% are shown. *Staphylococcus aureus* ATCC 12600^T (X68417) was used as the outgroup. Scale bars in panels A and B represent substitutions per nucleotide and nucleotide substitutions over the entire sequences, respectively.

