

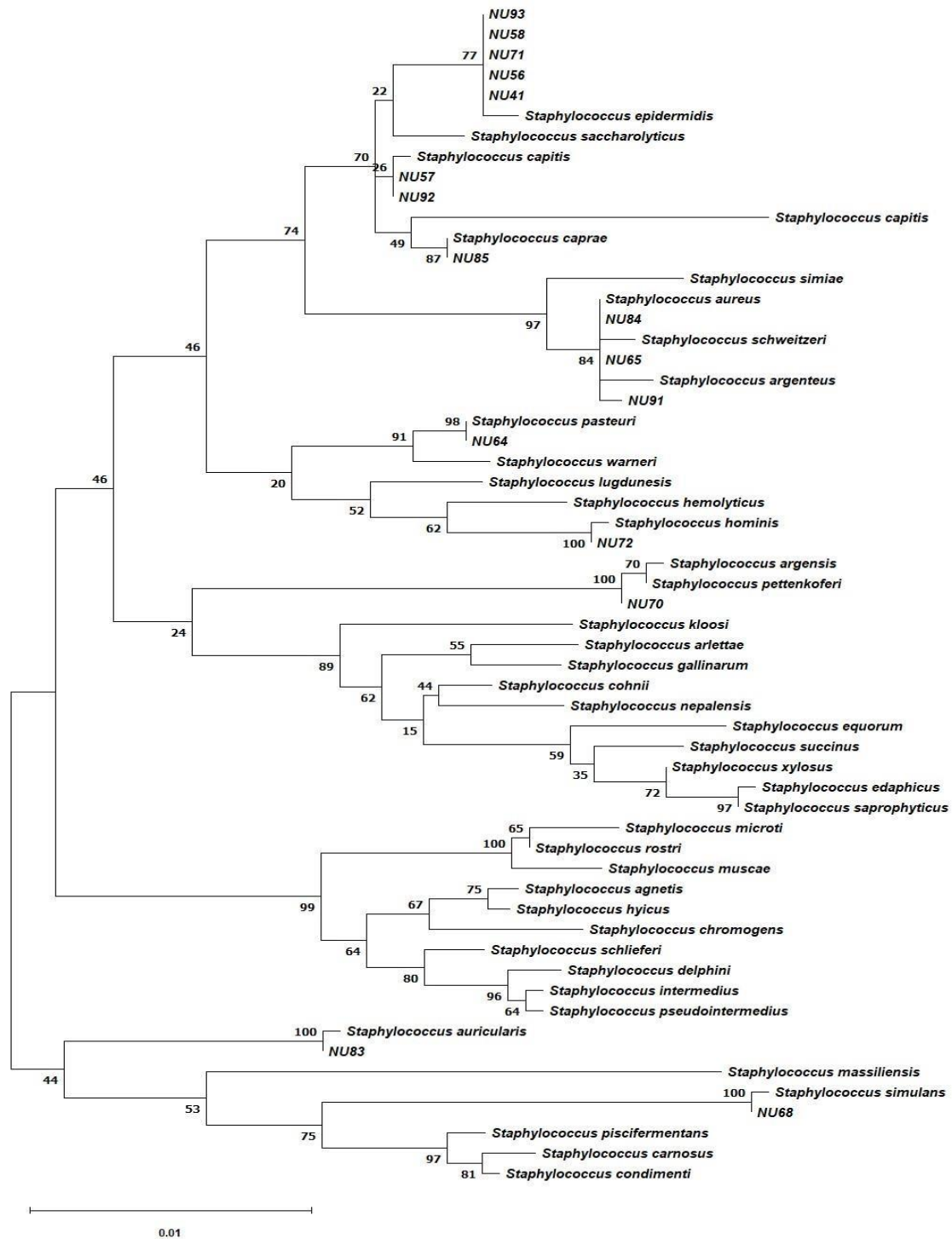


Figure S1: The 16S rRNA-based phylogenetic tree depicting the relationship between *Staphylococcus* species. The tree was constructed by using the maximum-likelihood method. In total, 1000 bootstrap replicates were used. Branch length indicates divergence and bootstrap support values are also shown.