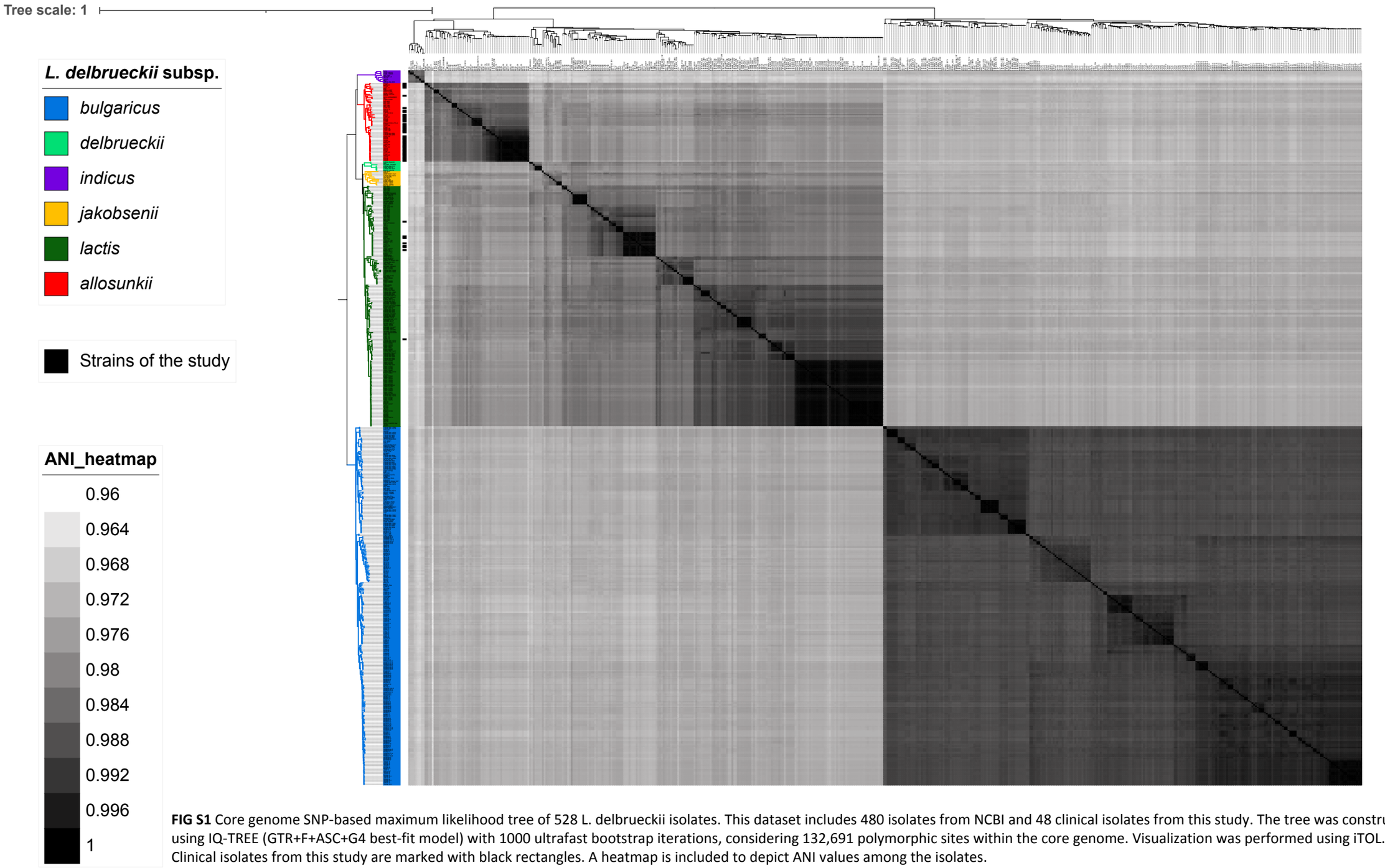

FIG S1 Core genome SNP-based maximum likelihood tree of 528 L. delbrueckii isolates. This dataset includes 480 isolates from NCBI and 48 clinical isolates from this study. The tree was constructed using IQ-TREE (GTR+F+ASC+G4 best-fit model) with 1000 ultrafast bootstrap iterations, considering 132,691 polymorphic sites within the core genome. Visualization was performed using iTOL. Clinical isolates from this study are marked with black rectangles. A heatmap is included to depict ANI values among the isolates.