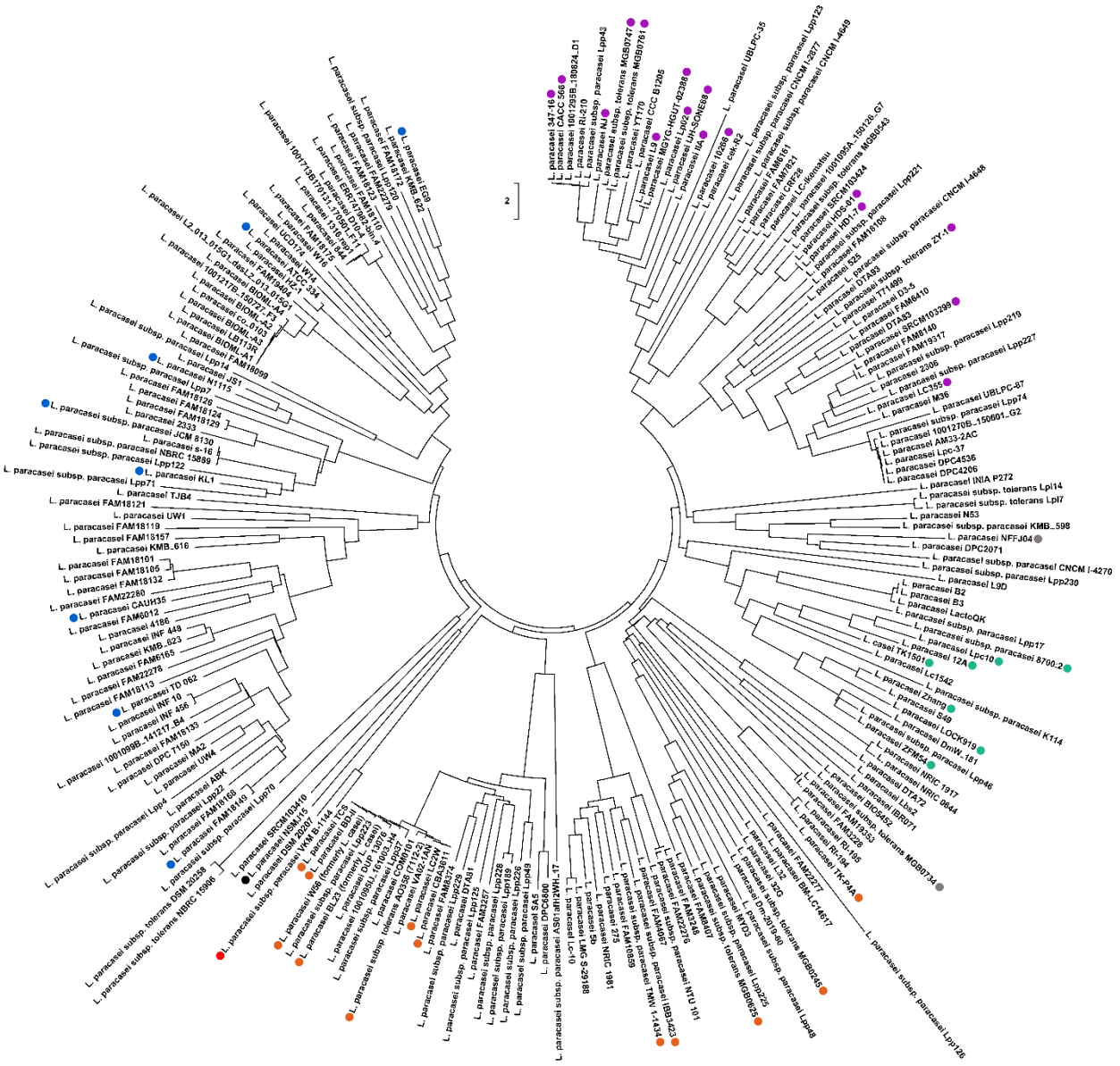

Supplementary Figure S1. Phylogenetic tree inferred from a pairwise distance matrix for 222 sets of 18-mers unique to the species *L. paracasei.* The tree was constructed in MEGA X software using the neighbor-joining method. The allocation of 47 genomes to the phylogroups identified in Figures 2 and 3, is indicated by colored circles. Scale bar shows the Sørensen distance as a percentage.