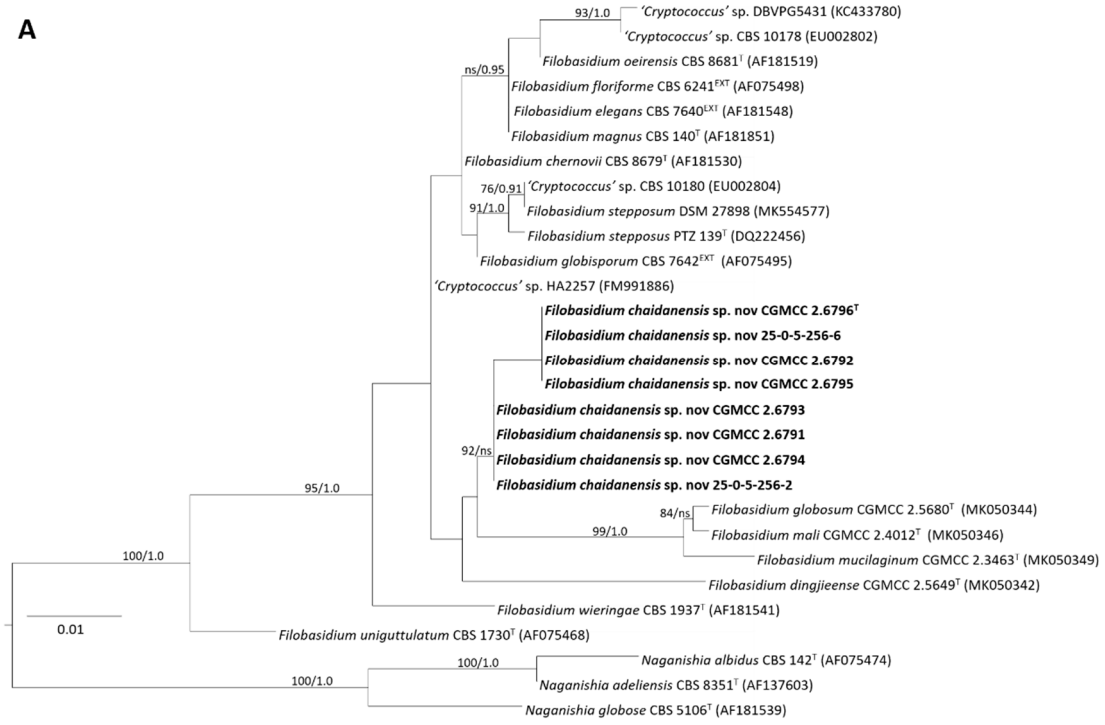
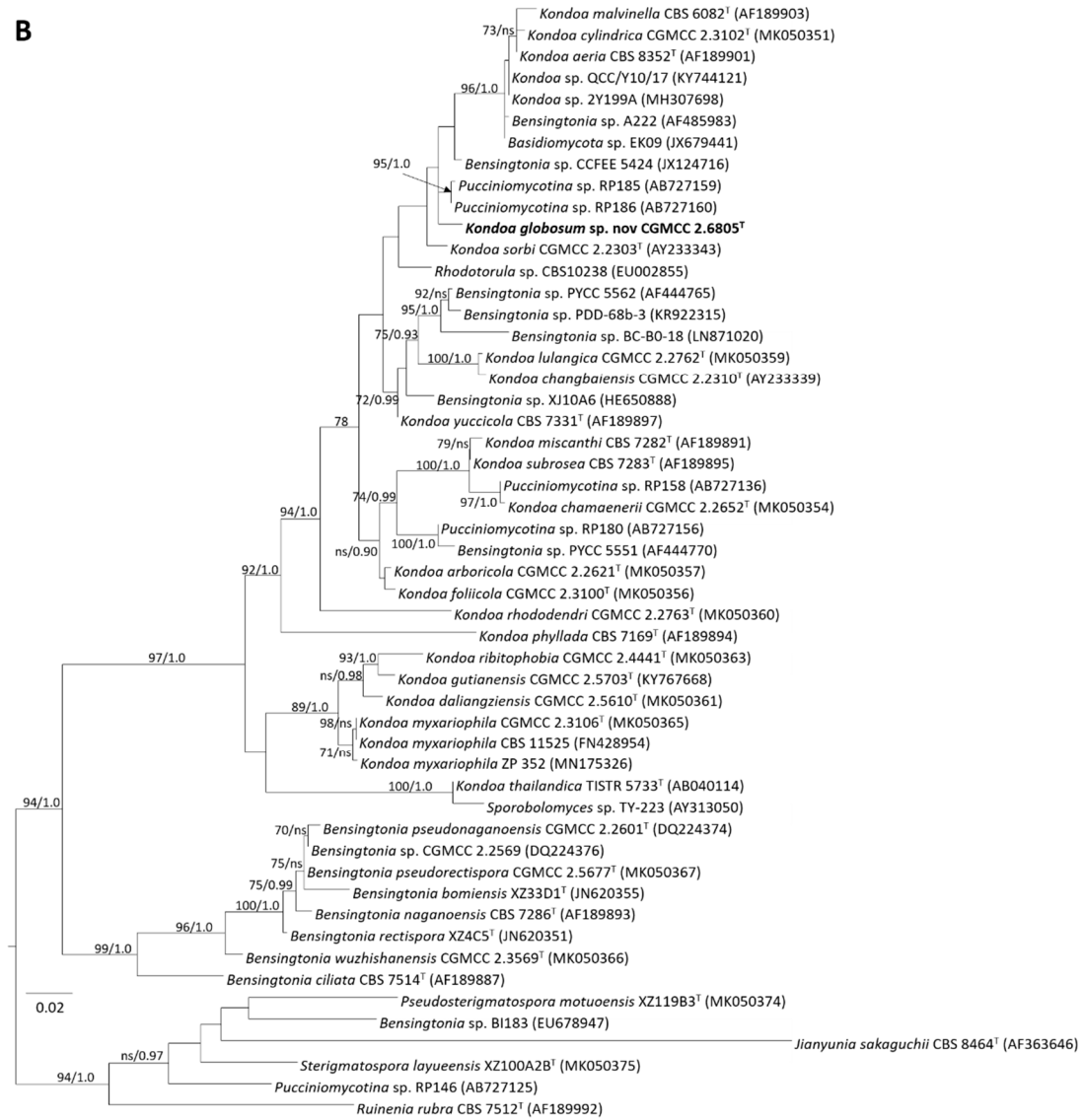


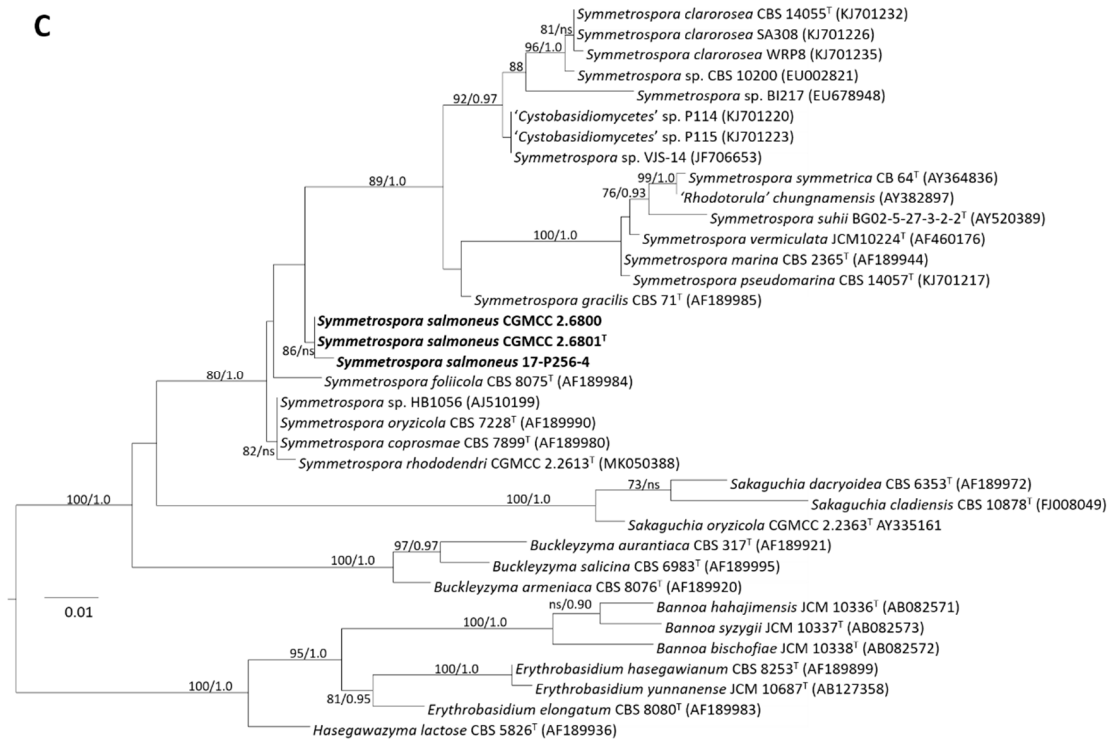
A



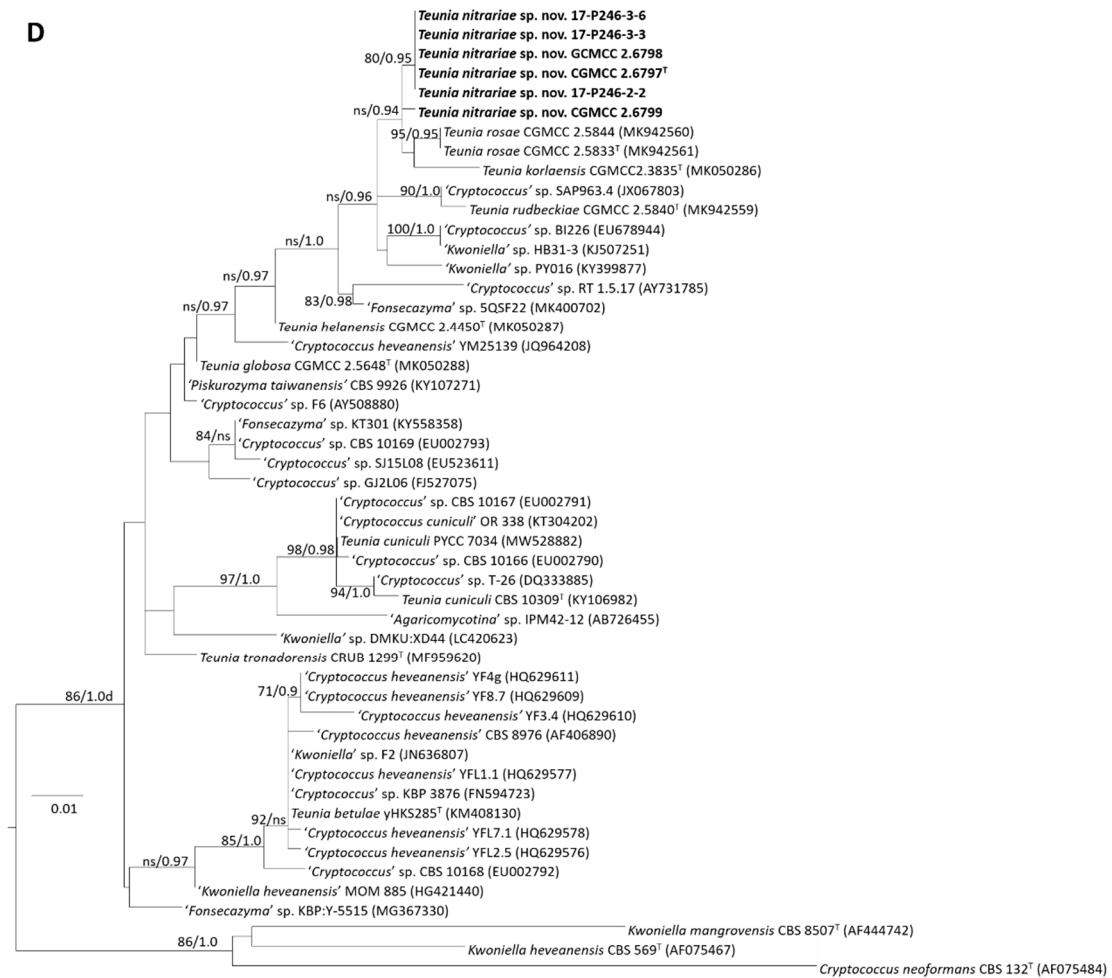
B



C



D



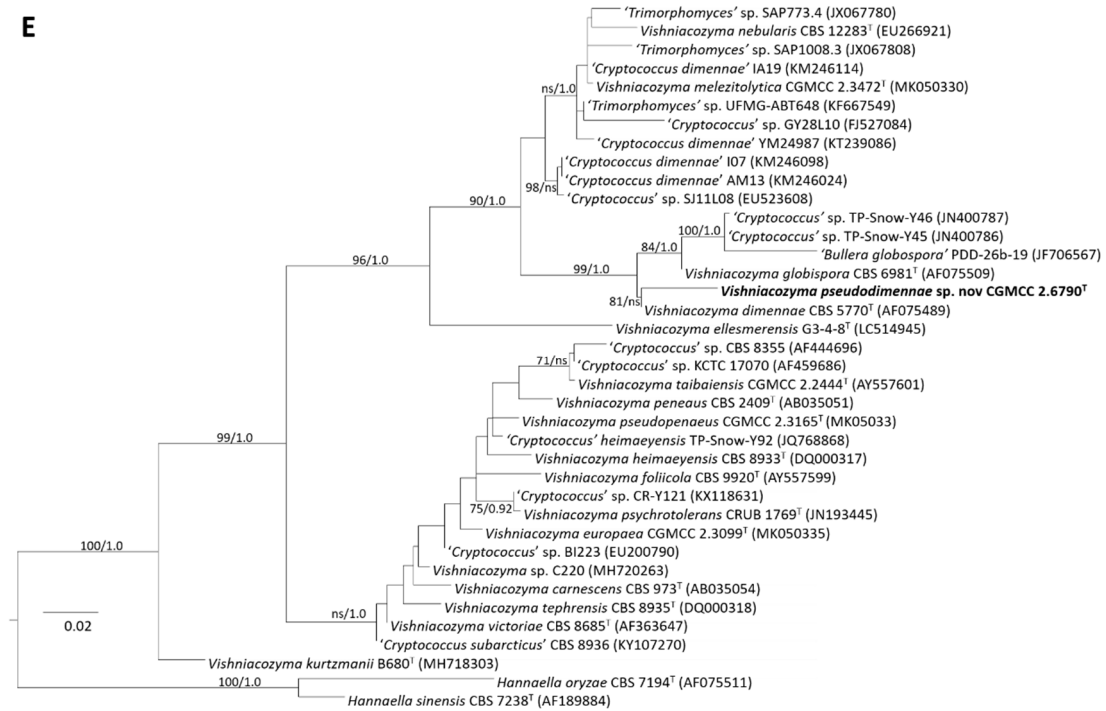


Figure S1. The Maximum likelihood tree of five new yeast species based on D1D2 sequence datasets: (A) *Filobasidium*; (B) *Kondoa*; (C) *Symmetrospora*; (D) *Teunia*; (E) *Vishniacozyma*. The tree backbone is constructed using RAxML and the numbers in each node represent bootstrap percentages (BP) of maximum likelihood from 1000 replicates and Bayesian posterior probabilities (PP). BP values ≥ 70 and PP values ≥ 0.9 were plotted on the branches of the tree. The clade of new species accepted in this study are in bold clades. Scale in 0.02 substitution per nucleotide position.

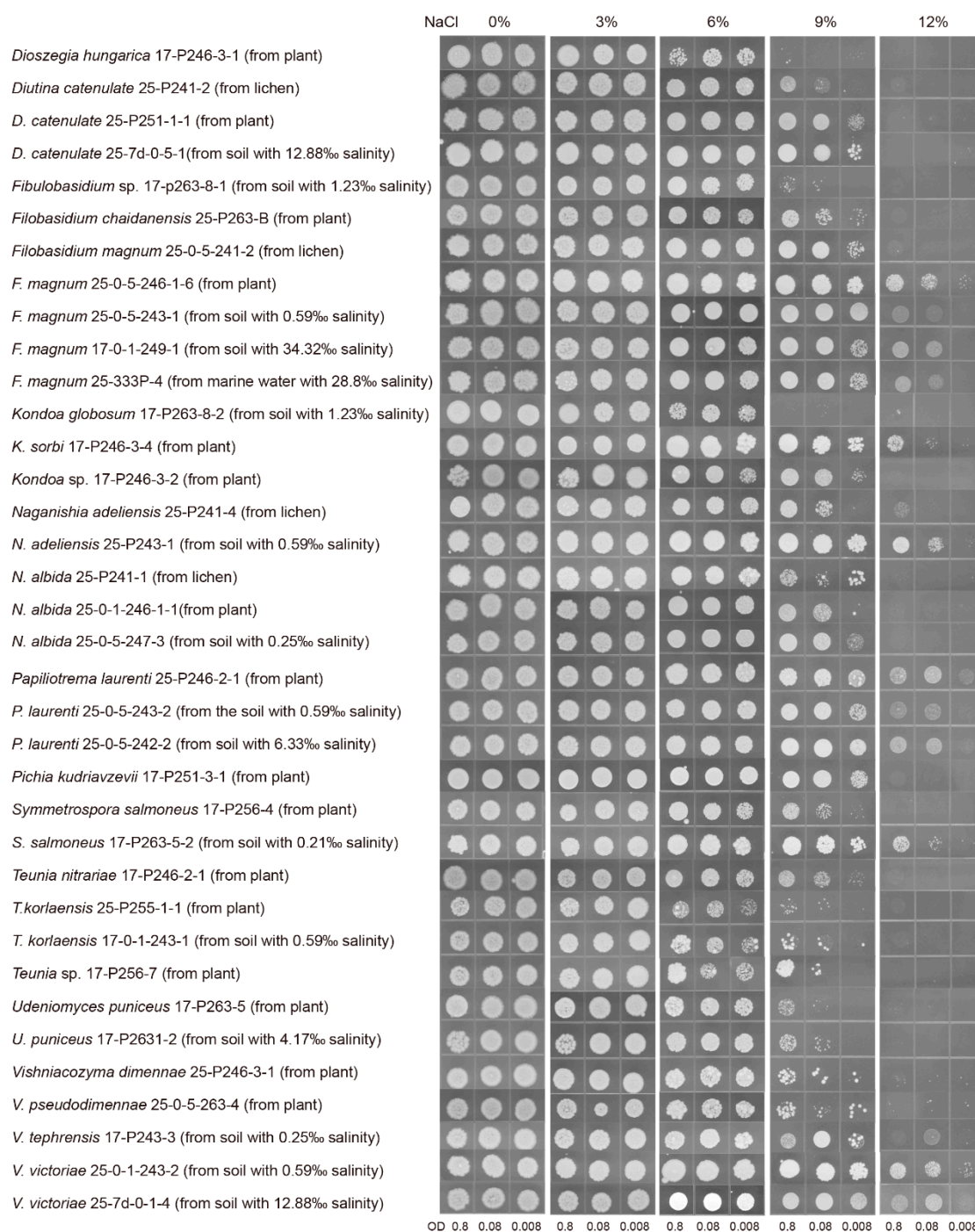


Figure S2. Growth of representative strains of all the species found in this study on YPD plates supplemented with 0%, 3%, 6%, 9%, and 12% (w/v) NaCl. All plates were incubated for 5 days at 20 °C.