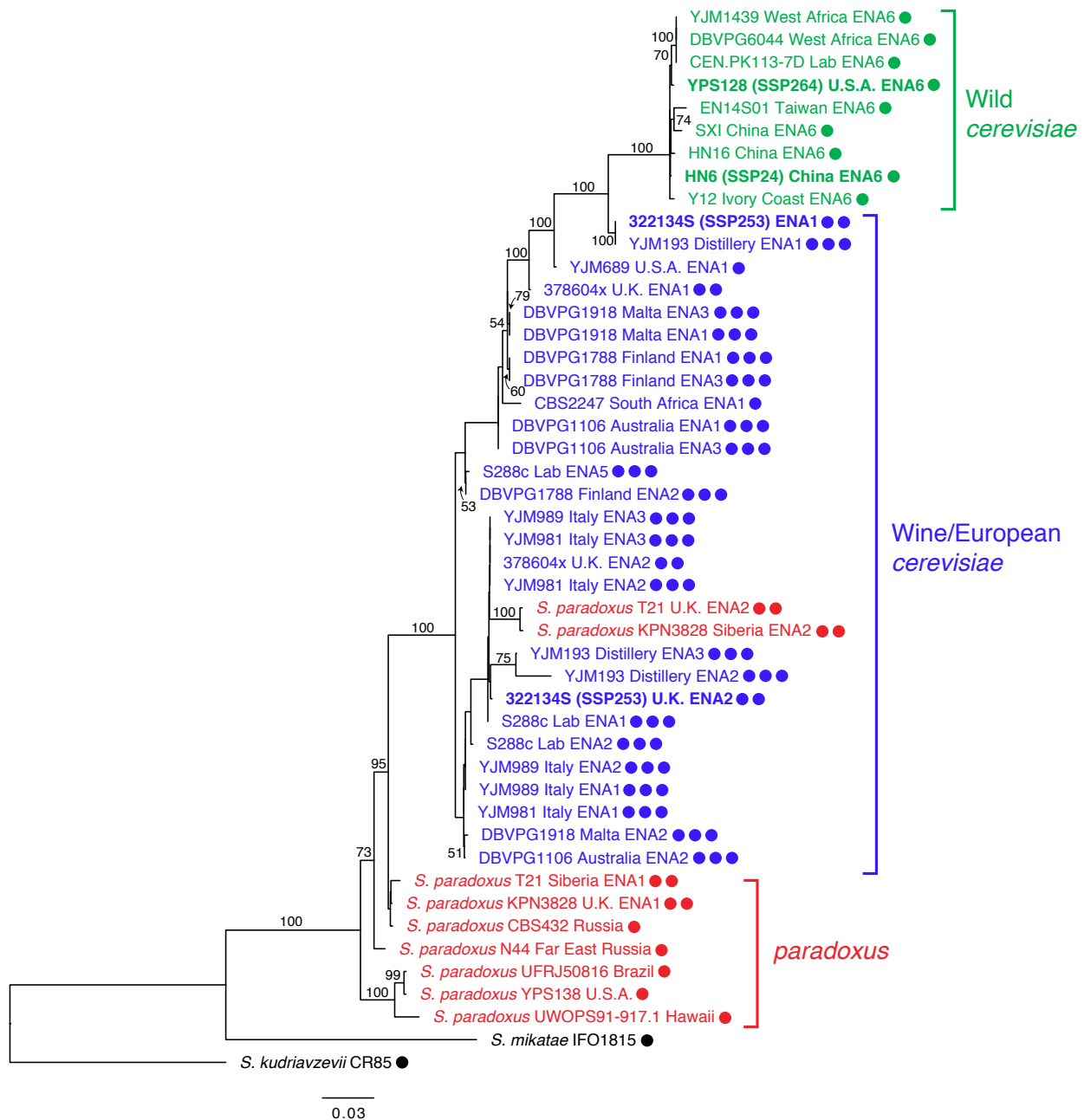




Suppl. Figure 5. Phylogeny of *ENA* genes from *S. cerevisiae* shows introgression related to amplification of copy numbers. Number of gene copies at the ChrIV location indicated as circles after each isolate. Strains used in this study are shown in bold. Data were derived from (GenBank, the 1,000 *S. cerevisiae* genomes project (Peter *et al.* 2018), and the Saccharomyces Genome Resequencing Project (Wellcome Trust Sanger Institute). The phylogeny was generated using a maximum likelihood approach (GTR + I + G model) implemented in PhyML 3.2 (Guindon and Gascuel 2003). Values above nodes indicate clades supported by 50% or more pseudo-replicates.