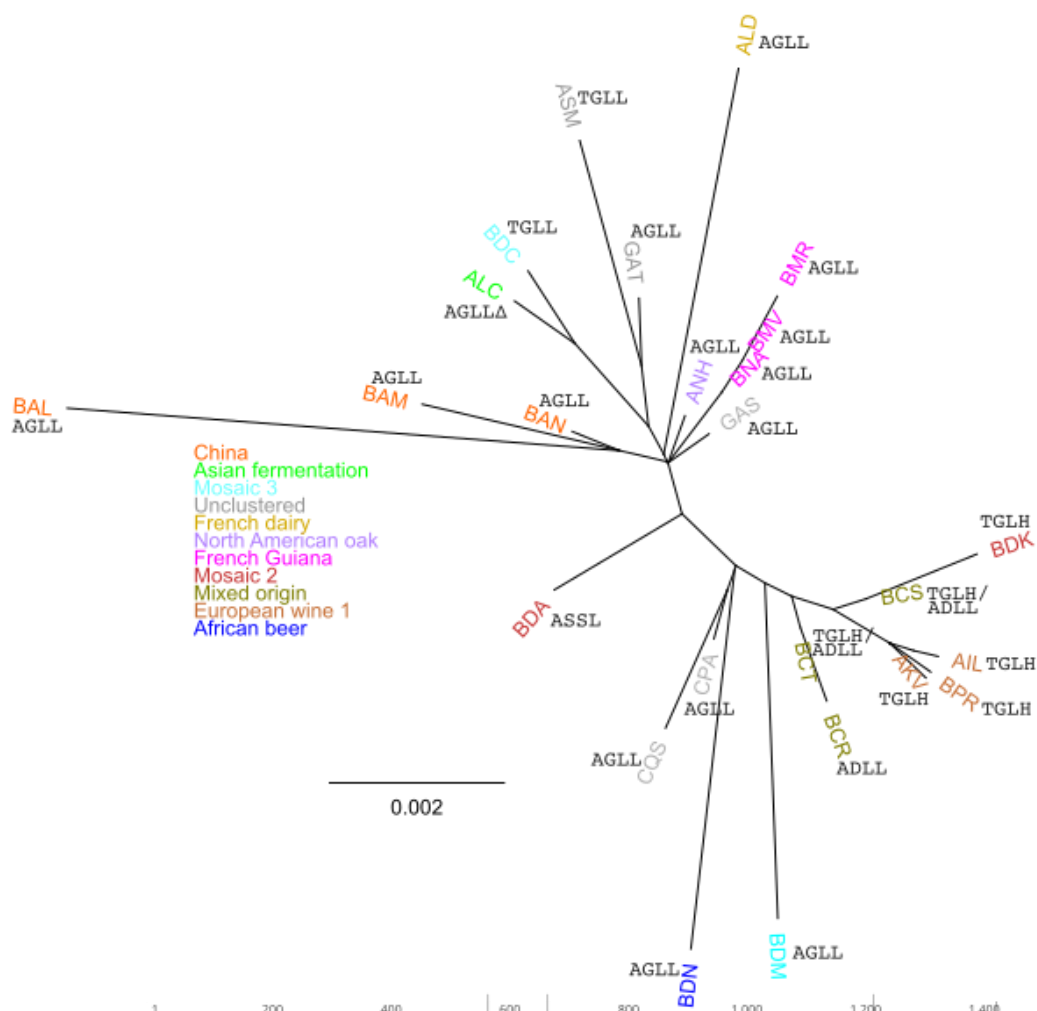


A



B

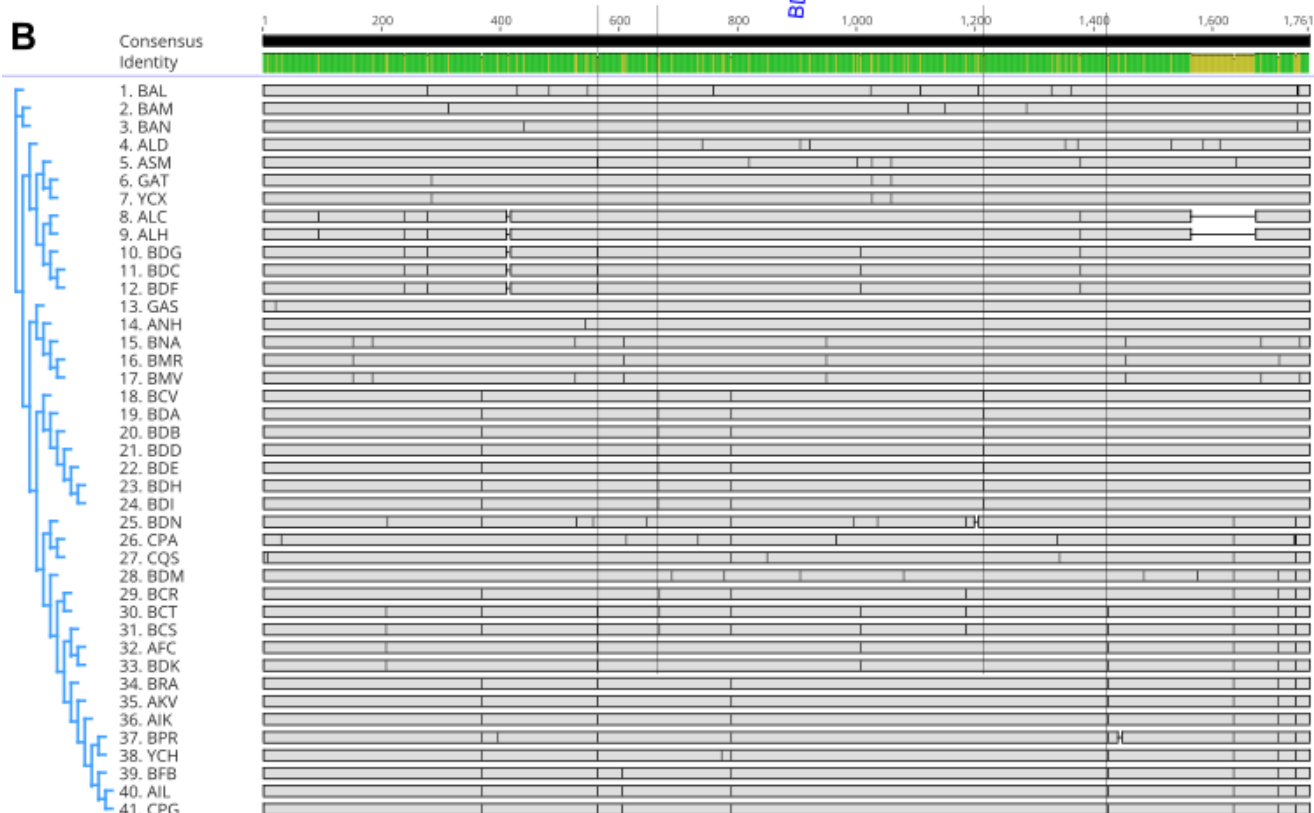


Figure S1. Phylogenetic relationships between natural *S. cerevisiae* isolates based on *HO* gene sequence

(A) Phylogenetic tree of the same 41 isolates mapped in Figure 2B, using the same code to represent the residues at key positions and the presence of the 36-residue deletion. Color coding shows which isolates belong to which clade, as defined in the 1,011 genomes study (Peter *et al.*, 2018). The three-letter names for each isolate are the same as assigned in that study (see Supplementary Table S1).

(B) Phylogenetic tree and DNA sequence alignment of *HO* coding regions of the same isolates. Vertical lines indicate the positions corresponding to codons 189, 223, 405, and 475.