

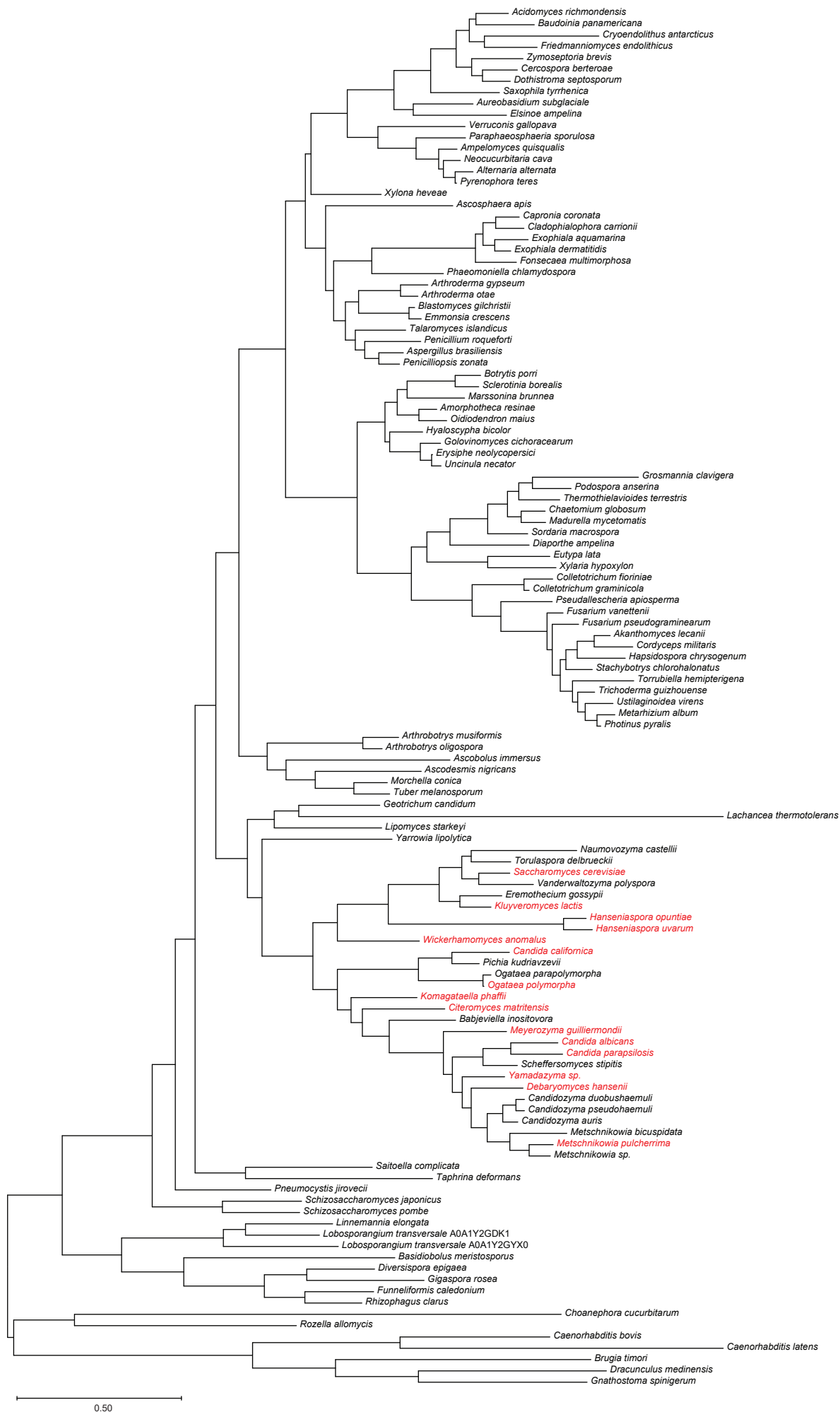


Figure S1. Phylogenetic tree representing the evolutionary relationships of 122 Taf14 proteins listed in Table S1. The tree was constructed using the Maximum Likelihood method. The scale bar indicates the number of amino acid substitutions per site; branch lengths are proportional to evolutionary distances. Taf14 orthologs from species indicated in red were used in functional complementation assays in *Saccharomyces cerevisiae*.