



**Figure S1.** Phylogenetic tree based on concatenated sequences of the SSU rRNA gene, the ITS region and the D1/D2 domain of the LSU rRNA gene showing the placement of *Trichosporiella flavificans*, *Candida ghanaensis* and *Crinitomyces reliqui* within the subphylum Saccharomycotina. The phylogenetic tree was constructed using the maximum likelihood

(ML) method with optimized models for 3 partitions (SSU, ITS region and LSU) in IQ-TREE. The numbers provided on branches are frequencies with which a given branch appeared in 1000 bootstrap replications. Bootstrap values of less than 50% are not shown. *Deakozyma indianensis* CBS 12903<sup>T</sup> was served as an outgroup species. Bar, 0.1 substitutions per site.