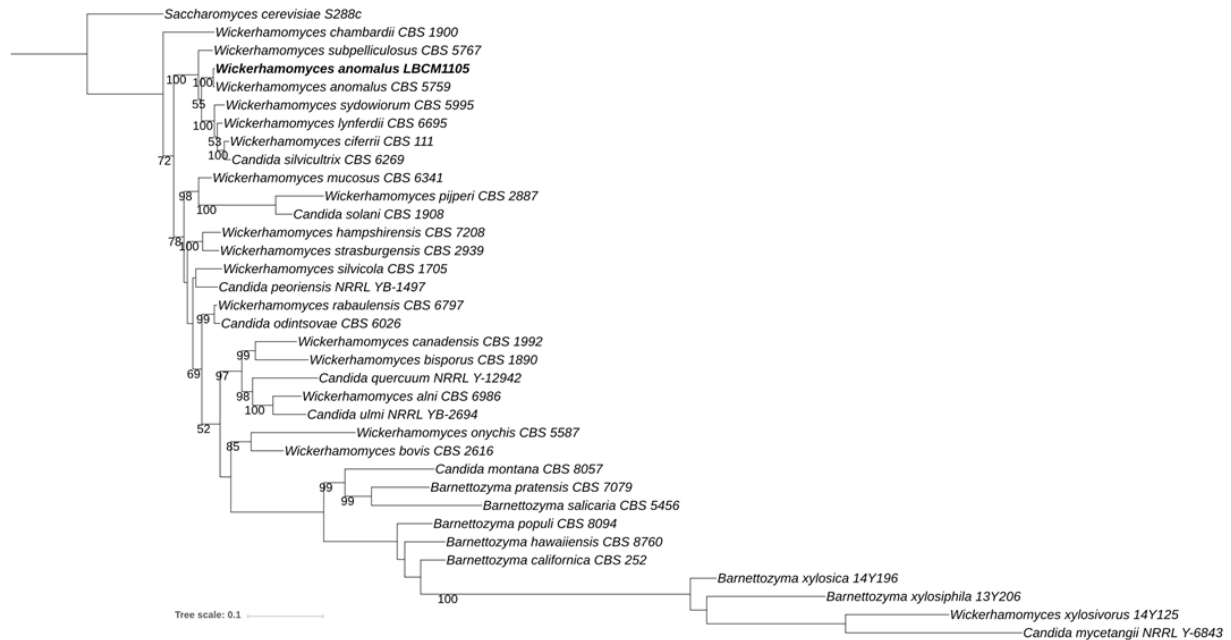


## Supplementary material to “Draft genome sequence of *Wickerhamomyces anomalus* LBCM1105, isolated from cachaça fermentation”



**Figure S1** - Maximum Likelihood (ML) phylogenetic tree based on DNA sequences from large ribosomal subunit (LSU), small ribosomal subunit (SSU) and Elongation Factor-1 $\alpha$  (EF-1 $\alpha$ ). The tree shows the placement of the strain LBCM1105 among strains representative of related species of *Barnettozyma*, *Wickerhamomyces* and *Candida*. The accession numbers of LSU, SSU and EF-1 $\alpha$  were described previously (Kobayashi, et al., 2017, doi.org/10.1099/ijsem.0.002233). ITS1 and ITS2 accession number are listed below. *Saccharomyces cerevisiae* (strain S288c) was used as the outgroup in order to root the phylogenetic tree. Bootstrap values (percentages) over 50% from 1,000 bootstrap replicates in ML tree are shown on branches. Accession numbers for the ITS sequences: *B. californica* - NR\_138212, *B. hawaiiensis* - NR\_153631, *B. populi* - NR\_153632, *B. pratensis* - NR\_153633, *B. xylosica* - NR\_154882, *B. xylosiphila* - LC012021, *C. montana* - NR\_153644, *C. mycetangii* - NR\_152475, *C. odintsovae* - NR\_077084, *C. peoriensis* - NR\_154960, *C. quercuum* - KX525668, *C. silvicultrix* - HM156509, *C. solani* - HM156501, *W. alni* - NR\_154966, *W. anomalus* CBS 5759 - NR\_111210, *W. bisporus* - KY105897, *W. canadensis* - KY105899, *W. chambardii* - NR\_154969, *W. ciferrii* - HM156508, *W. hampshirensis* - HM156504, *W. lynferdii* - HM156505, *W. mucosus* - NR\_154970, *W. onychis* - KY105910, *W. pijperi* - HM156502, *W. rabaulensis* - NR\_138207, *W. silvicola* - NR\_1550121, *W. strasburgensis* - NR\_154973, *W. subpelliculosus* - KY105921, *W. sydowiorum* - HM156507, *W. xylosivorus* - LC278379.