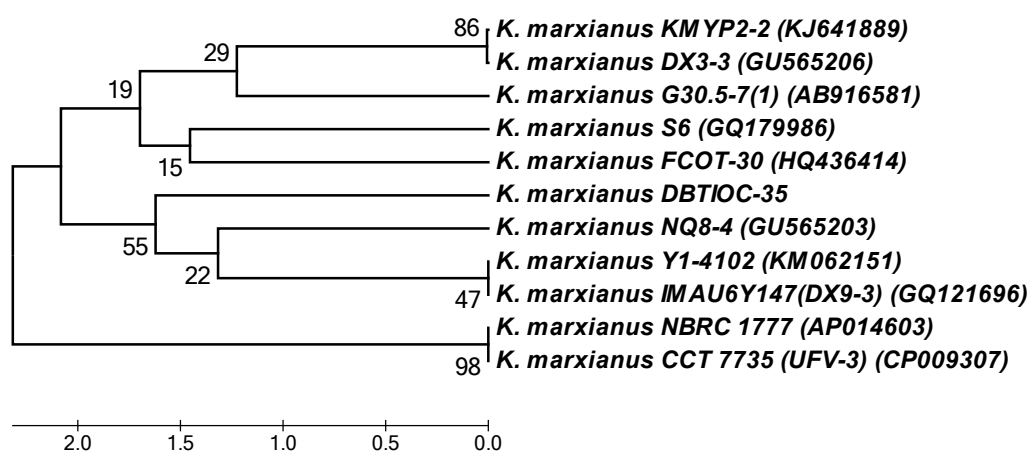


**Fig. S 1.** Evolutionary relationship of *K. marxianus* DBTIOC-35 with other related yeast based on analysis of published sequences of ITS–5.8S rRNA gene. The evolutionary history was inferred using the Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances which were computed using the Maximum Composite Likelihood method (units is number of base substitutions per site). There were a total of 618 positions in the final datasets, respectively. GenBank accession numbers are given in parentheses.



**Fig. S 2.** Evolutionary relationship of *K. marxianus* DBTIOC-35 with other related yeast based on analysis of published sequences of D1/D2 domain of 26S rRNA gene. The evolutionary history was inferred using the Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances which were computed using the Maximum Composite Likelihood method (units is number of base substitutions per site). There were a total of 493 positions in the final datasets, respectively. GenBank accession numbers are given in parentheses.