Supplementary Documents:
Reconstructing Yeasts Phylogenies and Ancestors from Whole Genome Data

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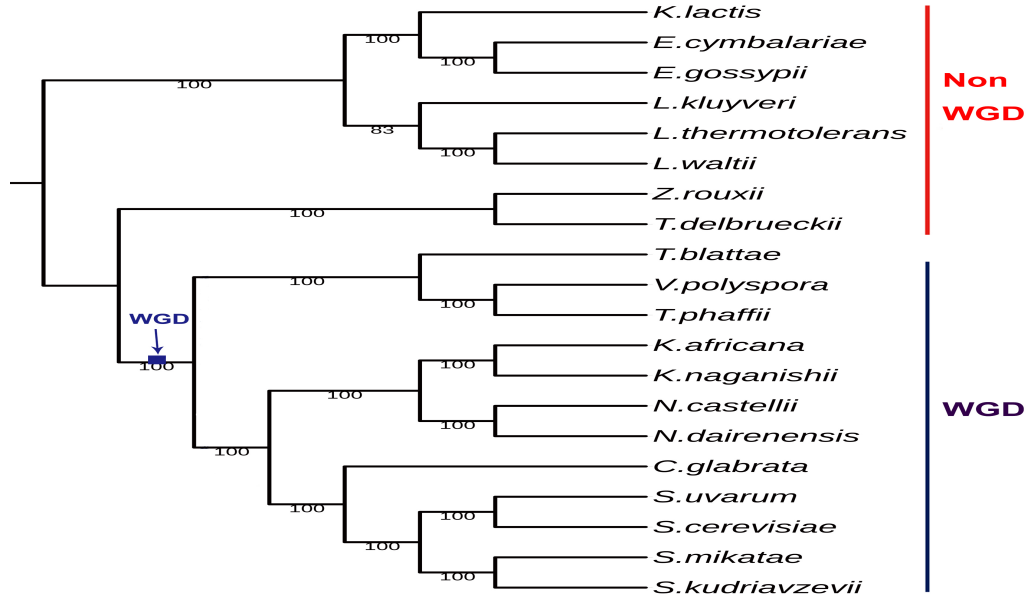
Supplementary Figure1. Yeasts phylogeny built from genome rearrangement events for 20 yeast species. All of the edges have a bootstrapping value of 100 except the branch between Lachancea genus and Eremothecium genus (bootstrapping value of 83). The red line on the right shows the non-WGD species, and the blue line on the right shows the post-WGD species. The blue bar on the left shows the

evolutionary step before yeasts' WGD event.

Code Package Downloading:

Please download the package and running examples using this link:

https://www.dropbox.com/sh/1pr4pbabykz15d9/AAD6_Hp7aKQAcwOjkvVP1liRa?dl=0

Supplementary Datasets 1-4 are provided in extra four xls files.

Supplementary Dataset 1: Ancestral genomes information reconstructed from 11 yeast species.

The reconstructed ancestral genomes information are provided in nine separate sheets.

Supplementary Dataset 2: Ancestral genomes information reconstructed from 20 yeast species.

The reconstructed ancesral genomes information are provided in 18 separate sheets.

Supplementary Dataset 3: Syntenic blocks analyses among ancestral genomes.

The syntenic blocks information among automated and manually reconstructed ancestral genomes are provided in four separate sheets.

Supplementary Dataset 4: Syntenic blocks analyses among ancestral genomes and present yeast genomes.

The syntenic blocks information among automated/manually reconstructed ancestral genomes and their shared five post-WGD descendants are provided in 20 separate sheets.