

Description of Additional Supplementary Files

Supplementary Data 1

Detection of SNPs in the genome sequence of *S. cerevisiae* DW1 by comparison with the reference genome of *S. cerevisiae* SY14

High-quality sequencing data from strain DW1 were aligned to the reference genome of *S. cerevisiae* SY14 using the bwa mem program (version 0.7.17-r1188) to detect SNPs in the DW1 genome. SNPs also present in the parental strains of DW1 were excluded. Corresponds to the SNPs in Supplementary Table 1.

Supplementary Data 2

Detection of Indels in the genome sequence of *S. cerevisiae* DW1 by comparison with the reference genome of *S. cerevisiae* SY14

High-quality sequencing data from strain DW1 were aligned to the reference genome of *S. cerevisiae* SY14 using the bwa (0.7.17-r1188) mem program to detect Indels in DW1 genome sequence. Indels also present in the parental strains of DW1 were excluded. Corresponds to the Indels in Supplementary Table 1.

Supplementary Data 3

Detection of long insertions and deletions in the consensus sequence of *S. cerevisiae* DW1 by comparison with the reference genome of *S. cerevisiae* SY14

Long DNA insertions and deletions in the DW1 genome were detected by aligning its consensus sequence with the reference genome of *S. cerevisiae* SY14 using the alignment tool in SnapGene software. Corresponds to the unique long insertion in the DW1 genome in Supplementary Table 1.

Supplementary Data 4

Detection of SNPs in the genome sequence of *S. cerevisiae* DW1 after growth of 800 generations

High-quality sequencing data from strains DW1-0G (cultured for 0 generations) and DW1-800G (cultured for 800 generations) were aligned to the reference genome of *S. cerevisiae* SY14 using the bwa program (version 0.7.17-r1188) to detect SNPs in each genome. Corresponds to the new SNPs in the DW1-800G genome in Supplementary Table 2.

Supplementary Data 5

Detection of Indels in the genome sequence of *S. cerevisiae* DW1 after growth of 800 generations

High-quality sequencing data from strains DW1-0G (cultured for 0 generations) and DW1-800G (cultured for 800 generations) were aligned to the reference genome of *S. cerevisiae* SY14 using the bwa program (version 0.7.17-r1188) to detect Indels in each genome. Corresponds to the new Indels in the DW1-800G genome in Supplementary Table 2.

Supplementary Data 6

Detection of SNPs in the genome sequence of *S. cerevisiae* DW2 and DW3 by comparison with the reference genome of *S. cerevisiae* SY14

High-quality sequencing data from strains *S. cerevisiae* DW2 and DW3 were aligned to the reference genome of *S. cerevisiae* SY14 using the bwa (0.7.17-r1188) mem program to detect SNPs in each genome. Corresponds to the SNPs in the DW2 and DW3 genome in Supplementary Table 3.

Supplementary Data 7

Detection of SNPs in the genome sequence of *S. cerevisiae* DW5 after growth of 1500 generations

High-quality sequencing data from strains DW5-0 G (cultured for 0 generations) and DW5-1500 G (cultured for 1500 generations) were aligned to the reference genome of *S. cerevisiae* SY14 using the bwa (0.7.17-r1188) mem program to detect SNPs in each genome. Corresponds to the new SNPs in the DW5-1500G genome in Supplementary Table 4.

Supplementary Data 8

Differential expression of telomere-proximal genes in DW strains relative to SY14

The log2FoldChange values, P-values, and annotations for genes located within 17 kb of the left and right telomeres are provided. Corresponds to Supplementary Table 5.

Supplementary Data 9

Detection of SNPs in the sequences of 21 original BAC plasmids and 5 assembled tos-YAC plasmids

High-quality sequencing data from 21 strains harboring the original BAC plasmids and 5 strains harboring the assembled *tos*-YAC plasmids were aligned to the reference sequence (a 2,767,012 bp sequence from silkworm chromosome 2) using the bwa (0.7.17-r1188) mem program to detect SNPs in each sequence. SNPs detected in both the original BACs and the assembled plasmids were considered inherited from the BACs and were excluded from the final list of variations. Corresponds to the SNPs in each *tos*-YAC plasmid in Supplementary Table 8.

Supplementary Data 10

Detection of Indels in the sequences of 21 original BAC plasmids and 5 assembled tos-YAC plasmids

High-quality sequencing data from 21 strains harboring the original BAC plasmids and 5 strains harboring the assembled *tos*-YAC plasmids were aligned to the reference sequence (a 2,767,012 bp sequence from silkworm chromosome 2) using the bwa (0.7.17-r1188) mem program to detect Indels in each sequence. Indels detected in both the original BACs and the assembled plasmids were considered inherited from the BACs and were excluded from the final list of variations. Corresponds to the Indels in each *tos*-YAC plasmid in Supplementary Table 8.