Supplementary Information

Telomere-to-telomere genome assembly of matsutake (*Tricholoma matsutake*)

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Supplementary Table S1 Assembly statistics for the two matsutake samples.
Supplementary Figure S1 Genomic DNA extracted from dried matsutake sporocarps. Lanes 1 and 2 indicate the genomic DNA of matsutake samples A and B, respectively. The three molecular weight markers used are as follows: Marker 7 GT (Nippongene, Tokyo, Japan), λ-HindIII digest (Thermo Fisher Scientific, Waltham, MA, USA), and 2.5 kb DNA Ladder (Takara Bio, Kusatsu, Japan).
**Supplementary Figure S2.** Estimation of the genome size of matsutake, based on $k$-mer analysis ($k = 21$) with the given multiplicity values.
Supplementary Figure S3 Validations of contig connections.

A. Sequence alignment of connected contigs of the sample A and contiguous sequences of the Sample B. Dots indicate sequences with a sequence identity of ≥75% between the two samples. B. Amplified DNA from the samples A and B. The primer pairs used in PCR are designed to bridge two contigs.