

Description of Additional Supplementary Files

Supplementary Data 1

Description: Evaluation of the accuracy of the assembled genomes using Illumina pair-end reads.

Supplementary Data 2

Description: Characteristics of genes identified in the assembled genomes.

Supplementary Data 3

Description: Detail information of TEs identified in the assembled genomes.

Supplementary Data 4

Description: Hox genes identified in subgenomes of three allotetraploids.

Supplementary Data 5

Description: Occupied genome length, gene number and TE sequences in A/B compartment in subgenomes of three allotetraploids.

Supplementary data 6

Description: Tissues of studied species used for RNA-Seq and Iso-Seq. Supplementary Data 7.
Hyperlinks for all data generated in this study.