

**Segmental Duplication of Chromosome 11 and its Implications for Cell Division  
and Genome-wide Expression in Rice**

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## **Supplementary Information**

**Figure S1.** The immunofluorescence analysis of OsCENH3 and FISH analysis of ChIP-DNA immunoprecipitated with anti-OsCENH3 antibody in rice.

**Figure S2.** Chromosome behavior at each stage of mitosis in variant YZG-5.

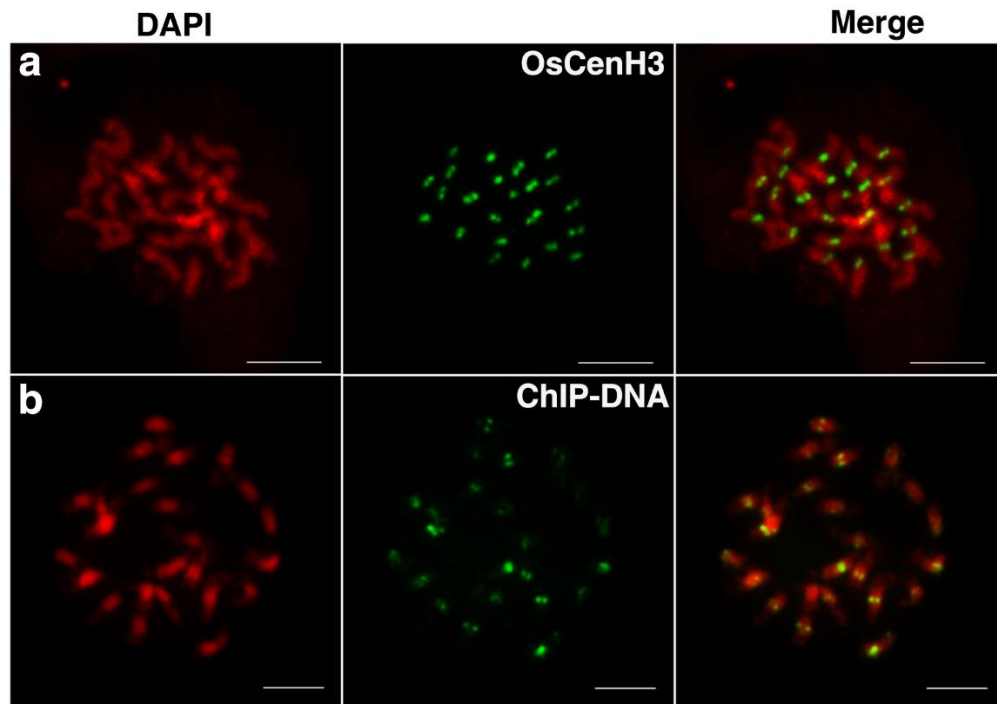
**Figure S3.** Gene expression level of each chromosome in YZG-5.

**Figure S4.** Ratio of differentially expressed genes to total genes on the corresponding chromosome.

**Figure S5.** The expression (fold change) values of ten genes on 11S-2 region in the seedlings of YZG-5 and the seedlings and roots of YZG-5 offsprings.

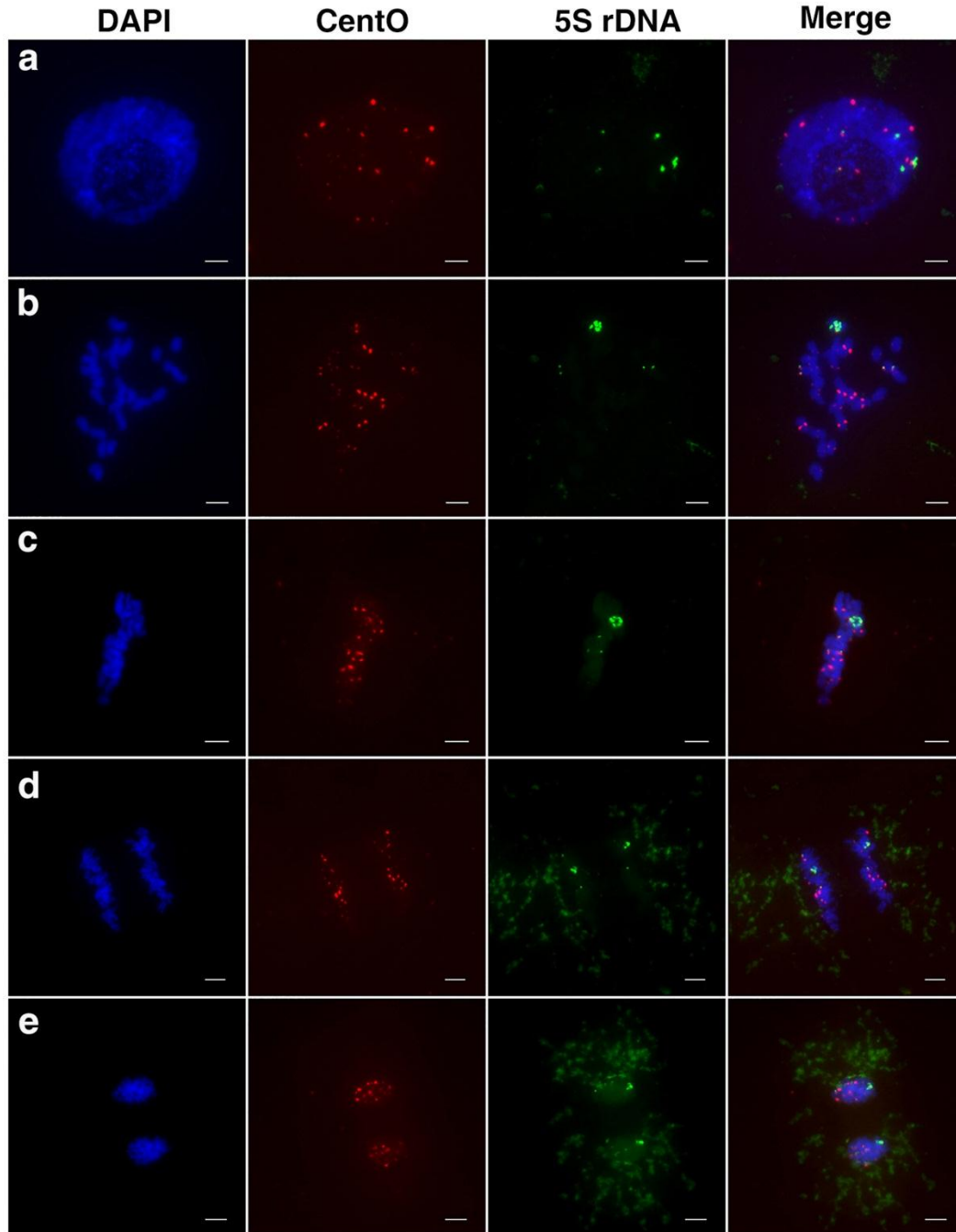
**Supplementary Table S1.** Primer pairs used for qPCR analysis of relative amounts of specific chromosome regions.

**Supplementary Table S2.** Primer pairs used for RT-qPCR analysis of ten genes on 11S-2 region.



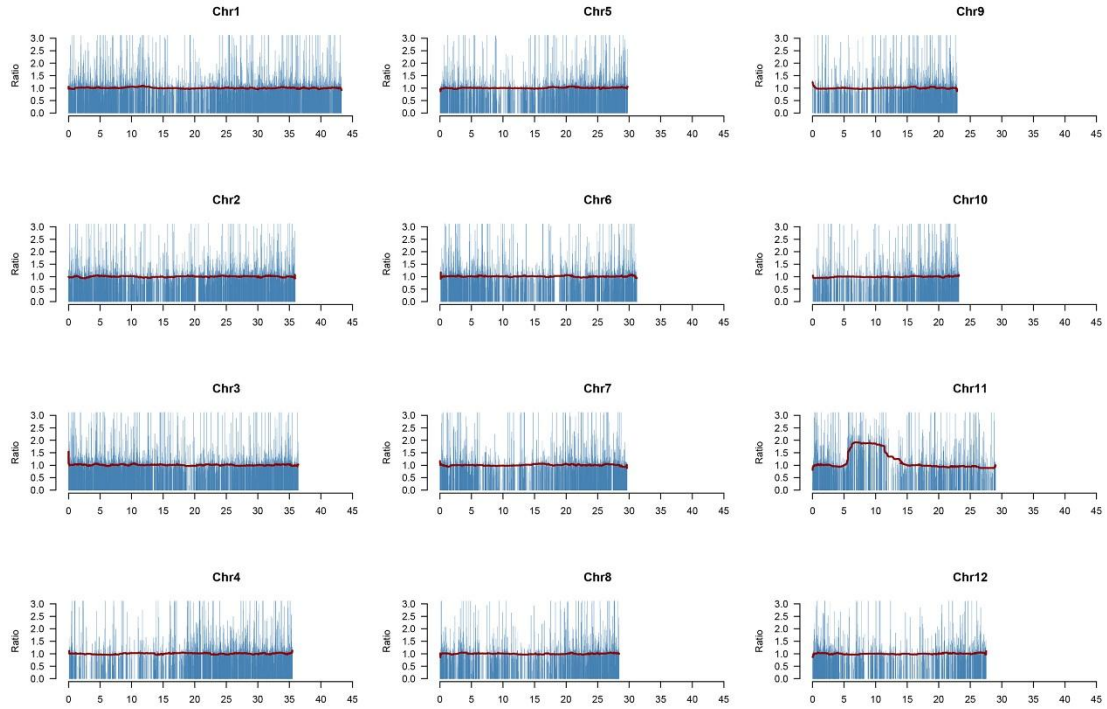
**Figure S1. The immunofluorescence analysis of OsCENH3 and FISH analysis of ChIP-DNA immunoprecipitated with anti-OsCENH3 antibody in rice.**

Chromosomes were counterstained with DAPI, indicated by red signals, and green signals indicate OsCENH3. Scale bars represent 5  $\mu\text{m}$  in all images. **(a)** The immunofluorescence analysis showed the signals of anti-OsCENH3 antibody were almost located at the centromere region of each chromosome. **(b)** FISH results showed the ChIP-DNA immunoprecipitated with anti-OsCENH3 antibody was located at the centromere region of each chromosome in rice.



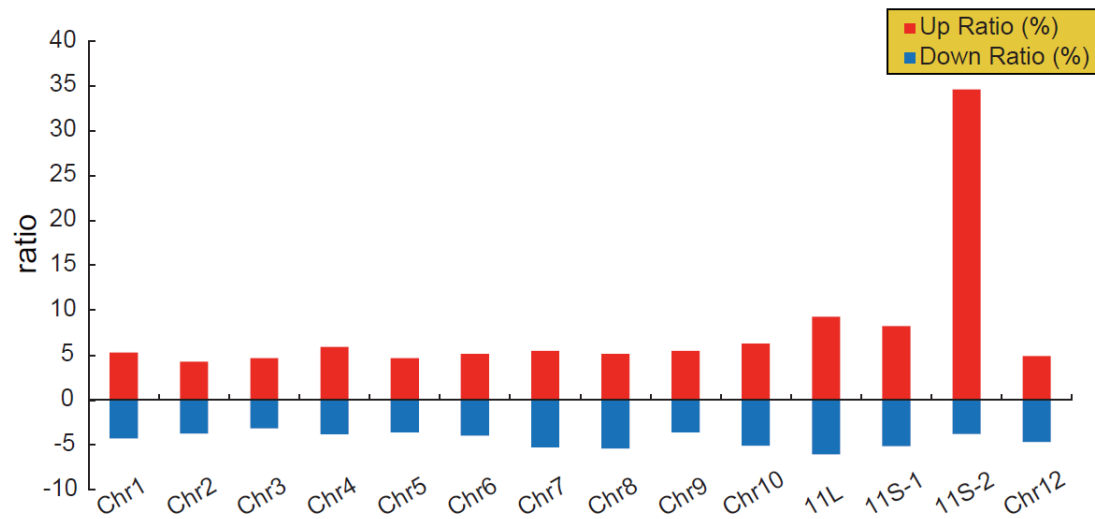
**Figure S2. Chromosome behavior at each stage of mitosis in variant YZG-5**

Chromosomes were counterstained with DAPI. Red signals indicate CentO and green signals indicate 5S rDNA. Scale bars represent 5  $\mu\text{m}$  in all images. **(a-b)** Mitotic interphase and prophase. **(c)** Mitotic metaphase. **(d-e)** Mitotic anaphase and telophase. At each stage of mitosis, the 5S rDNA signals divided normally, indicating that the tricentric chromosome 11S•11S•11S•11S has only one functional centromere at the middle position.



**Figure S3. Gene expression level of each chromosome in YZG-5**

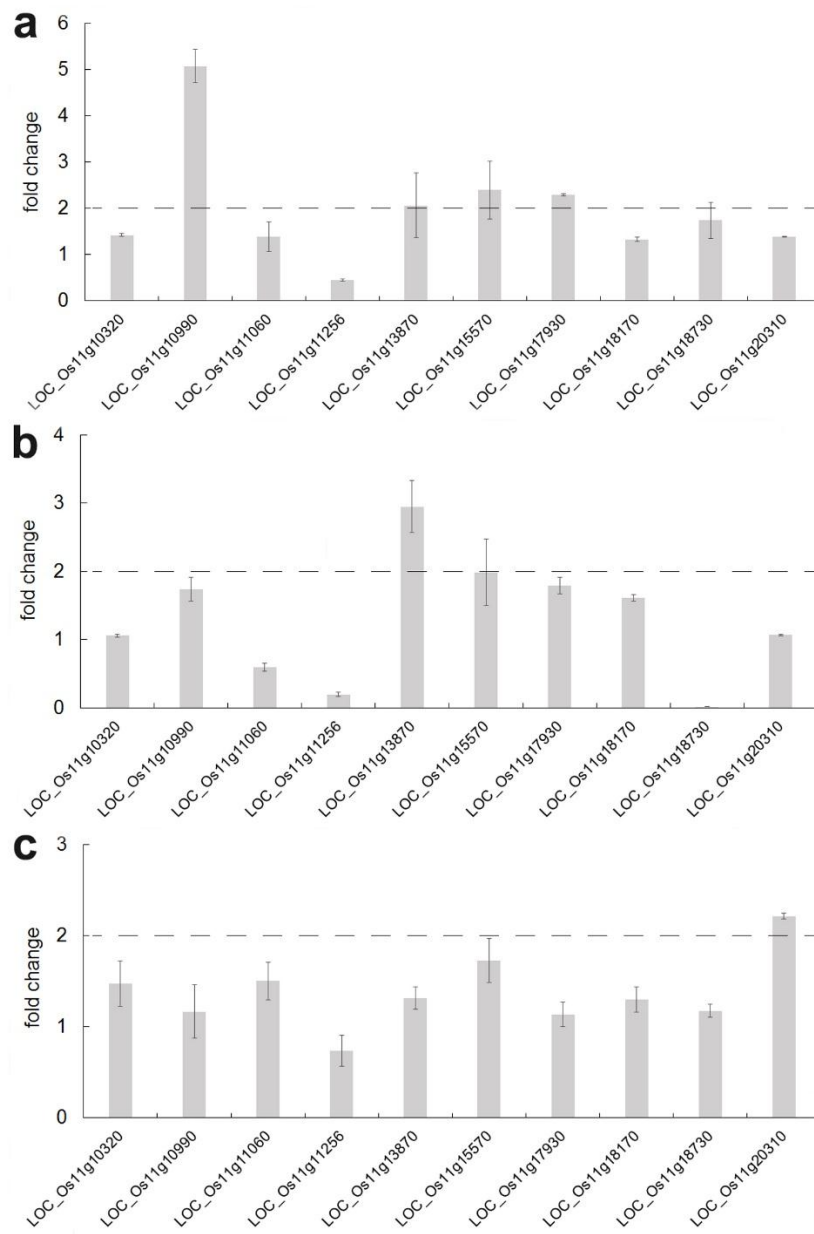
Blue bar represents expression level change of each expressed gene (FPKM>0) in whole rice genome of YZG-5. Red lines represent median score of expression level change in 100 genes sliding windows. X-axis represents genes loci.



**Figure S4. Ratio of differentially expressed genes to total genes on the corresponding chromosome**

Red bar indicates up-regulated genes, blue bar indicates down-regulated genes.

(Ratio=differentially expressed genes/all genes\*100)



**Figure S5. The expression (fold change) values of ten genes on 11S-2 region in the seedlings of YZG-5 and the seedlings and roots of YZG-5 offsprings**

(a) In the seedlings of YZG-5, four genes fold change of expression level are greater than 2.0 and only one gene fold change of expression level is less than 1.0. (b) In the leaves of YZG-5 offsprings, except one gene fold change of expression level is greater than 2.0, the remaining are less than 2.0. (c) In the roots of YZG-5 offsprings, nine out of ten genes fold change of expression level are less than 2.0.