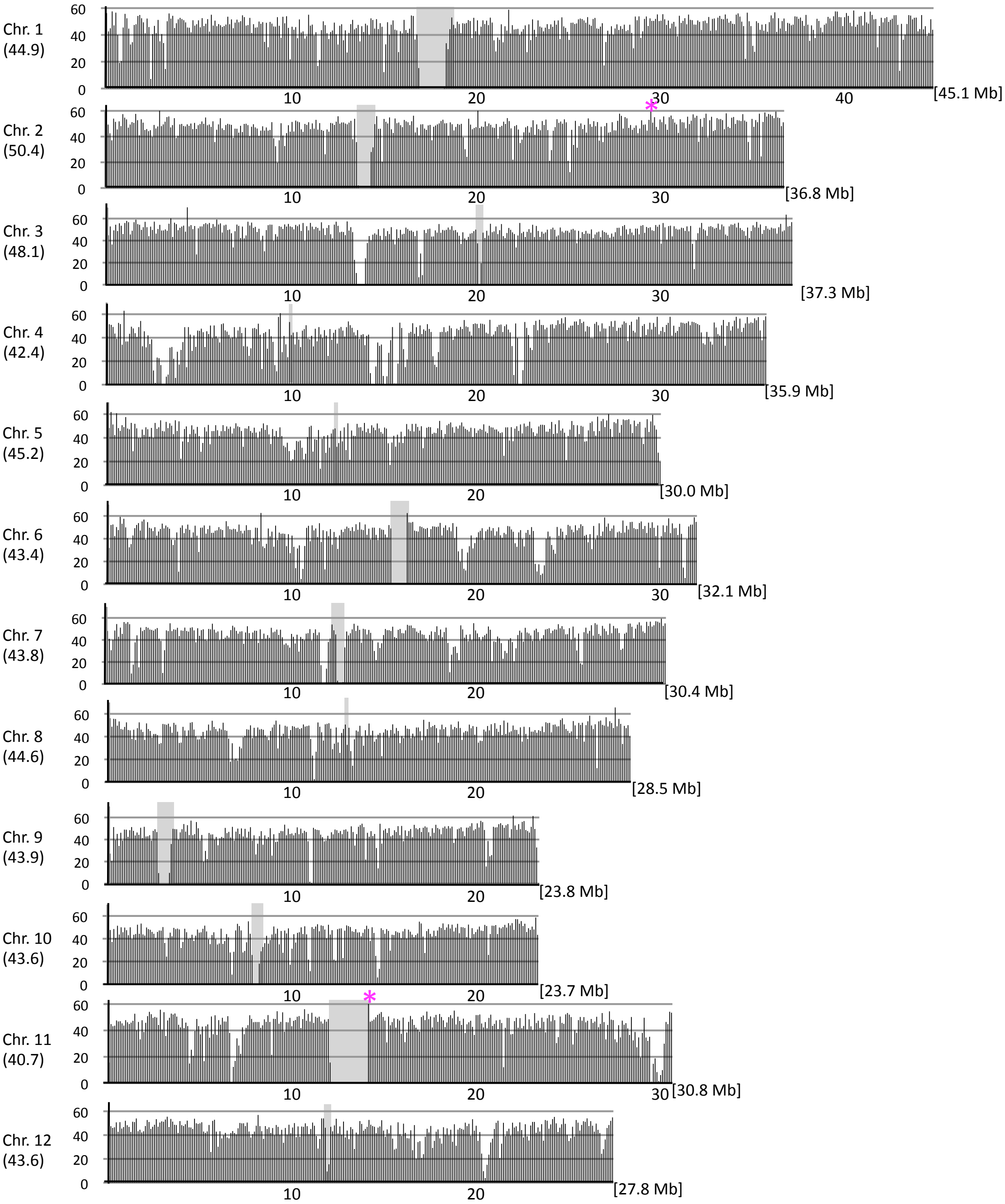

Supplementary Figure S1. Sequencing depth of the Omachi short reads generated using the GA sequencer with reference to the Nipponbare genome. The sequencing depth in each chromosome is shown in parentheses. The mean total sequencing depth was 45.0× the genome. The x-axis shows the physical distance along the Nipponbare genome. Total genome size of each chromosome is shown in brackets. The y-axis shows the sequencing depth, which represents the mean number of reads mapped in 100-kb windows. The grey areas show centromere regions. Read depths over 100 are indicated by red asterisks.