

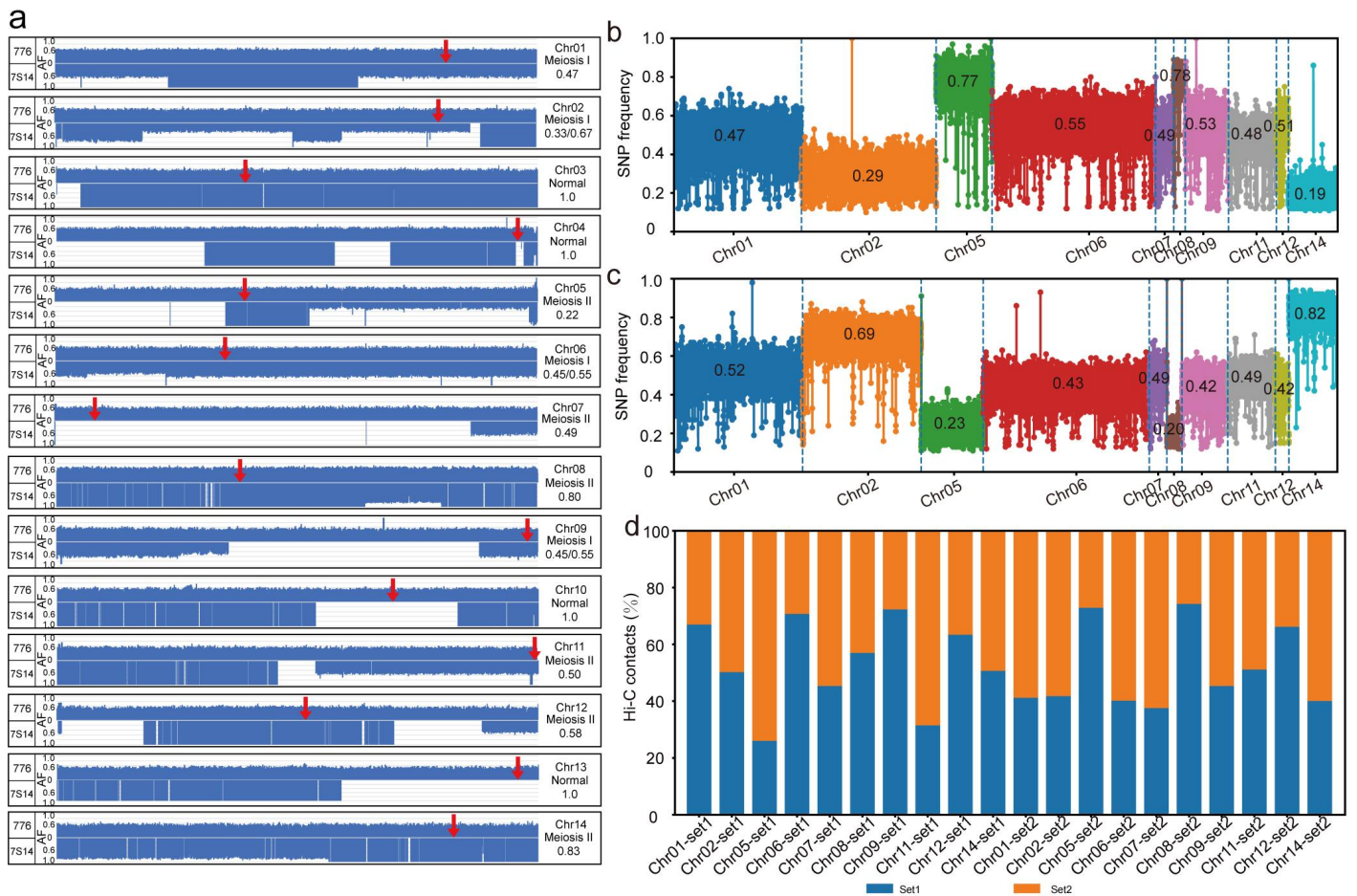


Figure S21. Genomic evidence for karyotype heterogeneity. (a), SNP allele-frequency analysis in progeny 7S14. Red arrows indicate putative centromere regions. All SNP sites identified in the parental strain are shown. Inferred mis-segregation stages and SNP allele-frequency are shown on the right. AF, allele frequency. (b), (c), SNP allele-frequency profiles of strain 7S14 obtained by mapping resequencing reads to set1 (b) and set2 (c). The numbers represent the average SNP frequency of the chromosomes and SNP frequencies of homologous chromosomes sum to approximately 1. Set1 and set2 refer to the two hifiasm-inferred putative chromosome assemblies of the 7S14 genome. These terms were used because extensive karyotype heterogeneity precluded reliable haplotype phasing. (d), Hi-C interaction patterns of heterozygous chromosomes in the 7S14 genome. The bar plot shows the proportion of interaction intensity between each chromosome and non-homologous chromosomes in set1 and set2.