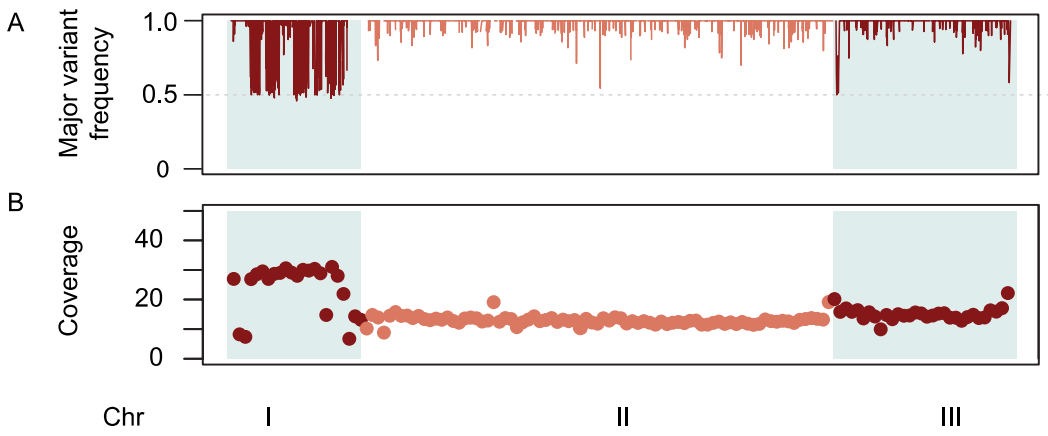

Figure S3 Chromosome I aneuploidy. (A) Major variant frequency along chromosomes I, II and III for one example segregant. The frequency of each base is counted at all polymorphic sites and the frequency of the most common one is plotted. (B) The depth of coverage of mapped reads for the same region and segregant. Coverage is averaged in non-overlapping windows of 10kb. An extra copy of a chromosome is manifested in a variant frequency pattern where parts of the chromosome have major variant frequencies close to 1 (homozygous stretches) while other parts have major variant frequencies fluctuating around 0.5 (heterozygous stretches), and a depth of coverage across the chromosome twice as high as that of the other chromosomes.