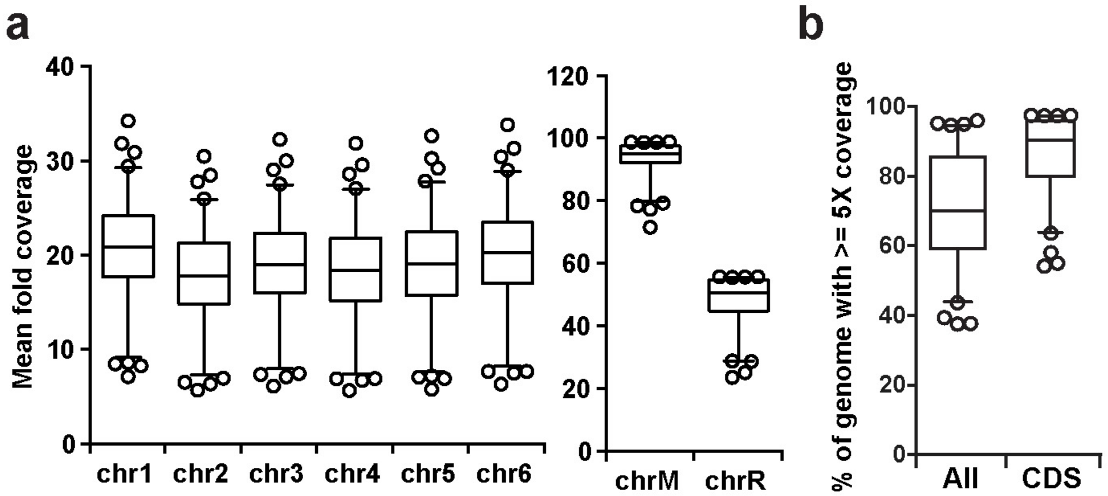

Supplementary Figure S1. Fold coverage of mapped sequence reads. (a) The sequence fold coverage of chromosomes 1-6, and the ribosomal and mitochondrial DNAs (n = 85, notice the different y-axes scales). **(b)** The proportion (%) of DNA covered by ≥5 reads (y-axis) in the entire genome (All, x-axis) and in the coding-DNA sequence (CDS, x-axis); n = 85. The edges of the boxes represent the 75th and 25th percentiles. The lines in the middle of the boxes represent the medians. Error bars are the 95% confidence intervals. The empty circles are outliers.