



**Figure S4.** The comparison of distributions for RHR obtained by simulations and observed RHR in Hot2 and Hot3. (a) The simulated distribution of heterozygosity from F<sub>1</sub> to F<sub>6</sub> of 193 lines. (b) The simulated distribution of recombination events per line from F<sub>1</sub> to F<sub>6</sub> of 193 lines. (c-d) *P* means the probability that the observed RHR in Hot2 and Hot3 come from the null distribution via simulation. 7.9% and 7.6% were the observed RHR in Hot2 and Hot3 respectively.