

Figure S1. Recombination landscapes of wild type and mutants for maize chromosomes 2 - 10. Y-axis is compressed to fit the map for the global 10x CO increase. Centromere positions are in blue.

CO Landscape

- 10x
- *ddm1*
- *ddm1/zmet2*
- *fancm*
- *recq4*
- wild type
- *zmet2*

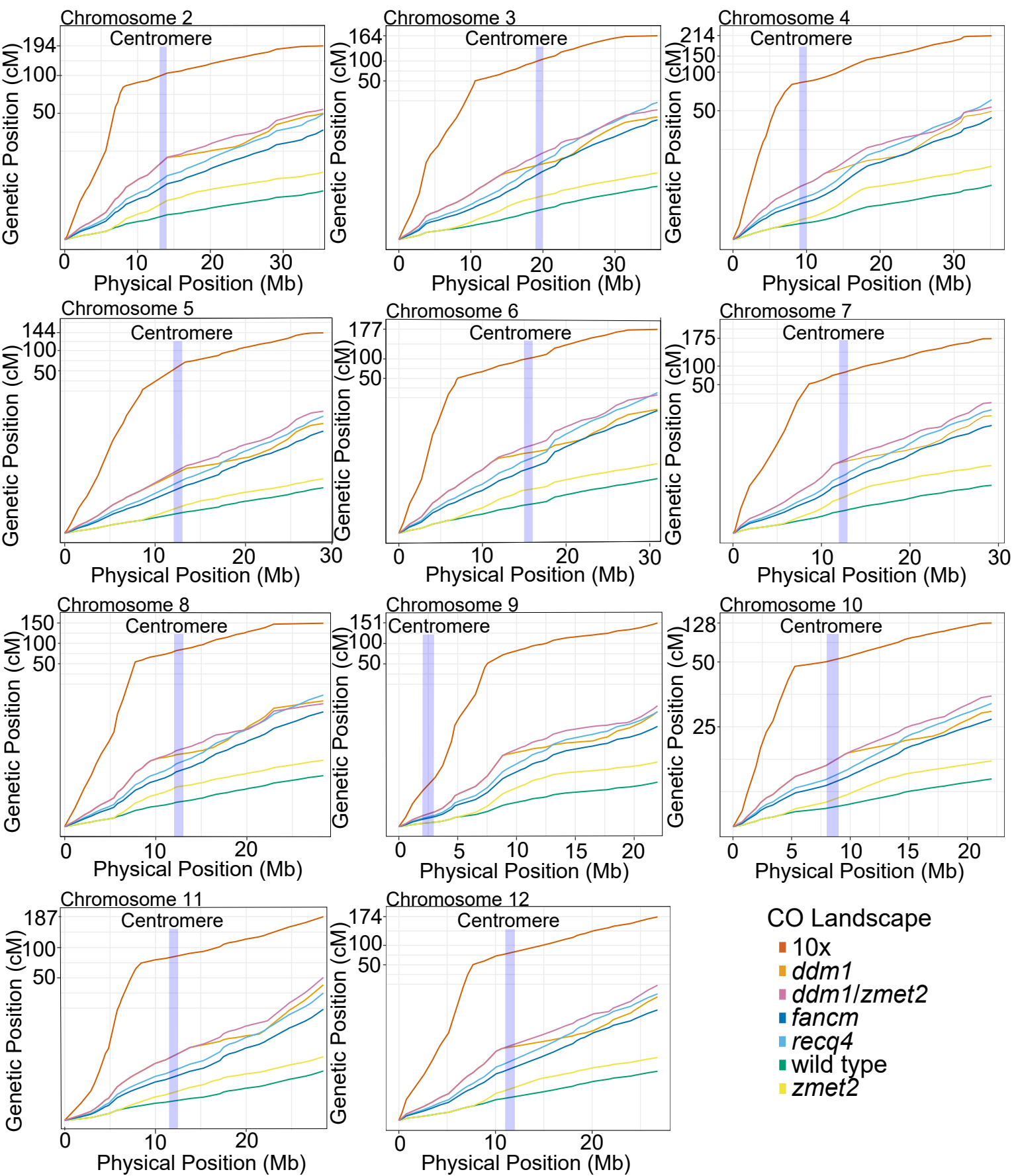


Figure S2. Recombination landscapes of wild type and mutants for rice chromosomes 2 - 12. Y-axis is compressed to fit the map for the global 10x CO increase. Centromere positions are in blue.

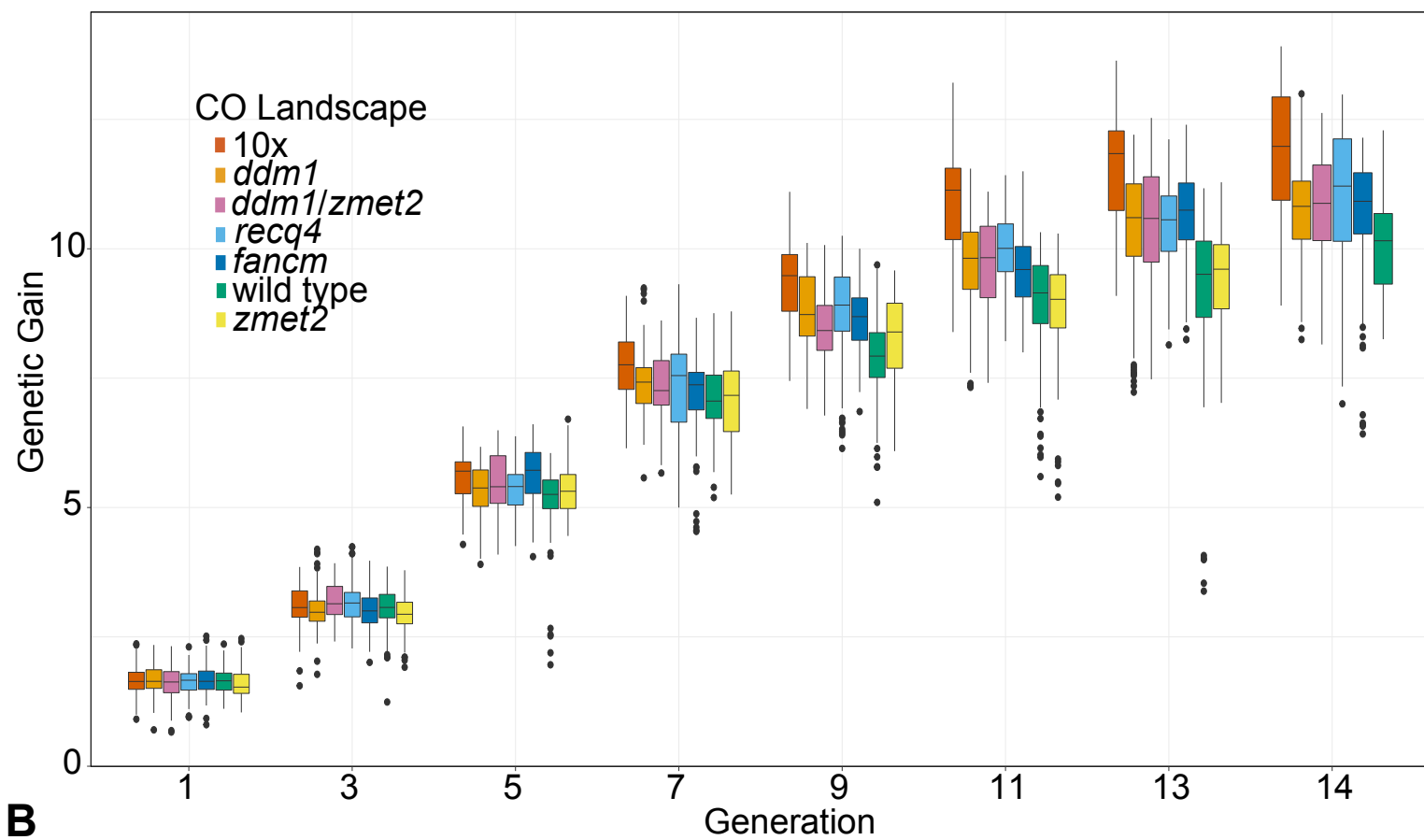
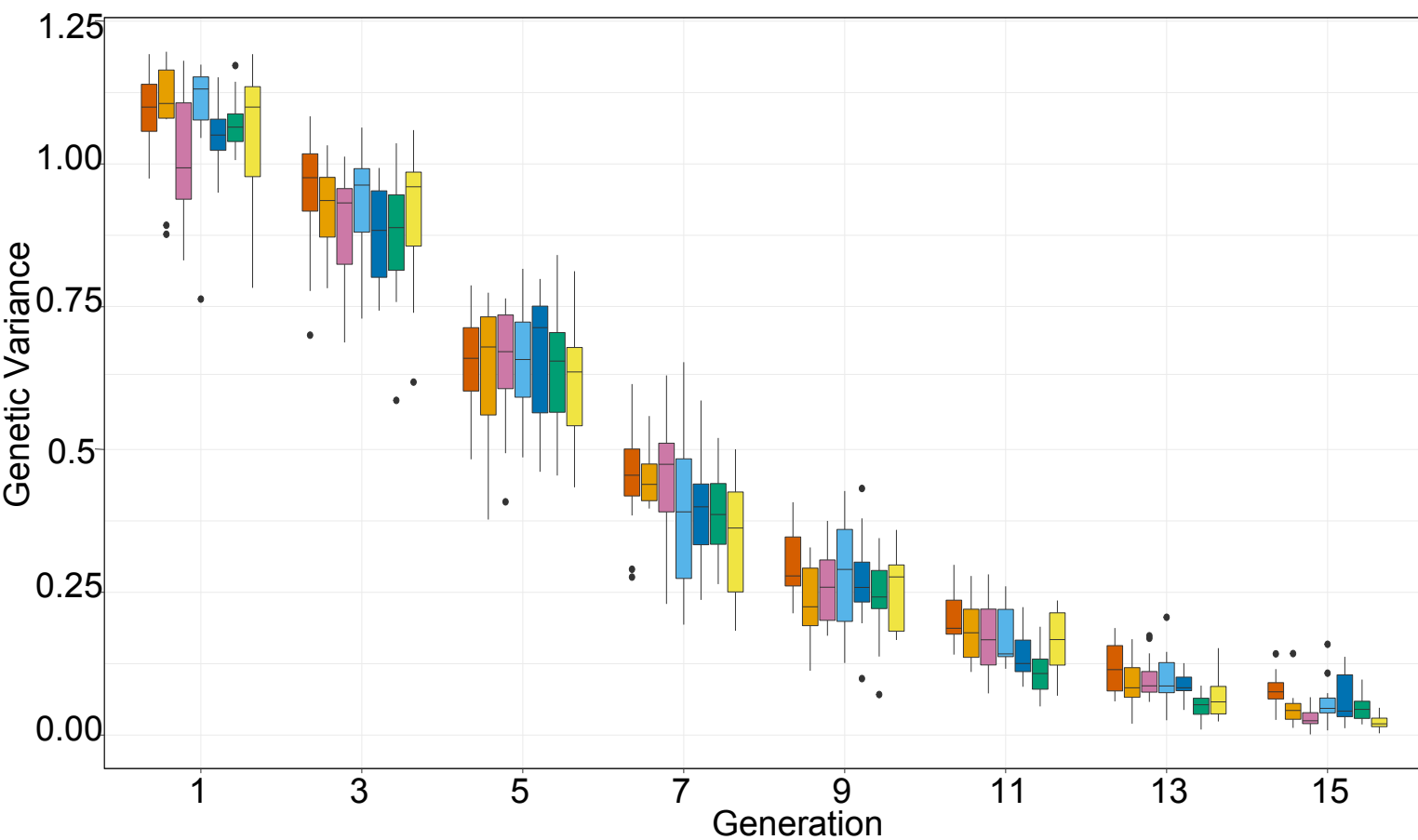
A**B**

Figure S3. Simulating a rice breeding population over 15 generations of recurrent selection. (A) Genetic gain. (B) Genetic variance.

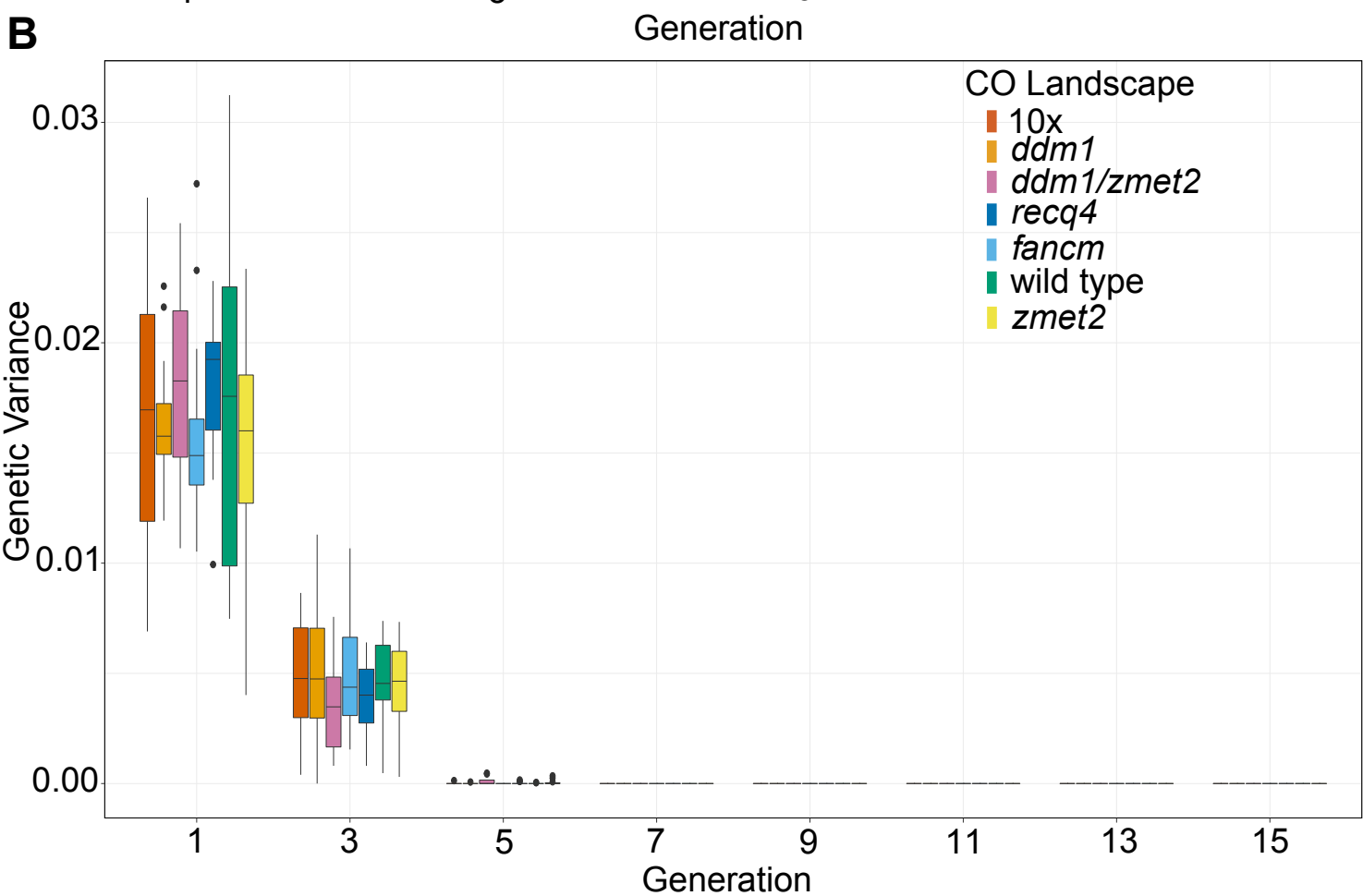
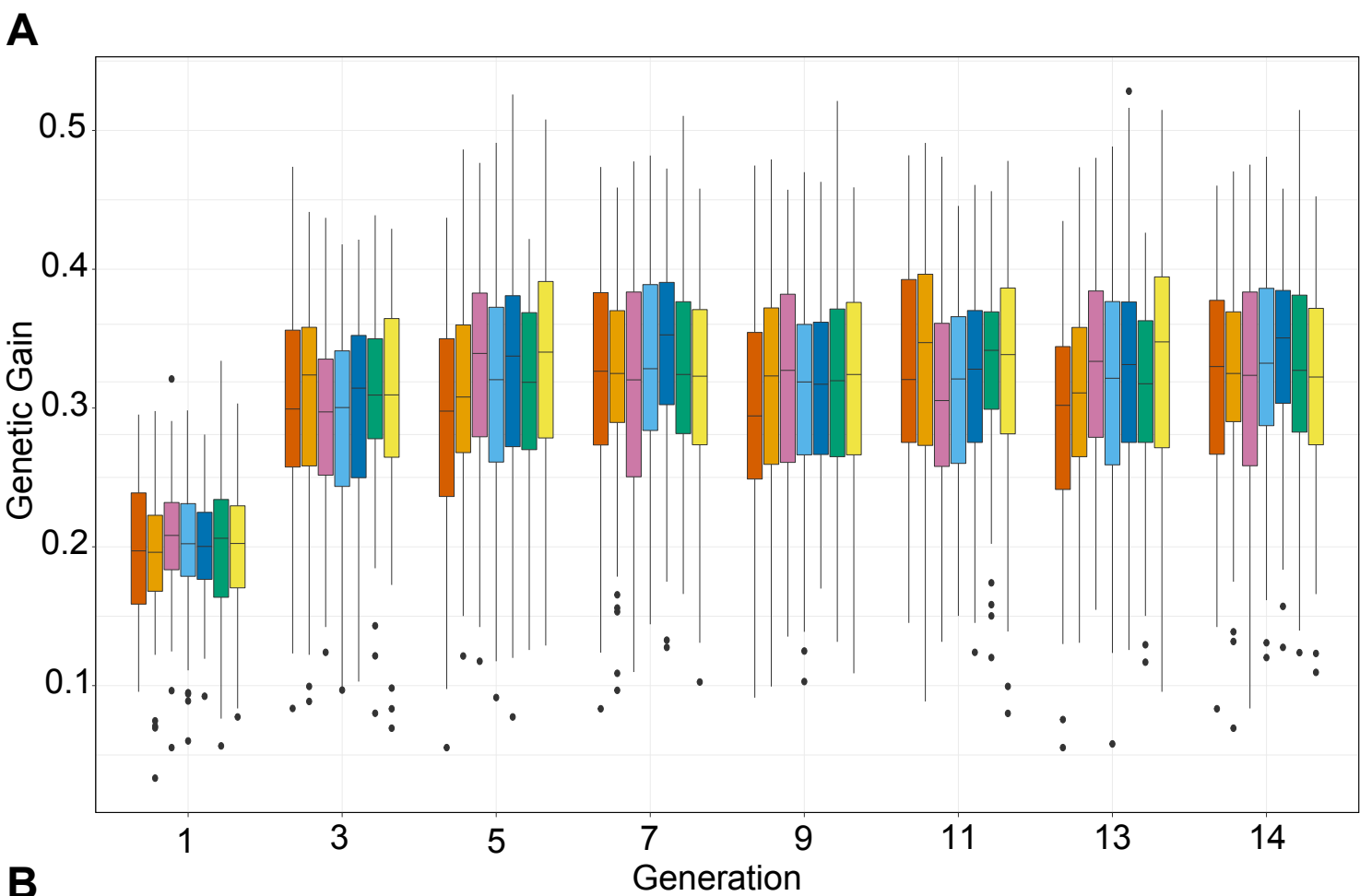


Figure S4. Simulating a maize breeding population over 15 generations of recurrent selection with an oligogenic trait. (A) Genetic gain. (B) Genetic variance.

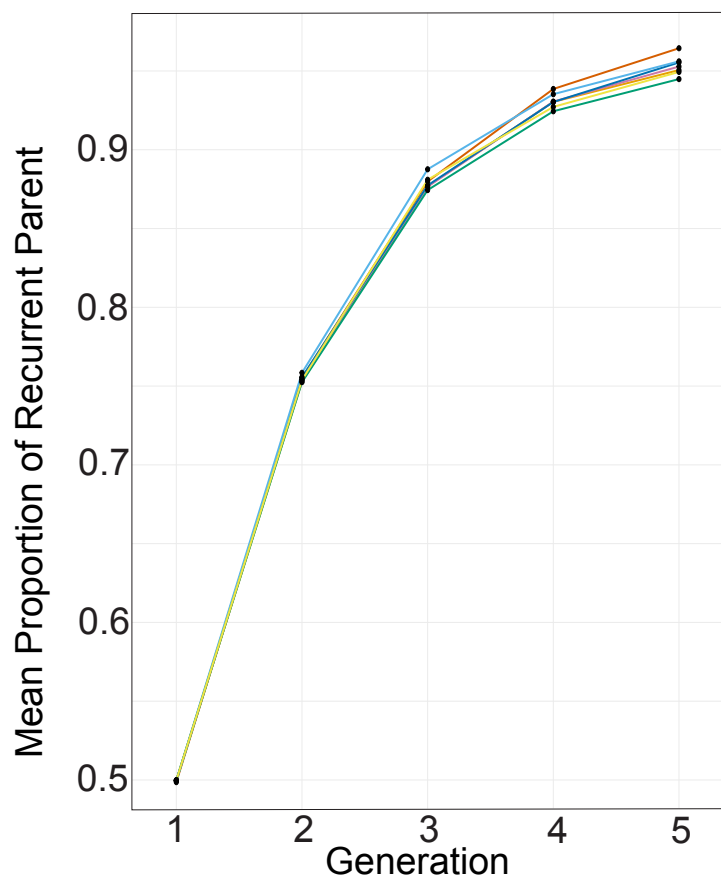
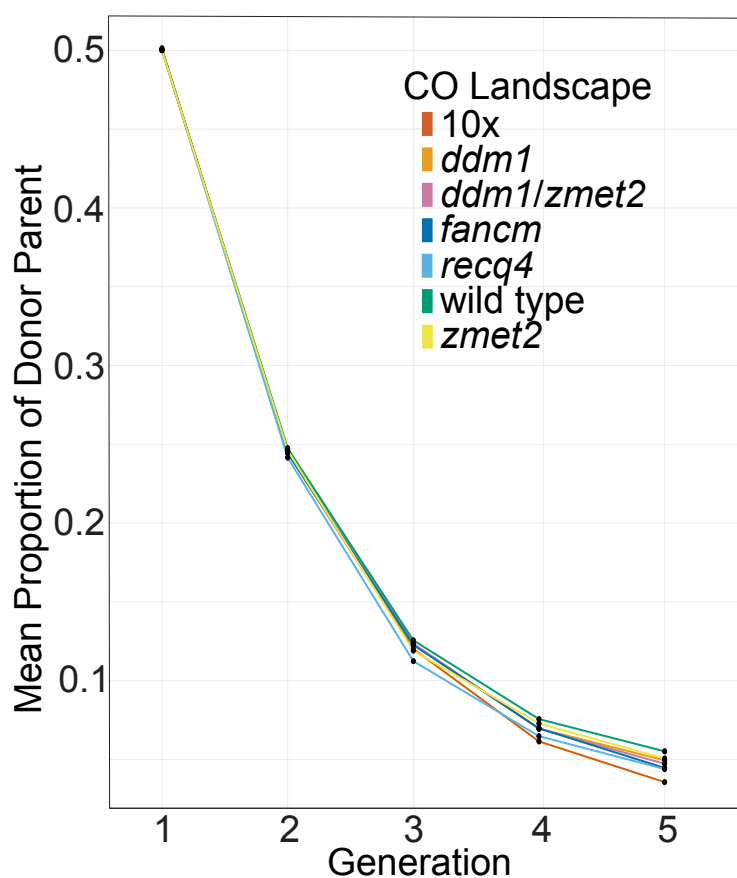
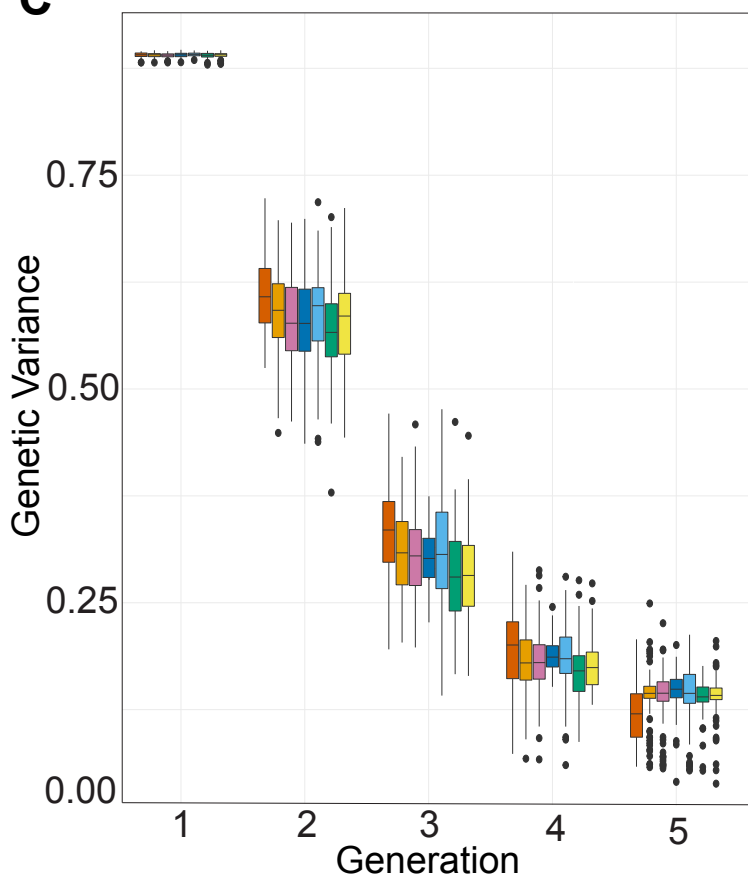
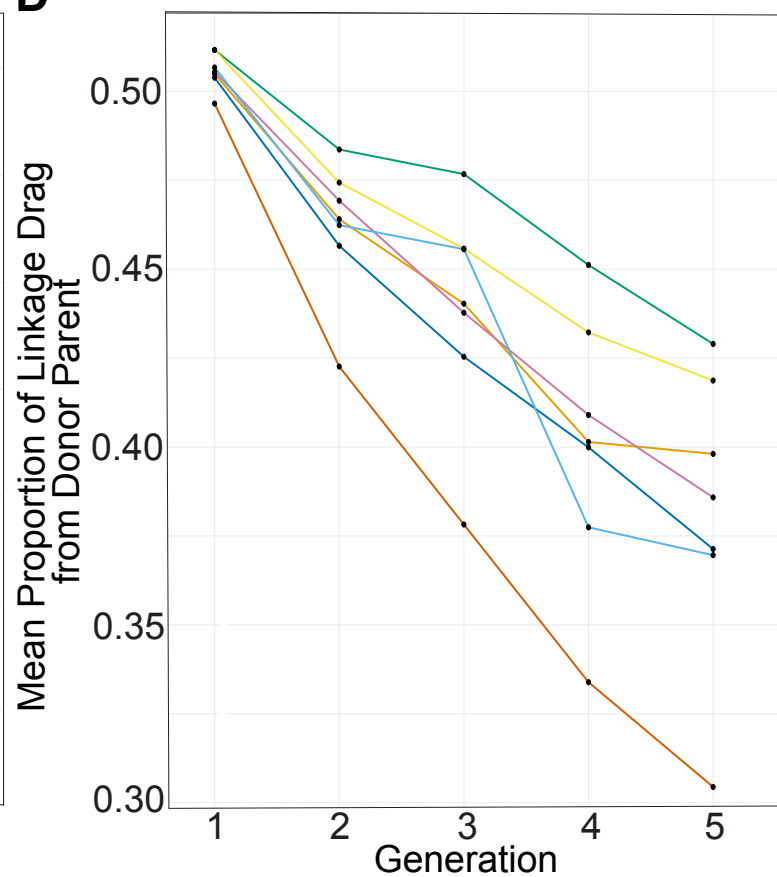
A**B****C****D**

Figure S5. Simulating introgression breeding in rice. Generation 1 represents F₁ progeny from the initial elite parent x wild parent cross. Generations 2 - 4 represent progenies from backcrossing to the elite parent. (A) Proportion of recurrent (elite) parent. (B) Proportion of donor (wild) parent. (C) Genetic variance. (D) Linkage drag around the introgression target (disease resistance) loci.

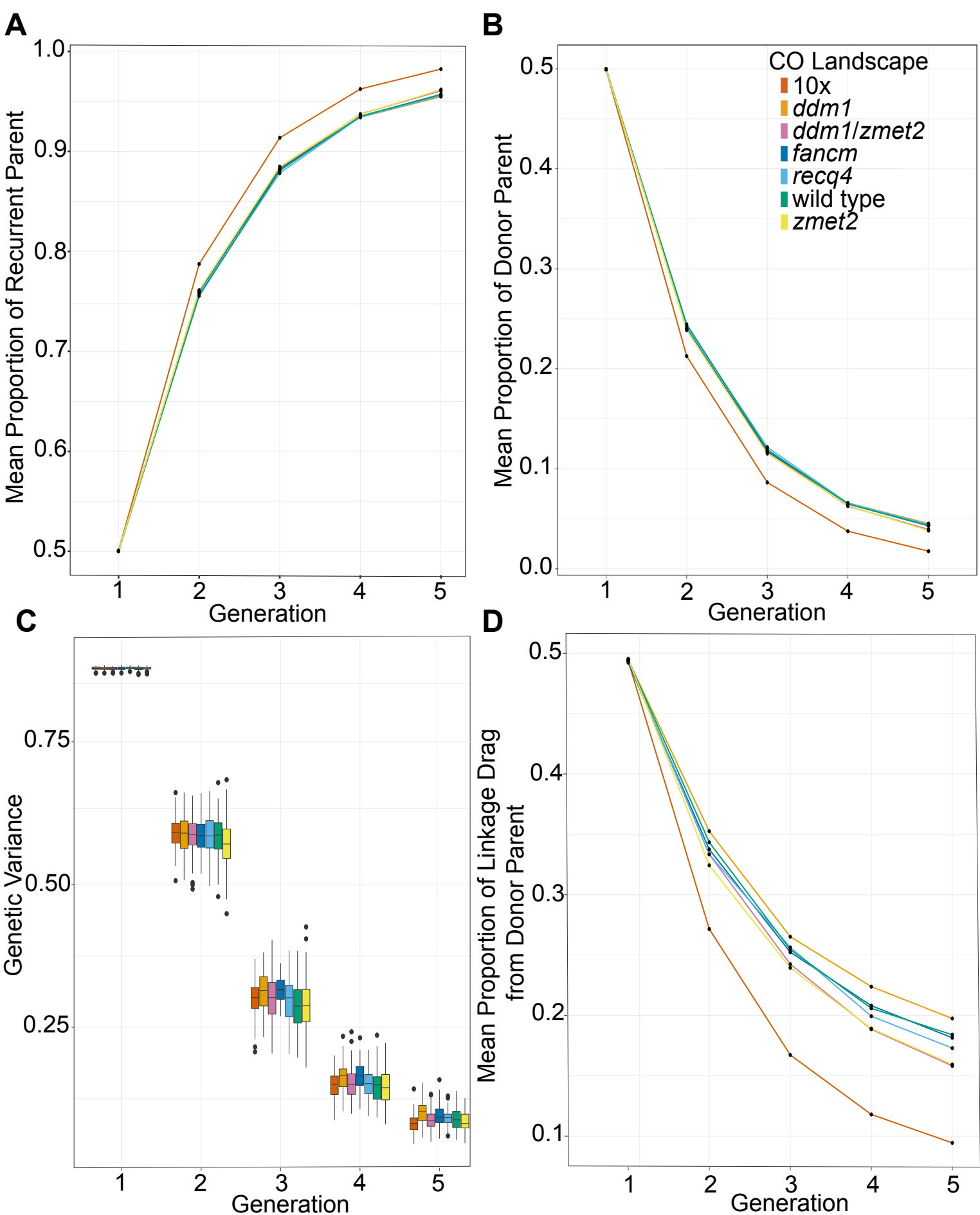


Figure S6. Simulating introgression breeding in maize with resistant QTLs in pericentromeric region. Generation 1 represents F_1 progeny from the initial elite parent x wild parent cross. Generations 2 - 4 represent progenies from backcrossing to the elite parent. (A) Proportion of recurrent (elite) parent. (B) Proportion of donor (wild) parent. (C) Genetic variance.

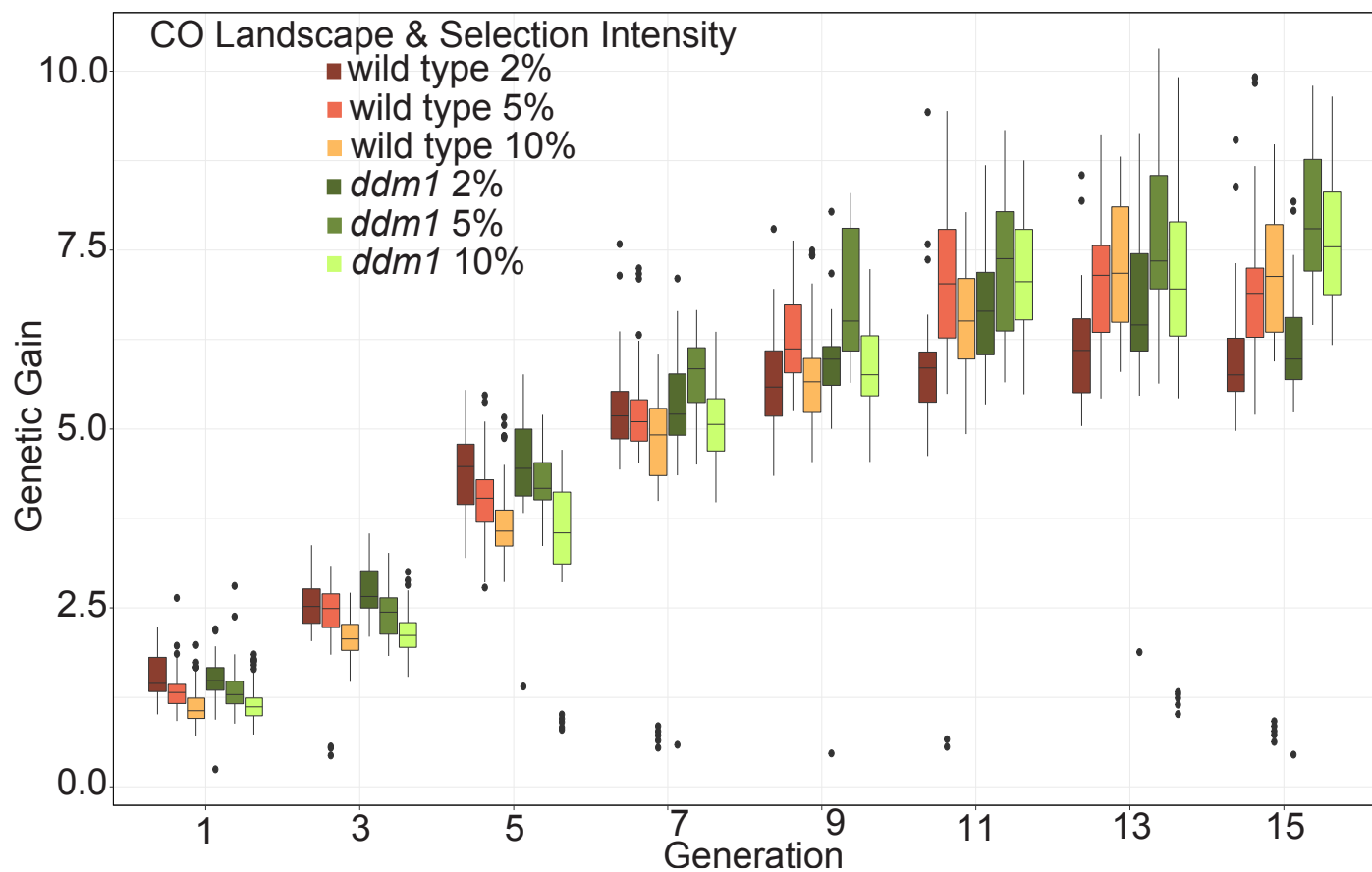
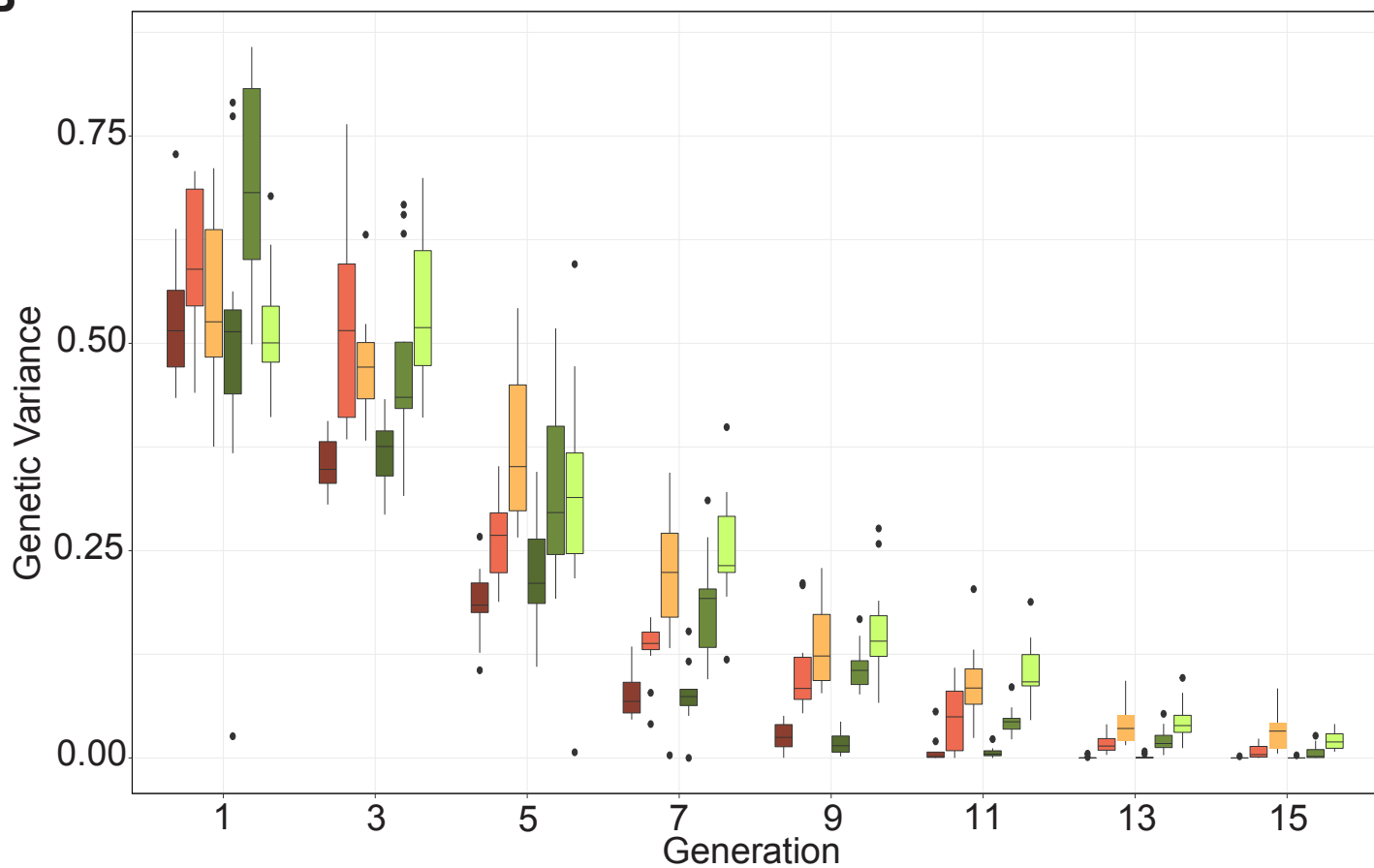
A**B**

Figure S7. Simulating recurrent selection with different selection intensities in wild-type maize and the *ddm1* maize mutant. (A) Genetic gain. (B) Genetic variance.

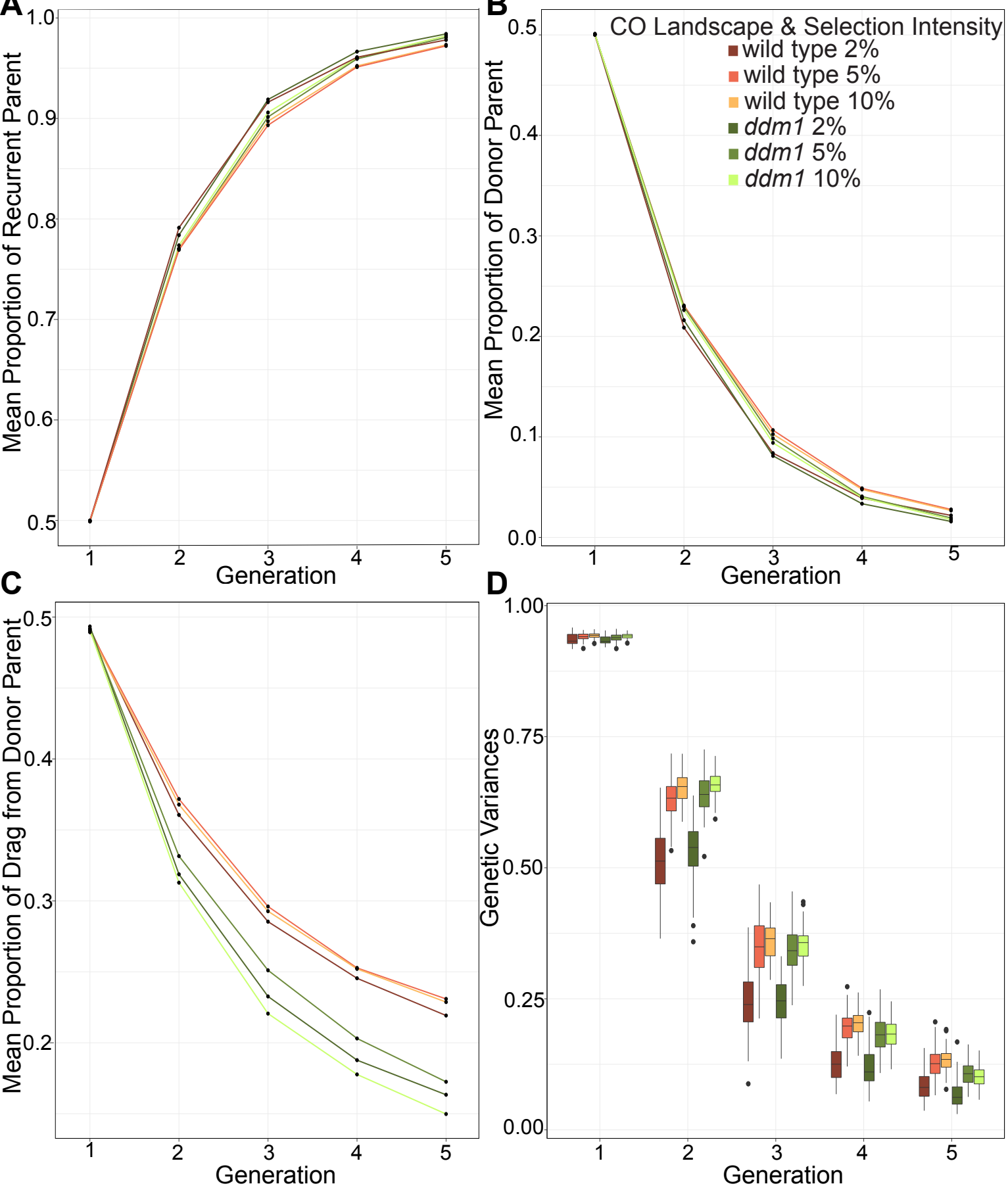


Figure S8. Simulating introgression of a resistance QTL on maize chromosome 1 with different selection intensities in wild-type maize and the *ddm1* maize mutant. Generation 1 represents F_1 progeny from the initial elite parent x wild parent cross. Generations 2 - 4 represent progenies from backcrossing to the elite parent. (A) Proportion of recurrent (elite) parent. (B) Proportion of donor (wild) parent. (C) Linkage drag around the introgression target (disease resistance) loci. (D) Genetic variance.

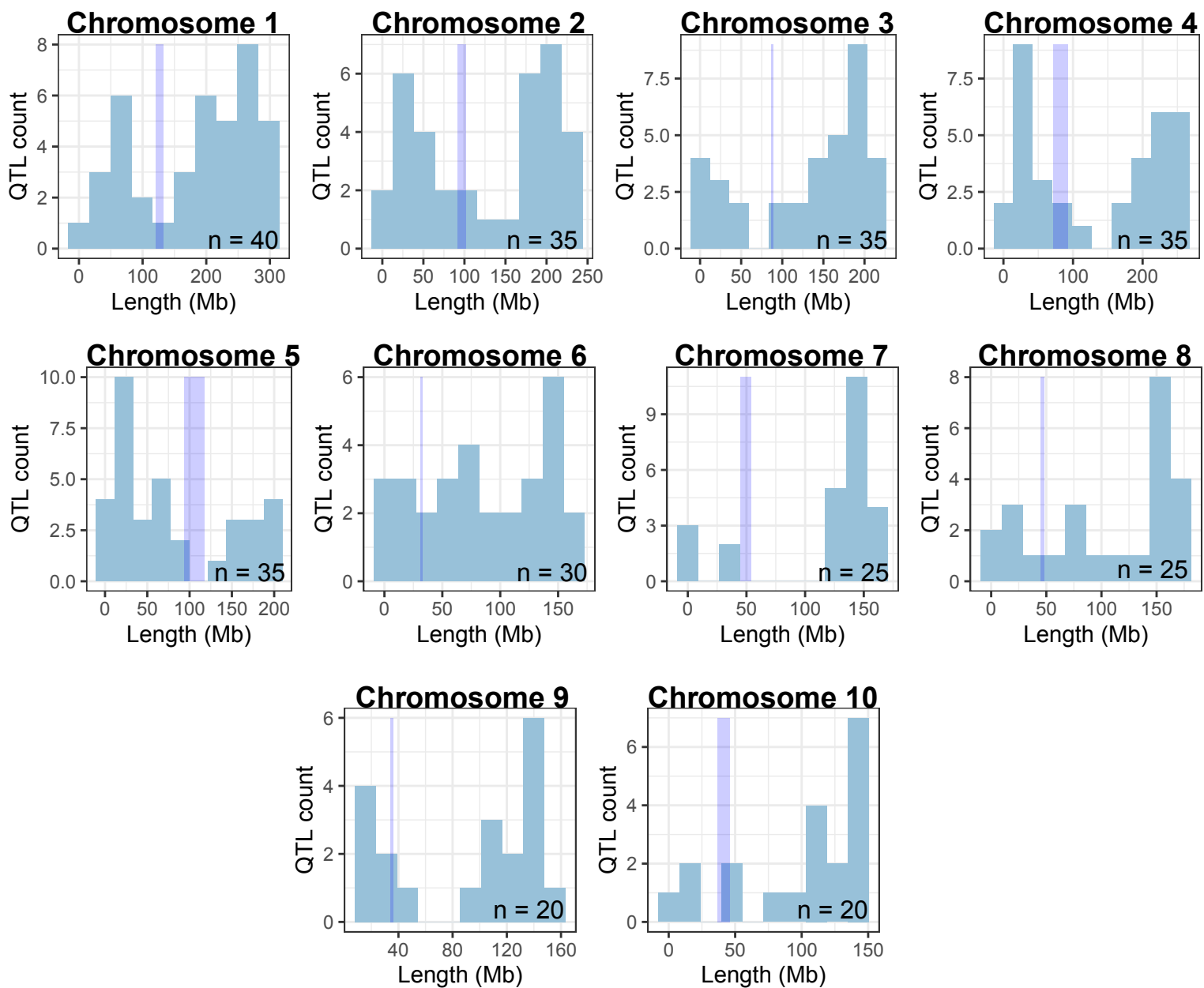


Figure S9. Histograms of 300 yield-like QTL distribution on maize chromosomes. Number of QTL per chromosome is in the bottom right corner of every histogram. Centromere positions are in purple.

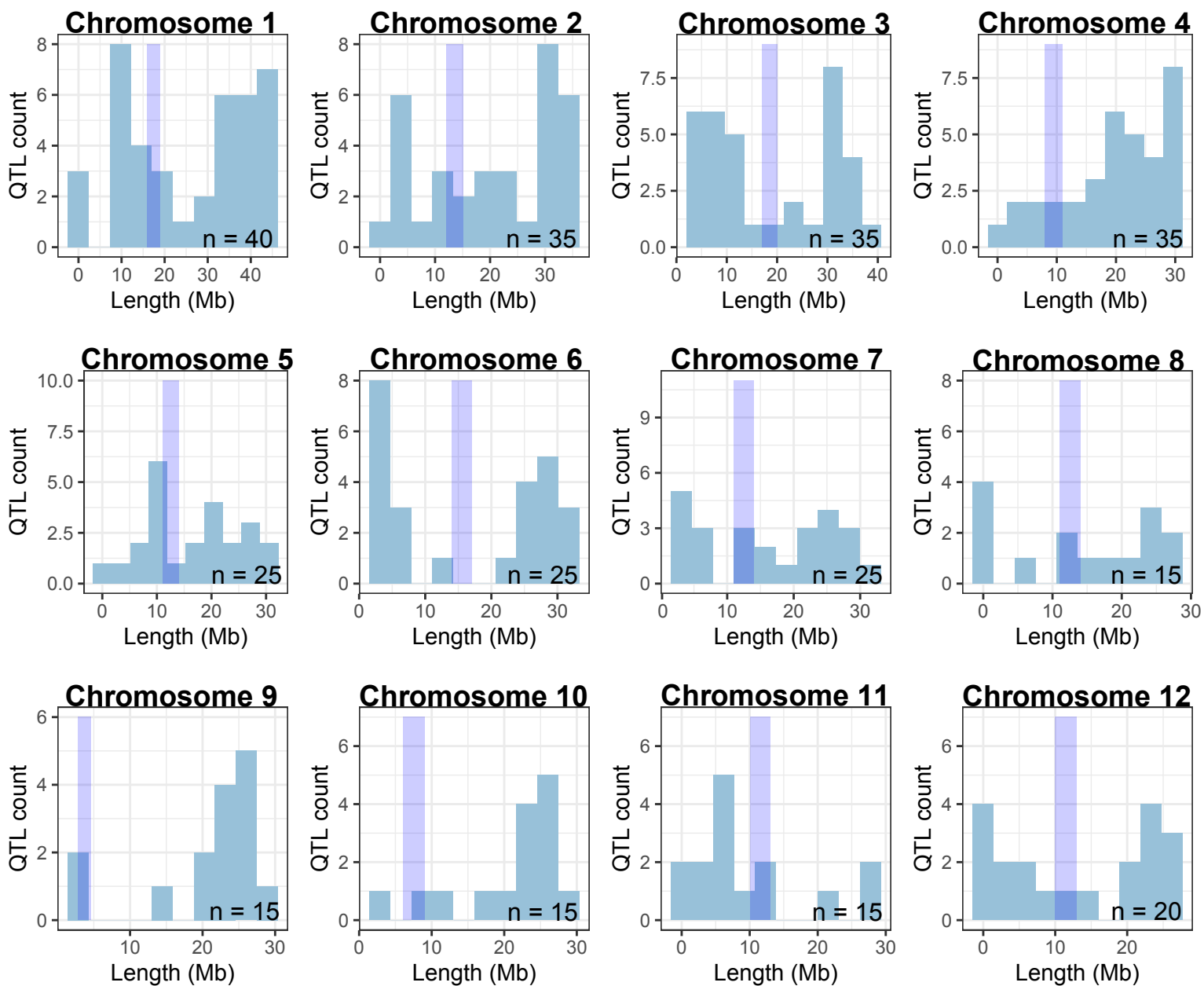


Figure S10. Histograms of 300 yield-like QTL distribution on rice chromosomes. Number of QTL per chromosome is in the bottom right corner of every histogram. Centromere positions are in purple.