Figure S1: Size of the QTL effect, for different numbers of QTLs.
Distribution for the size of the QTL effect depending on the number of QTLs per chromosome for *B. rapa*. The shape of the distribution is the same regardless of the number of QTLs; only the effect's size is modified.
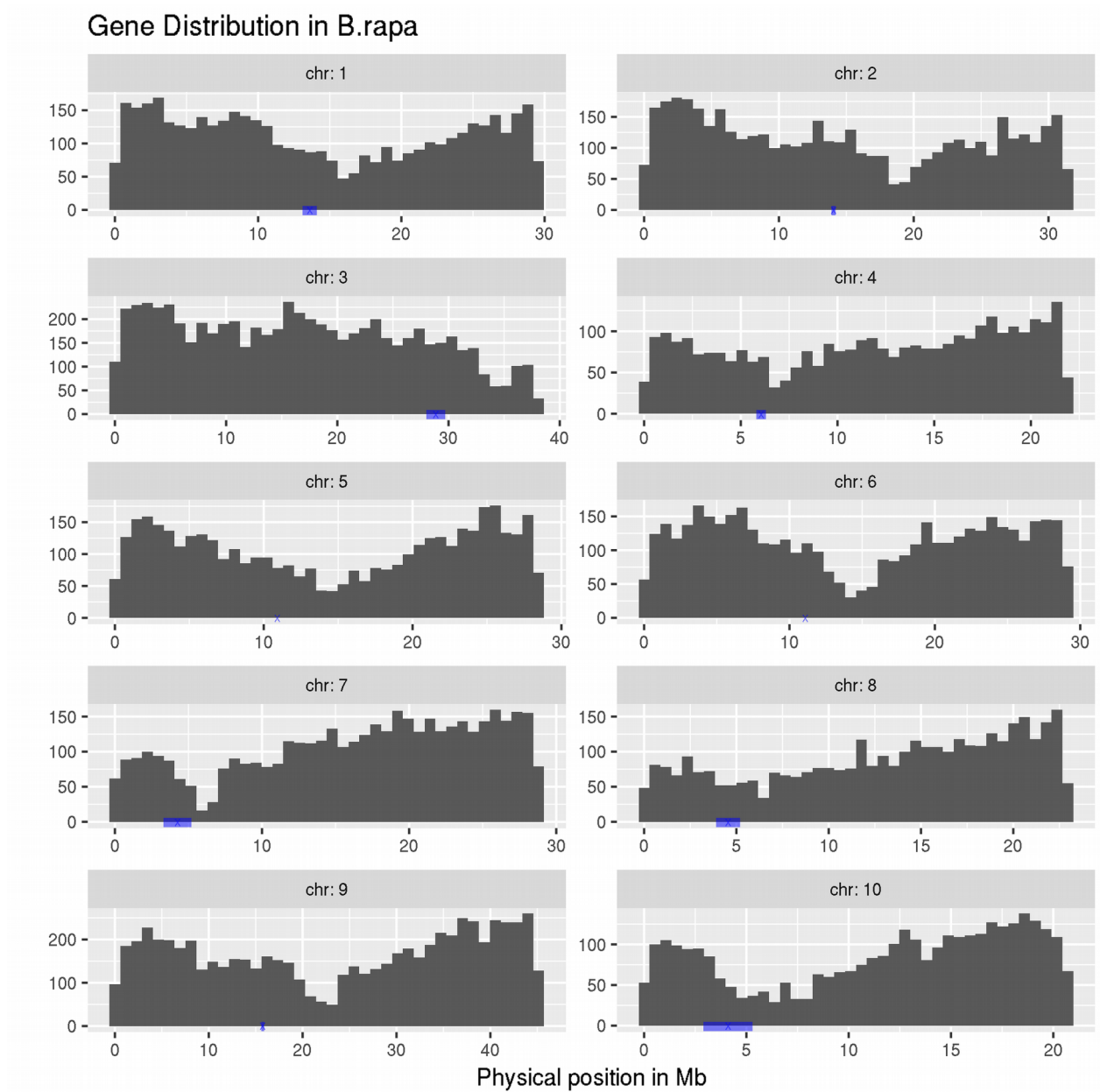
1

Figure S2: *B. rapa* **gene distribution.**
Gene distribution for each chromosome of *B. rapa*.
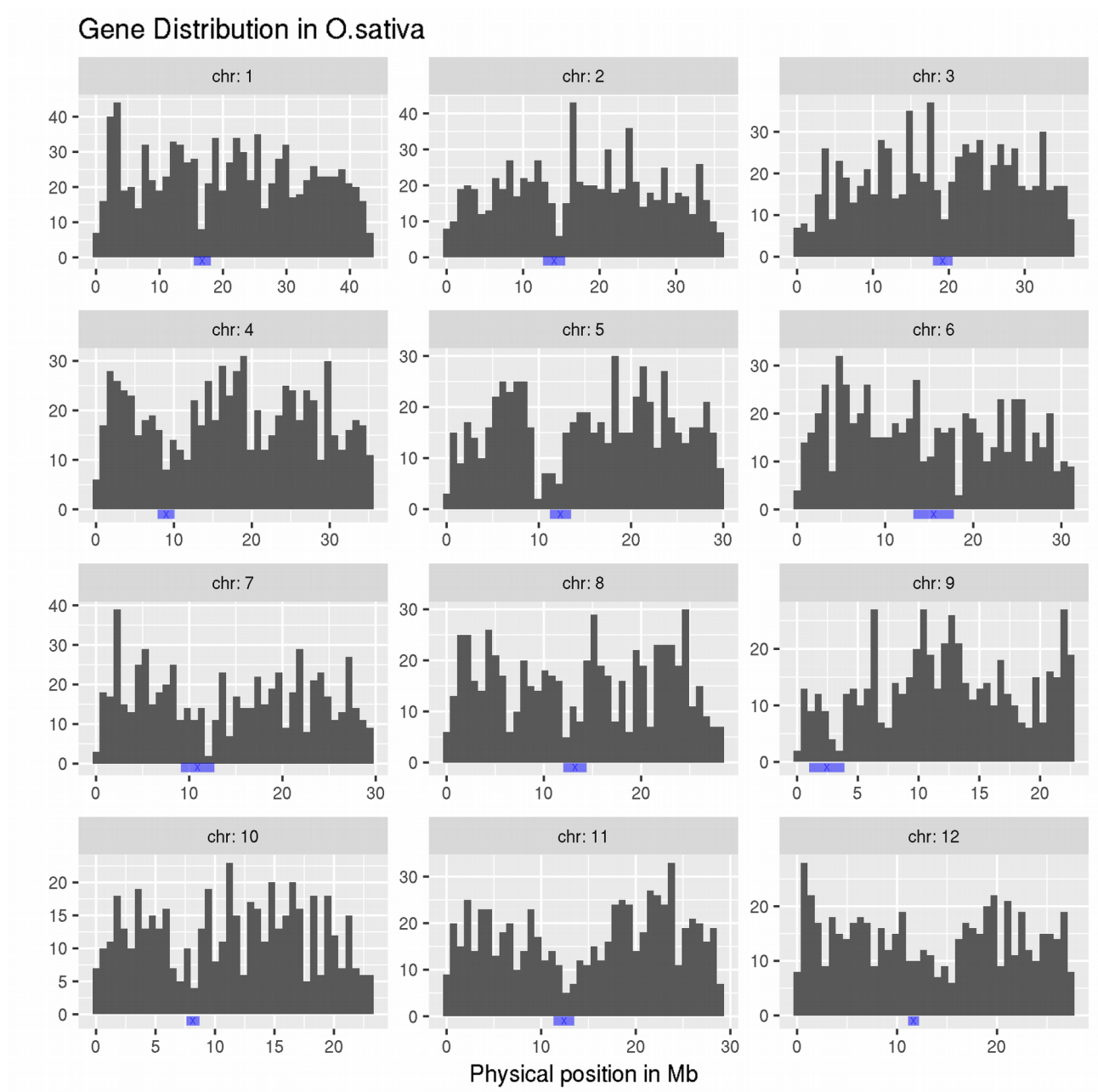In blue, *B. rapa* centromere positions from Mason *et al.* 2016.

Figure S3: *O. sativa* **gene distribution.**
Gene distribution for each chromosome of *O. sativa*.
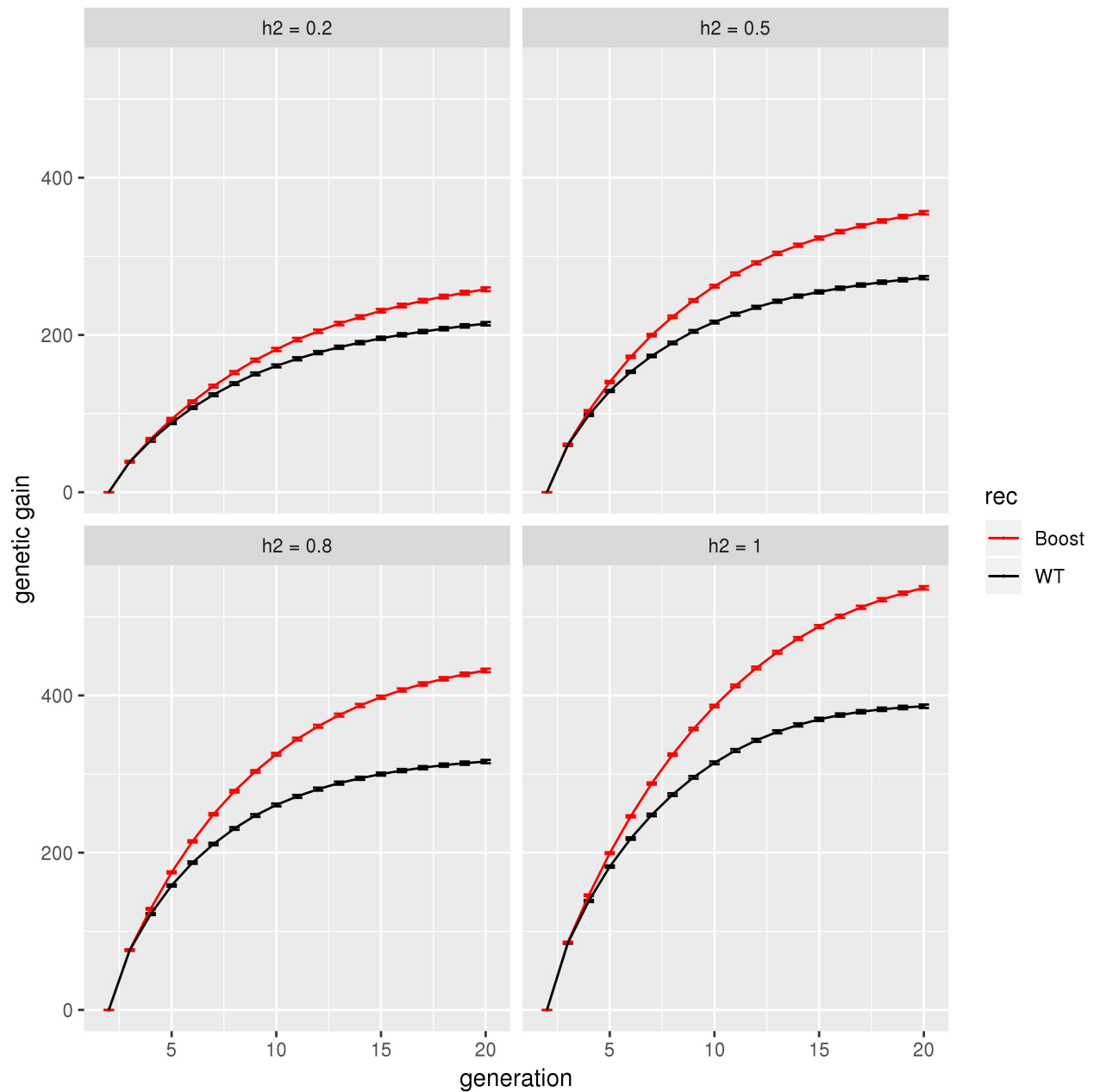In blue, the centromere positions taken from Mizuno *et al.*, 2018.

Figure S4: Genetic gain when using phenotypic selection for different heritabilities.
Genetic gain (sum of QTL effects) as a function of generation for four heritabilities (1, 0.8, 0.5, 0.2), for normal (black) and boosted (red) recombination for *B. rapa* under phenotypic selection, selection on heterozygotes with an intensity of 2%, 200 QTLs per chromosome, crossovers formed without interference, no coupling nor repulsion. The gain ratio between boosted and normal recombination, at g = 20, is 1.40 for $h^2 = 1$, 1.38 for $h^2 = 0.8$, 1.32 for $h^2 = 0.5$ and 1.24 for $h^2 = 0.2$. The first generation shown is the F2 generation (g = 2). The error bars represent 95% confidence interval on the mean.
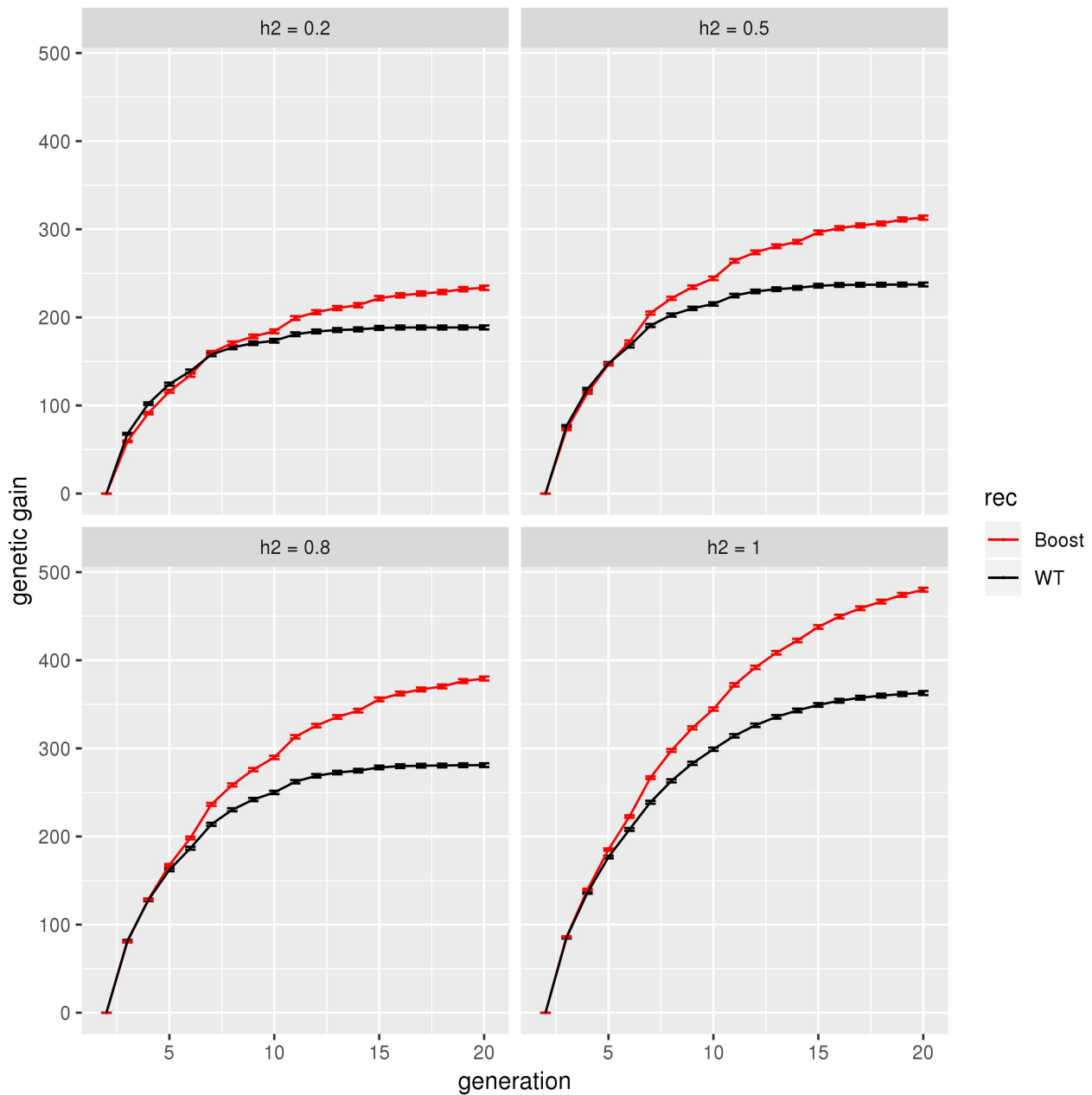
Figure S5: Genetic gain when using genomic selection for different heritabilities.
Genetic gain (sum of QTL effects) as a function of generation for four heritabilities (1, 0.8, 0.5, 0.2), for normal (black) and boosted (red) recombination for *B. rapa* under genomic selection with the marker effects estimated every fourth generation, selection on heterozygotes with an intensity of 2%, 200 QTLs per chromosome, crossovers formed without interference, no coupling nor repulsion. The gain ratio between boosted and normal recombination, at g = 20, is 1.33 for $h^2 = 1$, 1.37 for $h^2 = 0.8$, 1.34 for $h^2 = 0.5$ and 1.28 for $h^2 = 0.2$. The first generation shown is the F2 generation (g = 2). The error bars represent 95% confidence interval on the mean.
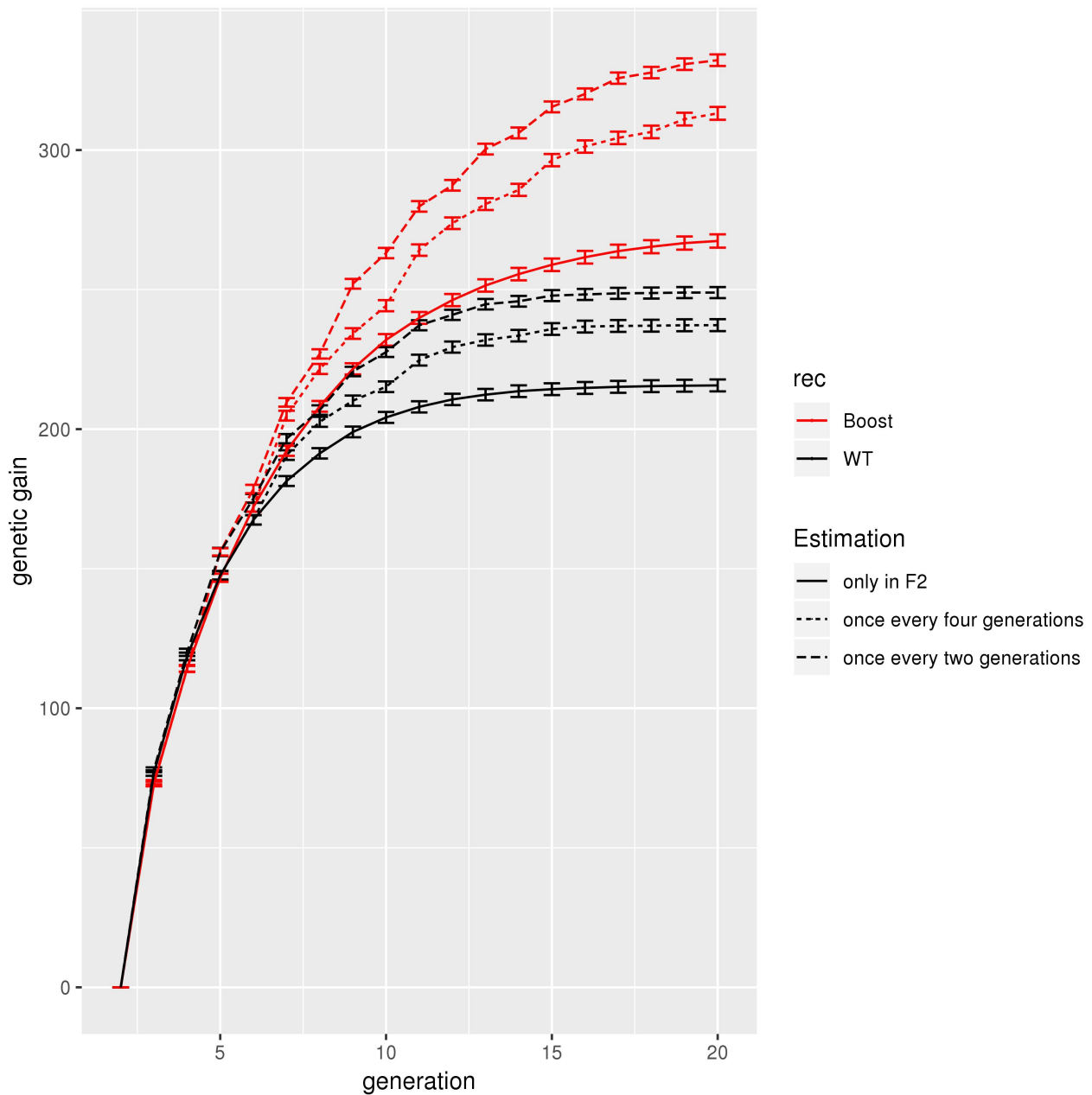
Figure S6: Genetic gain for different recalibration frequencies.
Genetic gain (sum of QTL effects) as a function of the generation, for different choices of the recalibration strategy in genomic selection, for *B. Rapa*, for genomic selection, a heritability of 0.5, selection on heterozygotes with an intensity of 2%, 200 QTLs per chromosome, crossovers formed without interference, no coupling nor repulsion. The different choices for recalibration are: an estimation in F2 only, recalibration every fourth generation and recalibration every second generation. The gain ratio between boosted and normal recombination, at g = 20, is 1.27 for an estimation only in the F2 generation, 1.34 when recalibrated every fourth generation, and 1.35 when recalibrated every second generation.
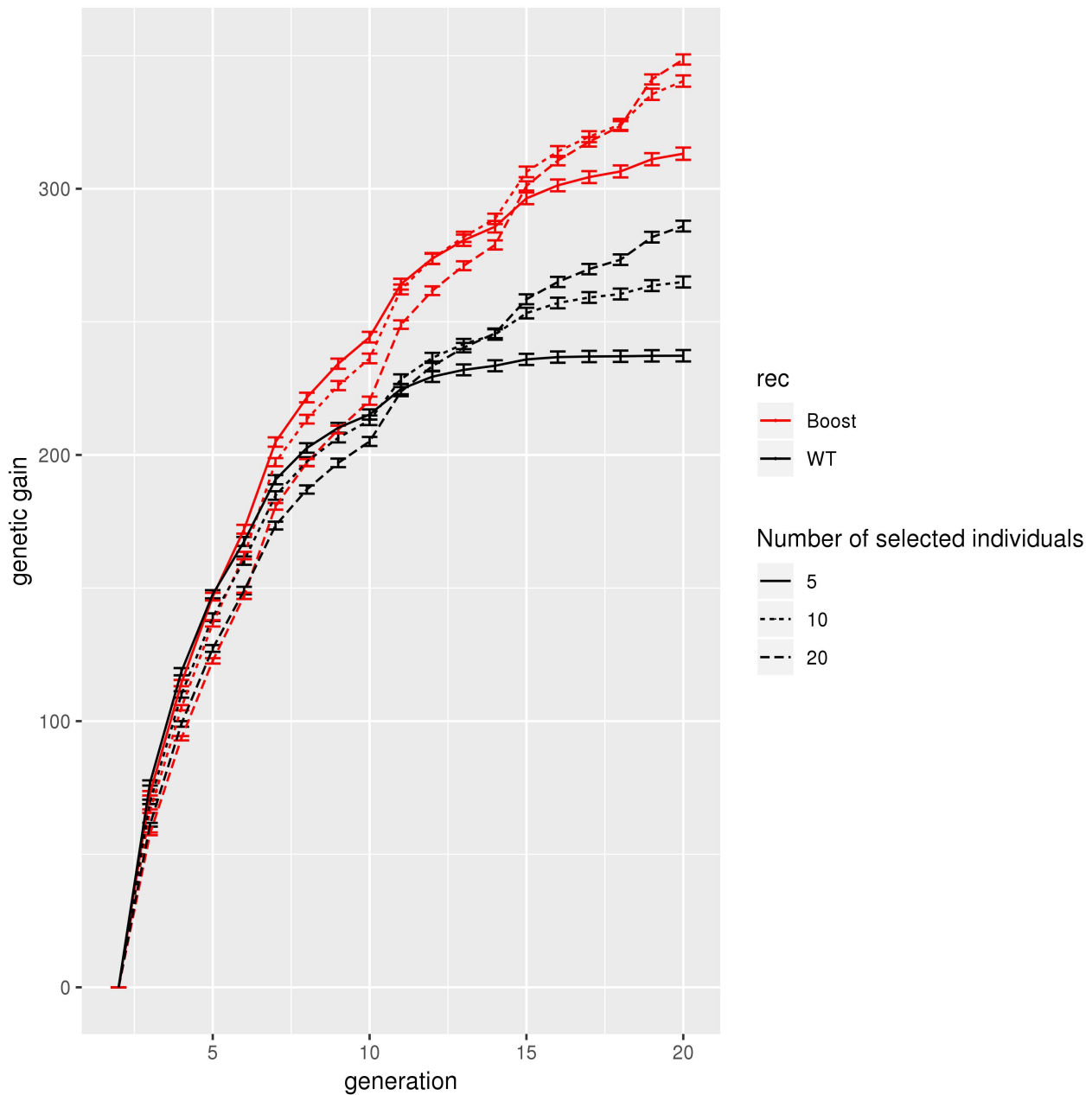
Figure S7: Genetic gain for different selection intensities
Genetic gain (sum of QTL effects) as a function of the generation, for different selection intensities, for *B. rapa*, for genomic selection with the marker effects estimated every fourth generation, a heritability of 0.5, selection on heterozygotes, 200 QTLs per chromosome, crossovers formed without interference, no coupling nor repulsion. The different selection intensities are 2% (selection of the 5 best individuals among the population of 250, based on their GEBV), 4% (selection of the best 10) and 8% (selection of the best 20), for normal (black) and boosted (red) recombination. The gain ratio between boosted and normal recombination, at g = 20, is 1.34 for a 2% selection, 1.30 for 4%, and 1.23 for 8%. The first generation shown is the F2 generation (g = 2). The error bars represent 95% confidence interval on the mean.
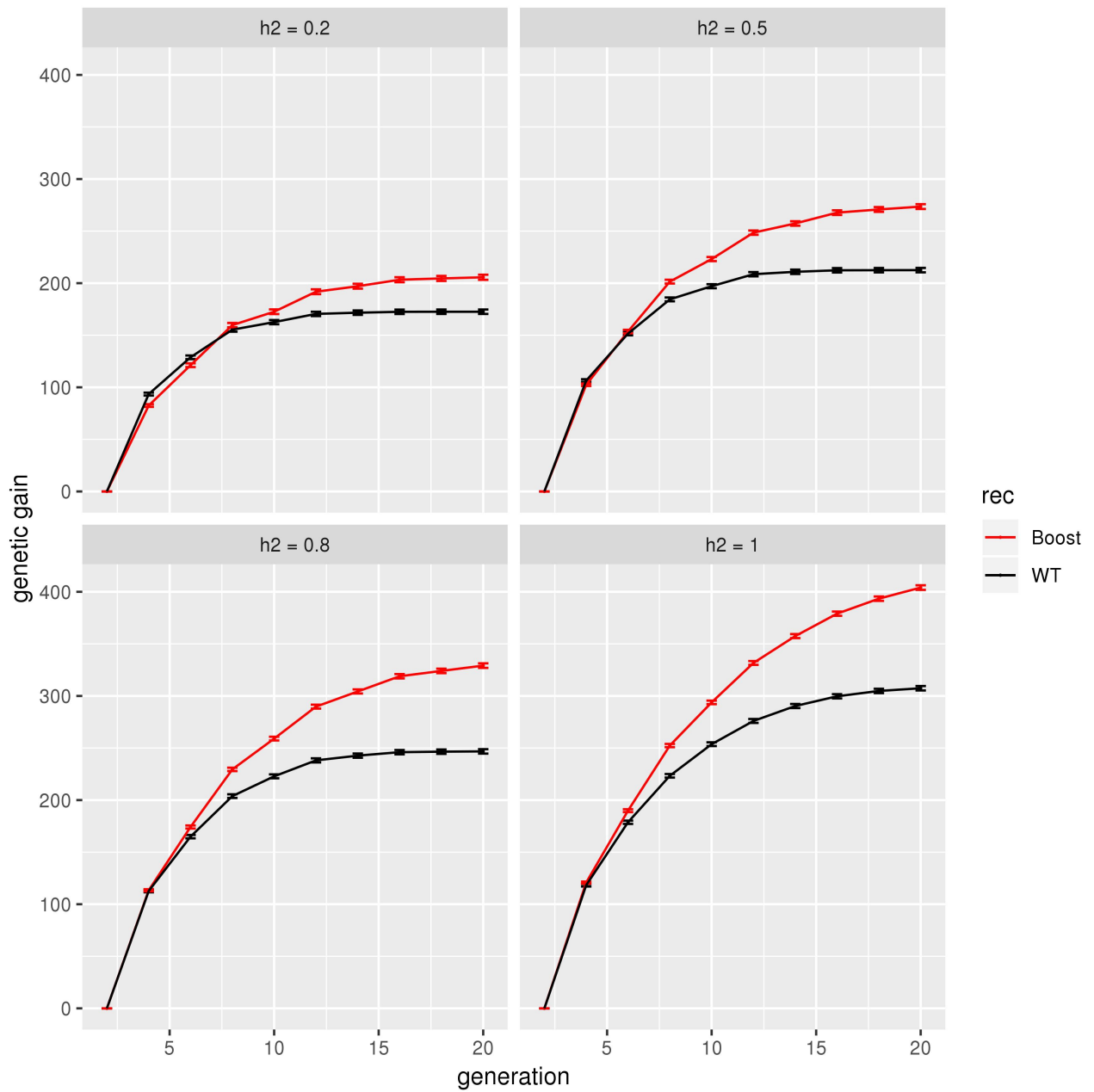
Figure S8: Genetic gain under DH selection scheme.
Genetic gain (sum of QTL effects) as a function of the generation for four heritabilities (1, 0.8, 0.5, 0.2), for normal (black) and boosted (red) recombination for *B. rapa* for genomic selection with the marker effects estimated every fourth generation, selection on homozygotes with an intensity of 2%, 200 QTLs per chromosome, crossovers formed without interference, no coupling nor repulsion. The gain ratio between boosted and normal recombination, at g = 20, is 1.33 for $h^2 = 1$, 1.35 for $h^2 = 0.8$, 1.31 for $h^2 = 0.5$ and 1.23 for $h^2 = 0.2$. The first generation shown is the F2 generation (g = 2). The error bars represent 95% confidence interval on the mean.
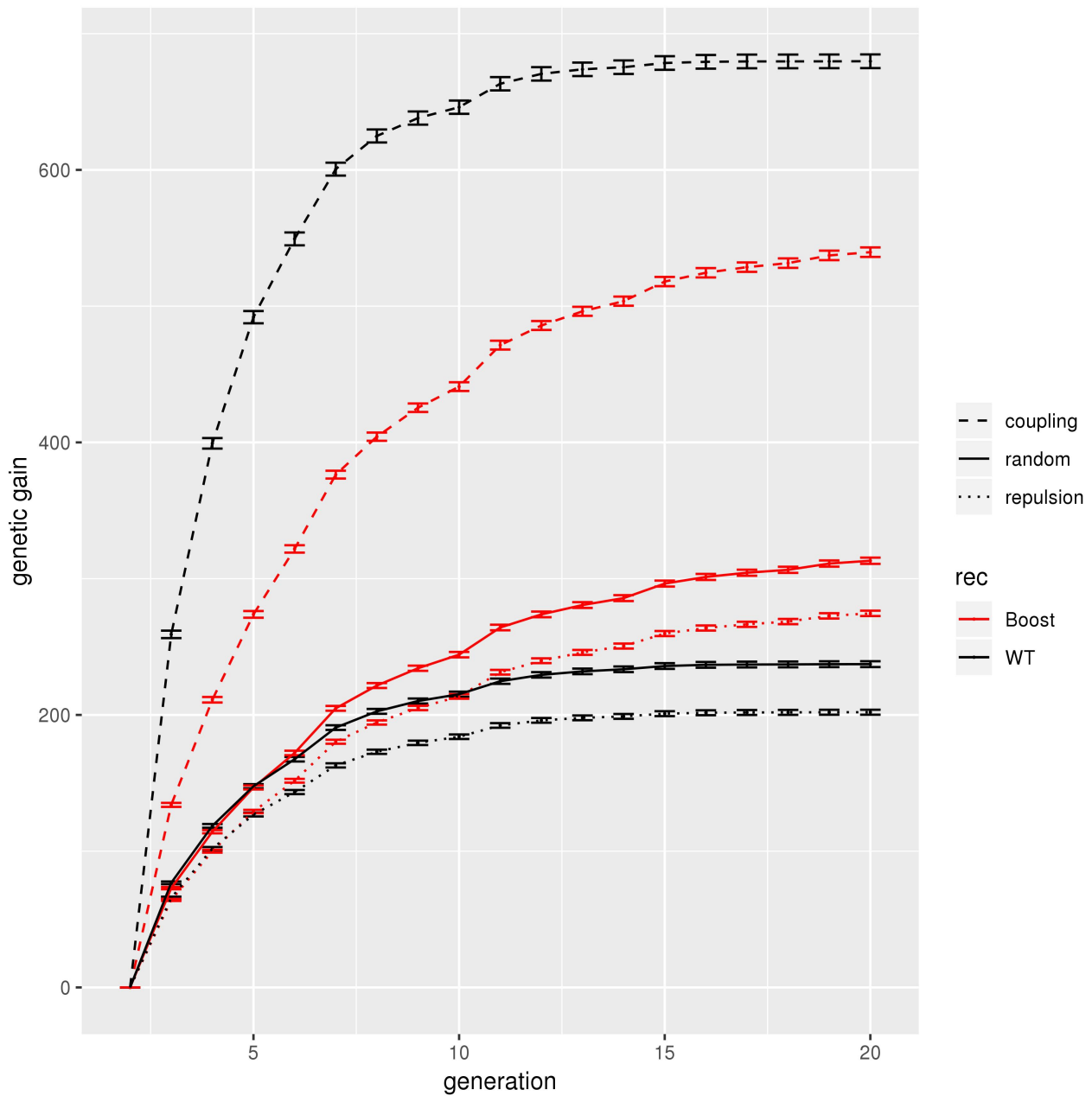
Figure S9: Genetic gain under coupling and repulsion
Genetic gain (sum of QTL effects) as a function of the generation, for QTLs under a moderate
coupling or repulsion (characteristic length of 5 cM, see Main text), for *B. rapa*, for genomic
selection with the marker effects estimated every fourth generation, a heritability of 0.5, selection
on heterozygotes with an intensity of 2%, 200 QTLs per chromosome, crossovers formed without
interference. The gain ratio between boosted and normal recombination, at g = 20, is 0.80 under a
coupling and 1.38 under repulsion. The first generation shown is the F2 generation (g = 2). The
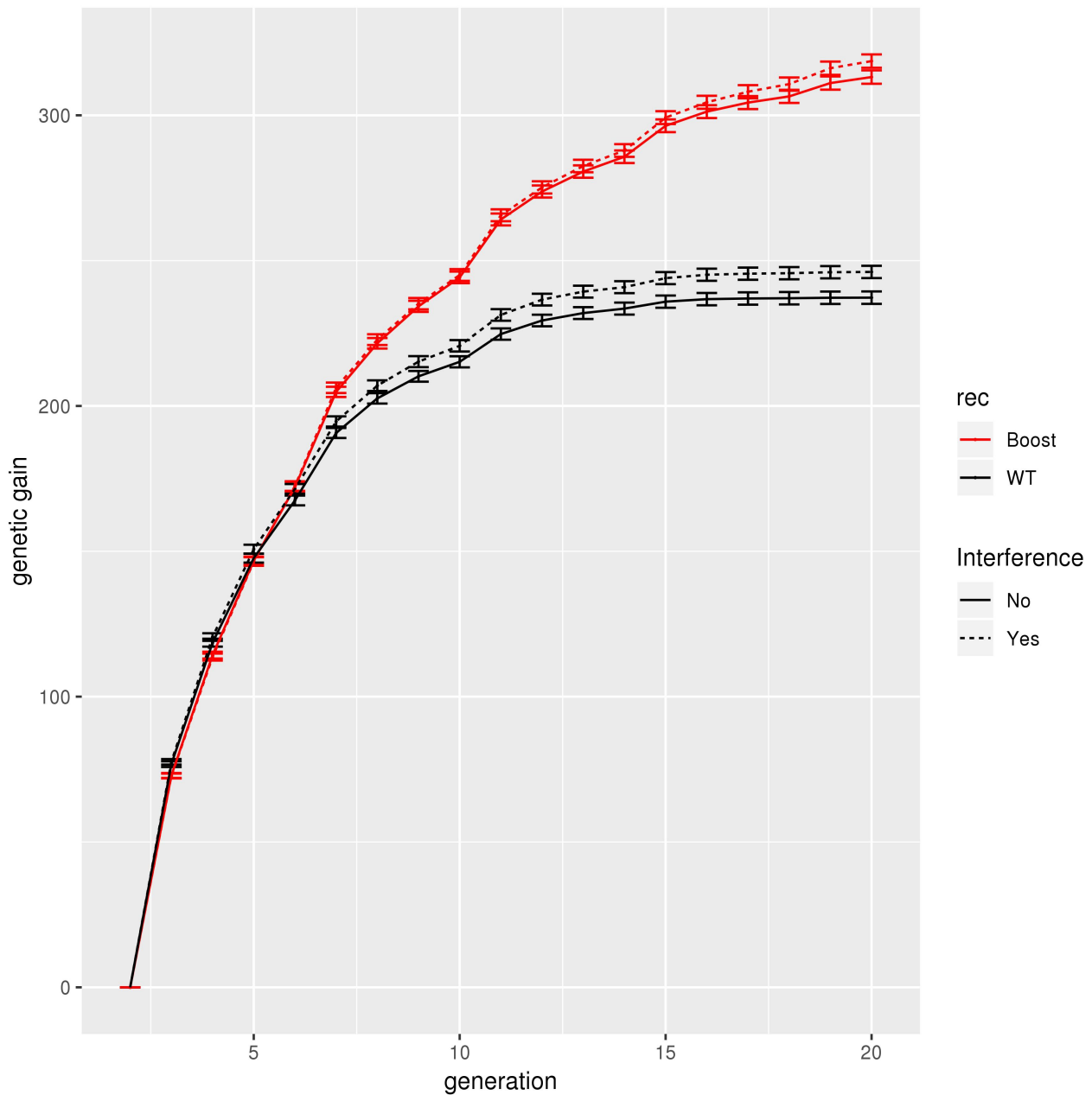error bars represent 95% confidence interval on the mean.

Figure S10: Genetic gain in the presence of crossover interference
Genetic gain (sum of QTL effects) as a function of the generation, when we allow for crossover interference, for *B. rapa*, for genomic selection with the marker effects estimated every fourth generation, a heritability of 0.5, selection on heterozygotes with an intensity of 2%, 200 QTLs per chromosome, without coupling nor repulsion. The gain ratio between boosted and normal recombination, at g = 20, is 1.31. The first generation shown is the F2 generation (g = 2). The error bars represent 95% confidence interval on the mean.