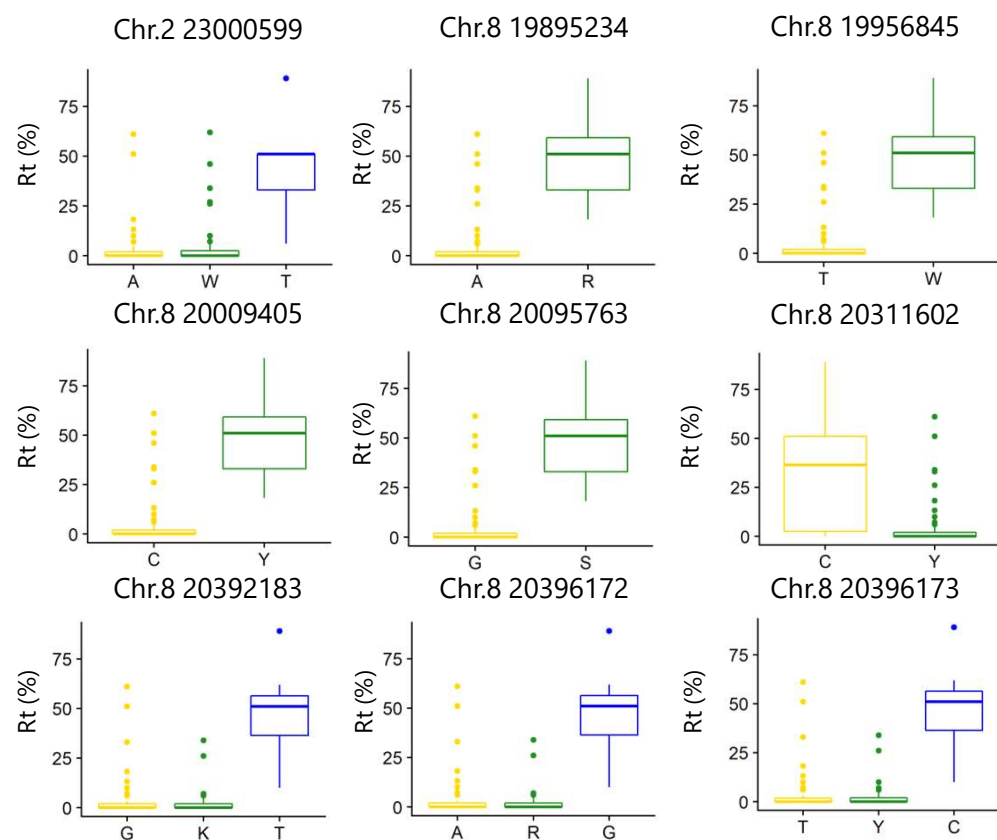


(A) Ratio of diseased fruits (Rt; %)



(B) Disease severity index (Sv)

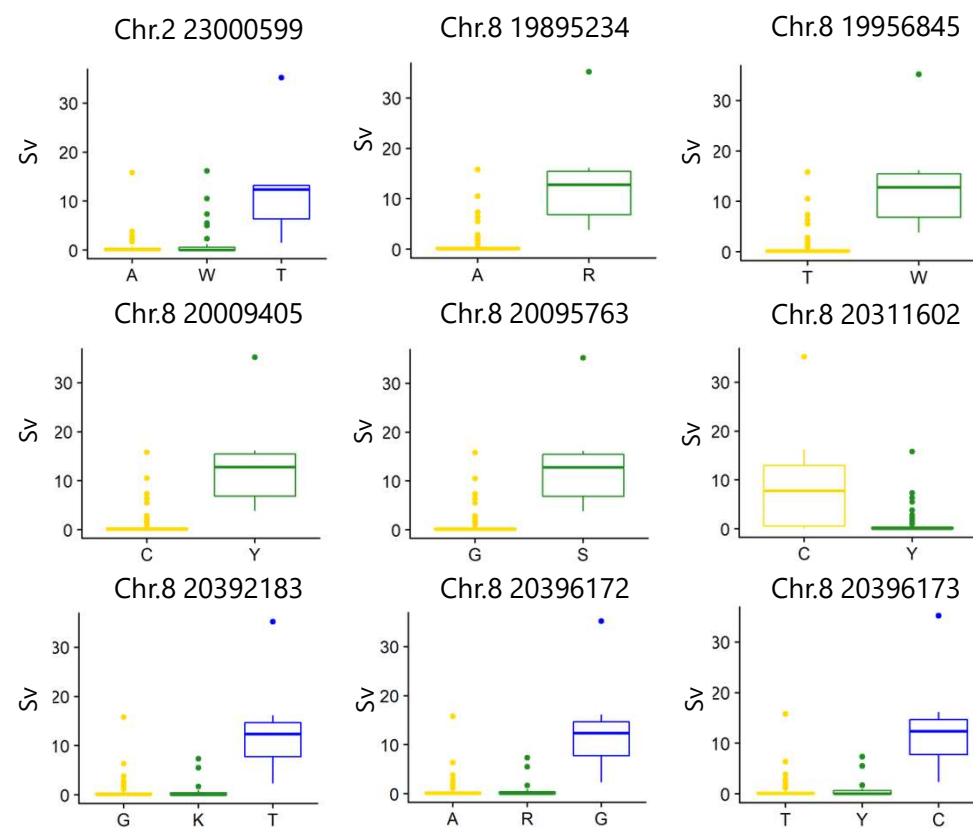
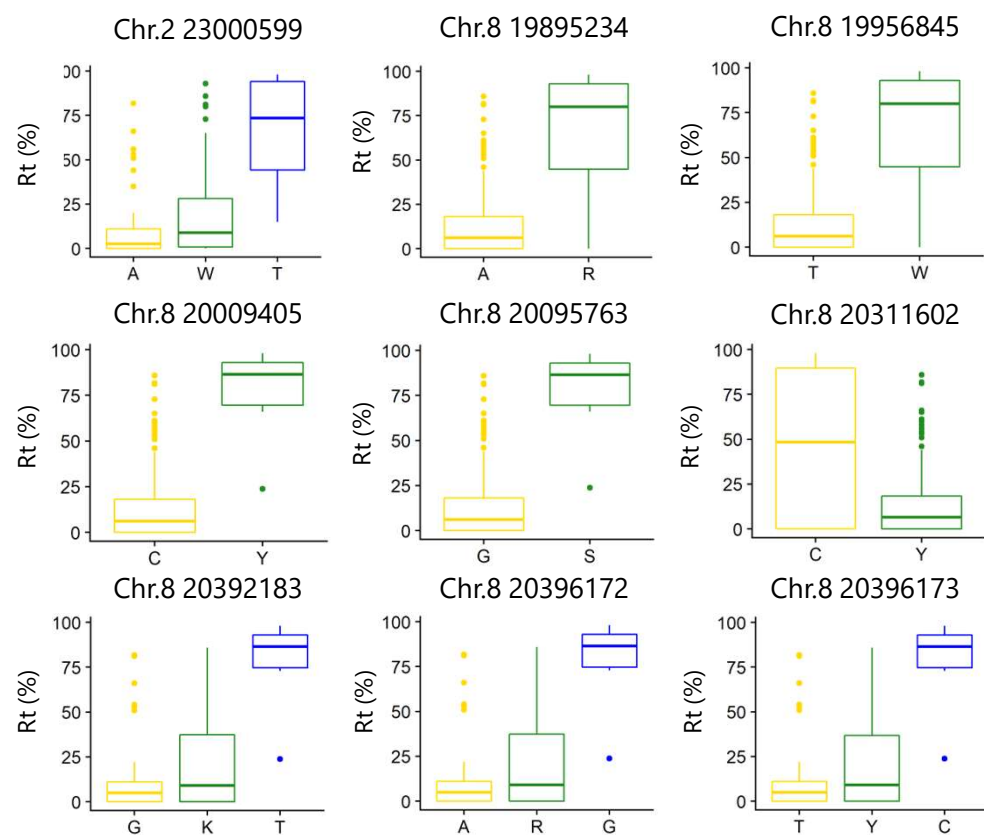


Figure S1. Box plots of trait values in 2017 for genotypes at 9 SNPs detected multiple years in GWAS. (A) Ratio of diseased fruits (Rt; %). (B) Disease severity index (Sv).

Genotypes: A, T, C and G: Homozygote for each base.

K, R, S, W and Y: Heterozygote of A/T, A/G, C/G, A/T and C/T, respectively.

(A) Ratio of diseased fruits (Rt; %)



(B) Disease severity index (Sv)

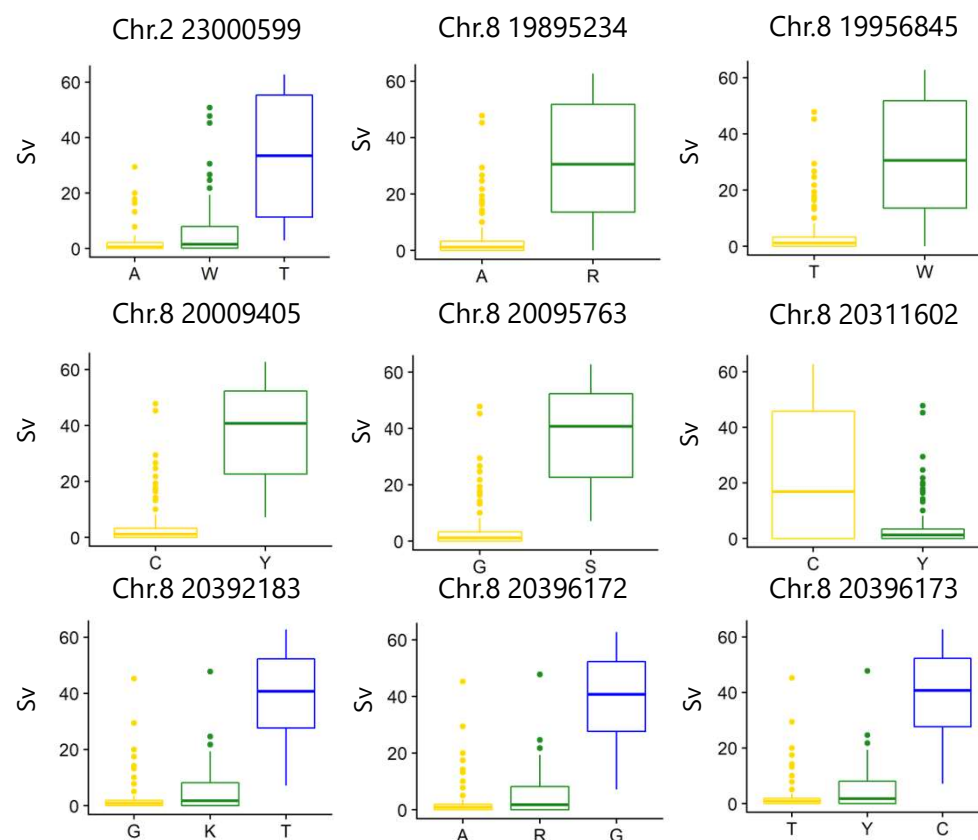
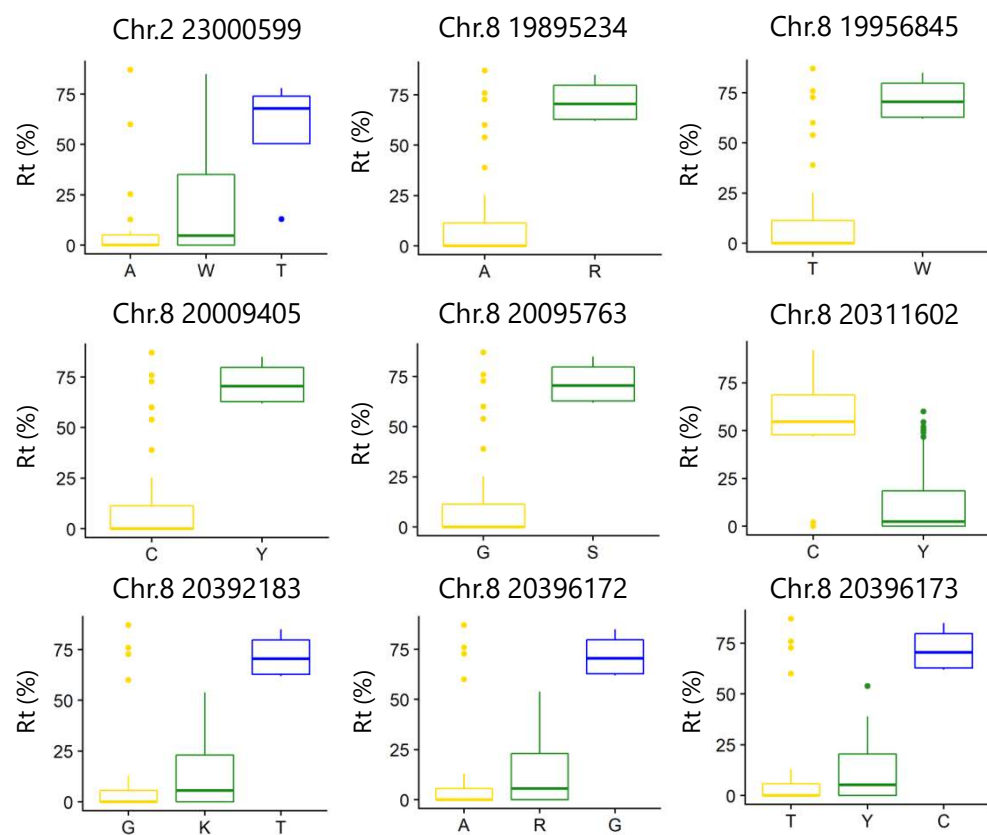


Figure S2. Box plots of trait values in 2018 for genotypes at 9 SNPs detected multiple years in GWAS. (A) Ratio of diseased fruits (Rt; %). (B) Disease severity index (Sv).

Genotypes: A, T, C and G: Homozygote for each base.

K, R, S, W and Y: Heterozygote of A/T, A/G, C/G, A/T and C/T, respectively.

(A) Ratio of diseased fruits (Rt; %)



(B) Disease severity index (Sv)

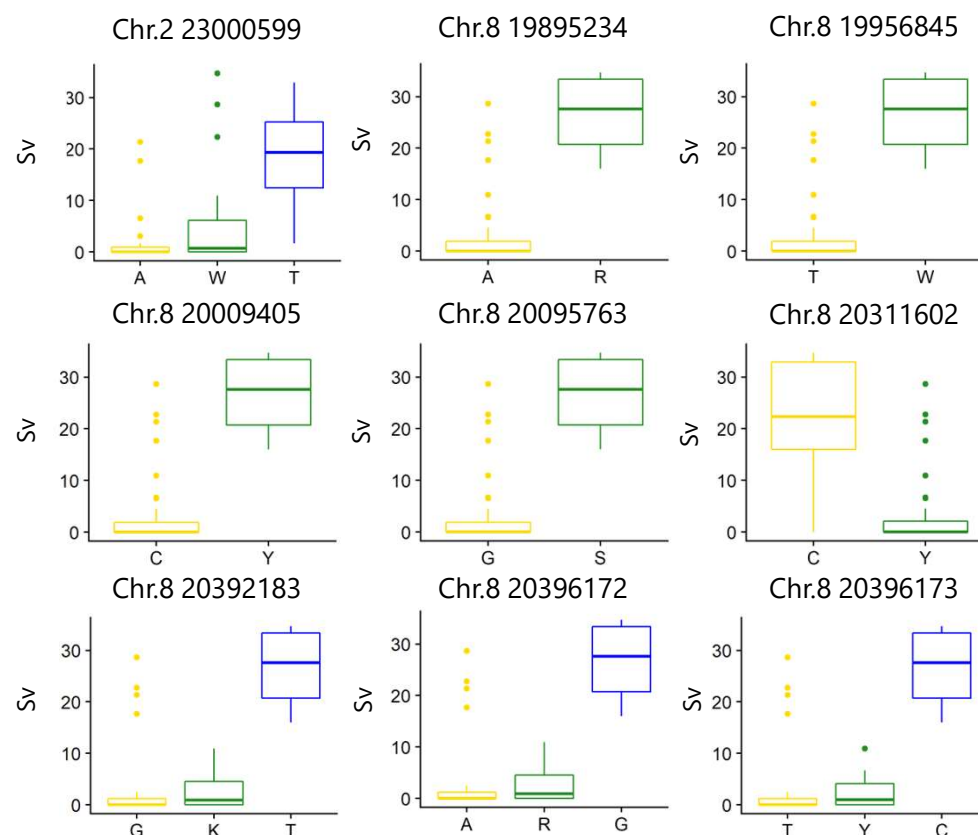


Figure S3. Box plots of trait values in 2019 for genotypes at 9 SNPs detected multiple years in GWAS. (A) Ratio of diseased fruits (Rt; %). (B) Disease severity index (Sv).

Genotypes: A, T, C and G: Homozygote for each base.

K, R, S, W and Y: Heterozygote of A/T, A/G, C/G, A/T and C/T, respectively.