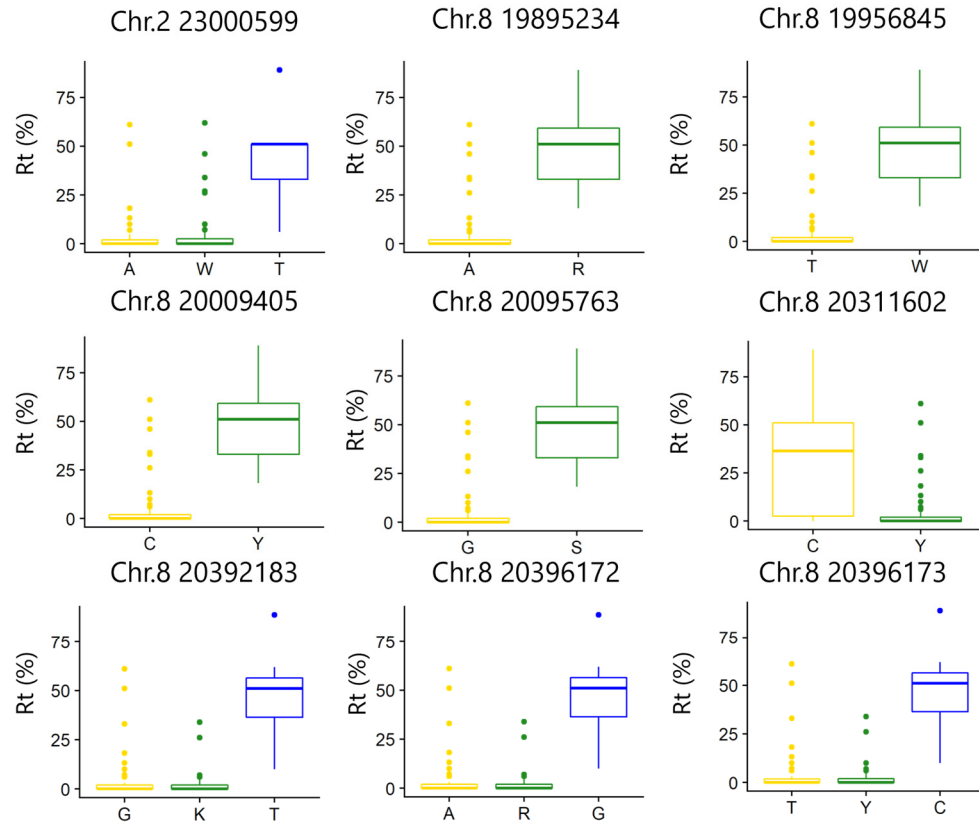


(a) Ratio of diseased fruits (Rt; %)



(b) Disease severity index (Sv)

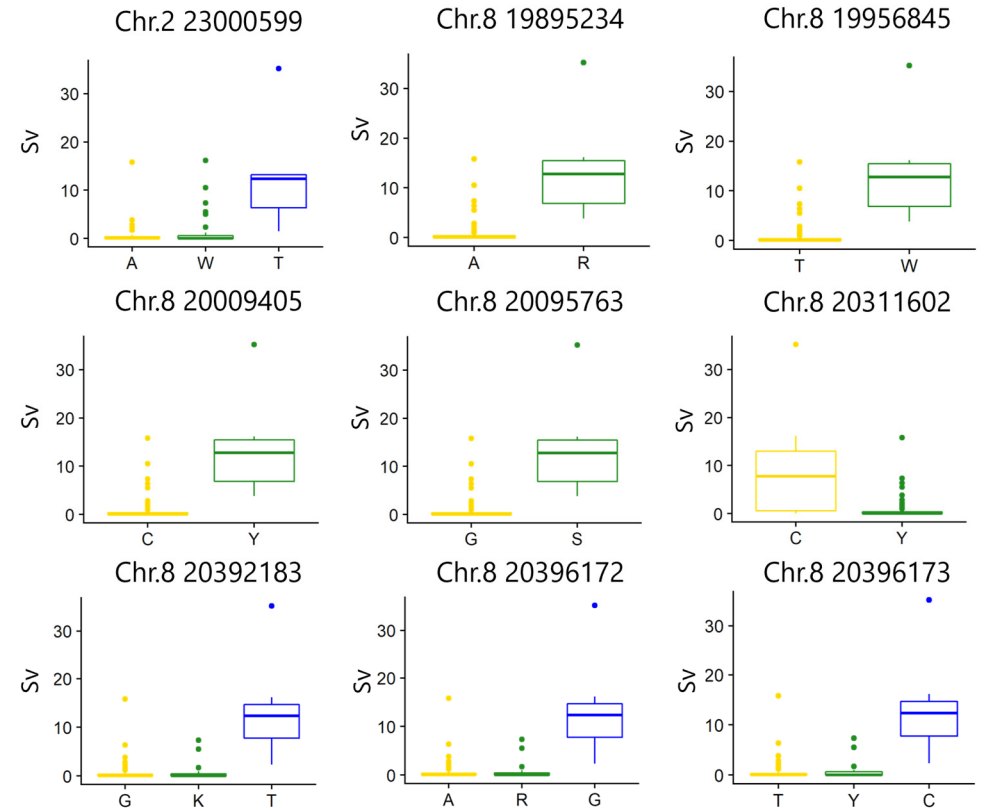
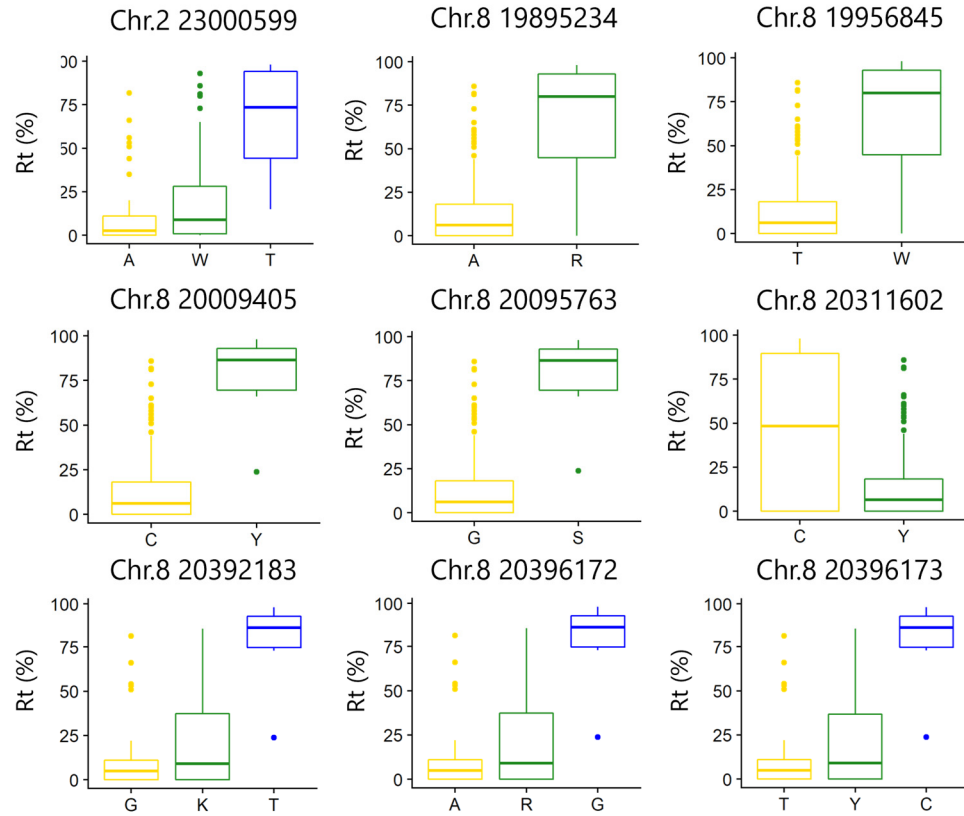


Figure S1. Box plots of trait values in 2017 for genotypes at nine SNPs detected in multiple years in GWAS. **(a)** Ratio of diseased fruits (Rt; %). **(b)** Disease severity index (Sv). Genotypes: A, T, C and G: Homozygote for each base. K, R, S, W and Y: Heterozygote of A/T, A/G, C/G, A/T and C/T, respectively.

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



(b) Disease severity index (Sv)

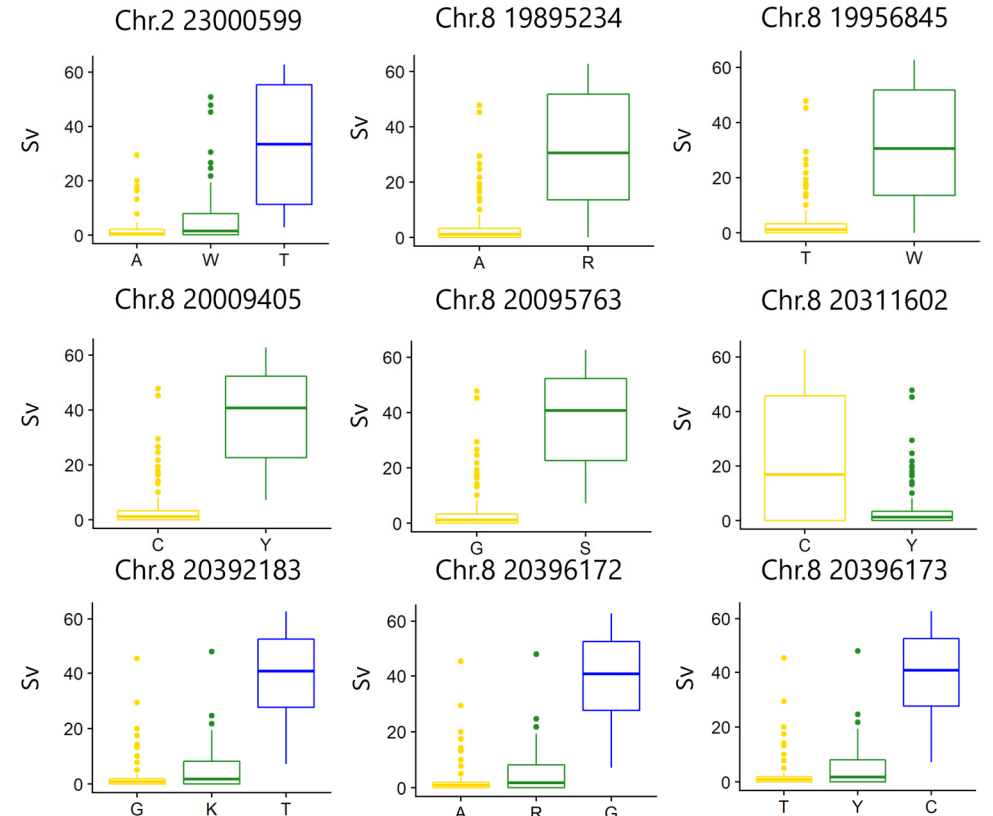
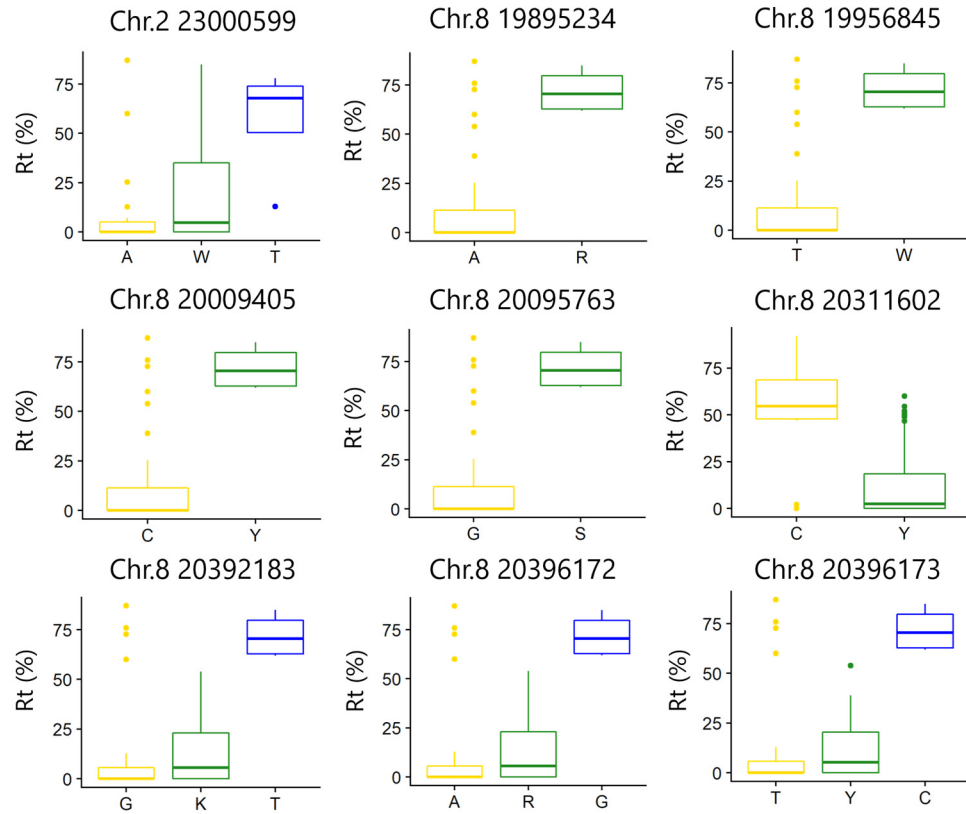


Figure S2. Box plots of trait values in 2018 for genotypes at nine SNPs detected in multiple years in GWAS. **(a)** Ratio of diseased fruits (Rt; %). **(b)** Disease severity index (Sv). Genotypes: A, T, C and G: Homozygote for each base. K, R, S, W and Y: Heterozygote of A/T, A/G, C/G, A/T and C/T, respectively.

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



(b) Disease severity index (Sv)

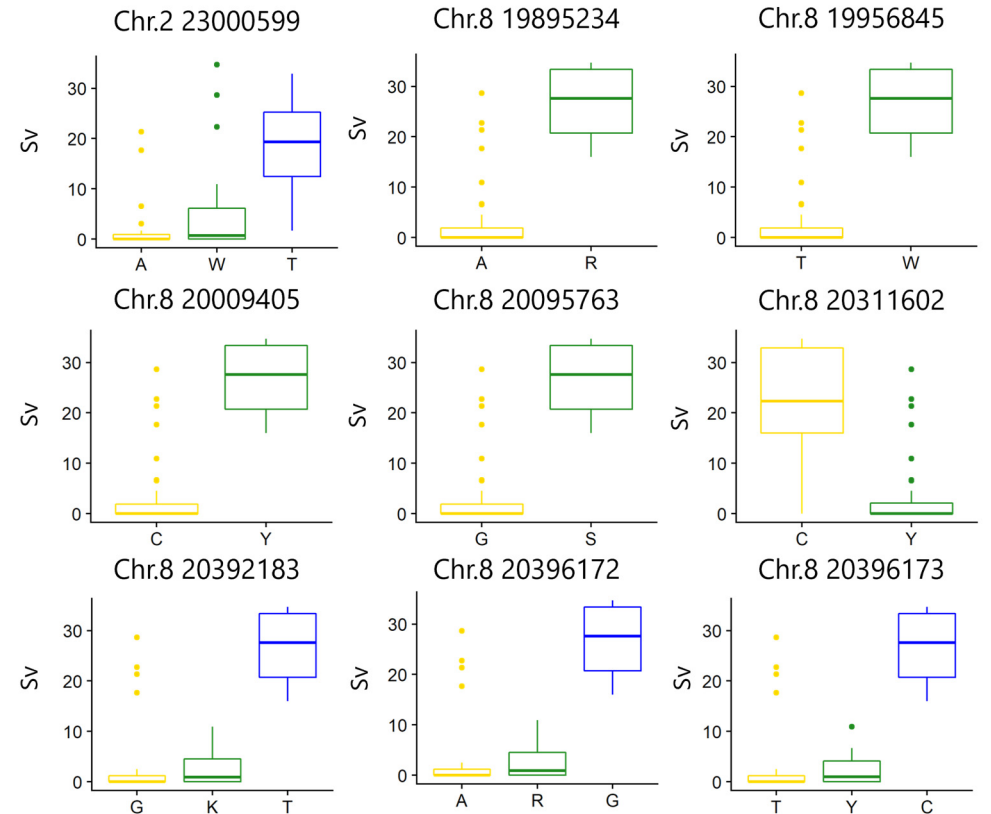


Figure S3. Box plots of trait values in 2019 for genotypes at nine SNPs detected in multiple years in GWAS. **(a)** Ratio of diseased fruits (Rt; %). **(b)** Disease severity index (Sv). Genotypes: A, T, C and G: Homozygote for each base. K, R, S, W and Y: Heterozygote of A/T, A/G, C/G, A/T and C/T, respectively.