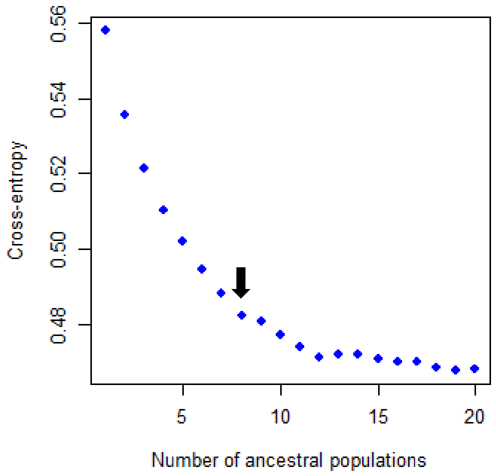
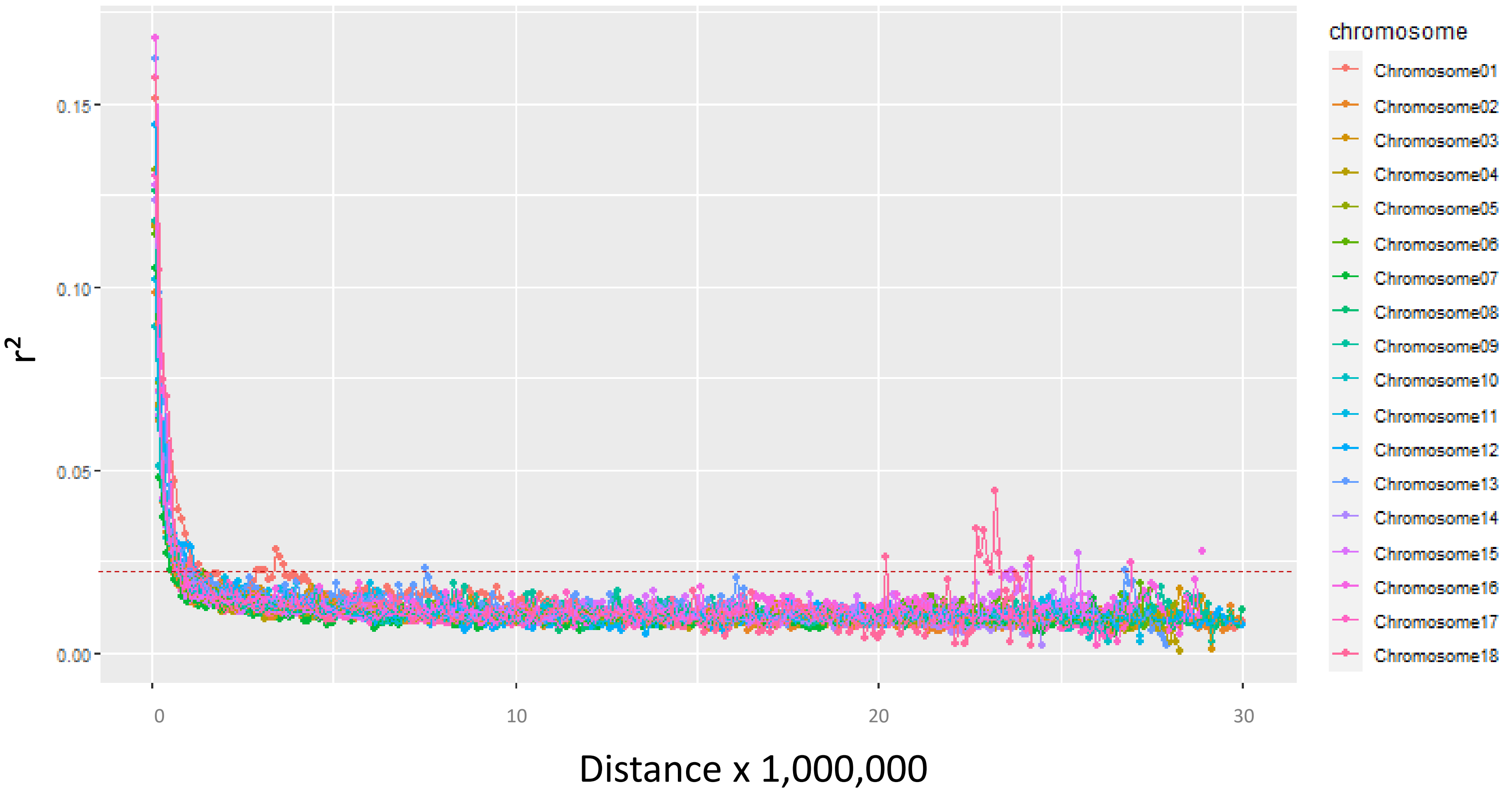
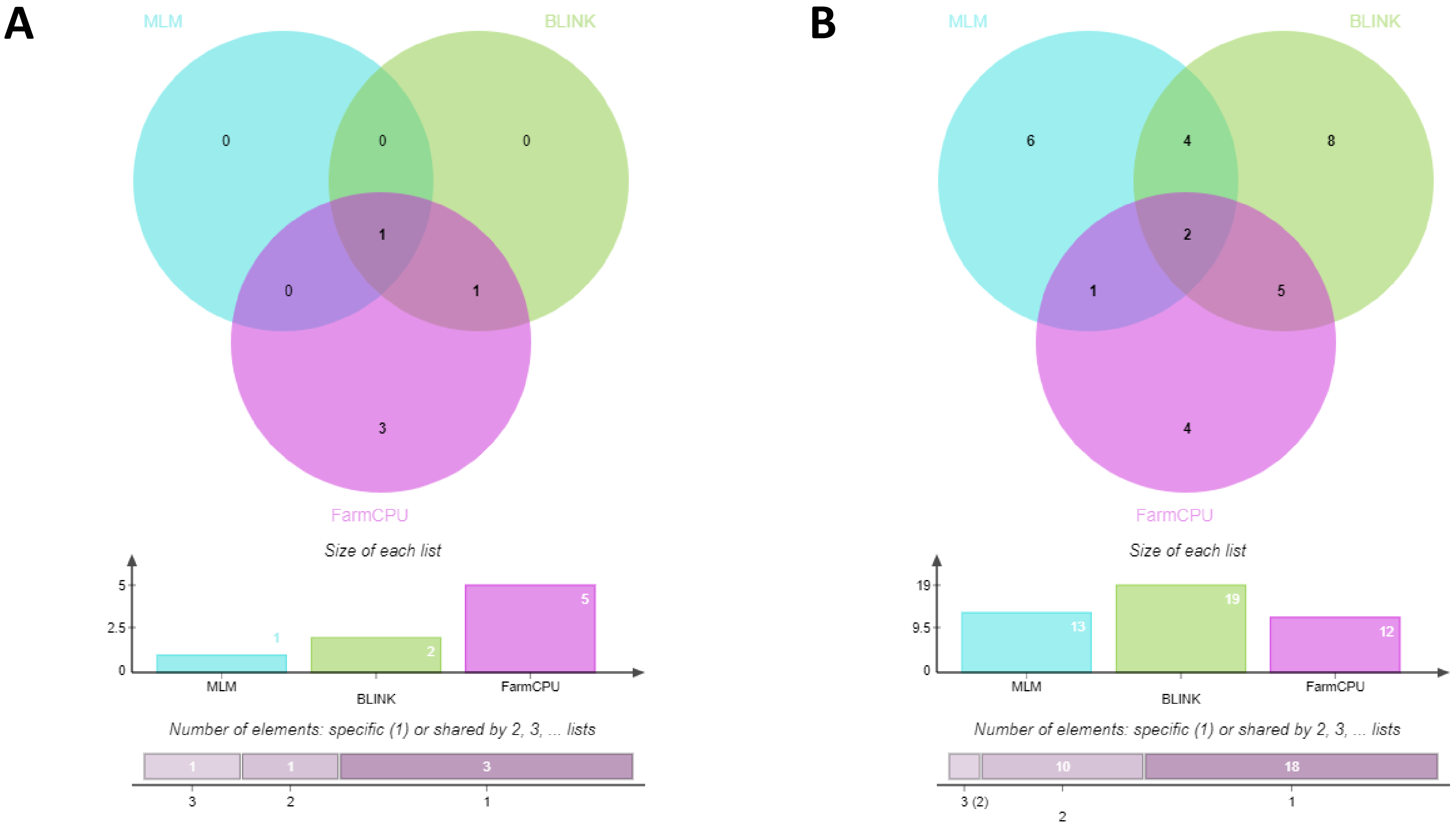


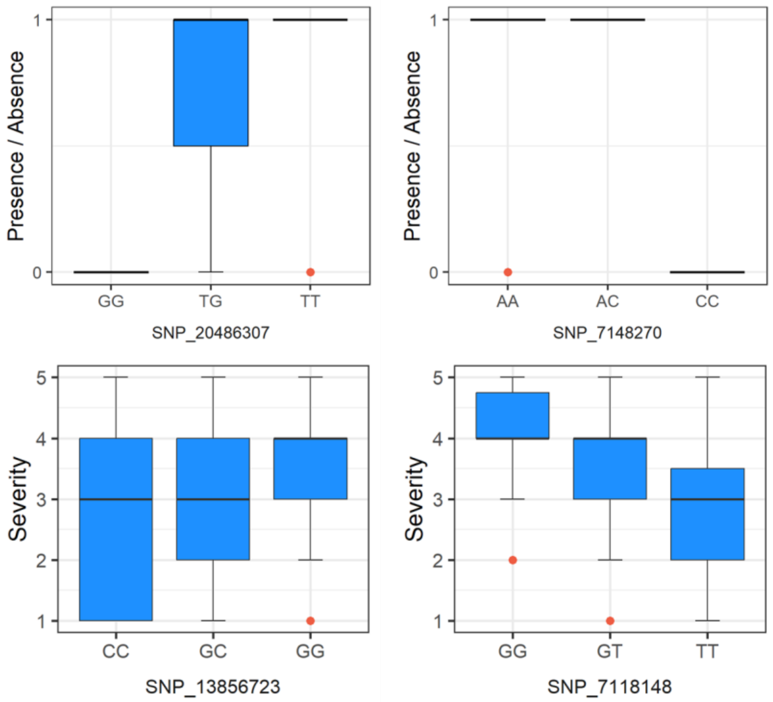
Supplementary Figure 1. Cross-entropy criterion as a function of the number of populations using snmf suggesting eight clusters.



Supplementary Figure 2. Genome-wide linkage disequilibrium (LD) decay, showing r^2 values plotted against physical distance (Mb) for each chromosome. The dashed line indicates the average genome-wide LD of 0.021.



Supplementary Figure 3. Venn diagrams showing the total number of significant associations identified by each model and the common ones. (**A**) significant associations identified with the CBSD severity phenotype, and (**B**) with the presence/absence of CBSV infection phenotype.



Supplementary Figure 4. Phenotypic distribution of the four significant markers. Above the two selected from the presence/absence of virus phenotype, and below the two for CBSD severity phenotype.