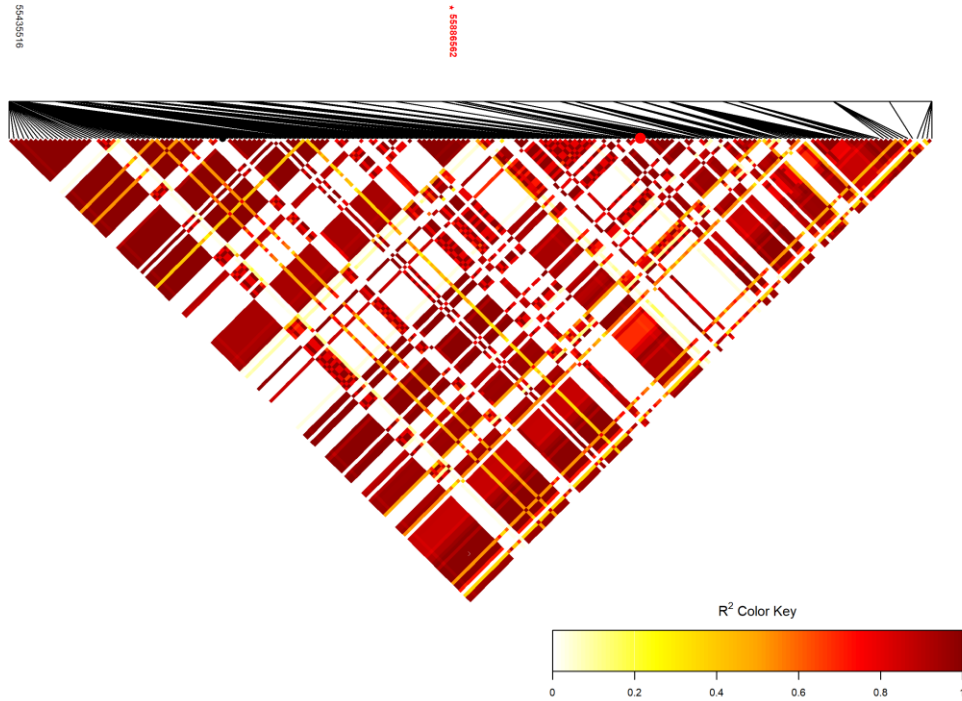


LD around SL4.0CH09:55,886,562 $\pm$ 5e+05 bp

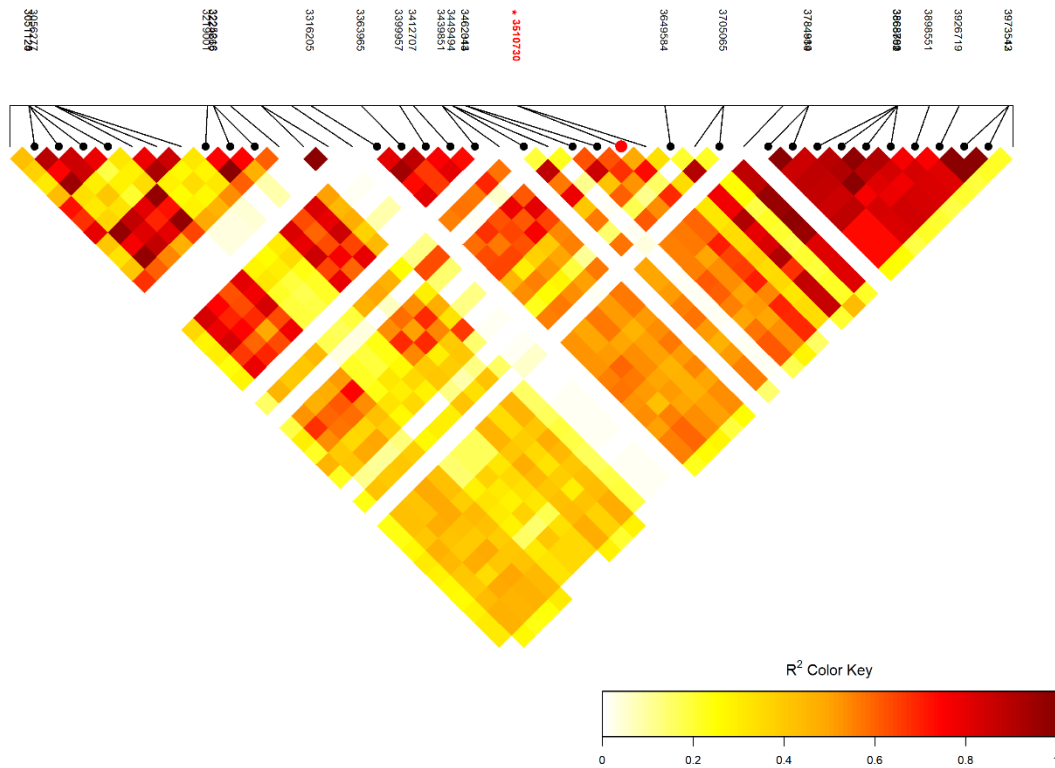
Physical Length:959.5kb



Supplementary data 3.1 - Linkage disequilibrium around the candidate SNP (55,886,562 bp) on chromosome 9 associated with TSWV mean symptoms. Linkage disequilibrium heatmap showing pairwise r^2 values among SNPs located within a $\pm$ 500 kb window around the lead SNP. The analysed region spans approximately 959.5 kb. Each diamond represents the LD value between a pair of SNPs, with colors ranging from white/yellow, indicating low LD, to red/dark red, indicating high LD. The lead SNP position is highlighted in red circle on the physical map. The region shows extensive but fragmented LD, with several blocks of strong association separated by low-LD gaps. Black-labeled positions on the physical map represent SNPs with high r^2 (> 0.5) with the peak SNP used to delimit the QTL and candidate gene mining. In this case it was SNP 55,435,516, located 451 kb upstream from the peak SNP.

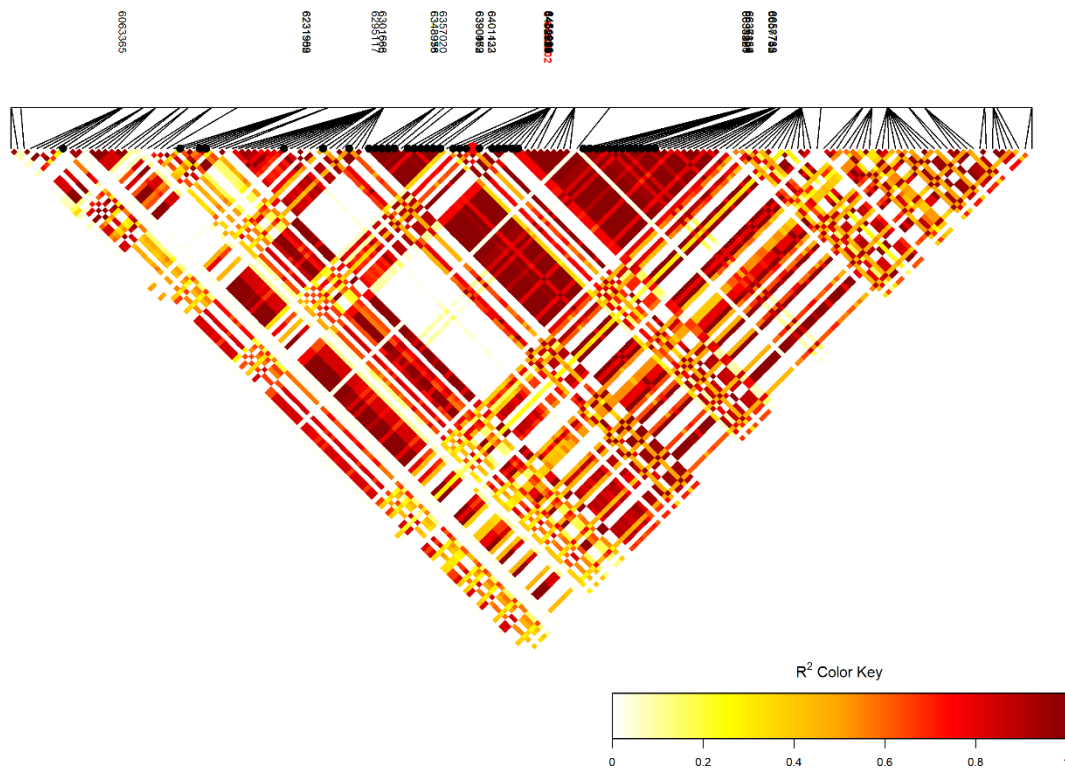
LD around SL4.0CH12:3,510,730 ± 5e+05 bp

Physical Length:944.2kb



Supplementary data 3.2 - Linkage disequilibrium around the candidate SNP (3,510,730 bp) on chromosome 12 associated with TSWV DAS-ELISA scores. Linkage disequilibrium heatmap showing pairwise r^2 values among SNPs located within a ± 500 kb window around the lead SNP. The analyzed region spans approximately 944.2 kb. Each diamond represents the LD value between a pair of SNPs, with colors ranging from white/yellow, indicating low LD, to red/dark red, indicating moderate to high LD. The lead SNP position is highlighted in red circle on the physical map. The region shows fragmented LD, with several blocks of strong association separated by low-LD gaps. Black-labeled positions on the physical map represent SNPs with high r^2 (> 0.5) with the peak SNP used to delimit the QTL and candidate gene mining. In this case, SNPs located in the interval between positions 3,412,707 and 3,926,719 bp had very high r^2 (> 0.7) with the peak SNP.

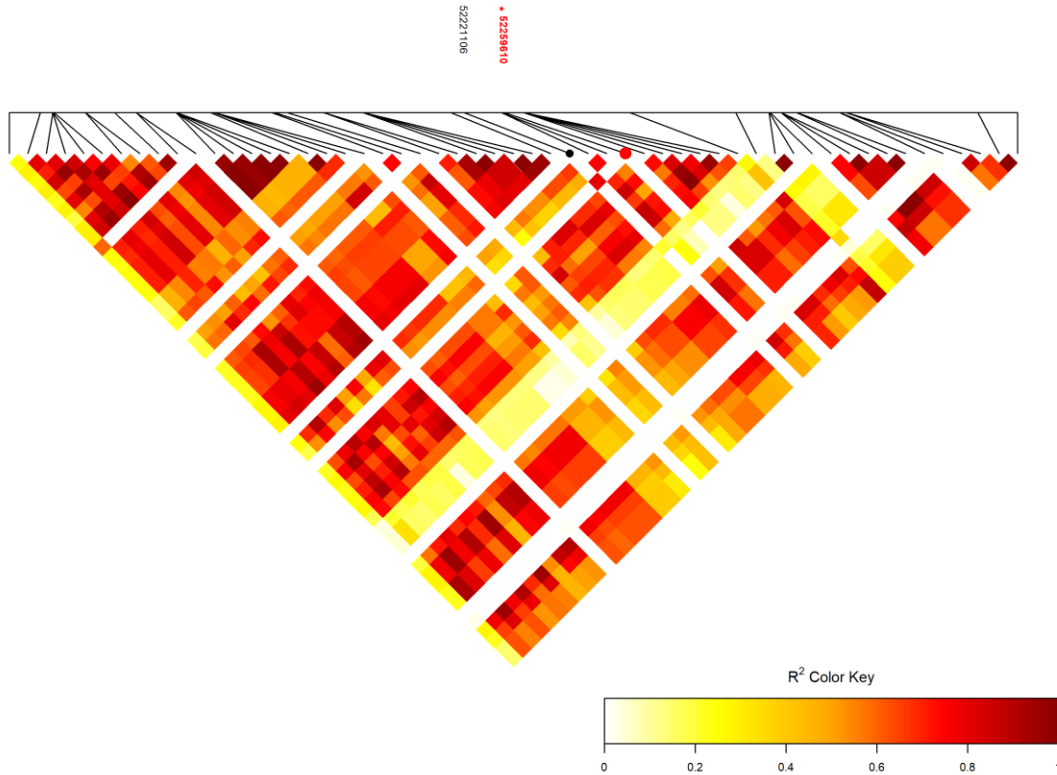
Physical Length:933.6kb



Supplementary data 3.3 - Linkage disequilibrium around the candidate SNP (6,452,902 bp) on chromosome 9 associated with ToMV symptoms and DAS-ELISA scores. Linkage disequilibrium heatmap showing pairwise r^2 values among SNPs located within a ± 500 kb window around the lead SNP. The analysed region spans approximately 933.6 kb. Each diamond represents the LD value between a pair of SNPs, with colors ranging from white/yellow, indicating low LD, to red/dark red, strong LD. The lead SNP position is highlighted in red circle on the physical map. The region shows fragmented LD, with several blocks of strong association separated by low-LD gaps. Black-labeled positions on the physical map represent SNPs with high r^2 (> 0.5) with the peak SNP used to delimit the QTL and candidate gene mining. In this case, SNPs located in the interval between positions 6,063,365 and 6,859,508 bp had very high r^2 (> 0.7) with the peak SNP.

LD around SL4.0CH11:52,259,610 $\pm$ 5e+05 bp

Physical Length:963.2kb



Supplementary data 3.4 - Linkage disequilibrium around the candidate SNP (52,259,610 bp) on chromosome 11 associated with ToMV symptoms. Linkage disequilibrium heatmap showing pairwise r^2 values among SNPs located within a $\pm$ 500 kb window around the lead SNP. The analysed region spans approximately 963.2 kb. Each diamond represents the LD value between a pair of SNPs, with colors ranging from white/yellow, indicating low LD, to red/dark red as strong LD. The lead SNP position is highlighted in red circle on the physical map. The region shows fragmented LD, with several blocks of strong association separated by low-LD gaps. Black-labeled positions on the physical map represent SNPs with high r^2 (> 0.5) with the peak SNP used to delimit the QTL and candidate gene mining. In this case, SNP 52,221,106 bp had very high r^2 (> 0.7) with the peak SNP.