Supplementary Material

Low-density SNP markers with high prediction accuracy of genomic selection to improve bacterial wilt resistance in tomato

Running title: Core sets of SNPs for genomic selection of bacterial wilt resistance in tomato

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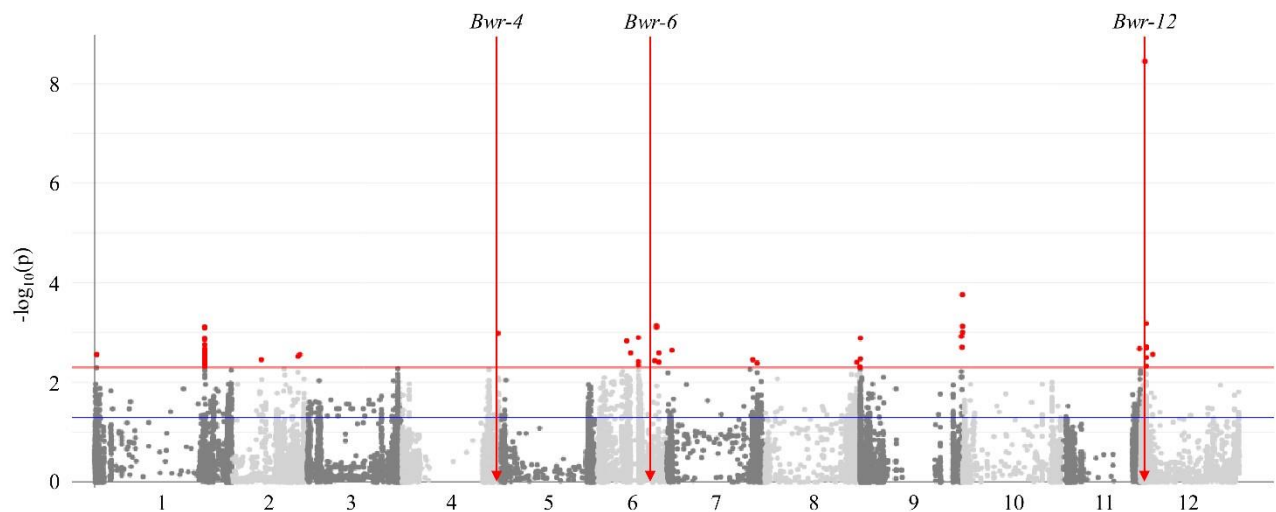*** Correspondence:** Sung-Chur Sim: sungchur@sejong.ac.kr

Figure S1. Manhattan plot of a genome-wide association study for bacterial wilt resistance in the combined population (n=353). The horizontal lines indicate two thresholds of $P < 0.005$ (red) and $P < 0.05$, (blue). A total of 31,142 genome-wide SNPs over 12 chromosomes are shown with gray dots and red dots represent SNPs significantly associated with bacterial wilt resistance at $P < 0.005$. The red arrows indicate the positions of SNPs associated with the major QTL, *Bwr-4*, *Bwr-6*, and *Bwr-12* (Nguyen et al., 2021).