



Figure S11 Plots of SNPs associated with relative total lesion length (RTLL) caused by inoculation with *Fusarium thapsinum* based on data for Ottawa locations. (a) Single-locus mixed model (marked in red; Bonferroni-corrected threshold of 0.05; dashed horizontal line); (b) Multi-locus mixed model (MLMM) identifies four SNPs on chromosomes 3, 4, 8 and 9 (marked in red) from the optimum model. The vertical axis indicates the $-\log_{10}$ of P-value scores, and the horizontal axis indicates chromosomes and physical positions of SNPs.