



**Figure S10** Plots of SNPs associated with relative total lesion length (RTLL) caused by inoculation with *Macrophomina phaseolina* 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 one SNP on chromosome 8 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.