



**Figure S4** Plots of SNPs associated with total lesion length (TLL) for *Macrophomina phaseolina* based on the combined analysis. (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 9 (marked in red) from the optimum model (b). The vertical axis indicates the  $-\log_{10}$  of P-value scores, and the horizontal axis indicates chromosomes and physical positions of SNPs.