

**Additional file 19: Figure S6.** Genome mapping statistics of the resistant line (R) and susceptible line (S). (a) Mean of the total clean reads obtained from samples by RNA-Seq; (b) mean mapping ratio aligned to the Williams 82 reference genome; and (c) mean number of total SNPs compared with the number in the reference genome. Statistical significance was detected by a two-tailed t-test. \* *P*<0.05; \* \* \* *P*<0.001.