**Supplementary Figure S1.** The workflow chart of this study. Up: The workflow of creation of m3; Down: the procedure of producing two F$_2$ populations.
**Supplementary Figure S2.** The changes of the wilted leaf numbers of *m*3 with time in 2016. Note: The ratio is figured by dividing the number of withered leaves by the total number of leaves.
Supplementary Figure S3. The distributions of SNP ED value on chromosome 11, which were identified by MutMap analysis.
**Supplementary Figure S4.** Expression levels of six candidate genes in the *m3* and WT at nine-leaf stage. The values were given as means ± SDs (n=3). The primers of qRT-PCR is shown in Supplementary Table S1 which marked in blue.