

Description of Additional Supplementary Files

Supplementary Data 1: Panicle phenotype in Wuhan 2016.

Supplementary Data 2: Known panicle development-related genes located in the vicinity of the QTL identified at the threshold of $1e-5$.

Supplementary Data 3: Summary of accessions for RNA sequencing.

Supplementary Data 4: Summary of SPP TWAS significant genes.

Supplementary Data 5: Summary of NPB TWAS significant genes.

Supplementary Data 6: Summary of PL TWAS significant genes.

Supplementary Data 7: Summary of GSEA results of TWAS significant genes.

Supplementary Data 8: Summary of GO enrichment results of TWAS significant genes.

Supplementary Data 9: Summary of transcription factor families enriched in TWAS significant genes.

Supplementary Data 10: Summary of enriched TF binding motifs of TWAS significant genes.

Supplementary Data 11: Summary of pQTL-eQTL hotspots of TWAS significant genes.

Supplementary Data 12: Summary of *cis*- & *trans*-ECAS significant genes.

Supplementary Data 13: Summary of significant associations between SPP TWAS-significant genes ($FDR < 0.01$) and the *cis*- and *trans*-EC of *OsMADS17* and *SDT*.

Supplementary Data 14: List of primers used in experiments.