

Supplementary Material

Genetic Mapping and Functional Analysis of a classical tassel branch number Mutant *Tp2* in maize

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Supplementary Figures



Supplementary Figure 1. The phenotypes of wild-type and mutant in the F_2 segregating population of Tp2. (**A-B**) Statistical analysis of plant height and ear height (**A**), ear leaf length and ear leaf width (**B**). The unit is centimeter and the significant difference is examined using a two tailed Student's t-test.



Supplementary Figure 2. The analysis of mRNA-Seq data. (**A-B**) The Spearman's rank correlation coefficient of the two biological replicates from RNA library of homozygous wild-type (**A**) and homozygous mutant (**B**). (**C**) Volcano plots in analyzing differentially expressed genes with mRNA sequencing.



Supplementary Figure 3. GO analysis of differentially expressed genes in tassel from wild type (WT) and Tp2/Tp2 of two biological replicates.



Supplementary Figure 4. The length distribution of sRNA in SAM from wild type (WT) and Tp2/Tp2 of two biological replicates.



Supplementary Figure 5. The Structure of the overexpression vector.



Supplementary Figure 6. Relative expression levels of *zma-miR156h* in OE-plants and their control via qRT-PCR assay, respectively. Double asterisks represent significance difference determined by the Student's t-test at P < 0.01.



Supplementary Figure 7. The data quality of tsCUT&Tag. (A) Scatter plots of *ZmSBP13* tsCUT&Tag data. (B-C) Distribution of peaks in genomic regions of the tsCUT&Tag. The Pearson correlations were calculated in deepTools (version 3.5.0).