

## Supplementary materials

### Supplementary Figures Captions

**Figure S1.** Pearson correlation coefficient heatmap of all gene expression between the two stages (-10 d before and 0 d) of stem gall formation. A. *U. esculenta*. B. *Z. latifolia*

**Figure S2.** Functional annotation of DEGs between the two stages (-10 d before and 0 d) of stem gall formation based on the *U. esculenta* genome. A. GO enrichment of DEGs. B. KEGG enrichment of DEGs

**Figure S3.** Functional annotation of DEGs between the two stages (-10 d before and 0 d) of stem gall formation based on the *U. esculenta* genome. A. GO classification. Each DEG was classified into at least one GO term and grouped into three categories: biological process, cellular component and molecular function. B. Pathway assignment based on KEGG. DEGs were grouped into cellular processes, environmental information processing, genetic information processing, metabolism, and organismal systems

**Figure S4.** Functional annotation of DEGs between the two stages (-10 d before and 0 d) of stem gall formation based on the *Z. latifolia* genome. A. GO enrichment of DEGs. B. KEGG enrichment of DEGs

**Figure S5.** Functional annotation of DEGs between the two stages (-10 d before and 0 d) of stem gall formation based on the *Z. latifolia* genome. A. GO classification of DEGs. B. Pathway assignment based on KEGG of DEGs

**Figure S6.** DEGs of plant disease resistance genes in the initial stage of stem gall formation

**Figure S7.** The complete protein sequences of 11 DEGs C2H2 zinc finger proteins were aligned by ClustalW

**Figure S8.** Structural analysis of the C2H2 zinc finger proteins family.

**Figure S9.** Validation of the RNA-Seq data in the cytokinin biosynthesis and signal pathway using qRT-PCR at the initial stage of stem gall formation.