

## Supporting Information

**Figure S1** Multiple amino acid sequences alignment of ZmAKIN $\beta\gamma$  and homologous in rice and *N. benthamiana*. Orange line indicated the CBM domain, and blue line indicated the first CBS domain.

**Figure S2** Analyses of the host-pathogen specificity of the interaction between P8 and AKIN $\beta\gamma$  by Y2H assay. (A) Interactions between P8 and OsAKIN $\beta\gamma$  or NbAKIN $\beta\gamma$  in yeast. (B) Interactions between ZmAKIN $\beta\gamma$  and SP8 of SRBSDV in yeast. The plasmid combinations indicated were co-transformed into yeast strain Y2H Gold, and the transformants were spotted on the selective medium SD/-Trp/-Leu and SD/-Trp/-Leu/-His/-Ade with 10-fold serial dilutions and grown at 30°C for 3-4 d.

**Figure S3** ZmAKIN $\beta\gamma$ -2 specifically interacted with P8 among tested nine proteins encoded by RBSDV. The plasmid combinations indicated were co-transformed into yeast strain Y2H Gold, and the transformants were spotted on the selective medium SD/-Trp/-Leu/-His/-Ade and grown at 30°C for 3-4 d.

**Figure S4** The phenotype on the back surface of the maize leaf. (A) and the accumulation levels of RBSDV P10 in the third true leaves of Mock-or RBSDV-inoculated maize plants at 20 dpi (B). The P10 accumulations were determined by western blotting. The orange arrow indicates the white swelling. CBB: Coomassie Brilliant Blue.

**Figure S5** The expression levels of *ZmAKIN $\beta\gamma$ -1* and *-2* were regulated by SCMV (A) or MCMV (B) infection. The second systemic infected leaves were collected from mock- and SCMV-or MCMV-inoculated maize plants at the indicated time points and subjected for RT-qPCR. Three independent experiments were conducted with at least three biological replicates per treatment. Error bars represented the means $\pm$ SE. Significant differences were indicated using Student's t-test: \* indicates  $P < 0.05$ , \*\* indicates  $P < 0.01$ .