

Supporting Information

A new adenylyl cyclase, ZmRPP13-LK3, participates in ABA-mediated heat stress resistance in Maize

Hao Yang^{1§}, Yulong Zhao^{1§}, Ning Chen¹, Shaoyu Yang¹, Hanwei Du¹, Wei Wang¹, Jianyu Wu¹, Fujun Tai¹, Feng Chen², Xiuli Hu^{1*}

The following Supporting Information is available for this article:

Fig. S1 Pie charts showing the distribution of DNP based on their predicted cellular components (a), molecular functions (b), biological processes (c) and the signaling pathways (d).

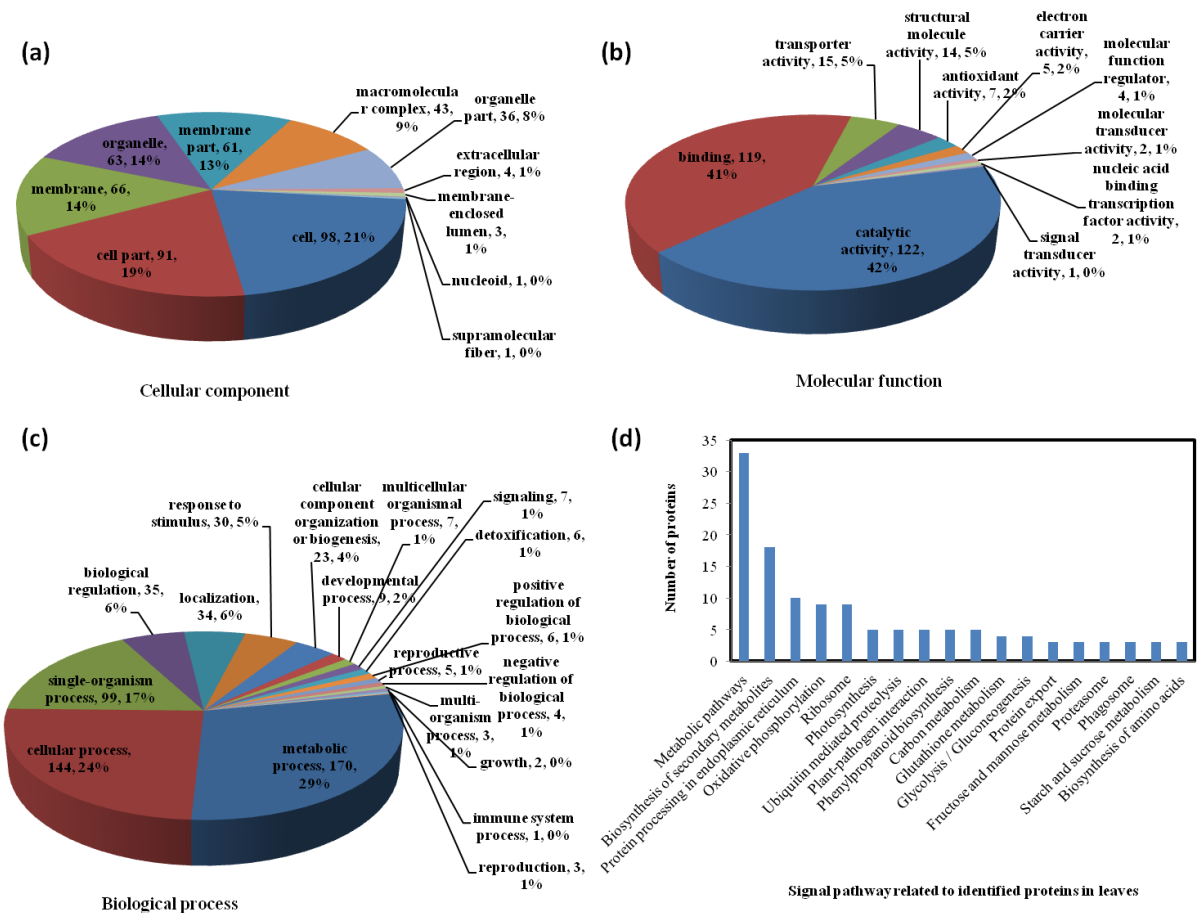


Fig. S2 Analysis of the protein-protein interaction network among 310 DEPs using STRING.

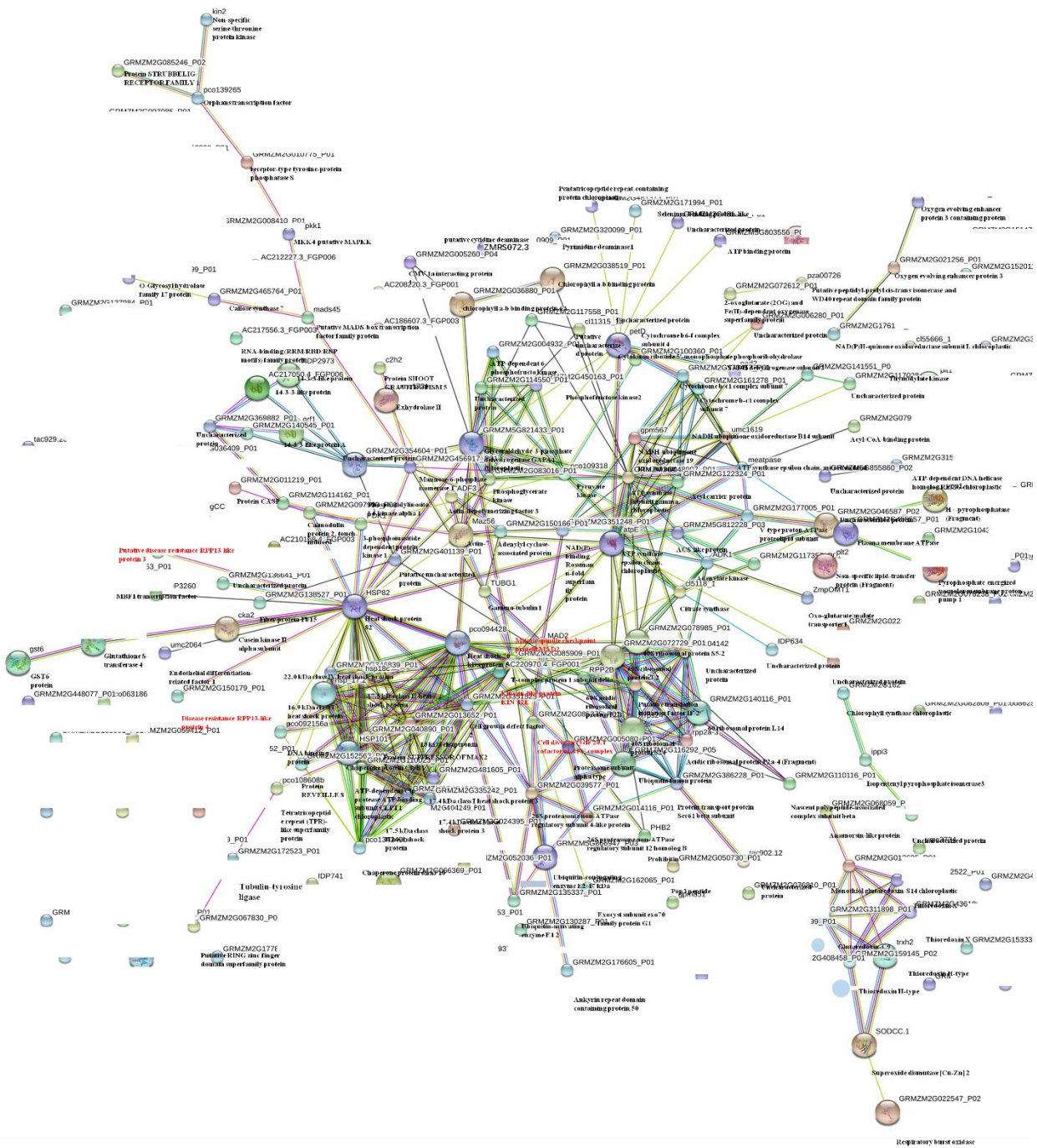


Fig. S3 Sequence alignments of ZmRPP13-LK3 with other known ACs in plants.

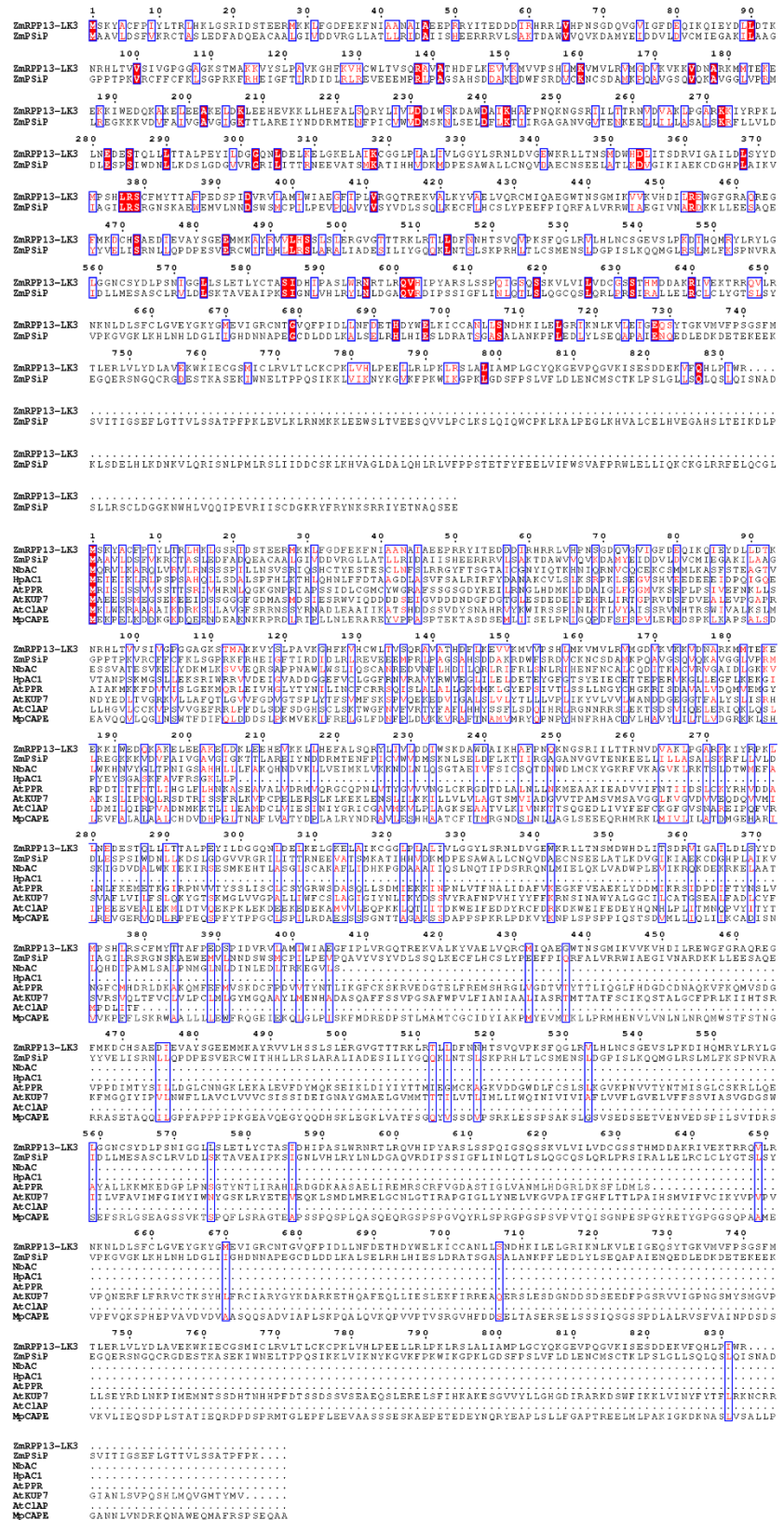


Fig. S4 HPLC method verifying cAMP production catalyzed by purified full-length ZmPSiP or ZmRPP13-LK3 when using AMP as substrate.

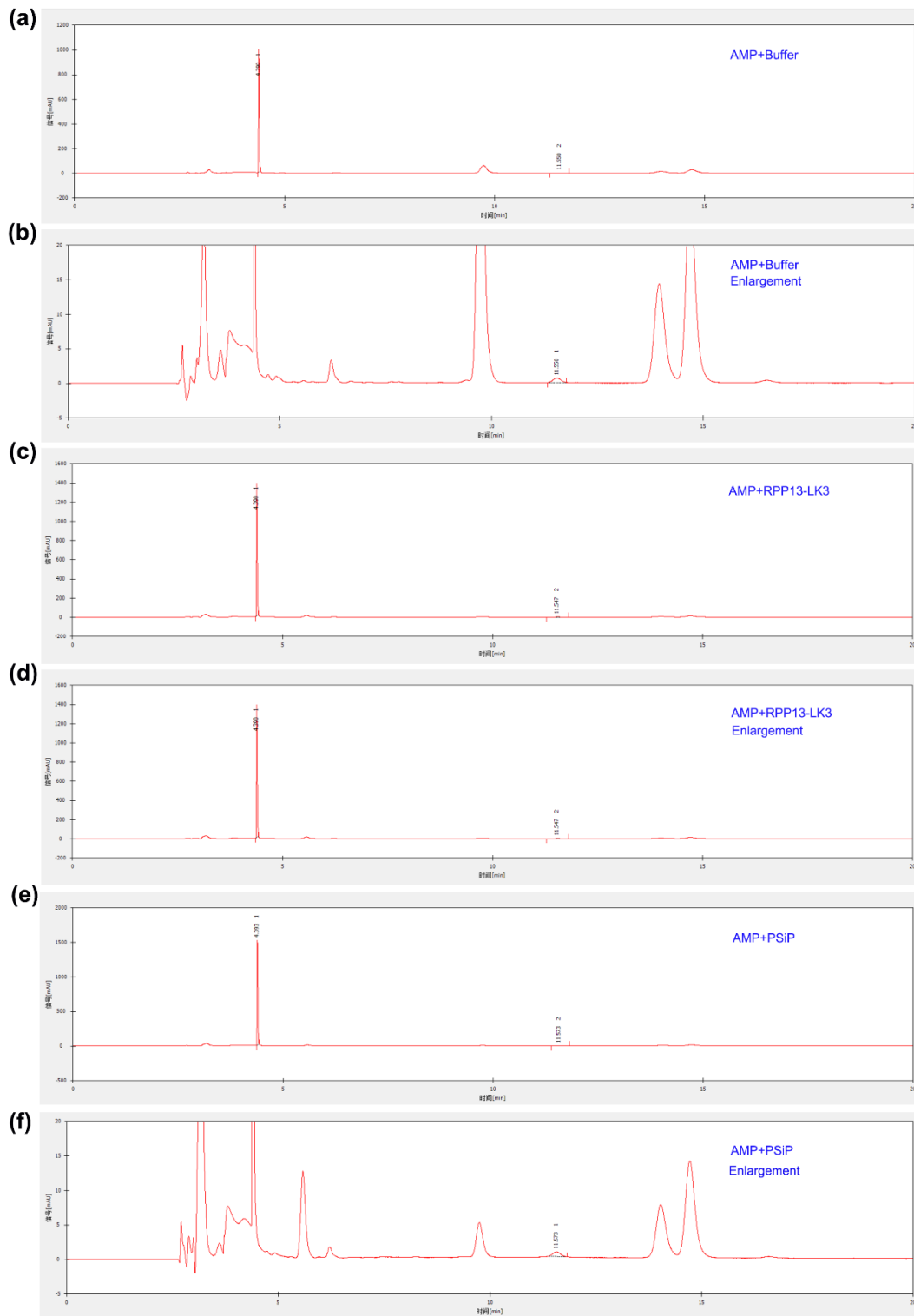


Fig. S5 HPLC method verifying cAMP production catalyzed by purified full-length ZmPSiP or ZmRPP13-LK3 when using ADP as substrate.

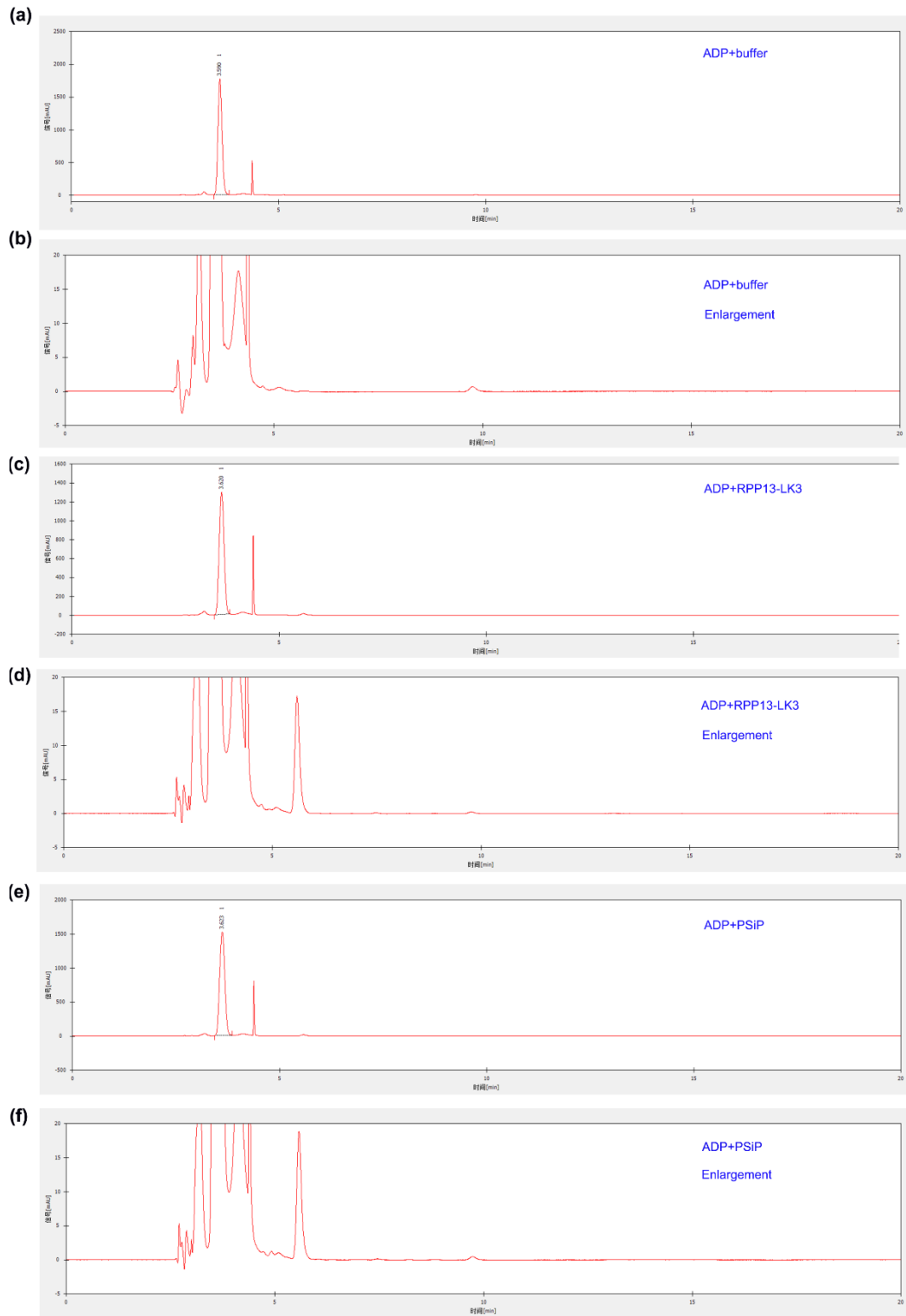


Fig. S6 Effect of RNAi against *ZmRPP13-LK3* or *ZmPSiP* in maize protoplasts. (a) and (b) PCR analysis of the effect of different concentration dsRNA on *ZmRPP13-LK3* and *ZmPSiP* gene expression in maize protoplasts. (c) and (d) qRT-PCR analysis of the effect of 25 μg dsRNA on *ZmRPP13-LK3* and *ZmPSiP* gene expression in maize protoplasts.

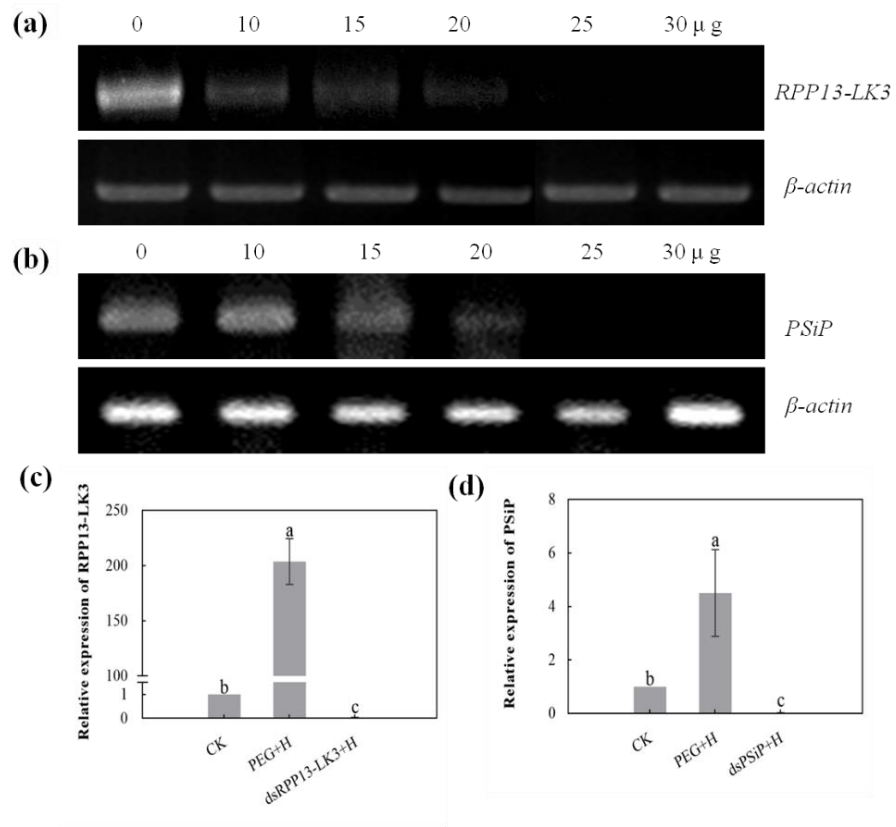


Fig. S7 The relationships between ZmRPP13-LK3 orthologues of several higher plants. A rooted phylogenetic tree was constructed using the maximum-likelihood method with the LG+ Gamma model. Numbers represent support values (> 50%) obtained with 100 bootstrap replicates using the MEGA7 software. The evolutionary distances were computed in units of the number of amino acid substitutions per site, as shown by the scale bar below the tree. The accession numbers of ZmRPP13-LK3 orthologues sequences used for phylogenetic analysis are shown in Table S3.

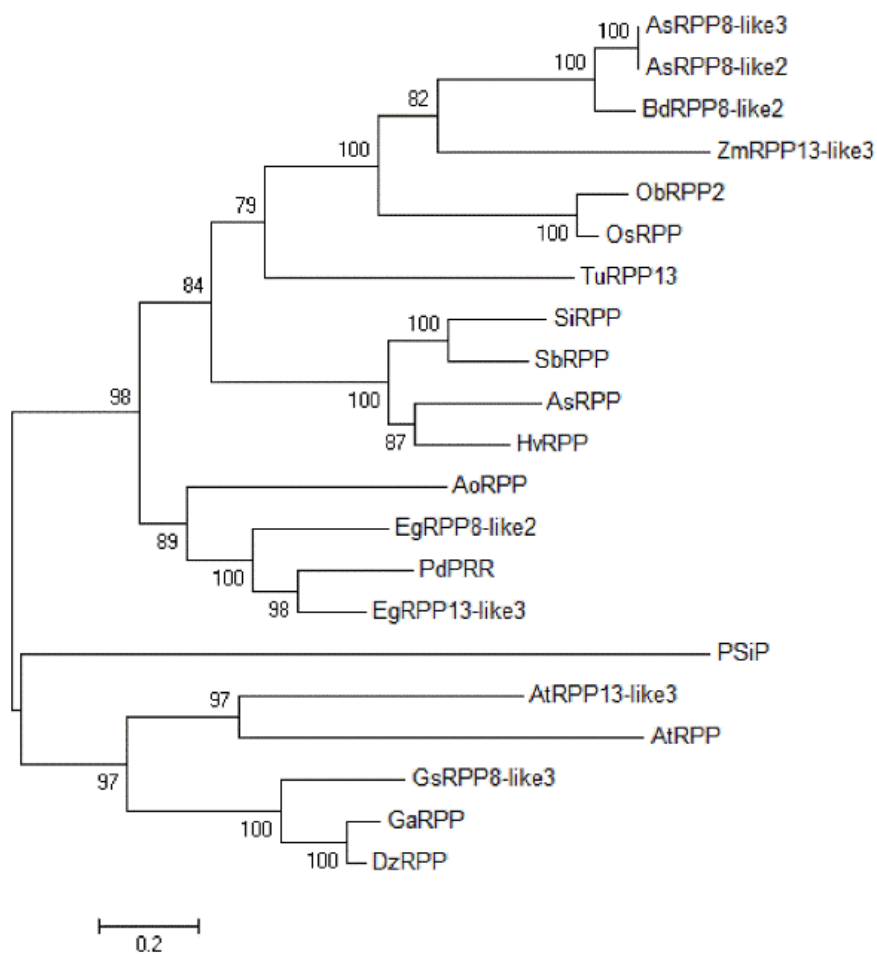


Fig. S8 The relative expressions of *ZmRPP13-LK3* and *ZmPSiP* in maize stems when inoculated with pathogen. Maize stems were inoculated with 5×10^6 spores/mL *Fusarium moniliforme* for 15 days, which can lead to stem rot disease. Total RNA was isolated from the stem for qRT-PCR analyses. Values represent means \pm SD from three biological replicates. The lowercase letters denote values significantly different from those of control ($p < 0.05$) determined by one-way ANOVA.

