

EXPLICIT-Kinase: a gene expression predictor for dissecting the functions of the *Arabidopsis* kinome

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SUPPORTING INFORMATION

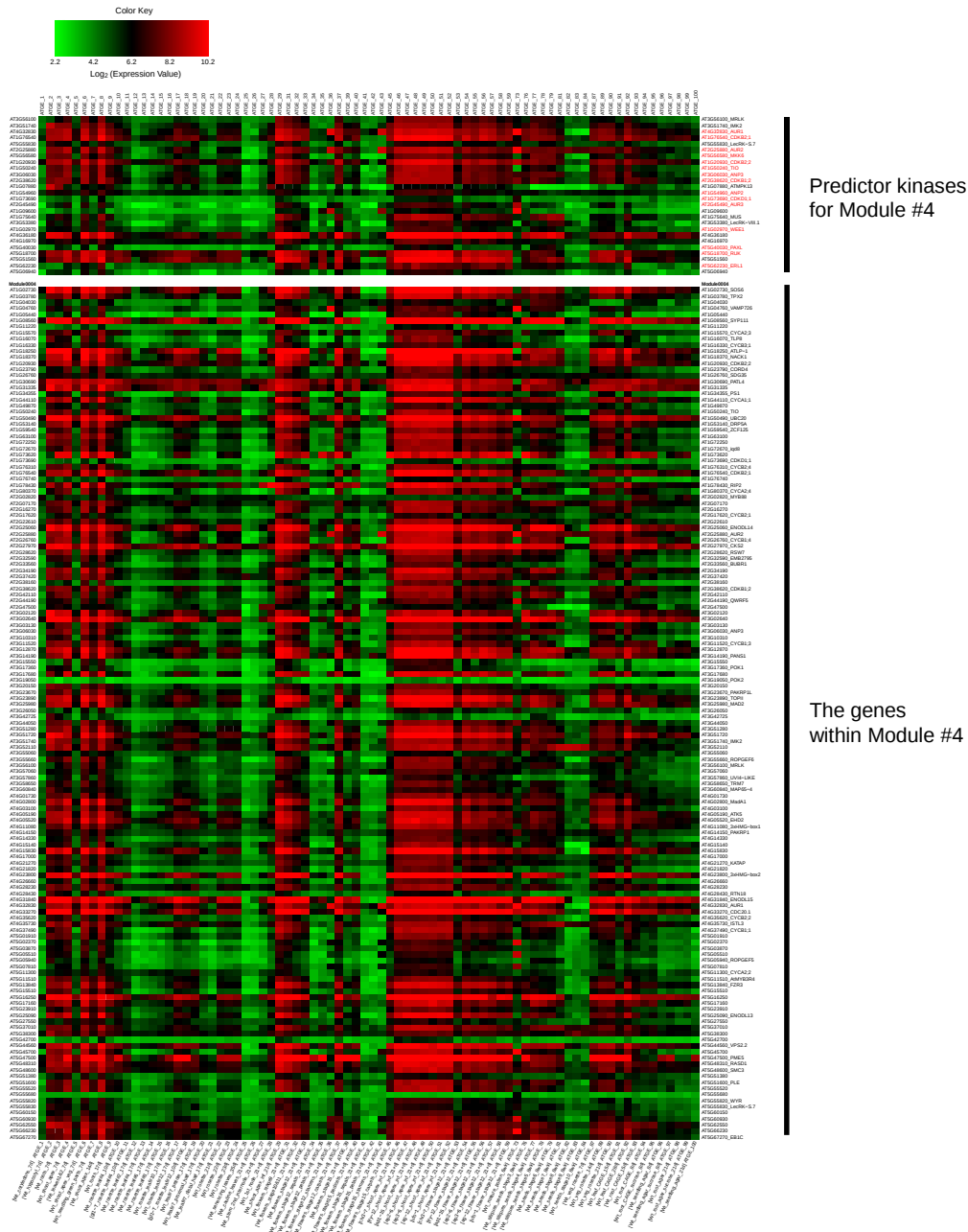


Figure S1. Tissue-specific expression patterns for the predictor kinases and the genes in the cytokinesis module

Expression data according to the AtGenExpress project.

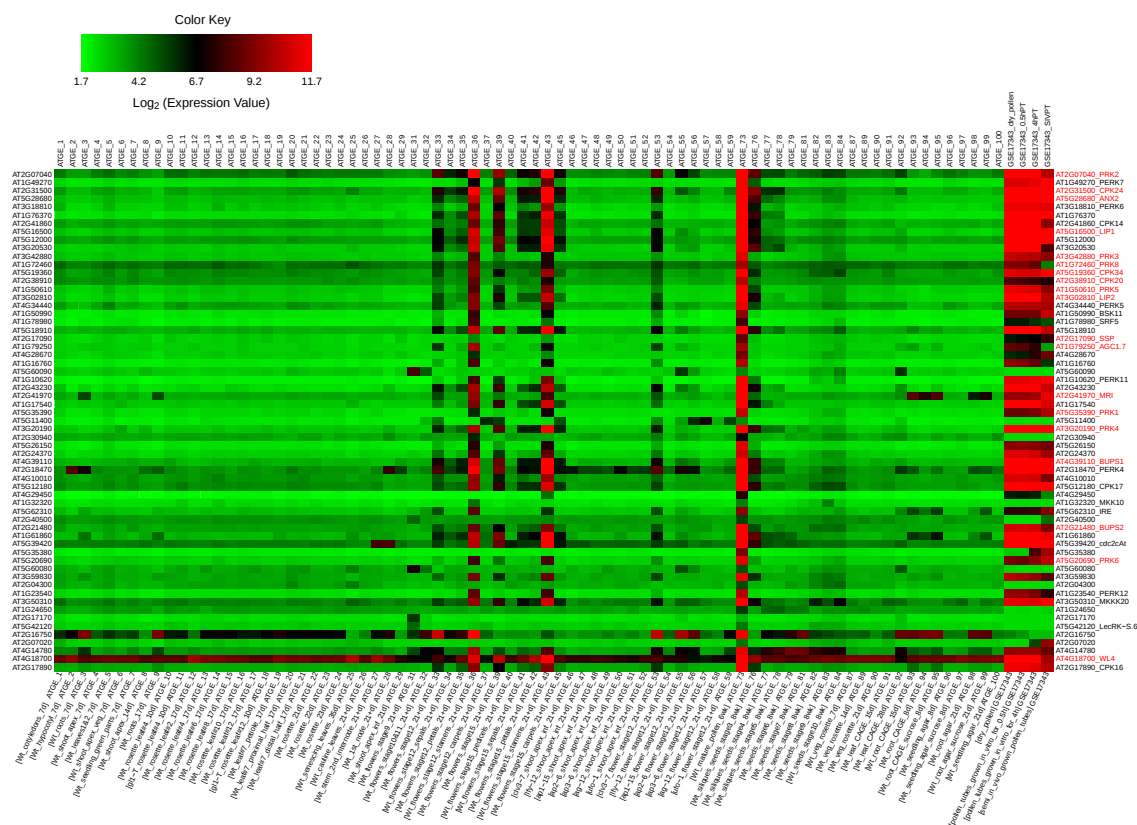


Figure S2. Tissue-specific expression patterns for the predictor kinases in the pollen tube development module

Expression data according to the AtGenExpress project and a pollen tube transcriptome analysis by Qin et al., 2009.

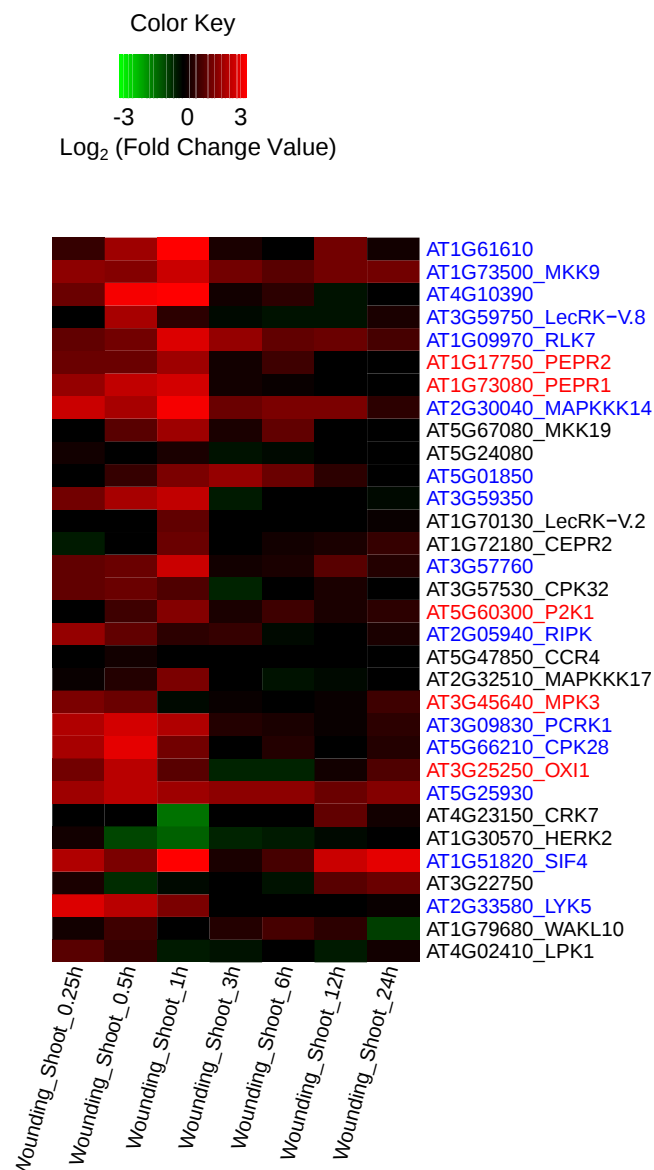


Figure S3. Gene regulation pattern upon wounding stress treatment for the predictor kinases in the wounding stress response GO regulon

Expression data according to the AtGenExpress project. Genes in red, known regulators of wounding stress response; genes in blue, uncharacterized kinase genes up-regulated by wounding stress.

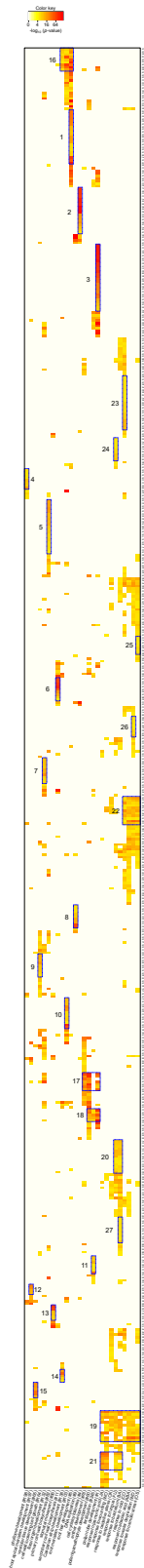


Figure S4. A detailed heatmap showing the shared and distinct predictor kinases among the gene modules and regulons

Zoom in the page to see the details. The boxes are the same as those in Figure 4C.

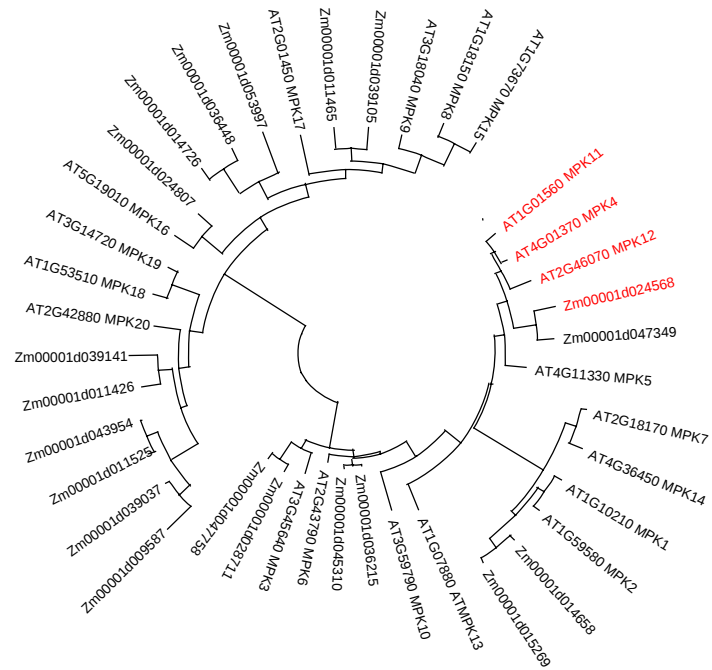


Figure S5. A phylogenetic tree of MAPKs from *Arabidopsis* and maize

Arabidopsis MPK4, MPK12, MPK11 and maize Zm00001d024568 are in the same sub-clade.

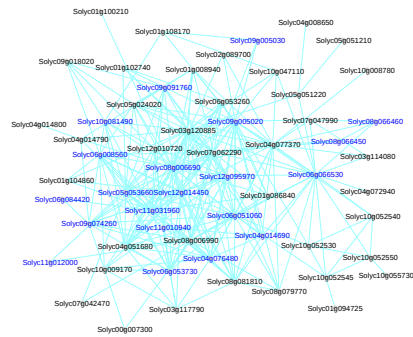
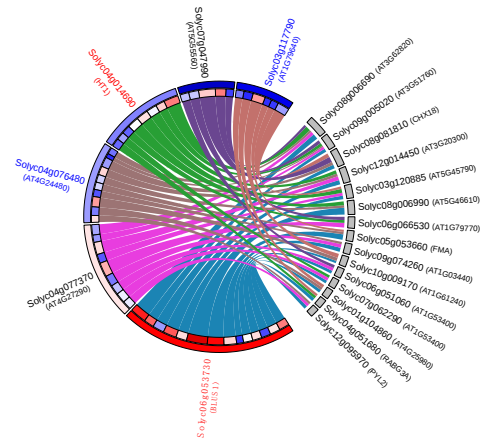
A**B**

Figure S6. Predictor kinases identified for the tomato gene module involved in stomatal movement

(A) The tomato gene co-expression modules involved in stomatal movement. The genes in blue are those with their *Arabidopsis* orthologues also identified from the *Arabidopsis* stomatal movement module. **(B)** Predictor kinases identified from the module. Legends are the same as Figure 5. Both AT2G24480 and AT1G79640 are conserved predictor kinases for the stomatal movement modules from tomato and *Arabidopsis*.

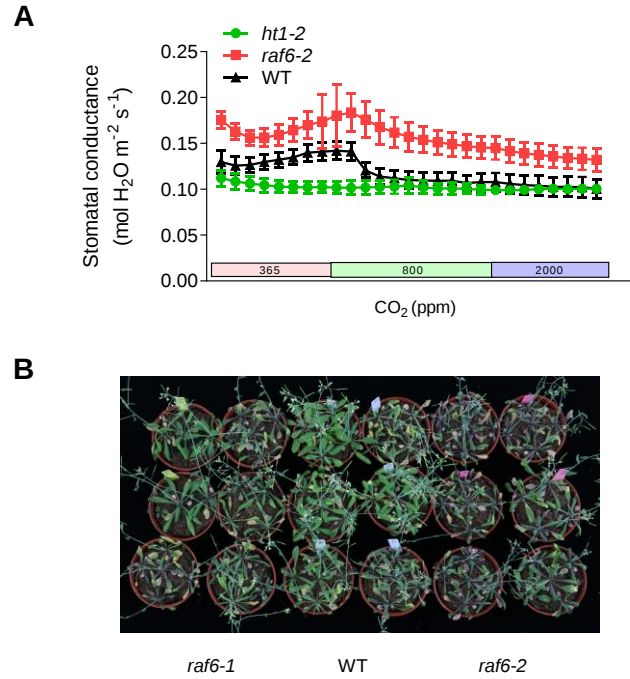


Figure S7. Additional phenotypes of the *raf6* mutants

(A) Stomatal conductance measured for WT and *raf6-2* plant leaves upon exposed to increased CO₂ concentration. The *ht1-2* mutant was used as a negative control for CO₂ response. Values represent means $\pm$ SE. WT and *raf6-2* had three replicates, and *ht1-2* had two replicates. **(B)** WT, *raf6-1*, and *raf6-2* plants after 10 days drought stress treatment. The plants were grown for three weeks under normal conditions, after which watering was stopped. The picture was taken 10 days later.

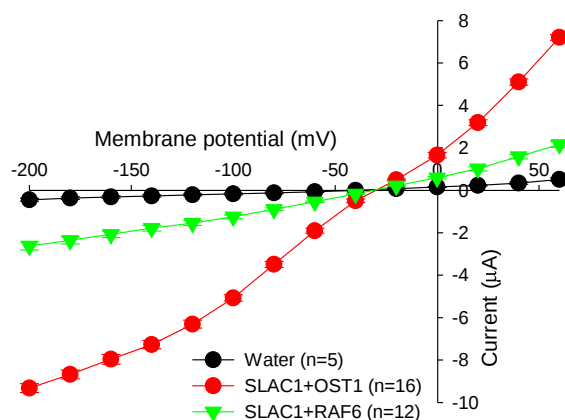


Figure S8. Regulation of SLAC1 activity by RAF6 and OST1

Electrophysiological analysis was performed on *Xenopus laevis* oocytes expressing SLAC1 with RAF6 or OST1. Water injection was used as a control. The I-V (current-voltage) relationship of the steady state whole-oocyte currents in oocytes are shown. The data are presented as mean $\pm$ SE.

Table S1. The significantly interacting kinase–non-kinase gene pairs

Table S2. The genes contained within the modules from the Arabidopsis GGM gene co-expression network

Table S3. Gene Ontology enrichment analysis results for the Arabidopsis GGM gene co-expression modules

Table S4. Predictor kinases identified for the Arabidopsis GGM gene co-expression modules

Table S5. References for the known predictor kinases identified for the Arabidopsis GGM gene co-expression modules

Table S6. Predictor kinases identified for the Arabidopsis GO regulons

Table S7. The genes contained within the modules from the maize GGM gene co-expression network

Table S8. Predictor kinases identified for the maize GGM gene co-expression modules