Supplementary File\_S1

The protein sequences used in this study

Supplementary File\_S2

Corrected Akaike Information Criterion (AICc), Akaike Information Criterion 2 (AIC2) and Bayesian Information Criterion (BIC) for the phylogenetic reconstruction

Supplementary File\_S3

Genomic and CDS sequences for AtCIPK16 orthologues used for intron-exon mapping

Supplementary Figure\_S4

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *C. sativa*

Supplementary Figure\_S5

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *C. rubella*

Supplementary Figure\_S6

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *A. alpine*

Supplementary Figure\_S7

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *B. stricta*

Supplementary Figure\_S8

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *B. oleraceae*

Supplementary Figure\_S9

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *E. salsugineum* (previously known as *Thellungiella halophila*)

Supplementary Figure\_S10

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *S. parvula* (previously known as *Thellungiella parvula*)

Supplementary Figure\_S11

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *L. alabamica*

Supplementary Figure\_S12

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *A. arabicum*

Supplementary Figure\_S13

Bi—species phylogenetic tree created by ML method with bootstrap value of 10,000 for CIPK protein sequences of *A. thaliana* and *T. hassleriana*

Supplementary Figure\_S14

Fully expanded phylogenetic tree for Figure 2. Please refer to the details from Figure 2

Supplementary Figure\_S14

Fully expanded phylogenetic tree for Figure 3. Please refer to the details from Figure 3