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Supplementary data

Global characterization for Arabidopsis protein interactome

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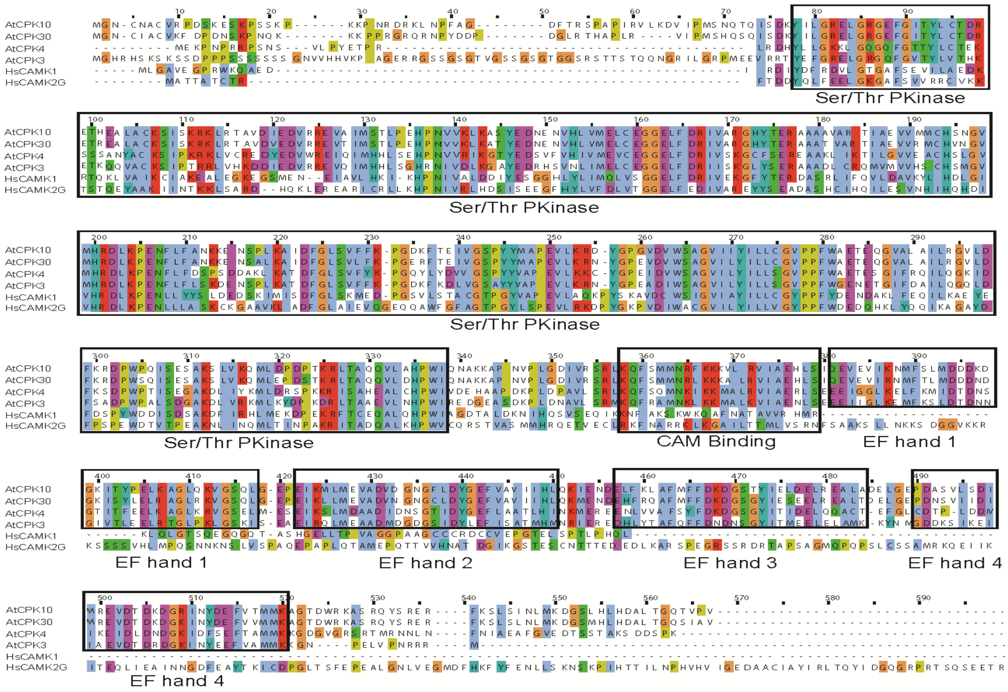
Supplemental Table 1. Detected methods of *Arabidopsis* protein interactions.

Detected method	Number of PPIs	Percent of PPIs
two hybrid	2373	69.14%
protein array	716	20.86%
anti bait coip	137	3.99%
affinity chromatography technologies	40	1.16%
coimmunoprecipitation	165	4.80%
experimental interaction detection	55	1.60%
pull down	121	3.52%
structure based prediction	47	1.36%
biochemical	96	2.79%
enzymatic study	55	1.60%
tap	59	1.71%
interaction detection	30	0.87%
far western blotting	30	0.87%



Supplemental Fig 1. Sequence alignment of 4 *Arabidopsis* CDPK family members with human CaMKs

The multiple sequence alignments are done using the ClustalW program (http://www.ebi.ac.uk/clustalw/) and are visualized by the Jalview program (http://www.jalview.org/). Amino acids are designated by single-letter codes and highlighted in different colors according to sequence similarity. Domains are boxed on the alignment. From top to bottom: AtCPK10, *Arabidopsis* CPK10 or CDPK1 (LocusID:At1g18890); AtCPK30, *Arabidopsis* CPK30 or CDPK1A (LocusID:At1g74740); AtCPK4, *Arabidopsis* CPK4 (LocusID:At4g09570); AtCPK3, *Arabidopsis* CPK3 or CDPK6 (locusID:At4g23650); HsCAMK1, human CaM kinase I alpha (Swiss-Prot:Q14012); HsCAMK2G, human CaM kinase II gamma chain (Swiss-Prot:Q13555). The alignment shows that several members of *Arabidopsis* CDPK family have high sequence identity and similar domain architecture with the human CaM kinase. The only difference is that, compared to the *Arabidopsis* CDPK family members, the human CaM kinases lack the EF-hand domains that are responsible for binding to Ca^{2+}. CDPK, Ca^{2+}-dependent protein kinase; CaMK, CaM kinase; Ser/Thr PKinase, Serine/threonine-protein kinase domain; CAM Binding, Calmodulin-binding domain; EF hand, EF-hand domain.