Supplemental material

Table S1: Primer sequences

SnRK2.4 CDS FL F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGACAAGTACGAGCTG
SnRK2.4 CDS FL R	GGGGACCACTTTGTACAAGAAAGCTGGGTAACTTATTCTCACTTCTCC
SnRK2.10 CDS FL F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGACAAGTACGAGCTT
SnRK2.10 CDS FL R	GGGGACCACTTTGTACAAGAAAGCTGGGTAACTGACTCGGACTTCTCC
SnRK2.6 CDS FL F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATCGACCAGCAGTG
SnRK2.6 CDS FL R	GGGGACCACTTTGTACAAGAAAGCTGGGTACATTGCGTACACAATCTC
PABD F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCTAAAGAATTTGCCAAGGG
PABD R	GGGGACCACTTTGTACAAGAAAGCTGGGTACGGTGTTTTGGCGTCAGC
Fragment A F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGACAAGTACGAGCTG
Fragment A R	GGGGACCACTTTGTACAAGAAAGCTGGGTAGAACCATGAATGTTTCTT
Fragment B F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTACTAAAGAATTTGCCAAGG
Fragment B R	GGGGACCACTTTGTACAAGAAAGCTGGGTAACTTATTCTCACTTCTCC
Fragment C F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTACTAAAGAATTTGCCAAGG
Fragment C R	GGGGACCACTTTGTACAAGAAAGCTGGGTATTCCTCTTTTCCATCTGC
Fragment D F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAGAGGAAGATGCAGAAGAC
Fragment D R	GGGGACCACTTTGTACAAGAAAGCTGGGTAACTTATTCTCACTTCTCC
Fragment E F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTACTAAAGAATTTGCCAAGG
Fragment E R	GGGGACCACTTTGTACAAGAAAGCTGGGTAAAGGGAGAAGGTTGGGTT
Fragment F F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTACAGACCGTTGAAGAGATC
Fragment F R	GGGGACCACTTTGTACAAGAAAGCTGGGTATTCCTCTTTTCCATCTGC
2.6 Kinase domain F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATCGACCAGCAGTG
2.6 Kinase domain R	GGGGACCACTTTGTACAAGAAAGCTGGGTAAAACCATTCATGGTTCCTTATTTCA
Mut R266A F	GAATTTGCCAGCTGAACTCACAGAG
Mut R266A R	GTGAGTTCAGCTGGCAAATTCTTTAGG
Mut K278A/ K279A F	GCATATTTCGCTGCTGAGAACCCAACC
Mut K278A/ K279A R	GGGTTCTCAGCAGCGAAATATGCAGC
Mut K294A/ K300A F	GAGATCATGGCTATAGTGGCTGACGCCGCTACACCGCCTCCTG
Mut K294A/ K300A R	GGCGGTGTAGCGGCGTCAGCCACTATAGCCATGATCTCTTC
Mut K294A/ K300A PABD F	GAGATCATGGCTATAGTGGCTGACGCCGCTACACCGTACCCAGC
Mut K294A/ K300A PABD R	GGGTACGGTGTAGCGGCGTCAGCCACTATAGCCATGATCTCTTC
Mut K27A F	CAAAAACTCTGCTGAACTTGTTGCC
Mut K27A R	CAAGTTCAGCAGAGTTTTTGACCTTCATGAGCC
Mut K222A F	CCAGTACGCTATCCCGGACTACGTCC
Mut K222A F	GTCCGGGATAGCGTACTGGACAGCC
attB4_UBQ10_F	GGGGACAACTTTGTATAGAAAAGTTGCTAGTCTAGCTCAACAGAGCTTTTAACCCAA
attB1r_UBQ10_R	GGGGACTGCTTTTTTGTACAAACTTGCCTGTTAATCAGAAAAACTCAGATTAATCGACAAATT

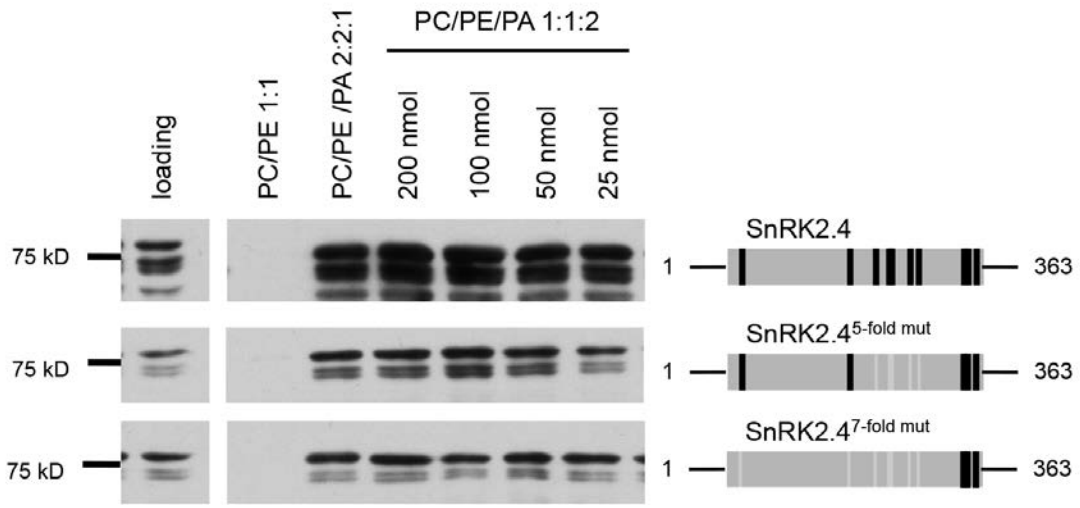

Figure S1. PA-binding in full length SnRK2.4 protein context is not abolished by mutations of conserved basic amino acids. Conserved basic amino acids in the PABD region or PABD region and kinase domain were mutated to Alanine in the full length SnRK2.4 (SnRK2.4^{R266A,K278A,K279A,K294A,K300A} or SnRK2.4^{K27A,K222A,R266A,K278A,K279A,K294A,K300A} respectively). GST tagged SnRK2.4, SnRK2.4^{R266A,K278A,K279A,K294A,K300A} or SnRK2.4^{K27A,K222A,R266A,K278A,K279A,K294A,K300A} were expressed in *E. coli* and purified. GST protein fusions were incubated with different amounts of liposomes ranging between 400 and 25 nmol containing either PC/PE 1:1, PC/PE/PA 2:2:1 or PC/PE/PA 1:1:2. The loading control is shown in the left panels and the proteins that bound to the liposomes are shown in the middle panels. On the right side a schematic overview of the location of the mutated amino acids is displayed.

Figure S2. Alignment between SnRK2.4 and SnRK2.10 protein sequence. The alignment was performed using Jalview software and MUSCLE alignment algorithm. PABD location is highlighted in red. The percentage of sequence identity is represented by different shades of grey .

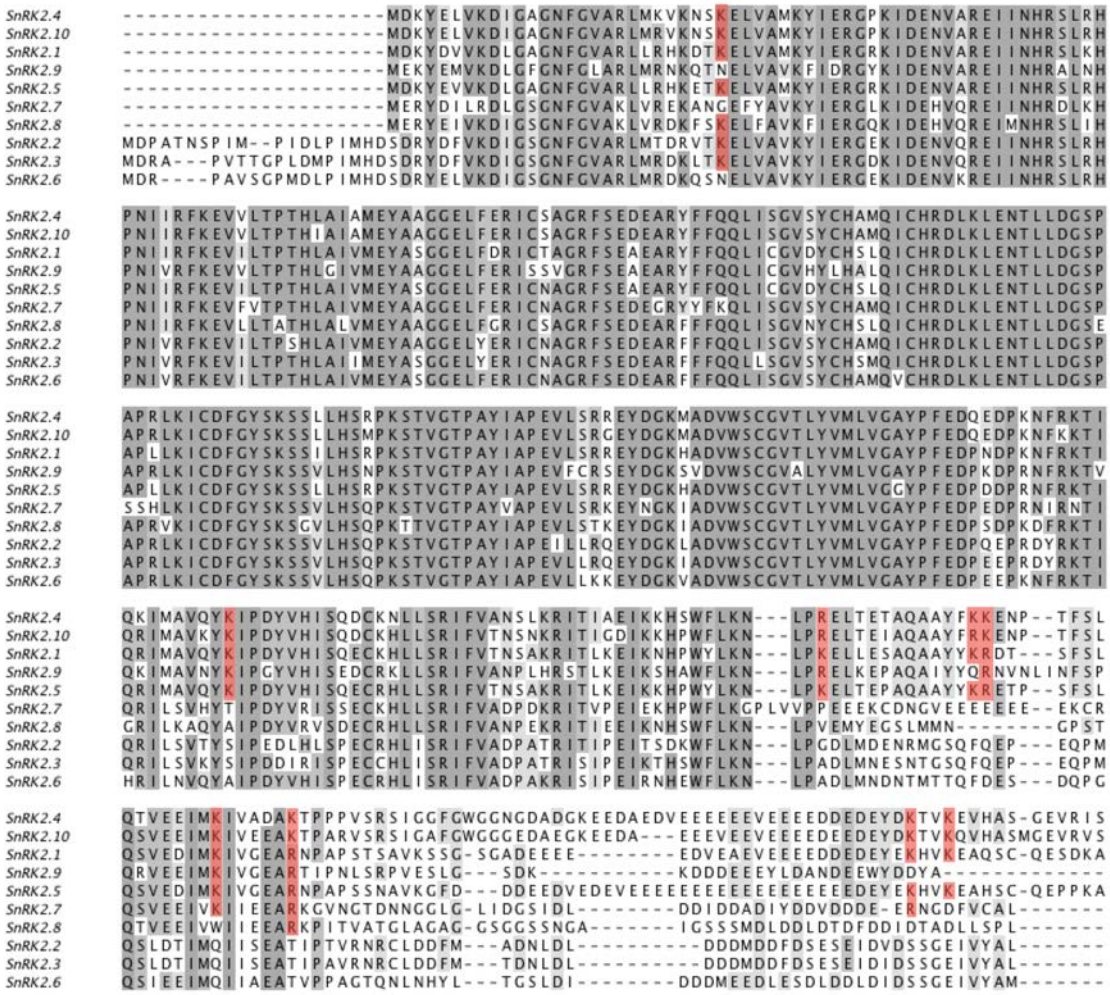

Figure S3. Alignment of protein sequences of all SnRK2 family members. The alignment was performed using Jalview software and MUSCLE alignment algorithm. The percentage of sequence identity is represented by different shades of grey. All basic amino acids being putative candidates responsible for PA-binding are highlighted in red. The basic amino acids responsible for PA-binding of PABD are conserved exclusively in SnRK2-class 1 proteins (SnRK2.4, SnRK2.10, SnRK2.1, SnRK2.9 and SnRK2.5)

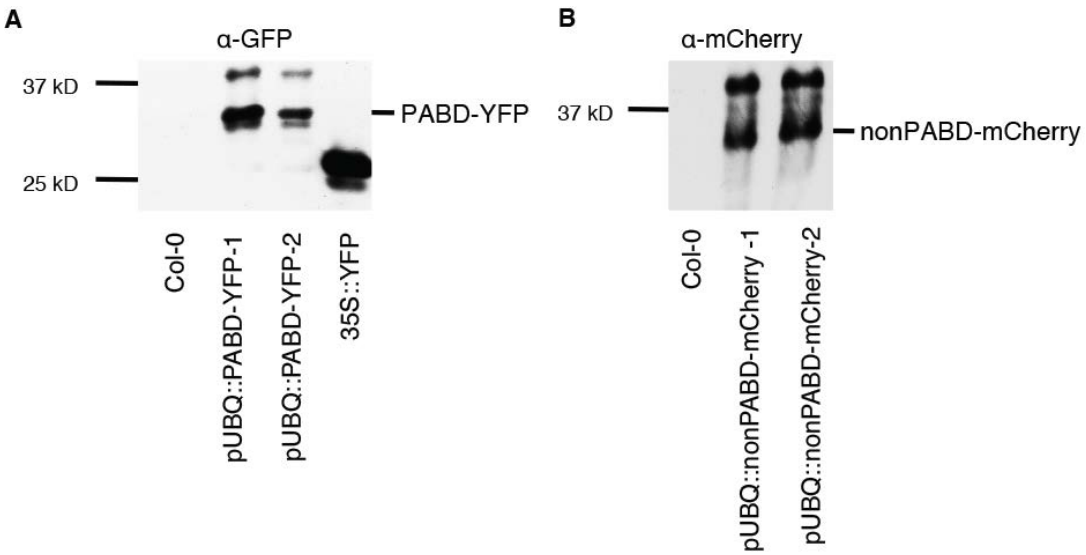

Figure S4. Identification of fusion proteins with YFP / mCherry. Lines overexpressing **a.** PABD-YFP and **b.** nonPABD-mCherry fusion proteins were examined for the size of the fusion proteins and the expression levels. Ten days old seedlings were used for the protein extraction. Protein extracts were quantified with Bicinchoninic Acid Protein Assay Kit, loaded on SDS-PAGE and proteins were detected with anti-GFP or anti-mCherry polyclonal antibodies (Invitrogen and Sicgen respectively) in Western analysis. Col-0 was used as a negative control. 35S::YFP line was used as a positive control for anti-YFP antibody.