



Supplementary Figure 1. Amino acid sequence alignment of TaIPK proteins. (A) Protein alignment of selected regions of TaIPK1s showing three conserved motifs. (B) Protein alignment of selected regions of TaIPKs showing inositol phosphate binding sites and ATP binding sites in the conserved domain. (C) Protein alignment of selected regions of TaPPIP5K1s showing PPIP5K1-specific ARK motif (highlighted in red color), inositol phosphate binding sites and ATP binding sites in the conserved domain. (D) Protein alignment of selected regions of TaITPKs showing conserved inositol phosphate binding sites and ATP binding sites. Highly conserved amino acids are represented in black color.