

**Figure S1.** Phylogenetic analysis and protein structures of the heavy-metal-associated isoprenylated plant protein (*HIPP*) gene family in common wheat and related *Triticeae* species. a-e indicates clade I- clade V, respectively. The left and the right represent the phylogenetic tree and protein structure, respectively. Multiple protein domains were represented by colored boxes. Legends are shown



**Figure S2**. Venn diagrams of differentially expressed *HIPPs* under different stresses. (a) *HIPPs* were up regulated under the stress of powdery mildew and yellow rust; (b) *HIPPs* were down regulated under the stress of powdery mildew and yellow rust; (c) *HIPPs* were no obvious expression change under the stress of powdery mildew and yellow rust; (d) *HIPPs* were up regulated under drought and heat stress; (e) *HIPPs* were down regulated under drought and heat stress; (f) *HIPPs* were no obvious expression change under drought and heat stress; (g) *HIPPs* were up regulated under four stresses; (h) *HIPPs* were down regulated under four stresses. Abbreviations: *Bgt*, powdery mildew; *Pst*, yellow rust; Up, up regulated; Down, down regulated; No, no obvious expression change.



**Figure S3.** Identification of positive transgenic plants for *HIPP1-V.* (a): Specific amplicon for *HIPP1-V* was present in five T0 transgenic lines. Yangmai158 and HIPP1-T0-1-4 were negative controls, and plasmid *pBI220*-*HIPP1-V* was used as positive control. M: DL2000 DNA ladder; 1: Yangmai158; 2: ddH2O; 3: HIPP1-T0-1-4; 4: OE-HIPP1-T0-10-2; 5: OE-HIPP1-T0-17-3; 6: OE-HIPP1-T0-27-3; 7: OE-HIPP1-T0-32-1; 8: OE-HIPP1-T0-39-3; P: pBI220-HIPP1-Vplasmid. (b):*HIPP1-V* expression in five *HIPP1-V*T0 positive transgenic lines (OE-HIPP1-T0-10-2, OE-HIPP1-T0-17-3, OE-HIPP1-T0-27-3, OE-HIPP1-T0-32-1 and OE-HIPP1-T0-39-3) and negative controls (HIPP1-T0-1-4 and Yangmai158).