Fig. S1 Structural classification of *Arabidopsis thaliana* type III and type IV J-proteins

In total, 92 type III J-proteins and 4 type IV J-like proteins have been identified in *Arabidopsis thaliana* genome. The highly diverged *Arabidopsis thaliana* type III J-proteins contain additional zinc-finger domains along with J-domain such as C2H2, A2L, DPH, PhnA, PHD, ZF-HYPF, PRIM ZN and ZN-CCHC, which are also included in the classification, designated by ZN2, ZN3, ZN4, ZN5, ZN6, ZN7, ZN8 and ZN9 respectively. They have been identified by using Pfam database. The C2H2 domain consists of the consensus sequence (F/Y)-X-C-X2-5-C-X3–Ψ-H-X3–4-H which is identified as a DNA binding domain. The A2L zinc-finger domain has the consensus sequence CX2CX13CX2C which specifically binds to zinc. Its function is unknown. The DPH (CSL) zinc-finger domain contains two CX(n)C motifs (in most cases n=2) as a consensus sequence which is involved in diphthamide biosynthesis. PHD fingers comprise C4HC3 signature which tend to be found in nuclear proteins that have a role in regulating chromatin. Zinc knuckle-CCHC has a consensus sequence CX2CX4HX4C which is involved in RNA binding. Transmembrane (TM), coiled coil (Cc) and tetratricopeptide (TPR) region were analyzed using different databases which are mentioned in figure 3. The domain region and total protein amino acid residue are also mentioned for each protein sequence. Type IV J-proteins contain 1 JLP2 and 3 JLP3/Magmas sequence where each sequence is represented by 3A, 3B and 3C.