

Fig S1 Gene position of *PbrLYPs*.

The characters in blue indicate the chromosome or scaffold number. The height of columns in red indicate the length of chromosome. The number on the right side of the chromosome indicate the start position of each gene.

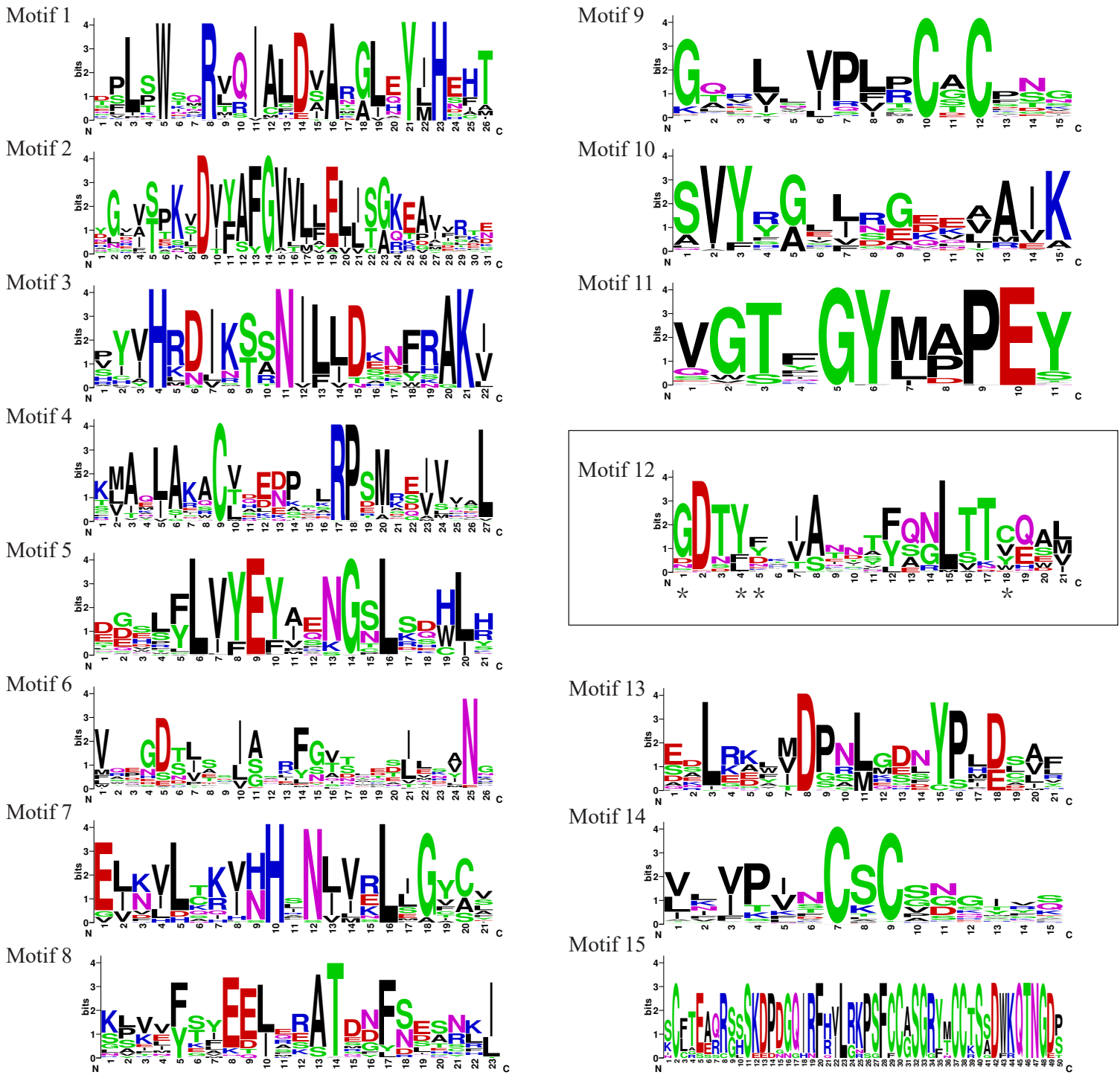


Fig S2 15 MEME motifs of LYPs

Over-represented motifs in *Arabidopsis* and the 8 Rosaceae species were identified using the MEME tool. The stack's height indicates the level of sequence conservation. The heights of the residues within the stack indicate the relative frequencies of each residue at that position. The star symbols under Motif 12 indicate the conservative positions for chitin binding.

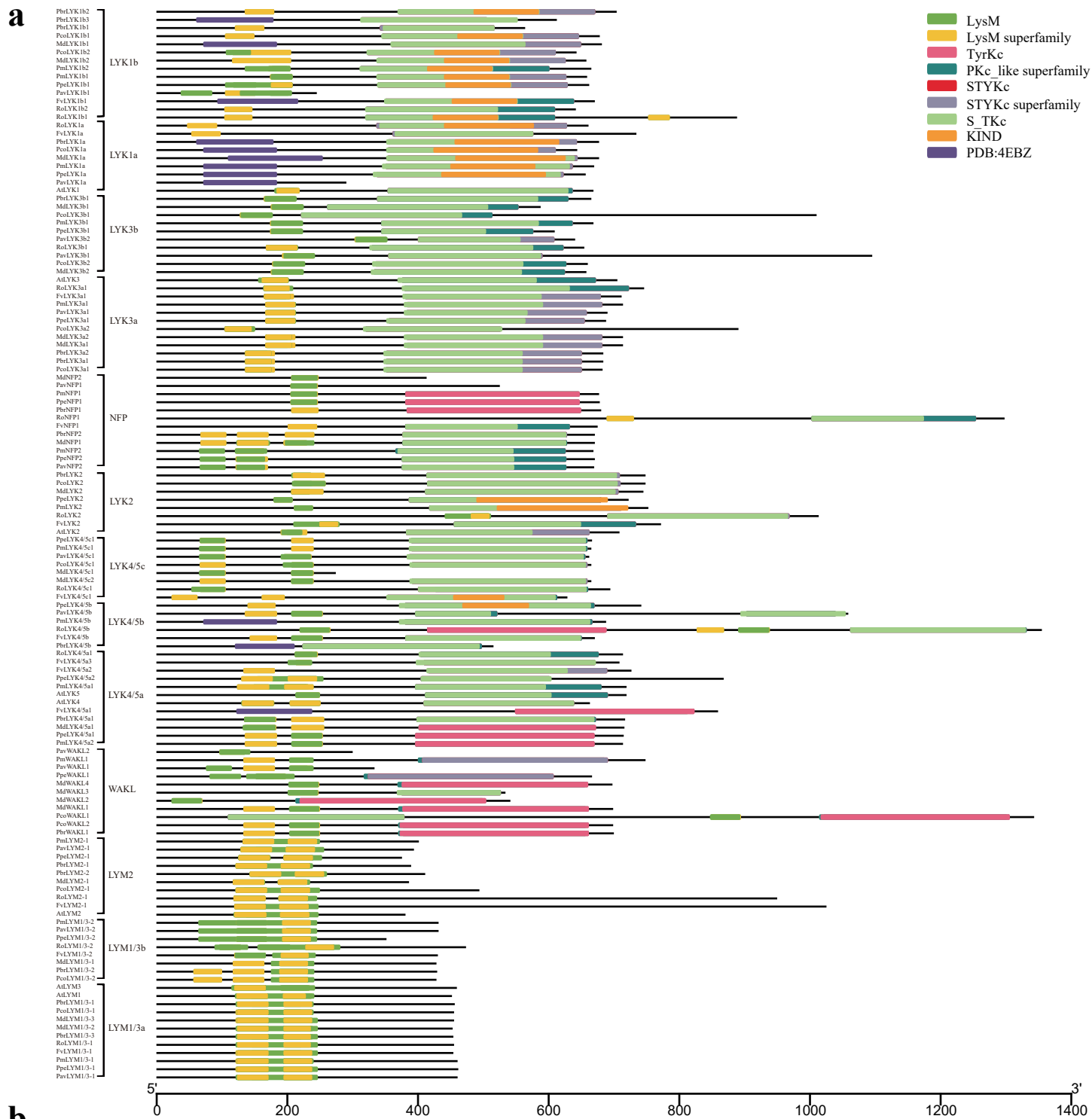


Fig S3 Schematic diagram and distribution of conserved motifs among the LYP proteins of *Arabidopsis* and 8 Rosaceae species.

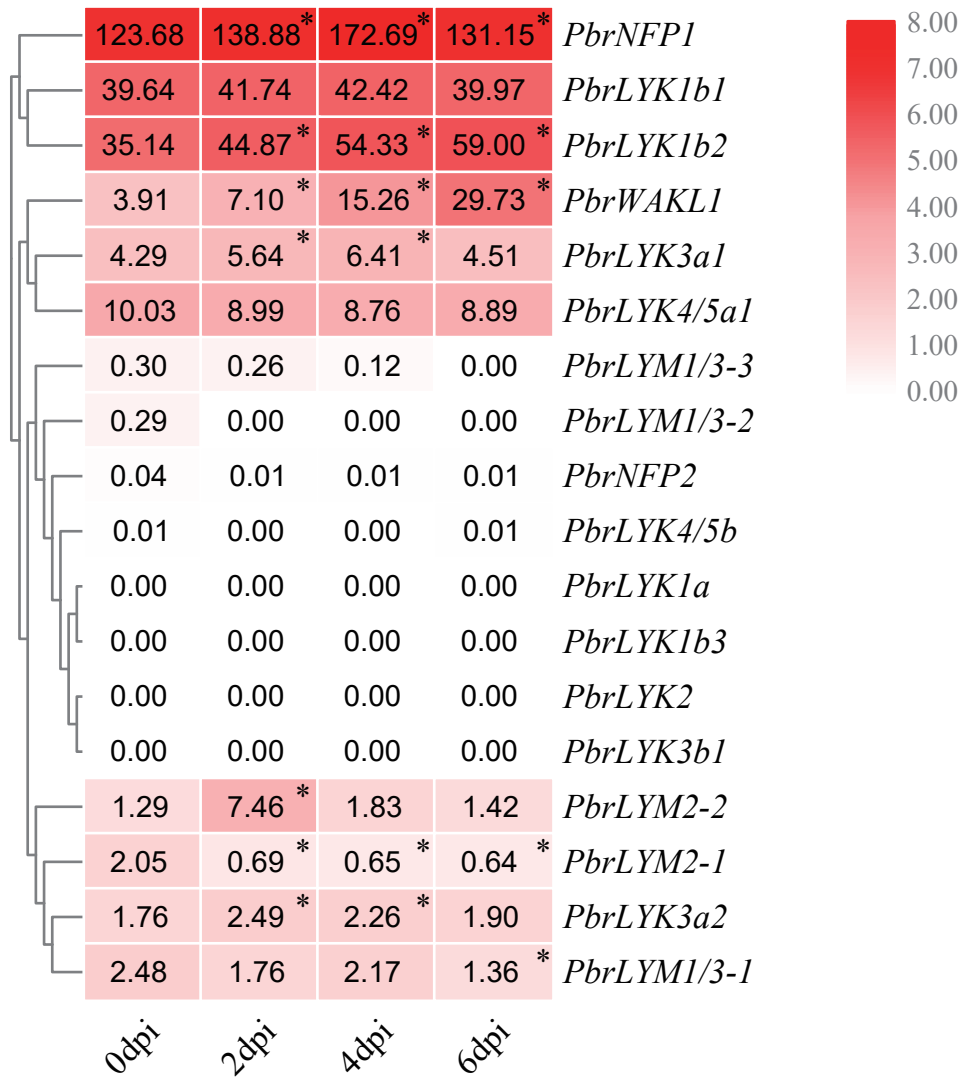


Fig S4 qRT-PCR analyses of the PbrLYP genes in Qiuzi pear leaves after *B. dothidea* infection. The pear actin was used as internal reference for the normalization. Asterisks indicated significant difference in statistics compared with 0dpi at the indicated time points (* $P < 0.05$).