

Supplementary Figures

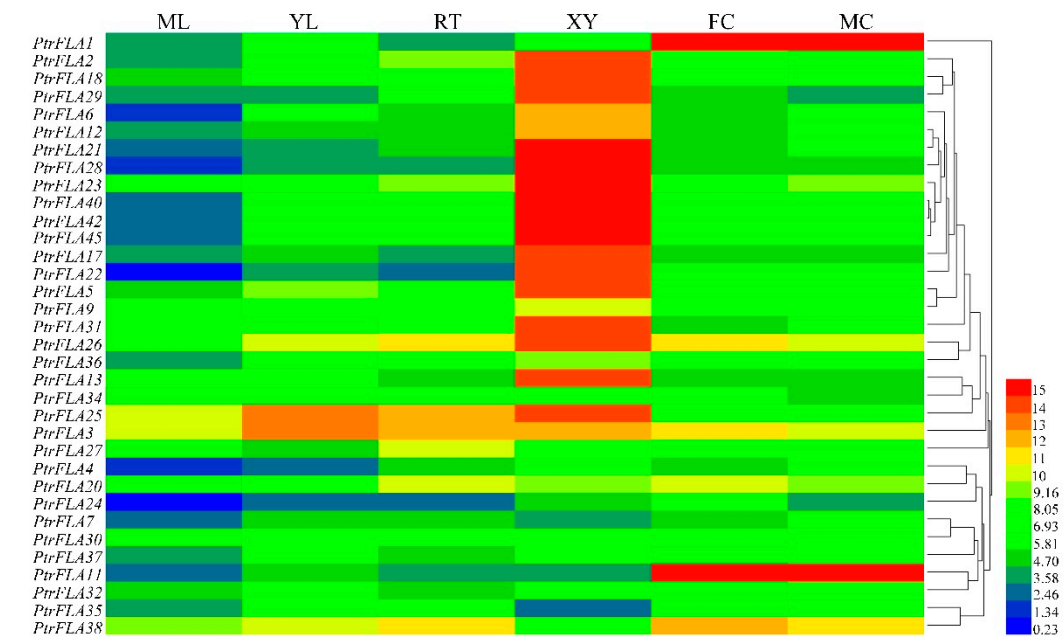


Figure S1. Hierarchical clustering of expression profiles of *PtrFLA* genes in different tissues. The microarray data were downloaded from the Poplar eFP browser. Color scale at the right of the dendrogram represents log<sub>2</sub> expression values. ML, mature leaf; YL, young leaf; RT, root; XY, xylem; FC, female catkin; MC, male catkin.

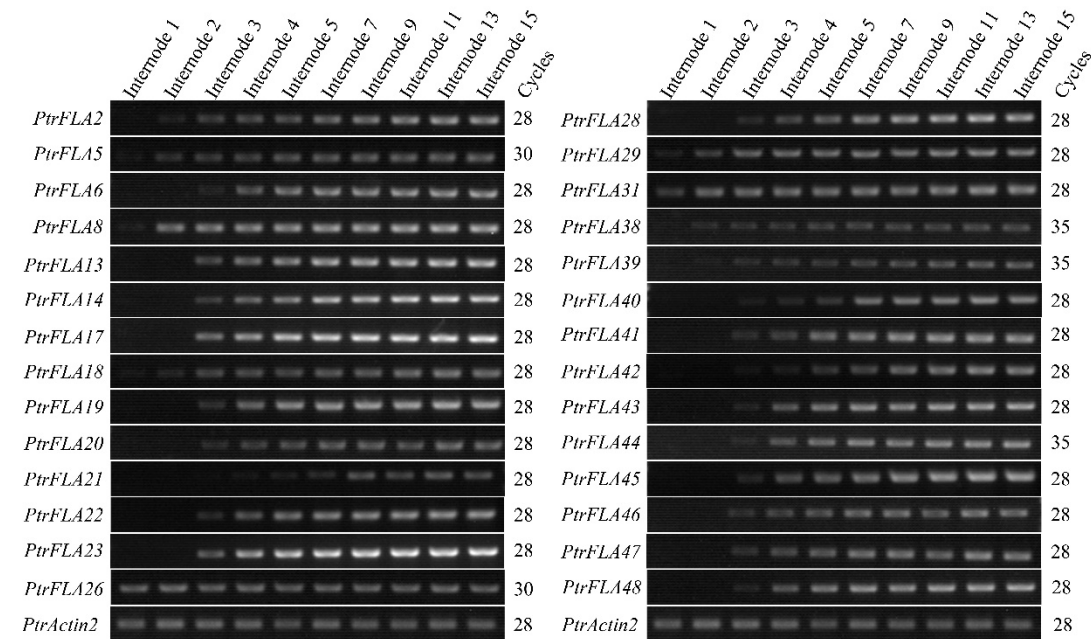


Figure S2. Gene expression of 28 *PtrFLA*s from group A in different stem internodes by RT-PCR analysis. Stem internodes included 1<sup>st</sup> to 5<sup>th</sup>, 7<sup>th</sup>, 9<sup>th</sup>, 11<sup>th</sup> and 12<sup>th</sup> internodes. The expression of *PtActin2* was used as an internal control.

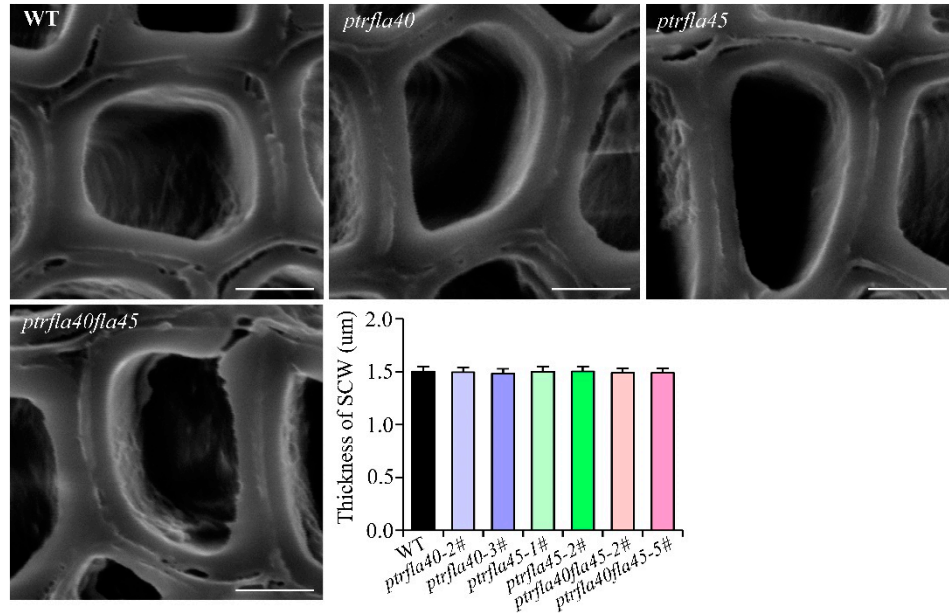


Figure S3. Wall thickness of secondary xylem mature fibers in 12<sup>th</sup> stem internodes of 4-month-old wild-type (WT), *ptrfla40*, *ptrfla45* and *ptrfla40fla45* mutants. Data are means  $\pm$  SD (n=50). Bars: 5 $\mu$ m.

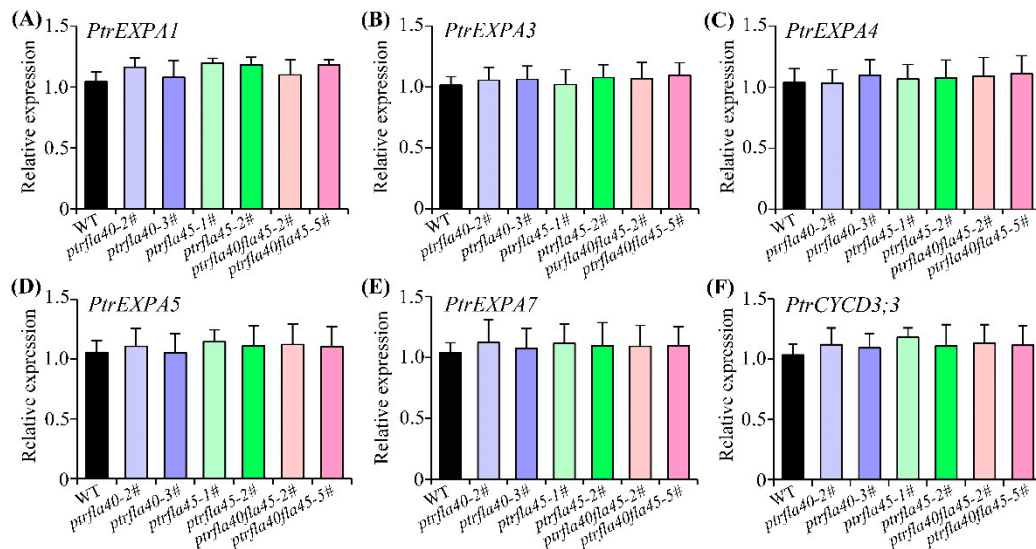


Figure S4. Transcription levels of five expansin genes and one cambial activity marker gene *PtrCYCD3;3* in wild-type (WT), *ptrfla40*, *ptrfla45* and *ptrfla40fla45* mutants by RT-qPCR analysis. The *PtActin2* was used as an internal control. Data are means  $\pm$  SD (n=3).