**The transcription factor PagLBD3 contributes to the regulation of secondary growth in *Populus***

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## Abstract

This dataset contains four parts of data described in the paper：“The transcription factor PagLBD3 contributes to the regulation of secondary growth in *Populus*. Journal of Experimental Botany 2021 Jul 27; erab351”.

The experiments investigated the role of transcription factor PagLBD3 in *Populus* secondary growth.

The first part (Fig.S1), we analyzed the expression pattern of *PagLBD3* in *Populus*. Table S1 listed primers used in all experiments.

The second part (Fig.S2), we obtained *PagLBD3* overexpression (*PagLBD3-OE,* L35 and L45) and dominant repression (*PagLBD3-SRDX,* L10 and L31)transgenic plants.

The third part (Fig.S3, Table S2-Table S5), we collected whole stem 9-12th internodes of *PagLBD3-OE* (L45) and WT plants, extracted RNA and performed RNA-seq to identify differentially expressed genes (DEGs) in *PagLBD3* overexpression versus WT plants in *Populus*. Three biological replicates were prepared for L45 and WT RNA-seq. “1” means up-regulated in L45 while “-1” means down-regulated in L45 in RNA-seq results.

The fourth part (Fig.S3, Table S6-Table S7), we collected whole stem 9-12th internodes of WT plants, extracted genomic DNA and performed DAP-seq to identify genes directly bound by PagLBD3 in *Populus*. We prepared three biological replicates of PagLBD3 DAP-seq (PagLBD3-r1, r2, r3) and input control (input-r1, r2, r3) for sequencing and data analysis.

We also integrated RNA-seq and DAP-seq to identify PagLBD3 putative direct target genes (DTGs) which were directly bound by PagLBD3 and differentially expressed in *PagLBD3* overexpression plants (Table S8-Table S9).

Main results: (1) *PagLBD3* expressed significantly higher insecondary phloem than secondary xylem. (2) *PagLBD3* overexpression increased stem secondary growth in *Populus* with significantly higher rate of cambial cells differentiated into phloem, while dominant repression of *PagLBD3* significantly decreased the rate of cambial cells differentiated into phloem. (3) we identified 1756 PagLBD3 genome-wide putative direct target genes (DTGs) through RNA sequencing (RNA-seq) coupled DNA affinity purification followed by sequencing (DAP-seq) assays and many of which are key regulators of secondary growth in *Populus*.

## Methods

The dataset was collected in growth chamber at Shandong Agriculture University and processed with methods described in a MS accepted for publication in Journal of Experimental Botany.

## Usage Notes

## The readme file contains an explanation of each experiment and information of detailed analysis can be found in the reference manuscript mentioned above.

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