Supplemental information

Two MADS-box genes regulate vascular cambium activity and secondary growth by modulating auxin homeostasis in *Populus*

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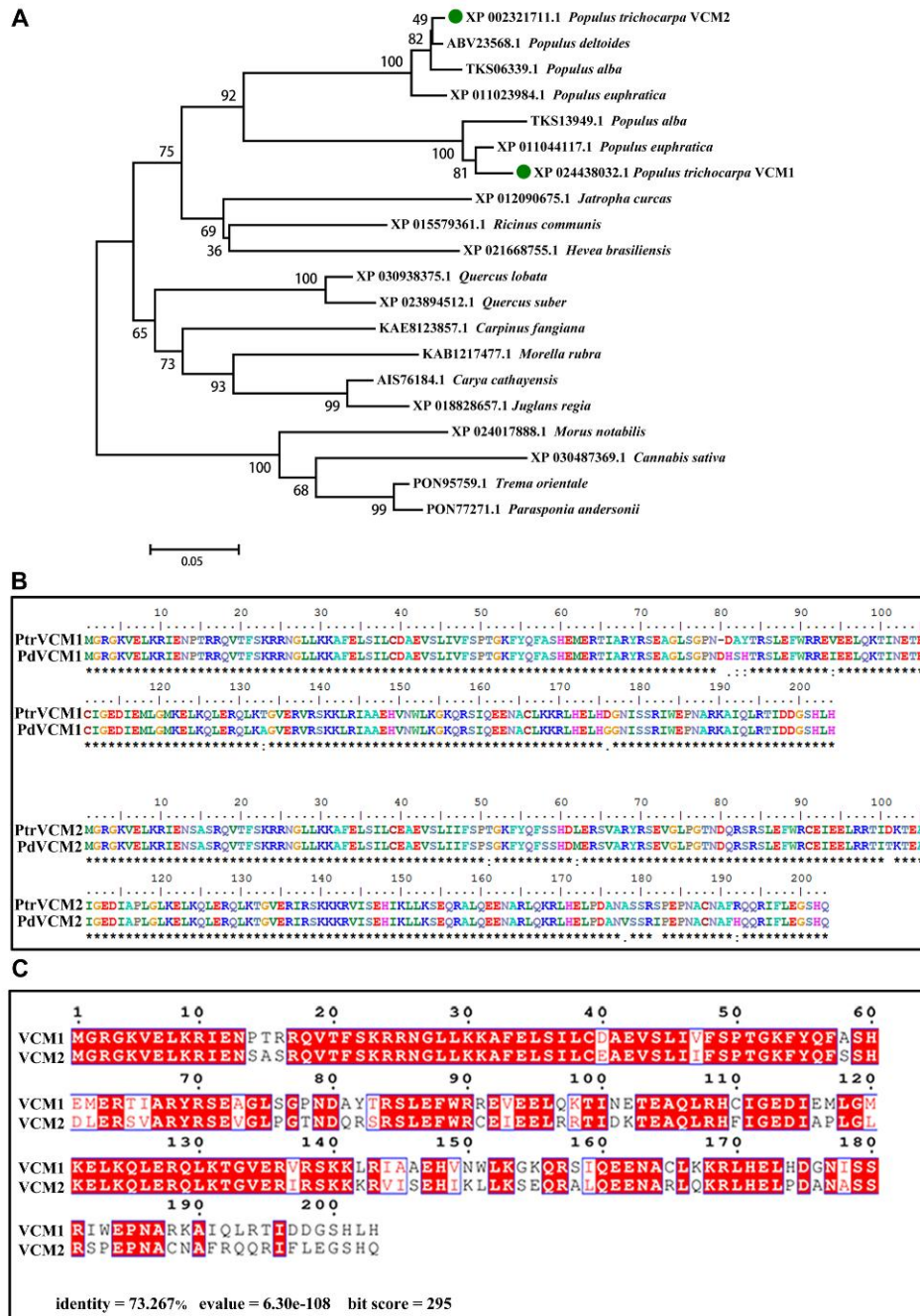
Supplemental Figures

Figure S1. Phylogenetic analysis of *VCM1* and *VCM2*.
(**A**) A neighbor joining tree of *VCM1 and VCM2* and their homologs in various woody plant species. N. bootstrap = 1000. (**B**) VCM1 and VCM2 protein sequences from *Populus trichocarpa* and *Populus deltoides* × *P. euramericana* cv. 'Nanlin895'. (**C**) Similarity of *VCM1 and VCM2* protein sequences.
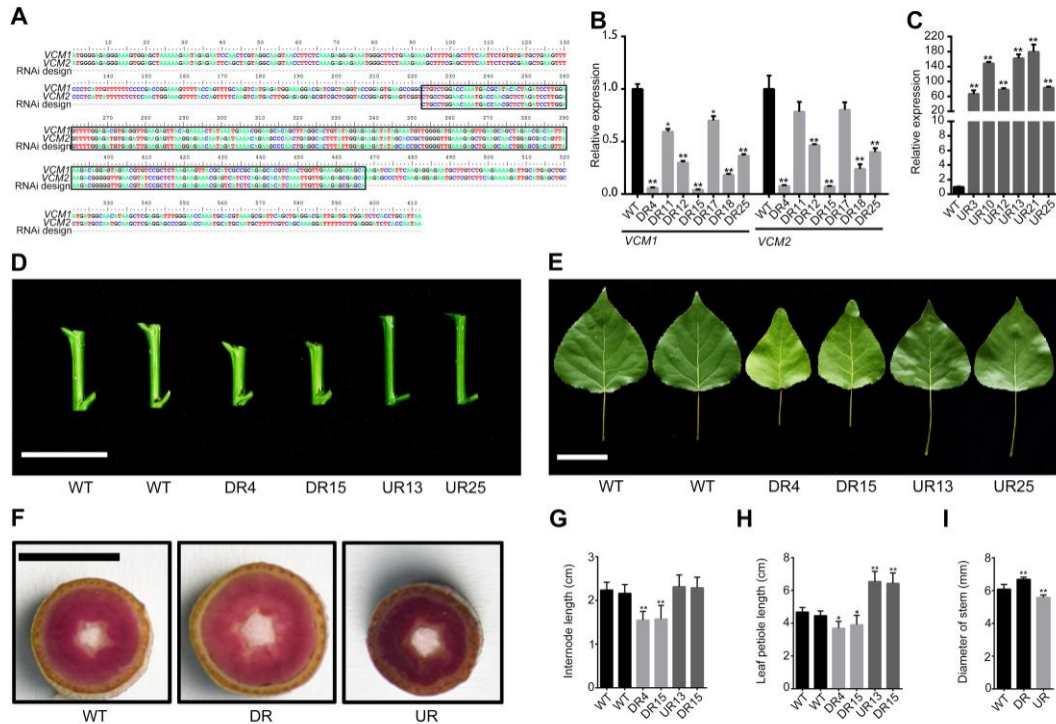
Figure S2. Regulation of *VCM1* and *VCM2* in *Populus*.
(**A**) RNAi fragment for downregulation of *VCM1& VCM2*. (B) A variety of *VCM1& VCM2* suppression in *DR* trangenics. (C) Expression of *VCM1* in *UR* trangenics. Values are means ±SD (n = 3 biological replicates). (D) The 10th internode of WT and transgenic, Scale bar = 2.5 cm. (E) Mature leaf from WT and transgenic, Scale bar = 5 cm. (F) Cross section of WT and transgenic, the position is 45 cm from the base in stem and plants were growth for more than five months. (G) Internode length (n = 10). (H) Leaf petiole length (n =10). (I) Stem diameter (n = 50). Statistical significance of differences was calculated based on two-tailed, two-sample student's t-test (**P <0.01, * P < 0.05).
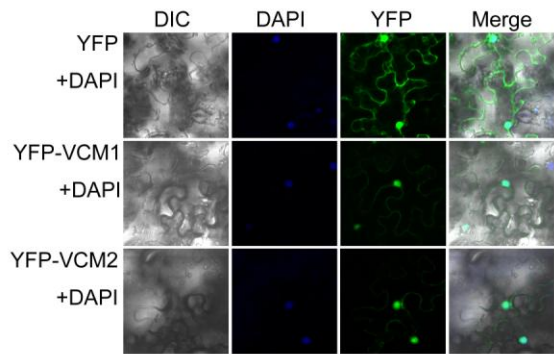
Figure S3. Subcellular localization of VCM1 and VCM2 in nucleus. Localization of VCM1 and VCM2 was examined in tobacco leaf epidermal cells. YFP was fused with VCM1 or VCM2 to form YFP-VCM1 or YFP-VCM2. DAPI is used as a nucleus marker.
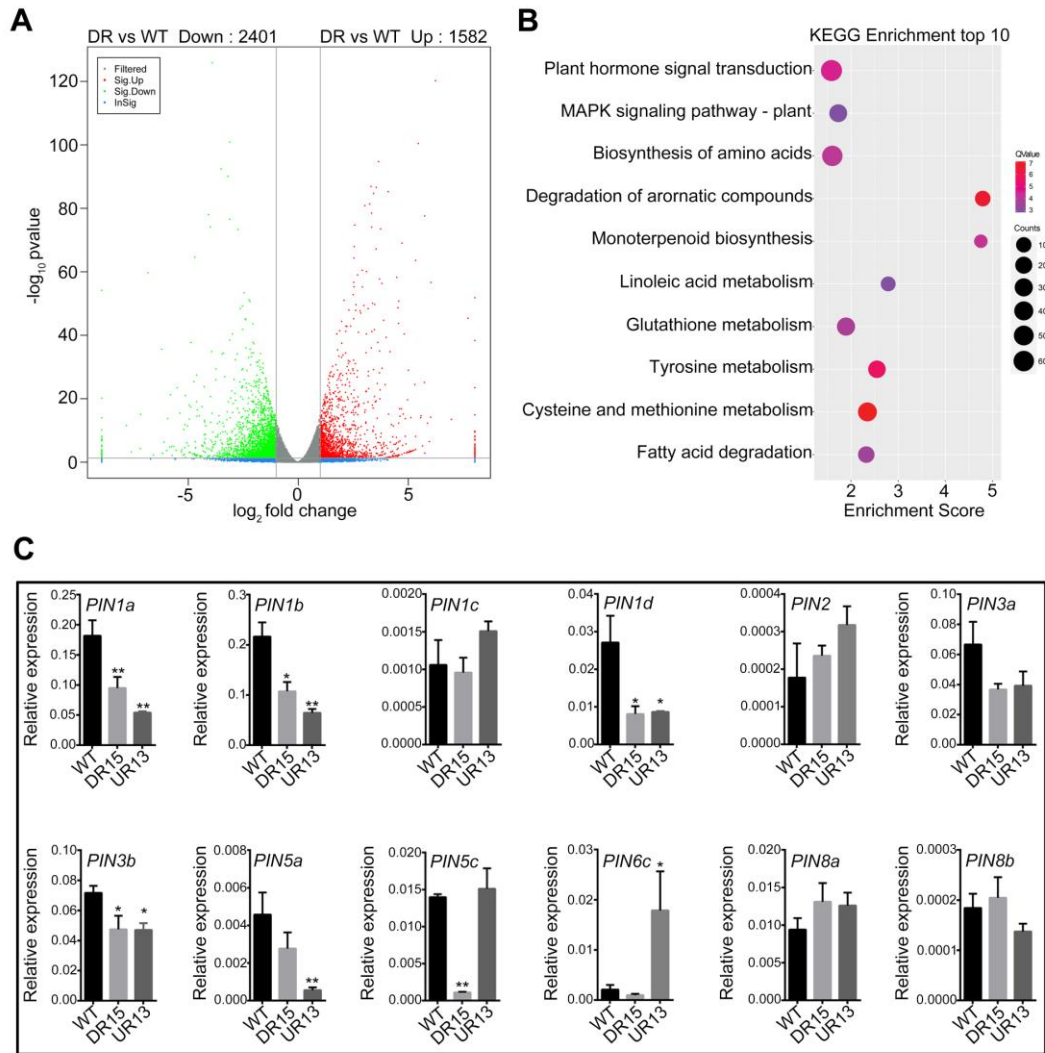
Figure S4. Differently expressed genes in downregulation of *VCM1& VCM2*.
(A) The transcriptome was substantially changed in downregulation of *VCM1&VCM2*.
(**B**) KEGG enrichment shows the top 10 biological processes changed in the
transcriptome. (**C**) qRT-PCR analysis of the *PIN* genes expression in regulation of
VCM1& VCM2. Values are means ±SD (n = 3 biological replicates). Statistical
significance of differences was calculated based on two-tailed, two-sample student's
t-test (**P < 0.01, * P < 0.05).