Supplementary Figure Legends:

Supplementary Figure S1. Comparison of tissue expression of the most relevant genes from WOX family of *Arabidopsis thaliana* and *Pinus pinaster* within different tissues and developmental stages. The selected genes belong to (i) WUS clade, such as *WOX3* gene in both Arabidopsis (A) and *Pinus pinaster* (B), sharing common patterns on SAM; and *WUS* gene in Arabidopsis (C) and *WOX5* gene in *Pinus pinaster* (D) with distinct expression pattern; (ii) intermediate clade, such as *WOX9* gene in Arabidopsis (E) and *WOXE* gene in *Pinus pinaster* (F), with common root expression patterns; and (iii) ancient clade, such as *WOX13* gene in both Arabidopsis (G) and *Pinus pinaster* (H), with shared expression patterns on SAM but specific RAM expression in *Pinus pinaster*. Developmental map from *Arabidopsis thaliana* comes from Arabidopsis eFP Browser (Winter et al. 2017), in case of *Pinus pinaster* developmental map comes from the exImage tool at ConGenIE.org (http://v22.popgenie.org/microdisection/) (Cañas et al. 2017).

Supplementary Figure S2. Comparison of tissue expression of the most relevant genes from KNOX family of *Arabidopsis thaliana* and *Pinus pinaster* within different tissues and developmental stages. The selected genes belong to (i) class I, such as *KNAT6* gene in Arabidopsis (A) and *KN2* gene in *Pinus pinaster* (B); and (ii) class II, such as *KN3* gene in Arabidopsis (C) and *KN5* gene in *Pinus pinaster* (D). Developmental map from *A. thaliana* comes from Arabidopsis eFP Browser (Winter et al. 2017), in case of *Pinus pinaster* developmental map comes from the exImage tool at ConGenIE.org (http://v22.popgenie.org/microdisection/) (Cañas et al. 2017).

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