Figure S1. Sequence alignment of walnut and *Arabidopsis AGL12* cDNA. The partial sequence of a walnut *AGL12* (*wAGL12,* accession number MF327581) cDNA was cloned by RT-PCR according to [50] and aligned with the *AtAGL12* cDNA sequence used for transformation. Briefly, after amplification and sequencing of the MADS-box sequences expressed in walnut roots, the 3′ end of the cDNA were amplified with the following gene specific primer (5′TAAGAAGGCCAAGGAGCTTT3′). The PCR products were cloned, sequenced and aligned with *AtAGL12* cDNA using Clustal Omega revealing 62.8% nucleotide identity (*) between both sequences. Translation initiation and termination codon are in bold characters.

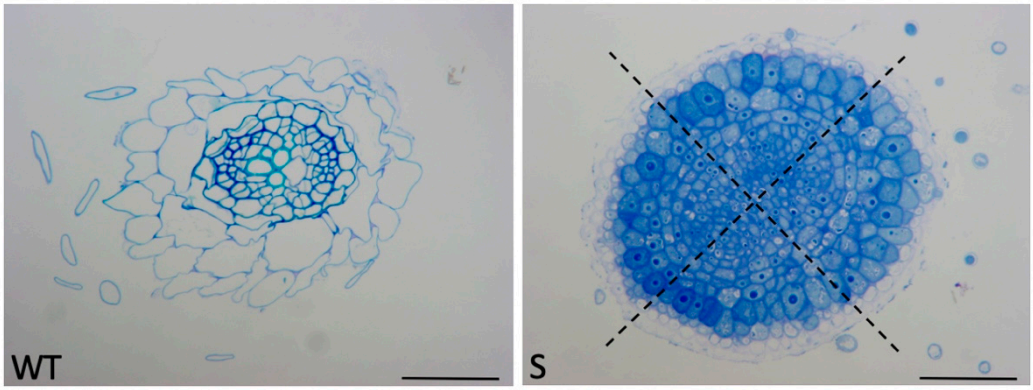

Figure S2. Transverse sections of WT (Col-0) and S T_1 *Arabidopsis* roots sampled 3 weeks after germination. The dotted lines represent two examples of perpendicular diagonals drawn for cell counting on root cross sections (equivalent to median planes on longitudinal sections, Figure 4). Scale bars: 100µm.

Table S1. List of primers and methods used for transgene detection in walnut. The table summarize the primers used to characterize the walnut tree transgenic lines and produce cDNA probes (*AtAGL12, gus and nptII)*. Kan^R embryonic lines were first screened by PCR and Southern-dot blot and further characterized by Southern- and/or northern blot hybridizations (mentioned in the last column of the table (P, Sd, S, and N, respectively).

Primer	Primer Sequence (5′-3′)	Annealing Temp. (°C)	Amplified Sequence (pb)	Method
d35S	gacgcacaatcccactatcc	60	S an AS constructs	P
agl12s	tctctgtgctctgtgatgcc			
agl12as	ttcacttggcattgttagcg	60	*AtAGL12* (500)	P, Sd, N
nptIIa	tgttccggctgtcagcgcag			
nptIIb	tcggcaagcaggcatcgcca	60	nptII (477)	P, Sd, S
gusa	tatacgccatttgaagccg			
gusb	aagccagtaaagtagaacggt	60	gus (550)	P, Sd
mcs1	ccaggctttacactttatgc			
mcs2	tcacgggttggggtttctac	50	*AtAGL12* promoter (>3000)	P
agrA	ccgtttccatttcgtcatatttc			
agrB	taaccgtgaacgtatagaccaccag	60	*Agrobacterium gDNA (560)*	P