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AtAGL12      AAATCATCAGATAGAAGGAAATATTC TGATTGAGAGATGGC TC GTGGAAGATTCAGCTTT
wAGL12      -----

AtAGL12      AAGAGGATTGAGAACCCGGTTTCACAGACAAGTGACTTTTTCGAAGAGGAGAAC TGGTCTTT
wAGL12      -----

AtAGL12      CTC AAGAAGGCTAAGGAGCTCTCTGTGCTCTGTGATGCCGAGATCGGTGTTGTGATCTTC
wAGL12      --TAAGAAGGCCAAGGAGCTTTCTGTGCTGTGTGATGCTGAAATGGAGTTATCATTTTC
          *****
AtAGL12      TCTCTCAGGGCAAGCTCTTTGAGCTCGCTACTAAAGGAAC AATGGAGGGAATGATTGAT
wAGL12      TCCTCCCATGGAAAGCTCTATGAGCTGGCCACC AAAGGAACCATGCAAGGGATTCAG
          ** * * * *
AtAGL12      AAGTACATGAAGTGTAAGTGGTGGTCTGTGTTCTTCTGCTACTTTTACTGCTCAA
wAGL12      AGGTACATGAAGTCTACAGGAGAGGTTTCAGCTGAACC-----A
          * * * * *
AtAGL12      GAACAACCTTAACCAACAAATCTTGATCCGAAAGATGAGATCAACGTGCTTAAGCAAGAG
wAGL12      GCCATTTGAAGCAACCCCTGCCCTGGATGCAAAAGAGGAATTAACATGCTGAACAAAGAG
          * * * * *
AtAGL12      ATTGAGATGCTTCAGAAAGGGATAAGCTATATGTTTGGAGGAGGAGATGGGGCTATGAAT
wAGL12      ATCGACATAC TCCAAAAGGCTTCAGGTATATGTTTGGAGGTGAGGTGCGACATGACG
          ** * * * *
AtAGL12      CTGGAAGAACCTCTTTTGCTTGAGAAGCATCTTGAGTATGGATTTCTCAGATTCGCTCT
wAGL12      TTGGATGAGTTAGATCTGCTTGAAAAGCACCTTGAGGTTTGGATTTGTAACATACGTTCA
          * * * * *
AtAGL12      GCTAAGATGAGTGTATGCTTTCAGAAATTCAGTCAATGAGGAAC AAGGAAGGAGTCTC
wAGL12      ACAAGATGAACATTAATGTTTC AAGAGATTC AACTTTTGGGAATAAGGAAGGAATGCTG
          * * * * *
AtAGL12      AAAAACCAAC AAGTATCTCTCTGACAAGATAGAGGAAAC AACAATAGCATATAGAT
wAGL12      AAAGCTGCAAAATAAGTATCTCTCAAGAT AAGATAGAAGATCATCAGAACAGTAGTACTACT
          *** * * * *
AtAGL12      GCTAACT-----TCGCAAGTCATGGAGACAAACTATT-----CCTATCCGCTAA-----CAATG
wAGL12      GCAATCACTGACTTTCGCACCAATTAATACCAC TAATTTCCATACC CACTAACCATAATG
          ** * *
AtAGL12      CCAAGTGAAATATTTTCAGTTC TAGACCATAGGGTATTTGAAGACTATGCTCACGAATTT
wAGL12      CAGAATGAGATATTTGAAATTC TAGCTAGGATGTCAT-----GATCTA
          * * * * *
AtAGL12      AAATAACCTTGCTAAGT-----ATAATATAGTGTGTTAAATCAC-----ACATAAT-----
wAGL12      GAATAAGCTGATCTACTGTTTTATGTACTACTGTTTTTAATTAAGGTCACGCGCTGTTTC
          *****
AtAGL12      ---TAAATAAAGCTGTGGAACCTTCGTAGCAGTTGAA-----AATCTATCCGTATGT
wAGL12      TGTTCCTCATGTAAGCCAATGTACGTAGCTGTATAGTATAAATTAAGTTCTTTCCGATGGA
          * * * *
AtAGL12      TTTATCTCTCTGTTTACATTTGTGTTGTGAAGATGAAA---T-GACTGC AAGTGTGGT
wAGL12      CAGACGTACGTACGTT---GTAATGCTGTATCATGATGATCAGGATGGGTACTTGCCA
          * * * *
AtAGL12      GTCTACTTATAACTCTTTCTACTTTCTATCTATGTTTGAATTTATGGATTT-----
wAGL12      TCCTAGCTAGTACTCTTACTACTTTTAGCAGCTTGATTGTAGTATATTAATGTTGACGT
          ** * *
AtAGL12      -----
wAGL12      ATGTGCTCTTGTGTTGCTATCAATAATGCTTGCATATATGCTGTGTCATGTTATTCAAAAA

AtAGL12      -----
wAGL12      AAAAAAAAAAAAAAAAAA

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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.

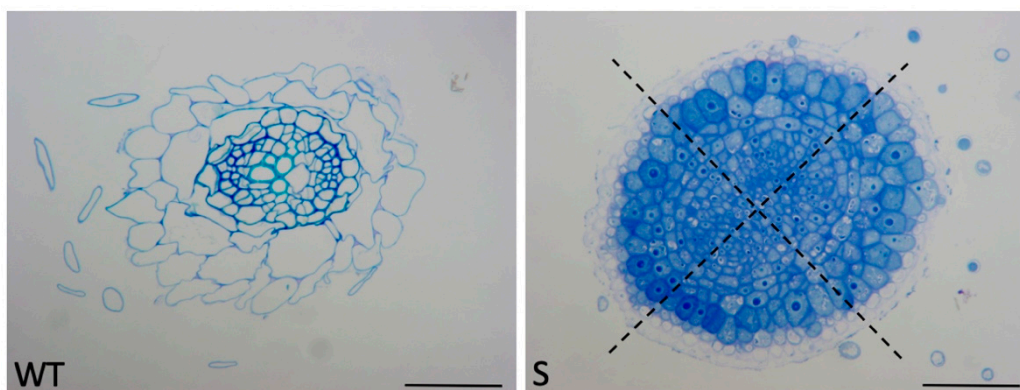


Figure S2. Transverse sections of WT (Col-0) and S T₁ *Arabidopsis* roots sampled 3 weeks after germination. The dotted lines represent two examples of perpendicular diagonals drawn for cell counting on root cross sections (equivalent to median planes on longitudinal sections, Figure 4). Scale bars: 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	<i>AtAGL12</i> (500)	P, Sd, N
nptIIa	tgttccggctgtcagcgcag			
nptIIb	tcggcaagcagcatcgcca	60	nptII (477)	P, Sd, S
gusa	tatacgccatttgaagccg			
gusb	aagccagtaaagtagaacggt	60	<i>gus</i> (550)	P, Sd
mcs1	ccaggctttacactttatgc			
mcs2	tcacgggttggggtttctac	50	<i>AtAGL12</i> promoter (>3000)	P
agrA	ccgtttccatttcgtcatatttc			
agrB	taaccgtgaacgtatagaccaccag	60	<i>Agrobacterium</i> gDNA (560)	P