

Supplementary material

Article

Transcriptome Dynamics of Rooting Zone and Leaves During *in vitro* Adventitious Root Formation in *Eucalyptus nitens*

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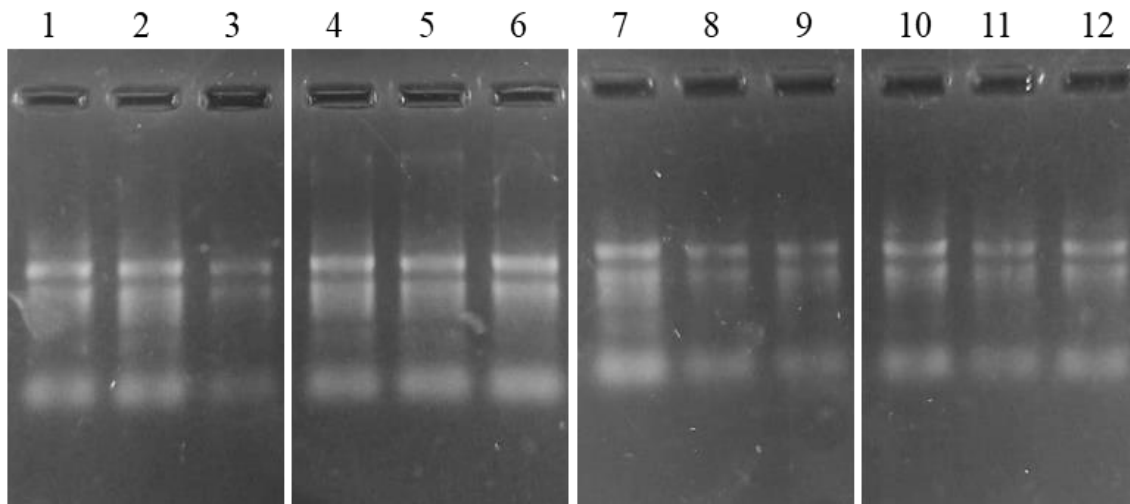


Figure S1. RNA integrity. Agarose gel electrophoresis of total RNA obtained from stems and leaves extracted before (S0) and after three/four (S3/4) days from IBA treatment. Three biological replicates per sample were used. Stem bases: S0, lanes 1, 2 and 3; S3/4, lanes 4, 5 and 6. Leaves: S0, lanes 7, 8 and 9; S3/4, lanes 10, 11 and 12).

RNA integrity was analyzed by horizontal 2% agarose gel electrophoresis and stained with GelGreen[®]. Total RNA concentrations varied between 436.4 and 1,301.1 ng/μL. The purity ratio A260/280 varied between 1.89 and 2.05, while A260/230 ranged between 1.86 and 2.08. No RNA degradation was observed.

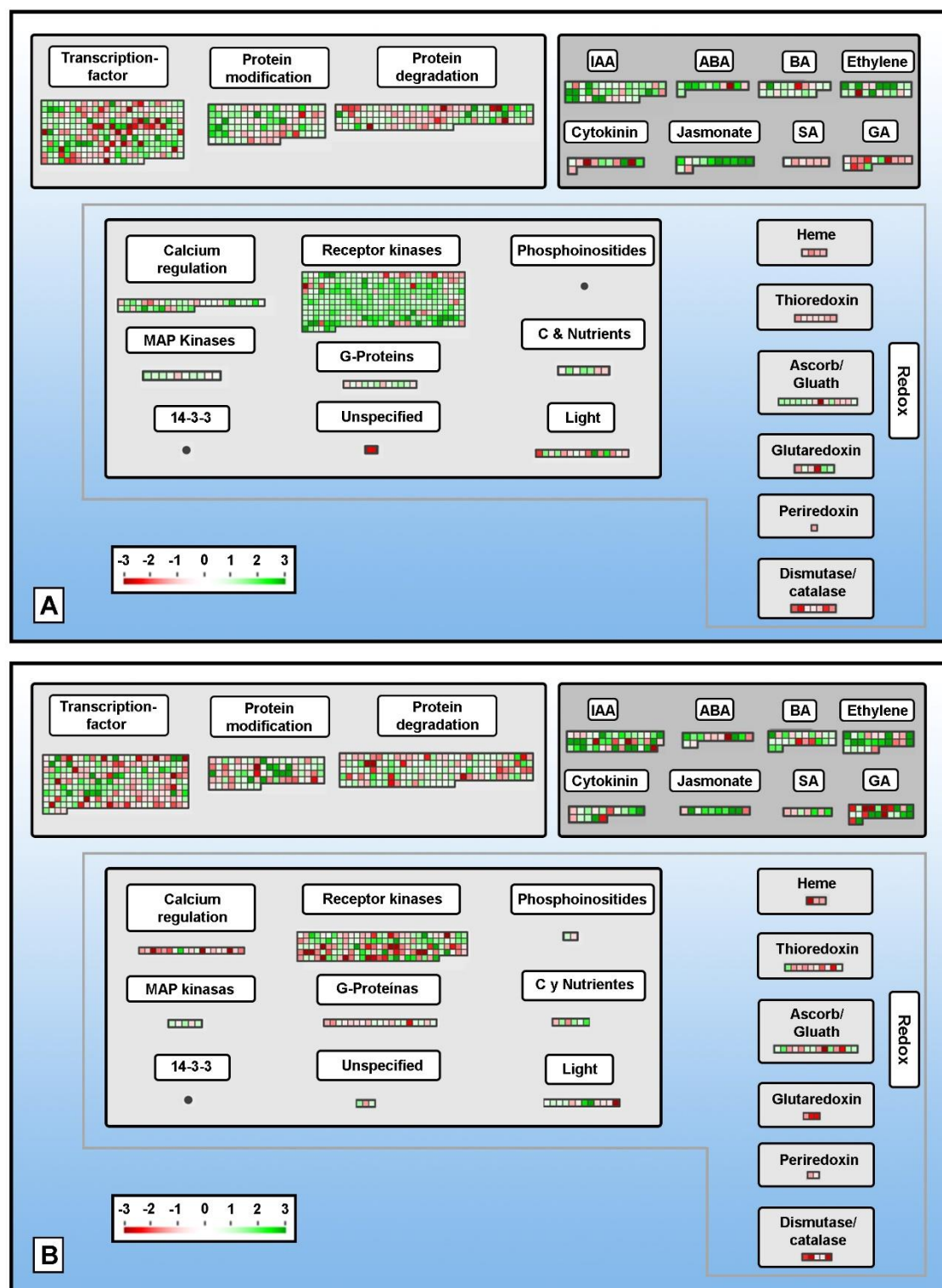


Figure S2. MapMan regulation overview of *E. nitens* leaves (**A**) and stem bases (**B**) gene expression during the early step of root formation. Each square corresponds to a gene. Red and green indicate lower and higher expression than the control, respectively. The scale bar is shown in log2. Sequences with a fold change (FC) ≥ 2 in its expression between treatments and FDR < 0.05 were assigned as a differentially expressed transcript.

Table S1. Gene expression fold changes on day three/four after the IBA treatment, determined by RT-qPCR and RNA-seq analysis.

Gene Name	qPCR	ARN-seq
<i>Endoglucanase 1 (Endo1)</i>	6,25	6,29
<i>Citokinin dehydrogenase (CitokDes3)</i>	4,75	5,36
<i>Ethylene-responsive transcription tactor (ERF003)</i>	2,46	4,46
<i>1-aminocyclopropane-1-carboxylate oxidase (ACO)</i>	-2,83	-1,81
<i>Fructose-bisphosphate aldolase (FBA)</i>	-4,64	-2,02
<i>Translation elongation factor 2 (EF 2)</i>	1	1
<i>Isoprene synthase, chloroplastic-like (ISC-like)</i>	-6,64	-5,18
<i>Gretchen hagen 3 (GH3-1)</i>	3,54	8,42
<i>Cellulose synthase A catalytic 8 (CSACat8)</i>	-4,05	-3,04
<i>Auxin response factors (ARF6)</i>	0,23	1,03
<i>Scarecrow (SCR)</i>	1,5	1,93

Table S2. Differentially expressed transcripts (DETs).

Sigla	Transcript	Annotation	Function	Log ₂ FC
Auxins metabolisms				
T1	tr3710_c79_g1	Acyl-CoA dehydrogenase/oxidase (IBR3)	IBA to IAA conversion	ns L
T2	tr1960_c212_g1	Enoyl-CoA hydratase (IBR10)	IBA to IAA conversion	↑ 1.0 L
T3	tr905_c81_g1	Enoyl-CoA hydratase (IBR10)	IBA to IAA conversion	↑ 1.1 L
T4	tr1960_c199_g2	Enoyl-CoA hydratase (IBR10)	IBA to IAA conversion	↑ 0.7 L
T5	tr5933_c23_g1	Enoyl-CoA hydratase 2 (ECH2)	IBA to IAA conversion	ns L
T6	tr496_c723_g1	GRETCHEN HAGEN 3 IAA-amida synthase GH3.1	IAA - amino acid conjugation	↑ 3.8 L ↑ 2.9 S
T7	tr1863_c28_g12	GRETCHEN HAGEN 3 IAA-amida synthase GH3.1	IAA - amino acid conjugation	↑ 7.2 L ↑ 8.4 S
T8	tr1863_c28_g8	GRETCHEN HAGEN 3 IAA-amida synthase GH3.1	IAA - amino acid conjugation	↑ 9.6 L ↑ 10.3 S
T9	tr4738_c576_g1	GRETCHEN HAGEN 3 IAA-amida synthase GH3.5	IAA - amino acid conjugation	↑ 1.1 L ↑ 1.0 S
T10	tr6569_c202_g1	GRETCHEN HAGEN 3 IAA-amida synthase GH3.5	IAA - amino acid conjugation	↑ 1.1 L ↑ 2.8 S
T11	tr1921_c236_g3	Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase UDP-glucosyltransferase	IAA - sugar conjugation	↑ 0.8 L
T12	tr1921_c245_g1	Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase UDP-glucosyltransferase	IAA - sugar conjugation	↑ 0.7 L
T13	tr268_c28_g1	Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase UDP-glucosyltransferase 75B1	IAA - sugar conjugation	↑ 0.8 L ↑ 1.1 S
T14	tr1939_c3_g1	Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase UDP-glucosyltransferase	IAA - sugar conjugation	↑ 0.7 L
T15	tr1921_c236_g9	Uridine 5'-diphosphate-glucose:indol-3-acetyl)-beta-D-glucosyl transferase UDP-glucosyltransferase	IAA - sugar conjugation	↑ 1.4 L
T16	tr268_c33_g3	Uridine 5'-diphosphate-glucose:indol-3-acetyl)-beta-D-glucosyl transferase UDP-glucosyltransferase 75B2	IAA - sugar conjugation	↑ 1.5 L ↑ 1.7 S
T17	tr3678_c14_g2	Uridine 5'-diphosphate-glucose:indol-3-acetyl)-beta-D-glucosyl transferase UDP-glucosyltransferase 74F1	IAA - sugar conjugation	↑ 2.3 S
T18	tr5846_c882_g1	IAR3/ILL2 hydrolase	Amide-bond cleavage	↑ 0.8 S
T19	tr4275_c68_g2	IAR3/ILL2 hydrolase	Amide-bond cleavage	↑ 0.9 S
T20	tr4002_c17_g2	IAR3/ILL2 hydrolase	Amide-bond cleavage	↑ 0.9 S
T21	tr5825_c150_g1	IAA carboxyl methyltransferase 1 (IAMT1).	IAA methylation	↑ 4.1 L ↑ 6.4 S
T22	tr2658_c159_g1	LIKE AUXIN RESISTANT2 (LAX2)	IAA influx carrier	↑ 1.6 L
T23	tr7297_c420_g1	PIN1	IAA efflux carrier	↑ 1.8 L ↑ 1.7 S
T24	tr3578_c13_g1	PIN1	IAA efflux carrier	↑ 1.1 L
T25	tr5015_c923_g1	PIN7	IAA efflux carrier	↑ 1.2 L ↑ 1.4 S
T26	tr2528_c174_g1	PIN3	IAA efflux carrier	↑ 1.0 S
T27	tr5878_c121_g1	PIN6	IAA efflux carrier	↑ 1.9 S
T28	tr2658_c159_g1	LIKE AUXIN RESISTANT3 (LAX3)	IAA/IBA influx carrier	↑ 2.8 S
T29	tr4959_c346_g1	ABCG36/ABCG37	IBA efflux carrier	↑ 3.1 L
T30	tr908_c134_g1	ABCG36/ABCG37	IBA efflux carrier	↑ 3.1 L
T31	tr7363_c12_g1	ABCG36/ABCG37	IBA efflux carrier	↑ 3.1 L

T32	tr5920_c209_g1	PXA1/ABCD1	IBA efflux carrier	↑ 2.2 H
Hormonal interactions and signaling				
T33	tr7325_c340_g1	Transport Inhibitor Response 1 (TIR1)	Auxin receptor	↓ -1.4 L
T34	tr5854_c681_g1	IAA6 transcription factor	Aux/IAA protein family gene	↑ 2.1 L
T35	tr2018_c21_g1	IAA13 transcription factor	Aux/IAA protein family gene	↑ 1.3 L
T36	tr3553_c114_g1	IAA34 transcription factor	Aux/IAA protein family gene	↑ 2.0 L
T37	tr3909_c8_g1	IAA33 transcription factor	Aux/IAA protein family gene	↓ -4.4 L
T38	tr2100_c21_g1	AHL20 transcription factor	Aux/IAA protein family gene	↓ -2.1 L
T39	tr4032_c79_g1	IAA14 transcription factor	Aux/IAA protein family gene	↑ 2.9 S
T40	tr937_c94_g1	IAA7 transcription factor	Aux/IAA protein family gene	↑ 2.4 L ↑ 1.0 S
T41	tr1963_c18_g1	IAA7 transcription factor	Aux/IAA protein family gene	↑ 1.3 S
T42	Tr1925_c27_g1	IAA8 transcription factor	Aux/IAA protein family gene	↑ 1.0 L ↑ 1.6 S
T43	tr5955_c127_g2	IAA8 transcription factor	Aux/IAA protein family gene	↑ 0.6 L
T44	3866_c90_g2	IAA10 transcription factor	Aux/IAA protein family gene	↑ 2.3 L ↑ 3.1 S
T45	tr1260_c1_g1	IAA10 transcription factor	Aux/IAA protein family gene	↑ 2.4 L ↑ 4.7 S
T46	tr1960_c281_g1	ARG4 transcription factor	Aux/IAA protein family gene	↑ 1.5 L ↑ 1.7 S
T47	tr1963_c17_g10	ARG4 transcription factor	Aux/IAA protein family gene	↑ 1.4 L ↑ 1.6 S
T48	tr1963_c17_g8	ARG4 transcription factor	Aux/IAA protein family gene	↑ 1.3 L ↑ 1.6 S
T49	tr4785_c211_g1.4	Auxin Response Factor ARF6	Mediate auxin responses	↑ 1.2 S
T50	tr5939_c74_g2	Auxin Response Factor ARF6	Mediate auxin responses	↑ 0.9 S
T51	tr5015_c534_g1	Auxin Response Factor ARF8	Mediate auxin responses	↑ 1.2 S
T52	tr5921_c82_g1	Auxin Response Factor ARF17	Mediate auxin responses	ns S
T53	tr4280_c47_g1	Auxin Response Factor ARF19	Mediate auxin responses	↑ 1.1 L ↑ 1.0 S
T54	tr5939_c74_g2	Auxin Response Factor ARF19	Mediate auxin responses	↑ 0.9 S
T55	Tr1963_c17_g6	SHY2/IAA3 transcription factor	Aux/IAA protein family gene	↑ 1.4 L ↑ 2.1 S
T56	tr7325_c339_g1	SHY2/IAA3 transcription factor	Aux/IAA protein family gene	↑ 1.9 L ↑ 5.5 S
T57	tr496_c1164_g2	Small Auxin Up RNAs. SAUR-like (SAUR68)	Auxin responsive genes. SAUR family	↑ 1.7 L ↑ 3.8 S
T58	tr496_c909_g3	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 1.0 L ↑ 1.4 S
T59	tr5943_c263_g2	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 1.7 L
T60	tr496_c1254_g9	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 3.0 S
T61	tr496_c1254_g7	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 3.1 S
T62	tr496_c1254_g10	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 2.1 S
T63	tr496_c750_g1	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 2.1 S
T64	tr5293_c0_g1	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 6.3 S
T65	tr496_c558_g2	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 2.2 S
T66	tr2672_c0_g1	Small Auxin Up RNAs. SAUR-like	Auxin responsive genes. SAUR family	↑ 1.2 S
T67	tr5839_c72_g1	Cyclin D-type (CCD3-1)	Cell cycle control	↑ 1.1 S

T68	tr530_c92_g1	Cyclin D-type (CCD3-1)	Cell cycle control	↑ 1.0 S
T69	tr5934_c173_g1	Cyclin-dependent kinase 1 (CKB1-1)	Cell cycle control	↑ 1.6 S
T70	tr4991_c487_g1	Cyclin-dependent kinase 1 (CKB1-1)	Cell cycle control	↑ 1.4 S
T71	tr931_c33_g1	Cyclin-dependent kinase 1 (CKS1)	Cell cycle control	ns S
T72	tr2103_c159_g1	Cyclin-dependent kinase 1 (CDKA1)	Cell cycle control	↑ 0.6 S
T73	tr5864_c693_g1	SCARECROW-like 5 (SCL5)	Transcriptional regulator. GRAS family	↑ 1.3 S
T74	tr6540_c351_g1	SCARECROW-like 13 (SCL13)	Transcriptional regulator. GRAS family	↓ -0,7 L
T75	tr7260_c339_g1	SCARECROW-like 13 (SCL13)	Transcriptional regulator. GRAS family	↓ -0,9 S
T76	tr3686_c605_g1	SCARECROW-like 14 (SCL14)	Regulador transcripcional familia GRAS	↑ 1.2 L ↑ 1.9 S
T77	tr972_c169_g3	SCARECROW-like 14 (SCL14)	Transcriptional regulator. GRAS family	↑ 0.9 L
T78	tr3686_c713_g1	SCARECROW-like 14 (SCL14)	Transcriptional regulator. GRAS family	↑ 0.6 L
T79	tr3686_c530_g1	SCARECROW-like 14 (SCL14)	Transcriptional regulator. GRAS family	↑ 0.9 L ↑ 1.1 S
T80	tr3686_c710_g1	SCARECROW-like 14 (SCL14)	Transcriptional regulator. GRAS family	↑ 1.3 L
T81	tr3686_c814_g5	SCARECROW-like 14 (SCL14)	Transcriptional regulator. GRAS family	↑ 0.8 S
T82	tr5916_c1149_g3	SCARECROW-like 21 (SCL21)	Transcriptional regulator. GRAS family	↑ 1.3 L
T83	tr4988_c126_g1	SCARECROW-like 21 (SCL21)	Transcriptional regulator. GRAS family	↑ 2.0 S
T84	tr4752_c258_g4	1-aminocyclopropane-1-carboxylate synthase 1 (ACC1)	Biosíntesis de etileno	↑ 1.1 L ↑ 2.5 S
T85	tr43_c3_g1	1-aminocyclopropane-1-carboxylate synthase 1 (ACC1)	Ethylene biosynthesis	↑ 1.2 L ↑ 2.7 S
T86	tr3461_c0_g2	1-aminocyclopropane-1-carboxylate synthase 1 (ACC1)	Ethylene biosynthesis	↑ 4.5 S
T87	tr6569_c89_g1	1-aminocyclopropane-1-carboxylate synthase 2 (ACC2)	Ethylene biosynthesis	↑ 3.1 L ↑ 4.4 S
T88	tr2886_c3_g2	1-aminocyclopropane-1-carboxylate synthase 2 (ACC2)	Ethylene biosynthesis	↑ 2.0 S
T89	tr4752_c258_g3	1-aminocyclopropane-1-carboxylate synthase 2 (ACC2)	Ethylene biosynthesis	↑ 2.1 S
T90	tr5955_c244_g1	1-aminocyclopropane-1-carboxylate synthase 4 (ACC4)	Ethylene biosynthesis	↑ 6.2 L ↑ 3.4 S
T91	tr1877_c23_g1	1-aminocyclopropane-1-carboxylate synthase 4 (ACC4)	Ethylene biosynthesis	↑ 4.6 L ↑ 3.2 S
T92	tr5020_c252_g1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↑ 1.4 L ↑ 1.9 S
T93	tr3855_c80_g1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↑ 6.3 L ↑ 5.7 S
T94	Tr1921_c200_g1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↑ 9.8 L ↑ 6.1 S
T95	tr4834_c160_g1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↑ 1.2 L
T96	Tr5534_c0_g1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↑ 1.1 L
T97	tr7260_c403_g2	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↑ 1.2 L
T98	tr4269_c56_g1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↓ -3.6 L

T99	tr7299_c221_g2	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↑ 0.9 S
T100	tr4991_c501_g1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	Ethylene biosynthesis	↓ -1.5 S
T101	tr7325_c185_g1	Ethylene receptor subfamily 1 (ERS1)	Ethylene receptor	↑ 0.8 S
T102	tr2039_c114_g1	Ethylene receptor, subfamily 2 (ERS2)	Ethylene receptor	↓ -0.7 L
T103	tr2100_c61_g1	Ethylene response 2 (ETR2)	Ethylene receptor	↑ 1.2 S
T104	tr566_c73_g1	Ethylene Response Factor. ABA REPRESSOR1 (ABR1)	Transcriptional regulator. AP2/EREBP family	↑ 1.3 L
T105	tr3742_c81_g1	Ethylene Response Factor. (ERF)	Transcriptional regulator. AP2/EREBP family	↑ 0.7 L
T106	tr5875_c146_g1	Ethylene Response Factor. (ERF)	Transcriptional regulator. AP2/EREBP family	↑ 3.0 L ↑ 4.5 S
T107	tr566_c73_g1	Ethylene Response Factor. (ERF)	Transcriptional regulator. AP2/EREBP family	↑ 0.9 S
T108	tr2674_c89_g1	Ethylene Response Factor 1 (ERF1)	Transcriptional regulator. AP2/EREBP family	↑ 1.3 S
T109	tr3743_c922_g1	Ethylene Response Factor 1 (ERF1)	Transcriptional regulator. AP2/EREBP family	↑ 1.2 S
T110	tr3961_c11_g1	Ethylene Response Factor 1 (ERF1)	Transcriptional regulator. AP2/EREBP family	↓ -2.8 S
T111	tr7299_c142_g1	Ethylene Response Factor 1 (ERF1)	Transcriptional regulator. AP2/EREBP family	↑ 1.4 L
T112	tr6442_c0_g1	Ethylene Response Factor 1 (ERF1)	Transcriptional regulator. AP2/EREBP family	↑ 1.6 L
T113	tr3743_c922_g1	Ethylene Response Factor 4 (ERF4)	Transcriptional regulator. AP2/EREBP family	↑ 1.1 L
T114	tr7297_c516_g1	Ethylene Response Factor 110 (ERF110)	Transcriptional regulator. AP2/EREBP family	↑ 1.6 L ↑ 3.5 S
T115	tr5854_c451_g1	Ethylene Response Factor 110 (ERF110)	Transcriptional regulator. AP2/EREBP family	↑ 1.2 L
T116	tr7316_c200_g1	Ethylene Response Factor 110 (ERF110)	Transcriptional regulator. AP2/EREBP family	↑ 1.9 S
T117	tr3743_c922_g1	Ethylene Response Factor 115 (ERF115)	Transcriptional regulator. AP2/EREBP family	↑ 1.1 L ↑ 1.2 S
T118	tr1877_c153_g9	AINTEGUMENTA (ANT)	Transcriptional regulator. AP2/EREBP family	↑ 1.6 L
T119	tr531_c93_g1	AINTEGUMENTA-like 6 (AIL6)	Transcriptional regulator. AP2/EREBP family	↑ 3.0 L ↑ 3.4 S
T120	tr3746_c101_g1	Factor de transcripción RAV (ABI3/VP1 2)	Transcriptional regulator. AP2/EREBP family	↑ 0.7 L
T121	tr4885_c0_g1	12-oxophytodienoate reductase 2 (12-Oxo-PDA-reductase)	Jasmonic acid biosynthesis	↑ 2.5 L ↑ 1.9 S
T122	tr4270_c63_g2	12-oxophytodienoate reductase 2 (12-Oxo-PDA-reductase)	Jasmonic acid biosynthesis	↑ 4.0 L
T123	tr4270_c63_g1	12-oxophytodienoate reductase 2 (12-Oxo-PDA-reductase)	Jasmonic acid biosynthesis	↑ 2.8 L ↑ 2.5 S
T124	tr4270_c63_g8	12-oxophytodienoate reductase 2 (12-Oxo-PDA-reductase)	Biosíntesis de ácido jasmónico	↑ 2.7 L ↑ 3.7 S
T125	tr4270_c63_g13	12-oxophytodienoate reductase 2 (12-Oxo-PDA-reductase)	Jasmonic acid biosynthesis	↑ 2.6 L ↑ 4.4 S
T126	tr4270_c63_g10	12-oxophytodienoate reductase 2 (12-Oxo-PDA-reductase)	Jasmonic acid biosynthesis	↑ 8.5 L ↑ 6.3 S
T127	tr4062_c0_g2	12-oxophytodienoate reductase 2 (12-Oxo-PDA-reductase)	Jasmonic acid biosynthesis	↑ 2.2 S
T128	tr3678_c490_g1	Type A Regulator Response 3 (ARR3)	Cytokinin signalling	↓ -2.6 S
T129	tr3743_c1776_g1	Type A Regulator Response 3 (ARR3)	Cytokinin signalling	↓ -1.1 S
T130	tr5015_c629_g1	Type A Regulator Response 3 (ARR3)	Cytokinin signalling	↓ -1.9 L
T131	tr7332_c101_g3	Type A Regulator Response 9 (ARR9)	Cytokinin signalling	↓ -1.3 T

T132	tr 3873_c119_g2	KNOTTED1-like homeobox gene 3 (KNAT3)	Regulador transcripcional familia Homeobox	↓ -0.9 S
T133	tr4751_c25_g1	KNOTTED1-like homeobox gene 7 (KNAT7)	Transcriptional regulator. Homeobox family	↓ -1.3 S
T134	tr3574_c196_g1	isopentenyltransferase 5 (IPT5)	Cytokinin biosynthesis	↓ -3.6 L ↓ -2.0 S
T135	tr7325_c211_g1	isopentenyltransferase 5 (IPT5)	Cytokinin biosynthesis	↓ -1.5 L
T136	tr5133_c4_g1	UDP-glucosyl transferase 76C1	Cytokinin conjugation	↑ 0.7 S ↑ 0.8 S
T137	tr979_c108_g1	UDP-glucosyl transferase 76C2	Cytokinin conjugation	↑ 1.8 S
T138	tr4966_c42_g1	UDP-Glycosyltransferase superfamily protein	Cytokinin conjugation	↑ 1.5 S
T139	tr3691_c13_g1	UDP-glucosyl transferase 85A3	Cytokinin conjugation	↑ 0.8 S
T140	tr2527_c912_g1	UDP-Glycosyltransferase superfamily protein	Cytokinin conjugation	↑ 1.3 S
T141	tr979_c108_g8	UDP-glucosyl transferase 76E1	Cytokinin conjugation	↑ 1.4 L ↑ 1.4 S
T142	tr2527_c914_g1	Cytokinin oxidase/dehydrogenase 1 (CKX1)	Cytokinin catabolism	↑ 2.4 S
T143	tr4029_c449_g1	Cytokinin oxidase/dehydrogenase 4 (CKX4)	Cytokinin catabolism	↑ 5.0 S ↑ 5.4 S
T144	tr4738_c764_g1	ent-kaurenoic acid hydroxylase (KAO2)	Gibberellin biosynthesis	↓ -2.9 S
T145	tr3921_c82_g9	2-oxoglutarate (2OG) and Fe (II)-dependent oxygenase superfamily protein	Gibberellin biosynthesis	↓ -5.6 S
T146	tr4278_c39_g28	2-oxoglutarate (2OG) and Fe (II)-dependent oxygenase superfamily protein	Gibberellin biosynthesis	↓ -3.0 S
T147	tr937_c208_g2	2-oxoglutarate (2OG) and Fe (II)-dependent oxygenase superfamily protein	Gibberellin biosynthesis	↓ -2.7 L
T148	tr937_c235_g1	GA3 oxidase	Gibberellin biosynthesis	↓ -2.3 L
T149	tr5854_c399_g1	GA3 oxidase	Gibberellin biosynthesis	↓ -1.3 L
T150	tr7292_c143_g1	GA20 oxidase	Gibberellin biosynthesis	↓ -1.6 L
T151	tr4738_c658_g1	GA20 oxidase	Gibberellin biosynthesis	↓ -2.2 S
T152	tr5846_c486_g1	GA2 oxidase	Gibberellin catabolism	↑ 0.8 L ↑ 3.4 S
T153	tr5831_c10_g1	GAs-regulated GASA/GAST/Snakin family protein (GAST1-homolog1)	Gibberellin-regulated family protein	↑ 6.9 S
T154	tr5884_c71_g5	GAs-regulated GASA/GAST/Snakin family protein (GAST1-homolog3)	Gibberellin-regulated family protein	↓ -1.4 L
T155	tr3743_c2135_g1	GAs-regulated GASA/GAST/Snakin family protein (GAST1-homolog4)	Gibberellin-regulated family protein	↓ -2.2 L ↑ 2.7 S
T156	tr7318_c93_g1	GAs-regulated GASA/GAST/Snakin family protein (GAST1-homolog4)	Gibberellin-regulated family protein	↓ -1.8 L ↑ 5.9 S
T157	tr5846_c761_g1	GAs-regulated GASA/GAST/Snakin family protein (GAST1-homolog5)	Gibberellin-regulated family protein	↑ 1.2 S
T158	tr7316_c167_g1	HVA22 homologue D	Dehydration response	↑ 2.5 L
T159	tr3743_c1615_g1	HVA22 homologue C	Dehydration response	↑ 1.3 L
T160	tr3996_c70_g1	Alcohol deshidrogenasa (ABA2)	ABA biosynthesis	↓ -3.0 L ↓ 1.6 S
T161	tr4991_c235_g2	UDP-glucosyl transferase 71B5 (UGT71B5)	ABA conjugation	↑ 2.0 L
T162	tr4991_c629_g1	UDP-glucosyl transferase 71B6 (UGT71B6)	ABA conjugation	↑ 1.3 L
T163	tr4991_c638_g1	UDP-glucosyl transferase 71B6 (UGT71B6)	ABA conjugation	↑ 2.8 L ↑ 1.7 S
T164	tr4991_c638_g2	UDP-glucosyl transferase 71B6 (UGT71B6)	ABA conjugation	↑ 2.7 L ↑ 2.0 S

T165	tr4991_c577_g2	UDP-glucosyl transferase 71B6 (UGT71B6)	ABA conjugation	↑ 1.1 L
T166	tr4991_c526_g1	UDP-glucosyl transferase 71B6 (UGT71B6)	ABA conjugation	↑ 2.2 L
T167	tr3964_c199_g1	AURORA1 (AUR1)	Microtubule-associated protein	↑ 1.9 L
T168	tr5020_c553_g1	MAP65-3	Microtubule-associated protein	↑ 1.6 L

References:

L, leaves; **S**, stem bases (rooting zone)

Table S3. Primers designed for qPCR validation of RNA-seq data.

Gene name	Primers	Sequences (5' → 3')	Amplicon size (pb)
<i>Endoglucanase 1 (Endo1)</i>	<i>Endo1_F</i> <i>Endo1_R</i>	GGGGACAACCCAGCCAAGAC TTGCACGAGATGCGGCTAGG	122
<i>Cytokinin dehydrogenase (CitokDes3)</i>	<i>CitokDes3_F</i> <i>CitokDes3_R</i>	CCGTCAGAGAAAAGCCCGGT CCCAAACCGCAGCAACGAAC	106
<i>Ethylene-responsive transcription factor (ERF003)</i>	<i>ERF003_F</i> <i>ERF003_R</i>	TCAAAGAGCGGGTGGGTGGTCA TGCTGAACACTGTTGTCTCCTTGGCCT	102
<i>Auxin response factors (ARFs) (ARF6)</i>	<i>ARF6_F</i> <i>ARF6_R</i>	TGTCGCTGGTTTTCTCCGGCA AGGGAGCCTCACGGTCACCACT	139
<i>Gretchen hagen 3 (GH3-1)</i>	<i>GH3_F</i> <i>GH3_R</i>	GTTCCGTTTTGTGTCGCTCT ACGATCCTGACCGAAATCAC	160
<i>1-aminocyclopropane-1-carboxylate oxidase (ACO)</i>	<i>ACO_F</i> <i>ACO_R</i>	AACTCCTCAAGGACGGCAAA AATAACCCGGTGCTCCACAC	125
<i>Fructose-bisphosphate aldolase (FBA)</i>	<i>FBA_F</i> <i>FBA_R</i>	CCTTCTCATTCGGGCGGGCG GCCCAGAGTGGCCTCGGAGT	128
<i>Cellulose Synthase A Catalytic 8 (CSACat8)</i>	<i>CSACat8_F</i> <i>CSACat8_R</i>	CCATCTCTTTGCCGTCTTCC TATCAGCAGCGTCGTCCACT	136
<i>Isoprene Synthase, Chloroplastic-like (ISC-like)</i>	<i>ISC-like_F</i> <i>ISC-like_R</i>	AGACGCTGTTTCGCAGATGGGACAT AGCCAGTTCGTTACGCAGTTGT	100

Table S4. Primers designed for the quantification of age-related gene expression.

Gene name	Primers	Sequences (5' → 3')	Amplicon size (pb)
<i>Gretchen hagen 3 (GH3-1)</i>	<i>GH3_F</i> <i>GH3_R</i>	GTTCCGTTTTGTGTCGCTCT ACGATCCTGACCGAAATCAC	160
<i>Auxin response factor (ARF6)</i>	<i>ARF6_F</i> <i>ARF6_R</i>	TGTCGCTGGTTTTCTCCGGCA AGGGAGCCTCACGGTCACCACT	139
<i>Arabidopsis response regulator 1 (ARR1)</i>	<i>ARR1_F</i> <i>ARR1_R</i>	CCCTCCTGTGATTGGGCTGC ATCCTGTTGCCGTGCTCCAC	107
<i>Transport Inhibitor Response 1 (TIR1)</i>	<i>TIR1_F</i> <i>TIR1_R</i>	GCATGTAAGCTGCTTGGTCA AAAATCAGGCATGTCGAACC	153
<i>Tryptophan aminotransferase in Arabidopsis 1 (TAA1)</i>	<i>TAA1_F</i> <i>TAA1_R</i>	GGGAACAGGTGACAAACTCAA GGCTTACATGGACCTGAAGA	157
<i>Scarecrow-Like 1 (SCL1)</i>	<i>SCL1_F</i> <i>SCL1_R</i>	AGGCGCTCTTCCATTATTCG CCTTCGCAGGCAATTACGTT	130
<i>Aintegumenta-Like 1 (AIL1)</i>	<i>AIL1_F</i> <i>AIL1_R</i>	AGGCACTGGCGTTGGTGGTG AGATGGCCGGGTCCCCCAAG	142