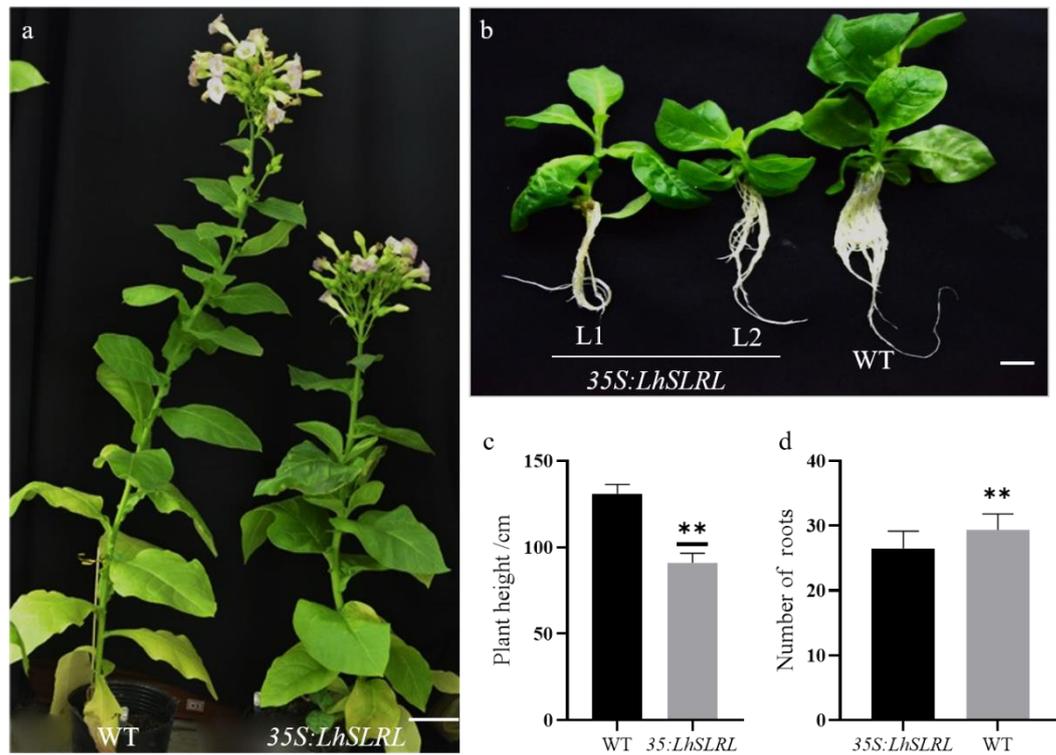


## Supplementary materials



**Figure S1. Morphological phenotypes of tobacco overexpressing *LhSLRL*.**

(a) Phenotypes of 5-month-old wild-type and transgenic plants.

(b) Phenotypes of the 1-month-old wild-type and transgenic plants.

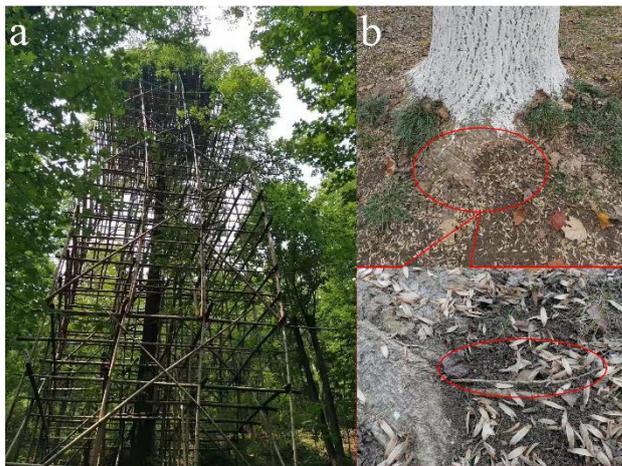
(c) Measurement of plant height in wild-type and transgenic lines (a). Error bars:  $\pm$  SD. \*P < 0.05; \*\*P < 0.01.

(d) Number of roots in wild-type and transgenic lines (b). Scale bars: 10 cm (a) and 1 cm (b).



**Figure 2. Morphological phenotypes of *Arabidopsis* overexpressing *LhRGA*.**

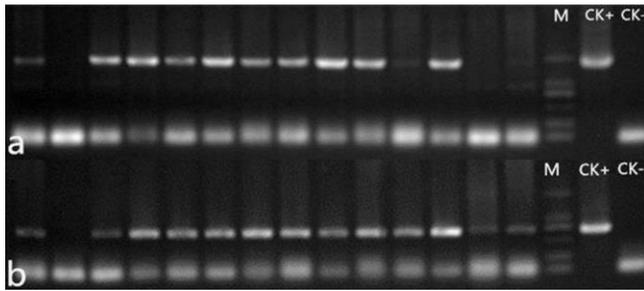
Phenotypes of the 60-day-old wild-type and transgenic plants. Scale bar = 1 cm.



**Figure S3. Sampling method.**

(a) The stems were collected from the top of the 25-year-old *Liriodendron* hybrids by scaffolding.

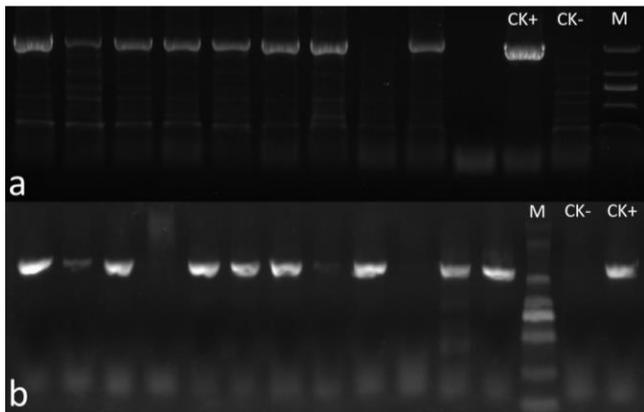
(b) *Liriodendron* hybrids is a shallow-rooted tree species, and its lateral roots are mainly distributed in the 0-20cm soil layer. The lateral roots of *Liriodendron* hybrids were used as q-PCR materials.



**Figure S4. PCR testing for *Arabidopsis* overexpressing *LhSLRL*.**

(a) Perform PCR using scf7 180-F and scf7 180-R. CK+: plasmid DNA, CK-: Wild-type DNA.

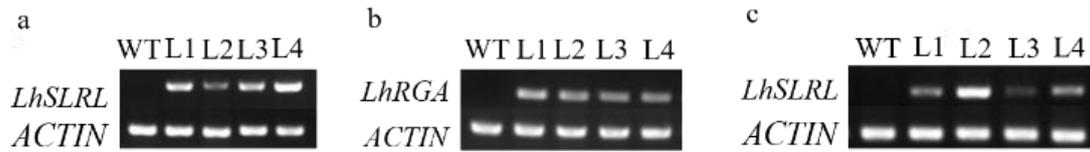
(b) Perform PCR using 35S-F and 35S:LhSLRL-R. CK+: plasmid DNA, CK-: Wild-type DNA.



**Figure S5. PCR testing for *Arabidopsis* overexpressing *LhRGA*.**

(a) Perform PCR using LOC 32933-F and LOC 32933-R. CK+: plasmid DNA, CK-: Wild-type DNA.

(b) Perform PCR using 35S-F and 35S:LhRGA-R. CK+: plasmid DNA, CK-: Wild-type DNA.

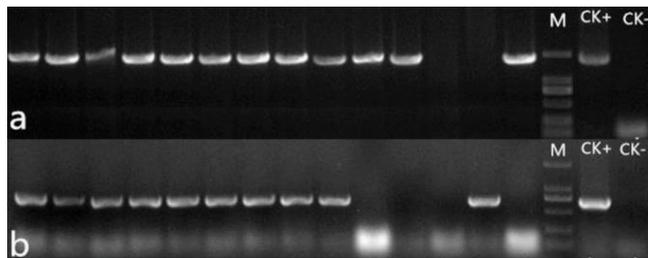


**Figure S6. RT-PCR analysis of wild types and *Arabidopsis*/tobacco overexpressing *LhDELLAs*.**

(a) RT-PCR analysis of wild types and *Arabidopsis* overexpressing *LhSLRL*.

(b) RT-PCR analysis of wild types and *Arabidopsis* overexpressing *LhRGA*.

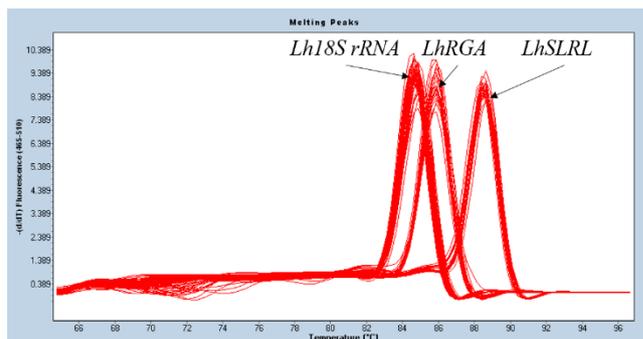
(c) RT-PCR analysis of wild types and tobacco overexpressing *LhSLRL*.



**Figure S7. PCR testing for tobacco overexpressing *LhSLRL*.**

(a) Perform PCR using scf7 180-F and scf7 180-R. CK+: plasmid DNA, CK-: Wild-type DNA.

(b) Perform PCR using 35S-F and 35S: *LhSLRL*-R. CK+: plasmid DNA, CK-: Wild-type DNA.



**Figure S8. The thermal profile of qRT-PCR****Table S1 DELLA proteins of different species**

Family	species	DELLA	The serial number
Poaceae Barnhart	<i>Brachypodium distachyon</i>	SLN1	XP_003560731.1
	<i>Oryza sativa</i>	SLR1	BAE96289.1
	<i>Zea mays</i>	D8	NP_001130629.2
		D9	NP_001296780.1
	<i>Hordeum vulgare</i>	SLN1	Q8W127.1
	<i>Triticum aestivum</i>	Rht	AGE81922.1
Brassicaceae Burnett	<i>Arabidopsis thaliana</i>	GAI	NP_172945.1
		RGA	NP_178266.1
		RGL1	NP_176809.1
	<i>Brassica campestris</i>	RGL2	NP_186995.1
		RGL3	NP_197251.1
		RGA1	XP_009101333.1
Cucurbitaceae	<i>Cucurbita maxima</i>	RGA2	Q5BN22.1
		GAIP	Q6EI06.1
Vitaceae Juss.	<i>Vitis vinifera</i>	GAIP-B	Q6EI05.1
Malvaceae Juss.	<i>Gossypium hirsutum</i>	GAI1	AEK06229.1
		SLR1a	AAV28970.1
Amborellaceae Pichon	<i>Amborella trichopoda</i>	SLR1b	AAO62757.1
		GAI1	XP_006826893.1
Nymphaeaceae	<i>Nymphaea colorata</i>	RHT-1	XP_006829673.3
		GAI1	XP_031491894.1
Solanaceae Juss.	<i>Solanum lycopersicum</i>	GAI1	XP_031497443.1
Funariaceae	<i>Physcomitrella patens</i>	GAI	NP_001234365.1
		DELLAa	XP_024361039.1
Selaginellaceae Willk.	<i>Selaginella kraussiana</i>	DELLAb	XP_024403888.1
		DELLA	ABU63412.1
Nelumbonaceae	<i>Nelumbo nucifera</i>	SLR1-like	XP_010249953.1
		GAI-like	XP_010254273.1
		GAI1	XP_010264458.1
		GAI1-like	XP_010274729.1
Ranunculaceae	<i>Aquilegia coerulea</i>	DELLA1	PIA63880.1
		DELLA2	PIA26570.1
		DELLA3	PIA65400.1

**Table S2 Primers used for gene cloning**

gene	Primer name	Primer sequence (5'-3')
LhSLRL	scf7 180-F	ATCTGCACATCCAAACACACCATTC
	scf7 180-R	ACAGCTTATTCTATTGTATCCCGAG
LhRGA	LOC 32933-F	TACATATATAGGCATGAACTCGTCC
	LOC 32933-R	TCAACCCGAGTCACTCTCTCCCGAA

**Table S3 Primers used for qRT-PCR, RT-PCR, and PCR testing**

Primer name	Primer sequence (5'-3')
Lh18SrRNA-F	TGTCGAGCAGGAAGCAGATCACAAC
Lh18SrRNA-R	TTGTTATTTATTGTCACCTACCTCCC
qRT-LhSLRL-F	TGTCGAGCAGGAAGCAGATCACAA
qRT-LhSLRL-R	GCCCAGGTGGAGTGGCTTGAAG
qRT-LhRGA-F	TCGACCGGTTCAATGAATCACTGC
qRT-LhRGA-R	CGTCTCATGTCGTTCCACTCGCTC
AtACTIN2-F	CAGTGTCTGGATCGGTGGTT
AtACTIN2-R	TGAACGATTCCTGGACCTGC
1RT-LhSLRL-F	GAAATCGCATTGGCTGGGTC
1RT-LhSLRL-R	GCTTGATTGGCGGTGAAGTG
RT-LhRGA-F	AGAACATCAGGACAGTCGCC
RT-LhRGA-R	TCCTGACCGTTGTACATGGC
NtACTIN-F	TGAGCTTCCAGATGGGCAAAT
NtACTIN-R	AGCCACCACTAAGCACAACG

2RT-LhSLRL-F CCAAGCTCTCGGAGATCGAC

2RT-LhSLRL-R GTTCTGTGGGTCCGAGAAGG

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35S-F TGAAGATAGTGGAAAAGGAAGGTG

35S: LhSLRL -R TGAGACGGTGGTGATTGGTG

35S: LhRGA -R GCAATCCGAGCCGTAAACTGATG

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**Table S4 Identity matrix for LhSLRL/LhRGA and five DELLA proteins in**

*Arabidopsis*

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Amino acid identity	AtGAI	AtRGA	AtRGL1	AtRGL2	AtRGL3
LhSLRL	39.74%	40.07%	37.95%	37.46%	35.83%
LhRGA	55.54%	55.37%	52.12%	51.63%	50.00%

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>LhSLRL

ATGGGACCATACGACACGGCCATCTCCCCACCACCACCAACTCCTCACC  
ATGCGGCCCATCCAAGCTCTCGGAGATCGACGGCCTCCTCGCAGGGGCGG  
GCTACCACATCCGGTCGTCGGATCTACGCCACGTGGCTCAGAGGCTGGAG  
CATCTGGAGTCAGCGATGGTCAACCAAGCTCCCGAGAACATCTCCAACCT  
AGCCACAGAGGCCGTACTACAACCCCTCCGACCTCGCGTCCTGGGTCCG  
AGTCCATGCTCTCCGAGTTCCACCAATCACCACCGTCTCAGCTCCTCCCC  
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CGACACCTGCACGGACCCGCTGCAGCAGCAGCAGCTGACGGTCATGGCGG  
CACTGGAGGAGGAGGACTCCGGCATCCGGCTCGTTCACCTGCTGATGACT  
TGCGCCGAGTCGATGCAACGTGGCGAAATCGCATTGGCTGGGTCTCTGAT  
CGACGAGATGCGCCTCCTCCTGACACGCGTCAACACCGGATGCGGCATCG  
GCAAGGTCGCGAGCTACTTCATAGACGCGCTAAGCCGGCGGCTCTTCTCA  
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CACGTCATCGACTTCAACCTGATGCACGGCCTGCAATGGCCCCGCCCTGAT  
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TGGGCCCTAGGGAAGCCGTGGCTGTCAATTCGGTAATGCAGCTCCACCGG  
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GCTACTGCGTGGAGGAGAACGGCGGGTGCCTGACCTTGGGCTGGCATAGC  
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>LhRGA

ATGAAAAGAGAACATCAGGACAGTCGCCGCAGCATGGCAACGACTGGGA  
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TCGAATCCATGCTCTCCGAATTC AATACGCCATCCGAACCGGCCATCTCC  
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GGCCATTCCCGGCGAGGTTGTTTATGGGAGAGGGGAATTAGATTTGGGCG  
AGCCAAGAGAGAAGAAACGGATGAGATTGGGGACTGCAGTGGCGGCCGC  
AGCTGAGTCGGCTCGCCAGTCGTCCTGGTCGACTCACAGGAGACCGGGA  
TCCGACTCGTTCATTGCTGATTGCCTGTGCCGAGGCCGTCCACCGGGACG  
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