

**Supplementary TABLE S1.** List of PCR primers

	Forward primer	Reverse primer
<b>Vector construction</b>		
35S::SPL13A	AAA tctaga AGTCATGGATTGGGATTTGAAG <u>TGCGCATTGAGCTTGTAAAGT</u> CACCCATCCAATCTCAAG	<u>ACTTAACAAGCTCAATGCGCA</u> ATCAGAGTCGTGAACATGGG GGT gagctc TACTGCCAAGAAAATGGAAGAG
35S::SPL13A(rSPL13A)-GFP	AAA tctaga AGTCATGGATTGGGATTTGAAG <u>GGTGCGGGAAGCGGCGGA</u> GGTAGTGCCGGAGGTAGCATGAGTAAAGGAGAAGAAC	<u>TGCGCGCTTCGCGCACCC</u> CTGCCAAGAAAATGGAAGAG ATT gagctc TTATTTGTATAGTTCATCCATG
35S::AtMIR156B	TTT tctaga TTTGACAAAACATCATGTCTCTCCA	TTC gagctc CTTCAAACCAAACGCAAAGACTTT
35S::AtMIR172B	ATC tctaga CTAGTCTTGTGTGCACCCATTTATGTG	CTC gagctc CTC AAGTCAAGATCAAAGGCAAAATAG
<b>qRT-PCR</b>		
SPL13A	ACAATCGGCGTCGACGCAAG	TGTGGAAGTGTGTTGCCTG
FT1	ATGGAGAATAGGAGTGATCCTTGCTG	TTCTCTAAGGTTGGTTACTTGG
FT8	GAGGGAGTATTTTTRCACTGGTTGGT	TAAAGATCAGAAAARTTCCGGGTA
MADS5	ACTCCAACAACAGAGCAGC	AAGCCCTCATCTTCTGGAAC
ACTIN	GGAGTGAGCCACACAGTTCC	ATAGCTTTCTCCACAGAGG
NPTII	TGAATGAACAGGACGAG	ATACTTTCTCGGACGAGCA
<b>Stem-Loop PCR</b>		
miR156, cDNA synthesis		GTTGGCTCTGGTGCAGGGTCCGAGGTATTGCACCAGAGCCAACGTGCTC
miR156, qRT-PCR	TCGCGTGACAGAAGAGAGT	GTGCAGGGTCCGAGGT
miR172A, cDNA synthesis		GTTGGCTCTGGTGCAGGGTCCGAGGTATTGCACCAGAGCCAACGTGCTC
miR172A, qRT-PCR	TCGCGAGAATCTTGATGATG	GTGCAGGGTCCGAGGT
miR172B, cDNA synthesis		GTTGGCTCTGGTGCAGGGTCCGAGGTATTGCACCAGAGCCAACATGCAG
miR172B, qRT-PCR	TCGCGAGAATCTTGATGATG	GTGCAGGGTCCGAGGT
U6, cDNA synthesis		CGATTTGTGCGTGTATCCTTGC
U6, qRT-PCR	CGGGGACATCCGATAAAAATTGGAACG	CGATTTGTGCGTGTATCCTTGC

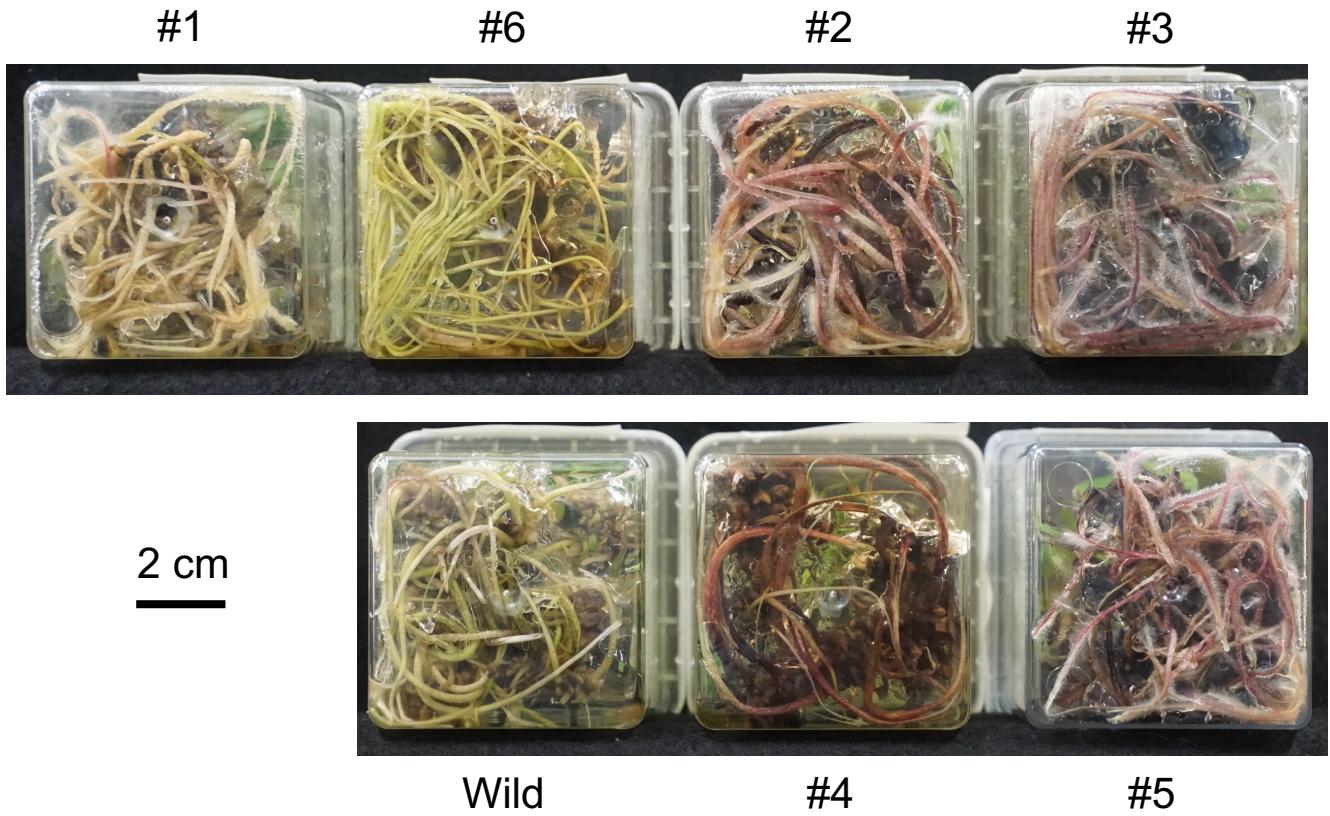
Lowercase letters indicate restriction sites. Overlapped regions are shown by underlines.

**Supplementary TABLE S2.** GenBank/DDBJ/EMBL accession numbers of Arabidopsis SPL sequences

SPL	Accession number
AtSPL13	NP_568731
AtSPL2	NP_199141
AtSPL10	NP_001323272
AtSPL11	NP_001077603
AtSPL8	NP_973738
AtSPL9	AY046007
AtSPL15	NP_191351
AtSPL6	NP_177077
AtSPL3	U50647
AtSPL4	NP_175723
AtSPL5	CAB56772
AtSPL7	OAO96340
AtSPL14	NP_173522
AtSPL16	NP_177784
AtSPL12	NP_191562
AtSPL1	NP_850468



**Supplementary Figure S1** The flower of the line #3 transformed plant (Figure 2D) consisted of (from left to right) four tepals, one pistil, and three stamens.



**Supplementary Figure S2** Root colors of transformed plants (lines #1–#6) and non-transformed plants (Wild) *in vitro*. Photographs were taken from the bottom of the culture vessels.



**Supplementary Figure S3** The transformed plants of lines #3 and #4, which were taken out of the pots (Figure 3). The line #3 plant consisted of an elongating shoot with 4 scaly leaves, and the line #4 plant consisted of an elongating shoot with 7 scaly leaves. The upper half of scaly leaves were deeply anthocyanin-pigmented in the line #4 plant.





**Supplementary Figure S4** Abaxial side of scaly leaves of the transformed plants from lines #5, #3, and #2, and of two non-transformed plants (Wild).



**Supplementary Figure S5** Appearances of a callus-derived non-transformed *L. formosanum* plant. Note that this bulb was subject to chilling to stimulate shoot elongation and flowering.