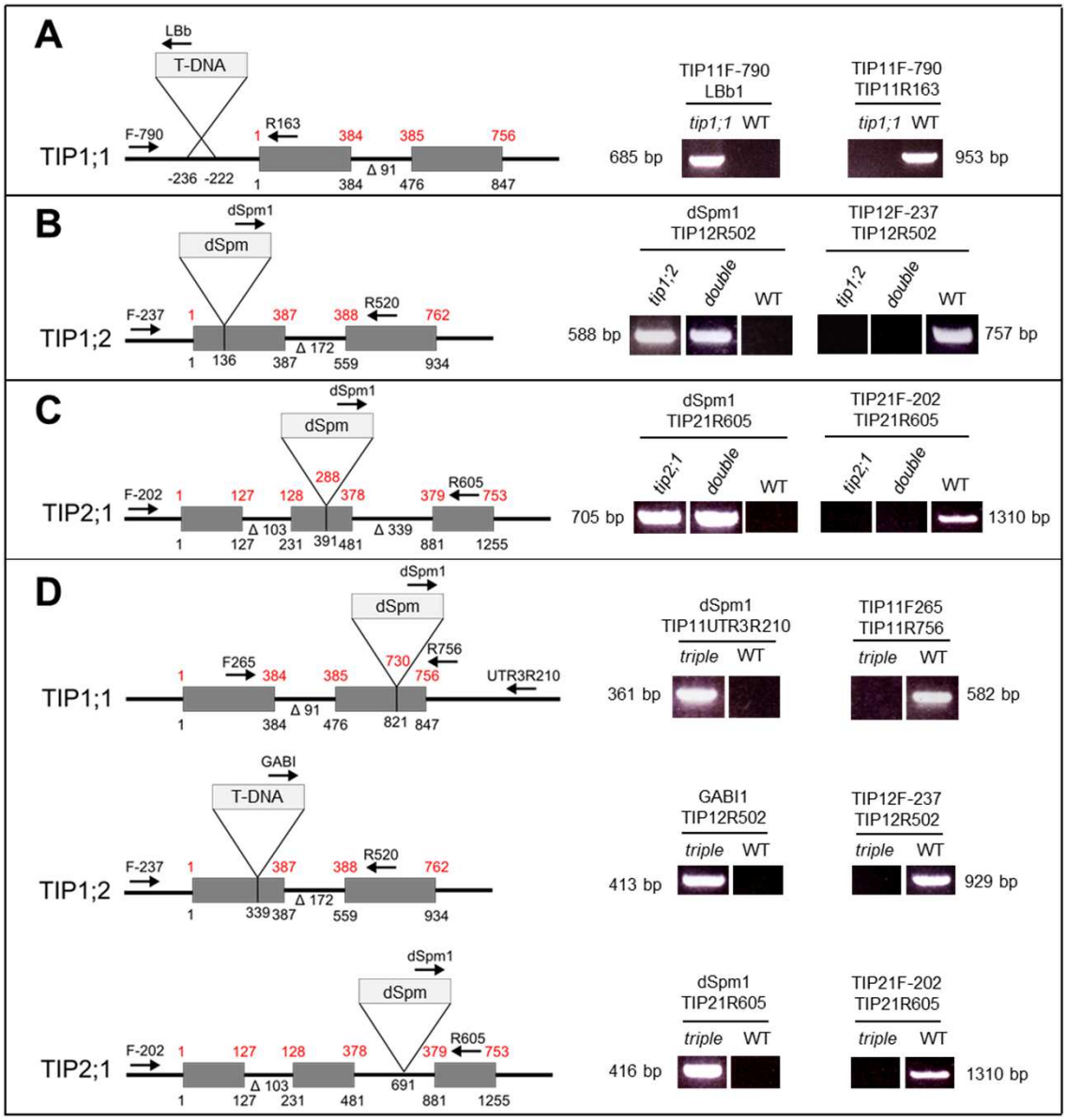
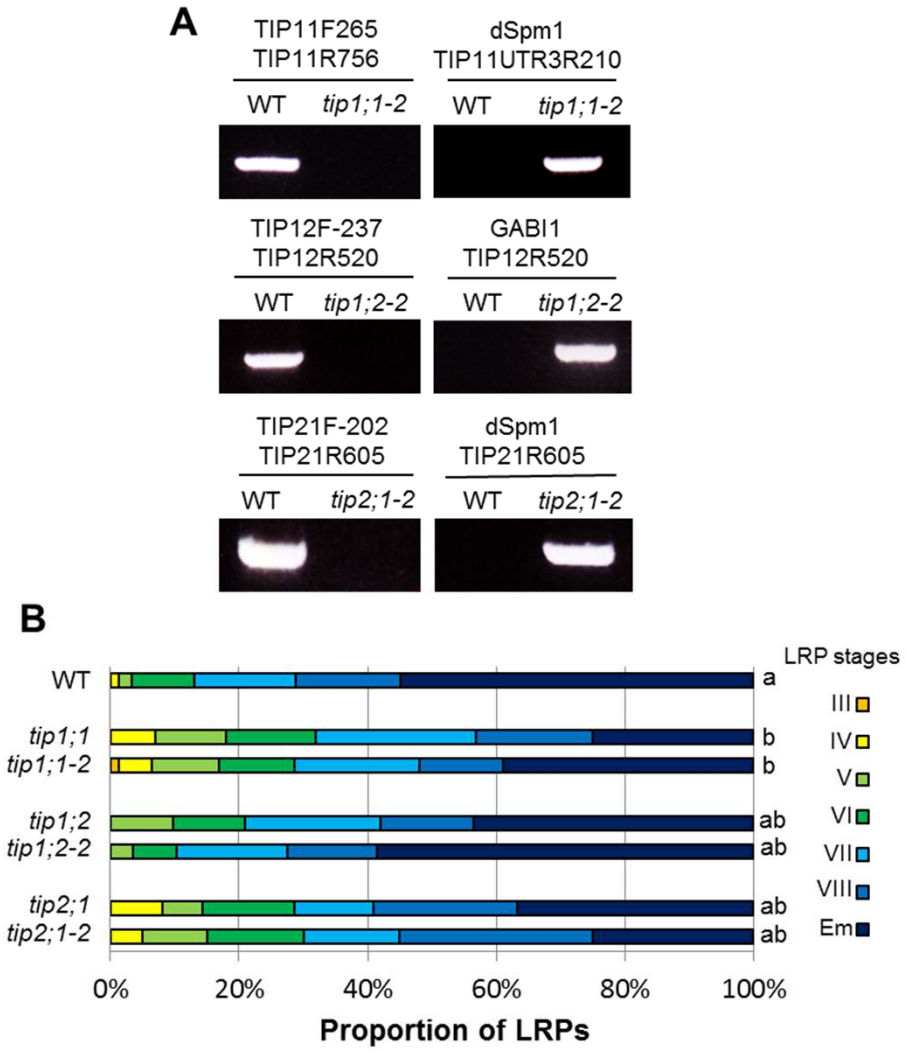


Supplemental Figure 1. Verification of the homozygosity of the insertion in the different *tip* mutant lines. Numbers in red and black indicate the position on the cDNA and the genomic DNA, respectively (position 1 starting at the start codon). Numbers on the primers refer to the cDNA positions. A, Insertion in the *tip1;1* single mutant. The T-DNA insertion induced the loss of 13 bp within the 5' non-coding region. B, Insertion in the *AtTIP1;2* gene of *tip1;2* single and *tip1;2 x tip2;1* double mutant. C, Insertion in the AtTIP2;1 gene of *tip2;*1 single and *tip1;2 x tip2;1* double mutant. D, Insertions in the *tip1;1 x tip1;2 x tip2;1* triple mutant. The left panels show the PCR analyses performed from the genomic DNA of the different wild-type and mutant lines using the indicated primers.



Supplemental Figure 2. Independent *tip* mutants exhibit delay in LRP development. A, Verification of the dSpm or T-DNA insertions in the second, independent batch of *tip* mutants: *tip1;1-2*, *tip1;2-2* (Schussler et al., 2008) and *tip2;1-2* (Schüssler and Schjoerring, unpublished data) by PCR using the primers given in Table1, according to the scheme shown in Figure 1. B, Developmental stage distribution (Developmental stage distribution (from III to VIII, Em: emerged; (Malamy and Benfey, 1997)) of LRP 42 h pgi. n = 20 – 77.Statistical analysis was performed using standard contingency tables to sequentially compare relevant lines (see Materials and Methods).

Supplemental information

Supplemental Table 1. Primers used to create multiple *tip* mutant lines and verify the obtained lines

Gene	Primer name	Primer sequence
AtTIP1;2	TIP12F-652	5'- CCGAAAAAGTTACCAGCCCAT -3'
	TIP12UTR3R 371	5'-AAAAACGGAAATGAAAACCAAAAA-3'
AtTIP2;1	TIP21F-683	5'-AATCACGTTAAACCGGCCATATTACTTA-3'
	TIP21F132	5'-GCTGACGTCGGACGCTGC-3'
	TIP21R395	5'- GAAATCAGCAGAAGCAAGAGGA-3'
	TIP21R729	5'-GAAATCAGCAGAAGCAAGAGGA-3'
	TIP21UTR3R 371	5'-ATAGGTTGTCATACAACAATTGCCAGAGT-3'
Transposon	dSpm1	5'-CTTATTTCAGTAAGAGTGTGGGGTTTTGG-3'

Supplemental Table 2. Primers used for RT-qPCR to determine the expression level of all *TIP* isoforms in the *tip* mutant lines and wild-type.

Gene name	Primer name	Primer sequence	Ref.
AtTIP1;1	TIP11F129	5'-CGGCGTTGGCTGAGTTCATTTC-3'	QP
	TIP11R195	5'-AAAGCCATGCCAGAGCCTGAAC-3'	
AtTIP1;2	TIP12F458	5'-TCGCCGCTTGTTTCCTCCTTAG-3'	QP
	TIP12R520	5'-AGAGACCGAACGCTGGAATTGG-3'	
AtTIP1;3	TIP13F517	5'-TCATTGCGCCTTTGGCGATTGG-3'	QP
	TIP13R594	5'-TCATCGATGCACCGTCGAAAGC-3'	
AtTIP2;1	TIP21F114	5'-TGCCATTGCCTACGCAAAGCTGAC-3'	A
	TIP21R211	5'-CGGCCACGAAGAGAGCAAAACCAT-3'	
AtTIP2;2	TIP22F370	5'-AATGGCGAGAGCGTACCGACTCAT-3'	A
	TIP22R519	5'-AGCAATGGTCCCGAGTGAACCTTT-3'	
AtTIP2;3	TIP23F358	5'-TCAGTGTCTTGGCTCCATCGTC-3'	QP
	TIP23R426	5'-GTCGGTACGCTCTTGCCATTAG-3'	
AtTIP3;1	TIP31F599	5'-GGCTCACAACAAACGGCATGAG-3'	QP
	TIP31R668	5'-AGTCCATTAACCGCTCCAACACC-3'	
AtTIP3;2	TIP32F123	5'-AGGCTCAATCCTCGCTCTAGACAA-3'	A
	TIP32R222	5'-TGCATGAGCTAACGCCACCAGA-3'	
AtTIP4;1	TIP41F323	5'-CCACATCAGCGTATTCCGTGCATT-3'	A
	TIP41R369	5'-TCCCATTCCTCCGGTGAGGTAACT-3'	
AtTIP5;1	TIP51F398	5'-AAAGTAACCGTCATGGAACAGCAC-3'	QP
	TIP51R466	5'-TGCTCCAAATCCAGTCATTTCTCC-3'	
ACT1	ActinF	5'-TGGAACTGGAATGGTTAAGGC-3'	S
	ActinR	5'-TCTCCAGAGTCGAGCACAATA-3'	
TUA4	a-Tubulin	5'-GGTCACCACCTGGAACAACT-3'	S
	a-Tubulin	5'-TGGCACCATCAAGACAAGACAAAGA-3'	
UBQ10	UbiquitinF	5'-CACACTCCACTTGGTCTTGCGT-3'	L
	UbiquitinR	5'-TGGTCTTTCCGGTGAGAGTCTTCA-3'	
MAF5	MAF5F	5'-TTTTTTGCCCCCTTCGAATC-3'	C
	MAF5R	5'-ATCTTCCGCCACCACATTGTAC-3'	

The numbers refer to the position of the nucleotide sequence compared to the ATG start codon. A: Alexandersson *et al*. (2005) C: Czechowski *et al*. (2005); L: Li *et al*. (2006); QP: Quantprime (Arvidsson *et al.*, 2008); S: Schussler *et al.* (2008).

Supplemental Table 3. Primers used for cloning.

Gene	Primer name	Primer sequence
AtTIP1;1	U-TIP11	5'-*GGCTTAAU*ATGCCGATCAGAAACATC-3'
	TIP11-U	5'-*GGTTTAAU*TCAGTAGTCTGTGGTTGG-3'
AtTIP1;2	U-TIP12	5'-*GGCTTAAU*ATGCCGACCAGAAACATC-3'
	TIP12-U	5'-*GGTTTAAU*TCAGTAATCGGTGGTAGG-3'
AtTIP2;1	U-TIP21	5'-*GGCTTAAU*ATGGCTGGAGTTGCCTTT-3'
	TIP21-U	5'-*GGTTTAAU*TTAGAAATCAGCAGAAGC-3'
YFP	U-YFP	5'-*GGCTTAAU*ATGGTGAGCAAGGGCGAG-3'
	UBOX-U	5'-*GGTTTAAU*TAAGGAATCCTTAATTAAGC-3'
gAtTIP1;2	attB1-S1	5’-GGGGACAAGTTTGTACAAAAAAGCAGCAGGCT TCTTCAGTCGCTGTGTCCA-3’
	attB2-S1	5’-GGGGACAAGTTTGTACAAAAAAGCTGGGTACC AGTAATCGGTGGTAGGCAAT-3’
gAtTIP2;1	attB1-D1	5’-GGGGACAAGTTTGTACAAAAAAGCAGGCTTCG AGAAAGATGCAAAGCAAA
	attB2-D1	5’-GGGGACAAGTTTGTACAAAAAAGCTGGGTAGA AATCAGCAGAAGCAAGAGGA

The sequences for the formation of the “sticky ends” during USER cloning are indicated in *italics. g* indicates that the primers were used to clone the genomic DNA (starting ~3kb upstream sequence of the translational start codon and ending before the stop codon)