Supplemental Material

Supplemental Table S1. List of PCR primers used in the present study.

Figure S1. DNA polymorphisms used for mapping. A, dCAPS marker to score a SNP in intron 3 of *GmTFL1a*.

Figure S2. Structure of the plasmids pMDC123-GFP and pMDC123-GFP-Dt1.

Figure S3. 139-bp sense and antisense sequences in exon 4 of *GmTFL1b* used for virus-induced gene silencing.

Figure S4. Stem growth habit of twenty-one indeterminate #6-22Dt1 plants that were infected with the recombinant viruses that contained 139-nucleotide sense or anti-sense sequences of exon 4 of the *GmTFL1b* gene.

Figure S5. Position of polymorphic sites and their flanking sequences in the *GmTFL1a* (A) and *GmTFL1b* (B) genomic sequences.

Supplemental Table S1 List of PCR primers used in the present study

Target gene (region/site)	Primer name	Primer sequence
Primers for isolation and sequence analysis		
GmTFL1a/b (Exons 1 to 4)	TFL1-F	5'-AAGAATGCCTTTAGAGCCTC-3'
	TFL1-R	5'-GTGCATTGAAGTAGACAGCA-3'
GmTFL1a (5' region)	TFL1a-ex1-R1	5'-GGACCTCATATCACCACCCTCAATCT-3'
	TFL1a-ex1-R2	5'-CCTTGGGCTTGGTGTTGACAGTGGAA-3'
GmTFL1a (3' region)	TFL1a-ex4-F1	5'-ACTCCACCCACTTCAAGGGACCACTT-3'
	TFL1a-ex4-F2	5'-GCAAATTCGCAGCAGAGAACGACCTT-3'
Primers for mapping/cosegreagion analysis		
GmTFL1a (SNP in intron 3)	TFL1a-in3-F	5'-GATATTGATGAGAGAGTGACG-3'
	TFL1a-R	5'-GTGCATTGAAGTAGACAGCA-3'
GmTFL1b (FLP/CAPS in intron 1	TFL1b-in1-F	5'-GAGTTACAACAAGAAGCAAGTT-3'
	TFL1b-in1-R	5'-GCACCGAAAAAGGGGGACATTT-3'
Primers for transformation		
GmTFL1b (4.216-bp region)	TFL1b-transform-F	5'-GAAGGGTCAATCCATCAAGTTAGC-3'
	TFL1b-transform-R	5'-CGGCAATTTAATGAGGATCA-3'
Primers for VIGS		
GmTFL1b (Exon 4)	TFL1b-sen-F	5'-TGTCCTGTTCAAGCAAAAGC-3'
	TFL1b-sen-R	5'-TACACGCGTCGTTTCCCTCTGTGCATTG-3'
	TFL1b-ant-F	5'-CTAAAGAGTACCCACTTCAAGGGACCACT-3'
	TFL1b-ant-R	5'-CCAGCAGCTACTTAGCTATAGC-3'
Primers for polymorphism analysis		
GmTFL1b (SNP in promoter)	TFL1b-pro-F	5'-CCATGCTTAATCGGCATCACT-3'
	TFL1b-pro-R	5'-GGTGGTGGCATAGTTTAATT-3'
GmTFL1b (SNP in exon 4)	TFL1b-ex4-F	5'-GGCTGCTGTCTACTTCAATGTCTAG-3'
	TFL1b-ex4-R	5'-GCCACATGTGAAGATCAACTTCCA-3'
Primers for RT-PCR		
cDNA synthesis	B26	5'-GACTCGAGTCGACATCGA-polydT$_{(17)}$-3'
GmTFL1a/b	TFL1a/b-RT-F	5'-AGGCACAACAGATGCCACAT-3'
GmTFL1a	TFL1a-RT-F	5'-GCTCCACTACCTCTTCTCTCTT -3'
	TFL1a-RT-R	5'-GGTTGAAGCAGTGGCAAAAT-3'
GmTFL1b	TFL1b-RT-F	5'-TTAGCTCCTCCTCTTCCTTG-3'
	TFL1b-realtime-F	5'-CAGATTGTGTTTCGCTGGTTGCA-3'
	TFL1b-RT-R	5'-GGCAAAACCAGCAGCTACTT-3'
β-tubulin	β-tub-F	5'-GACCCGATAACTTCGTGTTC-3'
	β-tub-R	5'-GAGCTTGAGTGTTCGGAAAC-3'
18S ribosomal RNA	SOY18SrRNA-861F	5'-TGATTAACAGGGACAGTCGG-3'
	SOY18SrRNA-1013R	5'-ACGGTATCTGATCGTCTTCG-3'

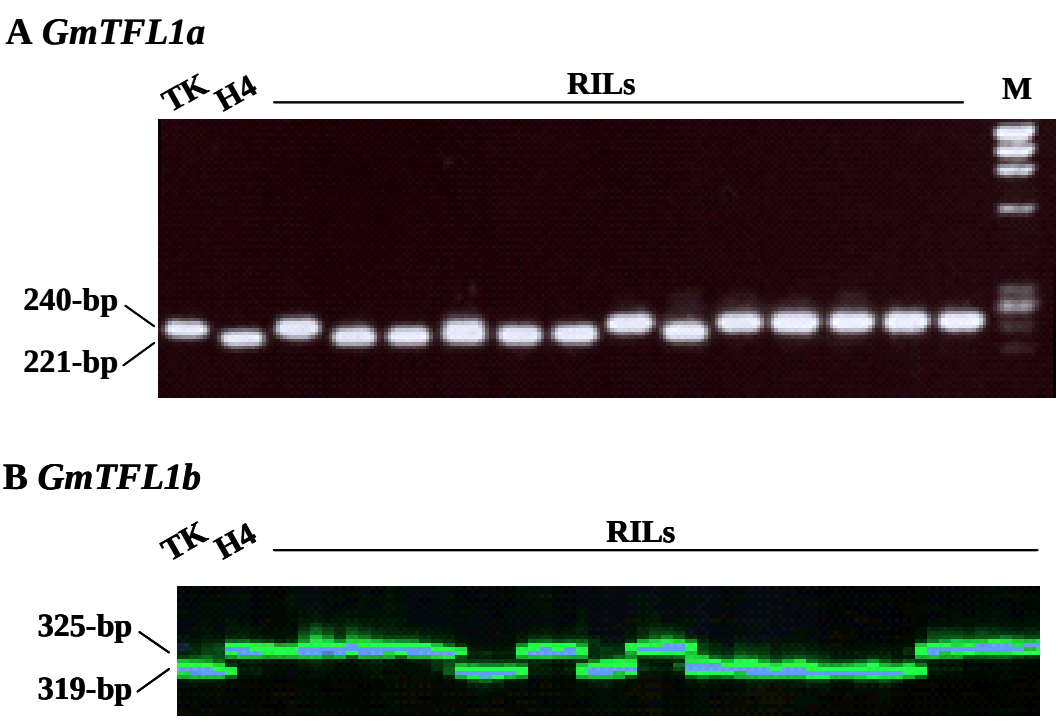
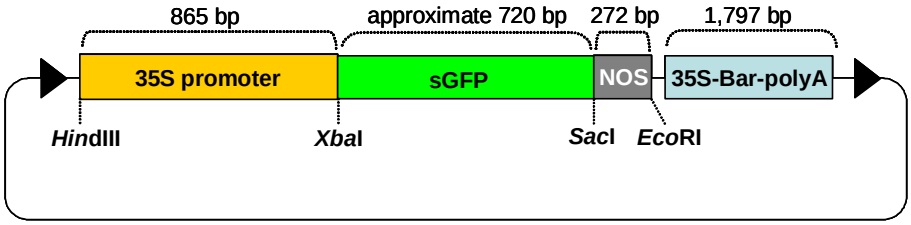
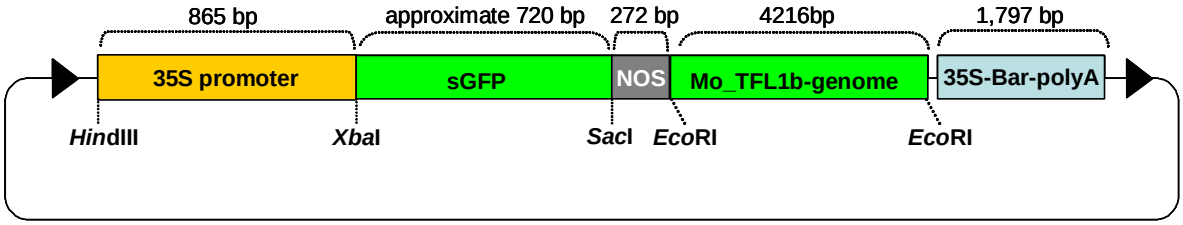


Figure S1. DNA polymorphisms used for mapping. A, dCAPS marker to score a SNP in intron 3 of *GmTFL1a*. Digestion with *Mae*II of amplified 240-bp fragments produced a 240-bp undigested fragment for TK and 221-bp and 19-bp digested fragments for H4. M; ØX174/*Hae*III digest, B, FLP marker to detect a six-nucleotide difference in length in intron 1 of *GmTFL1b*. The forward primer was labeled by a fluorescent dye. The FLP was detected by the ABI 377 sequencer with GeneScan software.



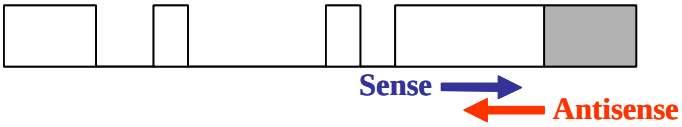
pMDC123-GFP



pMDC123-GFP-Dt1

Figure S2. Structure of the plasmids pMDC123-GFP and pMDC123-GFP-Dt1. A binary vector pMDC123-GFP was constructed by replacing the Gateway cloning site in pMDC123 with a green florescent protein gene (sGFP) controlled by CMV 35S promoter (Sato et al., 2007). A 4,216-bp genomic region that contained the putative promoter and coding region of *GmTFL1b* from an indeterminate cultivar Moshidou Gong 503 was inserted into the *Eco*RI site between the GFP and Bar (phosphinothricin resistance gene) cassettes in the pMDC123-GFP vector. NOS; *A. tumefaciens* nopaline synthase terminator.

A



B

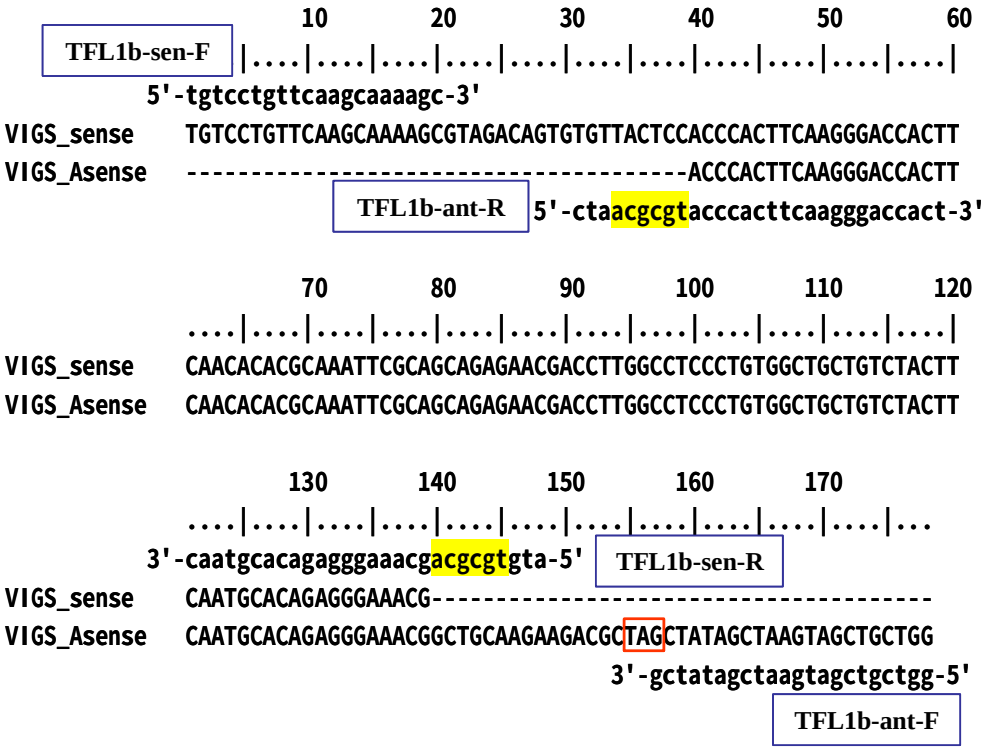


Figure S3. 139-bp sense and antisense sequences in exon 4 of *GmTFL1b* used for virus-induced gene silencing. A, Positions of 139-bp segments inserted in CMV-A1 vector. Sense and antisense segments are overlapped for an interval of 100 bp. Blank boxes and grey box indicate exons and 3' UTR, respectively. B, Inserted sequences and positions of primers used. A *Mlu*I site (ACGCGT) was attached in the 5' part of reverse primers for the subsequent plasmid construction. The stop codon is indicated by red square.

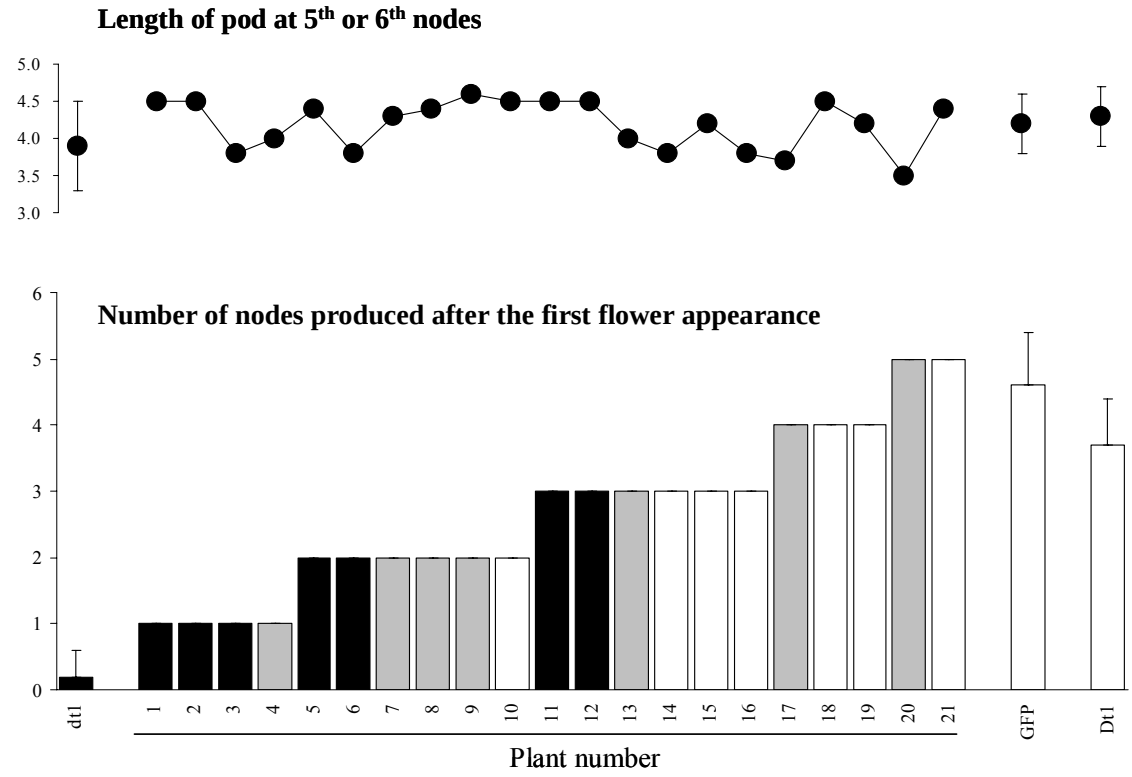


Figure S4. Stem growth habit of twenty-one indeterminate #6-22Dt1 plants that were infected with the recombinant viruses that contained 139-nucleotide sense or anti-sense sequences of exon 4 of the *GmTFL1b* gene. The infected plants produced one to five nodes after the first flower appearance (bottom panel). All of the plants produced pods of 3.5 to 4.5 cm in length at 5th or 6th nodes at 42 DAE (top panel). The determinate plants and some of 1-node, 2-node and 3-node plants (closed bar) produced almost the same-sized pods (more than 4.0 cm) at the terminal node (see Fig. 7C). Grey bars indicate the plants with pods of 1.0 to 2.0 cm at the terminal node. Blank bars indicate the plants with no pod at stem tips (see Fig. 7D).

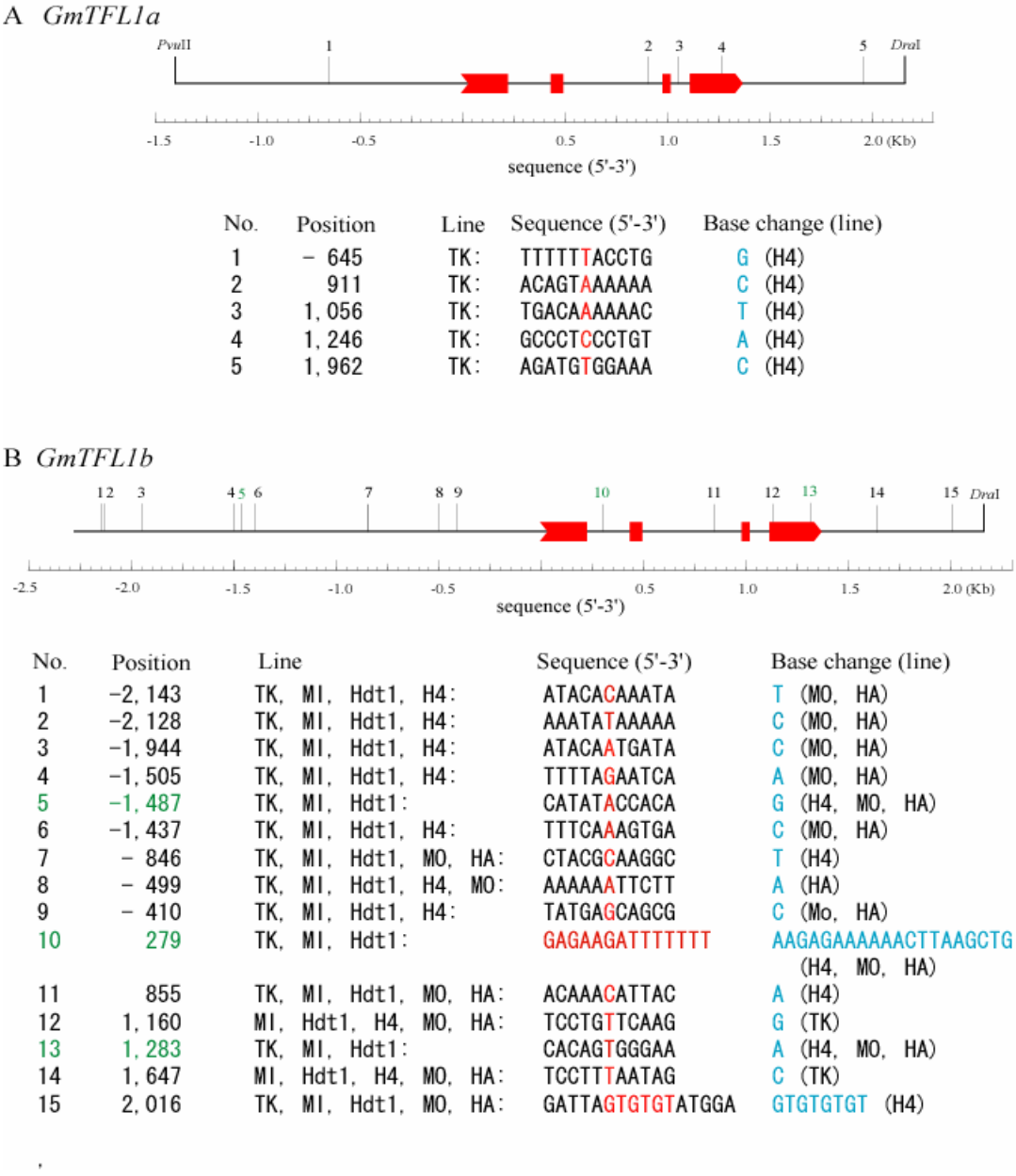


Figure S5. Position of polymorphic sites and their flanking sequences in the *GmTFL1a* (A) and *GmTFL1b* (B) genomic sequences. Red boxes indicate exons. Numerical numbers left of experimental lines refer to nucleotide positions from the Adenine of start codon. The lines listed left of flanking sequences possess the red-colored nucleotide(s) which is substituted by the blue-colored nucleotide(s) in the lines listed within parenthesis. The three mutations (Nos, 5, 10 and 13) in *GmTFL1b* were observed between determinate lines (TK, MI, Hdt1) and indeterminate lines (MO, HA, H4). MI; Misuzudaizu, MO; Moshidou Gong 503, TK; TK780, H4; Hidaka 4 (soja), HA; Harosoy, Hdt1; Harosoy NIL for *dt1*.