

Fig. S1. Phylogenetic analysis of cucurbits PEBP genes. Phylogram of 27 PEBP family proteins from cucumber (Csa), melon (MELO), watermelon (Cla) and *Arabidopsis* (At). The scale bar represents 0.1 substitutions per site, and the numbers next to nodes are bootstrap values from 1,000 replicates.

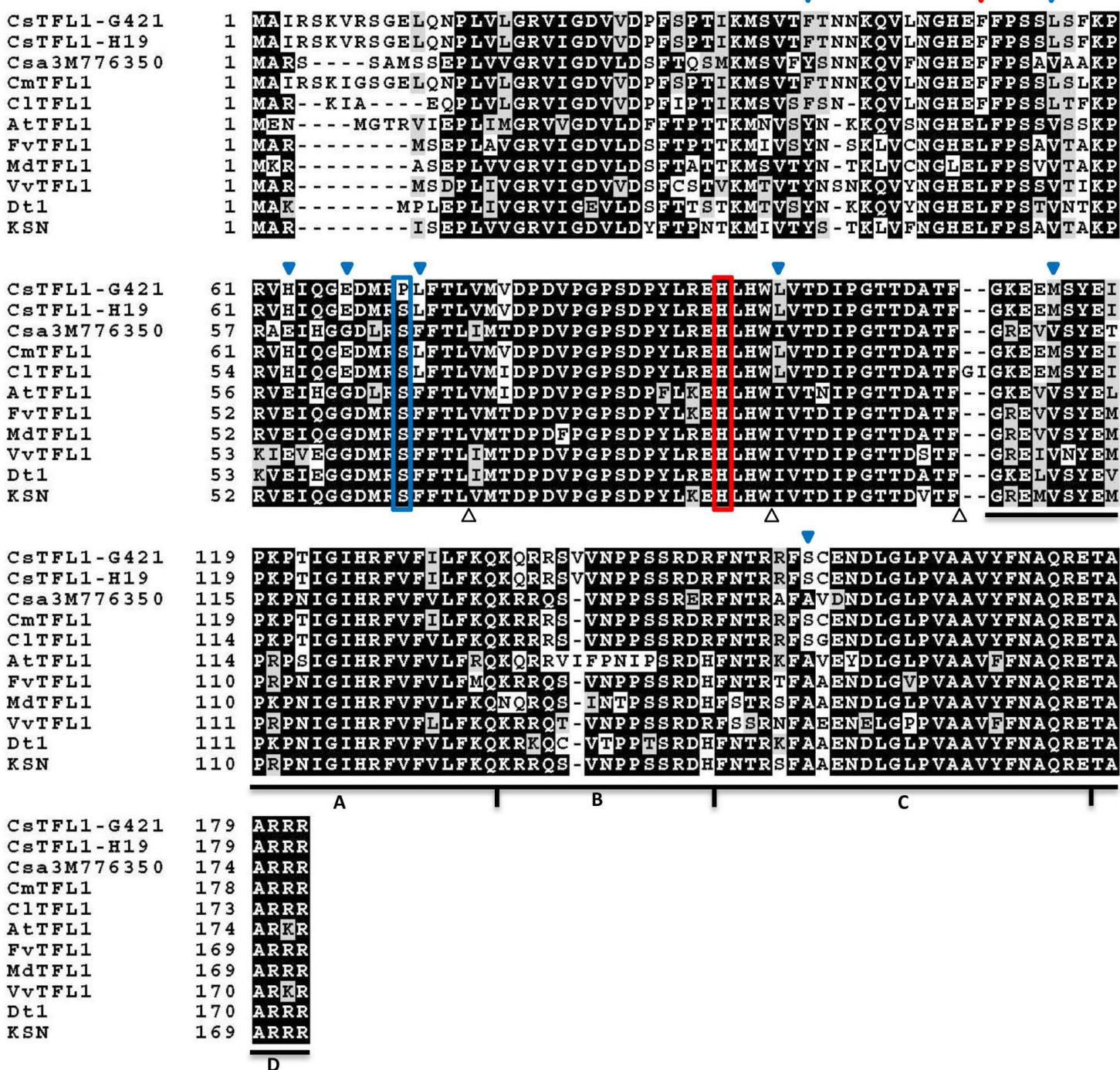


Fig. S2. Multiple alignments of CsTFL1 and TFL1-like genes in other species. Thin blue rectangle represents the SNP of S71P in G421. Thin red rectangle represents the conservative histidine in TFL1. Blue triangles represent the unconserved residues between Csa3M776350 and other cucurbits TFL1s. Red triangle represents the conserved residue in the cucurbit TFL1s. Open triangles represent the exon boundaries of TFL1. Four segments in the fourth exon of the TFL1s were shown as A, B, C and D. At, *Arabidopsis thaliana*; Cs, *Cucumis sativus*; Cm, *Cucumis melo L*; Cl, *Citrullus lanatus*; Fv, *Fragaria vesca*; Md, *Malus domestica*; Vv, *Vitis vinifera*; Dt1 is from *Glycine max*; KSN is from *Rosa chinensis*.

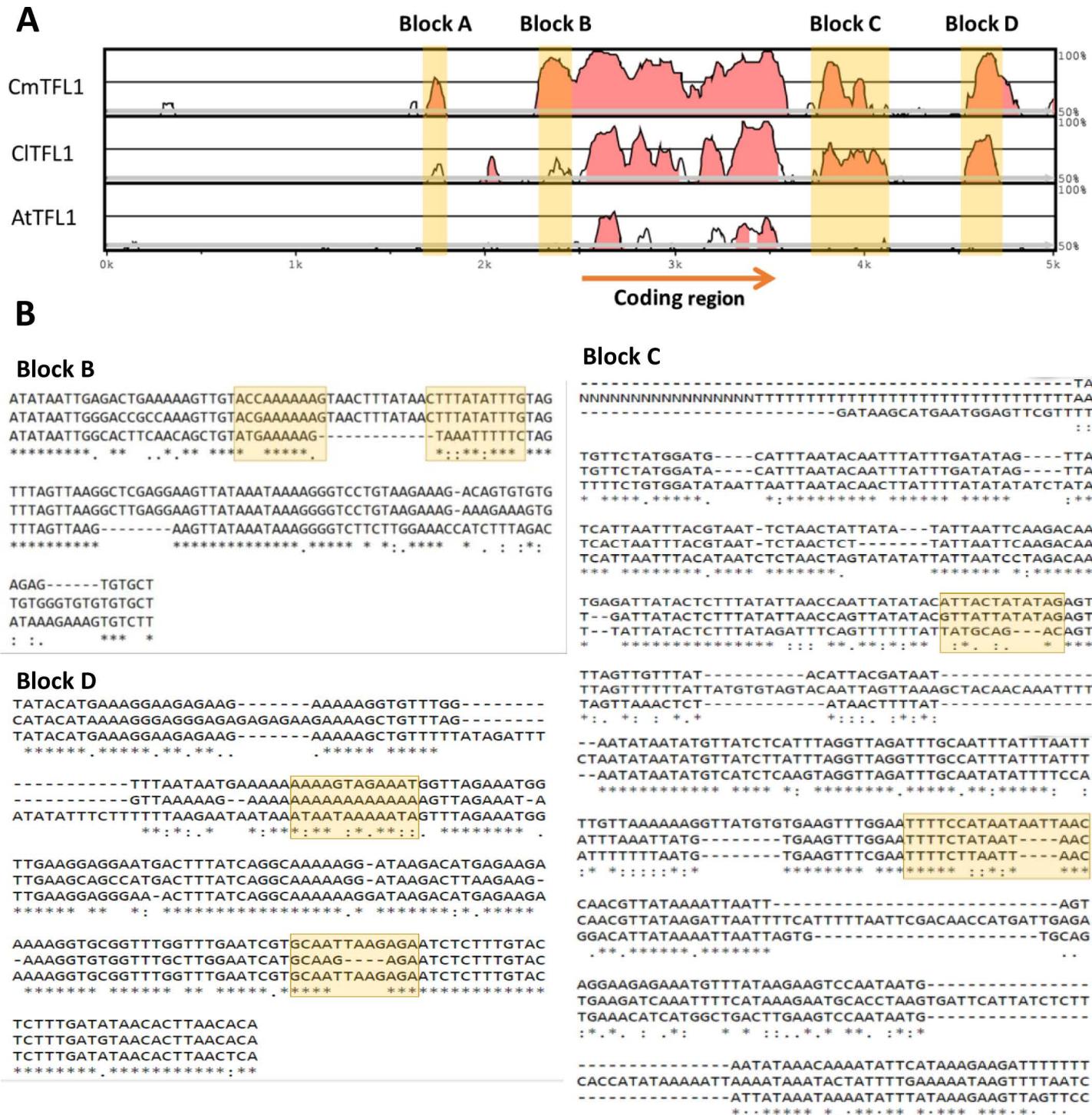


Fig. S3. Comparative analysis of the cucurbits TFL1s.(A) VISTA pairwise alignments of 5' and 3' region of melon *CmTFL1*, watermelon *CiTFL1*, and Arabidopsis *AtTFL1* against cucumber *CsTFL1*. Graphical output shows the base pair identity (50-100% range) in a sliding window of 100 bp. Regions with >50% similarity are in red and the four conserved blocks outside the coding region (indicated by the arrow) are highlighted in orange.(B) The sequence of four identified conserved blocks in the 5' and 3' region of the *CsTFL1*, *CmTFL1* and *CiTFL1* were aligned using the GenomeNet online ClusterW server (<http://www.genome.jp/tools-bin/clustalw>). Six potential MADS-box binding sites (CArG box) were identified by searching against the JASPAR database and highlighted in orange.

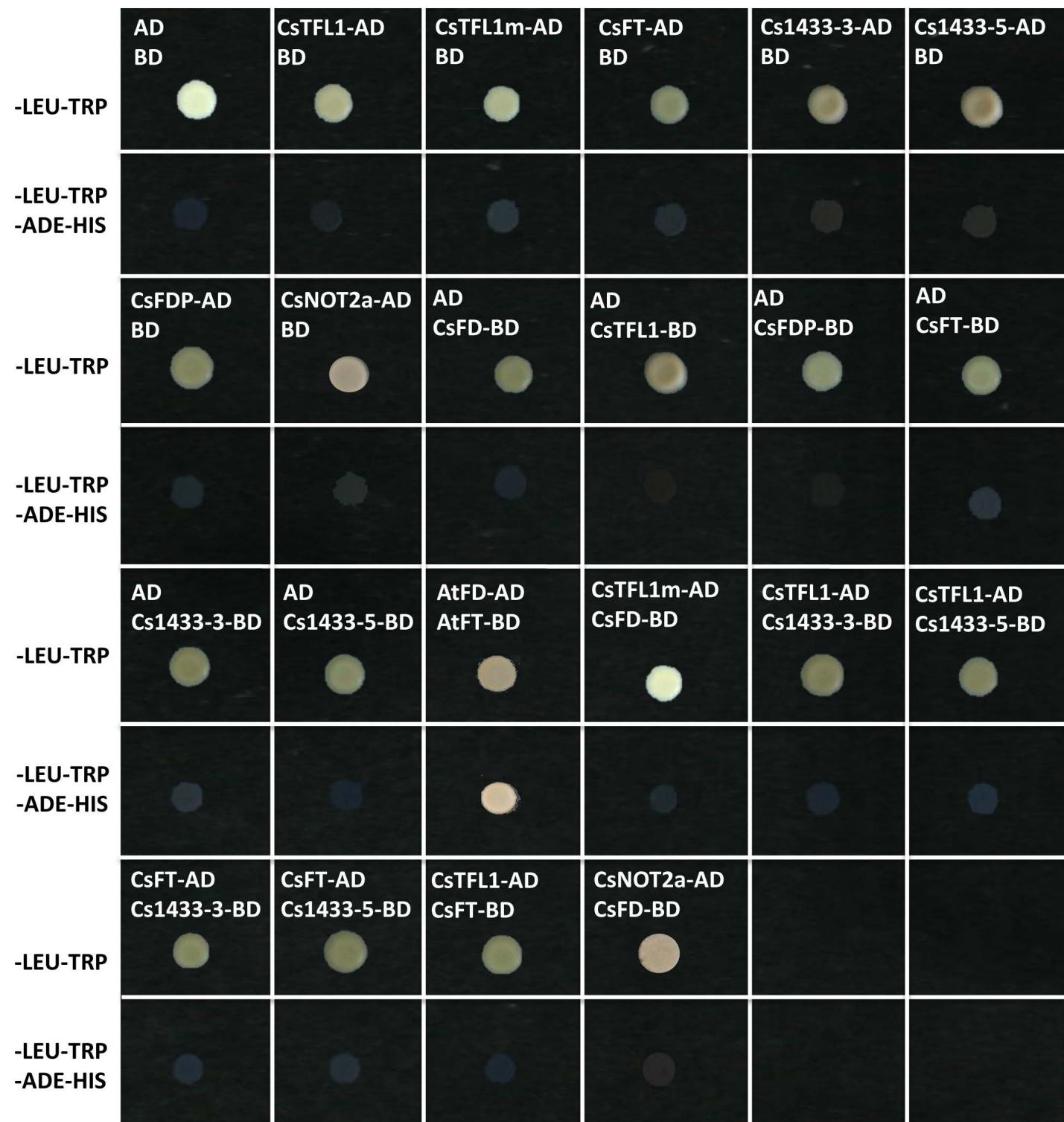


Fig. S4. Protein interactions as detected by yeast two-hybrid assays. The combination of empty vector pGBKT7 or pGADT7 was used as a negative control.

Table S1. Analysis of determinate traits in parental lines and segregation populations derived from G421 and H19

Year	Generation	Plants Tested	D: d Observed	D: d Ratio Tested	χ^2 ^a
3 years	H19	30	30:0	D	
	G421	28	0:28	d	
	F_1 H19×G421	42	42:0	D	
2010	RIL- F_8 H19×G421	139	72:67	1:1	0.18
2011	F_2 H19×G421	946	722:224	3:1	0.88

Table S2. Markers and genotype information used in this study.

[Click here to Download Table S2](#)

Table S3. Gene information used in this study

Gene name	Species	Gene ID in TAIR/ Cucurbit Database/ Genebank
AtTFL1	Arabidopsis	At5G03840
AtFT	Arabidopsis	At1G65480
AtBFT	Arabidopsis	At5G62040
AtMFT	Arabidopsis	At1G18100
AtCEN	Arabidopsis	At2G27550
AtTSF	Arabidopsis	At4G20370
AtFD	Arabidopsis	AT4G35900
AtHAN	Arabidopsis	AT3G50870
AtIND	Arabidopsis	AT4G00120
AtSPT	Arabidopsis	AT4G36930
CsFD	Cucumber	Csa3G002610
CsFDP	Cucumber	Csa6G051480
Cs1433-3	Cucumber	Csa2G369070
Cs1433-5	Cucumber	Csa4G094520
CsNOT21	Cucumber	Csa6G302150
CsLFY	Cucumber	Csa1G000050
CsSOC1	Cucumber	Csa6G076720
CsTEN	Cucumber	Csa5G644520
FvTFL1	<i>Fragaria vesca</i>	JN172097
MdTFL1	<i>Malus x domestica</i>	AB162040.1
VvTFL1	<i>Vitis vinifera</i>	AF378127
Dt1	<i>Glycine max</i>	ADF30943.1
KSN	<i>Rosa</i>	ADO64261.1

Table S4. Primer information used in this study

Primers for genetic mapping and cloning	
<i>SSR01698-F</i>	ACGATGAATTTGCCGTAGC
<i>SSR01698-R</i>	GAAGAATCACTGAACCCCGA
<i>SSR14859-F</i>	CAAACCTAGCCTAACCTTGG
<i>SSR14859-R</i>	AAACCTTTGACGTTGAAGGA
<i>SSR13251-F</i>	GGTCAATCCAAAAGAGAAAGCA
<i>SSR13251-R</i>	ATCAACACCATTGACGACCA
<i>SSR06632-F</i>	TCAGATGTTGATTGGCTCTCA
<i>SSR06632-R</i>	AGGGCCAACATTAAAGGGTC
<i>SSR01101-F</i>	TGTGACCACTCATTACACCCA
<i>SSR01101-R</i>	TTTATTGTTGGCCCATTCC
<i>SSR06653-F</i>	AAAGTTGGAAGGGTTGTGGTT
<i>SSR06653-R</i>	CTCTCTCGCGGATGTTTGT
<i>UW084417-F</i>	GGAAGAAACAAACCTGCTG
<i>UW084417-R</i>	TAGTGGGTGGAGGTGAAAGG
<i>UW085354-F</i>	TGGAGCATATAAGTAAGGTTAGGG
<i>UW085354-R</i>	TGGGCAAATAGTCATATTGAT
<i>SSR10449-F</i>	CACAATTCCCTCCGCTGTT
<i>SSR10449-R</i>	CCTTTCAGCTCTTCTAATTCTC
<i>UW085356-F</i>	GTGGAGATAGGAATTATTGGAGAG
<i>UW085356-R</i>	TGAATACTTGATTATCCAGGCTGT
<i>SSR17604-F</i>	TTGAAGTGGAGAGGAAGGA
<i>SSR17604-R</i>	TTCATTTGATATTGAAGTTAACACG
<i>UW085412-F</i>	ACGATCCATATGCTTGTGTT
<i>UW085412-R</i>	GATTCCAACGCACGTTTCT
<i>UW085076-F</i>	GTCCCCAACATCCTTCCTT
<i>UW085076-R</i>	TCATCGGTCAACCAATCAAT
<i>SSR14934-F</i>	ATACCTTGCAGGAGCCTTAT
<i>SSR14934-R</i>	ACTTTTCAGCAGAGCAGCC
<i>SSR15482-F</i>	AAAAACAGCAGGGCAGAAGA
<i>SSR15482-R</i>	GTTGAGCTGTCTATGGGGGA
<i>UW015248-F</i>	CCCGAAATTTCCTTACCCACA
<i>UW015248-R</i>	CTTGAAATTCCCTTACCCACA
<i>UW015253-F</i>	GACAAAATTCAAGAGTACAACACACC
<i>UW015253-R</i>	AAATGAAATGGATGATTAGATTGA
<i>TFL1-SNP-F</i>	GGGTCATATTCAAGGAGAAGATATGATATCATTGT
<i>TFL1-SNP-R</i>	GGAAATGGGTTCTCAAAGTTC
Primers for gene amplification and vector construction	
<i>CsTFL1-clone-F</i>	ATGGCAATTAGATCAAAAGTAAGAT
<i>CsTFL1-clone-R</i>	TTATGCCTCCTTGCAGCA
<i>CsTFL1-OE-F</i>	GCTCTAGAATGGCAATTAGATCAAAGTAAG
<i>CsTFL1-OE-R</i>	CCCCCCGGGTTATGCCTCCTGCAGC

<i>CsTFL1-Sense-F</i>	GGACTAGTCCATGGCAATTAGATCAAAAGTAA
<i>CsTFL1-Sense-R</i>	CGGGATCCCGCAATGGTCTCATATCTTCCT
<i>CsTFL1-Antisense-F</i>	TTGGCGGCCAATGGCAATTAGATCAAAAGTAA
<i>CsTFL1-Antisense-R</i>	CCATTAAATGGCAATGGTCTCATATCTTCCT
<i>CsTFL1-GFP-F</i>	GGACTAGTATGGCAATTAGATCAAAAGTAAAG
<i>CsTFL1-GFP-R</i>	TCCCCCGGGTGCCTCCTGCAGC

Primers for qRT-PCR

<i>CsTFL1-Q-F</i>	GCGTCGGTCAGTAGTGAATCCTCC
<i>CsTFL1-Q-R</i>	TTATGCCTCCTGCAGCAGTTT
<i>CsFT-Q-F</i>	AATCAACCAAGAGTCGAGATTGG
<i>CsFT-Q-R</i>	TTGCACCTGTTGTAGCTGGAATA
<i>Csa3M776350-Q-F</i>	AGCAATGTCCTCAGAACCTCTTG
<i>Csa3M776350-Q-R</i>	AGCAACAGCAGAAGGAAAGAACT
<i>CsUBIeq-Q-F</i>	CACCAAGCCAAGAAGATC
<i>CsUBI-eq-Q-R</i>	TAAACCTAATCACCAACCAGC
<i>ACTIN2-F</i>	CCTTCGTCTTGATCTTGCAGG
<i>ACTIN2-R</i>	AGCGATGGCTGGAACAGAAC

Primers for in situ probes

<i>CsTFL1-T7</i>	tgTAATACGACTCACTATAAGGCATGGTCTCATATCTTCCT
<i>CsTFL1-Sp6</i>	GATTAGGTGACACTATAGaattGCTATGGCAATTAGATCAAAAGTAA

Primers for yeast two-hybrid, BiFC and pull-down

<i>AtHAN-Y2H-F</i>	GGAATTCCATATGATGATGCAGACTCCGTACACT
<i>AtHAN-Y2H-R</i>	CGGGATCCCTGGTAAAGTCATGGACAAGAC
<i>AtFT-Y2H-F</i>	CGGAATTCATGTCTATAATATAAGAGACCCTTTAGTAAGC
<i>AtFT-Y2H-R</i>	CGGGATCCAAGTCTCTCCCTCCGCAG
<i>AtFD-Y2H-F</i>	CGGAATTCATGTTGTATCAGCTAACGATCAG
<i>AtFD-Y2H-R</i>	CGGGATCCAATGGAGCTGTGGAAGACCG
<i>CsTFL1-Y2H-F</i>	GGAATTCCATATGATGGCAATTAGATCAAAAGTAA
<i>CsTFL1-Y2H-R</i>	CGGGATCCCTATGCCCTTGCAGCAGT
<i>CsFT-Y2H-F</i>	GGAATTCCATATGATGCCAAGAGATCGTGACCC
<i>CsFT-Y2H-R</i>	CGGAATTCTTAATAATCATCTTGGACTCTTCT
<i>CsFD-Y2H-F</i>	GGAATTCCATATGATGGAAGAAGTTGGAAAGACATAAG
<i>CsFD-Y2H-R</i>	CGGGATCCCCTAAAACGGCGCCGTTGATG
<i>Cs1433-3-Y2H-F</i>	GGAATTCCATATGATGGCTGCCGCTCCTCTGT
<i>Cs1433-3-Y2H-R</i>	CCCCCCGGGCTGCTTCATCCTCACGCTT
<i>Cs1433-5-Y2H-F</i>	GGAATTCCATATGATGTCGCCGCTGATTCTCA
<i>Cs1433-5-Y2H-R</i>	CCCCCCGGGCTGCCATGCCCTCCCCCTGA
<i>CsFDP-Y2H-F</i>	CGGAATTCATGGGATTCAAACATGGGTC
<i>CsFDP-Y2H-R</i>	CGGGATCCGAACGGCGCTGACGATGTTCTCG
<i>CsNOT2a-Y2H-F</i>	CGGAATTCATGTCGGGTTACTTAATTCTCATCTC
<i>CsNOT2a-Y2H-R</i>	CGGGATCCATGTTGCGATAGAACTGGTCTC
<i>AtIND-BiFC-F</i>	TGCTCTAGAATGGAAAATGGTATGTATAAAAAG
<i>AtIND-BiFC-R</i>	CGCGGATCCGGGTTGGGAGTTGTGGTA

<i>AtSPT-BiFC-F</i>	TGCTCTAGAATGATATCACAGAGAGAAGAAAGA
<i>AtSPT-BiFC-R</i>	CGCGGATCCAGTAATTGATCTTTAGGTAG
<i>CsFT-BiFC-F</i>	GGACTAGTATGCCAAGAGATCGTGACCC
<i>CsFT-BiFC-R</i>	CCCCCCCAGATAATCATCTGGACTCTTCTCC
<i>CsFD-BiFC-F</i>	GGACTAGTATGGAAGAAGTTGGAAAGACATAAG
<i>CsFD-BiFC-R</i>	CCCCCCGGAAACGGCGCCGTTGATG
<i>CsI433-3-BiFC-F</i>	GGACTAGTATGGCTGCCGCTCCTCTGT
<i>CsI433-3 -BiFC-R</i>	CCCCCCCCTGCTTTCATCCTCACGCTT
<i>CsFDP-BiFC-F</i>	CGGGATCCATGGGATTCAAACATGGGTC
<i>CsFDP-BiFC-R</i>	CCCTCGAGGAACGGCGCTGACGATGTTCTCG
<i>CsNOT2a-BiFC-F</i>	CGGGATCCATGTCGGTTACTTAATTCATCTC
<i>CsNOT2a-BiFC-R</i>	CCCTCGAGATGTTGCGATAGAACTGGTCTC