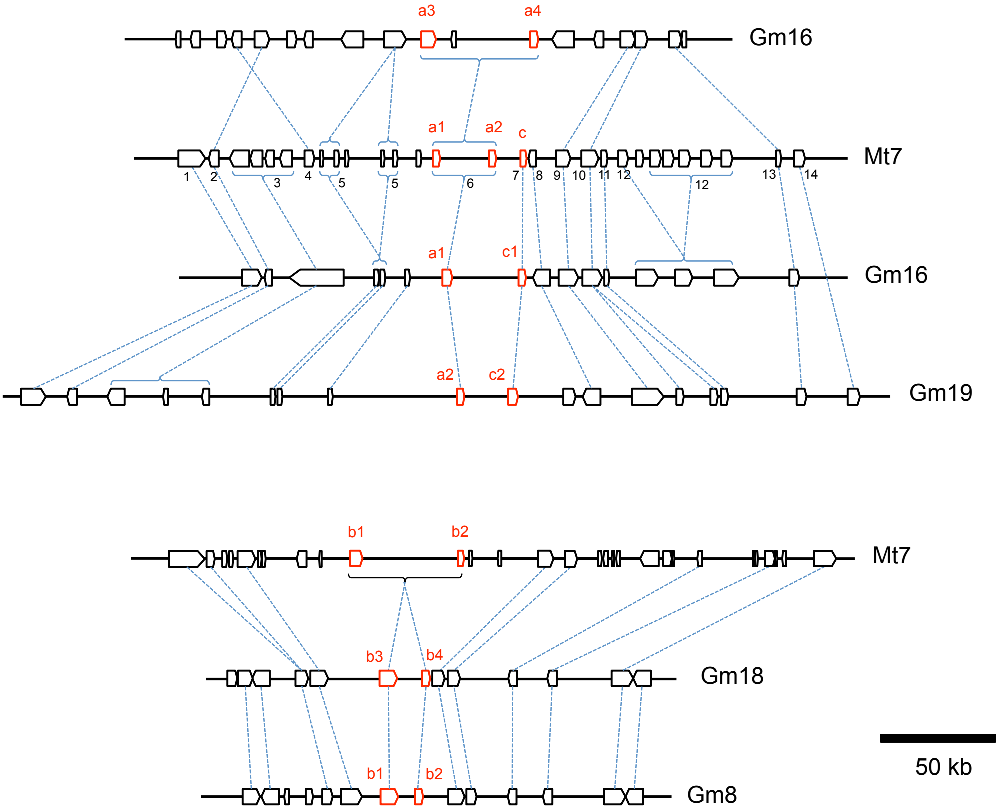
Supplemental Data.
Hecht et al. (2011). Plant Cell 10.1105/tpc.110.081042

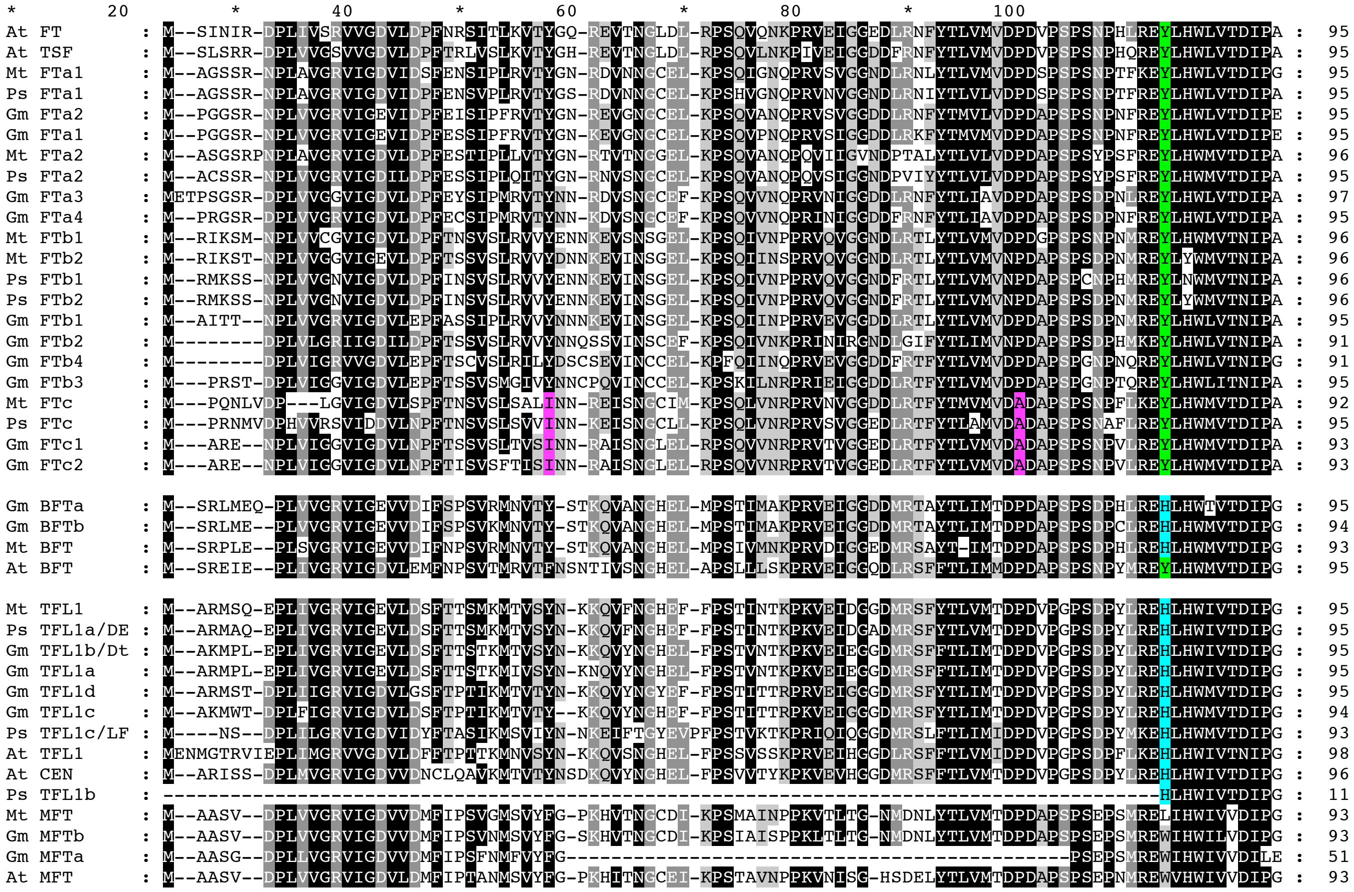


Supplemental Figure 1: Microsynteny around *FT* genes in Medicago and soybean.

Genes are represented as open boxes with the pointed end indicating putative direction of transcription. *FT* genes are shown in red, with letters indicating the identity of each gene. Full details are given in Supplemental Table 1. Genes with clear counterparts in more than one genomic region are connected by dashed blue lines. Numbers shown underneath genes in the region of the Mt *FTa*/*FTc* cluster refer to Supplemental Table 2.

Supplemental Figure 2 : Alignment of legume PEBP amino-acid sequences.

Alignments were generated with ClustalW and manually adjusted using Genedoc (Nicholas et al., 1997).
Sequence details are given in Supplemental Table 1.
Shading levels indicate degree of conservation – black = 90%, dark grey = 70%, light grey = 50%.
Red arrows indicate critical residues distinguishing FT (green) and TFL1 (blue) proteins (Ahn et al., 2006).
Distinguishing residues of FTc proteins are highlighted in purple.



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              *        20         *        40         *        60         *        80         *       100
At FT       : M--SINIR-DPLIVSRVVGDVLDPFNRSITLKVTYGQ-REVTNGLDL-RPSQVQNKPRVEIGGEDLRNFYTLVMVDPDVPSPSNPHLREYLHWLVTDIPA :  95
At TSF      : M--SLSRR-DPLVVGSVVGDVLDPFTRLVSLKVTYGH-REVTNGLDL-RPSQVLNKPIVEIGGDDFRNFYTLVMVDPDVPSPSNPHQREYLHWLVTDIPA :  95
Mt FTa1     : M--AGSSR-NPLAVGRVIGDVIDSFENSIPLRVTYGN-RDVNNGCEL-KPSQIGNQPRVSVGGNDLRNLYTLVMVDPDSPSPSNPTFKEYLHWLVTDIPG :  95
Ps FTa1     : M--AGSSR-NPLAVGRVIGDVIDPFENSVPLRVTYGS-RDVNNGCEL-KPSHVGNQPRVNVGGNDLRNIYTLVLVDPDSPSPSNPTFREYLHWLVTDIPA :  95
Gm FTa2     : M--PGGSR-NPLVVGRVIGEVIDPFEISIPFRVTYGN-REVGNGCEL-KPSQVANQPRVSVGGDDLRNFYTMVLVDPDAPSPSNPNFREYLHWLVTDIPE :  95
Gm FTa1     : M--PGGSR-NPLVVGRVIGEVIDPFESSIPFRVTYGN-KEVGNGCEL-KPSQVPNQPRVSIGGDDLRKFYTMVMVDPDAPSPSNPNFREYLHWLVTDIPE :  95
Mt FTa2     : M--ASGSRPNPLAVGRVIGDVLDPFESTIPLLVTYGN-RTVTNGGEL-KPSQVANQPQVIIGVNDPTALYTLVLVDPDAPSPSYPSFREYLHWMVTDIPA :  96
Ps FTa2     : M--ACSSR-NPLVVGRVIGDILDPFESSIPLQITYGN-RNVSNGCEL-KPSQVANQPQVSIGGNDPVIYYTLVLVDPDAPSPSYPSFREYLHWMVTDIPA :  95
Gm FTa3     : METPSGSR-DPLVVGGVIGDVLDPFEYSIPMRVTYNN-RDVSNGCEF-KPSQVVNQPRVNIGGDDLRNFYTLIAVDPDAPSPSDPNLREYLHWLVTDIPA :  97
Gm FTa4     : M--PRGSR-DPLVVGRVIGDVLDPFECSIPMRVTYNN-KDVSNGCEF-KPSQVVNQPRINIGGDDFRNFYTLIAVDPDAPSPSDPNFREYLHWLVTDIPA :  95
Mt FTb1     : M--RIKSM-NPLVVCGVIGDVLDPFTNSVSLRVVYENNKEVSNSGEL-KPSQIVNPPRVQVGGNDLRTLYTLVMVDPDGPSPSNPNMREYLHWMVTNIPA :  96
Mt FTb2     : M--RIKST-NPLVVGGVIGEVLDPFTSSVSLRVVYDNNKEVINSGEL-KPSQIINSPRVQVGGNDLRTLYTLVMVNPDAPSPSDPNMREYLYWMVTNIPA :  96
Ps FTb1     : M--RMKSS-NPLVVGNVIGDVLDPFINSVSLRVVYENNKEVINSGEL-KPSQIVNPPRVQVGGNDFRTLYTLVMVNPDAPSPCNPHMREYLNWMVTNIPA :  96
Ps FTb2     : M--RMKSS-NPLVVGNVIGDVLDPFINSVSLRVVYENNKEVINSGEL-KPSQIVNPPRVQVGGNDFRTLYTLVMVNPDAPSPSDPNMREYLYWMVTNIPA :  96
Gm FTb1     : M--AITT--NPLVVGRVIGDVLEPFASSIPLRVVYNNNKEVINSGEL-KPSQIINPPRVEVGGDDLRTLYTLVMVDPDAPSPSDPNMREYLHWLVTNIPA :  95
Gm FTb2     : M--------DPLVLGRIIGDILDPFTSSVSLRVVYNNQSSVINSCEF-KPSQIVNKPRINIRGNDLGIFYTLIMVNPDAPSPSDPHMKEYLHWLVTNIPA :  91
Gm FTb4     : M--------DPLVIGRVVGDVLEPFTSCVSLRILYDSCSEVINCCEL-KPFQIINQPRVEVGGDDFRTFYTLVMVDPDAPSPGNPNQREYLHWLVTNIPG :  91
Gm FTb3     : M---PRST-DPLVIGGVIGDVLEPFTSSVSMGIVYNNCPQVINCCEL-KPSKILNRPRIEIGGDDLRTFYTLVMVDPDAPSPGNPTQREYLHWLITNIPA :  95
Mt FTc      : M---PQNLVDP---LGVIGDVLSPFTNSVSLSALINN-REISNGCIM-KPSQLVNRPRVNVGGDDLRTFYTMVMVDADAPSPSNPFLKEYLHWMVTDIPA :  92
Ps FTc      : M---PRNMVDPHVVRSVIDDVLNPFTNSVSLSVVINN-KEISNGCLL-KPSQLVNRPRVSVGGEDLRTFYTLAMVDADAPSPSNAFLREYLHWMVTDIPA :  95
Gm FTc1     : M---ARE--NPLVIGGVIGDVLNPFTSSVSLTVSINN-RAISNGLEL-RPSQVVNRPRVTVGGEDLRTFYTLVMVDADAPSPSNPVLREYLHWMVTDIPA :  93
Gm FTc2     : M---ARE--NPLVIGGVIGDVLNPFTISVSFTISINN-RAISNGLEL-RPSQVVNRPRVTVGGEDLRTFYTLVMVDADAPSPSNPVLREYLHWMVTDIPA :  93

Gm BFTa     : M--SRLMEQ-PLVVGRVIGEVVDIFSPSVRMNVTY-STKQVANGHEL-MPSTIMAKPRVEIGGDDMRTAYTLIMTDPDAPSPSDPHLREHLHWTVTDIPG :  95
Gm BFTb     : M--SRLME--PLVVGRVIGEVVDIFSPSVKMNVTY-STKQVANGHEL-MPSTIMAKPRVEIGGDDMRTAYTLIMTDPDAPSPSDPCLREHLHWMVTDIPG :  94
Mt BFT      : M--SRPLE--PLSVGRVIGEVVDIFNPSVRMNVTY-STKQVANGHEL-MPSIVMNKPRVDIGGEDMRSAYT-IMTDPDAPSPSDPHLREHLHWMVTDIPG :  93
At BFT      : M--SREIE--PLIVGRVIGDVLEMFNPSVTMRVTFNSNTIVSNGHEL-APSLLLSKPRVEIGGQDLRSFFTLIMMDPDAPSPSNPYMREYLHWMVTDIPG :  95

Mt TFL1     : M--ARMSQ-EPLIVGRVIGEVLDSFTTSMKMTVSYN-KKQVFNGHEF-FPSTINTKPKVEIDGGDMRSFYTLVMTDPDVPGPSDPYLREHLHWIVTDIPG :  95
Ps TFL1a/DE : M--ARMAQ-EPLIVGRVIGEVLDSFTTSMKMTVSYN-KKQVFNGHEF-FPSTINTKPKVEIDGADMRSFYTLVMTDPDVPGPSDPYLREHLHWIVTDIPG :  95
Gm TFL1b/Dt : M--AKMPL-EPLIVGRVIGEVLDSFTTSTKMTVSYN-KKQVYNGHEL-FPSTVNTKPKVEIEGGDMRSFFTLIMTDPDVPGPSDPYLREHLHWIVTDIPG :  95
Gm TFL1a    : M--ARMPL-EPLIVGRVIGEVLDSFTTSTKMIVSYN-KNQVYNGHEL-FPSTVNTKPKVEIEGGDMRSFFTLIMTDPDVPGPSDPYLREHLHWIVTDIPG :  95
Gm TFL1d    : M--ARMST-DPLIIGRVIGDVLGSFTPTIKMTVTYN-KKQVYNGYEF-FPSTITTRPRVEIGGGDMRSFYTLIMTDPDVPGPSDPYLREHLHWMVTDIPG :  95
Gm TFL1c    : M--AKMWT-DPLFIGRVIGDVLDSFTPTIKMTVTY--KKQVYNGHEF-FPSTITTRPKVEIGGGDMRSFYTLIMTDPDVPGPSDPYLREHLHWMVTDIPG :  94
Ps TFL1c/LF : M----NS--DPLILGRVIGDVIDYFTASIKMSVIYN-NKEIFTGYEVPFPSTVKTKPRIQIQGGDMRSLFTLIMIDPDVPGPSDPYMKEHLHWMVTDIPG :  93
At TFL1     : MENMGTRVIEPLIMGRVVGDVLDFFTPTTKMNVSYN-KKQVSNGHEL-FPSSVSSKPRVEIHGGDLRSFFTLVMIDPDVPGPSDPFLKEHLHWIVTNIPG :  98
At CEN      : M--ARISS-DPLMVGRVIGDVVDNCLQAVKMTVTYNSDKQVYNGHEL-FPSVVTYKPKVEVHGGDMRSFFTLVMTDPDVPGPSDPYLREHLHWIVTDIPG :  96
Ps TFL1b    : -----------------------------------------------------------------------------------------HLHWIVTDIPG :  11
Mt MFT      : M--AASV--DPLVVGRVIGDVVDMFIPSVGMSVYFG-PKHVTNGCDI-KPSMAINPPKVTLTG-NMDNLYTLVMTDPDAPSPSEPSMRELIHWIVVDIPG :  93
Gm MFTb     : M--AASV--DPLVVGRVIGDVVDMFIPSVNMSVYFG-SKHVTNGCDI-KPSIAISPPKLTLTG-NMDNLYTLVMTDPDAPSPSEPSMREWIHWILVDIPG :  93
Gm MFTa     : M--AASG--DPLLVGRVIGDVVDMFIPSFNMFVYFG---------------------------------------------PSEPSMREWIHWIVVDILE :  51
At MFT      : M--AASV--DPLVVGRVIGDVLDMFIPTANMSVYFG-PKHITNGCEI-KPSTAVNPPKVNISG-HSDELYTLVMTDPDAPSPSEPNMREWVHWIVVDIPG :  93
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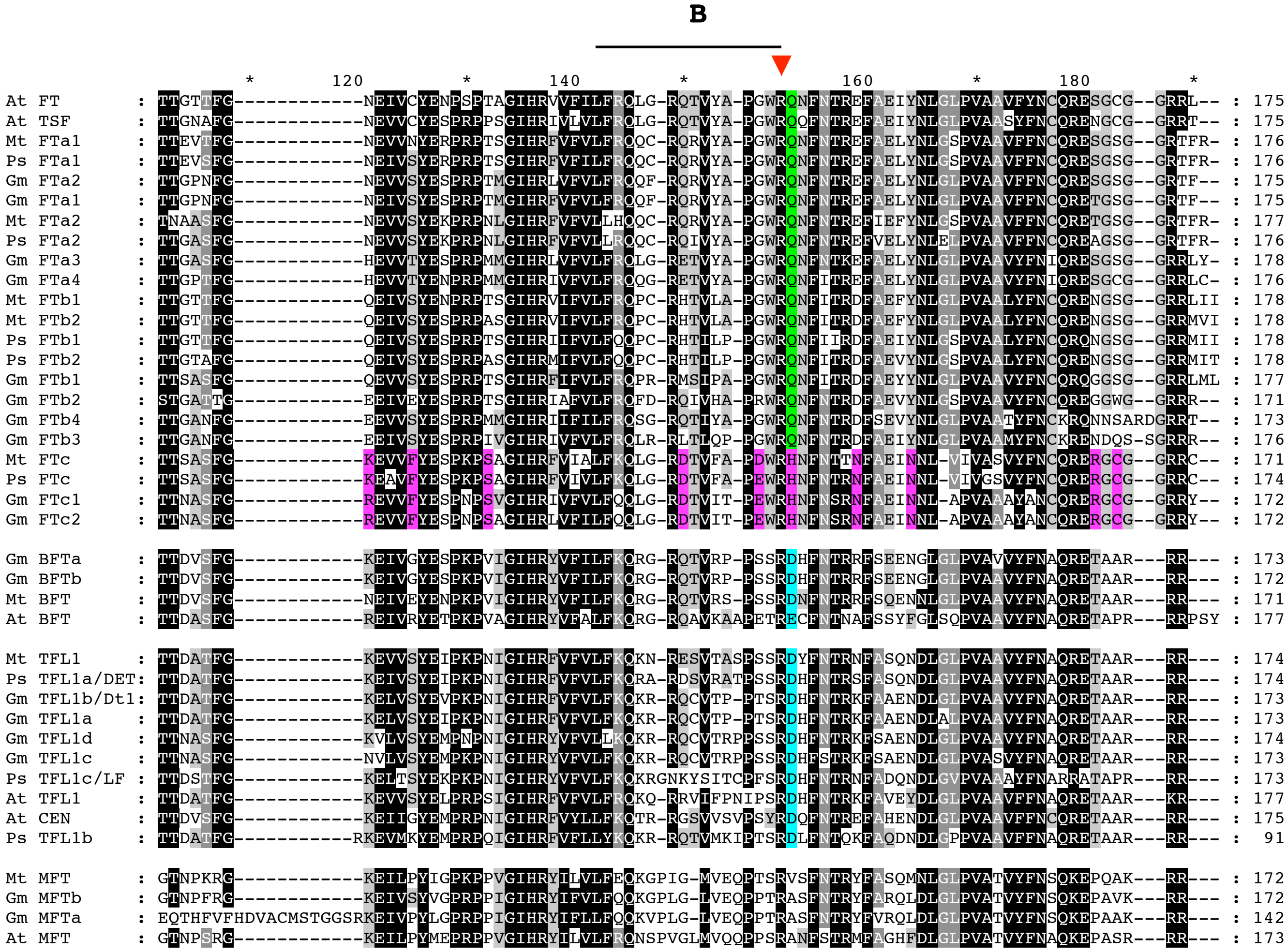

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                              *       120         *       140         *           160         *       180         *
At FT       : TTGTTFG------------NEIVCYENPSPTAGIHRVVFILFRQLG-RQTVYA-PGWRQNFNTREFAEIYNLGLPVAAVFYNCQRESGCG--GRRL-- : 175
At TSF      : TTGNAFG------------NEVVCYESPRPPSGIHRIVLVLFRQLG-RQTVYA-PGWRQQFNTREFAEIYNLGLPVAASYFNCQRENGCG--GRRT-- : 175
Mt FTa1     : TTEVTFG------------NEVVNYERPRPTSGIHRFVFVLFRQQC-RQRVYA-PGWRQNFNTREFAELYNLGSPVAAVFFNCQRESGSG--GRTFR- : 176
Ps FTa1     : TTEVSFG------------NEIVSYERPRPTSGIHRFVFILFRQQC-RQRVYA-PGWRQNFNTREFAELYNLGSPVAAVFFNCQRESGSG--GRTFR- : 176
Gm FTa2     : TTGPNFG------------NEVVSYESPRPTMGIHRLVFVLFRQQF-RQRVYA-PGWRQNFNTREFAELYNLGLPVAAVFFNCQRESGSG--GRTF-- : 175
Gm FTa1     : TTGPNFG------------NEIVSYESPRPTMGIHRFVFVLFRQQF-RQRVYA-PGWRQNFNTREFAELYNLGLPVAAVFFNCQRETGSG--GRTF-- : 175
Mt FTa2     : TNAASFG------------NEVVSYEKPRPNLGIHRFVFVLLHQQC-RQRVYA-PGWRQNFNTREFIEFYNLGSPVAAVFFNCQRETGSG--GRTFR- : 177
Ps FTa2     : TTGASFG------------NEVVSYEKPRPNLGIHRFVFVLLRQQC-RQIVYA-PGWRQNFNTREFVELYNLELPVAAVFFNCQREAGSG--GRTFR- : 176
Gm FTa3     : TTGASFG------------HEVVTYESPRPMMGIHRLVFVLFRQLG-RETVYA-PGWRQNFNTKEFAELYNLGLPVAAVYFNIQRESGSG--GRRLY- : 178
Gm FTa4     : TTGPTFG------------HEVVTYENPRPMMGIHRIVFVLFRQQG-RETVYA-PGWRQNFITREFAELYNLGLPVAAVYFNIQRESGCG--GRRLC- : 176
Mt FTb1     : TTGTTFG------------QEIVSYENPRPTSGIHRVIFVLFRQPC-RHTVLA-PGWRQNFITRDFAEFYNLGLPVAALYFNCQRENGSG--GRRLII : 178
Mt FTb2     : TTGTTFG------------QEIVSYESPRPASGIHRVIFVLFRQPC-RHTVLA-PGWRQNFITRDFAEFYNLGLPVAALYFNCQRENGSG--GRRMVI : 178
Ps FTb1     : TTGTTFG------------QEIVSYESPRPTSGIHRIIFVLFQQPC-RHTILP-PGWRQNFIIRDFAEIYNLGSPVAALYFNCQRQNGSG--GRRMII : 178
Ps FTb2     : TTGTAFG------------QEIVSYESPRPASGIHRMIFVLFQQPC-RHTILP-PGWRQNFITRDFAEVYNLGSPVAALYFNCQRENGSG--GRRMIT : 178
Gm FTb1     : TTSASFG------------QEVVSYESPRPTSGIHRFIFVLFRQPR-RMSIPA-PGWRQNFITRDFAEYYNLGLPVAAVYFNCQRQGGSG--GRRLML : 177
Gm FTb2     : STGATTG------------EEIVEYESPRPTSGIHRIAFVLFRQFD-RQIVHA-PRWRQNFNTRDFAEVYNLGSPVAAVYFNCQREGGWG--GRRR-- : 171
Gm FTb4     : TTGANFG------------EEVVSYESPRPMMGIHRIIFILFRQSG-RQTIYA-PGWRQNFNTRDFSEVYNLGLPVAATYFNCKRQNNSARDGRRT-- : 173
Gm FTb3     : TTGANFG------------EEIVSYESPRPIVGIHRIVFVLFRQLR-RLTLQP-PGWRQNFNTRDFAEIYNLGLPVAAMYFNCKRENDQS-SGRRR-- : 176
Mt FTc      : TTSASFG------------KEVVFYESPKPSAGIHRFVIALFKQLG-RDTVFA-PDWRHNFNTTNFAEINNL-VIVASVYFNCQRERGCG--GRRC-- : 171
Ps FTc      : TTSASFG------------KEAVFYESPKPSAGIHRFVIVLFKQLG-RDTVFA-PEWRHNFNTRNFAEINNL-VIVGSVYFNCQRERGCG--GRRC-- : 174
Gm FTc1     : TTNASFG------------REVVFYESPNPSVGIHRIVFVLFQQLG-RDTVIT-PEWRHNFNSRNFAEINNL-APVAAAYANCQRERGCG--GRRY-- : 172
Gm FTc2     : TTNASFG------------REVVFYESPNPSAGIHRLVFILFQQLG-RDTVIT-PEWRHNFNSRNFAEINNL-APVAAAYANCQRERGCG--GRRY-- : 172

Gm BFTa     : TTDVSFG------------KEIVGYESPKPVIGIHRYVFILFKQRG-RQTVRP-PSSRDHFNTRRFSEENGLGLPVAVVYFNAQRETAAR---RR--- : 173
Gm BFTb     : TTDVSFG------------KEIVGYESPKPVIGIHRYVFILFKQRG-RQTVRP-PSSRDHFNTRRFSEENGLGLPVAAVYFNAQRETAAR---RR--- : 172
Mt BFT      : TTDVSFG------------NEIVEYENPKPVIGIHRYVFILFKQRG-RQTVRS-PSSRDNFNTRRFSQENNLGLPVAAVYFNAQRETAAR---RR--- : 171
At BFT      : TTDASFG------------REIVRYETPKPVAGIHRYVFALFKQRG-RQAVKAAPETRECFNTNAFSSYFGLSQPVAAVYFNAQRETAPR---RRPSY : 177

Mt TFL1     : TTDATFG------------KEVVSYEIPKPNIGIHRFVFVLFKQKN-RESVTASPSSRDYFNTRNFASQNDLGLPVAAVYFNAQRETAAR---RR--- : 174
Ps TFL1a/DET: TTDATFG------------KEIVSYEIPKPNIGIHRFVFVLFKQRA-RDSVRATPSSRDHFNTRSFASQNDLGLPVAAVYFNAQRETAAR---RR--- : 174
Gm TFL1b/Dt1: TTDATFG------------KELVSYEVPKPNIGIHRFVFVLFKQKR-RQCVTP-PTSRDHFNTRKFAAENDLGLPVAAVYFNAQRETAAR---RR--- : 173
Gm TFL1a    : TTDATFG------------KELVSYEIPKPNIGIHRFVFVLFKQKR-RQCVTP-PTSRDHFNTRKFAAENDLALPVAAVYFNAQRETAAR---RR--- : 173
Gm TFL1d    : TTNASFG------------KVLVSYEMPNPNIGIHRYVFVLLKQKR-RQCVTRPPSSRDHFNTRKFSAENDLGLPVAAVYFNAQRETAAR---RR--- : 174
Gm TFL1c    : TTNASFG------------NVLVSYEMPKPNIGIHRYVFVLFKQKR-RQCVTRPPSSRDHFSTRKFSAENDLGLPVASVYFNAQRETAAR---RR--- : 173
Ps TFL1c/LF : TTDSTFG------------KELTSYEKPKPNIGIHRYVFVLFKQKRGNKYSITCPFSRDHFNTRNFADQNDLGVPVAAAYFNARRATAPR---RR--- : 173
At TFL1     : TTDATFG------------KEVVSYELPRPSIGIHRFVFVLFRQKQ-RRVIFPNIPSRDHFNTRKFAVEYDLGLPVAAVFFNAQRETAAR---KR--- : 177
At CEN      : TTDVSFG------------KEIIGYEMPRPNIGIHRFVYLLFKQTR-RGSVVSVPSYRDQFNTREFAHENDLGLPVAAVFFNCQRETAAR---RR--- : 175
Ps TFL1b    : TTDATFG-----------RKEVMKYEMPRPQIGIHRFVFLLYKQKR-RQTVMKIPTSRDLFNTQKFAQDNDLGPPVAAVFFNAQRETAAR---RR--- :  91

Mt MFT      : GTNPKRG------------KEILPYIGPKPPVGIHRYILVLFEQKGPIG-MVEQPTSRVSFNTRYFASQMNLGLPVATVYFNSQKEPQAK---RR--- : 172
Gm MFTb     : GTNPFRG------------KEIVSYVGPRPPIGIHRYIFVLFQQKGPLG-LVEQPPTRASFNTRYFARQLDLGLPVATVYFNSQKEPAVK---RR--- : 172
Gm MFTa     : EQTHFVFHDVACMSTGGSRKEIVPYLGPRPPIGIHRYIFLLFQQKVPLG-LVEQPPTRASFNTRYFVRQLDLGLPVATVYFNSQKEPAAK---RR--- : 142
At MFT      : GTNPSRG------------KEILPYMEPRPPVGIHRYILVLFRQNSPVGLMVQQPPSRANFSTRMFAGHFDLGLPVATVYFNAQKEPASR---RR--- : 173
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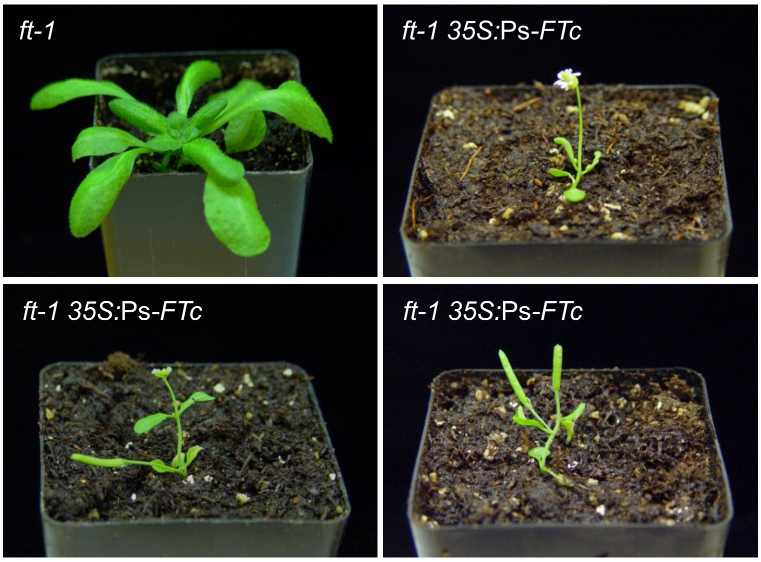
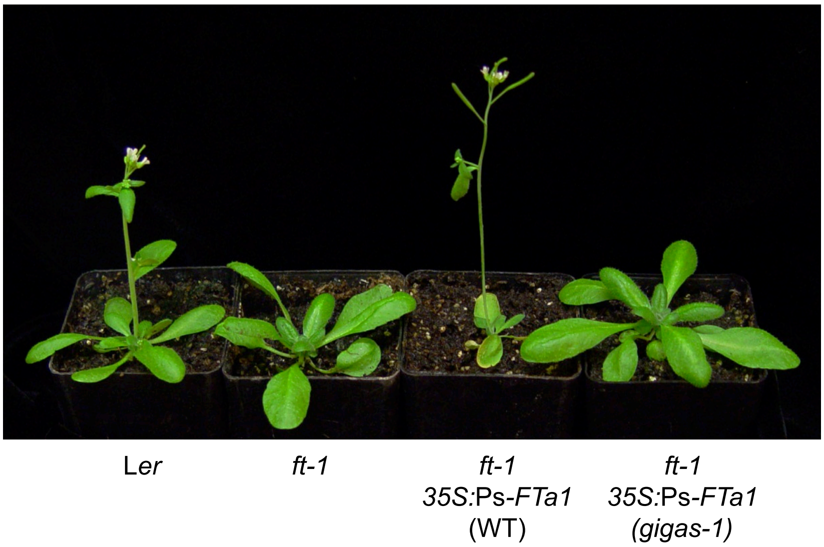


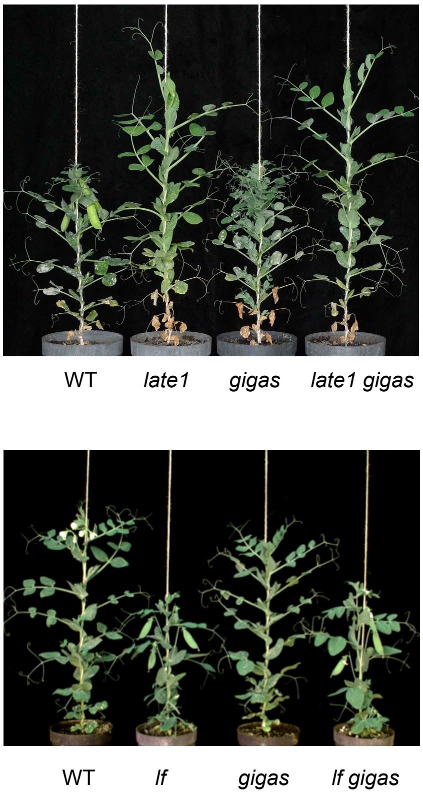
Supplemental Figure 3:

Overexpression of pea *FTc* in transgenic Arabidopsis results in extremely early flowering and and a tendency toward production of terminal flowers. Three representative primary transformants are shown.



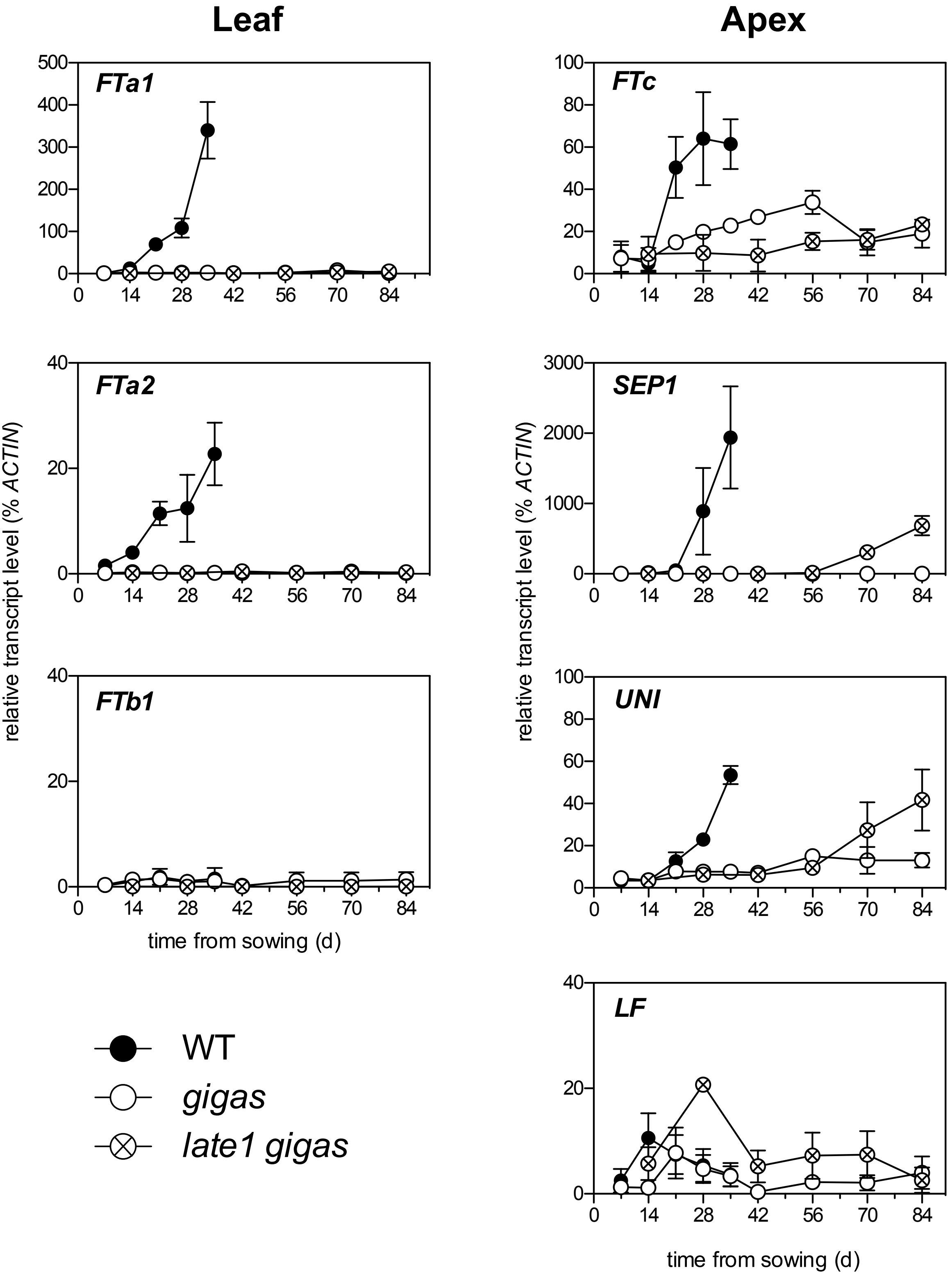
Supplemental Figure 4:

The *gigas-1* mutation completely impairs the activity of pea *FTa1* in transgenic Arabidopsis.



Supplemental Figure 5:

Photographs of representative plants of *late1-2 gigas-2* and *lf-22 gigas-2* double mutants, together with WT (NGB5839) and corresponding single mutants.
Plants were grown under LD conditions (16L/8D) in the phytotron.



Supplemental Figure 6: Gene expression in NGB5839 (WT), *gigas-2*, and the *late1-2 gigas-2* double mutant during development under LD conditions (16L/8D). Relative transcript levels were determined in dissected shoot apices (Apex) or the uppermost fully-expanded leaf (Leaf). Values are normalized to the transcript level of the *ACTIN* gene, and represent mean ± SE for n= 2-3 biological replicates, each consisting of pooled material from two plants.

Supplemental Table 1 Details of *FT*-like sequences in pea, Medicago and soybean. Gene models were identified in BLAST searches on on Mtr 3.0 at JCVI (Medicago, http://www.jcvi.org/cgi-bin/medicago/index.cgi) and Glyma1.0 at Phytozome (soybean, http://www.phytozome.net/soybean.php). The Medicago *FTa2* and *FTb2* genes are incorrectly annotated as three (*FTa2*) or two (*FTb2*) separate gene models in Mtr3.0. Several of the listed soybean gene models are also likely incorrectly annotated and have been corrected for the phylogenetic analyses in Figure 1 and Supplemental Figure 2. Gene models for soybean genes *FTa1*, *FTa3* and *FTb4* are missing the most likely translational start site whereas *FTb3* and *MFTa* have additional exons included. Conceptual translation of the corrected *MFTa* gene model reveals a frameshift and premature truncation resulting from a substitution and single base insertion in exon 3.

Species	Gene name	Gene model	Previous name	Accession # (cDNA / gDNA)
Pea	Ps *FTa1/GIGAS*			HQ538822 / HQ538830
	Ps *fta1 (gigas-1)*			HQ538821
	Ps *FTa2*			HQ538823
	Ps *FTb1*			HQ538824
	Ps *FTb2*		Ps *FTL*	HQ538825 / HQ538831
	Ps *FTc*			HQ538826 / HQ538832
	Ps *TFL1a/DET*			AY340579
	Ps *TFL1b*			AY340580
	Ps *TFL1c/LF*			AY343326
Medicago	Mt *FTa1*	Medtr7g099820	Mt *FTLa*	
	Mt *FTa2*	Medtr7g099850-70	Mt *FTLb*	
	Mt *FTb1*	Medtr7g006170	Mt *FTLd*	
	Mt *FTb2*	Medtr7g006200-10	Mt *FTLe*	
	Mt *FTc*	Medtr7g099890	Mt *FTLc*	
	Mt *TFL1*	Medtr7g127250		
	Mt *BFT*			AC146807_6.1
	Mt *MFT*	Medtr4g155400		
Soybean	Gm *FTa1*	Glyma16g04840		
	Gm *FTa2*	Glyma19g28390		
	Gm *FTa3*	Glyma16g26660		
	Gm *FTa4*	Glyma16g26690		
	Gm *FTb1*	Glyma08g47820		
	Gm *FTb2*	Glyma08g47810		
	Gm *FTb3*	Glyma18g53680		
	Gm *FTb4*	Glyma18g53690		
	Gm *FTc1*	Glyma16g04830		
	Gm *FTc2*	Glyma19g28400		
	Gm *TFL1a*	Glyma03g35250		
	Gm *TFL1b/Dt1*	Glyma19g37890		
	Gm *TFL1c*	Glyma13g22030		
	Gm *TFL1d*	Glyma10g08340		
	Gm *BFTa*	Glyma09g26550		
	Gm *BFTb*	Glyma16g32080		
	Gm *MFTa*	Glyma08g05650		
	Gm *MFTb*	Glyma05g34030		

Supplemental Table 2 Microsynteny in the *FTa*/*FTc* region in soybean (Gm) and Medicago (Mt). Fifteen genes present in the Medicago chromosome 7 region are listed along with their gene model numbers (Medtr7g) and those of their counterparts on soybean chromosome 19 (Glyma19g) and in two different regions of chromosome 16 (Glyma16g). Genes were identified as top hits in reciprocal tBLASTn searches using predicted peptide sequences on Mtr 3.0 at JCVI (Medicago, http://www.jcvi.org/cgi-bin/medicago/index.cgi) and Glyma1.0 at Phytozome (soybean, http://www.phytozome.net/soybean.php). The "Mt other" column lists the second top hits in Gm on Mt and Mt on Mt searches and suggests that no clear second region of microsynteny exists in Medicago. Ordinal numbering refers to the diagram in Supplemental Figure 1.

no.	**identity**	**Gm 16** Glyma16g	**Mt 7** Medtr7g	**Gm 16** Glyma16g	**Gm 19** Glyma19g	**Mt other**
1	AMP-dependent synthetase/ligase		099650	04910	28300	
2	peptidase	26600	099660	04890	28310	8g109470
3	importin-related		099680-720	04880	28320-50	
4	hypothetical protein	26570-90	099740			
5	transferase	26650	099760-800	04860-70	28360-70	3g150860
6	FTa	26660	099820	04840	28390	
7		26690	099850-70			
8	FTc		099890	04830	28400	
9	transmembrane		099900	04810	28420	
10	aquaporin	26720	099920	04800	28430	4g064600
11	nucleoside phosphatase	26730	099940	04790	28440-60	4g042800
12	pentatricopeptide repeat		099950	04780	28470	2g127200
13	nucleoside phosphatase		099970-100050	04770-50		
14	no apical meristem	26740	100100	04740	28500	2g110730
15	glycoamidase		100110		28480	

Supplemental Table 3 – primers

Gene	Accession	Purpose	Primers		Tm (ºC)
PsFTa1		Expression	FTLa-6F FTLa-2R	GCCCAAGCAACCCTACTTTT CCATCCTGGAGCGTAAACCC	60
		Full length cDNA	FTLa-9F FTLa-5R	CCACATATGGCAGGTAGTAGC CATAAAACGACACACACATGGA	60
PsFTa2		Expression	FTLb-3F FTLb-5R	GGAAATGACCCCGTGATCTA TGAATCCCTAAGTTGGGTCG	60
		Full length cDNA	FTLb-5F FTLb-R4	ATGGCCTGTAGTAGCCGGAATCC AGCACCATTGATGCAGTACC	60
PsFTb1		Expression	FTLe1-F4 FTLe1-R5	CCTTGTAATCCTCATATGAGAG CGTTGTTCCTGTAGTTGCTGG	62
		Full length cDNA	FTLe-2FF FTLe-2R	ATGCGTATGAAATCATCGAATCC ATTATATGATCATCCTCCTTCCACC	62
PsFTb2		Expression	FTLe2-F7 FTLe2-R7	CGACTACCGGGACAGCATTT CAGGTGAACCAAGGTTATAAAC	62
		Full length cDNA	FTLe-2FF FTLe-2R	ATGCGTATGAAATCATCGAATCC ATTATATGATCATCCTCCTTCCACC	62
PsFTc		Expression	FTLc-8F FTLc-7R	GATATTCCAGCCACAACAAGC TTATGACGCCACTCTGGAGCAA	62
		Full length cDNA	FTLc-9F FTLc-3R	ATGCCTAGGAATATGGTCGATCC GAACTAACCCCCGCCCACTTGG	60
ACT		Expression	ACT-F ACT-R	GTGTCTGGATTGGAGGATCAATC GGCCACGCTCATCATATTCA	59
PIM	AJ291298	Expression	PIM-4F PIM-6R	GCTTCAGAGTTTGGAACAGC GACTCCATGGTGGTTTGG	58
SEP1	AY884290	Expression	PM6-7F PM6-8R	GATTGCCTGTACTGATTTCG TTGTTGAGCTTGACTTGTGG	60
UNI	AF010190	Expression	UNI-1F UNI-2R	CATCAGAGCTGAAAGAAGG GCTTCCTTTTCACGTTGC	55
LF	AY343326	Expression	LF-CR2 LF-CR3	AAATAAGCAGCAGCAACAGGG CAGACATTCCAGGGACAACAG	60
DET	AY340579	Expression	TFL1a-1F TFL1a-2R	CGTTGGTAGAGTCATAGG AGGATCACTAGGGCCAGG	58
FD		Expression	FD-6F FD-3R	ATTTGATCCAAACGTCGGTGT ATCAACTTTTTGCTCCAGTTCG	60