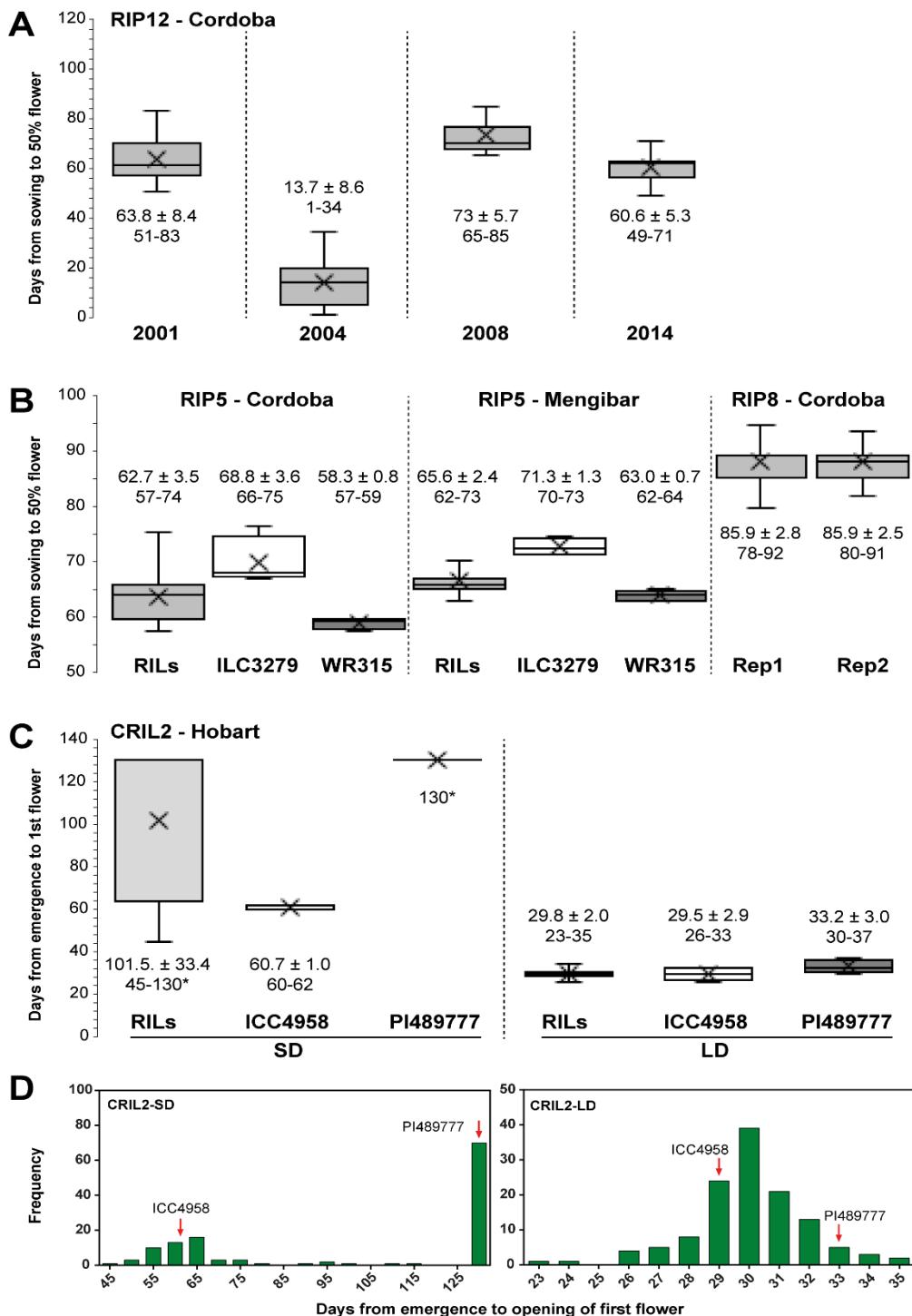
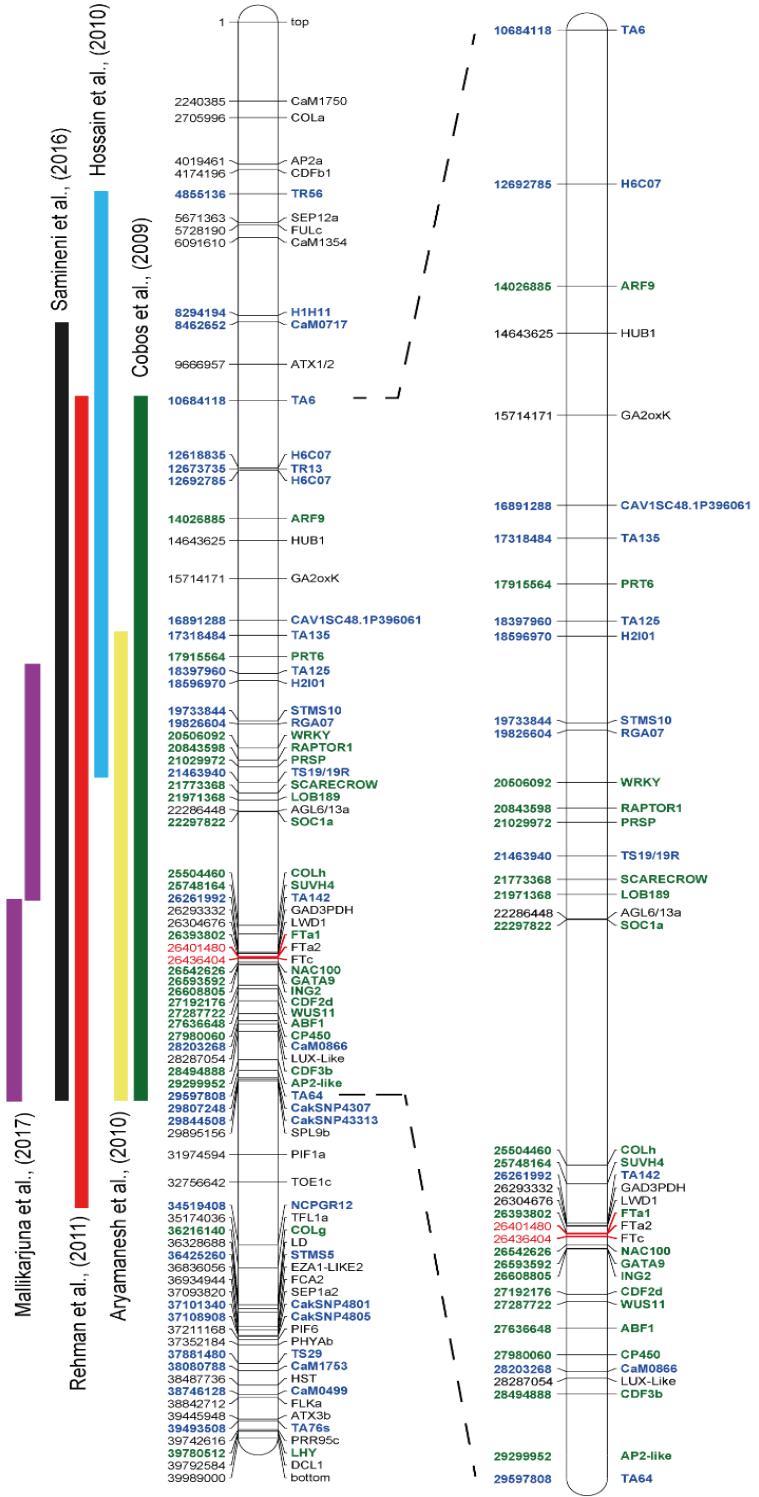


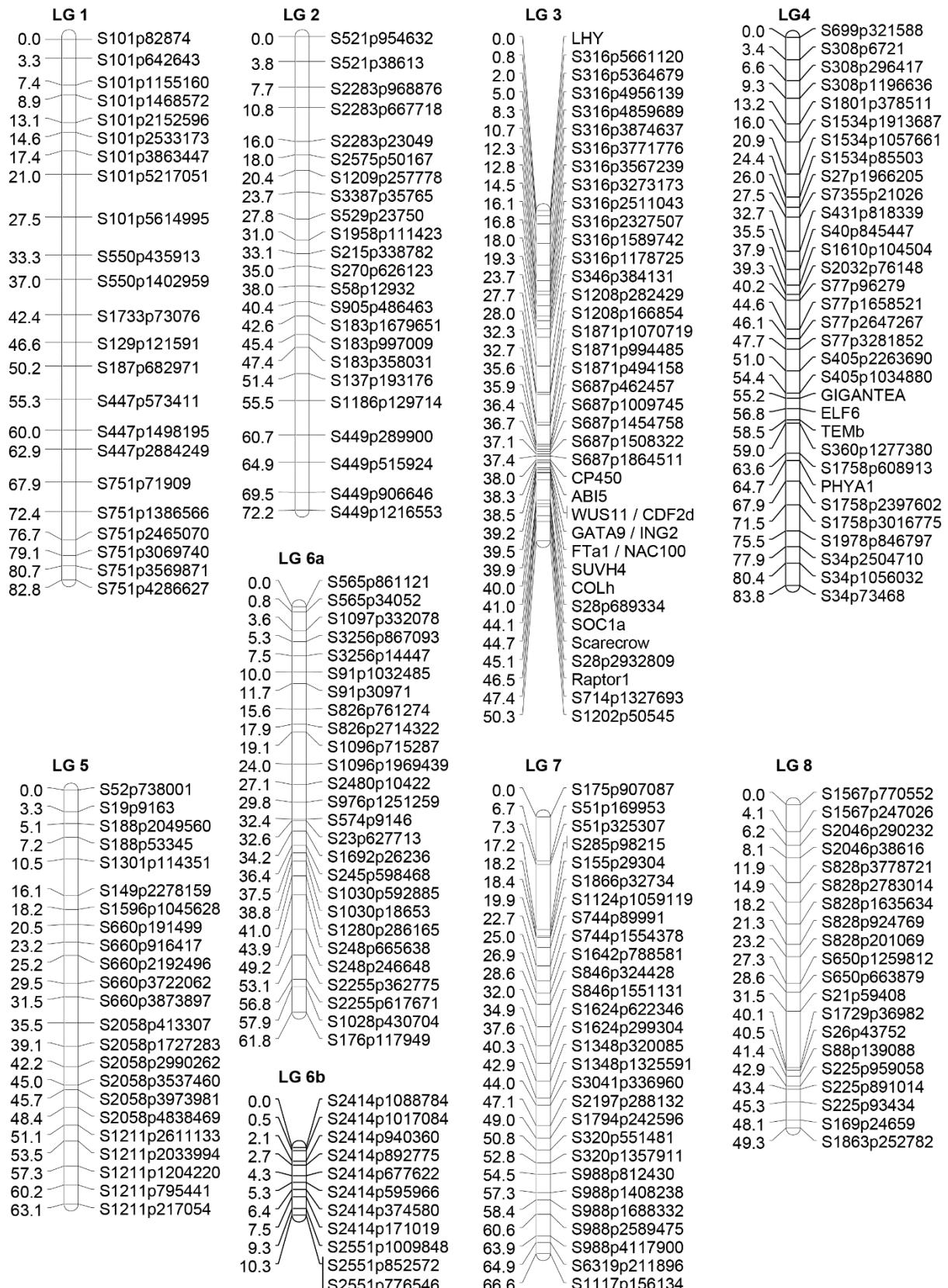
Supplementary Figure 1. High density linkage map of the chickpea interspecific population CRIL2, ICC4958 (*Cicer arietinum*) x PI489777 (*Cicer reticulatum*), which was used to select a subset of markers to construct genetic maps with the HRM markers designed in this study (Figure S4). The high density map is based on 2956 RAD-GBS SNP markers genotyped in 107 RIL lines (von Wettberg et al. 2018). It comprised nine linkage groups, with a total map length of 507.2cM. The map length of each linkage group varied from 9.1cM (LG9) to 78.4cM (LG4) with an average of 56.36cM (Inset table). A total of 2,956 markers were mapped on all of the 9 linkage groups. The number of markers mapped on an individual linkage group varied from 86 (LG3) to 495 (LG4) with an average of 328.44 markers/LG.



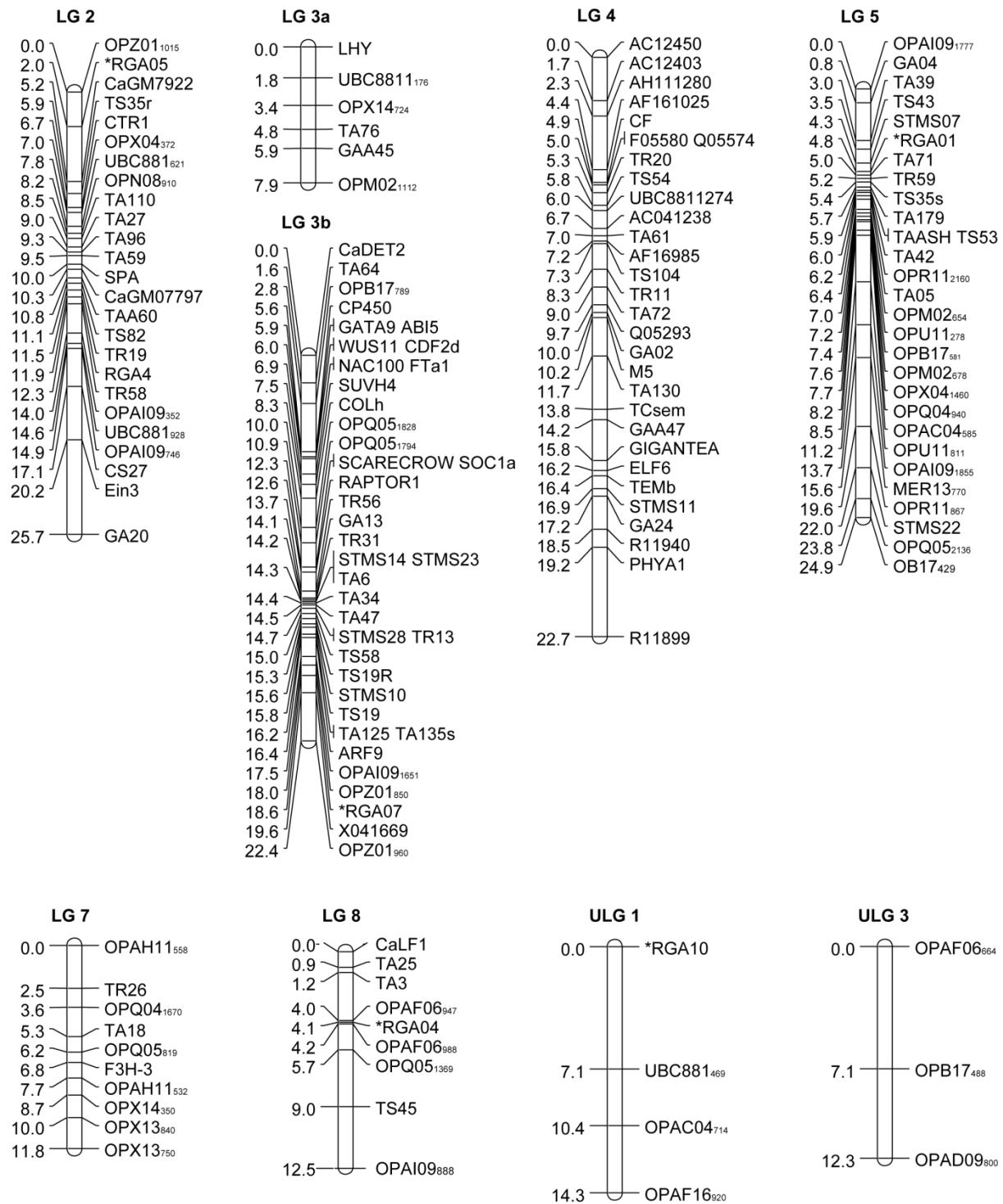
Supplementary Figure 2. Boxplot illustrating the variation in flowering time obtained in different environments for RIP12 (A), RIP5/RIP8 (B) and CRIL2 (C). Note that for RIP12, the flowering values during the 2004 season are relative: the date of the first visible flower in any RIL of the population was considered as day 1 and used as reference for the rest of the population. Box edges denote the lower and upper quantiles with mean (cross) and median (line) values in the middle of the box. Numbers under the boxes correspond to mean \pm standard deviation and range (minimum-maximum value). (D) Frequency distribution of flowering time variation measured in CRIL2 parents and RILs grown under long (LD) and short days (SD). Red arrows indicate the phenotypic values of the parental lines.



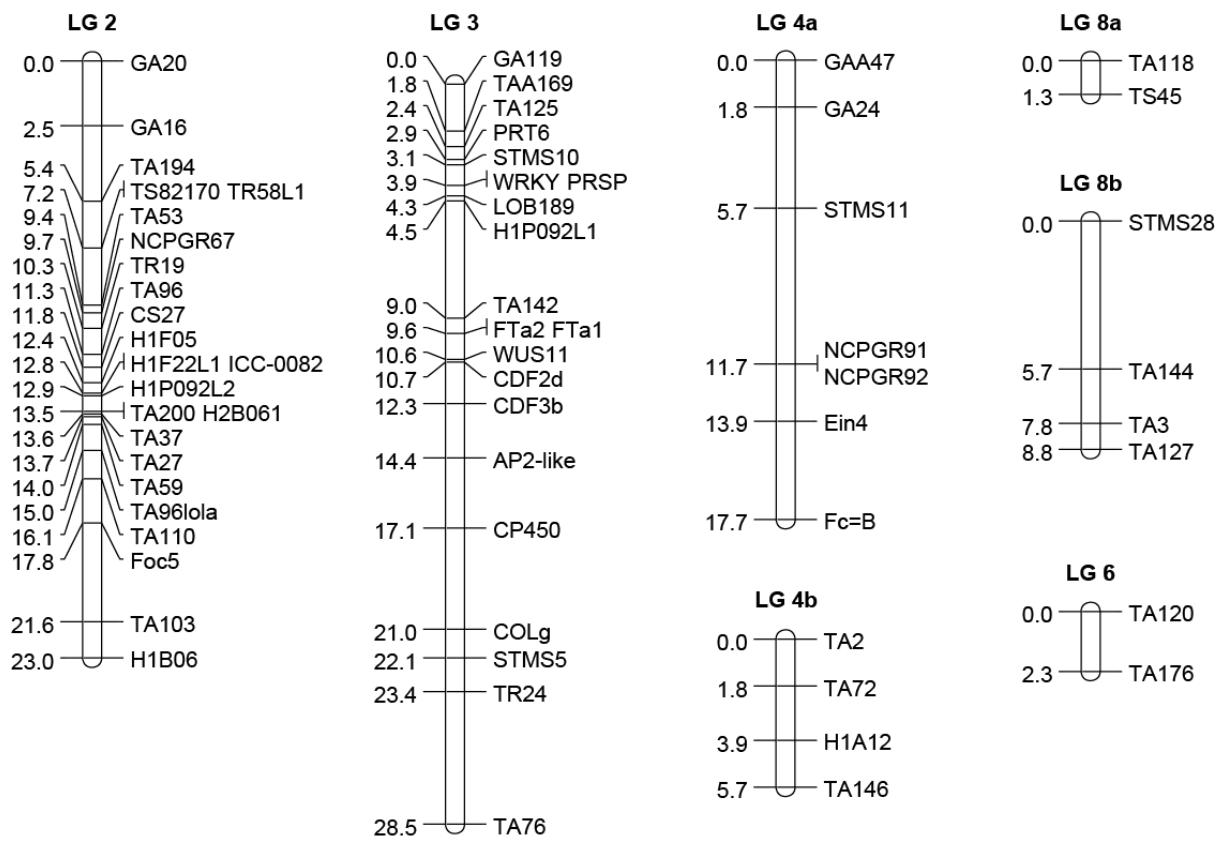
Supplementary Figure 3. Representation of the chickpea chromosome 3 and the region between markers TA6 and TA64, summarizing the different flowering QTL (vertical coloured bars) described to date in the region (Aryamanesh et al. 2010; Cobos et al. 2009; Mallikarjuna et al. 2017; Rehman et al. 2011; Samineni et al. 2016). Numbers on the left of the linkage group indicate physical position in bp, according to the genome assembly of cultivar CDC Frontier (ASM33114v1; Varshney et al., 2013). Interesting markers from previous reports are shown in blue and markers designed for this study are shown in green. Other interesting flowering-related genes are shown in black while the cluster of *FT* genes is highlighted in red.



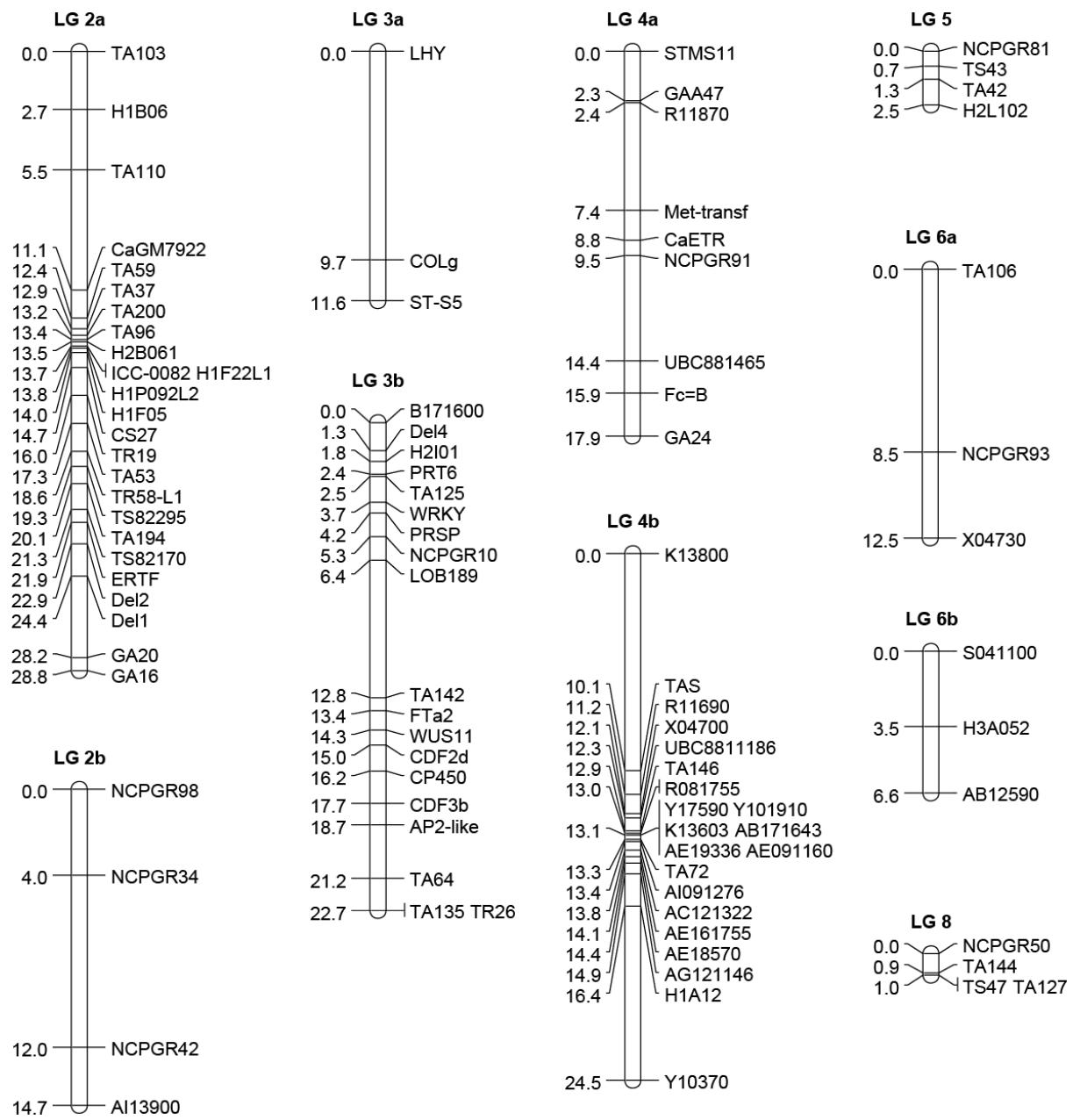
Supplementary Figure 4. Genetic linkage map constructed for CRIL2 (ICC4958 x PI489777). Numbers on the left of each linkage group represent the absolute distances in cM. The map comprises a total of 226 markers, grouped in 9 linkage groups covering a total distance of 540 cM, with an average inter-marker distance of 2.4 cM.



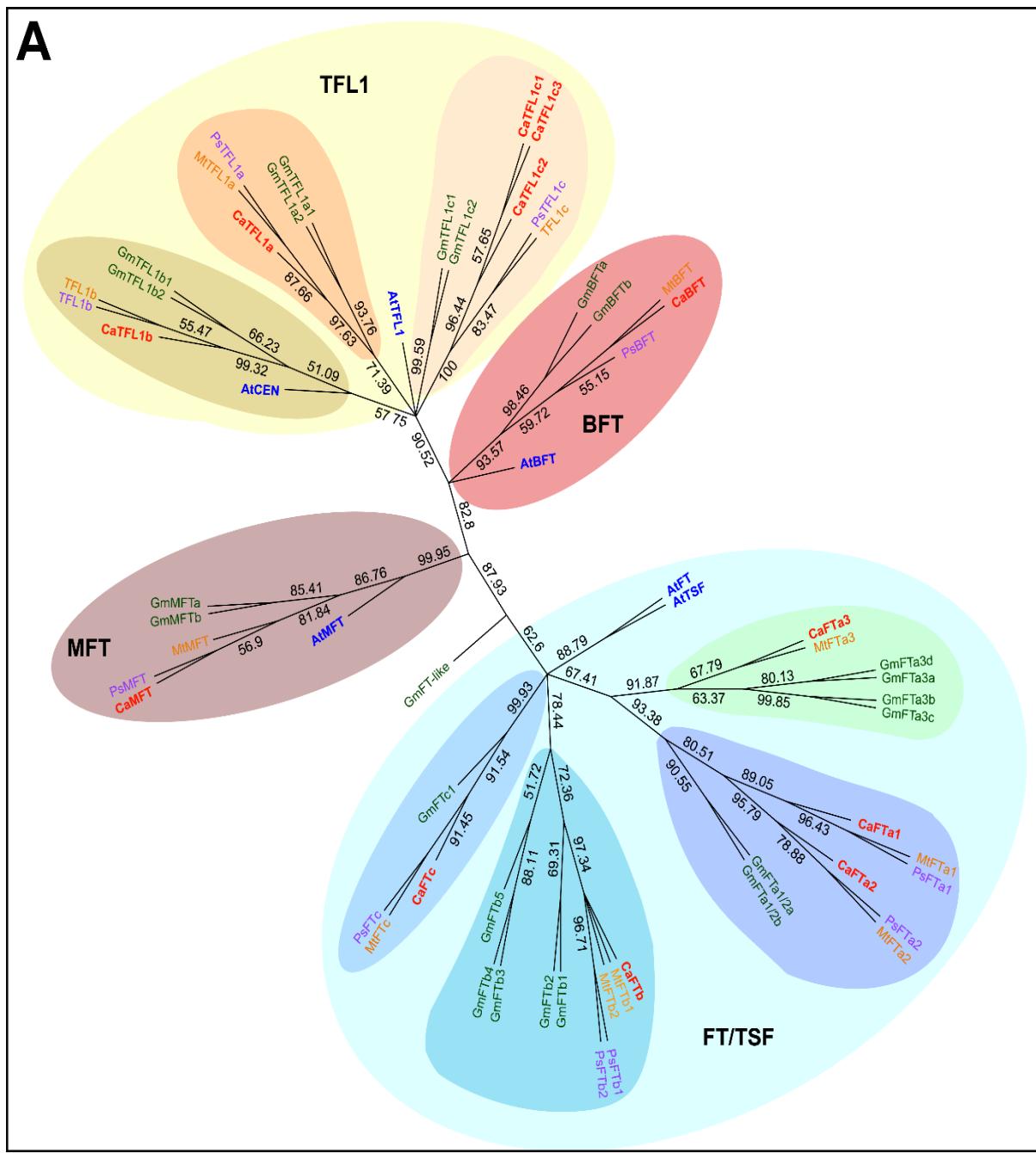
Supplementary Figure 5. Genetic linkage map constructed for RIP12 (ICCL81001 x Cr5-9). Numbers on the left of each linkage group represent the absolute distances in cm. The map comprises a total of 155 markers, grouped in 9 linkage groups covering a total distance of 154.5 cM, with an average inter-marker distance of 1.05 cM.



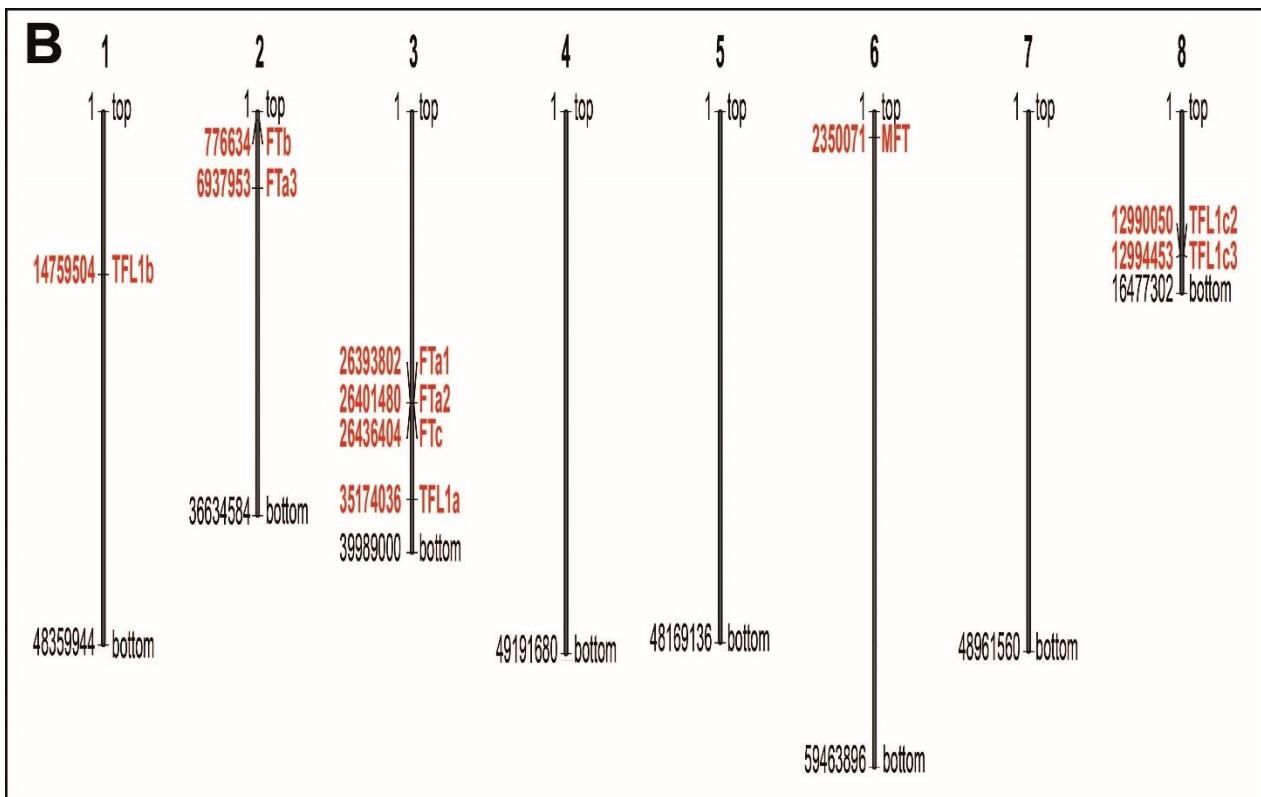
Supplementary Figure 6. Genetic linkage map constructed for RIP5 (WR315 x ILC3279). Numbers on the left of each linkage group represent the absolute distances in cM. The map comprises a total of 64 markers, grouped in 7 linkage groups covering a total distance of 87.3 cM, with an average inter-marker distance of 1.53 cM.



Supplementary Figure 7. Genetic linkage map constructed for RIP8 (ILC3279 x WR315). Numbers on the left of each linkage group represent the absolute distances in cM. The map comprises a total of 95 markers, grouped in 10 linkage groups covering a total distance of 142.7 cM, with an average inter-marker distance of 1.76 cM.



Supplementary Figure 8. (A) Maximum parsimony tree derived from the alignment of phosphatidylethanolamine-binding proteins (PEBP) in *Arabidopsis thaliana* (At, blue), *Cicer arietinum* (Ca, red), *Glycine max* (Gm, green), *Pisum sativum* (Ps, purple) and *Medicago truncatula* (Mt, orange). Accession number of the PEBP genes can be found in Supplementary Table 4. Sequences were aligned with MAFFT (full alignment can be found in Supplementary Figure 9) and the tree was build using PAUP* in Geneious 8 software. Numbers beside branches represent bootstrap support from 1000 replications. (B) In next page; Position of the PEBP genes (in red) in the chickpea reference genome. Bars represent chromosomes, with numbers indicated on top. *BFT* and *TFL1c1* are not included as they were located in an unplaced scaffold (NW_004516558.1 and NW_004516523.1, respectively).



Supplementary Figure 8 B.

Supplementary Figure 9. Multiple sequence alignment of the PEBP sequences from five species described in Supplementary Table 1. Proteins were aligned in Geneious 8 using MAFFT. Residues conserved in more than 80% of the sites are presented with black background/white letters. Those with a conservation between 60-80% show grey background/white letters and those between 40-60% with grey background/black letters.

	*	20	*	40	*	60	*	80					
AtMFT	:	-	-MAA-SV-	DPLVVGVIGDVV	-DNEIPPTANMSVYF	-GPKHITNCEI	-KPSIAVNPKVNIISG	:	57				
MtMFT	:	-	-MAA-SV-	DPLVVGVIGDVV	-DNEIPPSVGSVYF	-GPKHVTNCDI	-KPSIAINPPKVILTG	:	57				
PsMFT	:	-	-MMS-SA-	DPLVVGVIGDVV	-DNEIPPSVAMSVYF	-GPKHVTNCDI	-KPSIAINQPRIDLTG	:	57				
CaMFT	:	-	-MMAA-SV-	DPLVVGVIGDVV	-DNEIPPSVGSVYF	-GPKHVTNCDI	-KPSIAINPPRVILTG	:	58				
GmMFTA	:	-	-MRYLSLSTFSLLCITFVVMMAA-SV-	DPLVVGVIGDVV	-DNEIPPSVNSMSVYF	-GSKHVTNCDI	-KPSIAISPPLDITG	:	75				
GmMFTb	:	-	-MAA-SG-	DPLVVGVIGDVV	-DNEIPPSFNMFVYF	-	-	:	31				
AtBFT	:	-	-MSR-EI-E	DPLVVGVIGDVV	-EMENPNSVIMRVV	-EINSNTIVSNCHEL	-APSILLSKPRVBIGG	:	58				
MtBFT	:	-	-MSR-PL-	DPLVVGVIGDVV	-DLENPSVFMNVY	-STKQVANCHEL	-MPSTIVMNKPVRDVG	:	57				
PsBFT	:	-	-MSR-QL-	DPLVVGVIGDVV	-DLENPSVFMNVY	-STKQVANCHEL	-MPSTIVNKPRVBIGG	:	57				
CaBFT	:	-	-MSR-SL-	DPLVVGVIGDVV	-DLENPSVFMNVY	-STKQVANCHEL	-1PSIVVMNKPRVBIGG	:	57				
GmBFTA	:	-	-MSR-LMEQPLVVGVIGDVV	-DLESPSPVFMNVY	-STKQVANCHEL	-MPSTIMAKPRVBIGG	:	58					
GmBFTb	:	-	-MSR-LM-	DPLVVGVIGDVV	-DLESPSPVFMNVY	-STKQVANCHEL	-MPSTIMAKPRVBIGG	:	57				
AtTSF	:	-	-MSLS-RR-	DPLVVGSVVG	-VL-DPETRISSLKV	-Y-GHREVTNL	-RPSQVLNKPIVBIGG	:	58				
AtFT	:	-	-MSIN-IR-	DPLIVSVVGV	-DPENRSLTLKV	-Y-GQREVTNL	-RPSQVNPKPRVBIGG	:	58				
MtFTa1	:	-	-MAGS-SR-	DPLAVGVIGDV	-DSBENSIPLRV	-Y-GNRDVNN	-KPSQIGNQPRVSVGG	:	58				
PsFTa1	:	-	-MAGS-SR-	DPLAVGVIGDV	-DPEENSVBLRV	-Y-GSPDVNN	-KPSHVGNQPRVNMGG	:	58				
CaFTa1	:	-	-MASG-SR-	DPLVVGVIGDV	-DNEBENSIPLRV	-Y-GNREVN	-KPSQVANQPRASVGG	:	58				
MtFTa2	:	-	-MASG-SRP-	DPLAVGVIGDV	-DPEESTIPLL	-Y-GNKTIVT	-KPSQVANQPVHIGV	:	59				
PsFTa2	:	-	-MACS-SR-	DPLVVGVIGDV	-DPEESSIPLO	-Y-GNRRVNS	-KPSQVANQPOVSIGG	:	58				
CaFTa2	:	-	-MASG-SR-	DPLVVGVIGDV	-DPEESSIPLL	-Y-GNRRVNS	-KPSQVAKQPVQSVGG	:	58				
GmFTa1/2a	:	-	-MPGG-SR-	DPLVVGVIGDV	-DPEESSIPF	-Y-GNREVGN	-KPSQVANQPRVSVGG	:	58				
GmFTa1/2b	:	-	-MPGG-SR-	DPLVVGVIGDV	-DPEESSIPF	-Y-GNKEVGN	-KPSQVPNCPRVSVGG	:	58				
GmFT-like	:	-	-EEEDLIE	DVLIDDCNNF	-VGKLV	-Y-GST	-KPSQVTPNRCR	-TSDQTNDRPIVBIRG	:	50			
MtFTa3	:	-	-MSG-SR-	DPLVVGVIGDV	-VEFQSSIPR	-Y-NGKEELNN	-KPSQVWNQPRVSVGG	:	58				
CaFTa3	:	-	-MPGGST-SR-	DPLVVGVIGDV	-DLPQT	-Y-NGKDVTN	-KPSQVWNQPRVSVGG	:	60				
GmFTa3a	:	-	-MPGG-SR-	DPLVVGVIGDV	-DPEEYSIP	-Y-NNRDVSN	-KPSQVWNQPRVNINGG	:	58				
GmFTa3b	:	-	-MPRG-SR-	DPLVVGVIGDV	-DPFECSI	-Y-NNKDVSN	-KPSQVWNQPRVNINGG	:	58				
GmFTa3c	:	-	-MPRG-SR-	DPLVVGVIGDV	-DPFECSI	-Y-NNKDVSN	-KPSQVWNQPRVNINGG	:	58				
GmFTa3d	:	-	-	-	-	-	-	-	-				
MtFTc	:	-	-MPQN-LV-	DPL--GVIGDV	-SFETNSV	-SLSALI	-NNREISN	-KPSQVLNRPRVNVGG	:	55			
PsFTc	:	-	-MPRN-MV-	DPHVVR	-SVDGV	-NPFNTNSV	-SLSVI	-NNKDIISN	-KPSQVLNRPRVSVGG	:	58		
CaFTc	:	-	-MPRNNG-GV-	DPLVVGVIGDV	-NPFNTNSV	-SLSVI	-NNKEIISN	-KPSQVNRPRASVGG	:	60			
GmFTc1	:	-	-	-A-RE-	DPLVVGVIGDV	-NPFNTNSV	-SFTI	-I-NNRAISN	-KPSQVNRPRVTVGG	:	55		
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PsFTb1	:	-	-	-MRMK-SS-	DPLVVGVIGDV	-DPFIN	-SLSLRV	-VYENNKEVNS	-KPSQIVNPPRVOVGG	:	59		
MtFTb2	:	-	-	-MRIK-ST-	DPLVVGVIGDV	-DPEFTS	-SLRVV	-YDNNKEVNS	-KPSQIVNPPRVOVGG	:	59		
PsFTb2	:	-	-	-MRMK-SS-	DPLVGVVICDV	-DPEFTS	-SLRVV	-YDNNKEVNS	-KPSQIVNPPRVOVGG	:	59		
CaFTb	:	-	-	-MRSKITM-	DPLVVGVIGDV	-DPEFTD	-SLSLRV	-YDNNKEVNS	-KPSQIVNPPRVOVGG	:	60		
GmFTb1	:	-	-	-MAI-TT-	DPLVVGVIGDV	-EPFASS	-SIPR	-VYNNNKEVNS	-KPSQIINFPRVBVGG	:	58		
GmFTb2	:	-	-	-MVOAEVSI	-	-	-	-NICKV	-	:	15		
GmFTb3	:	-	-	-MPR-ST-	DPLVVGVIGDV	-EPFTSS	-SMGIV	-YNNCP	-KPSKILNRPRIBIGG	:	58		
GmFTb4	:	-	-	-M-DPLVGVVG	-DPEFTCS	-SLSLRV	-YDSCS	-VINCC	-KPSQIINCPRVBVGG	:	54		
GmFTb5	:	-	-	-MPI-SM-	DPLVLGRIIGDIL	-DPEFTS	-SLSLRV	-VYNNQSSV	-KPSQIVNKPRINIRG	:	58		
AtCEN	:	-	-MARI-SS-	DPLVVGVIGDV	-DNCLQA	-VKMTV	-YNSDKO	-VYNEH	-KPSVVITYKPKVBVHG	:	59		
AtTFL1	:	-	-MENMGTR-VI-E	DPLIMG	-RVGV	-DFTPT	-TKMNV	-SY-NKKO	-VYNEH	-FPSSVSSKPKVBVHG	:	61	
MtTFL1a	:	-	-MARM-SQ-	DPLIVGVIGDV	-DSEFT	-SMKMTV	-SY-NKKO	-VYNEH	-FPSTINTKPKVBIDG	:	58		
PsTFL1a	:	-	-MARM-AQ-	DPLIVGVIGDV	-DSEFT	-SMKMTV	-SY-NKKO	-VYNEH	-FPSTINTKPKVBIDG	:	58		
CaTFL1a	:	-	-MARM-SQ-	DPLIVGVIGDV	-DSEFT	-SMKMTV	-SY-NKKO	-VYNEH	-FPSTINTKPKVBIDG	:	58		
GmTFL1a1	:	-	-MARM-PL-	DPLIVGVIGDV	-DSEFT	-STKMIV	-SY-NKN	-VYNEH	-FPSTVNTKPKVBIEG	:	58		
GmTFL1a2	:	-	-MAKM-PL-	DPLIVGVIGDV	-DSEFT	-STKMIV	-SY-NKKO	-VYNEH	-FPSTVNTKPKVBIEG	:	58		
MtTFL1b	:	-	-MSI-VT-	DPLAIGVIGDV	-DFTPT	-TKM	-SY-NTKO	-VYNEH	-FPSSVTTKPKVQIHG	:	57		
PsTFL1b	:	-	-MSI-IT-	DPLAIGVIGDV	-DFTTT	-TKM	-SY-NTKO	-VYNEH	-FPSSLI	-TTKPKVQIHG	:	57	
CaTFL1b	:	-	-MMNIVV-LA-	DPLAIGVIGDV	-DFTNT	-TKM	-SY-YNNNT	-KOVYNEH	-FPSSL	-TIKPKVH	:	61	
GmTFL1b1	:	-	-	-SSCYREGDRCS	-GSFH	-NSCEN	-HCL	-QOYKOAYN	-VMSFPFL	:	40		
GmTFL1b2	:	-	-	-MNMI-SS-	DPLAIGVIGDV	-DFTPT	-TKM	-SY-NNK	-KOVYNEH	-FPSSVTTKPKVQIHG	:	58	
MtTFL1c	:	-	-	-MGSI-TS-	DPLILG	-RVGV	-DFTPT	-TKM	-SY-NNK	-EFP	-FPSSVTTKPKVTEIGG	:	58
PsTFL1c	:	-	-	-M-NS-	DPLILG	-RVGV	-DFTAS	-TKM	-SY-NNK	-EFP	-FPSSVTTKPKVQIQG	:	56
CaTFL1c1	:	-	-	-MGSI-SL-	DPLVLG	-KVGV	-DNTPS	-TKM	-SY-NNK	-EFP	-FPSTVSTRPRVBQG	:	58
CaTFL1c2	:	-	-	-MGSI-SL-	DPLVLG	-KVGV	-DNTPS	-TKM	-SY-NNK	-EFP	-FPSTVSTRPRVBQG	:	58
CaTFL1c3	:	-	-	-	-	-	-	-	-MFFNRBISW	:	9		
GmTFL1c1	:	-	-	-MARM-ST-	DPLIIGR	-VIGDV	-GSE	-TP	-TKM	-SYEF	-FPSTITTTRPRVBIGG	:	58
GmTFL1c2	:	-	-	-MAKM-WT-	DPLFIG	-VIGDV	-DS	-TPT	-TKM	-SYH	-FPSTITTTRPKVBIGG	:	57

Supplementary Figure 9. Continued

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AtMFT	:	-HSDEIYTLVMTDPDAPSPSEPNMRBWHWIVVDIPGG-----					TNPNSRGKEIIIPMEPREPVGIHRYIILVLFR			: 124
MtMFT	:	-NDNLTYLVMTDPPDAPSPSEPSMRELIHWIVVDIPGG-----					TNPKRCREIIPYIGPKEPVGIGHRIILVLFE			: 124
PsMFT	:	-NRSIYTLVMTDPDAPSPSEPSIIRFTHWIVVDIPGG-----					TNPKRCRGEIIIPYIGPKEPVGIGHRIILVLFE			: 124
CaMFT	:	-NDNLTYLVMTDPPDAPSPSEPSMRELIHWIVVDIPGG-----					TNPKRCREIIPYIGPKEPVGIGHRIILVLFK			: 125
GmMFTA	:	-NDNLTYLVMTDPPDAPSPSEPSMREBWHWIVVDIPGG-----					TNPFRGKEIVSYVGPREPIGIGHRYIFVLFQ			: 142
GmMFTb	:	-----GPSEPSMREWIHWIVVDILEEQTTHFVHDVACMSTGGSRKEIVPYLGPREPIGIGHRYIFLLFQ								: 94
AtBFT	:	QDLRSSEFTLIMMDPDAPSPSNPYRBYLHWIVTDIPGT-----					TDASFGEEIVYETPKBVAGIHRVFAFLFK			: 126
MtBFT	:	EDMRSAYT-IMTPDAPSPSDPHIREBLHWIVTDIPGT-----					TDVSFGNEIVEYENPKEVIGIHRIVFILFK			: 124
PsBFT	:	DDMRSAFTLIMMDPDAPSPSDPYIREBLHWIVADIPGT-----					TDVSFGKEIVEYENPKEVIGIHRIVFILFK			: 125
CaBFT	:	DDLRSAYTLMITDPDAPSPSDPYIREBLHWIVTDIPGT-----					TDVSFGKEIVEYENPKEVIGIHRIVFILFK			: 125
GmBFTA	:	DDMRSAFTLIMMDPDAPSPSDPHIREBLHWIVTDIPGT-----					TDVSFGKEIVGYESPKEVIGIHRIVFILFK			: 126
GmBFTb	:	DMRSAYTLMITDPDAPSPSDPCIREBLHWIVTDIPGT-----					TDVSFGKEIVGYESPKEVIGIHRIVFILFK			: 125
AtTSF	:	DDFRNEYTLVMVDPDVPSPSNPHOREBYLHWIVTDIPAT-----					TGNAFGNEVVYESPREPSGIHRIIVLVLFR			: 126
AtFT	:	EDLNEYTLVMVDPDVPSPSNPHIREBYLHWIVTDIPAT-----					TGTFGNEIVYENPKEVIGIHRIVFILFR			: 126
MtFTa1	:	NDLRLNEYTLVMDPDPSPSPSNPTFREBYLHWIVTDIPAT-----					TEVTFGNEVVYERPRRTSGIHRIVFILFR			: 126
PsFTa1	:	NDLRLNEYTLVMDPDPSPSPSNPTFREBYLHWIVTDIPAT-----					TEVSGFNEIVSAYERPRRTSGIHRIVFILFR			: 126
CaFTa1	:	NDMRNFYTLVMDPDPSPSPSNPTFREBYLHWIVTDIPAT-----					TGVSGFNEVVYERPRRTSGIHRIVFILFR			: 126
MtFTa2	:	NDPTA1YTLVMDPDPAPSPSPSPEPSFREBLHWIVTDIPAT-----					NAASFGNEVVYESKPRENLGIHRIVFVL LH			: 127
PsFTa2	:	NDPVIYTLVMDPDPAPSPSPSPEPSFREBLHWIVTDIPAT-----					TGASFGNEVVYESKPRENLGIHRIVFVL LR			: 126
CaFTa2	:	NDLRIFYTLVMDPDPAPSPSPNSPFRBYLHWIVTDIPAT-----					AGASFGNEVVYESKPRENLGIHRIVFVL FR			: 126
GmFTa1/2a	:	DDLRFNFTYTMVIVDPDVPSPSNPNFRBYLHWIVTDIPAT-----					TGPNFGNEVVYESPRETMGIHRLVFLFR			: 126
GmFTa1/2b	:	DDLRKFYTMVIVDPDVPSPSNPNFRBYLHWIVTDIPAT-----					TGPNFGNEIVSYESPRETMGIHRLVFLFR			: 126
GmFT-like	:	-DANFYTLYVMDPDPSPSPSRDKPTERBHLLCQYSSRGSNLRY-----					VLTQFFFGBEVVYEGPFPHRWHIRIVFVLFR			: 122
MtFTa3	:	DDLRFNFTYTMVIVDPDVPSPSNPNIREBLHWIVTDIPAT-----					TGPIFGHEVVYESPRESMGIHRIIVFVIFR			: 126
CaFTa3	:	DDLRFNFTYTMVIVDPDVPSPSNPNIREBLHWIVTDIPAT-----					TGPIFGNEVVYENPREFMGIHRIIFVVFQ			: 128
GmFTa3a	:	DDLRFNFTYTLIAVDPDVPSPSDPNIREBLHWIVTDIPAT-----					TGASFGHEVVYESPREMMGIHRIIVFVLFR			: 126
GmFTa3b	:	DDFRNFYTLIAVDPDVPSPSDPNIREBLHWIVTDIPAT-----					TGPIFGHEVVYESPREMMGIHRIIVFVLFR			: 126
GmFTa3c	:	DDFRNFYTLIAVDPDVPSPSDPNIREBLHWIVTDIPAT-----					TGPIFGHEVVYESPREMMGIHRIIVFVLFR			: 126
GmFTa3d	:	-----MMGIHRLVFLFR								: 13
MtFTc	:	DDLRFYTLVMDADAPSPSPSNPLKEYLHWIVTDIPAT-----					TSASFCKEIVVYESPKESAGIHRIVFILFK			: 123
PsFTc	:	EDLRFYTLVMDADAPSPSPSNPLKEYLHWIVTDIPAT-----					TSASFCKEIVVYESPKESAGIHRIVFILFK			: 126
CaFTc	:	EDLRFYTLVMDADAPSPSPSNPLKEYLHWIVTDIPAT-----					TSANFGKEVVYESPNSAGIHLVFLFR			: 128
GmFTc1	:	EDLRFYTLVMDADAPSPSPSNPLKEYLHWIVTDIPAT-----					TNASFGREVVYESPNSAGIHLVFLFQ			: 123
MtFTb1	:	NDLRLYTLVMDPDPGSPSPSNPNREBLHWIVTDIPAT-----					TGTFGQEIVSYESPRETSGIHRIVFVLFR			: 122
PsFTb1	:	NDFRSLYTLVMDPDPGSPSPSNPNREBLHWIVTDIPAT-----					TGTFGQEIVSYESPRETSGIHRIVFVLFQ			: 127
MtFTb2	:	NDLRLYTLVMDPDPGSPSPSNPNREBLHWIVTDIPAT-----					TGTFGQEIVSYESPREASGIHRIVFVLFR			: 127
PsFTb2	:	NDFRSLYTLVMDPDPGSPSPSNPNREBLHWIVTDIPAT-----					TGTAFGQEIVSYESPREASGIHRLMIFVLFQ			: 127
CaFTb	:	NDFRSLYTLVMDPDPGSPSPSNPNREBLHWIVTDIPAT-----					TGTFGQEIVSYESPRETSGIHRIVFVLFR			: 128
GmFTb1	:	DDLRLYTLVMDPDPGSPSPSNPNREBLHWIVTDIPAT-----					TSASFGEVVYESPRETSGIHRIVFVLFR			: 126
GmFTb2	:	-----R-----					TWILIGEQEVVYESQDETSGIHQ-----			: 39
GmFTb3	:	DDLRLYTLVMDPDPGSPGNPTOREBLHWLITNIPAT-----					TGANFGEEIVSYESPREIVGIHRIIVFVLFR			: 126
GmFTb4	:	DDFRSLYTLVMDPDPGSPGNPNQREBLHWLVTNIPAT-----					TGANFGEEIVVYESPREMMGIHRIIFVLF R			: 122
GmFTb5	:	NDIGIFYTLIMVNPDAPSPSPDPMKEYLHWLVTNIPAS-----					TGAATGEEIVVYESPRETSGIHLIAFVLFR			: 126
AtCEN	:	GDMRSSEFTLVMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVSFGCKEIIIGYEMPRENIIGIHRIVYLLFK			: 127
AtTFL1	:	GDMRSSEFTLVMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKEVVYESLPRENSIGIHRIVFVLFR			: 129
MtTFL1a	:	GDMRSSEFTLVMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKEVVYESIPKENIGIHRIVFVLFR			: 126
PsTFL1a	:	ADMRSSEFTLVMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKEIVSYEIPKENIGIHRIVFVLFR			: 126
CaTFL1a	:	GDMRSSEFTLVMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKEIVSYEIPKENIGIHRIVFVLFR			: 126
GmTFL1a1	:	GDMRSSEFTLIMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKELVSYEIPKENIGIHRIVFVLFK			: 126
GmTFL1a2	:	GDMRSSEFTLIMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKELVSYEIPKENIGIHRIVFVLFK			: 126
MtTFL1b	:	GDMRSSEFTLVMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKEVMSYEMPRENIIGIHRIVFLLYK			: 125
PsTFL1b	:	GDMRSSEFTLIMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKEVMSYEMPREQIGIHRIVFLLYK			: 125
CaTFL1b	:	GDMRSSEFTLIMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFCKEVMSYEMPRENIIGIHRIVFILYK			: 129
GmTFL1b1	:	SDMRSEFTLVMTDPPVPGPSDPYIKEYLHWLIVTDIPGT-----					TDAVFCNEVVYESIPRENIIGIHRIVFVLFK			: 108
GmTFL1b2	:	GDMRSSEFTLVMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TDAVFGNEVVEYEILRENIIGIHRIVFVLFK			: 126
MtTFL1c	:	VDMRSSEFTLIMIDPPVPGPSDPYMKBLHWIVTDIPGT-----					TDSIFGCKEILSYEKPKENIGIHRIVFVLFK			: 126
PsTFL1c	:	GDMRSSEFTLIMIDPPVPGPSDPYMKBLHWIVTDIPGT-----					TDSIFGCKEILSYEKPKENIGIHRIVFVLFK			: 124
CaTFL1c1	:	GDMRSSEFTLIMIDPPVPGPSDPYMKBLHWIVTDIPGT-----					TDSIFGCKEILSYEIPKENIGIHRIVFVLFK			: 126
CaTFL1c2	:	GDMRSSEFTLIMIDPPVPGPSDPYMKBLHWIVTDIPGT-----					TDSIFGCKEILSYEIPKENIGIHRIVFVLFK			: 126
CaTFL1c3	:	NFLFTIFLQIMIDPPVPGPSDPYMKBLHWIVTDIPGT-----					TDSIFGCKEILSYEIPKENIGIHRIVFVLFK			: 77
GmTFL1c1	:	GDMRSSEFTLIMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TNASFGKVVLVSYEMPNEENIGIHRIVFVLFK			: 126
GmTFL1c2	:	GDMRSSEFTLIMTDPPVPGPSDPYIKEYLHWIVTDIPGT-----					TNASFGNVLVSYEMPNEENIGIHRIVFVLFK			: 125

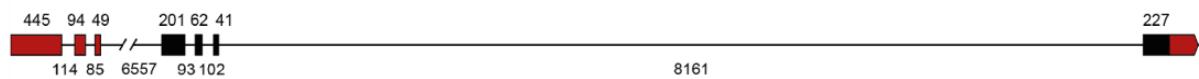
Supplementary Figure 9. Continued

	* 180 * 200 *	
AtMFT	: CNS--PVGLMVQQPPSRANE--STRMFAGHFDLGLPVATVYFNAAQKEPASRR----- : 173	
MtMFT	: QKG--PIGM-VEQPTSRVSE--NTRFASQMLGLPVATVYFNSQKEPQAKR----- : 172	
PsMFT	: QKG--PIGL-VEEPPSRVSE--NTRFASQDLGLPVATVYFNSQKEPQSKE----- : 172	
CaMFT	: QKG--PMGL-VEQPTSRVSE--NTRFASQDLGLPVATVYFNSQKEPQAKR----- : 173	
GmMFTA	: QKG--PLGL-VEQPPTRASE--NTRFARQLDLGLPVATVYFNSQKEPAVKR----- : 190	
GmMFTb	: QKV--PLGL-VEQPPTRASE--NTRFVRQLDLGLPVATVYFNSQKEPAAKR----- : 142	
AtBFT	: QRG--RQAV-KAAPETRECE--NTNAESSYFQLSQPVAAVYFNAAQRETAPRREPSY- : 177	
MtBFT	: QRG--RQIV-RSPSSRDHF--NTRBESQENNLGLPVAAVYFNAAQRETAAARR----- : 171	
PsBFT	: QRG--RQIV-RAPNSRDQE--NTRBESSENNLGLPVAAVYFNAAQRETAAARR----- : 172	
CaBFT	: QRG--RQIV-RSPTFRDHF--NTRBESQONSGLGPVAAVYFNAAQRETAAARR----- : 172	
GmBFTA	: QRG--RQIV-RPPSSRDHF--NTRBESSEENLGLGPVAAVYFNAAQRETAAARR----- : 173	
GmBFTb	: QRG--RQIV-RPPSSRDHF--NTRBESSEENLGLGPVAAVYFNAAQRETAAARR----- : 172	
AtTSF	: QLG--RQTV-YAPGWRQNF--NTRFAEIYNLGLPVAAVYFNQCQRENGCGERT-- : 175	
AtFT	: QLG--RQIV-YAPGWRQNF--NTRFAEIYNLGLPVAAVYFNQCQRENGCGERT-- : 175	
MtFTa1	: QOC--RQRV-YAPGWRQNF--NTRFAELYNLGLSPVAAVFFNCQCQRESGGGTFR- : 176	
PsFTa1	: QOC--RQRV-YAPGWRQNF--NTRFAELYNLGLSPVAAVFFNCQCQRESGGGTFR- : 176	
CaFTa1	: QOC--RQRV-YAPGWRQNF--NTRFAELYNLGLPVAAVFFNCQCQRESGGGTFR- : 176	
MtFTa2	: QOC--RQRV-YAPGWRQNF--NTRFAELYNLGLSPVAAVFFNCQCQRESGGGTFR- : 177	
PsFTa2	: QOC--RQIV-YAPGWRQNF--NTRFBEVLYNIELPVAAVFFNCQCQREAGGGTFR- : 176	
CaFTa2	: QOC--QQVV-FAPGWRQNF--NTRFAELNLDIELPVAAVFFNCQCQRESGGGTFR- : 176	
GmFTa1/2a	: QOF--RQRV-YAPGWRQNF--NTRFAELYNLGLPVAAVFFNCQCQRESGGGTFR- : 175	
GmFTa1/2b	: QOF--RQRV-YAPGWRQNF--NTRFAELYNLGLPVAAVFFNCQCQREIGSGGRTF- : 175	
GmFT-like	: MKS-CRIV-KAPEKRTNF--NTTEFMAKYEP-QDVAGVFFNSRRRG----- : 163	
MtFTa3	: QLG--RQIV-YAPGWRQNF--NTRFAELNMLGLPVAAVYFNQIREHGSGGRLL- : 175	
CaFTa3	: QLG--RQIV-YAPGWRQNF--NTRFAELYNLGLPVSSVYYNIQREAGSGGRRLC- : 178	
GmFTa3a	: QLG--RQIV-YAPGWRQNF--NTRFAELYNLGLPVAAVYFNQIRESGGGRLY- : 176	
GmFTa3b	: QQG--RQIV-YAPGWRQNF--ITRFAELYNLGLPVAAVYFNQIRESGCGGRRLC- : 176	
GmFTa3c	: QQG--RQIV-YAPGWRQNF--ITRFAELYNLGLPVAAVYFNQIRESGCGGRRL- : 175	
GmFTa3d	: QLG--RQIV-YAPGWRQNF--NTRFAELYNLGLPVAAVYFNQIRESGGGRLYH : 64	
MtFTc	: QLG--RDTV-FAPDWRHNF--NTTNEAEINNLV-IVASVYFNQCQRERGCGGRRC- : 171	
PsFTc	: QLG--RDTV-FAPEWRHNF--NTRNFAEINNLV-IVGSVYFNQCQRERGCGGRRC- : 174	
CaFTc	: QLG--RDTV-FAPEWRHNF-KTRNEAEINNLV-IVASVYFNQCQRERGCGGRRS- : 176	
GmFTc1	: QLG--RDTV-ITPEWRHNF-NSRNFAEINNLIA-PVARAYANCQRERGCGGRY- : 171	
MtFTb1	: QPC--RHTV-LAPGWRQNF-ITRFAEFYNLGLPVAAALYFNQCQRENGSGGRLII : 173	
PsFTb1	: QPC--RHTI-LPPGWRQNF-IIIRFAEIYNLGLSPVAAALYFNQCQRENGSGGCRMII : 178	
MtFTb2	: QPC--RHTV-LAPGWRQNF-ITRFAEFYNLGLPVAAALYFNQCQRENGSGGERMVI : 178	
PsFTb2	: QPC--RHTI-LPPGWRQNF-ITRFAEVYMLGLSPVAAALYFNQCQRENGSGGERMIT : 178	
CaFTb	: QPC--RHTI-LAPGWRQNF-VTRFAEVYMLGLPVAAALYFNQIREIGSGGCRMII : 179	
GmFTb1	: QPR--RMSI-PAPGWRQNF-ITRFAEYMLGLPVAAVYFNQCQROGGSGGRLML : 177	
GmFTb2	: -----ENVF-TSSGWQRQNMIMTRFEN--YNNLGLPVAAVYFNQCQROGGSGGERML : 86	
GmFTb3	: QLR--RLTL-QPPGWRQNF-NTRFAEIYMLGLPVAAAMYFNCKRENQDQSSRRR- : 176	
GmFTb4	: QSG--RQIV-YAPGWRQNF-NTRFSESEVYMLGLPVAAATYFNCKRQNNNSARDGRRT : 173	
GmFTb5	: QFD--RQIV-HAPGWRQNF-NTRFSEAEVYMLGLSPVAAVYFNQCQREGGWGCR- : 175	
AtCEN	: QTR--RGSV-VSVPGSRDQF--NTRFAHENDLGLPVAAVFFNCQCQREIAARR----- : 175	
AtTFL1	: QKQ--RVI-TPNIPSRDHF--NTRKFVEYDLGLPVAAVFFNCQCQREIAARR----- : 177	
MtTFL1a	: QKN--RESV-TASPSSRDYF--NTRFASQNDLGLPVAAVYFNQIREIAARR----- : 174	
PsTFL1a	: QRA--RDSV-RATPSSRDHF--NTRSFASQNDLGLPVAAVYFNQIREIAARR----- : 174	
CaTFL1a	: QKS--RESV-MTTPSSRDHF--NTRFASQNDLGLPVAAVYFNQIREIAARR----- : 174	
GmTFL1a1	: QKR--RQCV-TPPTSRDHF--NTRKFIAENDLALPVAAVYFNQIREIAARR----- : 173	
GmTFL1a2	: QKR--RQCV-TPPTSRDHF--NTRKFIAENDLGLPVAAVYFNQIREIAARR----- : 173	
MtTFL1b	: QKR--RQIV-MKIPTSRDHF--NTKKFIAQNDLGLPPVAAVFFNCQCQREIAARR----- : 173	
PsTFL1b	: QKR--RQIV-MKIPTSRDHF--NTQKFAQNDLGLPPVAAVFFNCQCQREIAARR----- : 173	
CaTFL1b	: QKR--RQIV-MKIPTSRDHF--NTKKFIAEDNDLGLPPVAAVFFNCQCQREIAARR----- : 177	
GmTFL1b1	: QKR--RQGV-LKTPTRDHF--NSRSTAEENLGLPPVAAVFFNCQCQREIAARR----- : 156	
GmTFL1b2	: QKR--RGSD--ENSNNKX----- : 140	
MtTFL1c	: QEKGMKHSI--VAPFSSRDHF--NTRFSAQNDLGVPVAAAYFNARRAPRERAS- : 177	
PsTFL1c	: QKRGNKYSI--TCPFSSRDHF--NTRFEDQNDLGLPVAAAYFNARRAPRER- : 173	
CaTFL1c1	: QKK--KHSI--TTPSSRDHF--NTRFSMQNNDLGVPVAAAYFNARRAPGRKPTYI- : 176	
CaTFL1c2	: QKK--KHSI--TTPSSRDHF--NTRFSMQNNDLGVPVAAAYFNARRPAAARKPTYI- : 176	
CaTFL1c3	: QKK--KHSI--TTPSSRDHF--NTRFSMQNNDLGVPVAAAYFNARRPAGRKPTYI- : 127	
GmTFL1c1	: QKR--RQCV-TRPPSSRDHF--NTRFSAENDLGLPVAAVYFNQIREIAARR----- : 174	
GmTFL1c2	: QKR--RQCV-TRPPSSRDHF--STRFSAENDLGLPVASVYFNQIREIAARR----- : 173	

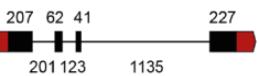
FTa1 3992 bp



FTa2 16510 bp



FTa3 2296 bp



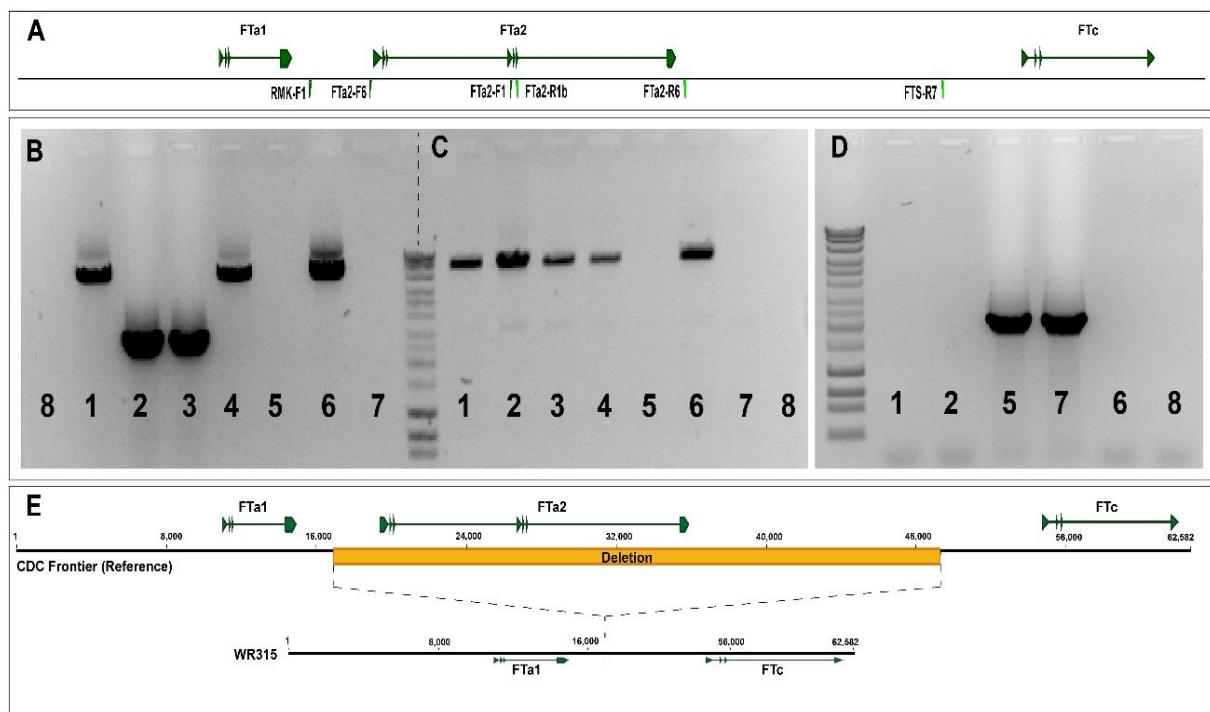
FTc 7257 bp



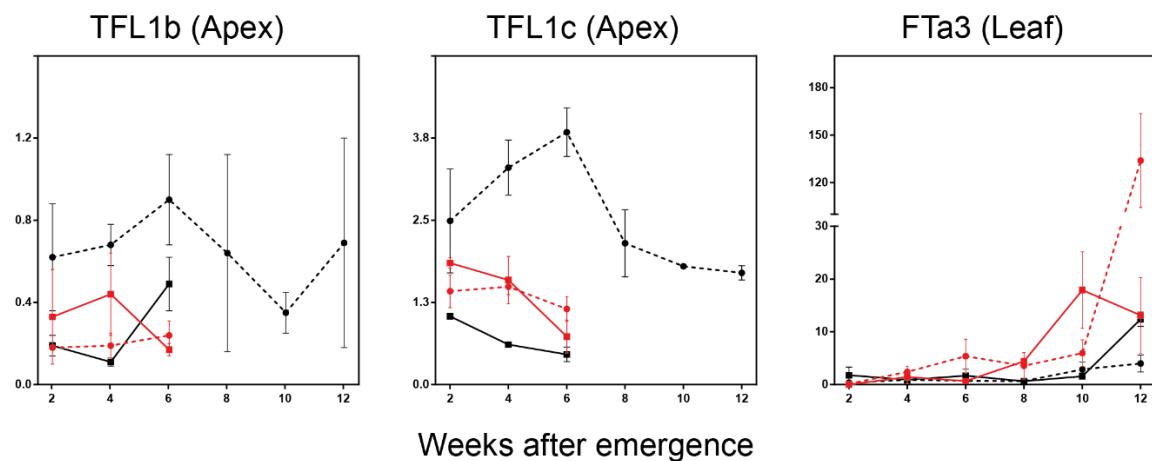
FTb 2898 bp



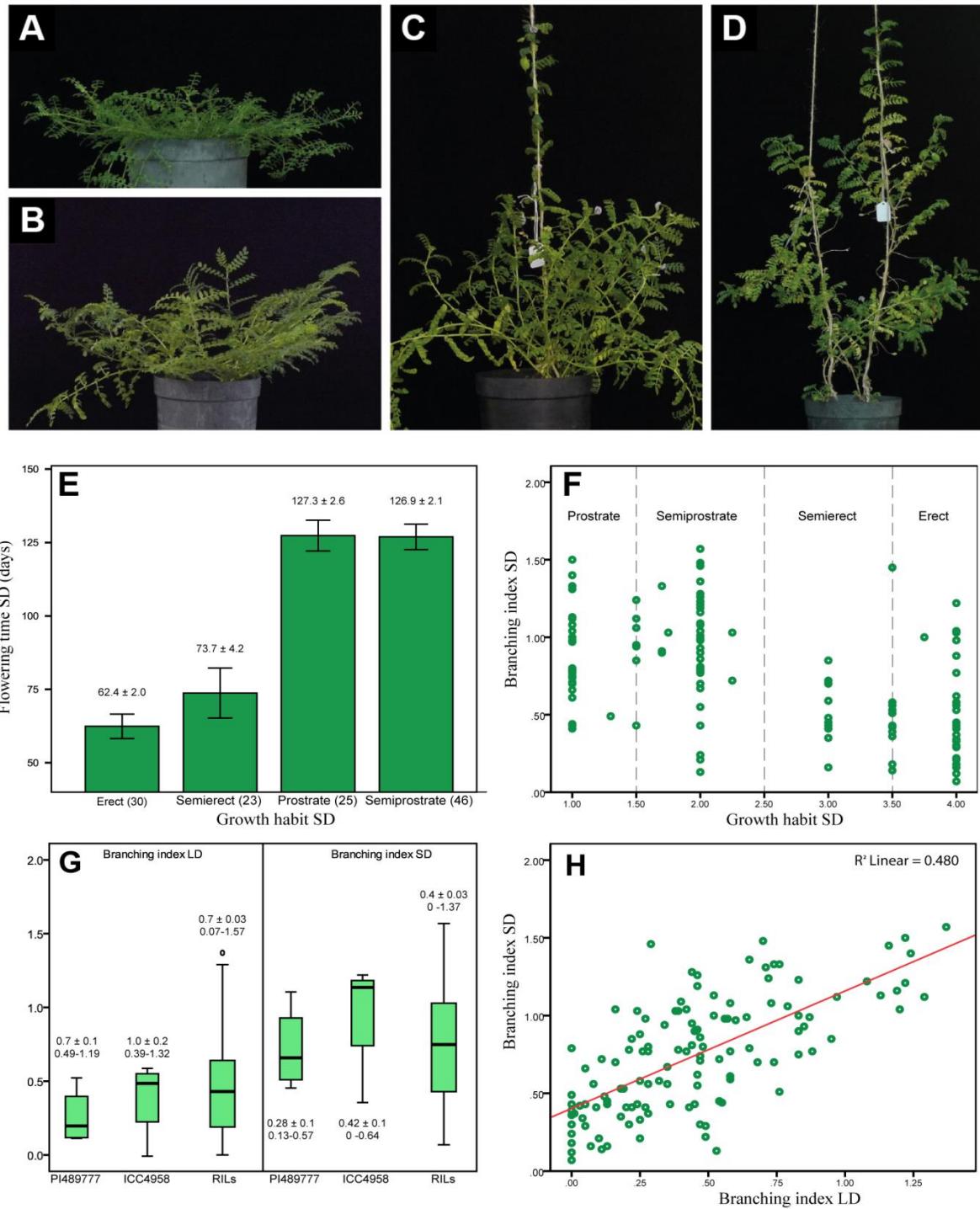
Supplementary Figure 10. Graphic representation of the genomic sequences of the five chickpea *FT* genes. Black boxes indicate exons (sizes over the line, in bp), red boxes the 5' and 3' untranslated regions and lines correspond to introns (sizes under the line).



Supplementary Figure 11. (A) Schematic diagram of the region of chromosome 3 containing the *FTa1-FTa2-FTc* cluster. The black line represents genomic DNA sequence with *FTa1*, *FTa2* and *FTc* gene models shown at top in green (triangles representing exons and line corresponding to introns). The position of the primers used are indicated below; forward and reverse primers are presented in dark and light green, respectively. The failure to amplify any region of *FTa2* in some lines, shown by the electrophoresis gel of the products obtained with primers *FTa2-F6/FTa2-R1b* (**B**) and *FTa2-F1/FTa2-R6* (**C**), suggested a deletion of the gene. 7 chickpea accessions were tested, as follows: 1-ICC4958; 2-PI489777; 3-Cr5-9; 4-CA2156; 5-WR315; 6-ILC3279; 7- ICCV2; 8-SDW. To determine the extent of the deletion, several primers were tested in the *FTa1-FTa2* and *FTa2-FTc* intergenic regions. The primer pair RMK-F1/FTS-R7 successfully yielded a band (**D**). Since the expected size of the amplicon in (**D**) is 33.7 kb according to CDC Frontier genome used as reference, the presence of a 2-3 kb band indicated a probable deletion spanning ~ 30kb. Sequencing of the band confirmed the deletion of 32kb that completely eliminates *FTa2* and includes part of the *FTa1-FTa2* and *FTa2-FTc* intergenic regions (**E**). All PCRs were performed in a final volume of 25 µL containing 50 ng template DNA, 5 µL of 5x reaction buffer, 10 mM dNTPs, 0.2 µM of each primer, 50 mM MgCl₂, 0.1 µL of MangoTaq™ DNA polymerase (Bioline, Australia) and autoclaved Milli-Q water to final volume. Reactions were performed in a thermal cycler using the following program: an initial denaturation of 5 min at 94°C, followed by 35-40 cycles (94°C for 40 seconds, 58°C annealing temperature and 10 min extension) and a final extension of 10 minutes at 72°C. Primers sequences: *FTa2-F6* AAGCCCACAACCCACCTAAGGG; *FTa2-R1b* ACTAGCCCCAGCAGTTGAAG; *FTa2-F1* TAGGCGGAAACGATCTCA GG; *FTa2-R6* GCCATAAACCTCTGCGAACGGC, *RMK-F1* ACTGTTCTGCACACAGTGGCTACC; *FTS-R7* AGGCCAAAGACAAGATCCCG.



Supplementary Figure 12. Relative expression of flowering-related chickpea genes in CRIL2 parental lines. ICC4958 and PI48977 are represented by red and black lines, respectively. Continuous lines/squares indicate long day condition while dashed lines/circles represent short day. TFL1b and TFL1c expression was measured only in apex and FTa3 expression was measured in both tissues but found only in leaf. The average \pm SE of 2 biological and 2 technical replicates is shown, and transcripts were normalized against ACTIN.



Supplementary Figure 13. Variation in growth habit (GH) observed in the CRIL2 population, illustrated by representative examples of the four categories used in the present study: Prostrate (**A**), semi-prostrate (**B**), semi-erect (**C**) and erect (**D**). (**E**) Relationship between GH and flowering phenotype (DTF) of the CRIL2 population grown under SD. Numbers over bars indicate mean DTF ± standard error and those between parentheses correspond to the number of RILs in each category. (**F**) Relationship between GH and branching index (BI) of the CRIL2 population grown under SD. Boxplot illustrating the variation in branching index displayed by CRIL2 parental lines and RILs under LD and SD (**G**). Box edges denote the lower and upper quantiles with median value in the middle of the box. (**H**) Relationship between BI of CRIL2 population grown under SD and LD photoperiod.

Supplementary Table 1. Details of the HRM markers developed in this study for each population, and identity (NCBI GenID) of the genes targeted by them.

Marker	Population	Fw Sequence	Rv Sequence	GeneID
LHY	CRIL2/RIP12	AAACCAACTAACGATACCCCT	TGAGCATCACTCATTCACCA	101500635
	RIPs8/5	CGTCACACTTGAATCTCATTCC	AGTTTCCCCCTTAATAATGTGG	
CP450	CRIL2/RIP12	CACAAAATAGAGAACATGACAGC	ACTTTCCCTTGATGTAGG	101502624
	RIPs8/5	AGAGTTGTATAGTTAAGGATG	GTGTGTGTGTTATCAATTAAAGC	
CDF2d	CRIL2/RIP12	TGGTTCCAATTAAAGTTCAAGTG	AGTCAAGTGTGGTAAGAGTTG	101500722
	RIPs8/5	AGTCGATGCTTAATCTAACAGC	AGATCTGCATAAAAGATGGTTCC	
WUS11	CRIL2/RIP12	CAGCCTGGAATTAACATGCATC	ATGATTTGAGCAATTATTCTGTG	101503157
	RIPs8/5	GCATAACCTAGAGTATCGAGC	CTACTCTGACTTAATGGGTTCG	
FTa1	CRIL2/RIP12	AATCATCCCAAGAGATCAA	TGCACAGTCATTGTGTTTCG	101497376
	RIPs8/5	ACTGTTCTGCACACAGTGGCTACC	AAAGAGATCTAACACATTTCG GAGGAACACGACGCCCTCC	
ING2	CRIL2/RIP12	CATCTCATGGCTCTAAAGAAAGG	ATTTCTTAAGCAATTCTCAATGG	101503708
SUVH4¹	CRIL2/RIP12	TTCGCCGTCACTACCTCG	GGAGATTAAGCTTCGGAGG	101508428
COLh	CRIL2/RIP12	TGCTACATCATTCACCTAGTAACA	TGCCATGATATAGGAAGTCTTAGTT	101504031
SOC1a	CRIL2/RIP12	AAACAAAGAAAAACGAATGTGTC	CGACATATAATTCTGTGGACCG	101510775
SCARECROW²	CRIL2/RIP12	GAGACATGTTGTTAACAGC	CTTGATGGCTCTAACAGC	101513767
RAPTOR1²	CRIL2/RIP12	CCCAATGCCATCCAATCGG	CACACAACAACAACTACCTAGGG	101514864
ARF9²	RIP12	GCAATATGGTGAGAAGAATTTC	TGAGATAGGCAATTAGTCCCTG	101491204
ABI5	CRIL2/RIP12	TTAGCACAAGAACGAGCGAGC	GTGAACGAAAAGGTGTATGAAGG	101490892
GATA9¹	CRIL2/RIP12	GAGGAATATGCTCTTCCATTCC	TGGAAGAGTAATTTCCTCCCTA	101503040
NAC100¹	CRIL2/RIP12	CAGGTCTTAGCAATGACACG	GCCCTATTCTCCCATGTC	101500623
GIGANTEA	CRIL2/RIP12	TGTTGAGTACTTGATTCTAGTTAC	TCAGTATAGATGCATACCTCAGC	101511540
ELF6	CRIL2/RIP12	ACCACCCATTTCAGTTGTTAC	CCAGGGTCAAATTATCATAGTCG	101509509
TEMB	CRIL2/RIP12	GAGTTGAGAAAATCTGTTCAGCG	AGGTTCCGGAAAAGACG	101492303
PHYA1	CRIL2/RIP12	ACAATTGCTTGTAAATGCC	GCCCAGAGATAACTGTCAG	101506511
CDF3b	RIPs8/5	AAACAACCGAAGAAAAATAGG	GAATTGTATAATGTTATCTCG	101499964
COLg	RIPs8/5	AGAGACTCTGAAGGTGTCCC	CAGTGGCTCGAGAAAAGTGG	101499146
AP2-like	RIPs8/5	AAACAAACATCGCACATCACC	CCTTGTCTATTAGTGTCTGC	101502947
LOB189	RIPs8/5	ACAAAATCAATACAAGCAAACC	TGCAACCGTTAGTTGTG	101508422
PRSP	RIPs8/5	GATACATTTCGCTCAAACATG	TGCGTTGAAAAGTGTGTTATTAGC	101491522
PRT6	RIPs8/5	AAATTTCATTCTCCTAAGACAGT	ACGGTCCAACCCAACGTATA	101506928
WRKY	RIPs8/5	TTCTGAGAGCACCGTATGG	AGCATCTCAACTGTAATTAAATG	101511519

(1) Primers designed by Saxena et al (2014)

(2) Primers designed for this study based on SNPs described by Saxena et al (2014)

Supplementary Table 2. Sequence and product size of the primers used to measure the expression of flowering related genes in chickpea

Gene	Fw primer	Rv primer	Product size (bp)		
			Genomic	cDNA	GeneID
<i>ACTIN</i>	ATTGTCTTGAAGTGGTGGTTCT	TTCCTCTCTGGTGGTGCTAC		(Verma et al. 2013)	
<i>PIM</i>	GAACTTCAAGTCCTGAAACAGC	CATTGTGCCTGTTGTTGAGC	472	188	101488241
<i>UNI</i>	TGCAACCGCTAACAGTGAACG	ACGAACAAATGCCGTGAGTTCTTG	660	169	101503680
<i>FTa1</i>	TGCCAATCAACCCAGAGCG	AGTGGGGTTACTTGGGCTAGG	236	101	101497376
<i>FTa2</i>	GTTCTGACGGTGGTTCTCTC	CGGAGGTTCACAAAGAAGG	297	183	101496618
<i>FTc</i>	TGTTGGTGGTGAAGATCTAAGG	ATTCTGCTGAAGGATTG	6616	186	101508200
<i>FTb</i>	GGTAGCTCAAACCCCTCCA	TCCCTCATATTGGGTCACTAGG	618	131	101505276
<i>FTa3</i>	CCATCCCGGAGCATAACACAGTC	TGCACCAAGGCCCTAGCAATCC	1460	196	101515383
<i>E1</i>	AACGACAACAACAAGGGATCGG	TGCAGCCAACAAGAGTCTGC	120	120	101497661
<i>TFLib</i>	TATACCGGGCACAACAGATG	GGAGGTCCAAGGTATTGTC	584	195	101508699
<i>TFL1c</i>	ACGTTCTGGCCAAGTGAT	TGGATCCCTATGTTAGGCTTG	1134	136	101491943

Supplementary Table 3. Description, physical position in the chromosome and GeneID of the 59 genes annotated between markers SUVH4 and GATA9, according to the genome assembly of cultivar CDC Frontier (ASM33114 v1; Varshney et al., 2013), available at the National Center for Biotechnology Information (NCBI; <https://www.ncbi.nlm.nih.gov>).

Marker	Position	GeneID	Description
SUVH4	25748486	101508428	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH4
	25765688	101509380	CLAVATA3/ESR (CLE)-related protein 4A-2-like
	25787922	101509702	uncharacterized protein LOC101509702
	25849917	101510346	protein Mpv17-like, partial
	25899924	101510883	N-alpha-acetyltransferase MAK3
	25908342	101511521	cytochrome b-c1 complex subunit Rieske-4, mitochondrial-like
	25911181	101511199	uncharacterized protein LOC101511199
	25920520	101511847	uncharacterized protein LOC101511847
	25929005	101512385	uncharacterized protein LOC101512385
	25945170	101512699	LRR receptor-like serine/threonine-protein kinase RPK2
	25987693	101513246	UPF0496 protein At3g19330-like
	26006715	101513575	putative serine/threonine-protein kinase isoform X2
	26029555	101514543	chalcone synthase
	26038727	101505971	uncharacterized protein LOC101505971
	26049105	101514869	jasmonate O-methyltransferase-like isoform X2
	26056836	101506278	jasmonate O-methyltransferase-like
	26073603	101506600	3,7-dimethylxanthine N-methyltransferase-like
	26105741	101515408	7-methylxanthosine synthase 1-like
	26119620	101506937	ethylene-responsive transcription factor LEP
	26135351	101515744	nudix hydrolase 12, mitochondrial
	26162323	101488713	calcium-binding mitochondrial carrier protein SCaMC-1-like
	26169052	101489051	uncharacterized protein LOC101489051
	26187333	101489383	histidine biosynthesis bifunctional protein hisIE, chloroplastic
	26191225	101489915	uncharacterized protein LOC101489915
	26198363	105851804	glycine-rich cell wall structural protein 1-like
	26211557	101490249	syntaxin-22-like
	26221867	101490568	syntaxin-22-like
	26223872	101490780	uncharacterized protein LOC101490780
	26228217	101491110	DNA cross-link repair protein SNM1 isoform X1
	26233285	101491643	uncharacterized protein LOC101491643
	26237155	101491949	uncharacterized protein LOC101491949
	26259086	101492622	uncharacterized protein LOC101492622
	26268535	101492953	probable xyloglucan endotransglucosylase/hydrolase protein B
	26275124	101493288	probable xyloglucan endotransglucosylase/hydrolase-like precursor
	26293522	101493610	glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic

Supplementary Table 3. Continued

	26300947	101493929	pentatricopeptide repeat-containing protein At3g26630, chloroplastic
	26304938	101494250	WD repeat-containing protein LWD1
	26309206	105851806	pentatricopeptide repeat-containing protein At3g26630, chloroplastic-like
	26315891	101494555	acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal
	26325185	101494873	eukaryotic peptide chain release factor subunit 1-3
	26331419	101495197	importin-13 isoform X2
	26353855	101495954	INO80 complex subunit D-like
	26365580	101496291	omega-hydroxypalmitate O-feruloyl transferase
FTa1	26393854	101497376	protein FLOWERING LOCUS T-like
	26409508	101496618	protein HEADING DATE 3A-like isoform X1
	26437711	101508200	protein FLOWERING LOCUS T-like
	26446273	101497706	transmembrane and coiled-coil domain-containing protein 1-like
	26454060	101498244	aquaporin SIP1-2-like
	26459034	101498578	apyrase 2-like
	26465157	101499141	pentatricopeptide repeat-containing protein At5g15010, mitochondrial
	26476855	101499461	nucleoside-triphosphatase-like
	26505866	101499961	NAC transcription factor 29
	26513981	101500308	uncharacterized protein LOC101500308
NAC100	26542626	101500623	NAC domain-containing protein 100-like
	26551883	101500931	U11/U12 small nuclear ribonucleoprotein 65 kDa protein
	26560819	101501672	thioredoxin-like 1-1, chloroplastic
	26568175	101501985	CCR4-NOT transcription complex subunit 3 isoform X1
	26586013	101503370	glucan endo-1,3-beta-glucosidase 8-like
GATA9	26593826	101503040	GATA transcription factor 9-like

Supplementary Table 4. Accession number of the PEBP genes from five plant species; *Arabidopsis thaliana*, *Medicago truncatula*, *Pisum sativum* (Pea), *Glycine max* (soybean) and *Cicer arietinum* (chickpea). Soybean accessions were obtained from Wang et al. (2015) and the protein sequences retrieved from the Soybean Knowledge Database [<http://soykb.org>; Joshi et al. (2012)]. Proteins sequences retrieved from the accessions listed were used in the alignment displayed in Supplementary Figure 10.

Arabidopsis		Medicago		Pea	Chickpea		Soybean	
MFT	AT1G18100	Medtr8g106840		PsCam040701	LOC101504081		GmMFTa	Glyma05g34030
							GmMFTb	Glyma08g05650
BFT	AT5G62040	Medtr0020s0120		PsCam044479	LOC101507903		GmBFTA	Glyma09g26550
							GmBFTb	Glyma16g32080
ATC	AT2G27550	-		-	-		-	-
TFL1	AT5G03840	TFL1a	Medtr7g104460	AY340579	TFL1a	LOC101506075	GmTFL1b1	Glyma12g30940
		TFL1b	Medtr2g086270	AY340580	TFL1b	LOC101508699	GmTFL1b2	Glyma13g39360
		TFL1c	Medtr1g060190	AY343326	TFL1c1	LOC101495644	GmTFL1a1	Glyma03g35250
					TFL1c2	LOC101491943	GmTFL1a2	Glyma19g37890
					TFL1c3	LOC101492277	GmTFL1c1	Glyma10g08340
							GmTFL1c2	Glyma13g22030
FT	AT1G65480	FTa1	Medtr7g084970	HQ538822	FTa1	LOC101497376	GmFTc1	Glyma19g28400
TSF	AT4G20370	FTa2	Medtr7g085020	HQ538821	FTa2	LOC101496618	GmFTa3a	Glyma16g26660
		FTa3	Medtr6g033040	-	FTa3	LOC101515383	GmFTa3b	Glyma16g04830
		FTb1	Medtr7g006630	HQ538824	FTb	LOC101505276	GmFTa3c	Glyma16g26690
		FTb2	Medtr7g006690	HQ538825			GmFTa3d	Glyma02g07650
		FTc	Medtr7g085040	HQ538826	FTc	LOC101508200	GmFTa1/2a	Glyma19g28390
							GmFTa1/2b	Glyma16g04840
							GmFTb1	Glyma08g47820
							GmFTb2	Glyma18g53670
							GmFTb3	Glyma18g53680
							GmFTb4	Glyma18g53690
							GmFTb5	Glyma08g47810
							GmFT-like	Glyma08g28470

Supplementary Table 5. Information about sunrise and sunset times (h = hours, m = minutes) in Cordoba, Spain (Latitude, Longitude: 37 52 51, - 4 46 44) and Jaen, Spain (Latitude, Longitude: 37 45 59, - 3 47 21) during the growing seasons of RIP12, RIP5 and RIP8. Source: Observatorio Astronómico Nacional, Instituto Geográfico Nacional, Ministerio de Fomento, Spain.

Cordoba, 2001												Cordoba, 2004												Cordoba, 2014													
Day	February		March		April		May		June		Day	February		March		April		May		June		Day	February		March		April		May		June						
	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset		Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset		Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset			
1	823	1843	751	1913	804	2042	723	2110	659	2136	1	824	1842	750	1913	804	2042	723	2110	658	2136	1	823	1842	751	1912	805	2042	723	2110	659	2136					
2	823	1844	749	1914	803	2043	722	2111	658	2136	2	823	1843	749	1914	803	2043	722	2111	658	2136	2	823	1843	750	1913	803	2043	722	2110	658	2136					
3	822	1845	748	1915	801	2044	721	2112	658	2137	3	822	1844	748	1915	801	2044	721	2112	658	2137	3	822	1845	748	1914	802	2044	721	2111	658	2137					
4	821	1846	747	1916	800	2045	720	2112	658	2138	4	821	1845	746	1916	800	2045	720	2113	657	2138	4	821	1846	747	1915	800	2045	720	2112	658	2137					
5	820	1847	745	1917	750	2046	719	2113	657	2138	5	820	1846	745	1917	758	2046	718	2114	657	2138	5	820	1847	745	1916	759	2046	719	2113	657	2138					
6	819	1848	744	1918	757	2047	718	2114	657	2139	6	819	1847	743	1918	757	2047	717	2115	657	2139	6	819	1848	744	1917	757	2046	718	2114	657	2139					
7	818	1849	742	1919	756	2048	717	2115	657	2139	7	819	1848	742	1919	755	2048	716	2115	657	2139	7	818	1849	742	1918	756	2047	717	2115	657	2139					
8	817	1850	741	1920	754	2048	716	2116	657	2140	8	818	1849	740	1920	754	2049	715	2116	657	2140	8	817	1850	741	1919	754	2048	716	2116	657	2140					
9	816	1851	739	1921	753	2049	715	2117	657	2140	9	816	1851	739	1921	752	2050	714	2117	656	2140	9	816	1851	740	1920	753	2049	715	2117	657	2140					
10	815	1853	738	1921	751	2050	714	2118	656	2141	10	815	1852	737	1922	751	2051	713	2118	656	2141	10	815	1852	738	1921	751	2050	714	2118	656	2141					
11	814	1854	736	1922	750	2051	713	2119	656	2141	11	814	1853	736	1923	749	2051	712	2119	656	2141	11	814	1853	737	1922	750	2051	713	2119	656	2141					
12	813	1855	735	1923	748	2052	712	2120	656	2142	12	813	1854	734	1924	748	2052	711	2120	656	2142	12	813	1855	735	1923	748	2052	712	2120	656	2142					
13	811	1856	733	1924	747	2053	711	2121	656	2142	13	812	1855	733	1925	746	2053	711	2121	656	2142	13	811	1856	734	1924	747	2053	711	2120	656	2142					
14	810	1857	732	1925	745	2054	710	2121	656	2143	14	811	1856	731	1926	745	2054	710	2122	656	2143	14	810	1857	732	1925	746	2054	710	2121	656	2143					
15	809	1858	730	1926	744	2055	709	2122	656	2143	15	810	1857	730	1927	744	2055	709	2123	656	2143	15	809	1858	731	1926	744	2055	709	2122	656	2143					
16	808	1859	729	1927	743	2056	708	2123	656	2143	16	809	1858	728	1927	742	2056	708	2123	656	2143	16	808	1859	729	1927	743	2056	708	2123	656	2143					
17	807	1900	727	1928	741	2057	707	2124	656	2144	17	807	1859	727	1928	741	2057	707	2124	656	2144	17	807	1900	728	1928	741	2057	708	2124	656	2144					
18	805	1901	726	1929	740	2058	707	2125	657	2144	18	806	1900	725	1929	739	2058	706	2125	657	2144	18	806	1901	726	1929	740	2058	707	2125	657	2144					
19	804	1902	724	1930	738	2059	706	2126	657	2144	19	805	1901	724	1930	738	2059	706	2126	657	2144	19	804	1902	724	1930	739	2058	706	2126	657	2144					
20	803	1903	723	1931	737	2059	705	2127	657	2144	20	804	1903	722	1931	737	2100	705	2127	657	2145	20	803	1903	723	1931	737	2059	705	2126	657	2144					
21	802	1904	721	1932	736	2100	704	2127	657	2145	21	803	1904	721	1932	735	2101	704	2128	657	2145	21	802	1904	721	1932	736	2100	705	2127	657	2145					
22	800	1905	720	1933	734	2101	704	2128	657	2145	22	801	1905	719	1933	734	2102	704	2128	657	2145	22	800	1905	720	1933	735	2101	704	2128	657	2145					
23	799	1906	718	1934	733	2102	703	2129	658	2145	23	800	1906	718	1934	733	2103	703	2129	658	2145	23	799	1906	718	1934	733	2102	703	2129	658	2145					
24	798	1907	717	1934	732	2103	702	2130	658	2145	24	799	1907	716	1935	731	2104	702	2130	658	2145	24	798	1907	717	1935	732	2103	703	2130	658	2145					
25	797	1908	716	1935	731	2104	702	2130	658	2145	25	797	1908	715	1936	730	2104	702	2131	658	2145	25	793	1904	712	1931	727	2100	659	2126	654	2141					
26	796	1909	714	1936	730	2105	702	2131	658	2145	26	796	1909	713	1937	729	2105	701	2132	659	2145	26	792	1905	710	1932	726	2100	658	2127	655	2141					
27	794	1910	713	1937	729	2106	701	2132	659	2145	27	795	1910	712	1938	728	2106	701	2132	659	2145	27	790	1906	709	1933	726	2108	700	2133	659	2145					
28	793	1911	711	1938	727	2106	701	2132	659	2145	28	793	1911	710	1939	726	2107	700	2133	659	2145	28	749	1907	707	1934	724	2102	657	2128	655	2141					
29	791	1913	726	2107	700	2133	659	2145	29	752	1912	709	1940	725	2108	700	2134	659	2145	29	706	1935	722	2103	656	2129	656	2141	29	804	2036	721	2104	656	2130	656	2141
30	808	2040	724	2109	659	2135	30	807	2040	724	2109	659	2134	30	806	2041	724	2109	659	2135	30	806	2041	725	2109	659	2134	30	806	2041	725	2109	659	2135			
31	807	2041	725	2109	659	2135	31	806	2041	725	2109	659	2135	31	806	2041	725	2109	659	2135	31	803	2037	720	2105	655	2131	31	803	2037	720	2105	655	2131			

Cordoba, 2003			
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