

Supplemental Figure 1: Phenotypes for key inflorescence mutants in pea.

This figure summarises the main phenotypic features of key pea mutants described in the introduction of this study. For each mutant, a diagram of inflorescence architecture (left), and schematic of the meristem transitions involved (right) are shown for the most severe mutant allele described.

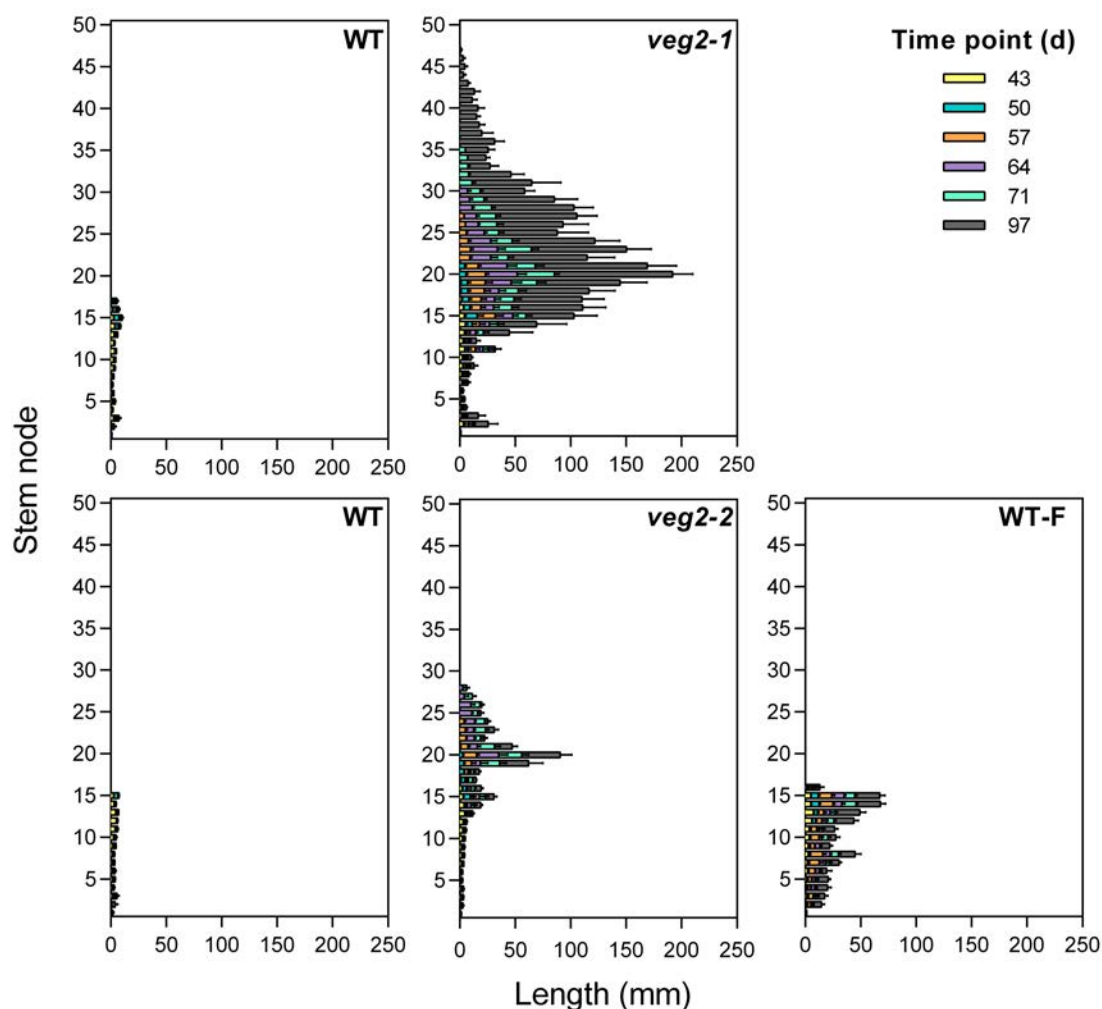
(A) Wild-type.

(B) The *pim* mutant, which bears proliferating secondary inflorescences (I_2 s) in the place of single flowers. After one or more iterations of I_2 structures, flowers are borne, usually with abnormal morphology (Taylor et al., 2002).

(C) The *det* mutant, which exhibits termination of the main stem in an ectopic I_2 (Singer et al., 1990).

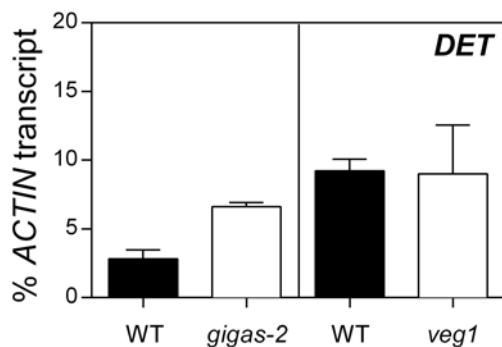
(E) The *veg1* and *gigas* mutants, which share a non-flowering phenotype with aerial branching under LD conditions (Beveridge and Murfet, 1996; Berbel et al., 2012).

In diagrams, arrows indicate the potential for indeterminate growth, green ovals are leaves, pink circles are flowers and blue triangles are stubs terminating each secondary inflorescence (I_2) axis. In schematics, straight arrows indicate meristem transitions and products, and circular arrows indicate meristem indeterminacy. Meristem abbreviations are as follows: vegetative meristem (VM), primary inflorescence meristem (I_1 M), secondary inflorescence meristem (I_2 M), floral meristem (FM).



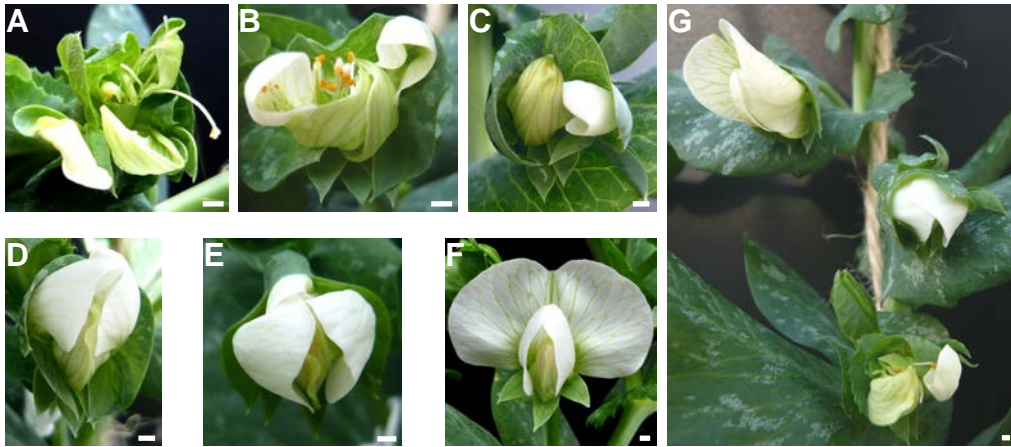
Supplemental Figure 2: Branching in the *veg2* mutants.

Characterisation of branch outgrowth throughout development for intact *veg2-1* and *veg2-2* mutant plants, and their associated wild-type (WT) lines (siblings of *veg2-1*, and line NGB5839, respectively), and deflowered wild-type plants (WT-F: line NGB5839, each flower removed after anthesis). Increase in length of the main lateral branch at each node was calculated from measurements taken at five weekly time points during development (43-71 days after sowing) and a final time point when wild-type plants were senescing (97 days after sowing). Stem node is shown on the y-axis and branch length on the x-axis to represent an upright plant with lateral branches. Branch length is not shown for reproductive nodes in wild-type and *veg2-2* plants as an I_2 was present as the main lateral structure at these nodes. Mean values \pm standard error are shown for $n = 5$ to 6 plants grown in LD (24 light), from the same experiment shown in Figure 2C.



Supplemental Figure 3: *DET* expression in non-flowering *gigas* and *veg1* mutants.

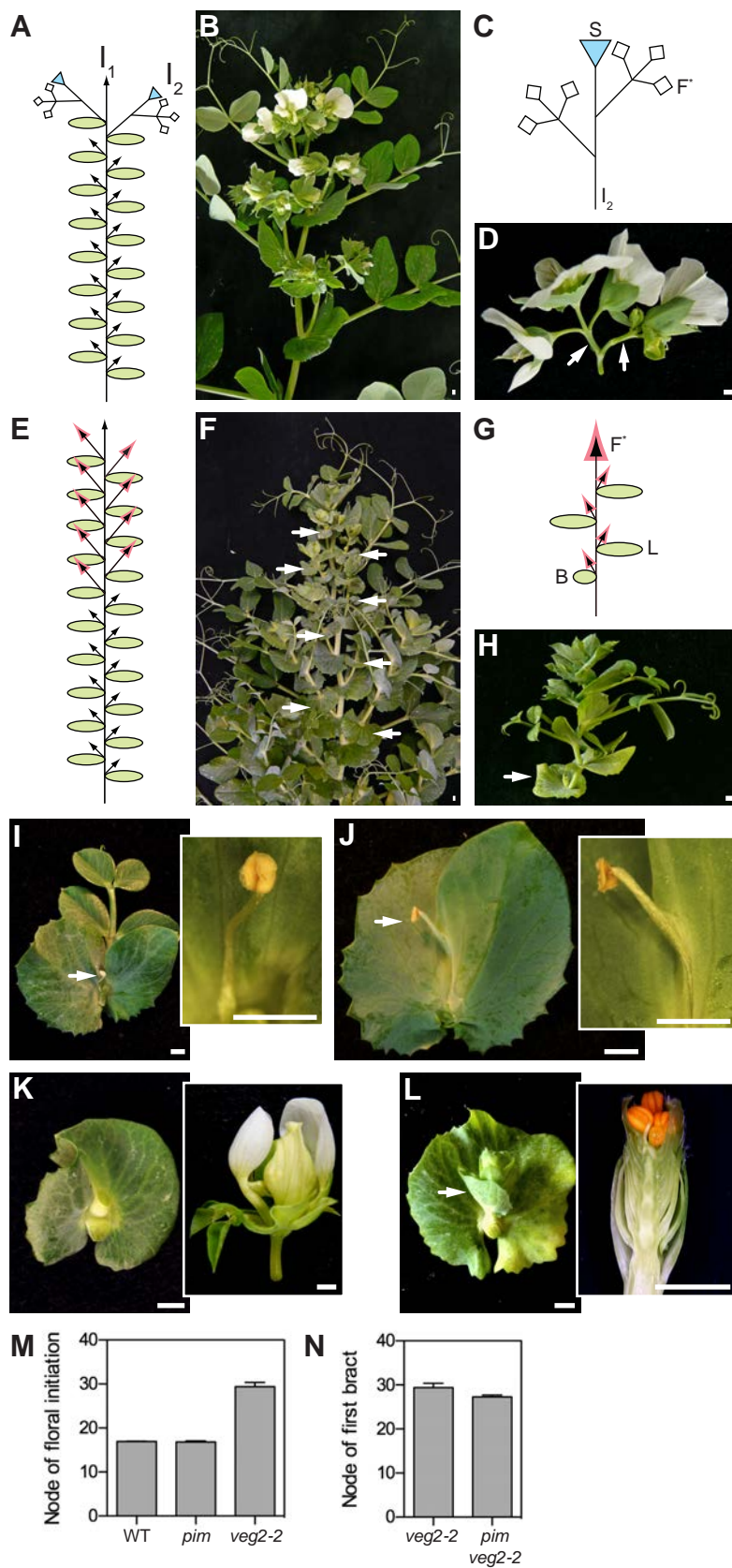
Relative expression of *DET* transcript as a marker of primary inflorescence (I_1) identity in dissected shoot apices during early floral development in wild-type (WT; line NGB5839 or wild-type sibling of *veg1*), 45 days after sowing under LD (18 light/6 dark) conditions, in the same experiment shown in Figures 2E and 6B. Note that expression of *DET* at levels equal to or higher than wild-type indicate acquisition of I_1 identity has occurred prior to this time point, similar to wild-type. Mean \pm standard error are shown for $n = 2$ to 3 biological replicates. For more detailed resolution of *DET* expression in these mutants, please refer to Hecht et al. (2011) and Berbel et al. (2012).



Supplemental Figure 4: Floral morphology in the *veg2-2* mutant.

(A-F) Examples of flowers exhibiting the range in severity of floral morphology defects observed in *veg2-2* mutant plants. Flowers range from **(A)** those defective in all whorls to **(F)** flowers with wild-type morphology.

(G) Photo of a *veg2-2* mutant plant exhibiting decreasing floral defects with increased reproductive node. Scale bars indicate 1mm.



Supplemental Figure 5: The *pim-2 veg2-2* double mutant phenotype. Legend over page.

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(A-D) The *pim-2* single mutant. **(A)** Diagram of the *pim* stem. **(B)** Photograph of aerial stem nodes. **(C)** Diagram and **(D)** photograph of the *pim* secondary inflorescence (I_2) with normal I_2 morphology but groups of proliferating abnormal I_2 structures borne in place of single flowers. Arrows indicate where the pedicel of a single flower would be in wild-type.

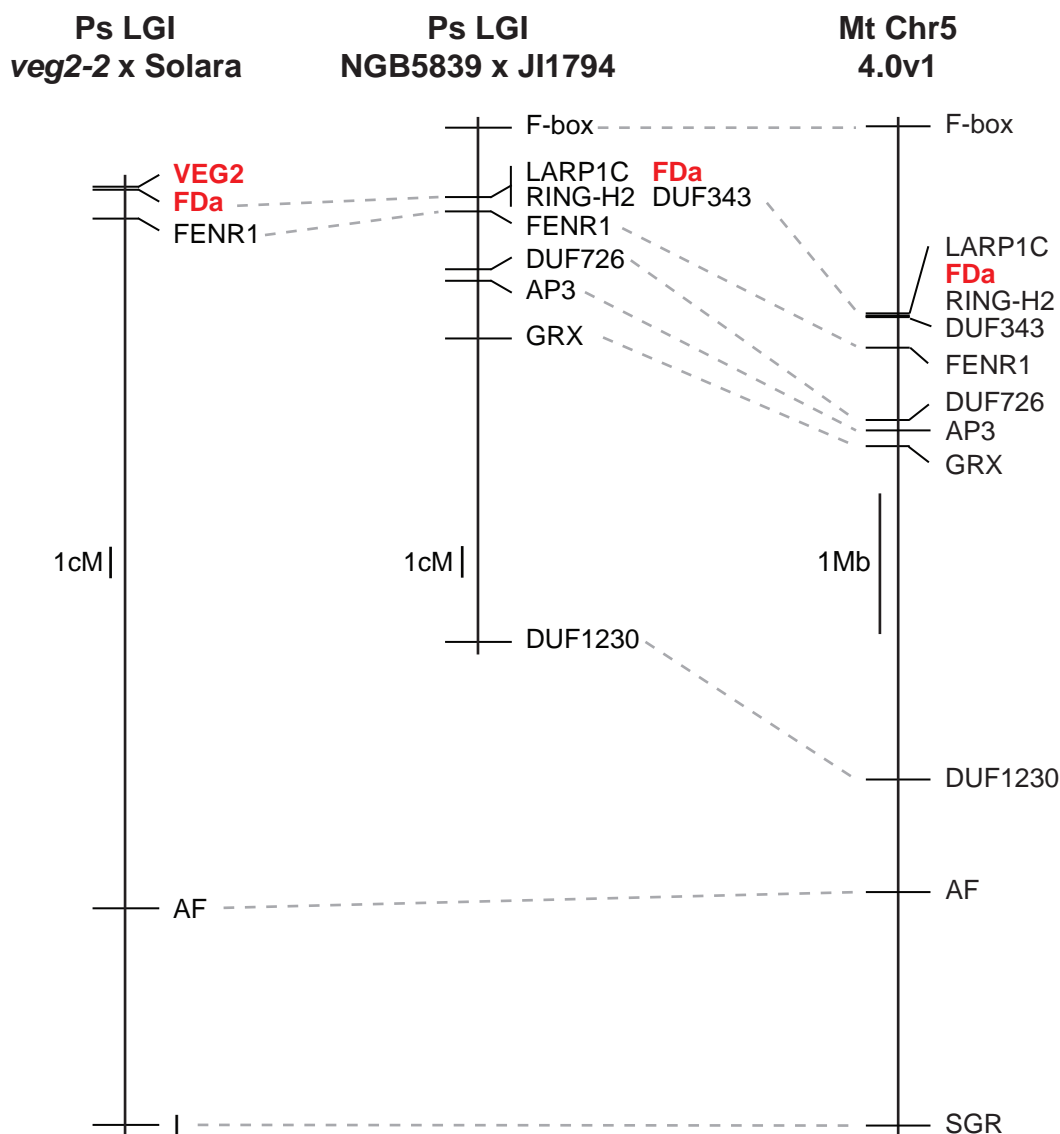
(E-J) The *pim-2 veg2-2* double mutant. **(E)** Diagram of the *pim veg2-2* stem. **(F)** Photograph of aerial stem nodes. Branches that had a bract present instead of a leaf at the first branch node (arrows in **F**) developed instead of I_2 structures at aerial nodes. The presence of a bract made these branches distinct from vegetative branches at lower nodes, but reminiscent of the ' I_2 ' structures in *veg2-2*, which have a bract subtending each flower. Once initiated, these branches were present at every subsequent aerial node, as is seen for I_2 structures in wild-type pea. *pim veg2-2* plants lacked recognisable flowers, but eventually produced floral organs at upper nodes on branches and/or the main stem. **(G)** Diagram and **(H)** photograph of a branch borne on the main stem of the *pim veg2-2* double mutant, which had a bract (B) at the first node (arrow in **H**), leaves (L) at subsequent nodes, and showed acquisition of partial floral identity at later nodes. **(I)** Leaf dissected from an upper node of a branch that acquired partial floral identity, with an axillary stamen (arrow; inset at higher magnification). **(J)** A reduced leaf (back) dissected from an upper branch node, with a stamen (arrow; inset at higher magnification) fused to the leaf in place of a rachis.

(K-L) Bracts and associated axillary structures in *veg2-2* and *veg2-2 pim*. **(K)** Bract dissected from a *veg2-2* ' I_2 ', where the bract subtended an axillary flower (removed for clarity and shown inset only). **(L)** Bract dissected from a *veg2-2 pim* aerial branch, shown subtending an axillary bud which also had a bract at the first node (arrow), and eventually acquired partial floral identity (stamens visible in dissected bud, inset).

(M-N) Comparison of **(M)** node of floral initiation in wild-type (WT), *pim* and *veg2-2* single mutants, and **(N)** node of first axillary structure borne from the main stem bearing a bract instead of a leaf at the first node. In *veg2-2* the node of floral initiation is the same as the node of first bract, as *veg2-2* I_2 structures have bracts subtending each flower. Values represent mean \pm standard error for $n = 11-14$ plants per genotype.

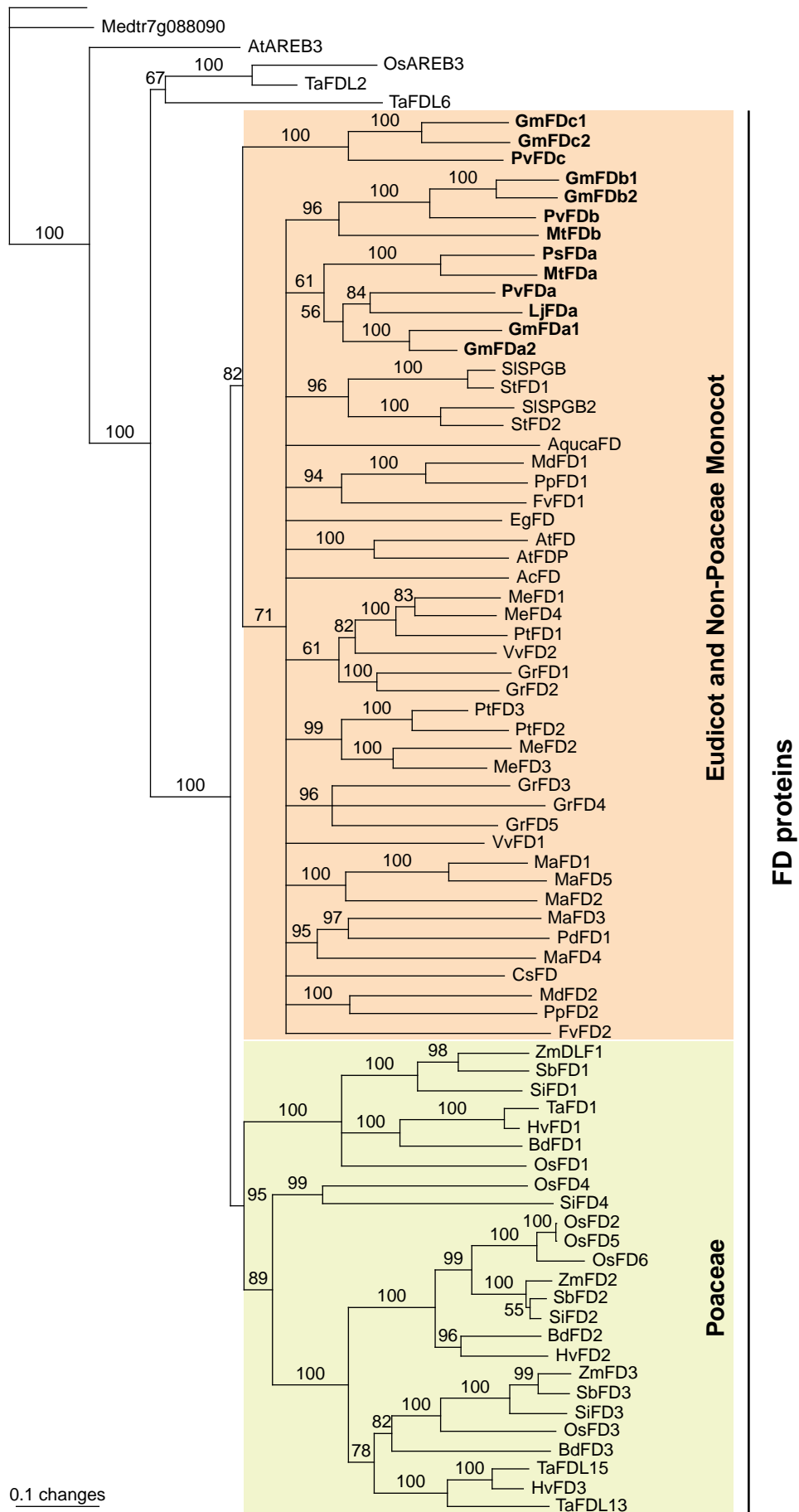
In diagrams, arrows indicate the potential for indeterminate growth, pink arrows indicate the acquisition of partial floral identity, white squares are abnormal flowers (F*), blue triangles are terminal stubs (S), and green ovals are leaves (L) or bracts (B).

Scale bars in photographs indicate 2mm.



Supplemental Figure 6: Comparative map for pea and Medicago showing relative locations of *VEG2/FDa* and surrounding genes.

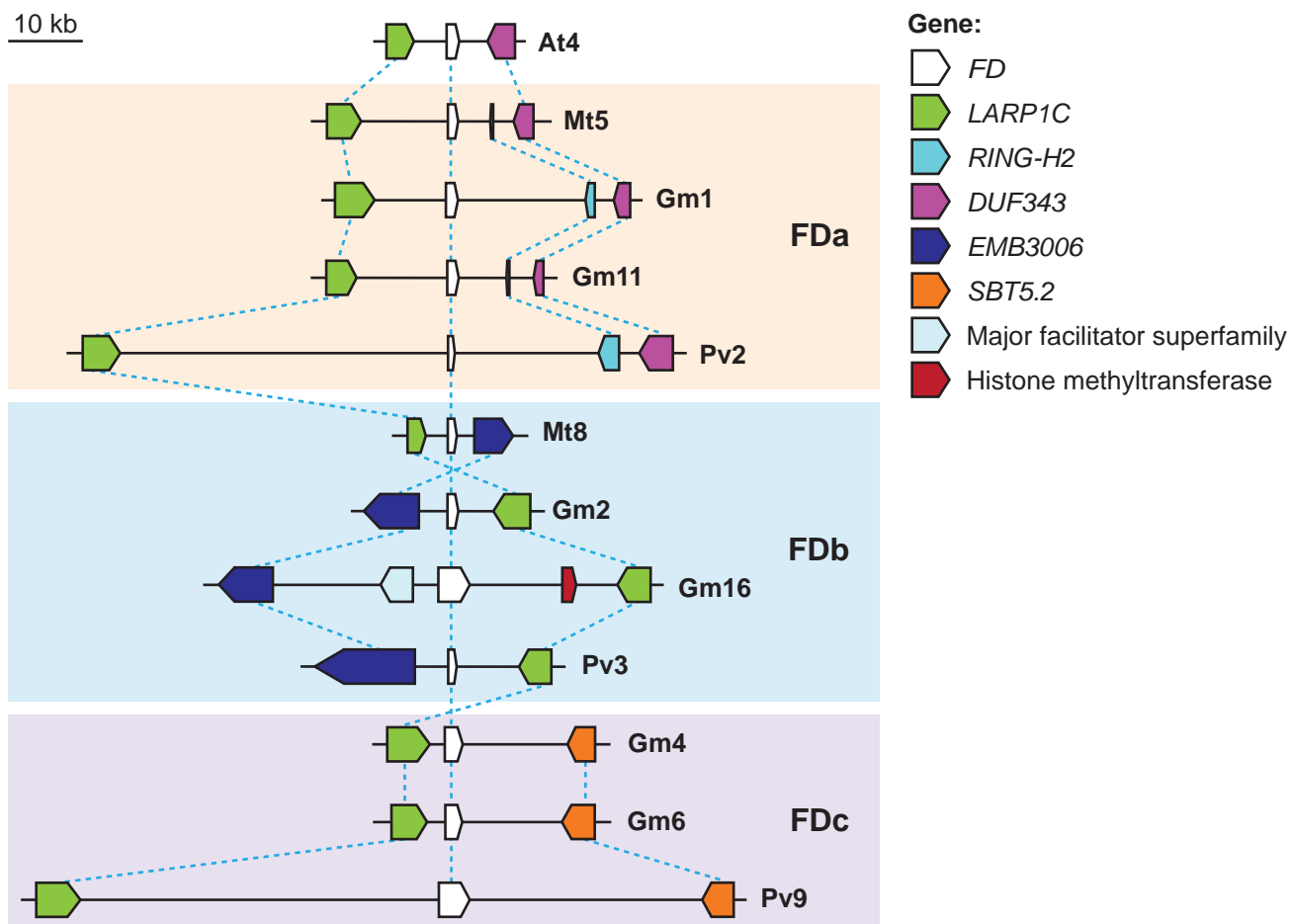
Corresponding genes are linked between pea linkage group I (Ps LGI) and Medicago chromosome 5 (Mt Chr5) by dashed lines. For pea, distances were estimated from the segregation data of two F_2 populations from crosses between *veg2-2* and Solara (114 plants), and NGB5839 and JI1794 (92 plants), using JoinMap software (v4; Kyazma B.V., Wageningen, Netherlands). There were no recombination events between *FDa* and *VEG2*, using a marker for *FDa* based on the G536A SNP (Figure 4), which co-segregated perfectly with *veg2-2* phenotype. Full details for markers and corresponding Medicago genes are given in Supplemental Table 1.



Supplemental Figure 7: Phylogram of the angiosperm FD family. Legend over page.

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Phylogram of FD proteins from diverse eudicot and monocot species. Proteins previously identified as FD-like that fall outside the core FD family (GmFDL19, Medtr7g088090, TaFDL2 and TaFDL6; Li and Dubcovsky, 2008; Pierre et al., 2008; Nan et al., 2014) and other related group A bZIP proteins (AtAREB3 and OsAREB3) are also included. Alternative names for previously identified soybean proteins GmFDL02 (GmFDb1), GmFDL04 (GmFDc1) and GmFDL0602 (GmFDc2) are adopted to better reflect wider phylogenetic relationships. Bootstrap values obtained from 10,000 trees are indicated as a percentage above each branch. Branches with bootstrap values <55% have been collapsed. Legume FD proteins are shown in bold. The analysis is based on the sequence alignment shown in Supplemental Dataset 2. Sequence details and species abbreviations are given in Supplemental Table 2.



Supplemental Figure 8: Microsynteny between genomic regions containing *FD* and flanking genes in *Arabidopsis* and legume species.

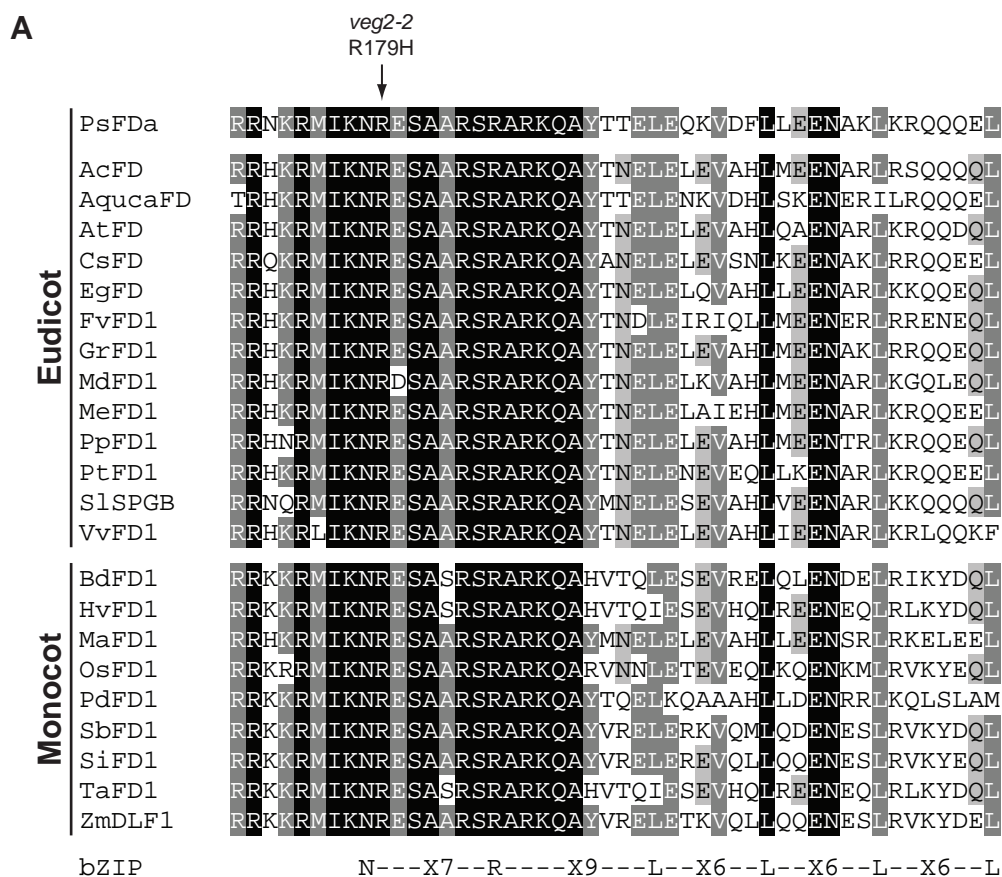
The genes flanking *FD* in *Arabidopsis* (At), and legume *FDa*, *FDb*, and *FDC* genes in *Medicago* (Mt), common bean (Pv) and soybean (Gm) are shown. Genes are represented as boxes with point showing putative direction of transcription. Gene details are given in Supplemental Table 4. Chromosome number is indicated for each species. Between species, corresponding genes are connected by dashed lines.

Supplemental Figure 9: Conserved nature of the amino acid altered by the *veg2-2* SNP.

(A) Alignment of predicted protein sequence for the bZIP domain showing conservation of the arginine altered in the *veg2-2* mutant between FD proteins from diverse eudicot species (Ac, Kiwifruit; Aquca, Aquilegia; At, Arabidopsis; Cs, Cucumber; Eg, Eucalyptus; Fv, Strawberry; Gr, Cotton; Md, Apple; Me, Cassava; Pp, Peach; Pt, Poplar; Sl, Tomato; Vv, Grape) and monocot species (Bd, Brachypodium; Hv, Barley; Ma, Banana; Os, Rice; Pd, Date palm; Sb, Sorghum; Si, Foxtail millet; Ta, Wheat; Zm, Maize).

(B) Alignment of the bZIP domain and surrounding region for all Arabidopsis bZIP family proteins, illustrating conservation of the arginine altered in the pea *veg2-2* mutant (arrow). Letters in parenthesis indicate group of bZIP protein as defined by Corrêa (2008).

Shading in alignments indicates degree of conservation: black = 100%, dark grey = 80%, light grey = 60%. Sequence details are given in Supplemental Table 2.



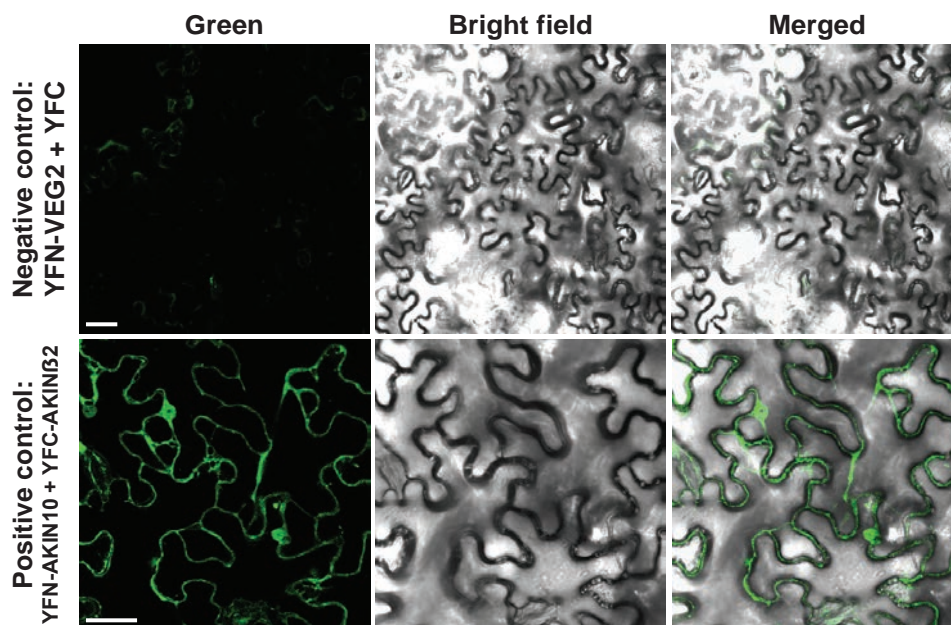
B

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AtFD      (A) GNRHRKRMIKNRESAARSRARKQAYTNEELEVVAHQAEENARLKR
AtFDP     (A) GDRRYKRMIKNRESAARSRARKQAYTNEELEIAHQTENARLKI
AtABF1    (A) VERRQKRMIKNRESAARSRARKQAYTLEEAETESKLVNQDLQK
AtABF2    (A) VERRQKRMIKNRESAARSRARKQAYTVEEAFAVAKKEENDELQR
AtABF3    (A) IERRQKRMIKNRESAARSRARKQAYTMEEAETIAQLKELNEELQK
AtABF4    (A) IERRQKRMIKNRESAARSRARKQAYTLEEAETEKKKTNQQLQK
AtABI5    (A) VERRQKRMIKNRESAARSRARKQAYTVEEAELNQLKEENAQLKH
AtAREB3   (A) VERRQKRMIKNRESAARSRARKQAYTHEEIKVSRTEENERLKR
AtbZIP13  (A) AAQRQRMIKNNRESAARSRERKQAYQVEEALAAKTEENELLSK
AtbZIP15  (A) VDKKLRKIKNRESAARSRARKQAYTMEVEVELENLKDYEEELK
AtDPBF2   (A) MERRQRMIKNNRESAARSRARQAYTVEEELNNTTEENTKQKE
AtDPBF4   (A) VERRQKRMIKNRESAARSRARKQAYTHEEIKVSRTEENELRRR
AtGBF4    (A) AAQRQRMIKNNRESAARSRERKQAYQVEEETLAAKTEENELLSK
AtbZIP17  (B) DEKKRARLMLNRESAQLSRQRKHYVEELEEKVRNMHSTITDNG
AtbZIP28  (B) DKRKLIRQIRNRESAQLSRLRKKQQTTEEERKVKSMNATIAELNG
AtbZIP49  (B) EKKNVRLVLRNRESAHLSRQRKHYVEELEDKVKNMHSTISELSS
AtbZIP9   (C) DLKRIREFMNSNRESAKRSRRRQOYLVDEETQVDSLKGDNSTLYK
AtbZIP25  (C) DVKRARRMLSNRESARRSRRRQEQMNEFDTQVQGLRAEHSTLIN
AtBZO2H1  (C) DVKKSRRMLSNRESARRSRRRQEQTSDLEETQVNDLKEGHSLLK
AtBZO2H3  (C) NVKRVKMLSNRESARRSRRRQAHLSEETQVSQLRVENSKLKMK
AtAHPB1B  (D) DQKTLRRLAQNREAAARKSRLRKKAYVQVEENSRLKLTQLEQELQR
AtbZIP21  (D) DAKTLRRLAQNREAAARKSRLRKKAYVQVEESSRIKLSQLEQELQR
AtbZIP50  (D) HDKMKRRLAQNREAAARKSRLRKKAYVQVEESRLKLSQLEQELK
AtbZIP65  (D) DPKTLRRLAQNREAAARKSRLRKKAYVQVEESCRKLTQLEQEIQR
AtOBF     (D) DQKTLRRLAQNREAAARKSRLRKKAYVQVEENSRLKLTQLEQELQR
AtPAN     (D) DQRTLRLAQNREAAARKSRLRKKAYVQVEENSRIRLAQLEELKR
AtTGA1    (D) PDKIQRRLAQNREAAARKSRLRKKAYVQVEETSRLKLTQLEQELDR
AtTGA3    (D) NDKMKRRLAQNREAAARKSRLRKKAHVQVEESRLKLSQLEQELVR
AtTGA4    (D) PDKIQRRLAQNREAAARKSRLRKKAYVQVEETSRLKLTQLEQELDR
AtTGA6    (D) DQKTLRRLAQNREAAARKSRLRKKAYVQVEENSRLKLTQLEQELQR
AtbZIP34  (E) DPKRVKRIILANRQSAQRSRVRKLYISEERSVTSLQAEVSVLSP
AtbZIP61  (E) DPKRVKRIILANRQSAQRSRVRKLYISEERSVTSLQTEVSVLSP
AtbZIP19  (F) GKKGEKPLGNREAVRKYREKAKAASLEDEVARLAVNQDLVK
AtbZIP23  (F) ESSGKRRPLGNREAVRKYREKAKAASLEDEVMLKAVNNQLK
AtbZIP24  (F) DSSNKRLCCNREAVRKYREKAKARTAYLEDEVMLQSLNEQFLR
AtbZIP16  (G) ELKRQRKQSNRESARRSRLRQAECEDEAQRAEVLEENENTNRA
AtbZIP68  (G) EIKRQRKQSNRESARRSRLRQAECEDEAQRAEVLENGENSSRA
AtGBF1    (G) ELKRQRKQSNRESARRSRLRQAECEQOQRVESLSENNQSLRD
AtGBF2    (G) EVKREKQSNRESARRSRLRQAETEQSVKVDALVAENMSLRS
AtGBF3    (G) ELKRERKQSNRESARRSRLRQAEETEARKEVEALTAENMALRS
AtHY5     (H) ENKRLKRLLRNRVSAQQAREKRYLSEENRVKDELKNSELEE
AtHYH     (H) EYRSLKRLLRNRVSAQQAREKRYVSDLESRANLEQNNNDQLEA
AtbZIP18  (I) DPKRAKRIILANRQSAARSKERKARYILEERKVQTLQTEATTLA
AtbZIP29  (I) DPKRVKRIILANRQSAARSKERKARYIVEEHKVQTLQTEATTLA
AtbZIP30  (I) DPKRVKRIILANRQSAARSKERKARYIIEEHKVQTLQTEATTLA
AtbZIP31  (I) DPKEVRIILKNRESAARSKQKMLQYMINDELKINLENKNASIFE
AtbZIP32  (I) DPKEVRIILKNRESAARHLKQKMLQYMINDEHRINVENENASIFE
AtbZIP33  (I) DPKKVRRIILKNRESAARSKQKMLKYMIDEHRKIFLENKNALIFE
AtbZIP52  (I) DPKRAKRIILANRQSAARSKERKARYIQEERKVQTLQTEATTLA
AtbZIP69  (I) DPKRAKRIILANRQSAARSKERKARYIAIEERKVQTLQTEATTLA
AtbZIP71  (I) DPNEVKRIILNRLDTRSKQKSLYIVDEGSRVIRHVMVNTSLYG
AtbZIP74  (I) DAKKYRMLANRQSAARSKENREKIRDMELRVETENTQASLFG
AtPosF21  (I) DPKRAKRIILANRQSAARSKERKARYIFIEERKVQTLQTEATTLA
AtVIP1    (I) DPKRAKRIILANRQSAARSKERKARYITGIEERKVQTLQTEATTLA
AtbZIP62  (J) EERRIRRIILANRESARQTIIRQAMCEESKKAADTYENENRRR
AtbZIP60  (K) VAKKRRRVRNRDAVRSREKKEYVQDEKKSKEYERECLELGR
AtbZIP76  (L) TYEADNTKRAKQFFAQRSRVRKLYISEERNVQTLQAEKGSVSA
AtbZIP77  (L) PGSKTDSKRIKHQNAHRAFLRLLEYLSDERTIQVLQVEGCEMSS
AtbZIP78  (L) ATSEADTKRAKQFFAQRSRVRKIQYIAIEERNVQTL-----
AtbZIP1   (S) DEKKRRKLSNRESARRSRLKQOKLMEDTIEISSERRIKENSE
AtbZIP3   (S) NERKQRMIKNNRESARRSRMRKQRHLDELSQVAVLRSENHQLLD
AtbZIP4   (S) DDKKRRRTISNRESARRSRMRKQKRFEEETEENRNLNIRNQELKN
AtbZIP5   (S) DERKKRRKLSNRESARRSREKQKHLLEMSIQLNQLKIQNQLKN
AtbZIP6   (S) DDRKRRKMSNRESARRSRMRKQRHIDNPKDEANRGLNRELAN
AtbZIP7   (S) DERKKRRKMSNRESARRSRMRKQRHIDNREOVNRLDENRELG
AtbZIP8   (S) NERKRRKVSNNRESARRSRMRKQRHMEELWSMLVQLINKKSLVD
AtbZIP42  (S) NERKQRMIKNNRESARRSRMRKQRHLDELSQVAVLRSENHQLLD
AtbZIP43  (S) NERKQRKISNRESARRSRMRKQRQVDELSQVAVLRDENHQLLR
AtbZIP44  (S) DERKKRRKQSNRESARRSRMRKQRHLDDTAQVTHLRKENAQIVA
AtbZIP48  (S) DERKQRMLSNRESARRSRMRKQRHLDELSQVAVLRNENNCID
AtbZIP53  (S) DERKKRRMISNRESARRSRMRKQKQLGDLINVTLLKNDNAKITE
AtbZIP58  (S) DERKQRMIKNNRESARRSRMRKQRHLDELSQVAVLRRTDNHCLMD
AtbZIP70  (S) EERRARRMVSNNRESARRSRMRKQKQIEEQQQVEQLMMLNHLSE
AtbZIP75  (S) EEKRLRRMASNRESARRSRMRERMMEKELQMQVKQLMAYNQFLYN
AtGBF5    (S) DERKKRRMLSNRESARRSRMRKQKHVDDTAQINQLSNDNRQILN
AtGBF6    (S) EQRKRRMLSNRESARRSRMRKQKLLDDTAQVNHKKENTEIVT
AtbZIP72  (S) DPKILKRIILSNRVAQRSRWKKVQYLDLAVKRSMEQREVSELRS
    
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bZIP consensus N---X7--R---X9---L--X6--L--X6--L



Supplemental Figure 10: Positive and negative BiFC controls.

Negative control comprising VEG2 fused to the N-terminal half of YFP (YFN-VEG2) co-expressed with the C-terminal half of YFP (YFC), and positive control with co-expression of constructs for a known interaction (Belda-Palazón et al., 2012). Photographs from left to right comprise the green channel image showing fluorescence of YFP, the bright field image and the merged YFP fluorescence and bright field images. Scale bars indicate 40 μ m.

Supplemental Table 1: Mapping locus details.

For mapping of *VEG2/FDa* and flanking genes for Supplemental Figure 6, existing morphological markers were supplemented with newly designed molecular markers targeted to introns of pea orthologs of genes identified in the relevant interval of the *Medicago truncatula* genome at Phytozome (phytozome.jgi.doe.gov; Goodstein et al., 2012). For cleaved amplified polymorphic sequence (CAPS) markers, the relevant restriction enzyme is shown in parentheses. The *VEG2* locus was mapped separately to, but later found to correspond to *FDa*. Populations are as follows: a, *veg2-2* x Solara; b, NGB5839 x JI1794.

Name	Marker type	Population	Primers	Tm (°C)	Accession number(s)	Corresponding Medicago locus (Mt4.0)
F-box SKIP31-like protein (F-box)	HRM	b	TGGAGCCCGATTTTGTAAG ATTATCTCCAAAAGGAAGAAAGC	55	KP751411; GAMJ01003933	Medtr5g025560
LA RELATED PROTEIN 1C (LARP1C)	HRM	b	CCGACTGTGCCCCAGTTGCTTTCT CCATGCAACTTCTTCAGGTC	55	JI919144, JI924790, JR963915	Medtr5g022790
FDa	CAPS (BspHI)	a	GATCATTTTCCCTTCGACACTC GGGAAAGATTCACAACCACAA	60	KP739949; KP739950	Medtr5g022780
	HRM	b	GCGGTAATCATTTTCGTACTCA TGTTTGGTGGGATAGGGCAATGTG	55		
VEG2	Morphological	a	-	-		
RING-H2 finger protein (RING-H2)	HRM	b	TTAATTGGCCTGGAAGAGGA CATGCGAACAAGGAAGAACA	55	KP739948	Medtr5g022770
Protein of unknown function (DUF343)	HRM	b	AGATGAAGATGCATCAAACCAGA GGAAGAGTGAGGGGAGGGCAACA	55	JI907170	Medtr5g022760
Ferredoxin-NADP reductase (FENR1)	CAPS (HpyCh4IV)	a, b	ATGCTTATGCCAAAAGATCCTAATGC CTCTGCTTACAGCAAAGTCAAGCCTGAAGTT	60	X12446	Medtr5g022300
Protein of unknown function (DUF726)	Size	b	GCTGCATTGCTTTCAGCTAC CTCTTGCTCCAAGTGAGTAACC	56	JI945542	Medtr5g021430
APETALA3 (AP3)	CAPS (PsiI)	b	TGGGGGATATTGATCTGTGG TCAAGCATTTTCTGCAGCCACACA	55	JN412098	Medtr5g021270
Glutaredoxin (GRX)	HRM	b	TTCAGTTTCCGCTTTCGTTT TGATCCACCAATATGCTTCC	55	JI899180	Medtr5g021090
Protein of unknown function (DUF1230)	HRM	b	TTCTTCATTAAGCAACAAGCAA CCGAGCTAGGATCTGC AAAA	55	GAMJ01037230	Medtr5g016100
AFILA (AF)	Morphological	a	-	-	-	Medtr5g014400
STAY-GREEN (I;SGR)	Morphological	a	-	-	AB303331; AM884277	Medtr5g011120

Supplemental Table 2: Details of sequences for FD proteins and related bZIP transcription factors used for phylogenetic analyses and alignments.

Asterisks indicate that an altered annotation was used (putative intron sequence was removed or annotation of exons was corrected based on transcript sequence or alignments between species). Where relevant, previous gene names are indicated. Sequences were obtained from GenBank (www.ncbi.nlm.nih.gov), Phytozome (phytozome.jgi.doe.gov; Goodstein et al., 2012), or alternative sources as indicated.

Species	Gene name	Accession number	Source	Reference(s)
<i>Actinidia chinensis</i> (kiwifruit)	AcFD	AGK89941	GenBank	Varkonyi-Gasic et al. (2013)
<i>Aquilegia coerulea</i>	AqucaFD	Aquca_075_00022*	<i>Aquilegia coerulea</i> Genome Sequencing Project assembly v1.1 at Phytozome	This study
<i>Arabidopsis thaliana</i>	AtABF1 (AtbZIP35)	NP_564551	GenBank	Jakoby et al. (2002)
	AtABF2 (AtbZIP36)	NP_849777		
	AtABF3 (AtbZIP37)	NP_567949		
	AtABF4 (AtbZIP38)	NP_566629		
	AtABI5 (AtbZIP39)	NP_565840		
	AtAHP1B (AtbZIP20)	NP_196312		
	AtAREB3 (AtbZIP66)	NP_191244		
	AtbZIP1	NP_199756		
	AtbZIP3	NP_197087		
	AtbZIP4	NP_176162		
	AtbZIP5	NP_566925		
	AtbZIP6	NP_179870		
	AtbZIP7	NP_195487		
	AtbZIP8	NP_177054		
	AtbZIP9	NP_568457		
	AtbZIP13	NP_199221		
	AtbZIP15	NP_199105		
	AtbZIP16	NP_850248		
	AtbZIP17	NP_565946		
	AtbZIP18	NP_181594		
	AtbZIP19	NP_567974		
	AtbZIP21	NP_563810		
	AtbZIP23	NP_179268		
	AtbZIP24	NP_190764		
	AtbZIP25	NP_567003		
	AtbZIP28	NP_187691		
	AtbZIP29	NP_849520		
	AtbZIP30	NP_179719		
	AtbZIP31	NP_178956		
	AtbZIP32	NP_178948		
	AtbZIP33	NP_565355		
	AtbZIP34	NP_565970		
	AtbZIP42	NP_189674		
	AtbZIP43	NP_198696		
AtbZIP44	NP_177672			
AtbZIP48	NP_178489			
AtbZIP49	NP_191225			
AtbZIP50	NP_565162			
AtbZIP52	NP_172170			
AtbZIP53	NP_191801			
AtbZIP58	NP_172817			
AtbZIP60	NP_174998			
AtbZIP61	NP_191371			
AtbZIP62	NP_173381			
AtbZIP65	NP_850784			
AtbZIP68	NP_174494			
AtbZIP69	NP_172097			
AtbZIP70	NP_200891			
AtbZIP71	NP_180011			
AtbZIP72	NP_196333			
AtbZIP74	NP_850010			

Species	Gene name	Accession number	Source	Reference(s)
<i>Arabidopsis thaliana</i> (continued)	AtbZIP75	NP_850791	GenBank	Jakoby et al. (2002); Abe et al. (2005); Wigge et al. (2005)
	AtbZIP76	AAU94427		
	AtbZIP77	AAM64869		
	AtbZIP78	NP_849319		
	AtBZO2H1 (AtbZIP10)	NP_192173		
	AtBZO2H3 (AtbZIP63)	NP_568508		
	AtDPBF2 (AtbZIP67)	NP_566870		
	AtDPBF4 (AtbZIP12)	NP_850341		
	AtFD (AtbZIP14)	BAC65864		
	AtFDP (AtbZIP27)	CAD29861		
	AtGBF1 (AtbZIP41)	NP_195391		
	AtGBF2 (AtbZIP54)	NP_192021		
	AtGBF3 (AtbZIP55)	NP_182150		
	AtGBF4 (AtbZIP40)	NP_171893		
	AtGBF5 (AtbZIP2)	NP_179408		
	AtGBF6 (AtbZIP11)	NP_195185		
	AtHY5 (AtbZIP56)	NP_568246		
	AtHYH (AtbZIP64)	NP_850605		
	AtOBF (AtbZIP26)	NP_196313		
	AtPAN (AtbZIP46)	NP_177031		
AtPosF21 (AtbZIP59)	NP_001031456			
AtTGA1 (AtbZIP47)	NP_851273			
AtTGA3 (AtbZIP22)	NP_564156			
AtTGA4 (AtbZIP57)	NP_196565			
AtTGA6 (AtbZIP45)	NP_566415			
AtVIP1 (AtbZIP51)	NP_564486			
<i>Brachypodium distachyon</i>	BdFD1	XP_003578537	GenBank	Tsuji et al. (2013)
	BdFD2	XP_003563257		
	BdFD3	XP_003570743		
<i>Cucumis sativus</i> (cucumber)	CsFD	Cucsa.322810	<i>Cucumis sativus</i> genome v1 at Phytozome	This study
<i>Eucalyptus grandis</i>	EgFD	Eucgr.J02482*	<i>Eucalyptus grandis</i> genome assembly v1.1 (Myburg et al., 2014) at Phytozome	This study
<i>Fragaria vesca</i> (strawberry)	FvFD1	mrna14556.1-v1.0-hybrid	<i>Fragaria vesca</i> genome v1.1 (Shulaev et al., 2011) at Phytozome	Tsuji et al. (2013)
	FvFD2	mrna08566.1-v1.0-hybrid		
<i>Glycine max</i> (soybean)	GmFDa1	Glyma01g36810*	Soybean genome v1.1 (Schmutz et al., 2010) at Phytozome	Jung et al. (2012); Tsuji et al. (2013); Nan et al. (2014); This study
	GmFDa2	not annotated; Chr11: 5997867-5996321		
	GmFDb1 (GmFDL02)	Glyma02g05100*		
	GmFDb2	not annotated; Chr16: 26917990-26913770		
	GmFdc1 (GmFDL04)	Glyma04g02420		
	GmFdc2 (GmFDL0602)	Glyma06g02470		
<i>Gossypium raimondii</i> (cotton)	GmFDL19	Glyma19g30230	Cotton genome v2.1 (Paterson et al., 2012) at Phytozome	This study
	GrFD1	Gorai.003G007000		
	GrFD2	Gorai.007G191800		
	GrFD3	Gorai.009G192500		
	GrFD4	Gorai.009G269300		
<i>Hordeum vulgare</i> (barley)	GrFD5	Gorai.002G122200	GenBank	Tsuji et al. (2013)
	HvFD1	BAK04622		
	HvFD2	AK249012		
<i>Lotus japonicus</i>	HvFD3	AK359958	<i>Lotus japonicus</i> genome assembly build 2.5 (Sato et al., 2008) at Kazusa DNA Research Institute (www.kazusa.or.jp/lotus)	This study
	LjFDa	chr2.CM0272.780.r2.m		
<i>Malus domestica</i> (apple)	MdFD1	MDP0000169473*	<i>Malus domestica</i> genome v1.0 (Velasco et al., 2010) at Phytozome	Tsuji et al. (2013)
	MdFD2	MDP0000636541*		

Species	Gene name	Accession number	Source	Reference(s)
<i>Manihot esculenta</i> (cassava)	MeFD1	cassava4.1_021397m*	Cassava genome v4.1 (Prochnik et al., 2012) at Phytozome	This study
	MeFD2	cassava4.1_029555m*		
	MeFD3	cassava4.1_023228m*		
	MeFD4	cassava4.1_021412m*		
<i>Medicago truncatula</i>	MtFDa	Medtr5g022780*	<i>Medicago truncatula</i> Genome Project v3.5 (Young et al., 2011) at Phytozome	Stanton-Geddes et al. (2013); This study
	MtFDb	Medtr8g075130*		
	Medtr7g088090 (prev. MtFD)	Medtr7g088090		
<i>Musa acuminata</i> (banana)	MaFD1	GSMUA_Achr1P02640_001*	The Banana Genome Hub (banana-genome.cirad.fr; D'Hont et al., 2012)	Tsuji et al. (2013); This study
	MaFD2	GSMUA_Achr5P11470_001*		
	MaFD3	GSMUA_Achr9P24090_001*		
	MaFD4	GSMUA_Achr9P21040_001		
	MaFD5	GSMUA_Achr5P11220_001*		
<i>Oryza sativa</i> (rice)	OsAREB3	LOC_Os05g41070	<i>Oryza sativa</i> genome, MSU Release 7.0, Rice Genome Annotation Project (rice.plantbiology.msu.edu ; Kawahara et al., 2013)	Tsuji et al. (2013)
	OsFD1	LOC_Os09g36910		
	OsFD2	LOC_Os06g50600		
	OsFD3	LOC_Os02g58670		
	OsFD4	LOC_Os08g43600		
	OsFD5	LOC_Os06g50830		
	OsFD6	CT843963		
<i>Phaseolus vulgaris</i> (common bean)	PvFDa	Phvul.002G105700*	<i>Phaseolus vulgaris</i> genome v1.0 (Schmutz et al., 2014) at Phytozome	This study
	PvFDb	Phvul.003G266100		
	PvFDc	Phvul.009G018700		
<i>Phoenix dactylifera</i> (date palm)	PdFD1	PDK_30s1175071g003	Date palm draft genome v3 (qatar- weill.cornell.edu/research/ datepalmGenome; Al- Dous et al., 2011)	Tsuji et al. (2013)
<i>Pisum sativum</i> (pea)	PsFDa	KP739950	GenBank	This study
<i>Populus trichocarpa</i> (poplar)	PtFD1	XP_002327643*	GenBank	Tsuji et al. (2013)
	PtFD2	XP_002307742		This study
	PtFD3	XP_002300691		
<i>Prunus persica</i> (peach)	PpFD1	ppa018386m*	Peach genome v1.0 (The International Peach Genome Initiative, 2013) at Phytozome	This study
	PpFD2	ppa021354m*		
<i>Setaria italica</i> (foxtail millet)	SiFD1	Si031077m	<i>Setaria italica</i> genome v2.1 (Bennetzen et al., 2012) at Phytozome	Tsuji et al. (2013)
	SiFD2	Si007412m		
	SiFD3	Si023448m		
	SiFD4	Si014546m		
<i>Solanum lycopersicum</i> (tomato)	SISPGB	Solyc02g083520	Tomato genome ITAG2.3 (Tomato Genome Consortium, 2012) at Phytozome	Pnueli et al.(2001); Park et al. (2014)
	SISPGB2	Solyc02g061990*		
<i>Solanum tuberosum</i> (potato)	StFD1	not annotated; Chr02:60345702..60350121	<i>Solanum tuberosum</i> genome annotation v3.4 at Phytozome (Potato Genome Sequencing Consortium, 2011)	Tsuji et al. (2013)
	StFD2	PGSC0003DMP400041309		
<i>Sorghum bicolor</i>	SbFD1	XP_002460587	GenBank	Tsuji et al. (2013)
	SbFD2	XP_002439039		
	SbFD3	XP_002453108		
<i>Triticum aestivum</i> (wheat)	TaFD1	CK206464	GenBank	Li and Dubcovsky (2008); Tsuji et al. (2013)
	TaFDL2	ABZ91908		
	TaFDL6	ABZ91910		
	TaFDL13	ABZ91911		
	TaFDL15	ABZ91912		
<i>Vitis Vinifera</i> (grape)	VvFD1	CBI19920	GenBank	Tsuji et al. (2013)
	VvFD2	XP_003635259		
<i>Zea mays</i> (maize)	ZmDLF1	NP_001105962	GenBank	Muszynski et al. (2006); Tsuji et al. (2013)





















Supplemental Table 3: Primer details.























Gene	Purpose/details	Primer names	Primer sequences (5' to 3')	Tm (°C)	Source
<i>ACT</i>	qRT-PCR	PsACT-F PsACT-R	GTGTCTGGATTGGAGGATCAATC GGCCACGCTCATATTTCA	59	Foo et al. (2005)
<i>AP3</i>	qRT-PCR	PsAP3-10F PsAP3-6R	TGGGGGATATTGATCTGTGG TCCAAC TCCAAACCACCTTCACCT	60	This study
<i>DET (TFL1a)</i>	qRT-PCR	PsTFL1a-1F PsTFL1a-2R	CGTTGGTAGAGTCATAGG AGGATCACTAGGGCCAGG	58	Hecht et al. (2011)
<i>FDa/VEG2</i>	Full-length coding sequence for BiFC construct	PsFD-7F PsFD-5R	ACCATGGAAGAGTTGTGGAAAG GGGAAAGATTCACAACCACAA	60	This study
	qRT-PCR	PsFD-6F PsFD-3R	ATTTGATCCAAACGTCGGTGT ATCAACTTTTTGCTCCAGTTCCG	60	
	<i>in situ</i> probe	PsFD-5F PsFD-6R	TTGCTGGAAGAGAATGCAAAG TCATTCAC TTTCCGCATGAA	60	
	PCR marker for isolation of full-length coding sequence for Figure 4D and <i>veg2-1</i> genotyping (presence/absence)	PsFD-7F PsFD-6R	ACCATGGAAGAGTTGTGGAAAG TCATTCAC TTTCCGCATGAA	56	
	CAPS marker (BspHI) for <i>veg2-2</i> genotyping	PsFD-4F PsFD-5R	GATCATTTTCCCTTCGACACTC GGGAAAGATTCACAACCACAA	60	
	PCR for fragment present in <i>veg2-1</i> for Figure 4D	PsFD-9F PsFD-12R	CGCAACTCATATCCGAAAGT CATAAGGCAACATGCAATGG	58	
	Attempted isolation of <i>FDa</i> from <i>veg2-1</i> . Primers were used in various combinations and are shown in order of location (5' → 3').	PsFD-1F	GACTCTCTCTCCCCCAATCTCTT	62	
		PsFD-7F	ACCATGGAAGAGTTGTGGAAAG	60	
		PsFD-1R	GGCCGAGTGTTTAAACTGAGAGC	62	
		PsFD-3R	ATCAACTTTTTGCTCCAGTTCCG	62	
		PsFD-5F	TTGCTGGAAGAGAATGCAAAG	60	
		PsFD-5R	GGGAAAGATTCACAACCACAA	60	
		PsFD-6R	TCATTCAC TTTCCGCATGAA	56	
PsFD-7R	TGCACTCATTTGTCATAGTTGG	62			
<i>FDb</i> (putative)	Attempted isolation. Primers were used in various combinations.	FD-1D	ATGGAAGAAGTDTGGAAWGAHATHAAYC TDKCTTC	60	This study
		FD-2D	CTAGCBCKKGAHCKWGCWGCAGAYTCYC KRTTCTTGATCA	60	
		FD-3D	MGRGARTCTGCWGCWMDTMMGVGCT AGRAARCAGG	60	
		MiFDP-1F	GACGACATAAGCGAATAATGAA	58	
		MiFDP-1R	AGCTCTTGATCGTGACGAG	62	
		MiFDP-2R	TGGAGCTGTTGATGTTCCGAT	58	
<i>FTa1</i>	Full-length coding sequence for BiFC construct	PsFTLa-9F PsFTLa-4R	CCACATATGGCAGGTAGTAGC AGCGTCTGTAGTGTAACGTGT	60	This study
	qRT-PCR	PsFTLa-6F PsFTLa-2R	GCCCAAGCAACCCTACTTTT CCATCCTGGAGCGTAAACCC	60	Hecht et al. (2011)
<i>FTa2</i>	Full-length coding sequence for BiFC construct	PsFTLb-5F PsFTLb-R4	ATGGCCTGTAGTAGCCGGAATCC AGCACCATTGATGCAGTACC	60	Hecht et al. (2011)
<i>FTb1</i>	Full-length coding sequence for BiFC construct	PsFTLe-2FF PsFTLe-2R	ATGCGTATGAAATCATCGAATCC ATTATATGATCATCTCCTTCCACC	62	Hecht et al. (2011)
<i>FTb2</i>	Full-length coding sequence for BiFC construct	PsFTLe-2FF PsFTLe2-1R	ATGCGTATGAAATCATCGAATCC GGTGCATGGATATGTTTAGAC	60	This study

Gene	Purpose/details	Primer names	Primer sequences (5' to 3')	Tm (°C)	Source
<i>FTc</i>	Full-length coding sequence for BiFC construct	PsFTLc-9F PsFTLc-3R	ATGCCTAGGAATATGGTCGATCC GAACTAACCCCGCCCACTTGG	60	Hecht et al. (2011)
	qRT-PCR	PsFTLc-8F PsFTLc-7R	GATATTCCAGCCACAACAAGC TTATGACGCCACTCTGGAGCAA	62	
<i>LARP1C</i>	Isolation of full-length coding sequence for Figure 4D	PsWiHe-1F PsHyp-1R	TCATCATCGGAGAGTCATCG TTCCCTCAGAGGCAGTAGGAAGC	55	This study
<i>LF (TFL1c)</i>	qRT-PCR	PsLF-CR2 PsLF-CR3	AAATAAGCAGCAGCAACAGGG CAGACATTCCAGGGACAACAG	60	Foucher et al. (2003)
<i>PIM</i>	CAPS marker (XmnI) for <i>pim-2</i> genotyping	PsPIM-F1 PsPIM-R1	ACCTCTTAACATTCTTTGG AAGTGAAGAAAAGAGAATATA	50	This study
	qRT-PCR	PsPIM-4F PsPIM-6R	GCTTCAGAGTTTGAACAGC GACTCCATGGTGGTTTGG	58	Hecht et al. (2011)
<i>RING-H2</i>	Isolation of full-length coding sequence for Figure 4D	PsZnFin-5F PsZnFin-3R	ACCACCCTTCCAAACCAAG CCATAGGCTGTGGTGGATTT	58	This study
<i>SEP1</i>	qRT-PCR	PsPM6-7F PsPM6-8R	GATTGCCTGACTGATTTTCG TTGTTGAGCTTGACTTGTGG	60	Hecht et al. (2011)
<i>SOC1a</i>	qRT-PCR	PsSOC1a-Q1 PsSOC1a-Q2	GAGTGTAAAGCACTGTTAGAGCAAG TCTCGGATGATCATTTGGCGGTGG	65	This study
<i>UNI</i>	qRT-PCR	PsUNI-1F PsUNI-2R	CATCAGAGCTGAAAGAAGG GCTTCCTTTTCACGTTGC	55	Hecht et al. (2011)
<i>VEG1 (FULc)</i>	qRT-PCR and <i>veg1</i> genotyping (presence/absence)	PsFULc-2F PsFULc-2R	CGATGCCTTGAAACCATAGG AATCCAATGACCCTCTTGC	58	Berbel et al. (2012)

Supplemental Table 4: Details for *FD* and flanking genes in *Arabidopsis* and legume species.

This table accompanies Figure 4B and Supplemental Figure 8. Details in this table are based on genome builds for *Arabidopsis* (TAIR10) from The Arabidopsis Information Resource (www.arabidopsis.org), and *Medicago* (Mt3.5), common bean (*Phvulv* v1.0), and soybean (*Glyma* v1.1) from Phytozome (www.phytozome.net). Single asterisks indicate incorrect annotation in online resources, as determined by alignments with expressed sequences and between legume species, which was corrected for the purposes of this study. Where possible, genes are named according to the closest related *Arabidopsis* homolog.

Species	Chromosome	Symbol	Gene	Locus ID	Chromosomal location
<i>Arabidopsis thaliana</i>	At4		<i>LARP1C</i>	AT4G35890	16997139-17000833
			<i>FD</i>	AT4G35900	17004595-17006287
			<i>DUF343</i>	AT4G35905	17007028-17008154
<i>Medicago truncatula</i>	Mt5		<i>LARP1C</i>	Medtr5g022790*	8775734-8771155
			<i>FDa</i>	Medtr5g022780*	8758327-8759707
			<i>RING-H2</i>	Medtr5g022770*	8754049-8754848
			<i>DUF343</i>	Medtr5g022760	8749173-8751848
	Mt8		<i>LARP1C</i>	Medtr8g075120	20220967-20223420
			<i>FDb</i>	Medtr8g075130*	20225953-20227169
		<i>EMB3006</i>	Medtr8g075140	20228872-20234066	
Common bean (<i>Phaseolus vulgaris</i>)	Pv2		<i>LARP1C</i>	Phvul.002G105500	21244748-21249771
			<i>FDa</i>	Phvul.002G105700*	21293640-21294548
			<i>RING-H2</i>	Phvul.002G105800	21312952-21315712
			<i>DUF343</i>	Phvul.002G105900	21317735-21322244
	Pv3		<i>LARP1C</i>	Phvul.003G266200	49298693-49303027
			<i>FDb</i>	Phvul.003G266100	49289696-49290831
			<i>EMB3006</i>	Phvul.003G266000	49272428-49285826
	Pv9		<i>LARP1C</i>	Phvul.009G018800	3474640-3480559
			<i>FDc</i>	Phvul009G018700	3423224-3427367
			<i>SBT5.2</i>	Phvul.009G018600	3474640-3480559

Soybean (<i>Glycine max</i>)	Gm1		<i>LARP1C</i>	Glyma01g36801	49220680-49225998
			<i>FDa1</i>	Glyma01g36810*	49235180-49236798
			<i>RING-H2</i>	Glyma01g36820	49253298-49254542
			<i>DUF343</i>	Glyma01g36830	49256522-49258723
	Gm2		<i>LARP1C</i>	Glyma02g05090	4130098-4135052
			<i>FDb1</i>	Glyma02g05100*	4139368-4140828
			<i>EMB3006</i>	Glyma02g05110	4144145-4151509
	Gm4		<i>LARP1C</i>	Glyma04g02405	1673134-1678845
			<i>FDc1</i>	Glyma04g02420	1680703-1683111
			<i>SBT5.2</i>	Glyma04g02431	1696836-1699749
	Gm6		<i>LARP1C</i>	Glyma06g02460	1632699-1637471
			<i>FDc2</i>	Glyma06g02470	1639376-1641643
			<i>SBT5.2</i>	Glyma06g02481	1654709-1659109
	Gm11		<i>LARP1C</i>	Glyma11g08500*	6008627-6013845
			<i>FDa2</i>	Not annotated	5997867-5996321
			<i>RING-H2</i>	Glyma11g08480*	5990036-5991373
			<i>DUF343</i>	Glyma11g08470	5986226-5987561
	Gm16		<i>LARP1C</i>	Glyma16g23170	26890147-26894598
			Histone methyltransferase gene	Glyma16g23191	26899881-26901749
			<i>FDb2</i>	Not annotated	26917990-26913770
		Major facilitator superfamily gene	Glyma16g23210	26920731-26925063	
		<i>EMB3006</i>	Glyma16g23220	26939014-26946253	

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