SUPPLEMENTARY MATERIALS AND METHODS

Phylogenetic analyses

Sequences were aligned using the MultAlin program (Corpet, 1988) and designed under ESPript3.0 (Robert and Gouet, 2014). For phylogeny analysis, amino acid sequences from UIF1 homologues were aligned using MUSCLE in the SEAVIEW program (Gouy et al., 2010). Homologous sites for phylogenetic reconstructions were determined automatically using Gblocks. Maximum Likelihood phylogenies were then generated from these alignments in PhyML (Guindon et al., 2009) using an LG evolutionary model. The PhyML options used to generate the tree were the default settings except the invariable sites that were optimized. Statistical support was provided by aLRT (SH-like).

Mutant allele genotyping

Genotyping of *uif1-1* and *uif1-3* T-DNA insertion mutants was performed using, for gene amplification, oUIF1-ADNT06-F / oUIF1-ADNT06-R (1123 pb amplification) and oUIF1-ADNT32-F/ oUIF1-ADNT32-R (1092 pb amplification) primers, respectively; and for the presence of *uif1-1* and *uif1-3* T-DNA insertions, oUIF1-ADNT06-R RP/ oLB2 (647 pb amplification) and oUIF1-ADNT32-F/ oLBb1.3 (918 bp amplification) primers, respectively (Suppl. Table S1). The *ult1-3* allele mutant was previously described (Carles et al., 2005). Putative *uif1-3 ult1-3* double-mutant plants were identified in the F2 generation and confirmed through segregation analysis in the F3 generation.

Constructs for transient assays and transgenic plants

Bacteria expression constructs

UIF1 (At4g37180) coding sequence (cds) was amplified from an *A. thaliana* inflorescence cDNA library, using the Phusion High Fidelity DNA Polymerase (Thermo Scientific) and the oETH1239 / oETH1240 primers (Suppl. Table S1). The amplified PCR product was subcloned into Zero Blunt (Life Technologies) and further transferred into pETM-33 at NcoI-XhoI cloning sites and into pETM-41 at NcoI-NotI cloning sites. This yielded respectively the pETH380 and pETH447 expression vectors. pETM-33 allows production of recombinant proteins with a N-terminus 6His tag followed by a GST tag and by a Precission cleavage site. pETM-41 allows production of recombinant proteins with a N-terminus 6His tag followed by a MBP tag and by a tobacco etch virus (TEV) cleavage site.

The DNA fragment coding for Myb domain of UIF1 (residues 206 to 270) was amplified from pETH380 (described above) using the Phusion High Fidelity DNA Polymerase (Thermo Scientific) and oETH1415 / oETH1416 primers. The obtained PCR product was subcloned into Zero Blunt (Life Technologies) and transferred into pETM-11 at NcoI-XhoI cloning sites to yield the pETH455 expression vector. pETM-11 allows production of recombinant proteins with a N-terminus 6His tag followed by a tobacco etch virus (TEV) cleavage site.

Yeast expression constructs

ULT1 (At4g28190) cds was transferred from pEZS-ULT1-CL (Carles et al., 2005) to pGBK-T7 (Clontech) using EcoRI-BamHI restriction sites, to yield pETH198 expression vector. UIF1 was amplified from pETH380 using the Phusion High Fidelity DNA Polymerase (Thermo Scientific) and oETH1368 / oETH1369 primers, and then cloned into pGAD-T7 at the EcoRI-BamHI sites to yield the pETH390 expression vector. pGBKT7 and pGAD-T7 yeast expression vectors are designed to express proteins fused to the GAL4 DNA binding domain and the GAL4 activation domain, respectively.

The DNA fragment coding for the N-terminus part (aa 1 to 193) of ULT1 was amplified from pBB134-NY-ULT1dBbox using the Phusion High Fidelity and oETH1381 / oETH1382 primers (Suppl. Table S1). The obtained PCR product was transferred into pGBK-T7 at EcoRI-BamHI cloning sites to yield the pETH403 expression vector.

The DNA fragment coding for the C-terminus part (aa 148 to 268) of ULT1 was transferred from pEZS-CL-YC-ULT1 vectors (BiFC construct) into pGBK-T7 at EcoRI-BamHI restriction sites to yield the pETH437 yeast expression vector.

The DNA fragment coding for the SAND domain (aa 12 to 152) was amplified from pETH198 using the Phusion High Fidelity and oETH1410 / oETH1411 primers (Suppl. Table S1). The obtained PCR product was subcloned into Zero Blunt (Life Technologies) and transferred into pGBK-T7 at EcoRI-BamHI cloning sites to yield the pETH446 expression vector.

The DNA fragment coding for the C-terminus part of UIF1 (aa 91 to 356) was amplified from pETH390 using the Phusion High Fidelity and oETH1383 / oETH1384 primers (Suppl. Table S1). The obtained PCR product was transferred into pGAD-T7 at EcoRI-BamHI cloning sites to yield the pETH404 expression vector.

Plant expression constructs

For subcellular localisation, *UIF1* (At4g37180) cds was amplified from an *A. thaliana* inflorescence cDNA library, using the Phusion High Fidelity DNA Polymerase (Thermo Scientific) and the (i) oUIF1-EcoR1.F /oUIF1-BamH1nostop.R (for C-terminus fusion to GFP) or (ii) oUIF1-EcoR1.F / oUIF1-BamH1.R (for N-terminus fusion to GFP) primers (Suppl. Table S1). Each amplified PCR product was subcloned independently into Zero Blunt (Life Technologies) and further transferred into non binary vector (i) pEZS-NL-ULT1 and (ii) pEZS-CL-ULT1 (Deepgreen Stanford: hht://deepgreen.stanford.edu) at EcoRI-BamHI cloning sites (pre-digested with EcoRI-BamHI to remove ULT1 cds (At4g28190) and correspond respectively to pEZS-NL-UIF1 and pEZS-CL-UIF1 vectors.

The vectors used for BiFC for transient expression were generated from the pEZS backbone and are gift from Bassem Al Sady (UC Berkeley, PGEC, USA). They each contain cds for one of the two split YFP forms (NY: aa 1 to 166; YC aa 167 to 265) under the control of a *CaMV35S* promoter, and for fusion at the N or C-terminus end the cds of interest (four vectors in total). A terminator of the transcription site (Osc) is located at the C-terminus end of the construct. The cds of *UIF1* and *ULT1* were amplified from an *A. thaliana* inflorescence cDNA library, using the Phusion High Fidelity DNA Polymerase (Thermo Scientific) and the UIF1salI.F / oUIF1-BamH1.R, ULT1-salI.F / oULT1-BamH1.R or UIF1-SalI.F / oUIF1-BamH1nostop.R, or ULT1-SalI.F / oULT1-BamH1nostop.R primer combinations (Suppl. Table S1). Truncated versions UIF1 93-364 and ULT1 1-193 (Fig. 1A) were amplified using UIF1dNTsalI.F / oUIF1-BamH1nostop.R, or UIF1dNTsalI.F / oUIF1-BamH1.R and or ULT1-SalI.F / oULT1dBbCTBamHI.R or ULT1-SalI.F / oULT1dBbCT-nostopBamHI.R primer combinations (Suppl. Table S1). Each PCR product was subcloned independently into Zero Blunt (Life Technologies), transferred into pEZS-CL-splitYFP vectors using Sal1-BamH1 then into the binary vectors pBB130 (nptII) and pBB134 (hptII) using XhoI-XbaI. pBB130 and pBB134 are derived from pART27 vectors (Gleave, 1992) in which the GFP fusion cassette from pEZS-NL (NotI fragment; Blanvillain et al., 2011) has been inserted and/or the NPTII resistance gene has been replaced by HPTII. The 2 separate resistance genes allow selection of doubly transformed Arabidopsis plants expressing two candidate interactors in fusion to each split-YFP. The transgenes were transferred into Arabidopsis using the *Agrobacterium tumefasciens*-mediated floral dip transformation.

For DLRA assays, *UIF1* WT or mutated cds versions were amplified from an *A.thaliana* inflorescence cDNA library, using the Phusion High Fidelity DNA Polymerase (Thermo Scientific) and the oUIF_FAscI / oUIF_RXbaI , oUIF_FAscI / oUIF_RdEARXbaI or oUIF-

ANANA_FAscI / oUIF_RdEARXbaI primer couples (Suppl. Table S1). Amplified PCR products were subcloned independently into Zero Blunt (Life Technologies) and further transferred into the pBB120 binary vector at AscI-XbaI cloning sites, allowing expression of a protein fused to the Gal4 DNA-binding domain (G4DBD), namely G4DBD-UIF-FL, G4DBD-UIF-dCT or G4DBD-UIF-ANANA-dCT.

Yeast-two-hybrid (Y2H) screen

The Y2H screen was performed using the Horwitz and Ma cDNA library (CD4-30), generated from mRNAs of inflorescence meristems, floral meristems and floral buds up to stage 8 or 9. An overnight culture of the AH109 strain (Clontech) carrying the Balt vector (ULT1 fused to the Gal4 DNA Binding Domain = pETH198 described below) was performed in 5 mL of YNB medium (MP Biomedicals) containing all essential amino-acids except tryptophane. The day of transformation, this culture was diluted in 100mL to obtain a final OD (600nM) of 0.3 and was grown again until it reached an OD (600nM) of 0.8. The culture was centrifuged two times. After the first centrifugation, the pellet was resuspended in 20 mL of water and after the second centrifugation, the pellet was resuspended in 20 mL of 100 mM Lithium Acetate. After the last resuspension, the culture was centrifuged and the pellet was resuspended in 1mL of 100mM Lithium Acetate and separated in five tubes. After an incubation of one hour at 28°C with gentle shaking, in each tube, the transformation reaction was performed by adding 200 µg of denaturated carrier DNA, 5 µg of cDNA library and 1.2 mL of solution B (100 mM LiAc, 40% PEG and 1xTE). After an incubation of 30 min at 28° C with gentle shaking, a heat shock was performed in a water bath at 42°C during 15 min. After the heat shock, 700 µl of YNB medium was added to each tube to dilute the PEG. After a centrifugation, each pellet was resuspended in 1 mL of YPGA medium and incubated 1 h at 28°C. A last centrifugation was performed and each pellet was resuspended in 800 µL of YNB medium. With each tube, 2 plates of YNB with all essential amino acids excepted leucine, tryptophan, adenine and histidine were plated and incubated at 30°C. For all the colonies that grew on these plates, three successive isolations were made on YNB selectives plates, and a plasmid extraction was performed from the last yeast cultures. After extraction the plasmids were transformed into *E. coli* (HB101 strain), and grown in liquid LB medium. An extraction of plasmid was performed and the cDNA insert was sequenced.

Protein extraction and western blot on mated Y2H diploids:

A yeast culture of 5mL (OD =3) was used for the extraction of proteins from each of the Y2H diploids. Protein extraction was adapted from Volland et al. (1994). Each culture was pelleted and resuspended in 500µL of water before addition of 50µL of NaOH 1.85N and 10 minutes incubation on ice. After addition of 50µL TCA 50% and 10 minutes incubation on ice, a centrifugation was performed for 10 minutes at 13000 rpm. The pellet was washed with 500µL of Tris-HCl 1M pH8. After a centrifugation of 10 minutes at 13000rpm, the pellet was resuspended in 50µL of buffer containing 50mM Tris-HCl pH 6.8, 2mM EDTA, 2% SDS, 10% Glycerol, bromophenol blue, 2% β-Mercaptoethanol. After a denaturation step of 5 minutes at 95°C, 10µL of each sample were loaded on a gel to perform a western blot. The proteins were transfered onto a PVDF membrane (GE Healthcare) that had been previously activated in methanol for 1min. The transfer was performed during 1h at 100V in buffer containing Laemli 1x and Ethanol 20%.

For detection of the Gal4-AD fusions (western-blot with an anti-HA antibody), the membrane was blocked overnight at 4°C in a solution of TBS-T 1x (TBS and 0.1% Triton X-100) containing 10% milk. After 3 washes of 5 minutes in TBS-T, the membrane was incubated with an anti-HA antibody (Roche) at a 1:10,000 dilution. After 3 washes of 5 minutes in TBS-T, the membrane was incubated with a rat secondary antibody coupled to HRP (Sigma-Aldrich) at a 1:5,000 dilution. After 3 washes of 5 minutes in TBS-T, the detection was performed with the Clarity ECL Western Substrate kit (Biorad) using the Chemidoc MP (Biorad). For detection of the Gal4-BD fusions (western-blot with an anti-c-Myc antibody), the membrane was blocked overnight at 4°C in a PBS-T 1x (PBS and 0.6% Tween 20) solution containing 10% milk. After 3 washes of 5 minutes in PBS-T, the membrane was incubated with an anti-c-Myc antibody (clone 9e10, Covance) at a 1:5,000 dilution, in a PBS-T solution containing 10% SVL. After 3 washes of 5 minutes in PBS-T, the membrane was incubated with a mouse secondary antibody coupled to HRP at a 1:5,000 dilution. After 3 washes of 5 minutes in PBS-T, the detection was performed with the Clarity ECL Western Substrate kit (Biorad) using the Chemidoc MP (Biorad).

Cut-off score for selection of UIF1 binding sites in candidate genes from the PBM-obtained matrices

Binding matrices corresponding to the three top-scoring motifs were used for prediction of UIF1 binding sites using Morpheus. The cut-off score was defined from a scan through all *A. thaliana* 3-kb promoter sequences (TAIR10 database), using the three UIF1 matrices (UIF1_1ary, UIF1_2ary UIF1_3ary): frequencies in the genome of a 0-score are 2.38×10^{-6} [UIF1_1ary and UIF1_3ary], 1.12×10^{-5} [UIF1_2ary]; of a -1-score: 1.09×10^{-4} [UIF1_1ary], 2.85×10^{-4} [UIF1_2ary], 3.42×10^{-4} [UIF1_3ary]; of a -2-score: 5.31×10^{-4} [UIF1_1ary], 7.43×10^{-4} [UIF1_2ary], 1.36×10^{-3} [UIF1_3ary]; of a -3 score: 1.48×10^{-3} [UIF1_1ary], 1.77×10^{-3} [UIF1_2ary], 3.92×10^{-3} [UIF1_3ary]). A cut-off score of -3 allows selecting only high confidence UIF1 binding sites (p-value < 0.01). A score was assigned to each binding site found in candidate target genes (*WUS*, *AG*, *CUC1-3*), and only those with a score ranging from -2 to 0 were considered for further EMSA analyses.

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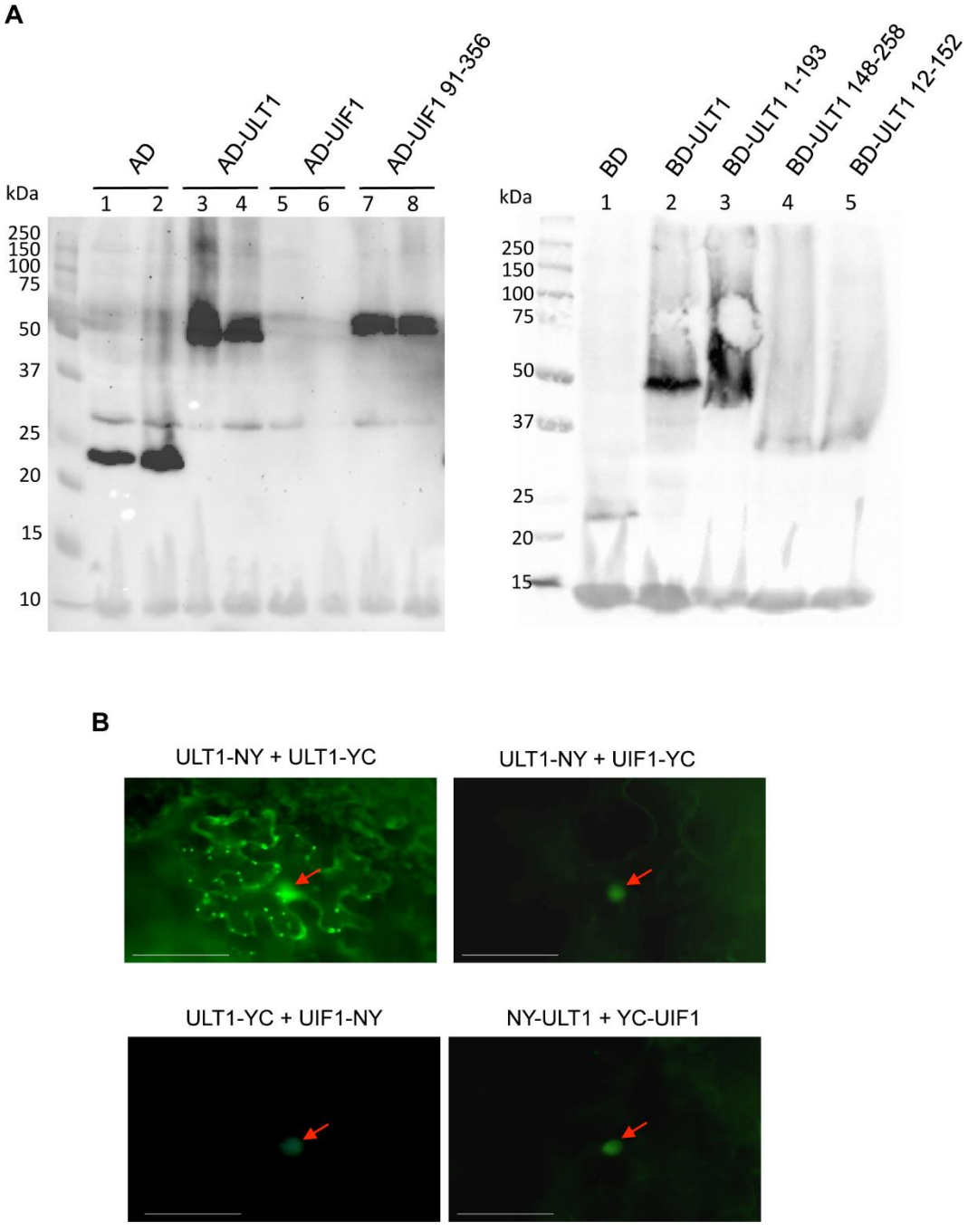
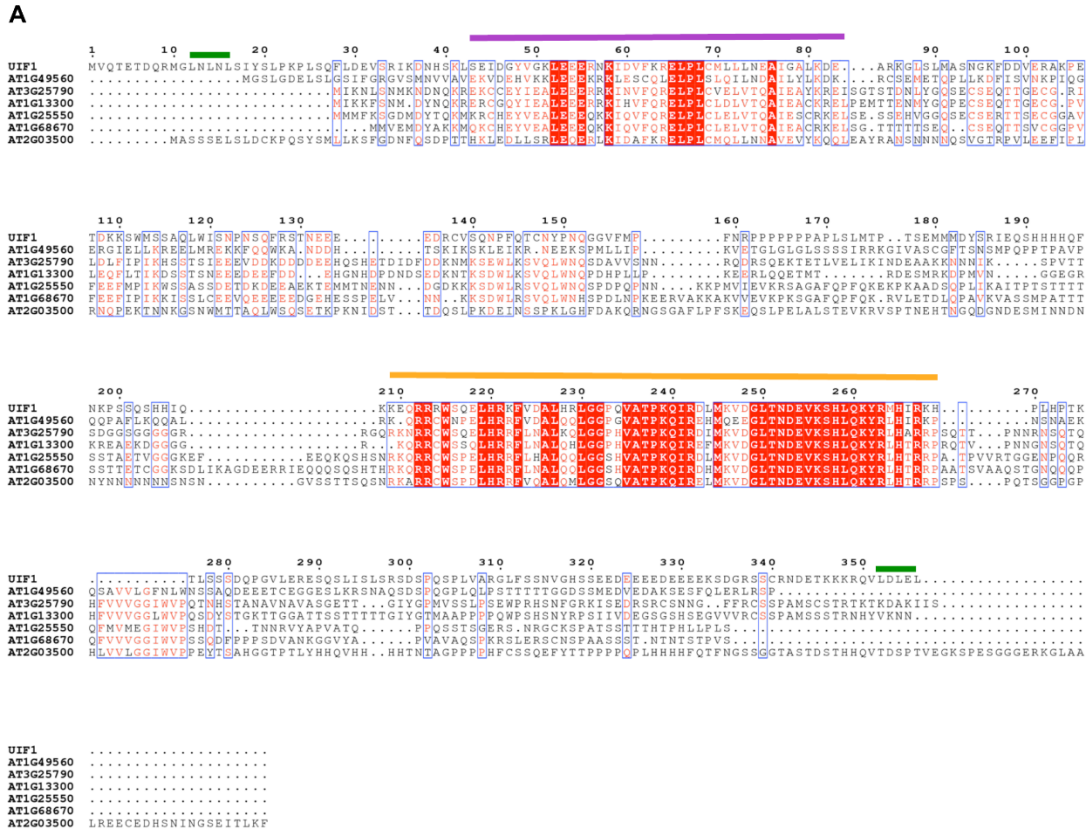
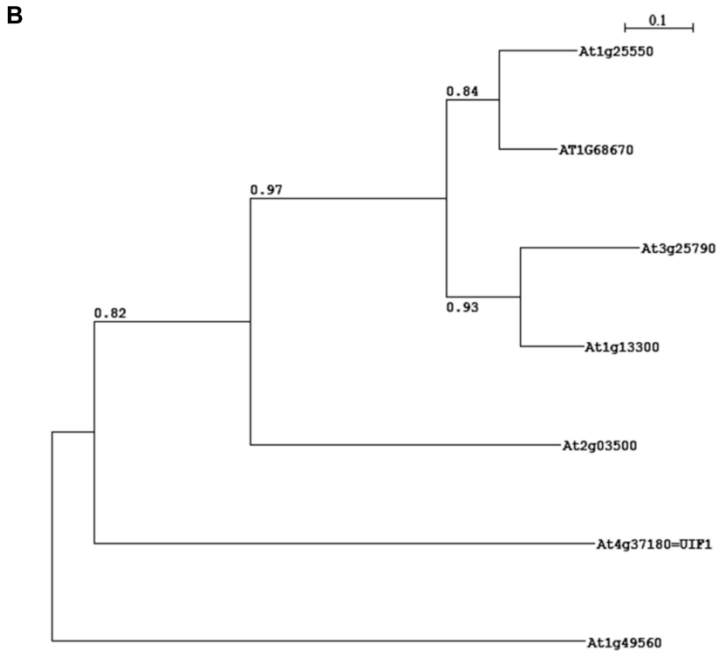
SUPPLEMENTARY DATA

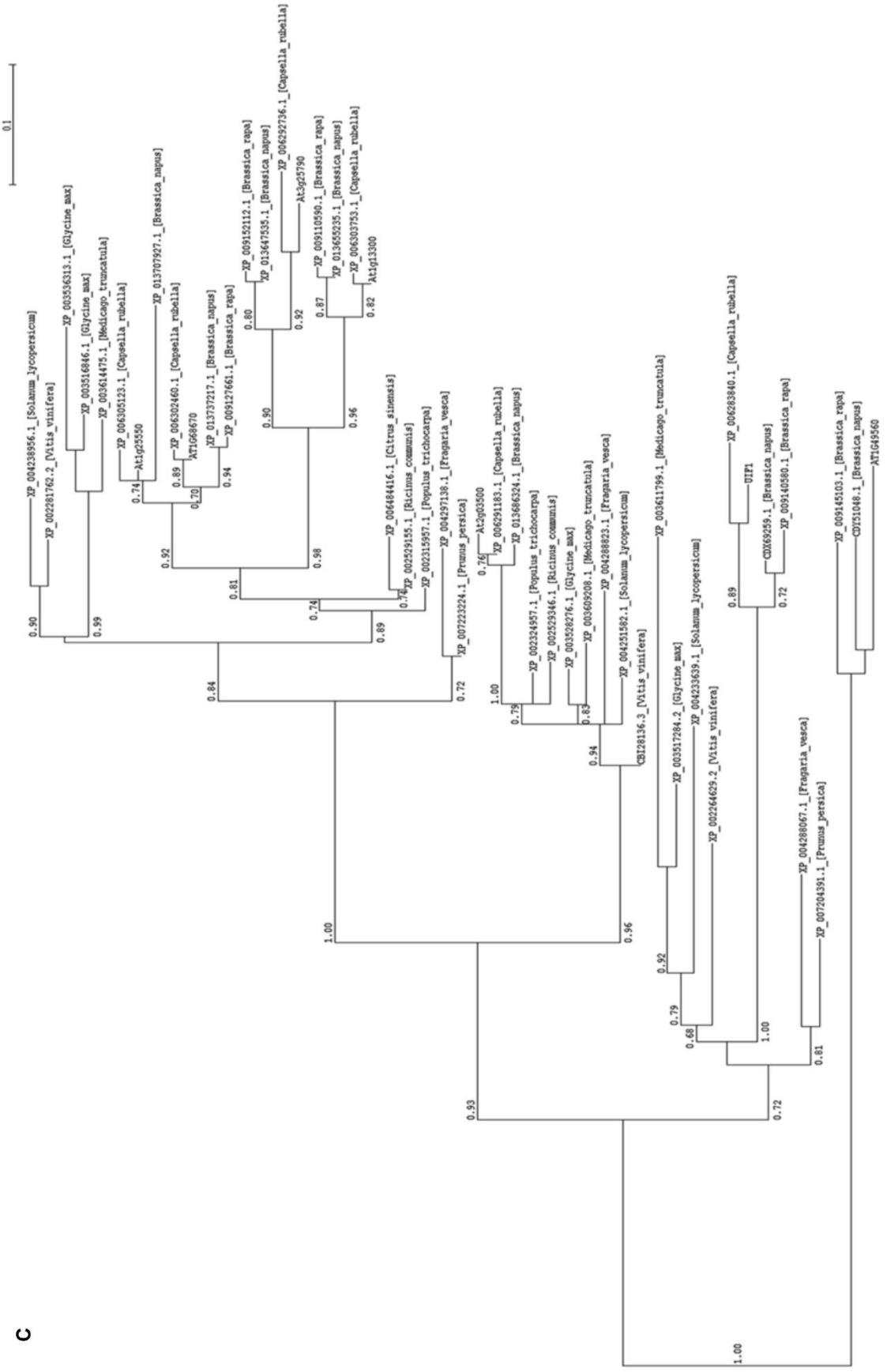


Supplementary Figure S1. Supplemental dataset for ULT1-UIF1 interaction, as tested by (A) Y2H or (B) BiFC experiments. (A) Western-blot analyses were performed on diploids obtained from mated yeast strains for co-expression of *ULT1* and *UIF1* constructs. (left) Western-blot on yeast extracts using an anti-HA antibody for detection of Gal4-AD fusions. Lane 1: mating between Gal4 DBD and Gal4 AD expression clones, lane 2: mating

between Gal4 DBD – ULT1 and Gal4 AD expression clones, lane 3: mating between Gal4 DBD and Gal4 AD – ULT1 expression clones, lane 4: mating between Gal4 DBD – ULT1 and Gal4 AD – ULT1 expression clones, lane 5: mating between Gal4 DBD and Gal4 AD – UIF1 expression clones, lane 6: mating between Gal4 DBD – ULT1 and Gal4 AD – UIF1 expression clones, lane 7: mating between Gal4 DBD and Gal4 AD - UIF1 (aa. 91 to 356) expression clones, lane 8: mating between Gal4 DBD - ULT1 and Gal4 AD - UIF1 (aa. 91 to 356) expression clones. (right) Western blot on yeast extracts using an anti-C-myc antibody, for detection of Gal4-DBD fusions. Lane 1 : mating between Gal4 DBD and Gal4 AD expression clones, lane 2 : mating between Gal4 DBD – ULT1 and Gal4 AD expression clones, lane 3 : mating between Gal4 DBD – ULT1 (aa. 1 to 193) and Gal4 AD expression clones, lane 4 : mating between Gal4 DBD – ULT1 (aa. 148 to 258) and Gal4 AD expression clones, lane 5 : mating between Gal4 DBD – ULT1 (aa. 12 to 152) and Gal4 AD expression clones. BD: DNA binding domain, AD: activation domain. (B) Supplemental dataset for ULT1-UIF1 interaction in the nucleus of tobacco cells by BiFC experiments. Cells of tobacco leaves were transiently co-infiltrated with protein fused at their C and N-ter part to N-ter part of YFP (NY) or C-ter part of YFP (YC) respectively: ULT1-NY and ULT1-YC (as control); ULT1-NY and UIF1-YC; ULT1-YC and UIF1-NY; NY-ULT1 and YC-UIF1. Tissues were observed 3 days after infiltration under Zeiss Axioplan fluorescent microscope with YFP filter (Green fluorescence) under 40 x objectives. The YFP signal detected in the nuclei of tobacco cells was reproducibly obtained in multiple independent experiments and with four different combinations of split YFP fusions to ULT1 and UIF1 proteins (Fig.1 and this Suppl. Fig. S1). Red arrows indicate cell nuclei. Scale bars: 2 µm.



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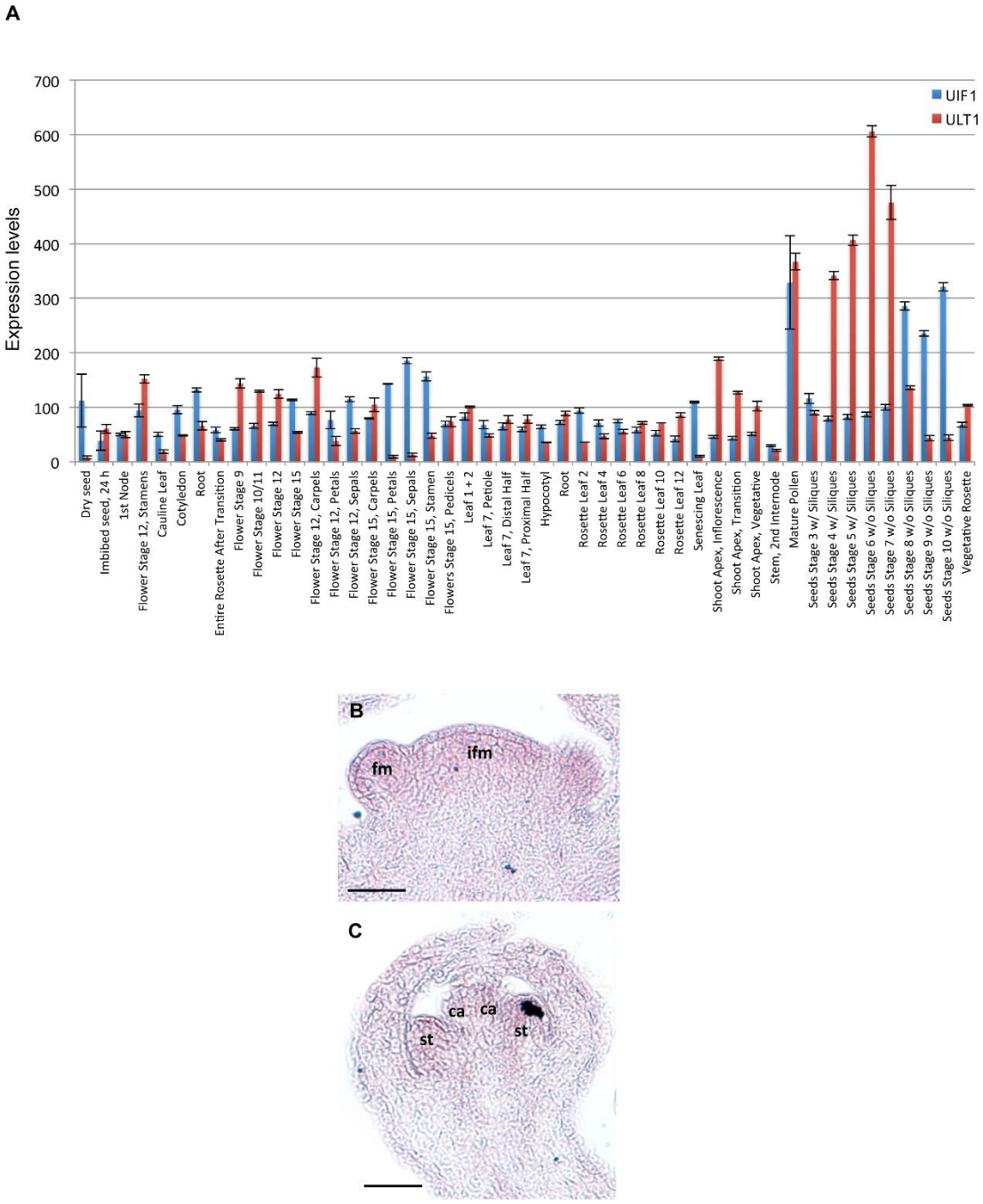
C

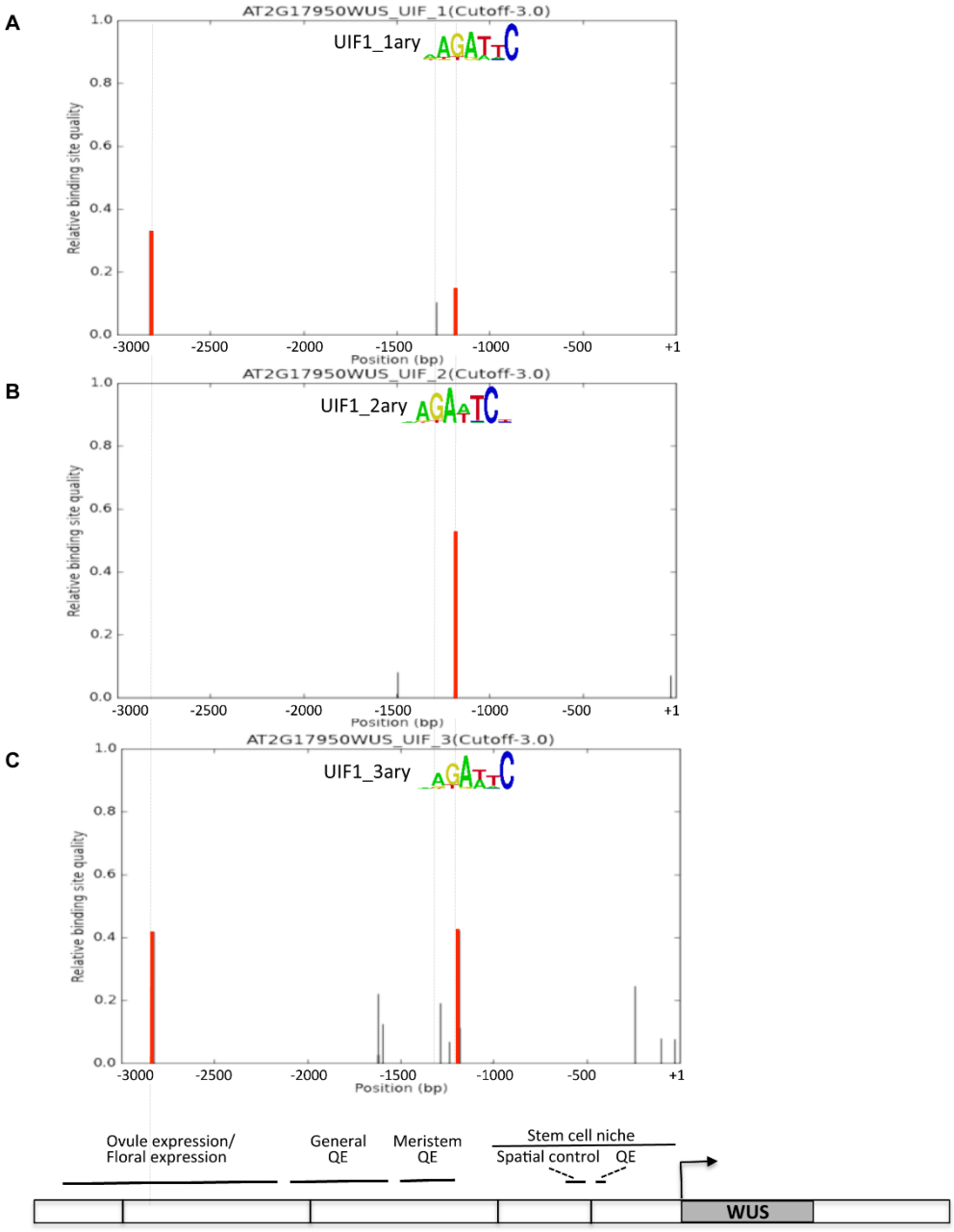
Supplementary Figure S2. Phylogenetic analyses of UIF1 and its homologues in *A. thaliana*. (A) Alignment of predicted amino acid sequences of UIF1 (AT4G37180.1) and UIF1-like homologues in *A. thaliana* (https://blast.ncbi.nlm.nih.gov/). Conserved aa are colored in red (100% identity), or boxed in blue (>50% identity) and non-conserved aa appear in black. The alignment shows that both the hydrophobic region (purple line) and the Myb domain (orange line) are conserved, while the EAR-like motifs (green lines) are specific to UIF1. (B,-C) Phylogenetic reconstructions from (A) UIF1 paralogues and (B) UIF1 orthologues in eudicots. Amino acid sequences were aligned using CLUSTALO in the SEAVIEW program (Gouy et al., 2010). Homologous sites for phylogenetic reconstructions were determined automatically using Gblocks. Maximum Likelihood phylogenies were then generated from these alignments in PhyML (Guindon et al., 2009) using an LG evolutionary model. The PhyML options used to generate the tree were the default settings except the invariable sites that were optimized. Statistical support was provided by aLRT (SH-like). Bootstraps support values superior to 0.6 are indicated at corresponding nodes.



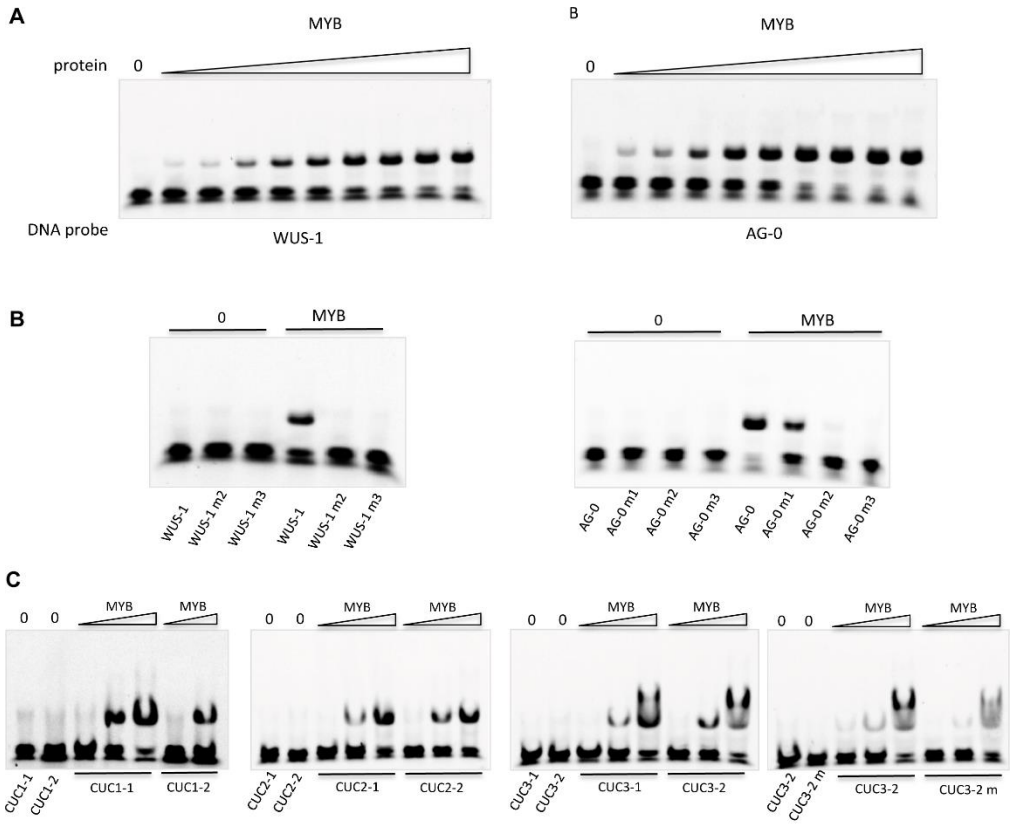
Supplementary Figure S3. UIF1 and ULT1 expression data. (A) Graphic representation of *UIF1* and *ULT1* expression levels in all tissues and organs of the *Arabidopsis thaliana* plant at different developmental stages (extracted from the eFP Browser dataset; http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi). *ULT1* expression level (red bars) is slightly higher than the one of *UIF1* (blue bars) until stage 12 of flower development (pre-anthesis) and then, this ratio is reversed from post-anthesis stages on. Regarding relative

expressions in individual floral organs, *UIF1* expression is higher than that of *ULT1* in sepals and petals, while *ULT1* expression is higher in carpels. In seeds and siliques, *ULT1* expression is much higher than *UIF1* expression during early embryogenesis but this tendency shifts drastically during later stages of embryogenesis with *UIF1* expression being higher than *ULT1* expression. Expression levels are expressed in absolute values as in e-FP Browser, standard errors are represented by vertical bars. (B-C) RNA *in situ* hybridization control for Fig. 2 D-F, using an *UIF1* sense probe hybridized to WT L*er* tissues. Longitudinal sections (B) through the inflorescence meristem (ifm) and adjacent floral meristems (fm) or (C) through a stage 6-7 flower. st: stamen primordia; ca: carpel primordia. Scale bars: 50 µm.

Supplementary Figure S4. *uif1-1* and *3* allelic mutants display loss of floral organ identity. (A-C) Flower phenotypes of eight week-old *uif1-1* (C) and *uif1-3* (A-B) mutant plants. *uif1-1* and *uif1-3* mutant alleles produced flowers with (A-B) stamens in the third whorl (red arrows) that partially lose their identity and become petaloid (white arrow) (A, zoom in B), or (C) branching stamens (white arrow) only fused along the filament (red arrow). Scale bars: 500µm.



Supplementary Figure S5. Morpheus analysis result on *WUS* promoter sequence. *WUS* promoter sequences were submitted to analyses through the Morpheus program (http://biodev.cea.fr/morpheus/) to predict the probability of potential UIF1 binding sites using UIF1_1ary (A), UIF1_2ary (B) and UIF1_3ary (C) matrices, with a cut-off score of -3. The two best UIF1 binding sites motifs in *WUS* promoter are represented by a red bar *and correspond to* GTAGATTCCT (*WUS-1*: score -1.73107) *and TAGAATATTT* (*WUS-2*: score -1.74376) motifs (position refers to *Baurle and Laux, 2005; WUS promoter elements are indicated at the bottom)*. Other UIF1 binding sites, with a negative score lower than -2, are represented by black bars.



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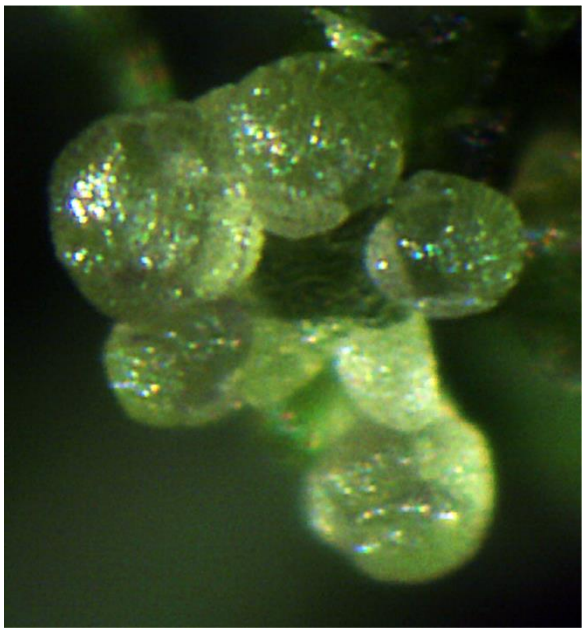
Gene	Binding site	Position^{ATG}	oligonucleotides
WUS-1	GTAGATTCCT	- 1182	oETH1433 / oETH1434
mutant m1	GTAGcTTCCT		oETH1466 / oETH1467
mutant m2	GTAGtTTCCT		oETH1491 / oETH1492
mutant m3	GTAGATTgCT		oETH1493 / oETH1494
AG-0	AAGAATCTTT	1922	oETH1435 / oETH1436
mutant m1	AAGcATCTTT		oETH1495 / oETH1496
mutant m2	AAGAATgTTT		oETH1497 / oETH1498
mutant m3	AAGcATgTTT		oETH1504 / oETH1505
CUC1-1	ATGATTCTCT	-1245	oETH1437 / oETH1438
CUC1-2	GTAGAATCCC	- 335	oETH1439 / oETH1440
CUC2-1	AAAGATACAA	- 616	oETH1445 / oETH1446
CUC2-2	ACAGATTCCT	- 333	oETH1447 / oETH1448
CUC3-1	CTGATTCTTT	-1677	oETH1462 / oETH1463
CUC3-2	ATAGAATCAA	-1344	oETH1464 / oETH1465
mutant m	ATAGtATCAA		oETH1501 / oETH1502

Supplementary Figure S6. Electrophoretic mobility shift assay (EMSA). (A-B) The binding properties of UIF1 *MYB* domain (*6*His-*GST*-UIF1-Myb) were tested for binding sites identified in *WUS* and *AG*, (A) using *a gradient of protein concentration (0;* 4 nM; 7.8 nM; 15.6 nM; 31.3 nM; 62.5 nM; 125 nM; 250 nM; 500 nM; 1000 nM) or (B) mutant versions of identified binding sites. In (B), 125 nM of recombinant protein were used. (C) The binding properties of UIF1 *MYB* domain (*6*His-*GST*-UIF1-Myb) were tested for binding sites identified in the *CUC* genes, using *a gradient of protein concentration (*15.6 nM;125nM;1000nM) or mutant versions of identified binding sites. (D) Information on the binding sites and corresponding oligonucleotides used for the EMSA assays.



Supplementary Figure S7. Type of dissected inflorescence used in the RT-qPCR experiment shown in Figure 5D. Picture, taken under a dissecting microscope, of a Col-0 inflorescence after removal of flower primordia older than stage 5.

Table S1. List of oligonucleotides used in this study and referred to in the methods.

Purpose	Primer name	Sequence 5'-3'
***uif1* T-DNA lines genotyping**	oUIF1-ADNT06-F	AACATGCAAATCTCGTGGAAG
	oUIF1-ADNT06-R	TGATGCTCTTCATAGGCTTGG
	oLB2	GATATAATAGGAAGC
	oUIF1-ADNT32-F	CATACACGGTTATGCCCATTC
	oUIF1-ADNT32-R	GATCCTCGACACTTCATCGAG
	oLBb1.3	GTTCCGAAATCGGCAAAAT
RT-PCR and RT-qPCR	oUIF1_cDNA_F1	ATGGTTCAAACAGAAACCG
	oUIF1_cDNA_F2	GCTCTTCATAGGCTTGGAGGGCC
	oUIF1_cDNA_R2	GGCCCTCCAAGCCTATGAAGAGC
	oUIF1_cDNA_R1	TCAAAGCTCAAGATCC
	oWUS_cDNA_F	GCAAGCTCAGGTACTGAATGTGGTG
	oWUS_cDNA_R	GACCAAACAGAGGCTTTGCTCTATCG
BiFC	oUIF1sall.F	GTCGACATGGTTCAAACAGAAACCG
	oUIF1-BamH1.R	GGATCCTCAAAGCTCAAGATCC
	oUIF1-BamH1nostop.R	GGATCCCAAAGCTCAAGATCC
	oULT1 sall.F	GTCGACATGGCGAACAATGAGGGAGAGATGC
	oULT1-BamH1.R	GGATCCTCAAGCTTTGACATTGCT
	oULT1-BamH1nostop.R	GGATCCAGCTTTGACATTGCT
	oUIF1dNTsall.F	GTCGACTTATGGCATCTAATGGG
	oULT1dBbCTBamHI.R	GGATCCTCACACCTTCCTGCTCCCTC
	oULT1dBbCT-nostopBamHI.R	GGATCCCACCTTCCTGCTCCCTC
DLRA	oUIF_FAscI	GGCGCGCCGTTCAAACAGAAACCGATC
	oUIF_RXbaI	TCTAGATTAAAGCTCAAGATCCAACACTTG
	oUIF_RdEARXbaI	TCTAGATTACACTTGTCTCTTCTTCTTTGTTTC
	oUIF-ANANA_FAscI	GGCGCGCCGTTCAAACAGAAACCGATCAAAGGATGGGTGCG AAT GCG AATGCG TCTATCT
Subcellular localisation	oUIF1-EcoR1.F	GAATTCATGGTTCAAACAGAAACCG
	oUIF1-BamH1nostop.R	GGATCCCAAAGCTCAAGATCC
	oUIF1-BamH1.R	GGATCCTCAAAGCTCAAGATCC
RNA *in situ* hybridization	oISH_UIF_F1	ACCGATCAAAGGATGGGTCT
	oISH_UIF_R1	TAATACGACTCACTATAGGGTCAGTTTCCGGTTTTGCCCT
	oT7 promoter.R	TAATACGACTCACTATAGGG
Bacteria expression constructs	oETH1239	TACCATGGTTCAAACAGAAACC
	oETH1416	CCATGGCACAGAAGAAAGAGCAG
Yeast expression constructs	oETH1368	CCATTCGAATTCATGGTTCAAACAGAAACC
	oETH1369	GAATGGGGATCCTCAAAGCTCAAGATCCAA
	oETH1381	TATGCTGAATTCATGGCGAACAATGAGGGA
	oETH1382	GCAGCAGGATCCTCACCTGCTCCCTCTCTC
	oETH1410	GAATTCATGGCATCCATGTTGTTT
	oETH1411	GGATCCTCACTTCTTTGATGATTC
	oETH1383	TATCAAGAATTCATGGCGAACAATGAGGGA
	oETH1384	TCACTAGGATCCTCACCTGCTCCCTCTCTC
	oETH1490	GAATTCATGGTTCAAACAGAAACC
	oETH1240	ATCTCGAGTCAAAGCTCAAGATC

EMSA	*WUS-1*	oETH1433	GTATGAAATTTGTAGATTCCTAAAAAAATCT
		oETH1434	AGATTTTTTTAGGAATCTACAAATTTCATA
	AG-0	oETH1435	GGTCTTTGTTAAAGAATCTTTGATCACGTCA
		oETH1436	TGACGTGATCAAAGATTCTTTAACAAAGAC
	CUC1-1	oETH1437	GGTCGGCGGAGATGATTCTCTCATCCACCAC
		oETH1438	GTGGTGGATGAGAGAATCATCTCCGCCGAC
	CUC1-2	oETH1439	GTTAGGCTGACGTAGAATCCCCTGAATTTCA
		oETH1440	TGAAATTCAGGGGATTCTACGTCAGCCTAA
	CUC2-1	oETH1445	GAGATAAAAAAAAAGATACAATCTGAATCCT
		oETH1446	AGGATTCAGATTGTATCTTTTTTTTATCT
	CUC2-2	oETH1447	GAGAGAAAACCACAGATTCCTATGAAAGAGT
		oETH1448	ACTCTTTCATAGGAATCTGTGGTTTTCTCT
	CUC3-1	oETH1462	GATCTTTTTACCTGATTCTTTTGTATCATTC
		oETH1463	GAATGATACAAAAGAATCAGGTAAAAAGAT
	CUC3-2	oETH1464	GGAGGAAGAGTATAGAATCAACCGAACCAAC
		oETH1465	GTTGGTTCGGTTGATTCTATACTCTTCCTC
	WUS-1 m1	oETH1466	GTATGAAATTTGTAGCTTCCTAAAAAAATCT
		oETH1467	AGATTTTTTTAGGAAGCTACAAATTTCATA
	WUS-1 m2	oETH1491	GTATGAAATTTGTAGTTTCCTAAAAAAATCT
		oETH1492	AGATTTTTTTAGGAAACTACAAATTTCATA
	WUS-1 m3	oETH1493	GTATGAAATTTGTAGATTGCTAAAAAAATCT
		oETH1494	AGATTTTTTTAGCAATCTACAAATTTCATA
	AG-0 m1	oETH1495	GGTCTTTGTTAAAGCATCTTTGATCACGTCA
		oETH1496	TGACGTGATCAAAGATGCTTTAACAAAGAC
	AG-0 m2	oETH1497	GGTCTTTGTTAAAGAATGTTTGATCACGTCA
		oETH1498	TGACGTGATCAAACATTCTTTAACAAAGAC
	AG-0 m3	oETH1504	GGTCTTTGTTAAAGCATGTTTGATCACGTCA
		oETH1505	TGACGTGATCAAACATGCTTTAACAAAGAC
	CUC3-2 m1	oETH1501	GGAGGAAGAGTATAGTATCAACCGAACCAAC
		oETH1502	GTTGGTTCGGTTGATACTATACTCTTCCTC