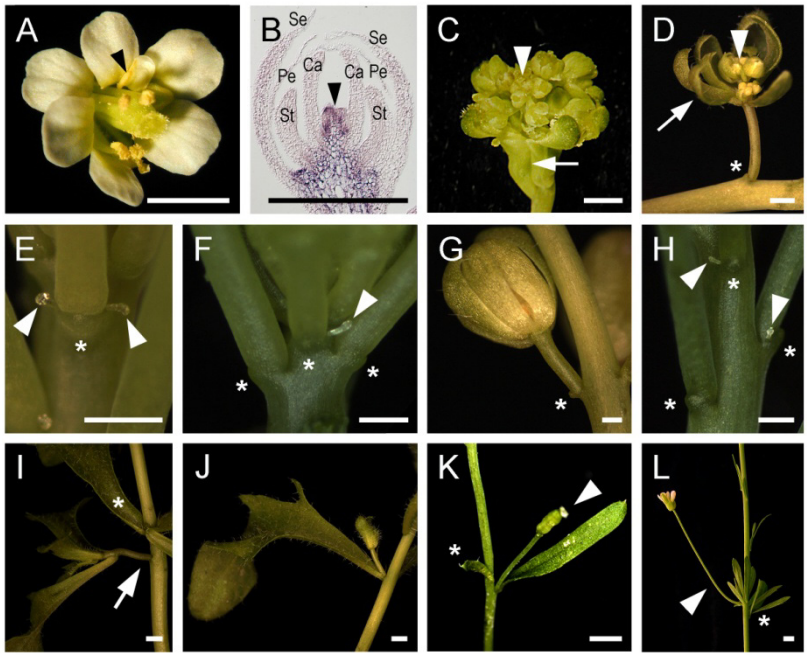
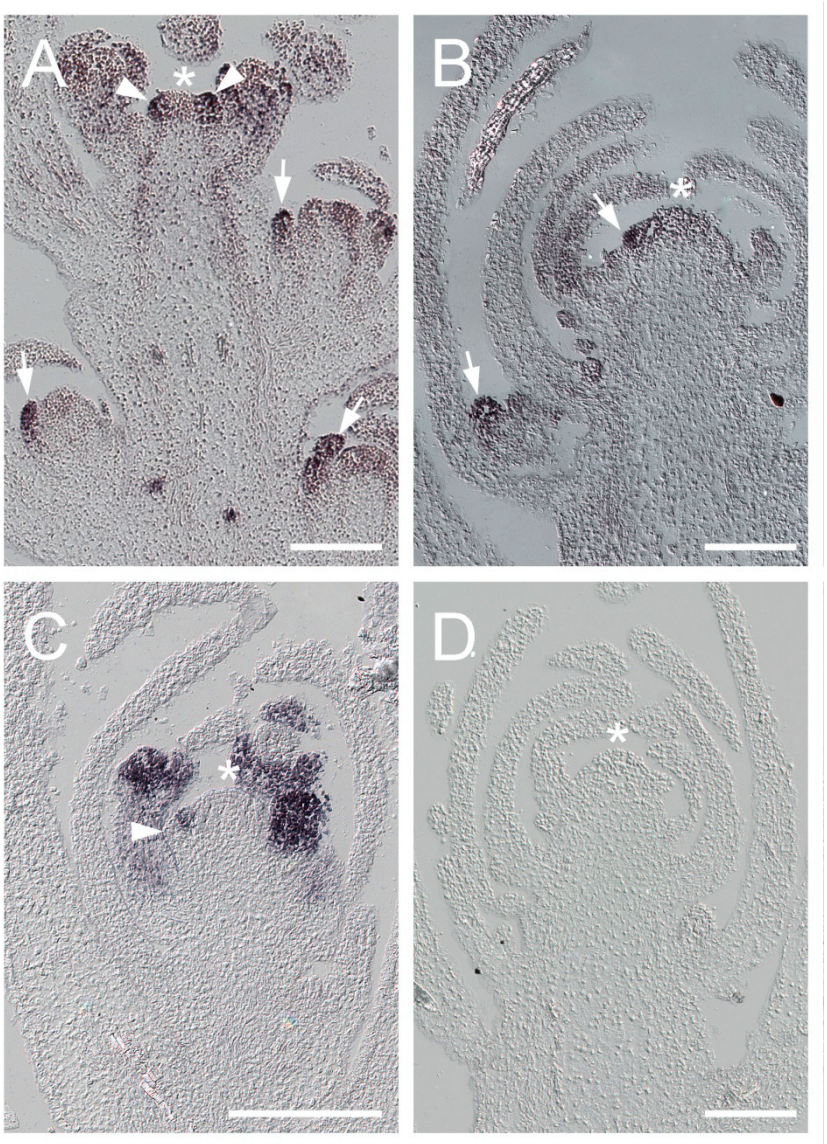
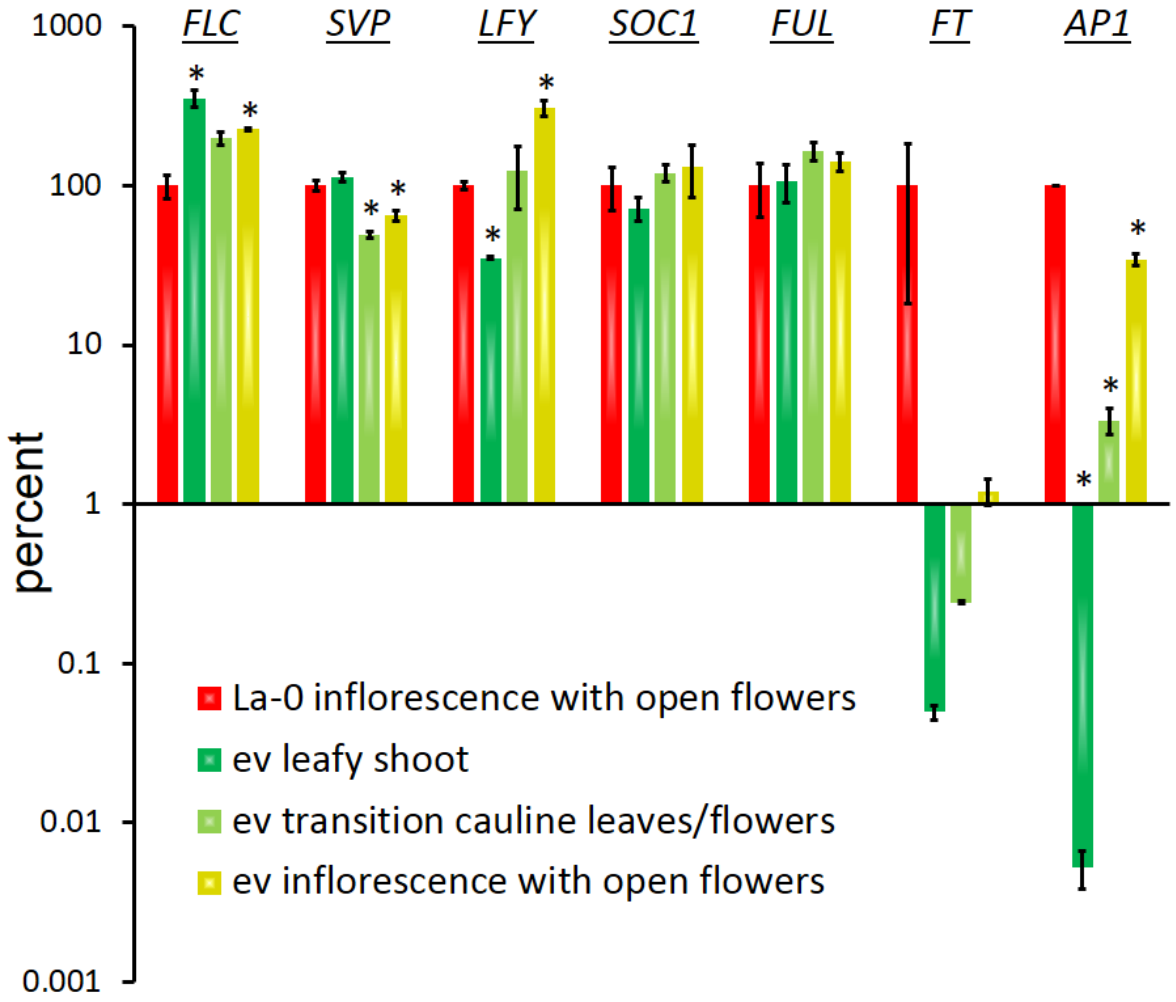
Supplemental Figure 1. Phenotypes of *iCLF* (*clf-28 swn-7 CLF$_{pro}$:CLF-GR*) plants. **A**, Late rescue of *iCLF* plants by renewed DEX treatment; senescent inflorescence with elongated siliques (arrow; 90 DAG, 30 days after Dexamethasone treatment, LD). **B**, untreated *iCLF* flowers are largely sterile in LD, approximately 1% of *iCLF* plants show flower reversions indicated by a single paraclade without cauline leaf (arrow). **C**, *iCLF* plants under continuous SD, 82 DAG. The growth habits of the plants varied from plants producing flowers with strongly reduced internode elongation (arrowhead) to plants with an elongated stem producing many cauline leaves (arrow). Inlay box, top view of the apex of the plant on the right side which still produces cauline leaves. Note the absence of elongated paraclades. **D**, *iCLF* plant 65 DAG, shifted from LD to SD 29 DAG; arrowheads mark flowers between the last normal leaf/paraclade metamer and the reversion nodes (arrow). All *iCLF* plants were grown on MS agar plates with 10 µM DEX for 10 days before they were transferred to soil. Scale bars, 10 mm. See also Supplemental Tables 1 and 2 for detailed organ counts.



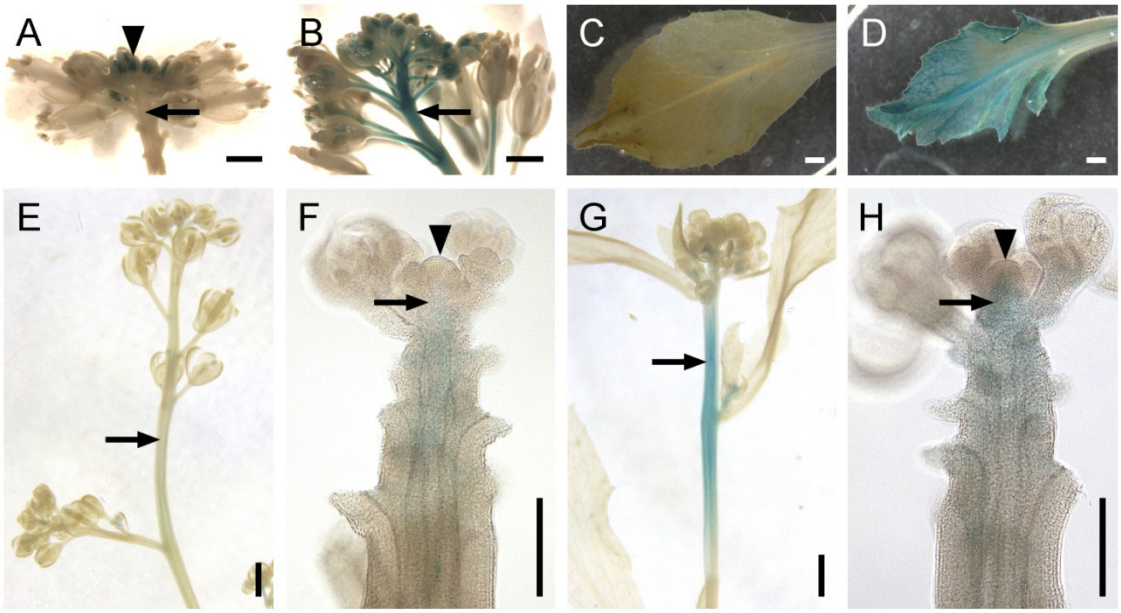
Supplemental Figure 2. Floral phenotype, rudimentary bracts and classes of reversion nodes. A, *emf2-10 vrn2-1* flower with additional flower organs (seven petals instead of four in the wildtype). One of the petals shows a partial homeotic transformation to stamen identity (arrowhead). **B**, RNA *in situ* hybridisation with *STM* antisense probe. Longitudinal section of *emf2-10 vrn2-1* mutant flower at stage 13. The arrowhead marks an indeterminate FM, which will give rise to an ectopic fifth whorl (present in all *emf2-10 vrn2-1* mutant flowers independent of day-length conditions). Se, Sepal; Pe, Petal; St, Stamen; Ca, Carpel. **C, D**, FM to IM reversions after the formation of sepals in floral stage 3 (**D**) or even carpels (**C**); LD to SD shifted *emf2-10 vrn2-1* plants (also seen in *iCLF*, *emf2-10 vrn2-1*, *emf2-10 vrn2-1 flc-5*, *emf2-10 vrn2-1 svp-32* and *emf2-10 vrn2-1 flc-5 svp-32,* less than 10% of all FM to IM reversions). **C**, An ectopic paraclade (arrowhead), is bursting out of a silique (arrow). **D**, Sepaloid leaves (arrow) surround a paraclade (arrowhead); Asterisk: rudimentary bract. **E-H**, rudimentary bracts (asterisks) at the base of pedicels, some with stipules (arrowheads). **E**, La-0, continuous SD; **F**, Col-0 shifted from LD to SD; **G**, *iCLF*, shifted from LD to SD, **H**, *ft-10*, continuous LD. **I-K**, different classes of reversion nodes in *iCLF* shifted from LD to SD. **I**, paraclade without cauline leaf (arrow) and leaf without paraclade or flower (asterisk), **J**, paraclade with cauline leaf, **K**, cauline leaf at the base of a pedicel (arrowhead marks the silique; asterisk: empty leaf). **L**, *emf2-10 vrn2-1* shifted from LD to SD, single leaf/flower node (arrowhead) between empty cauline leaves. Note the strongly reduced internode elongation (asterisk). Scale bars, **A-D** and **I-L**, 2 mm; **E-H,** 1 mm.



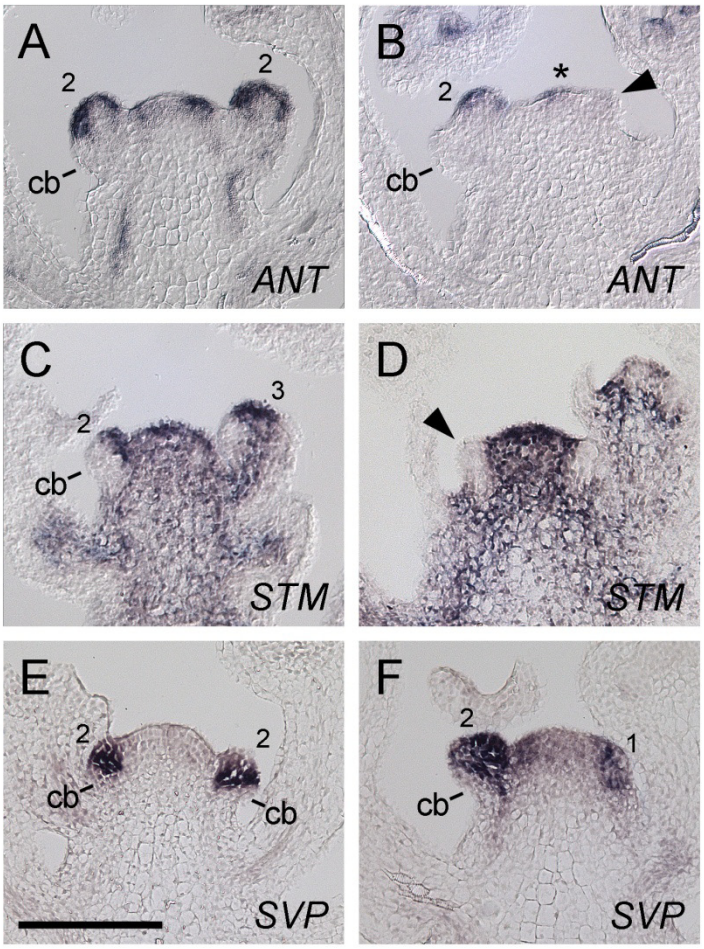
Supplemental Figure 3. *LFY* (A, B) and *AP1* expression (C, D) in wild-type inflorescences (A, C) and leafy *emf2-10 vrn2-1* shoots (B, D) in SD. RNA *in situ* hybridisations with antisense probes. **A**, Primary wild-type inflorescence. *LFY* is strongly expressed in floral (arrowheads) and leaf (arrows) primordia. **B,** In *emf2-10 vrn2-1* leafy shoots, *LFY* is expressed in leaf primordia (arrow) of the primary and the secondary tSAMs. **C,** Secondary wild-type inflorescence. *AP1* is expressed in floral primordia and young flowers but not in leaves. The arrowhead marks the cryptic bract of a stage 2 floral primordium. **D,** *AP1* is undetectable in leafy *emf2-10 vrn2-1* shoots. Asterisks mark the primary IM (A, C) or tSAM (B, D), respectively. Scale, 100µm.



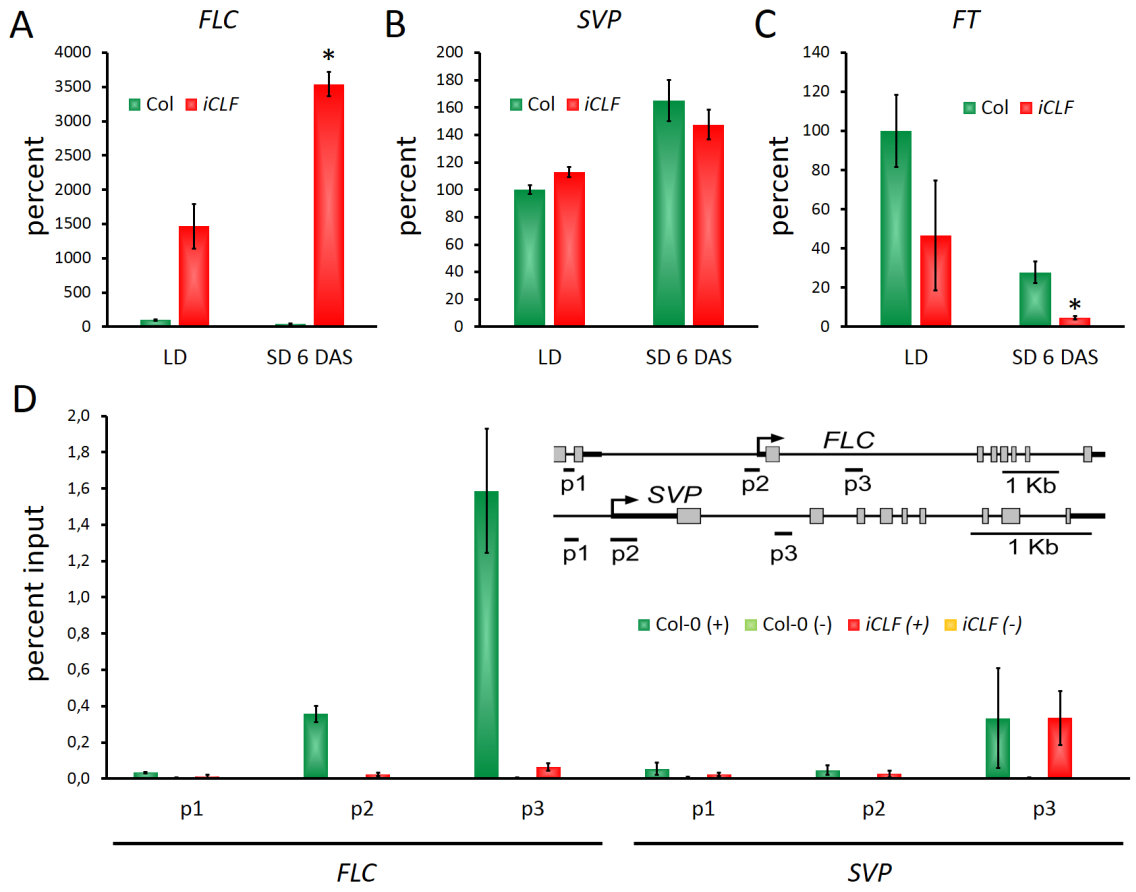
Supplemental Figure 4. Gene expression of flowering time and meristem identity genes in wild-type (La-0) and *emf2-10 vrn2-1* (*ev*) inflorescences in SD. Gene expression was measured in wild-type inflorescences and in three developmental stages of *emf2-10 vrn2-1* inflorescences. Each bar represents the mean of two biological replicates, ± s.e.m.; Asterisks: significant changes of expression (Student´s *t*-test: p≤ 0.05) compared to wildtype inflorescence apices. mRNA expression was quantified by qRT-PCR, normalized to *eIF4a*; relative expression to wild-type (La-0) is shown. Note logarithmic scaling. Inflorescence apices were harvested 8 hours after lights on and based on morphological appearance and height of stem: La-0 inflorescence with open flowers (flower primordia up to stage 13), >15 cm stem height; ev leafy shoot, 1-5 cm stem height; ev transition cauline leaves/flowers (cauline leaves and flower primordia up to stage 13), 15-25 cm; ev inflorescence with open flowers (flower primordia up to stage 13), >25 cm.



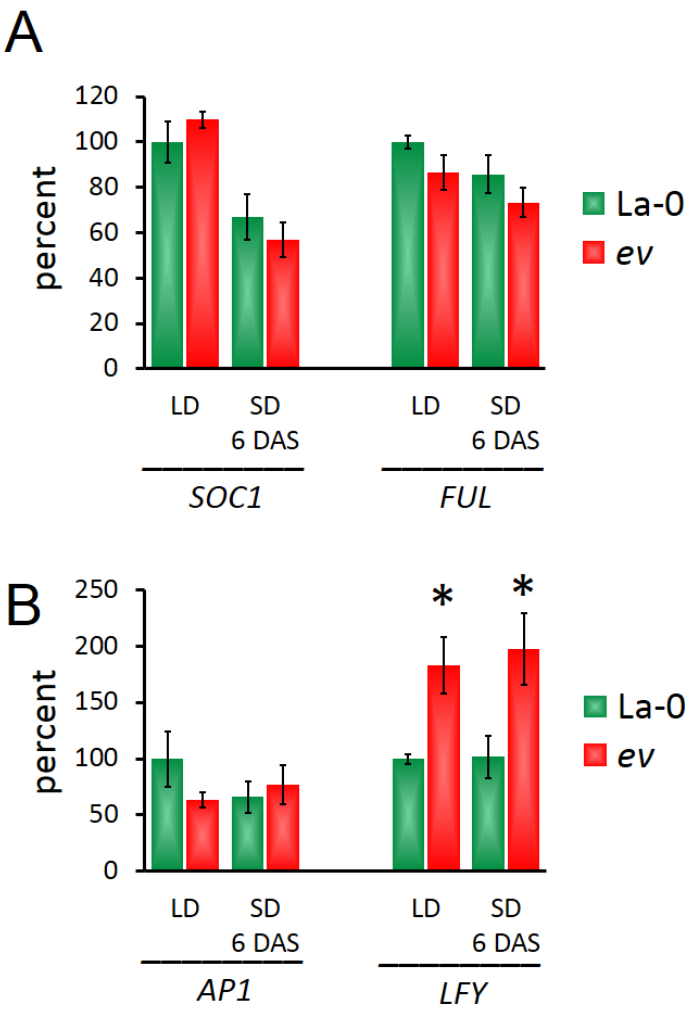
Supplemental Figure 5. *FLC$_{pro}$:GUS* expression in wild type, *emf2-10 vrn2-1* mutants and *iCLF*. **A-D**, *FLC$_{pro}$:GUS* lines in continuous SD. **A**, Wild-type inflorescence, *FLC$_{pro}$:GUS* expression is restricted to anthers in young flower buds (arrowhead); **B**, *emf2-10 vrn2-1* inflorescence, staining is visible in the stem (arrow) and pedicels. **C-D**, Accumulation of *FLC$_{pro}$:GUS* staining in *emf2-10 vrn2-1* mutant cauline leaves (**D**) compared to wild-type (**C**). **E-H**, *iCLF FLC$_{pro}$:GUS* plants (40 DAG) grown under continuous LD (**E, F**) or six days after shift from LD to SD (**G, H**); Arrowhead, IM; arrow, GUS staining in stem. Scale bars: **A-E, G**, 1 mm; **F, H**, 200 µm.



Supplemental Figure 6. Gene expression in inflorescences and cryptic bracts in wild-type and *emf2-10 vrn2-1* mutant floral primordia. RNA *in situ* hybridisation with antisense probes. **A, C, E,** wild-type (La-0) IMs flanked by FMs, 27 DAG, continuous LD. **B, D, F,** *emf2-10 vrn2-1* IMs flanked by FMs, 27 DAG, 6 DAS from LD to SD. **A, B,** *AINTEGUMENTA* (*ANT*), a classical indirect marker for cryptic bracts (Long and Barton, 2000). Note in (**B**) the size of the cryptic bract (cb) and the unusual shape of the IM (asterisk) and an early stage primordium (arrowhead). **C, D,** *STM* is a classical marker for meristem tissue and is not expressed in cryptic bracts in wildtype (**C**). **D**, in *emf2-10 vrn2-1* inflorescences some floral primordial are entirely unstained (arrowhead) indicating a complete switch to leaf fate of the primordia. **E, F,** *SVP* probe. The *SVP* expression pattern is fairly similar in *emf2-10 vrn2-1* (**F**) compared to wild-type (**E**), but expanded to the IM and pre-vascular tissue in *emf2-10 vrn2-1*. Scale bar: 100 µm.



Supplemental Figure 7. Expression analyses of *FLC, SVP* and *FT* and H3K27me3 ChIP for FLC and SVP in *iCLF* vs. wild type. qRT-PCR analyses of *FLC* (**A**), *SVP* (**B**) and *FT* (**C**) in inflorescence apices (5 DAS, harvested from 34 days old plants, 8 hours after lights on) normalized to *eIF4*, relative expression to Col-0 (LD). Each bar represents the mean of three biological replicates, ± s.e.m.; Asterisks: significant changes of expression (Student´s *t*-test: $p \leq 0.05$) compared to the equally treated wild type (Col). **D**, ChIP assay: *FLC* and *SVP* chromatin are enriched for H3K27me3 in inflorescence apices of wild type (Col-0). Like in *emf2-10 vrn2-1*, H3K27me3 is strongly reduced at the *FLC* locus in *iCLF* but not at *SVP*. (+) H3K27me3 antibody; (-) no-antibody control. Data represent mean of two biological replicates, ± s.e.m.



Supplemental Figure 8. qRT-PCR analyses of *LFY*, *SOC1*, *FUL* and *AP1* in *emf2-10 vrn2-1 (ev)* and wild-type inflorescence apices. Quantitative RT-PCR normalised to *eIF4*, relative expression to La-0 (LD), ± s.e.m. **A,** *SOC1* and *FUL* are essential for the maintenance of flowering and prevent floral reversion (Melzer et al. 2008), their expression is not altered in *emf2-10 vrn2-1* inflorescences relative to wild-type (La-0) suggesting that floral reversion observed in Pc-G mutants is not caused by reduced *SOC1* and *FUL* expression. **B,** The expression of the FT target *AP1* is unchanged, while *LFY* is upregulated in *emf2-10 vrn2-1* inflorescence independently of the day-length. *, Significant change of expression compared to the equally treated wild-type (Student's *t*-test, $p \leq 0.05$). Biological replicates per bar: N = 6. Samples were harvested 27 DAG, 6 DAS (for LD to SD shifted plants), harvested 8 hours after lights on.

Supplemental Table 1 | Flowering time of *iCLF* and *ft-10* mutants measured by leaf number.

	LD					SD				
	N	RL	CL	TL	RL/CL Ratio	N	RL	CL	TL	RL/CL Ratio
Col-0	24	11.2 ± 0.4	2.9 ± 0.2	14.1 ± 0.6	3.8	15	42.2 ± 2.0	9.3 ± 0.5	51.5 ± 2.0	4.5
iCLF	18	13.8 ± 0.6	5.3 ± 0.3	19.1 ± 0.8	2.6	18	47.3 ± 1.5	29.6 ± 3.8	76.9 ± 3.8	1.6
ft-10	18	40.2 ± 0.7	8.8 ± 0.7	49.0 ± 1.0	4.5	18	52.3 ± 1.9	26.1 ± 0.6	78.4 ± 2.2	2.0

± s.e.m.
iCLF and ft-10 show significantly more rosette and cauline leaves than Col-0 under both LD and SD (Student's *t*-test): $p \leq 0.05$

RL, rosette leaves
CL, cauline leaves
TL, total leaves

Supplemental Table 2 | Strong reversion nodes at main shoot of *iCLF*.

	N	PC without CL	CL	CL with PC	CL with F	Σ
Col-0	20	0	0	0	0	0
iCLF	45	2.8 ± 0.5 #	8.8 ± 1.0 #	9.2 ± 1.3 #	2.6 ± 0.3 #	23.4 ± 2.2 #

± s.e.m.

Significantly more than Col-0 (Student's *t*-test): # $p < 0.001$

CL, cauline leaves
PC, paraclades
F, flowers

Supplemental Table 3 | Suppression of floral reversion in *ev* by high *FT*.

	- estradiol		+ estradiol, leaves		+ estradiol, apex	
	R.N.	N	R.N.	N	R.N.	N
line 1	8.0 ± 1.2	6	0.8 ± 0.8 **	5	0.7 ± 0.7 **	7
line 2	10.0 ± 0.9	6	5.3 ± 2.3	7	0.0 ± 0.0 **	7
∑	9.0 ± 0.7	12	3.4 ± 1.5 *	12	0.4 ± 0.4 **	14

± s.e.m.

R.N.: strong reversion nodes at main shoot per plant
N: number of plants

Significantly fewer reversion nodes than untreated plants (Student's *t*-test):
* P ≤ 0.01, ** P ≤ 0.001

Plants from two independent transgenic lines were shifted to SD after three weeks in LD. Each day after shift, a drop of 10 µM Estradiol was placed either on up to three leaves or on the inflorescence apex. Treatment was repeated for seven days and organs counted three weeks after shift.

Supplemental Table 4 | RT-PCR Primer

AP1	5′-GCTTTCTAAACAGATCAAGGAG-3′	5′-TAAACGGGTTCAAGAGTCAG-3′
EiF4A	5′-TTCGCTCTTCTCTTTGCTCTC-3′	5′-GAACTCATCTTGTCCCTCAAGTA-3′
FLC	5′-CGGTCTCATCGAGAAAGCTC-3′	5′-CCACAAGCTTGCTATCCACA-3′
FT	5′-CCTCAGGAACTTCTATACTTTGGTTATGG-3′	5′-CTGTTTGCCTGCCAAGCTGTC-3′
FUL	5′-TACTTGAACGCTATGATCGCT-3′	5′-TAGCTTGGTTCTTTCTTGACCT-3′
LFY	5′-TCTCCCAAGAAGGGTTATCTG-3′	5′-TCTTCATCTTTCCTTGACCTG-3′
SOC1	5′-ACGAGAAGCTCTCTGAAAAGTGGG-3′	5′-CTTGGGCTACTCTCTTCATCACCT-3′
SVP	5′-CAAGGACTTGACATTGAAGAGCTTCA-3′	5′-CTGATCTCACTCATAATCTTGTCAC-3′

Supplemental Table 5 |ChIP PCR Primer

FLC-p1	5′-TCGCCATCGATCTTTCTTCT-3′	5′-TGAGTCAGGAACGAGTCACG-3′
FLC-p2	5′-TTCAAGTCGCCGGAGATACT-3′	5′-CGTGGCAATCTTGTCTTCAA-3′
FLC-p3	5′-GAGGCACCAAAGAAACAAGG-3′	5′-TCGCCCTTAATCTTATCATCG-3′
SVP-p1	5′-CAAAAATGAAAATACGTTGTAGCCC-3′	5′-AGTTGTCTCACTTTGTTCACTTATACTCCT-3′
SVP-p2	5′-CTCATCCTTCACCAATCAAAACCT-3′	5′-ACACACTCAGTCTTTTGTGAGAAGAATT-3′
SVP-p3	5′-AGATACGATTTTGGATTTTTGACCCACTAG-3′	5′-CCACAAAACACATTTAATCCCAAACATG-3′