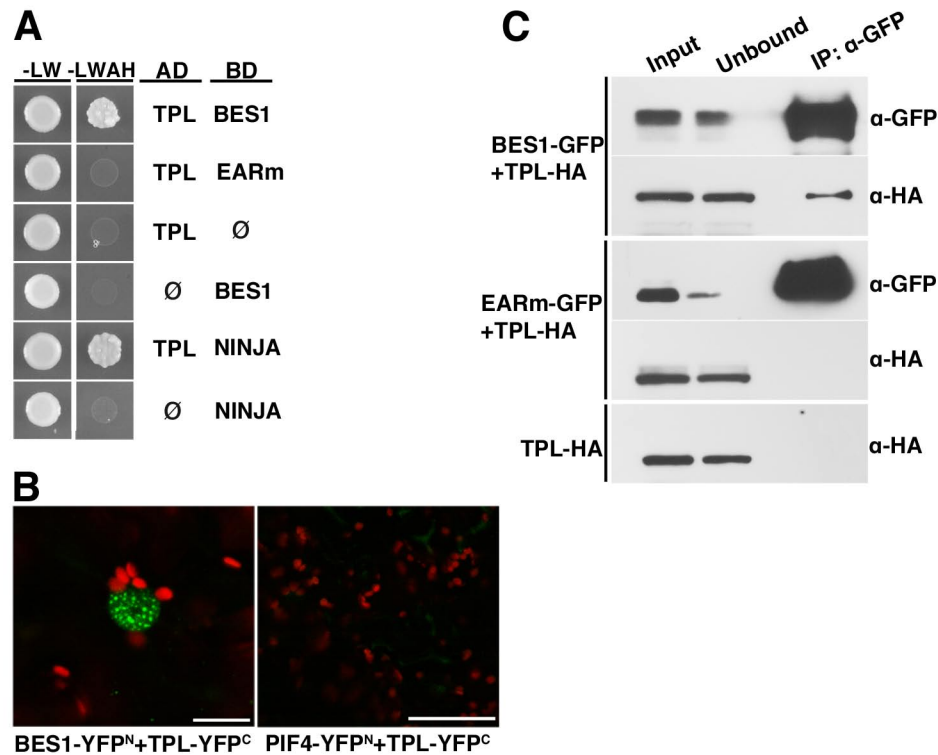
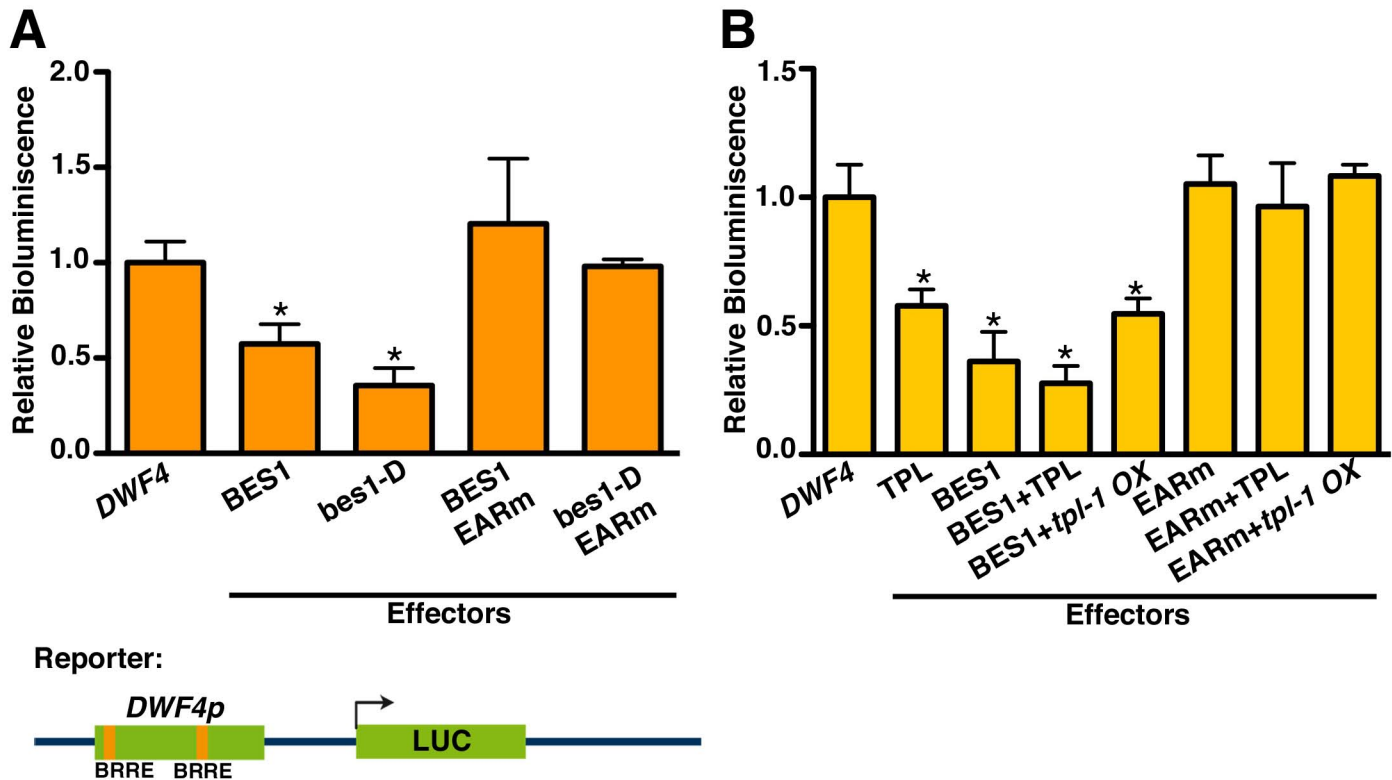


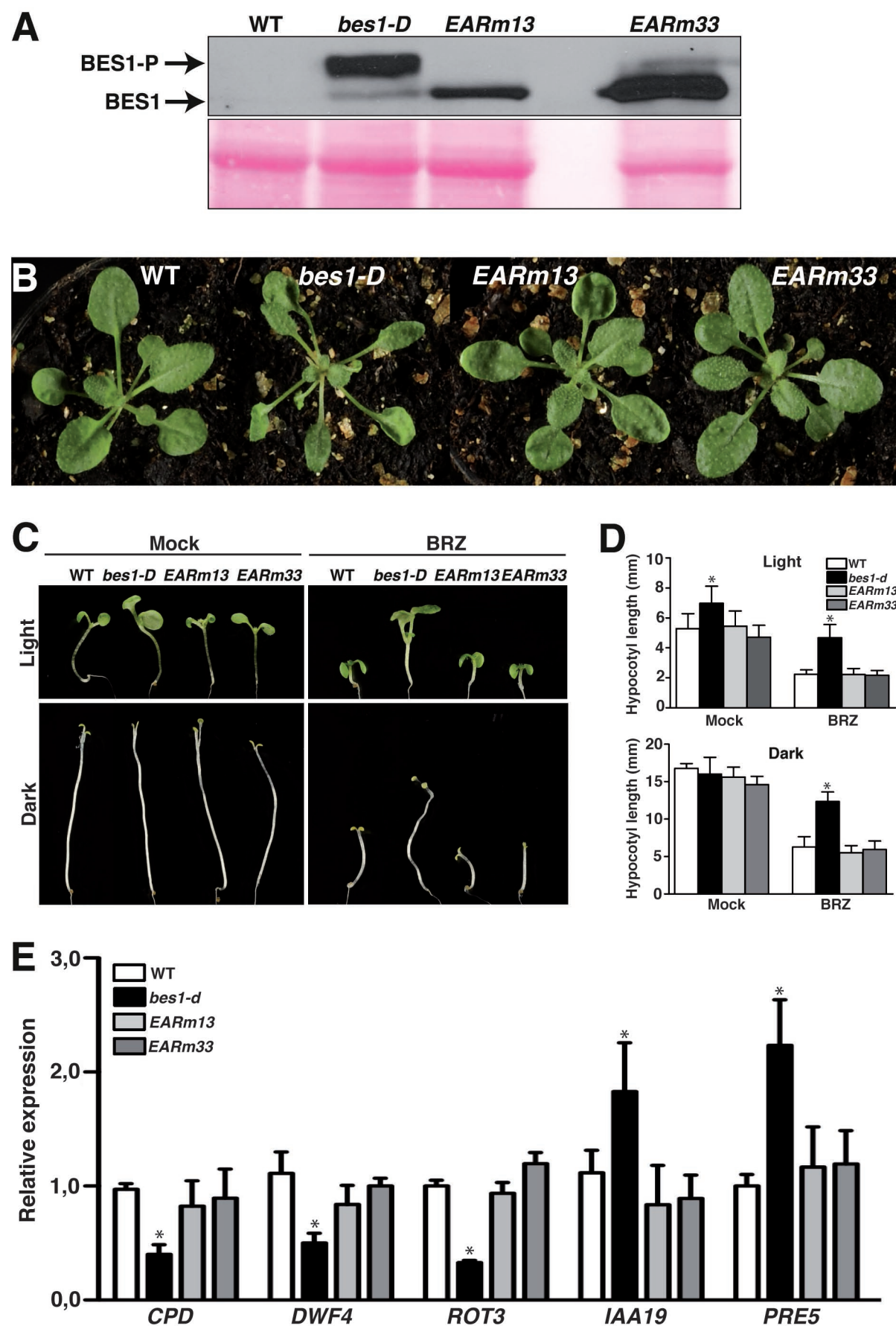
**Fig. S1**

**Fig. S1.** BES1 interacts with TPL through the EAR domain. (A) Yeast two-hybrid assay showing TPL and BES1 interaction. TPL interacts with the intact BES1 protein but not with BES1-EARM (EARM), where core Leucine residues in the EAR motif (LXLXL) were substituted by Alanine. TPL interaction with NINJA is included as a positive control. Yeast cells were grown on the synthetic dropout minimal medium lacking Leu and Trp (-LW), or synthetic dropout without Leu, Trp, His and Ade (-LWAH). (B) BiFC showing BES1 and TPL interaction. Nuclear YFP fluorescence is observed in *N. benthamiana* leaves infiltrated with the BES1-eYFP<sup>N</sup> and TPL-eYFP<sup>C</sup> constructs. PIF4-eYFP<sup>N</sup> and TPL-eYFP<sup>C</sup> are included as a negative control. Red fluorescence corresponds to chlorophyll. Scale bars represent 14 µm in the BES1-TPL panel and 50 µm in the PIF4-TPL panel. (C) Co-IP assay. TPL-HA is pulled-down by immunoprecipitation of GFP-tagged BES1, but not by BES1-EARM (EARM-GFP). *N. benthamiana* leaves were agroinfiltrated with BES1-GFP, BES1-EARM-GFP and TPL-HA. Two days after agroinfiltration, total protein extracts were immunoprecipitated with an anti-GFP antibody. TPL-HA was detected in these fractions with an anti-HA antibody.

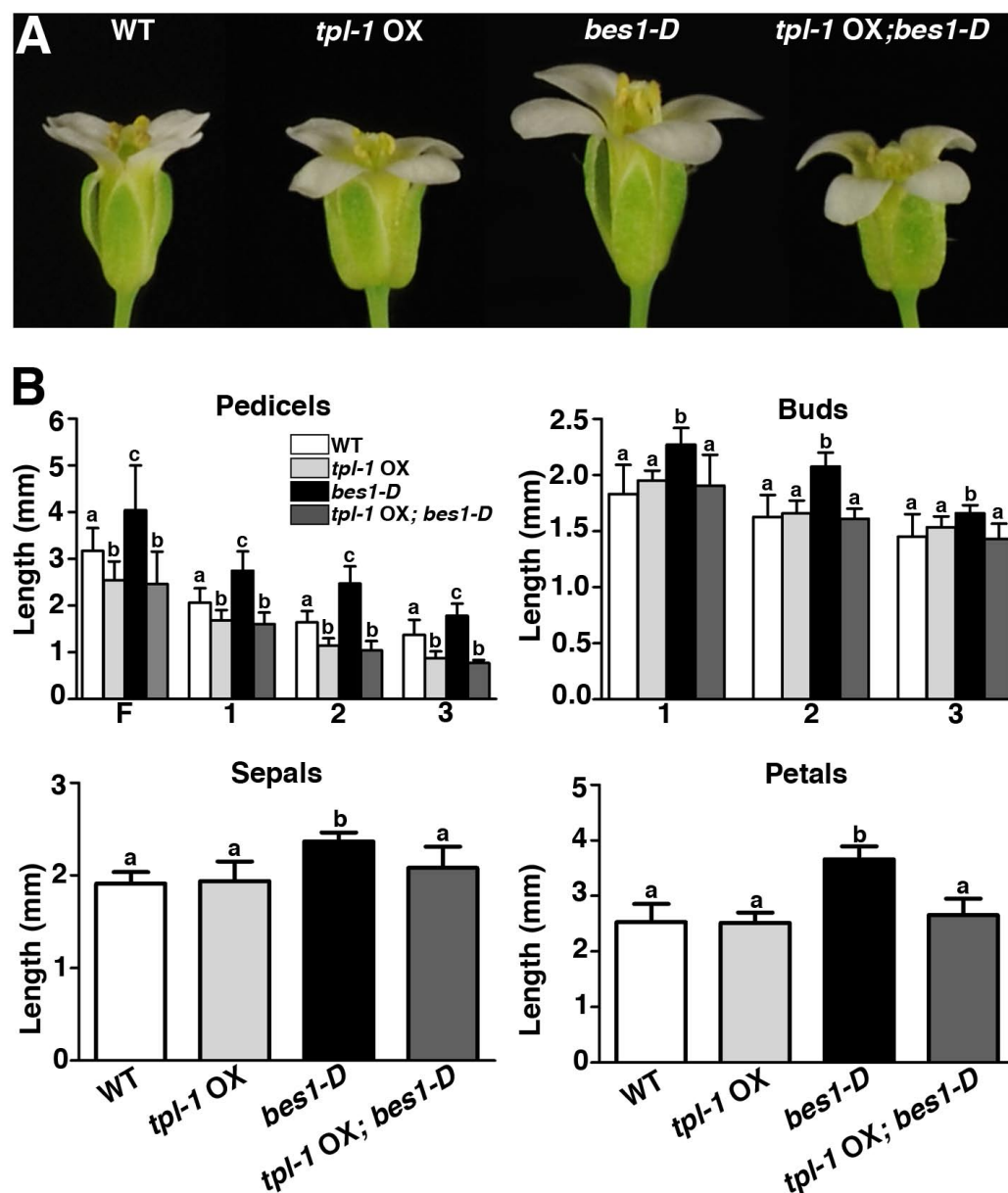
**Fig. S2**

**Fig. S2.** The EAR domain is required for the repressor activity of the BES1 factor. (A) The *DWF4* promoter containing two BRRE elements was fused to the *LUC* reporter gene and co-transfected with the *35S::BES1*, *35S::bes1-D*, *35S::BES1-EARm* or *35S::bes1-D-EARm* effector constructs into *N. benthamiana* leaves. (B) TPL regulation of *DWF4* expression. Leaves were co-infiltrated with the *DWF4* reporter and combinations of *Agrobacteria* expressing the *pTPL::TPL*, *35S::BES1*, *35S::BES1+pTPL::TPL*, *35S::BES1+tpl-1 OX*, *35S::BES1-EARm*, *35S::BES1-EARm+ pTPL::TPL* or *35S::BES1-EARm+ tpl-1 OX*, as indicated. Leaf discs were collected 48 hours after infiltration and luciferase activity was measured. Error bars represent SD (n=20). Schematic representation of the reporter construct shows the position of the BRRE elements. Asterisks indicate significant difference compared to the *DWF4* reporter ( $p < 0.05$ , Student's t-test).

Fig. S3

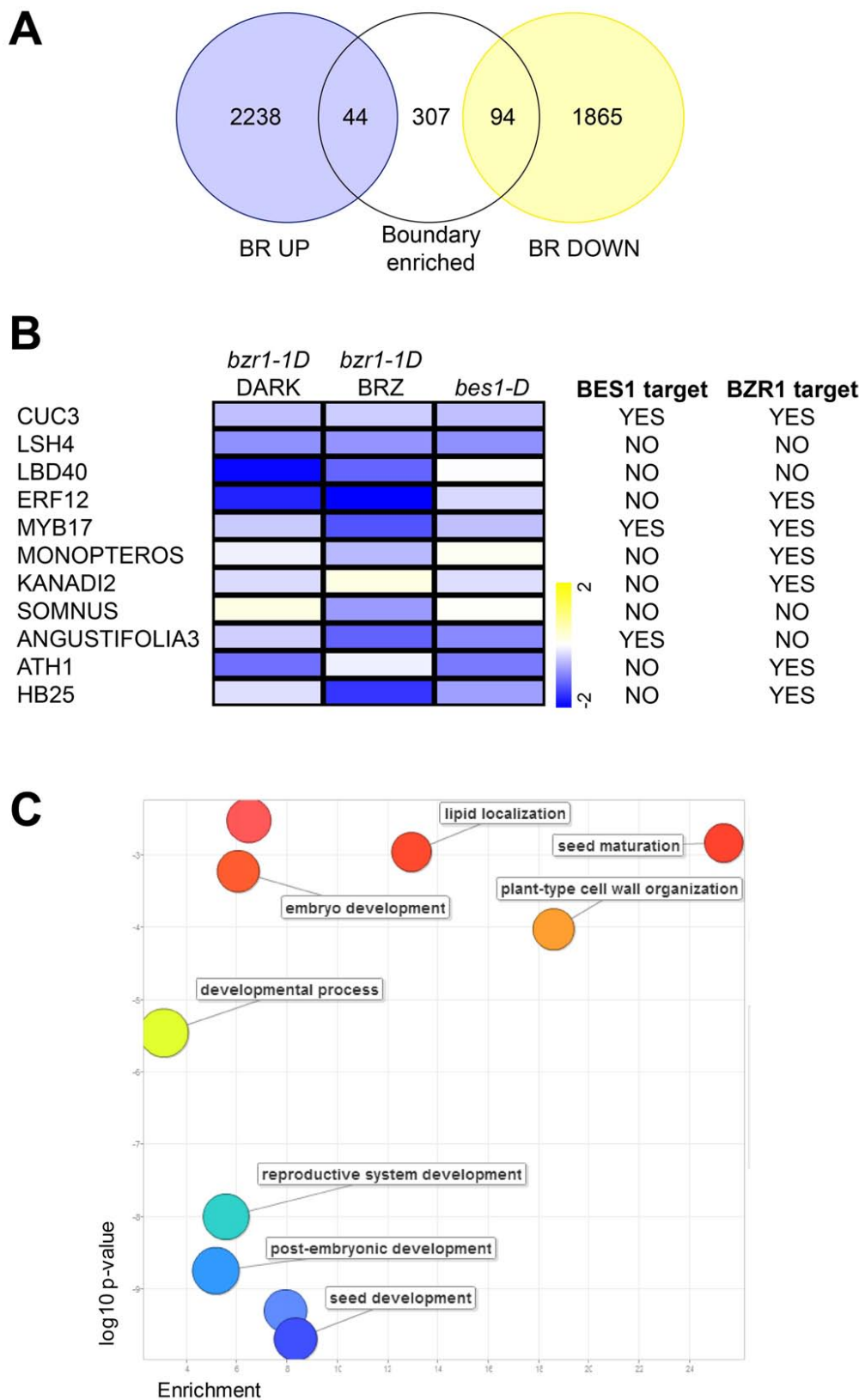


**Fig. S3.** The EAR domain is essential for BES1 function. (A) Western blot of 2-weeks old WT, 35S::*bes1-D*-GFP (*bes1-D*) and 35S::*bes1-D*-EARm transgenic seedlings (EARm13 and EARm33). (B) Phenotype of adult WT, 35S::*bes1-D*-GFP and 35S::*bes1-D*-EARm-GFP plants. Plants were grown for 4-weeks under long day conditions (16h light/8h dark). (C) Phenotype of WT, 35S::*bes1-D*-GFP and 35S::*bes1-D*-EARm-GFP seedlings grown on BRZ. Seedlings were grown for 6 days under short day conditions (Light) or in continuous dark (Dark) in MS growth media (Mock) or MS media supplemented with 0.5  $\mu$ M brassinazole (BRZ). (D) Hypocotyl length measurements of plants grown in (C). Bars represent s. d. (n=20). Similar results were obtained in three independent experiments. Asterisks indicate significant difference compared to the WT genotype ( $p < 0.05$ , Student's t-test). (E) Expression levels of the *CPD*, *DWF4*, *ROT3*, *IAA19* and *PRE5* genes in plants grown in short day conditions as in (D). Samples were taken at ZT0. Bars represent the standard deviation of three independent biological replicates. Asterisks indicate significant difference compared to the WT genotype ( $p < 0.05$ , Student's t-test).

**Fig. S4**

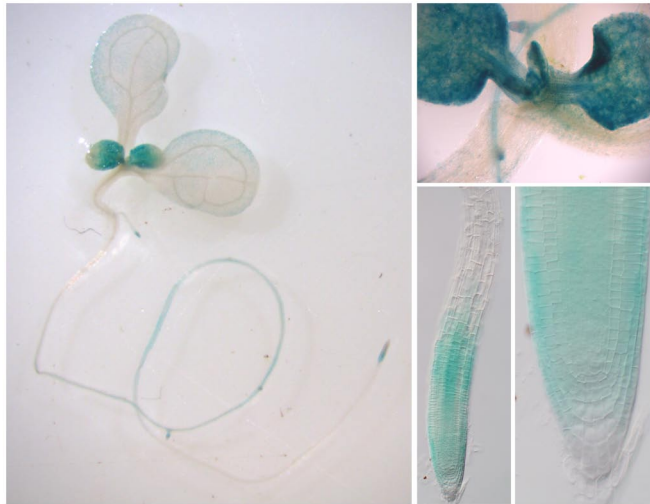
**Fig. S4.** Phenotypic characterization of the inflorescences. Significant differences by the Tukey's multiple comparison test are indicated by letters above bars ( $P < 0.05$ ). (A) A representative flower of the indicated genotypes. (B) Measurement of the pedicel, bud, sepal and petal length of flowers in the primary inflorescences ( $n=10$  plants and 20 flowers of each genotype). F: first open flower; 1, 2 and 3: three oldest buds.

Fig. S5



**Fig. S5.** Boundary-enriched BES1/BZR1-repressed targets include several boundary and patterning regulators. (A) Venn diagram showing the overlap of BR differentially expressed genes (Goda et al., 2004; Vert et al., 2005; Sun et al., 2010; Oh et al., 2012) and boundary enriched transcripts (Tian et al., 2014). BR-induced genes are not significantly enriched (44 found, 33 expected, hypergeometric test, p-value >0.01), while BR-repressed genes are strongly enriched in boundary-specific transcripts (94 found, 26 expected, hypergeometric test, p-value =  $1.5 \times 10^{-25}$ ). (B) Heat-map representation of the expression profiles of the BR-repressed, boundary expressed transcription factors: *bzr1-ID* (Sun et al., 2010), *bzr1-ID* BRZ (Oh et al., 2012) and *bes1-D* (our own data). 8 out of 11 transcription factors were identified as direct BES1- or BZR1- targets (Sun et al., 2010; Yu et al., 2011). (C) Gene ontology analysis of the 94 boundary enriched, BR-repressed genes visualized with ReviGO.

**Fig. S6**



**Fig. S6.** TPL is expressed in the shoot and root meristems. GUS staining of 6-day old *pTPL::GUS* seedlings. In the root, GUS staining was strong in the cell division and elongation zones. In aerial tissues, strong GUS staining was observed in the SAM and young, actively growing tissues.

**Supplemental Table 1.** Percentage of flowers that contain altered petal number.

<b>Genotype</b>	<b>n</b>	<b>3 petals</b>	<b>5 petals</b>	<b>% more or less petals</b>
<i>Col-0</i>	152	1	0	0.7
<i>pTPL::TPL</i>	142	4	12	11.9
<i>bes1-D</i>	145	5	4	6.2
<i>pTPL::TPL;bes1-D</i>	159	3	11	8.8
<i>tpl1-OX</i>	120	0	1	0.8
<i>tpl1-OX;bes1-D</i>	105	0	0	0

**Supplemental Table 2.** List of primers used in this study.

Primers used for constructs	
BES1-F	CACCATGACGTCTGACGGAGCAAC
BES1-R	ACCCGGGCAACTATGAGCTTTACCATTTC
TPL-F	CACCATGTCTTCTCTTAGTAGAGAGCTC
TPL-R	TCTCTGAGGCTGATCAGATGC
PIF4-YFP-F	CACCATGGAACACCAAGGTTGG
PIF4-YFP-R	TCCGTGGTCCAAACGAGAACCGTC
BES1-EARm-R	TCAACTATGAGCTTTACCATTTCAGCCGTGGCCTCTGCATCCTCCATAGCC
pDWF4-F	CACCGAATTACCGGTTGTTATGTAAATATAG
pDWF4-R	TGGAGCTAGTTTCTCTCTCTCTCACT

Primers used for RT-qPCR	
CPD-F	TGAAACAACCTCCACGATCA
CPD-R	TGCCCTAATCTTTTCATGCTCT
DWF4-F	CGACGTGGGGAAACAACACTAC
DWF4-R	CTGAACCAGCACATAGCCTTG
ROT3-F	ATCCGTGGAGATGGGACA
ROT3-R	AACCAGGACATAGCCTTTGC
IAA19-F	GAGCTGAGATTGGGGCTTC
IAA19-R	CCGACGACGTCATATTCATCT
PRE5-F	TGCTTCGAGGATCTCCGATGACCA
PRE5-R	GCCGTTCGTGAATCTCCGGCA
SAUR15-F	AAGGGAATCATCGTCGACAC
SAUR15-R	AAGTATGAAACCGGCACCAC

Primers used for ChIP-PCR	
CUC3p-F	TGCATAGTCGTGCCAATTACTAA
CUC3p-R	TACTGGGACAGACGAAGCCTT
CUC3 ORF-F	ACAGAGCAGTCTTCGAACGGTA
CUC3 ORF-R	GCTGGAATCCTAAAGGACATGG
PP2A-F	GCCTTAAGCTCCGTTTCCTACTT
PP2A-R	CGGCTTTCATGATTCCCTCT
DWF4p-2F	GCCAAAAGTCTACGGGTTTG
DWF4p-2R	TATGGGAAAAGGGTGGGCTC
BRAVOp-F	GCACGTGTAGAGAGAGAGAGC
BRAVOp-R	AACCGCACGAAAACATTAAATATTC