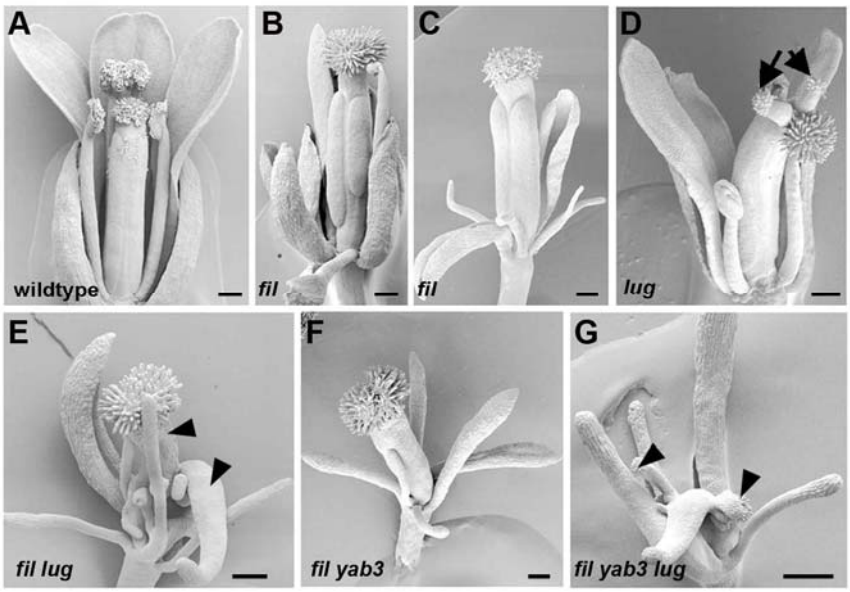
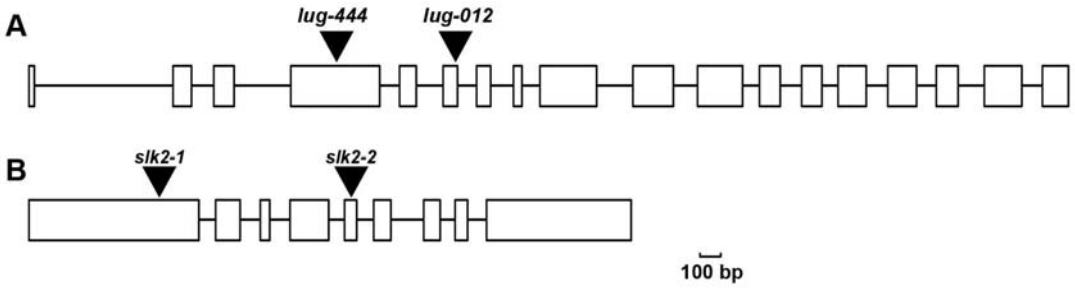
Supplemntal Data. Stahle et al. (2009). YABBYs and the transcriptional co-repressors LEUNIG and LEUNIG HOMOLOG maintain leaf polarity and meristem activity in *Arabidopsis.*



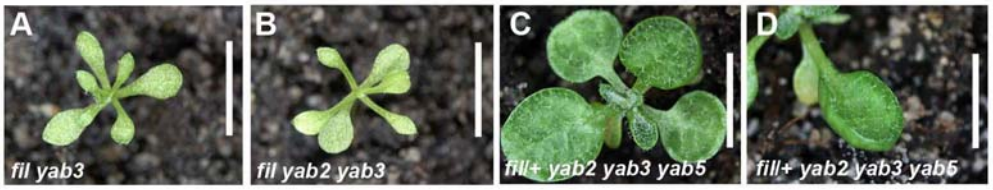
Supplemental Figure 1. Floral phenotypes of *fil lug* and *fil yab3 lug* mutants.

(A) to **(G)** Representative flowers from wild type **(A)**, *fil-8* (**[B]** and **[C]**), *lug-1* **(D)**, *fil-8 lug-1* **(E)**, *fil-8 yab3-2* **(F)** and *fil-8 yab3-2 lug-1* **(G)** plants. Note several outer whorl organs have been removed from **(A)** and **(D)**. Stigmatic horns that are a characteristic feature of *lug* flowers are indicated with arrows in **(D)**. Splitting of the gynoecium caused by enhanced patterning defects of *fil-8 yab3-2* and *fil-8 yab3-2 lug-1* carpels is indicated with arrowheads in **(E)** and **(G)**.

Bar = 100μm.



Supplemental Figure 2. Structure of T-DNA insertion alleles used in this study. Schematic diagram of the *LUG* **(A)** and *SLK2* **(B)** genes. Boxes represent exons and lines represent introns. The positions of T-DNA insertions are indicated with arrowheads (see methods for details).

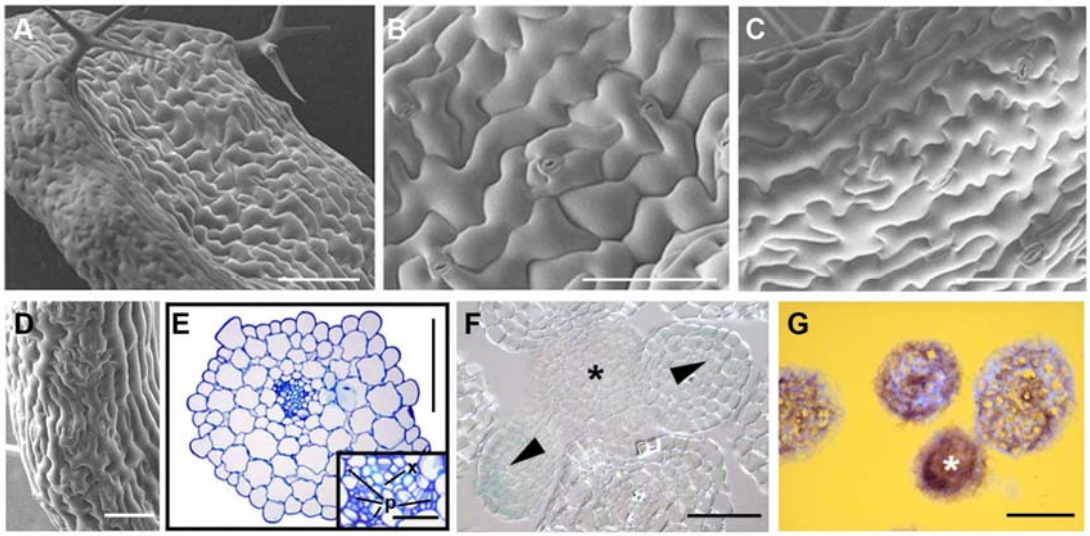


Supplemental Figure 3. Vegetative phenotypes of *yab* mutants.

(A) to **(C)** 16-day-old *fil-8 yab3-2* **(A)**, *fil-8 yab2-1 yab3-2* **(B)** and 28-day-old *fil-8*/+ *yab2-1 yab3-2 yab5-1* **(C)** plant.

(D) Side view of a *fil-8*/+ *yab2-1 yab3-2 yab5-1* leaf.

Bar = 0.5cm.



Supplemental Figure 4. Polarity defects of *fil yab3 lug luh*/+ leaves.

(A) to **(C)** Adaxial (**[A]** and **[B]**) and abaxial **(C)** epidermis of narrow *fil-8 yab3-2 lug-1 luh-4*/+ leaves.

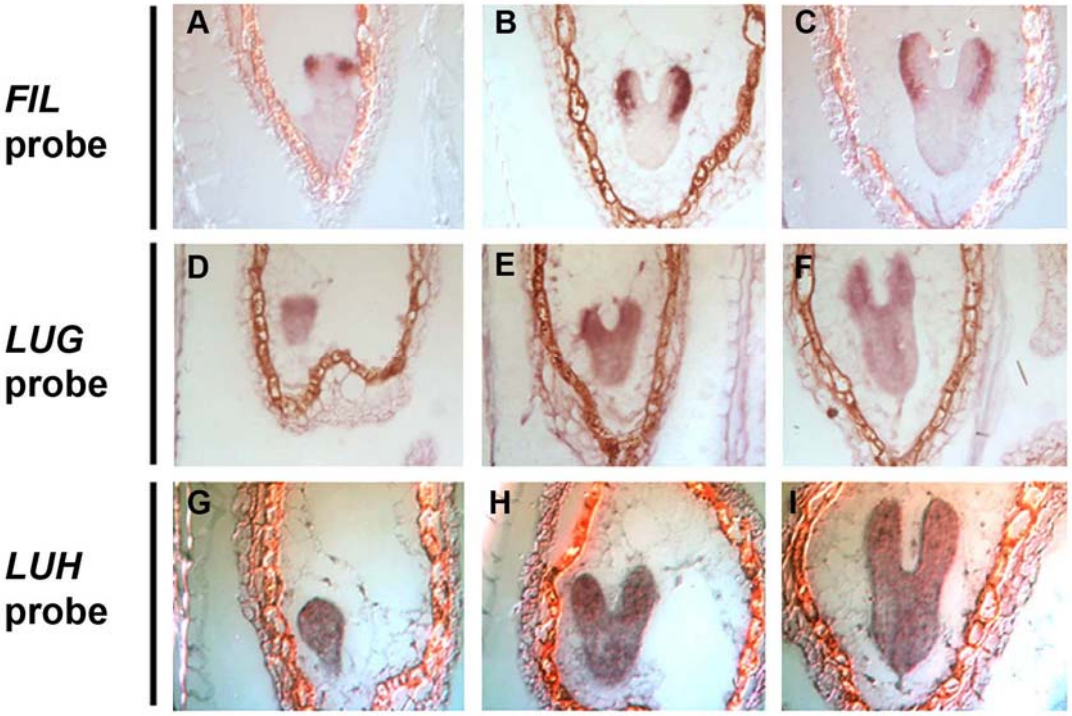
(D) SEM of a *fil-8 yab3-2 lug-1 luh-4*/+ needle showing a patch of abaxial like cells (arrow) amongst rectangular epidermal cells.

(E) Transverse section through a *fil-8 yab3-2 lug-1 luh-4*/+ needle. Inset: vasculature of leaf shown in **(E)** with phloem partially surrounding xylem.

(F) Histochemical localization of GUS activity in a transverse section through a *fil-8 yab3-2 lug-1 luh-4*/+ apex. Arrowhead indicates faint GUS staining and asterisk indicates SAM.

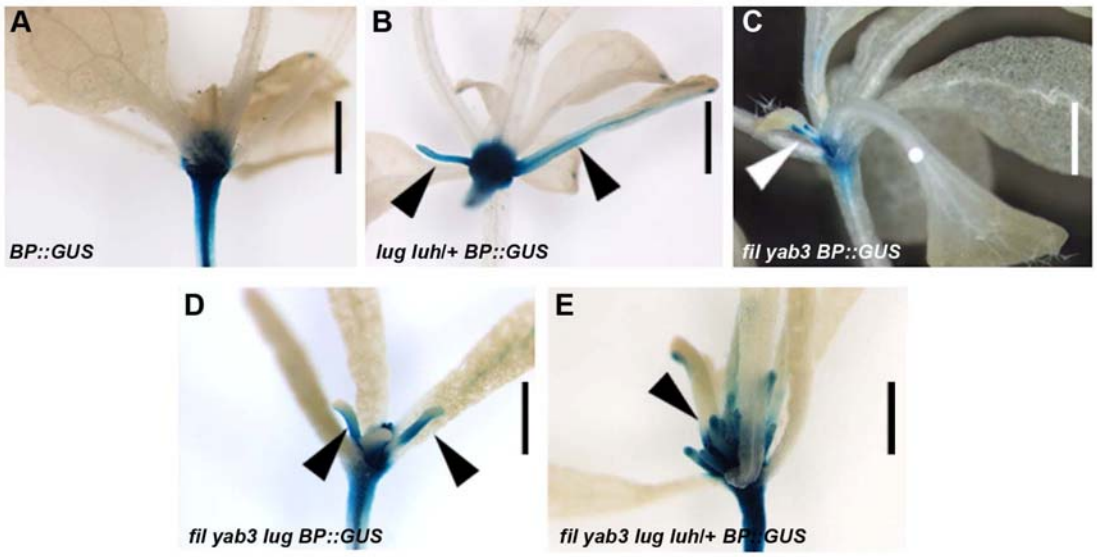
(G) RNA *in situ* hybridisation detects ectopic *PHB* expression in the abaxial domain of *fil-8 yab3-2 lug-1 luh-4*/+ leaves.

p, phloem; x, xylem. Bar = 100 μm in **(A)** to **(E)**, 50 μm in **(F)** and **(G)** and 20 μm in the inset in **(E)**.



Supplemental Figure 5. RNA *in situ* hybridisation showing the pattern of *FIL*, *LUG* and *LUH* expression in wildtype embryos.

(A) to **(I)** Expression of *FIL* (**[A]** to **[C]**), *LUG* (**[D]** to **[F]**) and *LUH* (**[G]** to **[I]**) in embryos at the globular (**[A]**, **[D]** and **[G]**), heart (**[B]**, **[E]** and **[H]**) and torpedo (**[C]**, **[F]** and **[I]**) stage of development.



Supplemental Figure 6. Ectopic *KNOX* expression in mutants.

(A) Histochemical localization of GUS activity in BP_{pro}*:GUS* plants shows that *BP* expression is confined to the shoot apex.

(B) and **(C)** Ectopic *BP* expression in leaves of *lug-444 luh-2*/+ BP_{pro}*:GUS* **(B)**, *fil-5 yab3-1* BP_{pro}*:GUS* **(C)**, *fil-5 yab3-1 lug-1* BP_{pro}*:GUS* **(D)** and *fil-5 yab3-1 lug-444 luh-4*/+ BP_{pro}*:GUS* **(E)** plants as indicated with arrowheads.

Scale = 1mm

Supplemental Table 1. Defining the dimerization domain of FIL.

DB / AD	Empty	FIL 1-229 (Full length)	FIL 1-109 (Zn finger)	FIL 1-146 (Zn + P-rich)	FIL 120-229 (YABBY)
LUG	-[a]	+	+	+	-

[a] α-Gal assay measuring activity of the LacZ reporter in three separate samples. Colour change after 4 hrs (++), colour change after 24 hrs (+) and no colour change after 24 hrs (–).

Supplemental Table 2. Interactions between SEU, SLK and the co-repressors LUG and LUH in yeast.

AD / DB	Empty	SEU	SLK1	SLK2	SLK3
LUG	-[a]	++	++	++	+
LUH	-	+	+	++	++

[a] α-Gal assay measuring activity of the LacZ reporter in three separate samples. Colour change after 4 hrs (++), colour change after 24 hrs (+) and no colour change after 24 hrs (–).

Supplemental Table 3. Dimensions of wildtype and mutant leaves.

Genotype	# of plants[a]	width[b]	length[c]
L*er*	17(5)	10.2 ± 0.27	22.7 ± 0.80
fil-8	20(5)	8.89 ± 0.24[d]	19.7 ± 0.61[d]
lug-1	23(5)	9.42 ± 0.21[d]	25.4 ± 0.6[d]
fil-8 lug-1	19(5)	7.79 ± 0.17[d,e]	17.2 ± 0.47[d,e]
fil-8 yab3-2	20(5)	3.44 ± 0.08[d]	10.2± 0.32[d]
fil-8 yab3-2 lug-1	20(5)	2.09 ± 0.08[d,f]	9.45 ± 0.31[d]
Col	20(8)	14.2 ± 0.16	44.8 ± 0.64
lug-444	14(8)	13.9 ± 0.27[d]	42.4 ± 1.1
luh-3	20(8)	13.3 ± 0.18[d]	39.5 ± 0.82[d]
lug-444 luh-3/+	19(8)	9.3 ± 0.31[d]	30.5 ± 0.95[d]
Col *er*	10(8)	12.4 ± 0.03	27.6 ± 0.06
yab2-1	8(8)	11.4 ± 0.03	25.8 ± 0.06
yab5-1	10(8)	10.3 ± 0.02[g]	16.5 ± 0.04[g]

[a] a fully mature leaf from either the 5th or 8th node, indicated (5) or (8) respectively, was measured per plant.

[b] measurements taken from widest point of the leaf, values are in mm ± SE.

[c] as measured from the leaf tip to base of petiole.

[d] values are significantly different from wildtype (Student's t-test, $P<0.05$).

[e] values are significantly different from *fil* and from *lug* (Student's t-test, $P<0.05$).

[f] values are significantly different from *fil yab3* (Student's t-test, $P<0.05$).

[g] values are significantly different from Col *er* (Student's t-test, $P<0.001$).

Supplemental Table 4. Plant material used in this study.

Allele	Background	Reference
fil-5	L*er*	Chen *et al.*, 1999
fil-8	L*er*	Kumaran *et al.*, 2002
lug-1	L*er*	Liu and Meyerowitz, 1995
lug-3	L*er*	Liu and Meyerowitz, 1995
lug-444	Col	SALK_126444, Alonso *et al.*, 2003
lug-012	Col	SALK_113012, Alonso *et al.*, 2003
luh-1	Col *er*	Sitaraman *et al.*, 2008
luh-3	Col	Sitaraman *et al.*, 2008
luh-4	Col	SALK_097509, Alonso *et al.*, 2003
seu-2	L*er*	Franks *et al.*, 2002
seu-4	Col	Pfluger and Zambryski, 2004
slk2-1	Col	SALK_089954, Alonso *et al.*, 2003
slk2-2	Col	SALK_093829, Alonso *et al.*, 2003
yab2-1	Col *er*	CS93680, Till *et al.*, 2006
yab3-1	Ws	Siegfried *et al.*, 1999
yab3-2	L*er*	Kumaran *et al.*, 2002
yab5-1	Col *er*	CS90062, Till *et al.*, 2006
BP_{pro}*:GUS*	Col	Ori *et al.*, 2000
$CLV3_{pro}$*: YFP-ER*	L*er*	Lenhard and Laux, 2003
$CYCB1_{pro}$*:GUS*	Col	Doerner *et al.*, 1996

Supplemental Table 5. RT-PCR primers used in this study.

Name	Primer sequence 5'>3'
SEU-QF1	AGCAGAGAAACACGAACAGG
SEU-QR1	CTGGTCCTTCTCCTCAGCAA
SLK3Y2H-F	CCGGAATTCATGCAGAGGAGCAGTGGCAT
SLK1-R1	GATGTGCTTGCCAGACTAATTG
SLK2-QF1	TGATTGACTTTTGCCGTGAC
SLK2-QR1	CTGGTAAACCTCAGATGCAGG
TUB7-QF1	CATTTGCTTCCGTACACTCAA
TUB7-QR1	CCAGGGAACCTAAGACAGCA