Fig S1. The *jba-1D/+* shoot apical meristem gradually enlarges. (**A**) A *jba-1D/+* inflorescence stem cut into four segments, with the most basal segment shown on the left and the most apical segment on the right. The width of the stem gradually increases. (**B**) *jba-1D/+ er-20* IM with four cauline leaves emerging at the same time. Scale bar: 2 mm.

Fig S2. The *jM1* single mutant plants resemble the wild-type L*er* accession. (**A-E**) 20-day-old plants of the designated genotypes. (C) *er-2* (D) Wild-type plant segregating from *jba-1D/+* selfed seeds. (E) *jM1* single mutant plant (*er-20*) segregating from *jba-1D/+ er-20* selfed seeds. (**F-J**) Top view of inflorescences of the designated genotypes. Scale bar: 2 mm

Fig. S3. ***jba-1D/+ er-20* plants carrying a *proER::ER* transgene.** (**A-D**) *jba-1D/+ er-20* transgenic plants carrying the genomic fragment of the *ER* promoter and gene at 5 weeks after bolting. (A, B) Partially rescued plant that displays some stigmatic tissues and carpeloid sepals. (C, D) Fully rescued plants that resemble *jba-1D/+* and lack ectopic carpels. Scale bar: 2 mm.

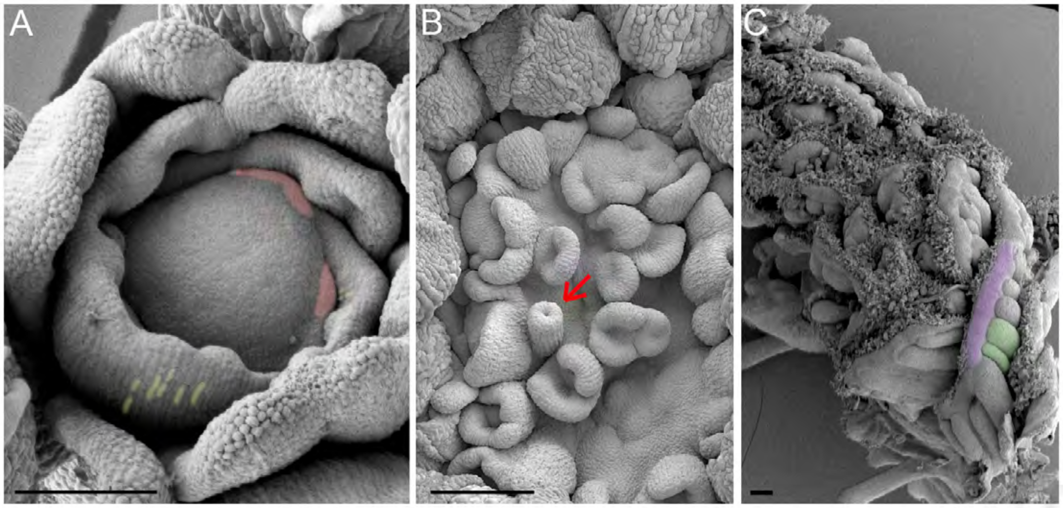

Fig S4. SEM of *jba-1D/+ er-20* inflorescence structures. (A) The IM forms carpel primordia at the periphery [marked in pink]**.** Periclinal cell divisions of cells elongating in an upward direction contribute to the longitudinal growth of the carpel [marked in yellow]**.** (**B**) In some cases, typical cylindrical gynoecium structures protrude from the center of the IM, some forming open ended tubes typical of wild-type gynoecia [red arrow]. (**C**) Elongated structure consisting of multi-fused carpels within carpels at the top of the inflorescence stem. Each consists of the distinct tissues typical of wild-type carpels, with a valve [green] flanked with valve margin and style [purple] bearing stigmatic papillae. Scale bars: 500 mM.

Fig S5. *jba-1D/+ er-20* inflorescences at sixteen weeks after bolting. (**A-C**) The *jba-1D/+ er-20* IM retains activity and produces numerous carpels in an indeterminate manner after the rest of the plant has undergone senescence. (A) Side view. (B) Top view. (C) Higher magnification of the inflorescence showing green and vivacious tissues

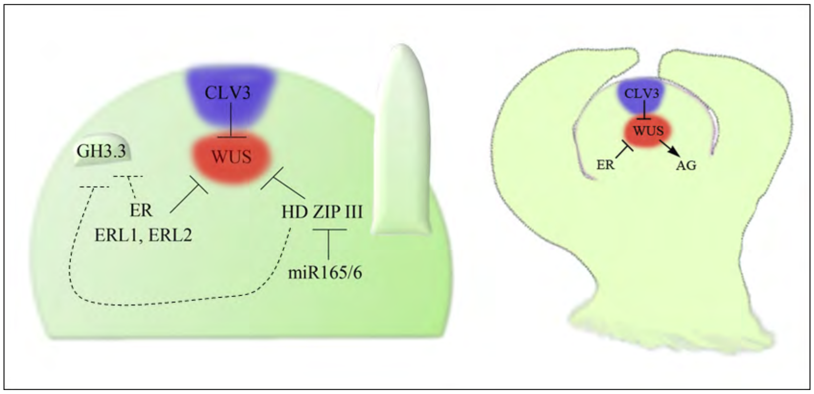

Fig S6. Schematic diagram of ERECTA (ER) family regulation of *WUS* and *AGAMOUS* at the vegetative shoot apical meristem (SAM) and the flower meristem (FM). In the vegetative SAM the ER family negatively regulates *WUS* transcription in parallel with the CLV3 and HD-ZIPIII pathways. ER and the HD-ZIPIII pathway also indirectly negatively regulate GH3.3. In the FM WUS positively regulates *AGAMOUS* (*AG*). On the left the vegetative SAM, on the right the flower meristem. Blue and red represent the *CLV3* and *WUS* expression domains, respectively. Solid lines signify direct regulation. Dashed lines indicate indirect regulation.

Table 1. Selected upregulated genes in *jba-1D/+er-20* compared with *jba-1D/+* IMs

AGI	Gene annotation/description	*jba+/−* (RPKM)	*jba-1D/+ er-20* (RPKM)	Fold change
AT2G21650	*MATERNAL EFFECT EMBRYO ARREST 3, MEE3* (involved during early morphogenesis)	0.03	15.5	512
AT5G09750	*HEC3, AGL5* (involved in transmitting tissue development, carpel formation, regulation of transcription)	0.17	41	223
AT2G01500	*WUSCHEL RELATED HOMEOBOX, WOX6* (gene that delays differentiation and maturation of primordia and regulates ovule patterning)	0.03	6.3	194
AT2G21450	*CHROMATIN REMODELING 34, CHR34*	0.34	9.78	28
AT1G25330	*CES*, *CESTA* (a positive regulator of brassinosteroid biosynthesis)	0.28	22.4	78
AT2G42830	*SHATTERPROOF 2, SHP2, AGL5* (involved in fruit development and a putative direct target of AG)	0.54	35.7	65
AT5G65080	*AGL68* (regulates flowering time)	0.22	13.3	56
AT4G09960	*AGL11, STK* (TF expressed in the carpel and ovules)	0.24	46	40
AT2G33880	*WUSCHEL RELATED HOMEOBOX, WOX9, STIP* (required for meristem growth and development and acts through positive regulation of WUS)	1.93	75.5	39
AT3G62820	Plant invertase/pectin methylesterase inhibitor superfamily protein	1.9	49.4	26
AT5G18000	*VERDANDI, VDD* (a direct target of the MADS domain ovule identity complex)	0.78	17.3	22
AT5G23260	*AGAMOUS-LIKE 32, AGL32* (shown to be necessary for determining the identity of the endothelial layer within the ovule)	0.09	2.15	23
AT3G50330	*HEC2* (involved in ovary septum development, transmitting tissue development, carpel formation, regulation of transcription)	0.89	15.3	17
AT5G21150	*ARGONAUTE 9* (AGO9-dependent sRNA silencing is crucial to specify cell fate in the *Arabidopsis* ovule)	5.98	98.6	16
AT5G41410	*BELL 1* (homeodomain protein required for ovule identity)	0.83	12.5	15
AT2G26440	Plant invertase/pectin methylesterase inhibitor superfamily	5.5	53.7	
AT3G51060	*STYLISH 1* (promotes gynoecium, stamen and leaf development)	1.2	11.3	9
AT1G23420	*INNER NO OUTER, INO* (may be required for polarity determination in the central part of the ovule)	0	5.4	5
AT4G18960	*AGAMOUS, AG* (specifies floral meristem and carpel and stamen identity)	9.4	70	7
AT3G58780	*SHATTERPROOF 1, SHP1* (required for fruit dehiscence. Controls dehiscence zone differentiation)	7.2	49	7
AT1G69180	*CRABS CLAW, CRC* (putative TF involved in specifying abaxial cell fate in the carpel)	22	142.3	7
AT3G18010	*WUSCHEL RELATED HOMEOBOX, WOX1* (encodes a WUSCHEL-related homeobox gene family member)	1.78	10.7	6
AT1G66350	*RGL1* (negative regulator of GA responses, member of GRAS family of transcription factors; involved in flower and fruit development)	10.5	53	5
AT3G23130	*SUPERMAN, SUP* (flower-specific gene controlling the boundary of the stamen and carpel whorls)	2.15	9.25	5
AT3G22880	*ARLIM15* (expression is restricted to pollen mother cells in anthers and to megaspore mother cells in ovules)	6.5	28.3	5
AT5G15800	*SEPALLATA1, SEP1* (encodes a MADS box transcription factor involved flower and ovule development)	22.3	96	4
AT5G11320	*YUCCA4, YUC4* (belongs to the YUC gene family. Involved in auxin biosynthesis and plant development)	2.2	8.8	4
AT3G57670	*NO TRANSMITTING TRACT, NTT* (TF specifically expressed in the transmitting tract and involved in transmitting tract development and pollen tube growth)	4.9	19.8	4
AT2G17950	*WUSCHEL, WUS* (homeobox gene controlling the stem cell pool; required to keep the stem cells in an undifferentiated state)	1.2	4.9	4
AT1G24260	*SEPALLATA3, SEP3* (member of the MADs box transcription factor family; SEP3 is redundant with SEP1 and 2)	28.7	103.7	4
AT5G66350	*SHORT INTERNODES, SHI* (function synergistically with other SHI-related genes promote gynoecium, stamen and leaf development)	1.8	5.8	3.3
AT5G62230	*ERECTA-LIKE 1, ERL1* (encodes a receptor-like kinase; along with *ERL2* functionally compensates for loss of ER during integument development)	16.6	48.2	3
AT4G36920	*APETALA 2, AP2* (involved in the specification of floral organ identity, establishment of floral meristem identity, suppression of floral meristem indeterminancy, and development of the ovule and seed coat)	7.7	29.9	3.9
AT2G23170	*GH3.3* (encodes an IAA-amido synthase that conjugates Asp and other amino acids to auxin *in vitro*)	10.6	26.7	2.5
AT5G17810	*WUSCHEL RELATED HOMEOBOX, WOX12* (encodes *WUSCHEL RELATED HOMEOBOX* gene family member with 65 amino acids in its homeodomain)	2.8	9.7	3.5
AT3G02310	*SEPALLATA 2, SEP2* (MADS-box protein, binds K domain of AG *in vivo*)	56.6	155.7	2.8
AT1G68640	*PERIANTHIA, PAN* (encodes bZIP-transcription factor, and is essential for AG activation in early flowers of short-day-grown plants)	15.1	32	2

Gene names and descriptions are from TAIR (http://www.arabidopsis.org/index.jsp).
RPKM, reads per gene kilobase per million reads.

Table S2. List of AG directly bound and immediate target genes that are upregulated in *jba-1D/+ er-20* IMs when compared with *jba-1D/+* IMs

AGI	**Gene name**	**Fold change**
Directly bound		
AT1G69180	*CRC*	6.5
AT3G11000	*GDA-2*	3.6
AT3G47730	*GA4*	1.8
AT1G24260	*SEP3*	3.6
AT1G47610		3.6
AT1G13400	*JGL*	2.5
Immediate target genes		
At1G80450		2.1

Bound genes are according to Gomez-Mena et al. (Gomez-Mena et al., 2005).