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SUPPLEMENTAL FILES:

Figure S1. Related to Figure 2.

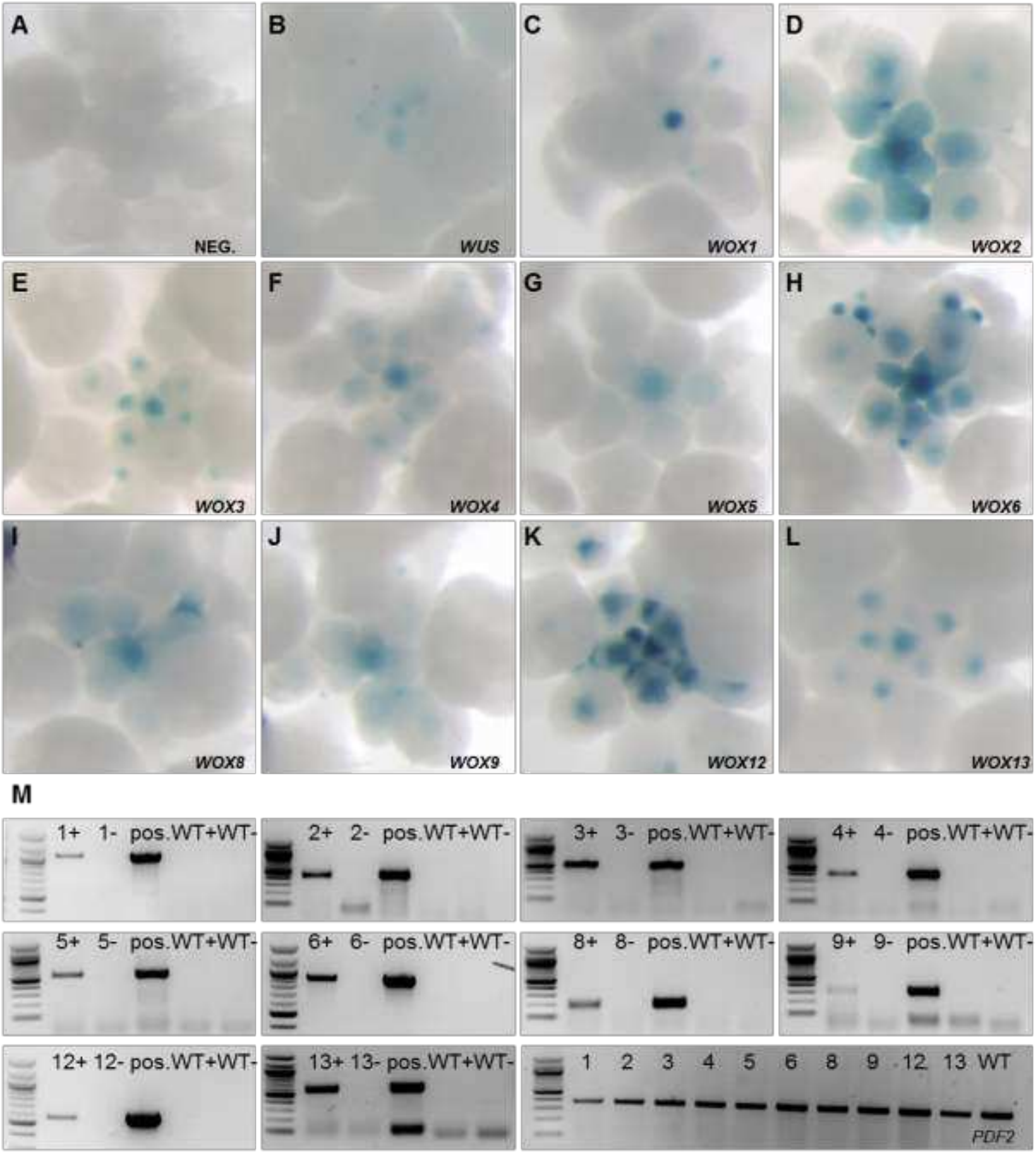

Figure S1. Related to Figure 2. Expression analysis of different *WOX* genes
(A-L) Expression levels of different *WOX* cDNAs visualized by expression of a tandem *GUS* reporter (blue).
(M) *WOX* transgene expression levels determined by RT-PCR. *WOX* genes are indicated by numbers. „+” samples prepared with RNA polymerase, „-” without RNA polymerase as negative control, „pos.” is transgene DNA as positive control. Lower right: expression of the *PDF2* gene as internal control.
Scale bar: (A-L) 0,5mm

Figure S2. Related to Figure 2.

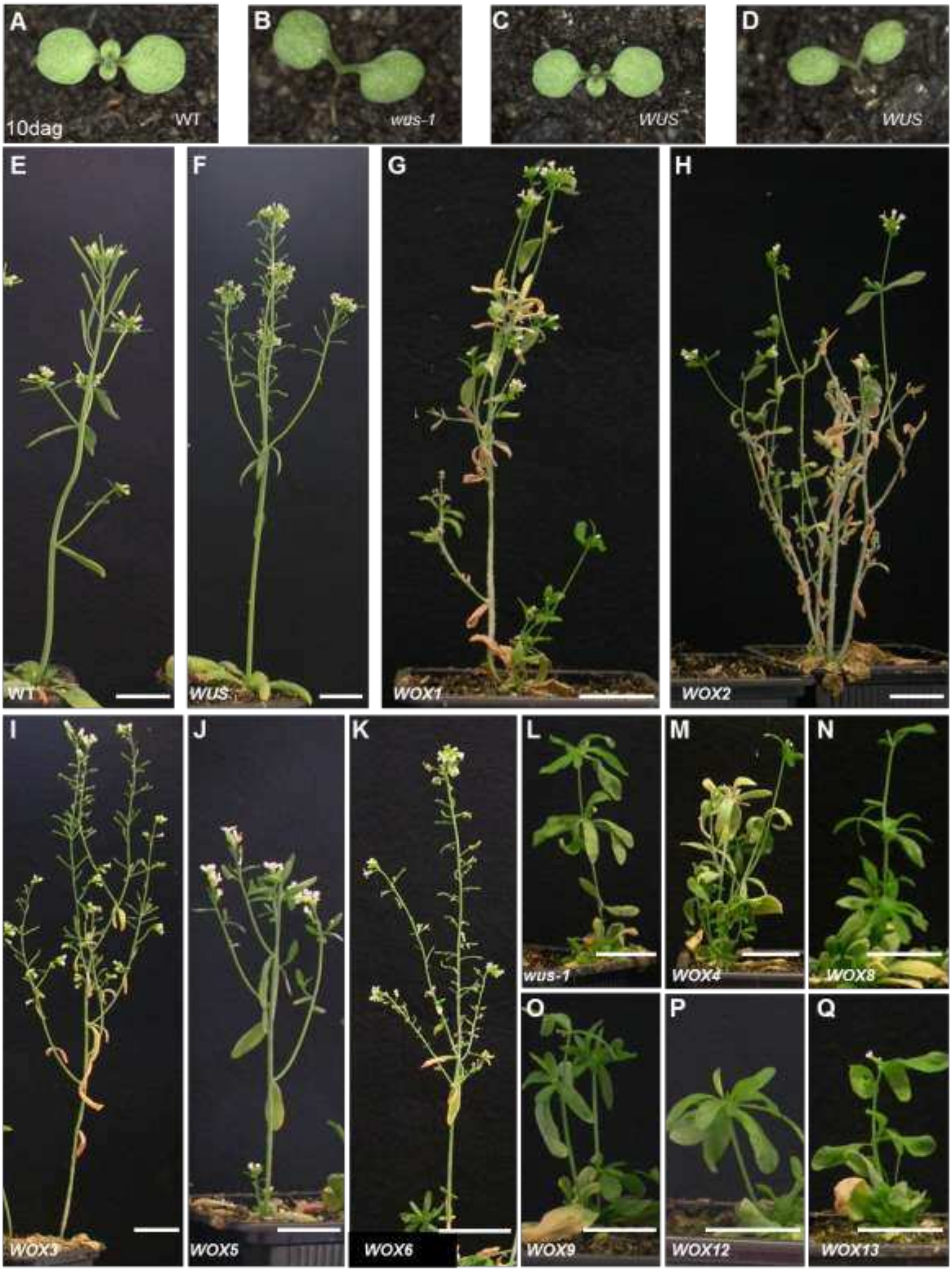

Figure S2. Related to Figure 2. Complementation of *wus-1* stem cell defects by different *WOX* genes

(A-D) 10-day-old seedling phenotypes.

(E-Q) 40-day-old transgenic plants in comparison to untransformed *wus-1* -/- mutants (L).

Scale bars: (A-D) 3mm, (E-Q) 2cm

Figure S3. Related to Figure 2.

Figure S3. Related to Figure 2. Two copies of *pWUS::WOX2* provide an enhanced complementation of *wus-1* defects

(A) Comparison of a 40-day-old *wus-1* mutant plant, where adventitious shoots terminated prematurely in an aerial rosette and a *wus-1* plant expressing homozygously *pWUS::WOX2* which produces an indeterminate shoot with many flowers.

(B) Flower of *wus-1* plant homozygous for *pWUS::WOX2* forming all floral organs.

(C) Comparison of gynoecia of wild-type and *wus-1* plants homozygous for *pWUS::WOX2*, which never elongate to the wild-type level.

Scale bars: (A) 1cm, (B-C) 3mm

Figure S4. Related to Figure 3 and Figure 4

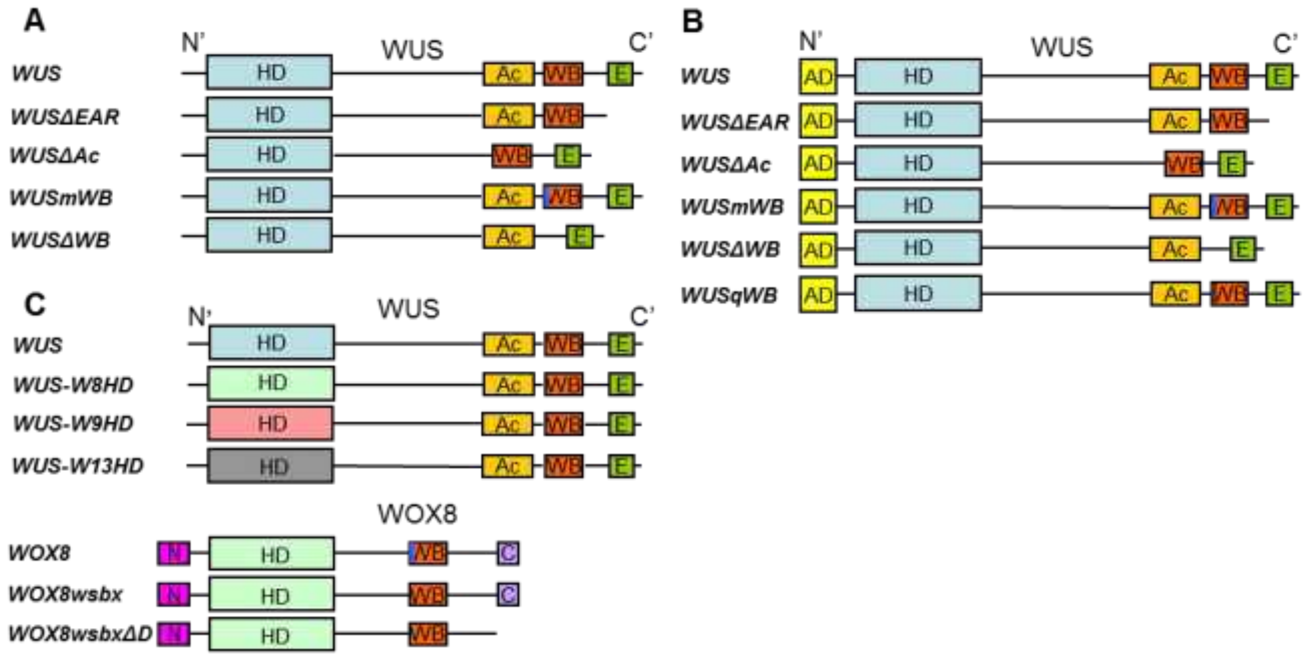

Figure S4. Related to Figure 3 and Figure 4. Schematic representation of variants of WUS used in different experiments

(A) Schematic representation of protein variants used in Figure 3A-C

(B) Schematic representation of variants of WUS used as bait in yeast two-hybrid experiments (compare to Figure 3D).

(C) Schematic representation of constructs used for Figure 4.

Boxes represent WOX protein domains: Ac, acidic domain; AD, Gal4 activation domain; C, WOX8 clade C-terminal domain; E, EAR domain; HD, homeodomain (different colors represent HDs from different WOX proteins); N, WOX8-type N-terminal domain; WB, WUS-box; blue strap in WUS-box, „AG" residues; dark red strap in WUS-box, "Q" residue exchange as in WOX5.

Figure S5. Related to Figure 3 and Figure 4

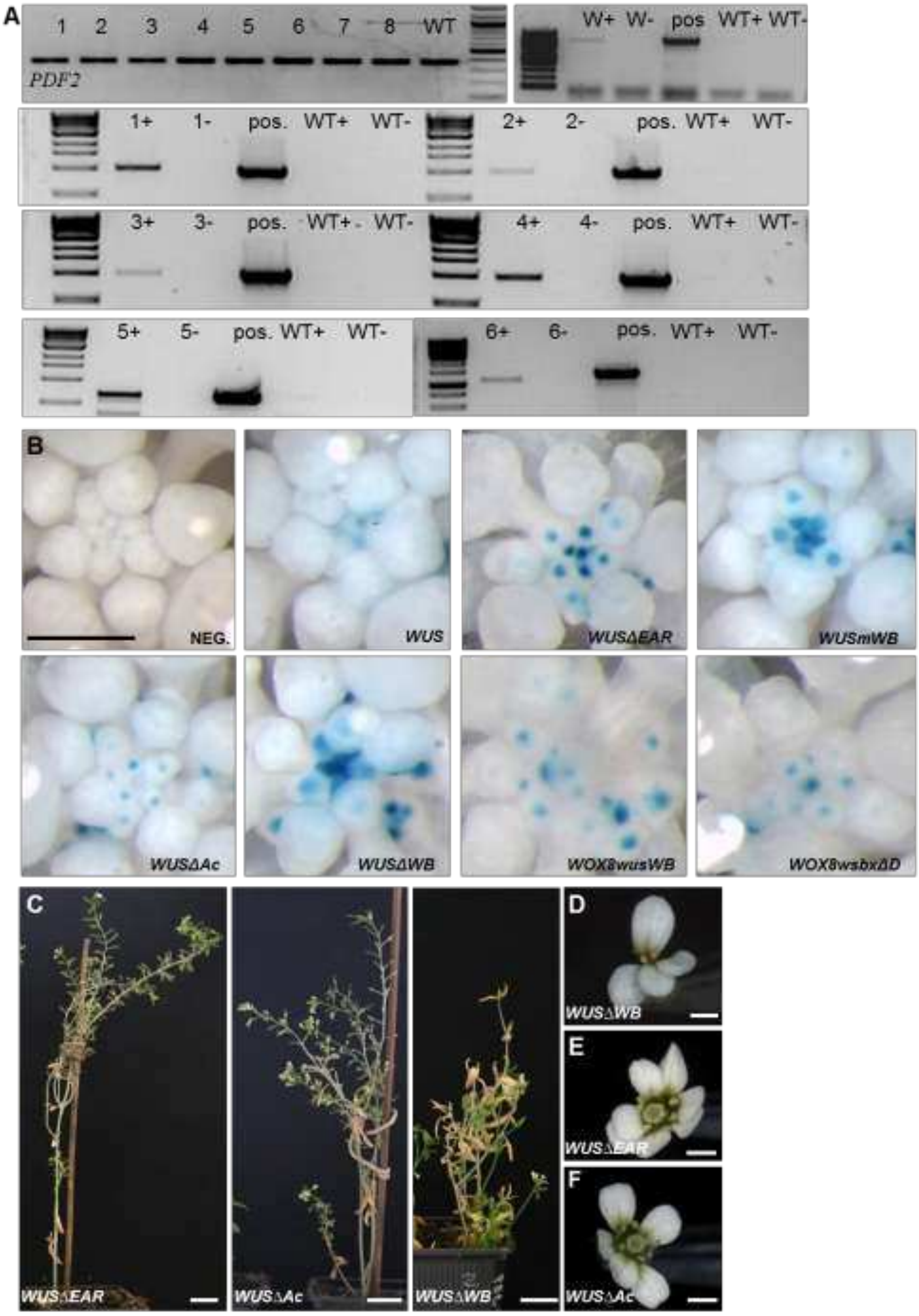

Figure S5. Related to Figure 3 and Figure 4. Expression controls of chimeric *WUS* and *WOX8* constructs

(A) RT-PCR of transgene expression levels. 1, *WUSΔEAR*; 2, *WUSΔAc*; 3, *WUSΔWB*; 4, *WUSmWB*; 5, *WOX8wusWB*; 6, *WOX8wsbxΔD*. „WT" is a neg control without constructs, „+" reaction with polymerase, „-" without polymerase, „pos." is the respective cDNA as pos control. Upper left: expression of the *PDF2* gene as internal control.

(B) Expression levels of different constructs as indicated, visualized by the tandem *GUS* reporter (blue).

(C) 40-day-old *wus-1* plants expressing chimeric *WUS* transgenes as indicated.

(D-F) Comparison of flowers formed in *wus-1* mutant plants expressing chimeric *WUS* genes as indicated.

Scale bar: (B) 0,5mm; (C) 2cm; (D-F) 1mm

Figure S6. Related to Figure 4.

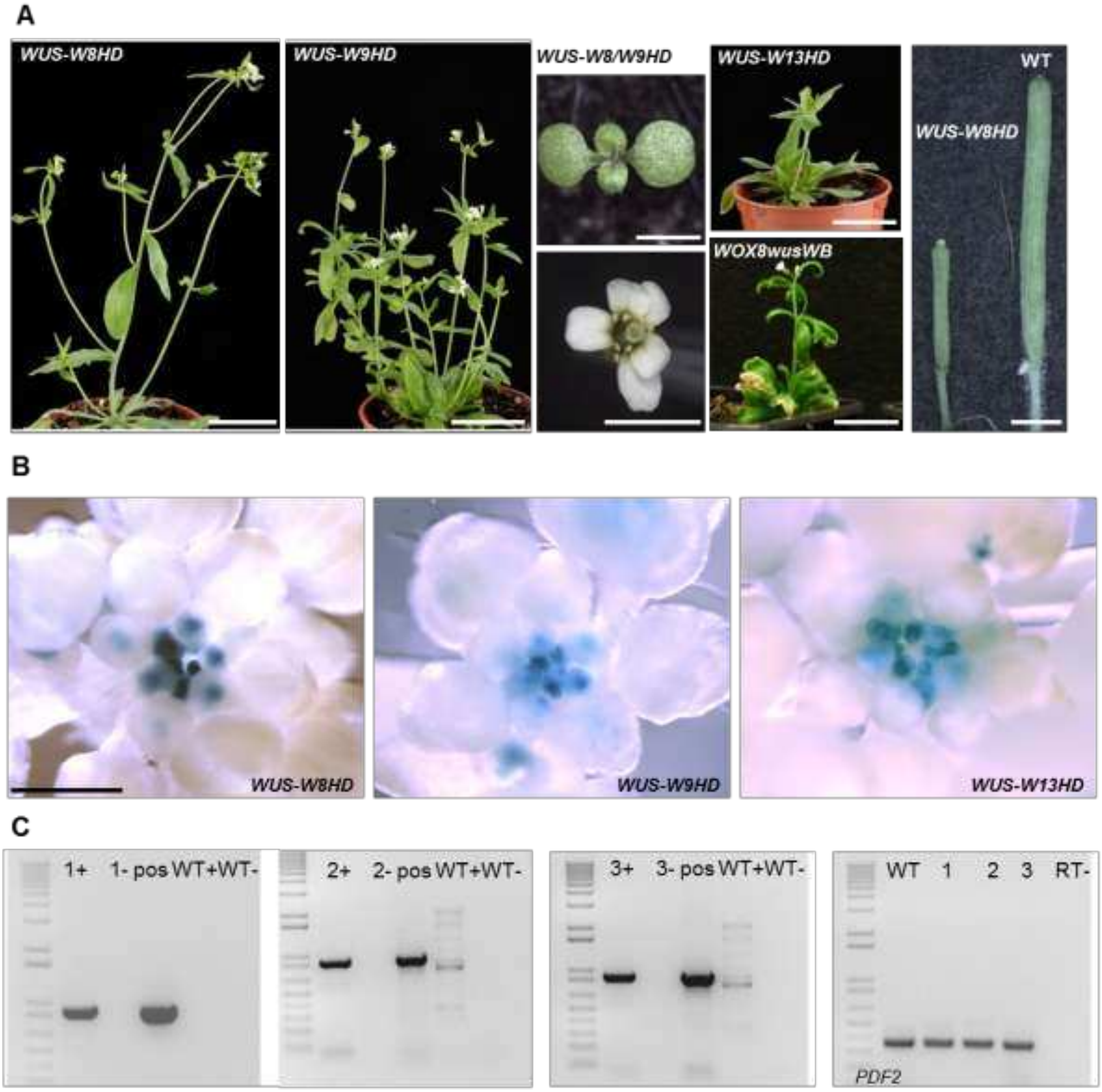

Figure S6. Related to Figure 4. Complementation of *wus-1* stem cell defects by different homeodomain constructs
(A) Comparison of *wus-1* plants expressing the indicated constructs.
(B) Comparison of expression levels of the different transgenes, visualized by tandem *GUS* reporter expression (blue).
(C) Expression levels of transgenes by RT-PCR as indicated. 1, *WUS-W8HD*; 2, *WUS-W9HD*; 3, *WUS-W13HD*. „WT" is a neg control without constructs, „+" reaction with polymerase, „-" without polymerase, „pos." is a transgene DNA as positive control. Lower right: expression of the *PDF2* gene as internal control.
Scale bars: (A – adult plants) 2cm; (A – seedling, flower and siliques) 3mm; (B) 0,5mm

Table S1. Related to Figure 3.
Seed production requires the acidic WUS domain

female	male	carpel lenght (mm)		viable seeds	n
		median	m.d.		
wild-type	wild-type	11,50	0,74	+	10
wild-type	not pollinated	3^{***}	0,0	-	11
wus-1-/- pWUS:WUSΔAc	*wus-1-/- pWUS:WUSΔAc*	3^{***}	0,74	-	25
wus-1-/- pWUS:WUSΔAc	not pollinated	3^{**}	0,37	-	9
wus-1-/- pWUS:WUSΔAc	wild-type	3^{***}	0,74	-	21
wild-type	*wus-1-/- pWUS:WUSΔAc*	11,75	1,11	+	10

Gynoecia of wild type (wild-type) plants or *wus-1-/-pWUS:WUSΔAc* transgenic plants were pollinated as indicated.

n, number of gyneocia crossed.

Plants statistically different to wild-type control (line 1) with P<0,01 **, <0,001 *** (line 1). Unmarked combinations, statistically not significant.

Probabilities determined using Kruskal-Wallis with Dunn's post-hoc test and corrected for multiple testing using the Holm method. m.d., mean absolute deviation.

Table S2. Mutant and transgenic lines used in the study

genotype	**background**	**reference**
wus-1-/+	L*er*	(Laux *et al*., 1996)
wox8 wox9/+	Col	(Breuninger *et al*,. 2008)
wus-1-/+ pWUS:LhG4 pOp:WUS pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX1 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX2 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX3 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX4 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX5 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX6 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX8 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX9 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX12 pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX13 pOp:GUS	L*er*	This study
*wus-1-/+ pWUS:LhG4 pOp:WUS*Δ*WB pOp:GUS*	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WUS mWB pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WUSΔEAR pOp:GUS	L*er*	This study
*wus-1-/+ pWUS:LhG4 pOp:WUS*Δ*Ac pOp:GUS*	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WUS-W8HD pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WUS-W9HD pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WUS-W13HD pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX8wusWB pOp:GUS	L*er*	This study
wus-1-/+ pWUS:LhG4 pOp:WOX8wsbxΔD pOp:GUS	L*er*	This study
wox8 wox9/+ pWOX9:WOX8	L*er*	This study
wox8 wox9/+ pWOX9:WOX8-wusWB	L*er*	This study
wox8 wox9/+ pWOX9:WUS	L*er*	This study

Table S3. Sequence of oligonucleotides used for RT-PCR

construct	**Forward Primer**	**Reverse Primer**
PDF2	CGTTACTGCCAGCCATTGTAGAA	CCGCAGGTAAGAGTTTGGAACAT
pOp:WUS *pOp:GUS*	CTAGCTTATCGATACCGTCG	CATACTTCCAGATGGCACCA
pOp:WOX1 *pOp:GUS*	CTAGCTTATCGATACCGTCG	TTGGAGCAATCTTCATGTTGTTCTTGATC
pOp:WOX2 *pOp:GUS*	CTAGCTTATCGATACCGTCG	TGGAGGAGGCGATTGAAGTAAGCC
pOp:WOX3 *pOp:GUS*	CTAGCTTATCGATACCGTCG	GGTGATGATGATAAGGATTGTG
pOp:WOX4 *pOp:GUS*	CTAGCTTATCGATACCGTCG	CCTATCTGTTCTTGAGTCGG
pOp:WOX5 *pOp:GUS*	CTAGCTTATCGATACCGTCG	CGTCGTGGTGGTCTCTCGAAT
pOp:WOX6 *pOp:GUS*	CTAGCTTATCGATACCGTCG	CCTGATGATGAATCCTTGACGTCT
pOp:WOX8 *pOp:GUS*	CTAGCTTATCGATACCGTCG	TAGGATCTGGTATCCGATCTGAGG
pOp:WOX9 *pOp:GUS*	CTAGCTTATCGATACCGTCG	AATCCTACATCTCGTTTTTCTTGAG
pOp:WOX12 *pOp:GUS*	CTAGCTTATCGATACCGTCG	CCATTGTTGTTCTCACACCC
pOp:WOX13 *pOp:GUS*	CTAGCTTATCGATACCGTCG	CCAGAAGAACCTCCACCATGC
pOp: WUS∆WB *pOp:GUS*	CTAGCTTATCGATACCGTCG	CGTACGCTTCCTCTCTTCCC
pOp: WUS mWB *pOp:GUS*	CTAGCTTATCGATACCGTCG	CGTACGCTTCCTCTCTTCCC
pOp: WUSΔEAR *pOp:GUS*	CTAGCTTATCGATACCGTCG	TCTGGGAACTACTCACAC
pOp: WUS∆Ac *pOp:GUS*	CTAGCTTATCGATACCGTCG	CGTACGCTTCCTCTCTTCCC
pOp: WUS-W8HD *pOp:GUS*	GGCTTCTTGAGATCCTTCA	CATACTTCCAGATGGCACCA
pOp: WUS-W9HD *pOp:GUS*	CTAGCTTATCGATACCGTCG	CATACTTCCAGATGGCACCA
pOp: WUS-W13HD *pOp:GUS*	CTAGCTTATCGATACCGTCG	CATACTTCCAGATGGCACCA
pOp:WOX8wusWB *pOp:GUS*	CTAGCTTATCGATACCGTCG	CGTACGCTTCCTCTCTTCCC
pOp:WOX8wsbxΔD *pOp:GUS*	CTAGCTTATCGATACCGTCG	CGTACGCTTCCTCTCTTCCC