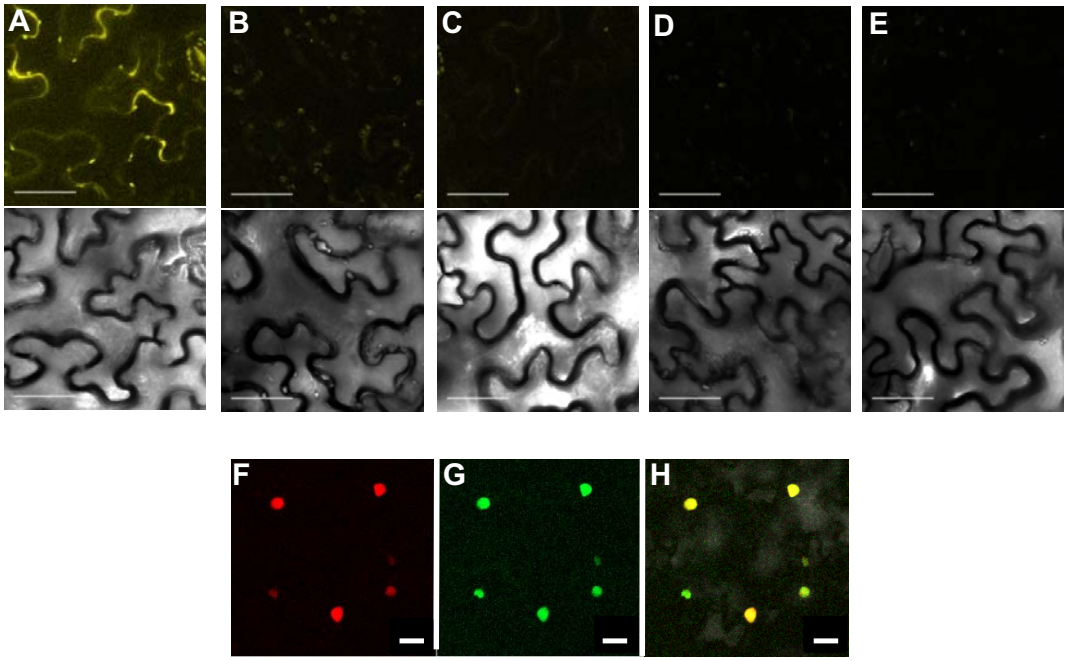

Supplemental Figure 1. **ARF8 and BPEp proteins interact *in vivo* and co-localize in the nucleus.**

(A-E) ARF8 and BPEp proteins interact in vivo. Bimolecular fluorescence complementation (BiFC) assay reveals that the C-terminal domains of BPEp (SD^{BPEp}) and ARF8 (CTD^{ARF8}) interact in tobacco leaf cells. SD^{BPEp} fused to the N-terminal domain of the YFP and CTD^{ARF8} fused to the C-terminal of the YFP were transiently expressed in *Nicotiana benthamiana* leaf cells. Four days post-infiltration, tobacco leaf cells were analyzed on an Axiovert100M LSM-510 laser-scanning Zeiss confocal microscope. SD^{BPEp} and CTD^{ARF8} interact in the cytoplasm of tobacco leaf cells **(A)**. Note that because SD^{BPEp} and CTD^{ARF8} lack the nuclear localization signals of BPEp and ARF8, a cytoplasmic interaction is observed in tobacco cells. SD^{BPEp} mutants R250A **(B)**, D253A **(C)**, F260A **(D)** and R250A/S251A/D253A **(E)** lost their ability to interact with ARF8, thus in agreement with the yeast data. For each panel, a fluorescent image (top) and a transmission image (bottom) is presented. Scale bars: 50µm.

(F-H) ARF8 and BPEp co-localize in the nucleus of the tobacco cells. BPEp-GFP and mOrange-ARF8 fusion proteins were transiently expressed in *Nicotiana benthamiana* as above, and their cellular localization was analyzed using confocal microscopy. **(F)** Transient expression of mOrange-ARF8 fusion protein. **(G)** Transient expression of BPEp-GFP fusion protein. **(H)** Overlay of **(F)** and **(G)** images showing the co-localization of mOrange-ARF8 and BPEp-GFP fusion proteins in the nucleus. Scale bars: 20 µm.

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YVKVSMDGAPYLRKIDLKMYKNYPELLKALENMF      IAA1
YVKVSMDGAPYLRKIDLKTYKNYPELLKALENMF      IAA2
YVKVSMDGAPYLRKIDLSCYKGYSELLKALEVMF      IAA3
YVKVSMDGAPYLRKIDLTMYKQYPELMKSLENMF      IAA4
YVKVSVDGAAFLRKIDLEMYKCYQDLASALQILF      IAA5
YMKVSMDGAPYLRKIDLCLHKGYLELALALEKLF      IAA6
FVKVSMDGAPYLRKVDLRSYTNYGELSSALEKMF      IAA9
YVKVSMDGVPYLRKMDLGSSQGYDDLAFALDKLF      IAA19
FVKVSMDGAPYLRKIDLRMYKSYDELSNALSNMF      IAA17
YVKVSMEGAPYLRKIDLKTYKSYLELSSALEKMF      IAA27
LVKVSMDGAPYLRKVDLKMYKSYQDLSDALAKMF      IAA7
FVKVSMDGAPYLRKVDLRTYTSYQQLSSALEKMF      IAA8
KQYMFLSRYSRGRSLDVYAVRSFKHCNKRSDLCF271   SDBPEp
FVKVYK-SGSVGRSLDISRFSSYHELREELGKMF      ARF8
FVKVYK-SGSFGRSLDISKFSSYHELRSELARMF      ARF6
HCKVFMESEDVGRTLDLSVIGSYQELYRKLAEMF      ARF10
HCKVFMESDDVGRTLDLSVLGSYEELSRKLSDMF      ARF16
CTKVHKQGIALGRSVDLSKFQNYEELVAELDRLF      ARF2
YTKVQKTGS-VGRSIDVTSFKDYEELKSAIECMF      ARF5
YTKVQKRGS-VGRSIDVNRYRGYDELRHDLARMF      ARF7
YTKVQKRG-SVGRSIDVTRYSGYDELRHDLARMF      ARF19
CTKVHMQGSAVGRAIDLTRSECYEDLFKKLEEMF      ARF1
CTKVHKQGSQVGRAIDLSRLNGYDDLLMELERLF      ARF4
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RIKVQMQGTAVGRAVDLTLLRSYDELIKELEKMF      ARF11
RTKVQMQGIAVGRAVDLTLLKSYDELIDELEEMF      ARF18
CTKVQMQGVTIGRAVDLSVLNGYDQLILELEKLF      ARF12
CTKVQMQGVTIGRAVDLSVLNGYDQLILELEKLF      ARF14
CTKVQMQGVTIGRAVDLSVLNGYDQLILELEKLF      ARF15
CTKVQMQGVTIGRAVDLSVLNGYDQLILELEKLF      ARF20
CTKVQMQGVTIGRAVDLSVLNGYDQLILELEKLF      ARF21
CTKVQMQGVTIERAVDLSVLNGYDQLILELEELF      ARF22
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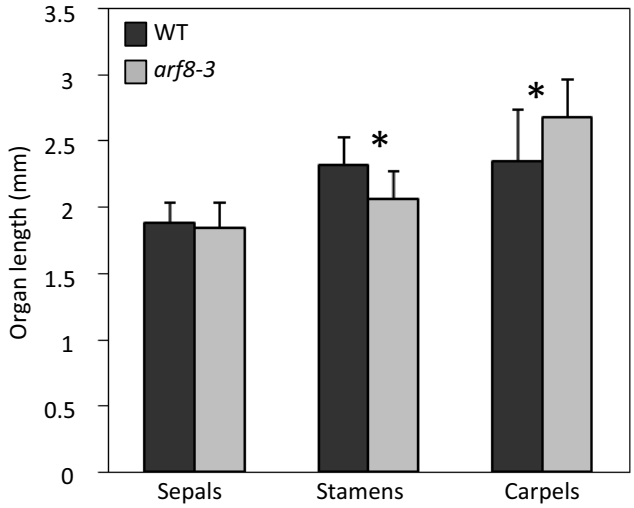
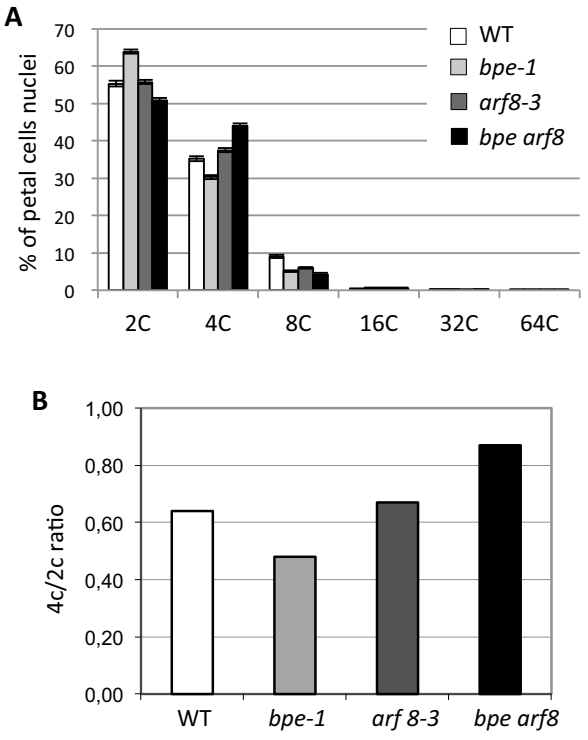
Supplemental Figure 2. Alignment of motif III of ARF and Aux/IAA C-terminal domains with the GRSLD motif of SD^{BPEp}.

Conserved amino acids of the GRSLD motif are highlighted in black background. In grey background are marked amino acids showing high similarity.



Supplemental Figure 3. Sepal, stamen and carpel size in *arf8-3* and wild-type plants.

Sepal, stamen and carpel organ length measurements performed using flowers at development stage 14. Values are given as mean ± standard error. For each value measurements were performed using at least 60 organs from at least 8 young plants (mutants and wild-type with no mature siliques) of the same age and grown under the same conditions. Asterisks indicate significant differences between wild-type and *arf8-3* with P value < 0.001 (t-test).



Supplemental Figure 4. DNA content of petal cell nuclei.

Nuclei were stained with propidium iodide before analysis of DNA content via flow cytometry.

(A) Distribution of nuclei passed on DNA content for each genotype as indicated. Confidence interval of the proportion of each type of nuclei showing significant difference ($P<0.05$, t-test) is shown.

(B) 4c /2c nuclei ratio indicative of a first endocycle.

These nuclear DNA content analyses reveal no enhanced endoreduplication in petals of *bpe* or *arf8* single mutants. A slight increase in 2C content is observed in *bpe-1*. Conversely, a slight increase in 4C nuclei is observed in petals of the *bpe arf8* double mutant compared to the wild type. This increased ploidy is however not confirmed with additional endocycle.

Supplemental Table 1 : Sequence of primers used in this study

Primer	Gene	Sequence	Experiment
At SAUR r	*SAUR-AC1*	TATTGTTAAGCCGCCCATTG	qRT-PCR
At SAUR l	*SAUR-AC1*	AAGGGAATCATCGTCGACAC	qRT-PCR
At IAA 1 R	*Aux/IAA1*	TGGACGGAGCTCCATATCTC	qRT-PCR
At IAA 1 F	*Aux/IAA1*	ACCGACCAACATCCAATCTC	qRT-PCR
At IAA 3 R	*Aux/IAA3*	TGATTGGATGCTCATTGGTG	qRT-PCR
At IAA 3 F	*Aux/IAA3*	CAACCCAAGCACAGACAGAG	qRT-PCR
At IAA 9 R	*Aux/IAA9*	GAGCTGCTGGGAAGGATATG	qRT-PCR
At IAA 9 F	*Aux/IAA9*	GCTGCAGCTAACCCAATAGC	qRT-PCR
At IAA 17 R	*Aux/IAA17*	AGGGTTCTCAGAGACGGTTG	qRT-PCR
At IAA 17 F	*Aux/IAA17*	TTGATTTTTGGCAGGAAACC	qRT-PCR
At IAA 19 F2	*Aux/IAA19*	GACTCGGGCTTGAGATAACG	qRT-PCR
At IAA 19 R2	*Aux/IAA19*	CGTGGTCGAAGCTTCCTTAC	qRT-PCR
ACT8 Q5	*ACT8*	GGTAACATTGTGCTCAGTGGTGG	qRT-PCR
ACT8 Q3	*ACT8*	AACGACCTTAATCTTCATGCTGC	qRT-PCR
TUB4 Q5	*TUB4*	AAGGCTTTCCTTCATTGGTACA	qRT-PCR
TUB4 Q3	*TUB4*	CTCTCCGGCTGTAGCATCTT	qRT-PCR
TCTP-F	*TCTP*	CACCCAAGCTCAGCGAAGAA	qRT-PCR
TCTP-R	*TCTP*	CATGCATACCCTCCCCAACAA	qRT-PCR
ARF8-5	*ARF8*	GACATGAAGCTGTCAACATCTGG	qRT-PCR
ARF8-m3	*ARF8*	TAGGTTGCTTACTCGGTATCC	qRT-PCR
BPEp-F	*BPEp*	CTGCTCCCCAAAAACAGAACTT	qRT-PCR
BPEp-R	*BPEp*	TGCTTAGATGAACTAATAGCGACTCCT	qRT-PCR
SD-D253-A-3	*BPEp*	CGAACCGCATAAACAGCGAGACTCCTACCCCGAGA	Site directed mutagenesis Asp^{253}
SD-D253-A-5	*BPEp*	TCTCGGGGTAGGAGTCTCGCTGTTTATGCGGTTCG	Site directed mutagenesis Asp^{253}
SD-F260-A-3	*BPEp*	CGTTTATTGCAATGCTTAGCTGACCGAACCGC	Site directed mutagenesis Phe^{260}
SD-F260-A-5	*BPEp*	GCGGTTCGGTCAGCTAAGCATTGCAATAAACG	Site directed mutagenesis Phe^{260}
SD-R250-A-3	*BPEp*	GCATAAACATCGAGACTCGCACCCCGAGAATACCTCG	Site directed mutagenesis Arg^{250}
SD-R250-A-5	*BPEp*	CGAGGTATTCTCGGGGTGCGAGTCTCGATGTTTATGC	Site directed mutagenesis Arg^{250}
BPEpORF-F	*BPEp*	GATTAAGTCCATGGATCCGAGTGGG	Cloning of *BPEp* ORF in pAS2.1
BPEpORF-R	*BPEp*	ATCCGCCCGGGAATTCAAGAAAACAAAACAGATTTTTGA	
SDBPE-F	*BPEp*	CCGGAATTCGGGAAAGAGGTGATGATTCTCATGATC	Cloning of SD^{BPEp} in pAS2.1
BPEpORF-R	*BPEp*	ATCCGCCCGGGAATTCAAGAAAACAAAACAGATTTTTGA	
ARF8CTD-F	*ARF8*	CACCCAAGACACAACTCATGAGT	Cloning of ARF8 in BiFC vector pBIFP3
ARF8CTD-R	*ARF8*	CTAGAGATGGGTCGGGTTTTGC	
SDBPEBiFC-F	*BPEp*	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAGGGGTAATGATTCTCATGATCATC	Cloning of BPEp in BiFC vector pBIFP2
SDBPEBiFC-R	*BPEp*	GGGGACCACTTTGTACAAGAAAGCTGGGTATCAAGAAAACAAAACAGATT	
BPEpGFP-F	*BPEp*	GGGGACAAGTTTGTACAAAAAAGCAGGCTGATGGATCCGAGTGGGATG	BPEp-GFP fusion Cloning
BPEpGFP-R	*BPEp*	GGGGACCACTTTGTACAAGAAAGCTGGGTATCAAGAAAACAAAACAGATT	
ARF8mOrang-F	*ARF8*	GGGGACAGCTTTCTTGTACAAAGTGGCTAAGCTGTCAACATCTGGA	mOrange-ARF8 fusion Cloning
ARF8mOrang-R	*ARF8*	GGGGACAACTTTGTATAATAAAGTTGCCTAGAGATGGGTCGGGTT	
BPEpSplicMut-F	*BPEp*	CCACCCAAAGAAGTAATGATTCTC	Mutagenesis of splice donor site for BPEp intron V
BPEpSplicMut-R	*BPEp*	GAGAATCATTACTTCTTTGGGTGG	