

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.

YVKVSMDGAPYLRKID	LKMYKN <mark>Y</mark>	PELLKALENM	1	IAA1
YVKVSMDGAPYL <mark>R</mark> KID	LKTYKN <mark>Y</mark>	PELLKALENM <mark>F</mark>	1	IAA2
YVKVSMDGAPYLRKID	LSCYKG <mark>y</mark>	SELLKALEVM <mark>e</mark>	2	IAA3
YVKVSMDGAPYL <mark>R</mark> KID	LTMYKQ <mark>y</mark>	PELMKSLENM <mark>F</mark>	1	IAA4
YVKVSVDGAAFL <mark>R</mark> KID	LEMYKC <mark>y</mark>	QDLASALQIL <mark></mark>	1	IAA5
YMKVSMDGAPYLRKID	LCLHKG <mark>Y</mark>	LELALALEKL <mark>f</mark>	1	IAA6
FVKVSMDGAPYLRKVD	LRSYTN <mark>Y</mark>	GELSSALEKM <mark>e</mark>		IAA9
YVKVSMDGVPYLRKMD	LGSSQ <mark>G</mark> Y	DDLAFAL <mark>D</mark> KL <mark>f</mark>		IAA19
FVKVSMDGAPYLRKID	lrmyk <mark>sy</mark>	DELSNALSNM	2	IAA17
YVKVSMEGAPYLRKID	lktyk <mark>sy</mark>	LELSSALEKM <mark>e</mark>		IAA27
LVKVSMDGAPYLRKVD	l kmyk <mark>sy</mark>	QDLSDALAKM		IAA7
FVKVSMDGAPYLRKVD	lrtyt <mark>sy</mark>	QQLSSALEKM		IAA8
KQYMFLSRYSRGRSLD	VYAVRSE	KHCNKRSDLCE	271	SD
FVKVYK-SGSVGRSLD	I SRFS <mark>S</mark> Y	HELREELGKM <mark>F</mark>	1	ARF8
FVKVYK-SGSFGRSLD	I SKFS <mark>S</mark> Y	HELRSELARM <mark>e</mark>		ARF6
HCKVFMESEDVGRTLD	LSVIG <mark>S</mark> Y	QELYRKLAEM <mark>e</mark>		ARF10
HCKVFMESDDVGRTLD	LSVLG <mark>S</mark> Y	EELSRKLSDM		ARF16
CTKVHKQGIALGRSVD	LSKFQN <mark>Y</mark>	EELVAEL <mark>D</mark> RL <mark>F</mark>		ARF2
YTKVQKTGS-V <mark>GRS</mark> ID	VTSFKDY	EELKSAIECMF	1	ARF5
YTKVQKRGS-VGRSID	VNRYRG	DELRHDLARM <mark>f</mark>		ARF7
YTKVQKRG-SVGRSID	VTRYSG <mark>Y</mark>	DELRHDLARM <mark>E</mark>		ARF19
CTKVHMQGSAVGRAID	LTRSEC	EDLFKKLEEM <mark>f</mark>	1	ARF1
CTKVHKQGSQVGRAID	LSRLNG	DDLLMELERL <mark>f</mark>	1	ARF4
RTKVQMQGVPVGRAVD	LNALKGY	NELIDDIEKL <mark>F</mark>	1	ARF9
RIKVQMQGTAV <mark>GR</mark> AVD	L T L L R <mark>S Y</mark>	DELIKELEKM <mark>f</mark>		ARF11
RTKVQMQGIAVGRAVD	LTLLK <mark>S</mark> Y	DELIDELEEM <mark>e</mark>		ARF18
CTKVQMQGVTI GRAVD	LSVLNG	DQLILELEKL <mark>e</mark>		ARF12
CTKVQMQGVTI GRAVD	LSVLNG <mark>Y</mark>	DQLILELEKL <mark>f</mark>	1	ARF14
CTKVQMQGVTI GRAVD	LSVLNG <mark>Y</mark>	DQLILELEKL <mark>f</mark>	1	ARF15
CTKVQMQGVTI GRAVD	LSVLNG <mark>Y</mark>	DQLILELEKL <mark>f</mark>		ARF20
CTKVQMQGVTI GRAVD	LSVLNG <mark>Y</mark>	DQLILELEKL <mark>f</mark>		ARF21
CTKVQMQGVTIERAVD	LSVLNG <mark>Y</mark>	DQLILELEEL		ARF22

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 \pm 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.

AL SAUR - SAUR-ACI XAUR-ACI XAUR-ACI XAUR-ACI XAUR-ACI XAUR-ACI XAUR-ACI XAURACCIA QRT-PCR AL IAA I R Aux/IAAI TGATGGAACTCCATATCTC QRT-PCR QRT-PCR AL IAA I R Aux/IAAI TGATGGAACCAACTCCAACTCC QRT-PCR AL IAA J R Aux/IAAI TGATGGATGCTCATTGTG QRT-PCR AL IAA J P Aux/IAAI GACCTCCTGGGAACGAACTCC QRT-PCR AL IAA J P Aux/IAAI GACCTCCTGGGAACGAACCAC QRT-PCR AL IAA J P Aux/IAAI GAGTGCTGGGAAGGAACCC QRT-PCR AL IAA J P Aux/IAAI GAGTGCTGGGAAGCACCC QRT-PCR AL IAA J P Aux/IAAI GAGTGCTGGAAGCTCCTACC QRT-PCR AL IAA J P Z Aux/IAAI GAGTGCTGGAAGCTCCTACC QRT-PCR AL IAA J P Z Aux/IAAI GAGTGGTGGAAGCTTGCTACC QRT-PCR ACTB Q5 ACTB GACTGTGGGAAGCTTGCTACCC QRT-PCR ACTB Q5 ACTB ACTGTGGGAAGCTTGCTACCCACCACACACAGCA QRT-PCR TUB4 Q3 TUB4 Q3 CTUAA AGGCCTTACCTAGGCAAGCACCACACACACACA QRT-PCR TUF-R TCTP CACCCAAGCCACAACACACACT QRT-PCR QRT-PCR TUB4 Q3 TUB4 AGACCCTAAGCACTTACTACACACACACACACACACACAC	Primer	Gene	Sequence	Experiment	
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BPEDSDICMUL-R BPED GAGAATCATTACTTCTTGGGTGG for BPED intron V	BPEpSplicMut-F	BPEn	CCACCCAAAGAAGTAATGATTCTC	Mutagenesis of splice dopor site	
	BPEpSplicMut-R	BPEp	GAGAATCATTACTTCTTTGGGTGG	for BPEp intron V	

Supplemental Table 1 : Sequence of primers used in this study