

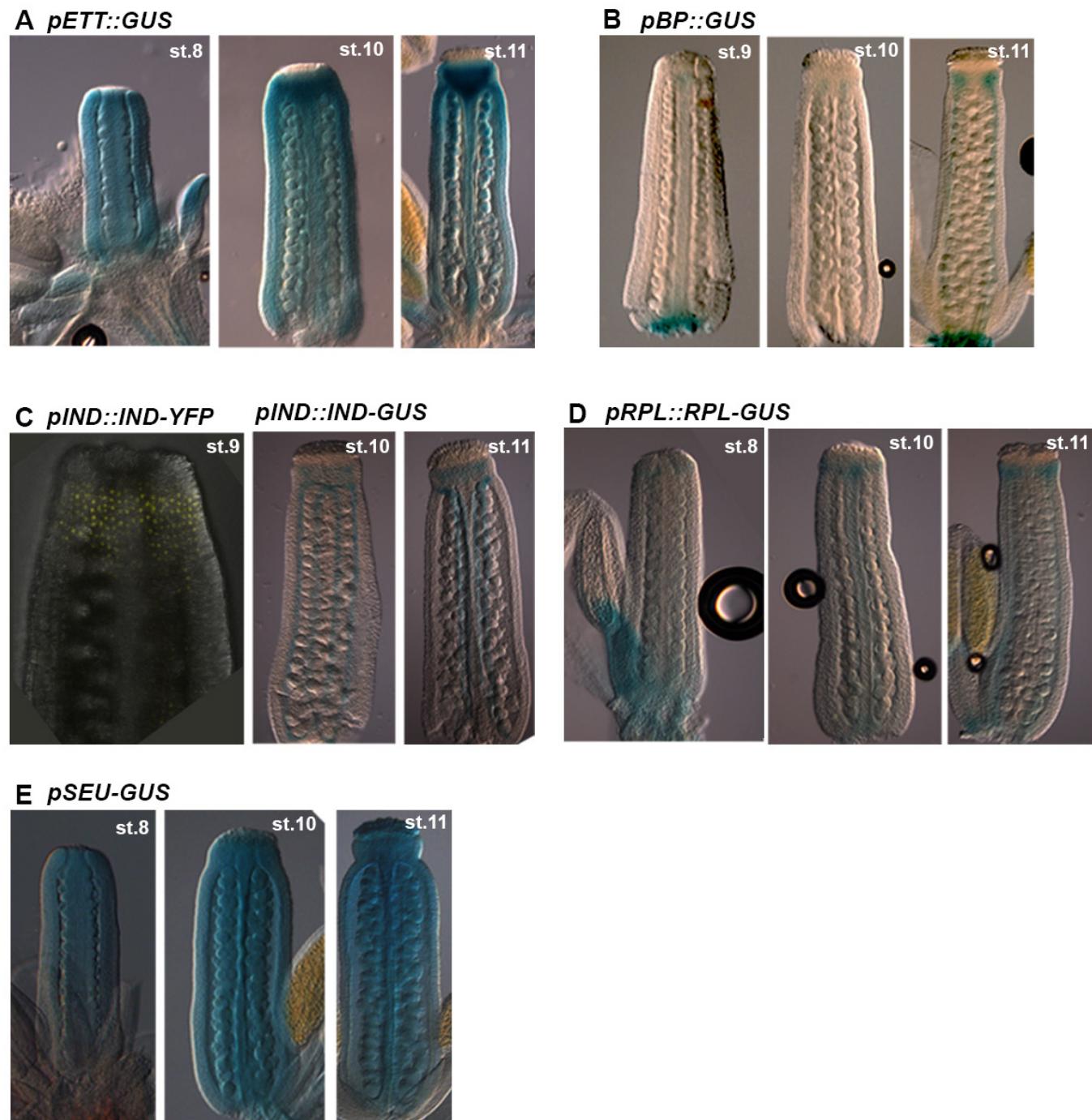
**Table S1.** Nomenclature for *B. rapa* genes.

<i>ETT</i>	<i>BraA.ETT.a, BraA.ETT.b</i>
<i>IND</i>	<i>BraA.IND.a</i>
<i>RPL</i>	<i>BraA.RPL.a, BraA.RPL.b, BraA.RPL.c</i>
<i>BP</i>	<i>BraA.BP.a</i>
<i>SEU</i>	<i>BraA.SEU.a</i>

**Table S2.** Primers used in this manuscript.

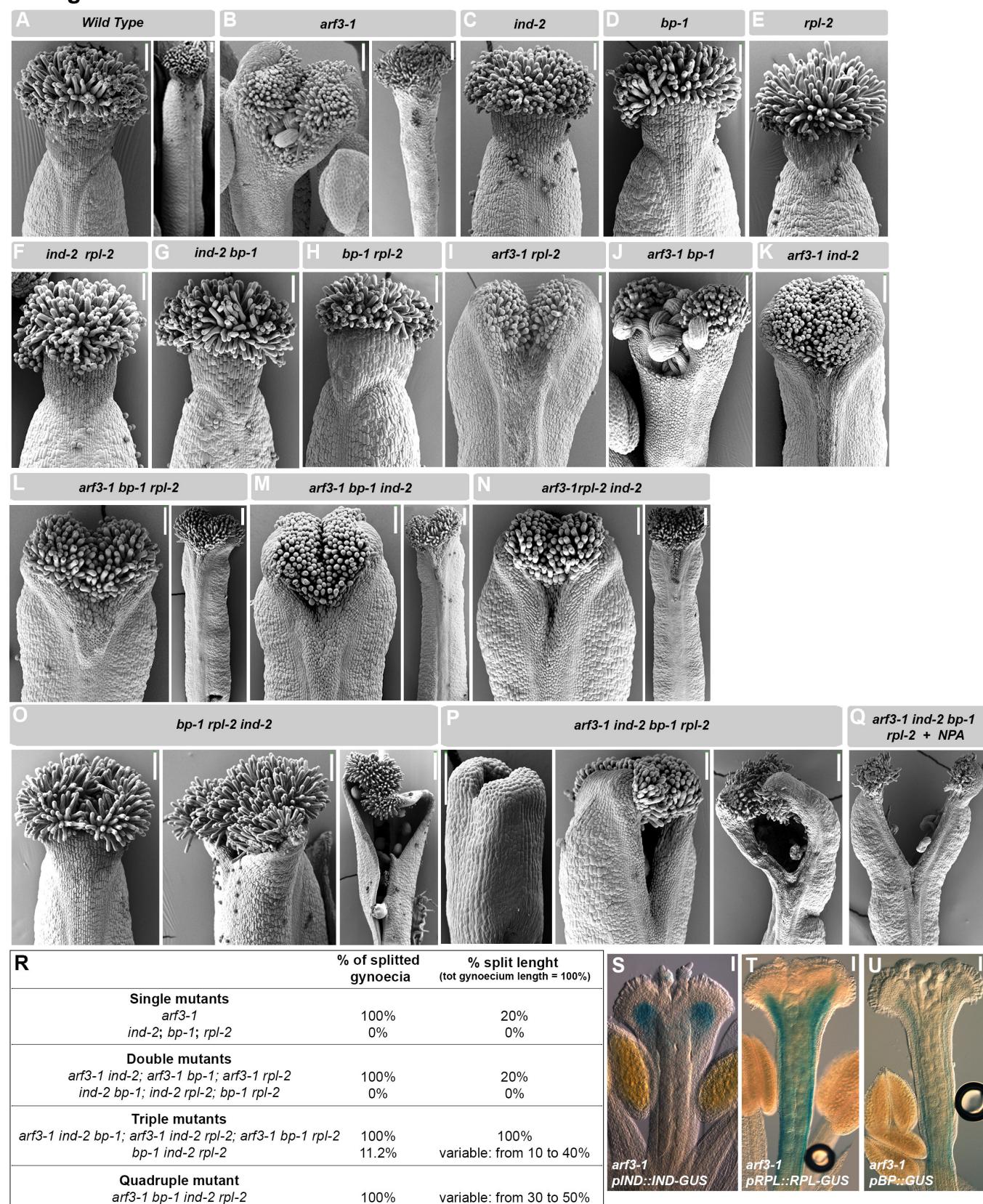
Arabidopsis ETT for Y2H and BiFC	ggggacaagttgtacaaaaaaggcaggcttcATGGGTGGTTAACGATCTG GGGGACCACTTGTACAAGAAAGCTGGGTGCTAGAGAGCAATGTCTAGCA
Arabidopsis RPL for Y2H and BiFC	ggggacaagttgtacaaaaaaggcaggcttcATGGCTGATGCATCGAGCC GGGGACCACTTGTACAAGAAAGCTGGGTCTAACCTACAAATCATGTAGAAC
Arabidopsis BP for Y2H and BiFC	ggggacaagttgtacaaaaaaggcaggcttcATGAAATATAATCGAGATTAAATAG GGGGACCACTTGTACAAGAAAGCTGGGTGTTATGGACCGAGACGATAAGGTCCATC
Arabidopsis IND for Y2H and BiFC	ggggacaagttgtacaaaaaaggcaggcttcATGATGGAGCCTCAGCCTCAC GGGGACCACTTGTACAAGAAAGCTGGGTGTCAGGGTGGAGTTGTGGT
Arabidopsis SEU for Y2H and BiFC	ggggacaagttgtacaaaaaaggcaggcttcATGGTACCATCAGAGCCGCTAATCC GGGGACCACTTGTACAAGAAAGCTGGGTGATGGTACCATCAGAGCCGCTAATCC
<i>B.rapa</i> ETT.a for Y2H	ggggacaagttgtacaaaaaaggcaggcttcatgggtggtaattgtatctgaacg GGGGACCACTTGTACAAGAAAGCTGGGTGctagagagcaatgttagcaacatatac
<i>B.rapa</i> ETT.b for Y2H	ggggacaagttgtacaaaaaaggcaggcttcATGGGTGGCTTAATCGATCTG GGGGACCACTTGTACAAGAAAGCTGGGTCTAGAGAGCAATGTCTAGCAAC
<i>B.rapa</i> RPL.a for Y2H	ggggacaagttgtacaaaaaaggcaggcttcATGCCGATGCTTACGAGCC GGGGACCACTTGTACAAGAAAGCTGGGTCTAACCTACAAATCATGTAGAAC
<i>B.rapa</i> BP for Y2H	ggggacaagttgtacaaaaaaggcaggcttcATGAAGAAATATCAACATGAAAGC GGGGACCACTTGTACAAGAAAGCTGGGTGTTATGGTCCAAGACGATAAGGGCC
<i>B.rapa</i> IND for Y2H	ggggacaagttgtacaaaaaaggcaggcttcATGTCTGGCTCAAAGCAGATGC GGGGACCACTTGTACAAGAAAGCTGGGTGTCAGACATAGGAGCTCCAAGCTG
<i>B.rapa</i> SEU for Y2H	ggggacaagttgtacaaaaaaggcaggcttcatggtgccatcagaggcgccaaatcc GGGGACCACTTGTACAAGAAAGCTGGGTGtgcgttccaatcacgctgaaaattg
Arabidopsis UBQ10 for QTRPCR	AGAACTCTGCTGACTACAATATCCAG ATAGTTTCCCAGTCAACGTCTAAC
Arabidopsis XTH7 for QTRPCR	ATTGACGGAGGCAGAGCCATT TCTTCGAAGCAAATCCACATCCTG

### S1 Figure.



**S1 Figure. Expression profile of ETT, IND, BP, RPL and SEU at different gynoecium developmental stages.**

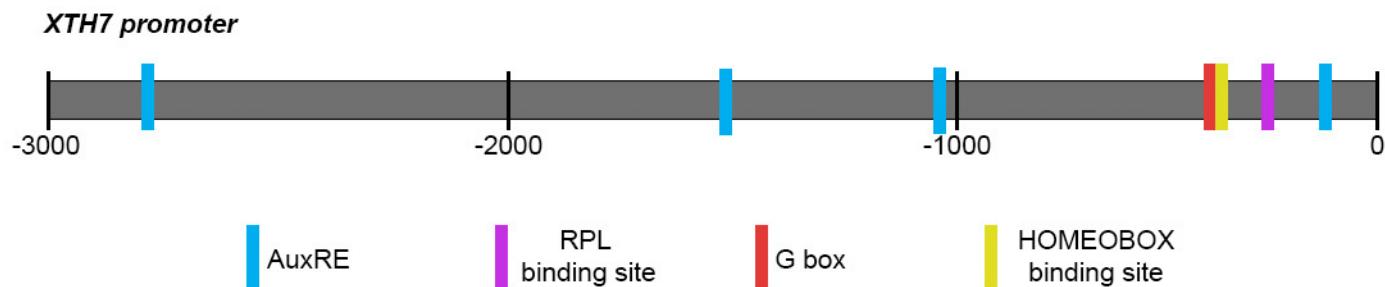
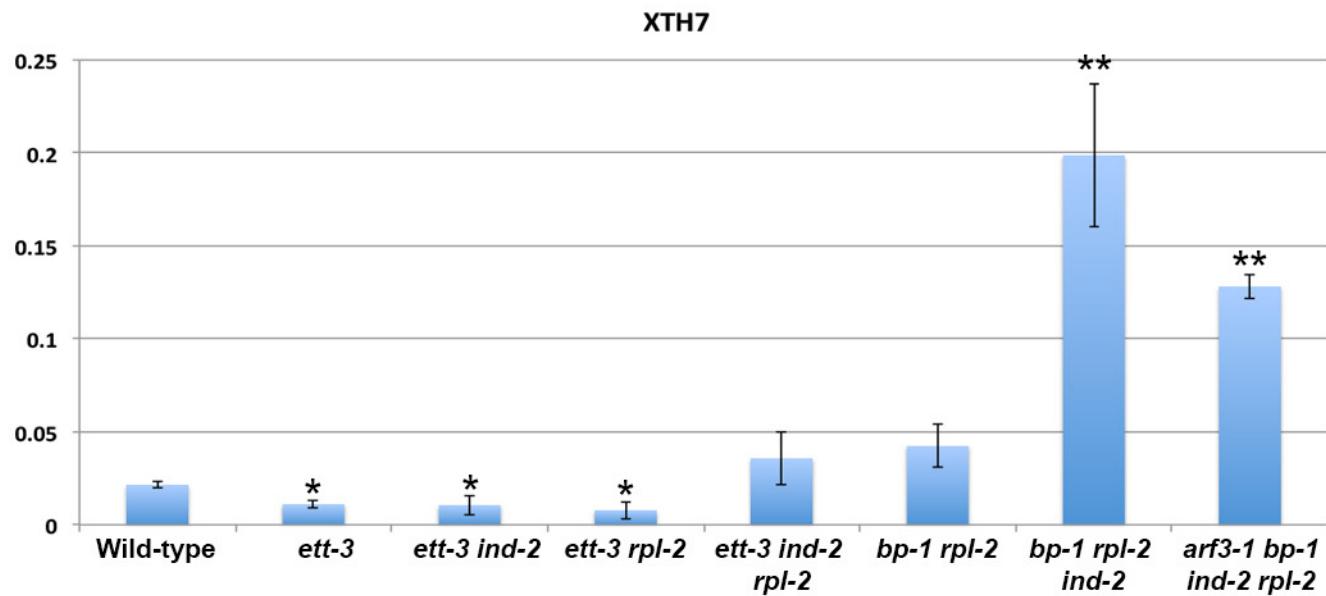
- (A) Expression profile of pETT::GUS marker line at stages 8, 10 and 11 of gynoecium development.
- (B) Expression profile of pBP::GUS marker line at stages 9, 10 and 11 of gynoecium development..
- (C) Expression profile of pIND::IND-YFP (left panel, stage 9) and pIND::IND-GUS marker line (right, stages 10 and 11) at stages 9, 10 and 11 of gynoecium development.
- (D) Expression profile of pRPL::RPL-GUS marker line at stages 8, 10 and 11 of gynoecium development..
- (E) Expression profile of pSEU::GUS marker line at stages 8, 10 and 11 of gynoecium development.

**S2 Figure.****S2 Fig. Genetic interactions between ETT, BP, RPL and IND**(A-E) SEM images of wild-type (A), *arf3-1* (B), *ind-2* (C), *bp-1* (D) and *rpl-2* (E) single mutants.(F-K) SEM images of *ind-2 rpl-2* (F), *ind-2 bp-1* (G), *bp-1 rpl-2* (H), *arf3-1 rpl-2* (I), *arf3-1 bp-1* (J) and *arf3-1 ind-2* (K) double mutants.(L-O) SEM images of *arf3-1 bp-1 rpl-2* (L), *arf3-1 bp-1 ind-2* (M), *arf3-1 rpl-2 ind-2* (N) and *bp-1 rpl-2 ind-2* triple mutant.(P-Q) SEM images of *arf3-1 bp-1 rpl-2 ind-2* quadruple mutant before (P) and after (Q) NPA treatment.

(R) Percentage of splitted gynoecia and split length in the single, double, triple and quadruple mutant combinations.

(S-U) GUS staining of *pIND::IND-GUS* (S), *pRPL::RPL-GUS* (T) and *pBP::GUS* (U) in *arf3-1* mutant background.

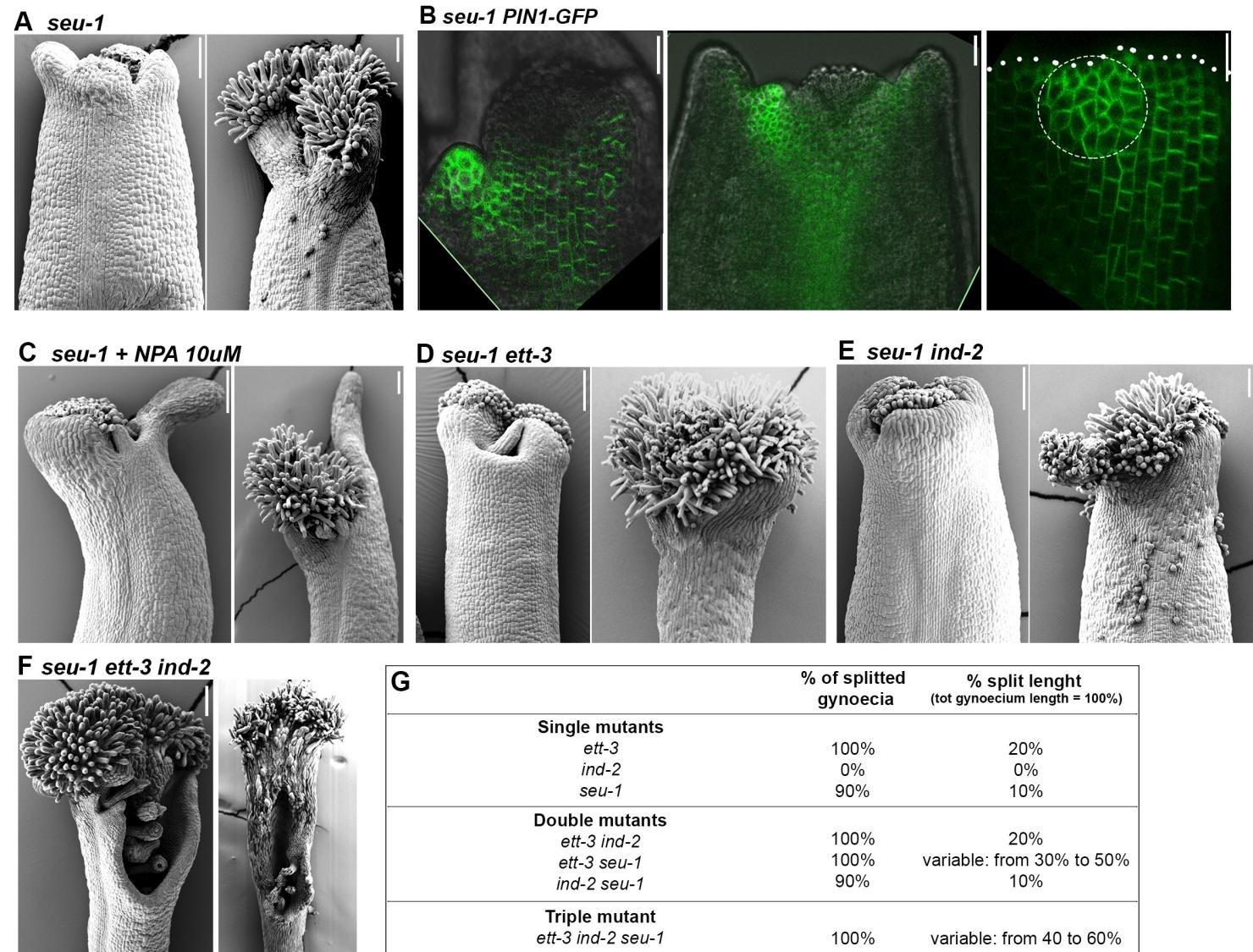
Scale bar: 100μm

**S3 Figure.****A****B****Figure S3. Expression analysis of XTH7.**

(A) Schematic representation of potential binding sites for ARFs (AuxRE; ETT), bHLH (G box; IND), RPL and HOMEOBOX (BP) factors contained in the *XTH7* promoter.

(B) Expression analysis by quantitative PCR of *XTH7* in the indicated mutant combinations.

\* is  $p < 0.05$ ; \*\* is  $p < 0.01$

**S4 Figure.****S4 Fig. Genetic interaction between ETT, IND and SEU and PIN1-GFP expression in *seu-1* mutant.**(A) SEM images of gynoecium apices of *seu-1* mutant.(B) Confocal images of *pPIN1::PIN1-GFP* in *seu-1* mutant with focus on the top part of the gynoecium. Areas of PIN1 apical versus apolar localization can be seen adjacent to the developing cleft. Dotted circle in the third panel encircles an area where the cells present severely affected division plane.(C-F) SEM images of gynoecium apices of *seu-1* mutant NPA-treated (C), *seu-1 ett-3* (D), *seu-1 ind-2* (E), *seu-1 ett-3 ind-2* triple mutant (F).

(G) Percentage of splitted gynoecia and lenght of the split in the single, double and triple mutant combinations.

Scale bar: 100μm

**S5 Figure.****brIND (Bra000979), *ind* mutant line - JI3-0395a.35**

107Q &gt; stop

bHLH domain

**brBP (Bra000638), *bp* mutant line - JI3-0579b**

74R &gt; stop

**brRPL.a (Bra005703), *rpl.a* mutant line - JI3-0278.15**

12Q &gt; stop

**brRPL.b(Bra009618), *rpl.b* mutant line - JI3-0753.9**

67P &gt; S

**brRPL.c(Bra028883), *rpl.c* mutant line - JI3-0573b**

77G &gt; R

**brSEU (Bra032192), *seu* mutant line - JI3-0822a**

E245 &gt; stop

**brETT.a (Bra005465)**

splice-acceptor

> introduce premature stop codon  
(JI3-2298b)S450 > F E480 > stop P484 > L P506 > S H539 > T  
(JI3-3427a) (JI3-3329b) (JI3-32170) (JI3-1778a) (JI3-2477a)

ES domain

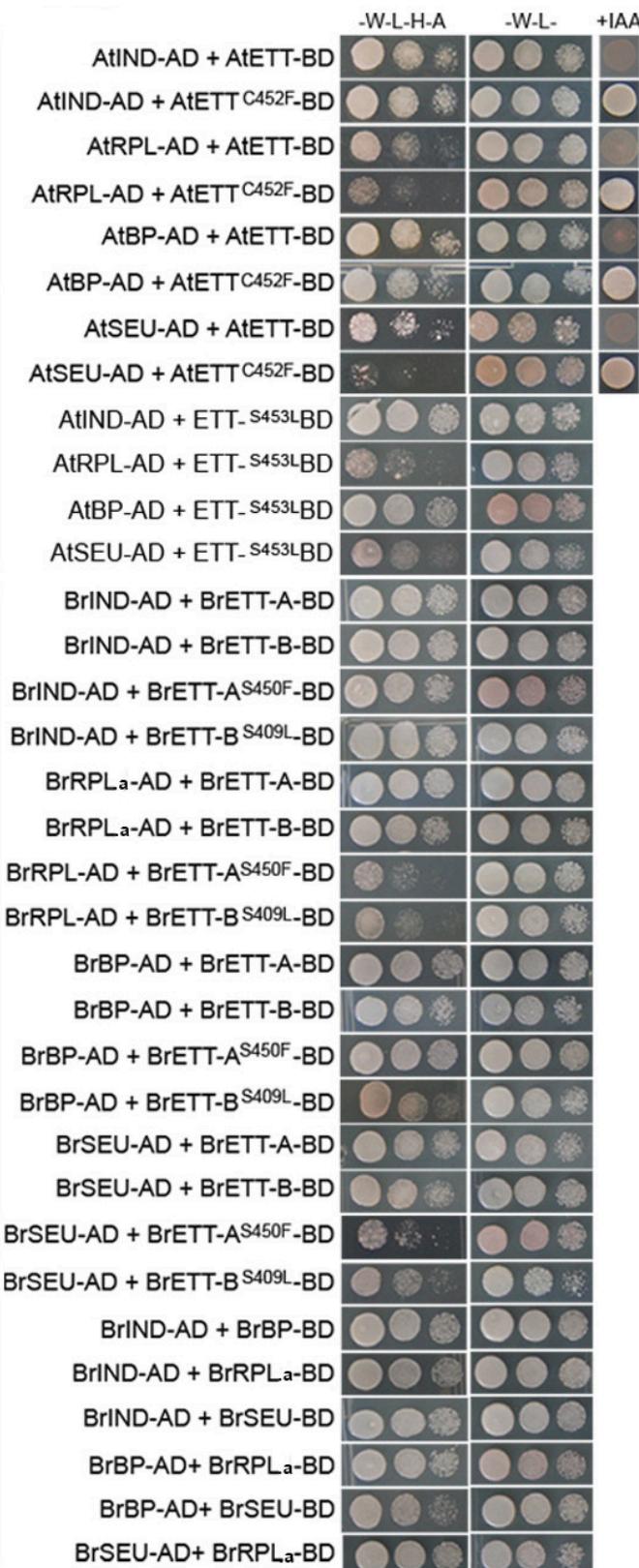
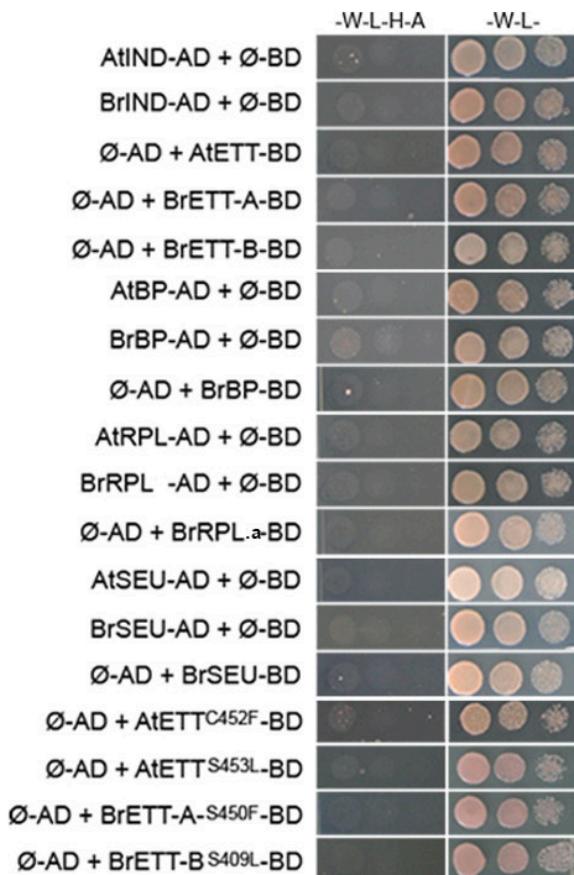
**brETT.b (Bra021885)**

splice-acceptor

> introduce premature stop codon  
(JI3-2221a)P402 > S S409 > L G426 > D P442 > L M489 > I  
(JI3-2224a) (JI3-1096a) (JI3-2075b) (JI3-1457b) (JI3-1449a)

ES domain

**S5 Figure.** Schematic representation of *Brassica rapa* exome capture mutant lines analysed in this manuscript.

**S6 Figure.***Arabidopsis**Control**Brassica rapa*

## S7 Figure.

A BrETT.a

MGGLDLNTEEQQEETTPSSGSGSLSPCDSSSSASAFCVGSSSSGVCLEWHAAGPLSLPKRGSVLVYFPQGHLEQAPDFSAAIYGLPPHVFCRLDVKLHAETADTDEVYAQVSLPES  
EDVERKVREGVIDVDGGEEDYEVVKRTNTPHMFCKTLTAASDTSTHGGFSPRRAECDFFPLDYQTQPRPSQELLARDLHGLEWRFRHIYRGQPRRRHLTTGWSAVFKKKLVSGDAFLRL  
GDDGKLRGLVRASSQIEGAGASFSSQYNOHMNNHFAEVHAIATNSAFIYNNPKASWSNFIIAPAKFLKTVDYPCIGMRKFARKASEDESARSPGIIYDNDLPIRWPGSKWCRLLVRD  
DTDANGHHQQRSPWIEPEPSGSISSSGFSITTPGKRSRIGFGSSGPDKDIPVSGSAGTDEEFLSRFQVRLLQGQEIHFGINTSDGGAGARRFRKGTEFGDYSGFHKVLQQGETVPAPEMMDQ  
RHQGMSQRNIWCGPFQNFSRILPPSSVQVSSPLPSSGPVRMEEHHGGSGRCLRGFGPLRDETAVGSGMVVGPCVEGNGSSIRGGVASQSSHGRDIFYGMRDMLLDIAL\*

B BrETT.b

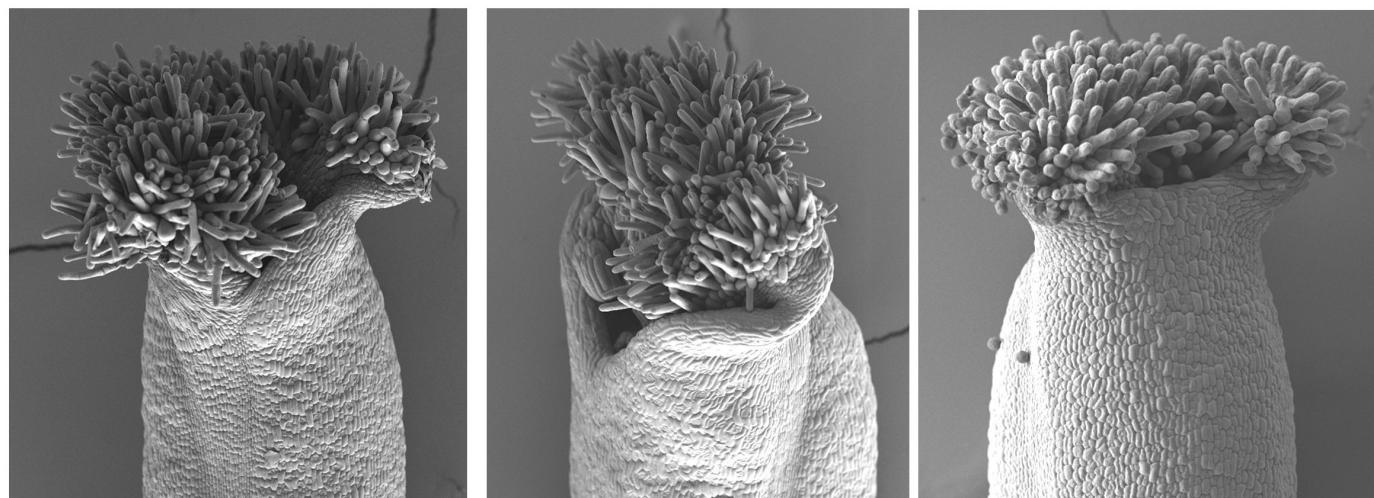
MGGLIDLNVTEEEDETLSASGSLSTSNSSSAFVANGSSSSSSGVCLELWHACAGPLISLPKRGSLVLYFPQGHLEQQAPGFSAAIYGLPPHVFCRILDVKLHAETDTDEVYAQVSLLPES  
EDIERKLREGVIDVWDGGDQEYEVVKRSNTPHMFCKTLTASDTSTHGGFSVRRAEADCFPPLDYSKPRPSQUELLARDLHGLEWRFRHIYRGQPRRRHLTTGWSGFVNKKLVSGDAFLFL  
RGDDGKRLGVRRARSQFEGASAQFSNAQYQNNTNNFSEVAHISTANSFAIINYNPKSLGIITGSDLDPRWPGSKWRC1LVRWDNEANRHQQRVSPWEIEPSGSISSSGSFMTTGPKRSR  
EFGDPDVPEGIATDFEESLRFQRLVQGQKEKPGFIINTSSDGAGGARRRKFGKGTEFGDSYGFHKVLQQGETVPAYSMTAHQHQHGLSQQGNFSSRFLLPPLSVHSSSPSSLVLTNSNRPNGL  
EEHQGGSGSCRLFQFPLRDESTAMVPCVEGQKGVGQSNSHHHSQGRGIYGMRDMLLDIAL\*

C

### S7 Figure. ETT Protein alignment.

**(A-B)** Sequences of ETT proteins from *B. rapa* BrETT.a (A) and BrETT.b (B).

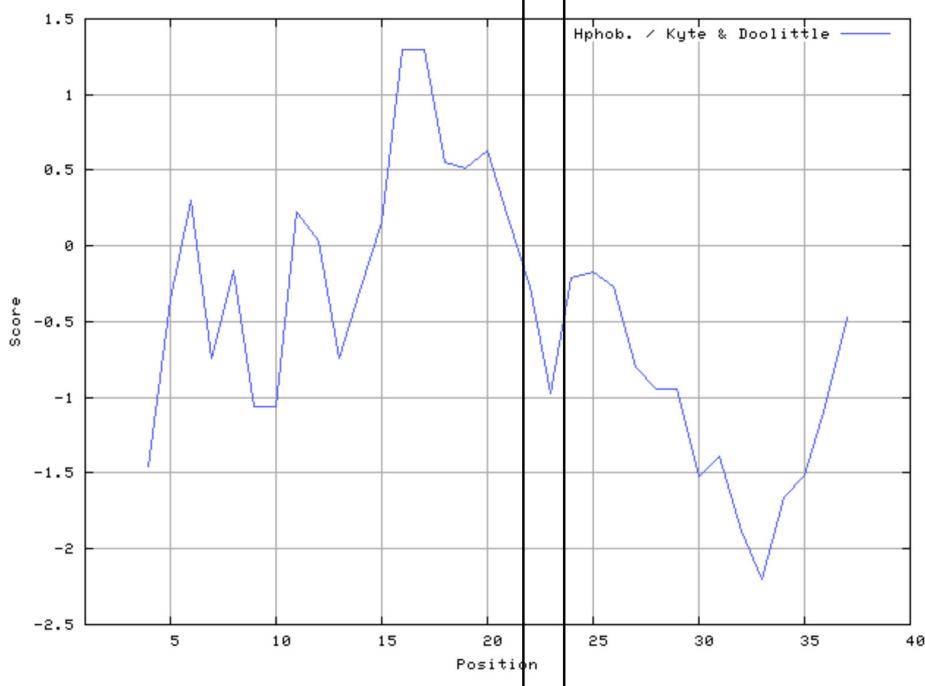
**(C)** Protein alignment between AtETT, BrETT.a, BrETT.b. Black vertical bar delimits the DBD domain (on the left) and the ES domain (on the right).

**S8 Figure.****A ett-3 pETT::ETT-C452F****B**

Amino acid	R	K	N	D	E	Q	H	P	Y	W	S	T	G	A	M	C	F	L	V	I
Kyte & Doolittle Hydrophobicity Scale	-4.5	-3.9	-3.5	-3.5	-3.5	-3.5	-3.2	-1.6	-1.3	-0.9	-0.8	-0.7	-0.4	+1.8	+1.9	+2.5	+2.8	+3.8	+4.2	+4.5
Physicochemical Meaning																				

More Hydrophilic      More Hydrophobic

10                          20                          30                          40  
 ESLRFQRVILQ GQEIFPGFIN TCS DGGAGAR RGRFKGTEFG

**S8 Fig. Analyses of C452F substitution in AtETT**

(A) SEM images of gynoecium apices of *ett-3* plants transformed with the pETT::ETT\_C452F construct.

(B) Hydrophobicity analyses by ProtScale of the ETT subdomain where the C452F and S453L substitutions are located. The substitutions fall in a region which shows tendency to hydrophilicity with values below 0.