

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

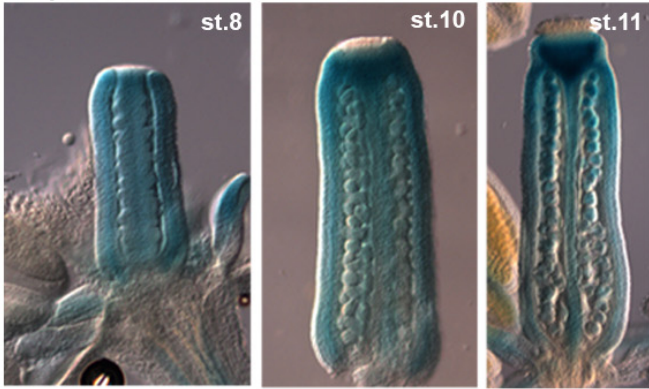
<i>ETT</i>	<i>BraA.ETT.a</i> , <i>BraA.ETT.b</i>
<i>IND</i>	<i>BraA.IND.a</i>
<i>RPL</i>	<i>BraA.RPL.a</i> , <i>BraA.RPL.b</i> , <i>BraA.RPL.c</i>
<i>BP</i>	<i>BraA.BP.a</i>
<i>SEU</i>	<i>BraA.SEU.a</i>

Table S2. Primers used in this manuscript.

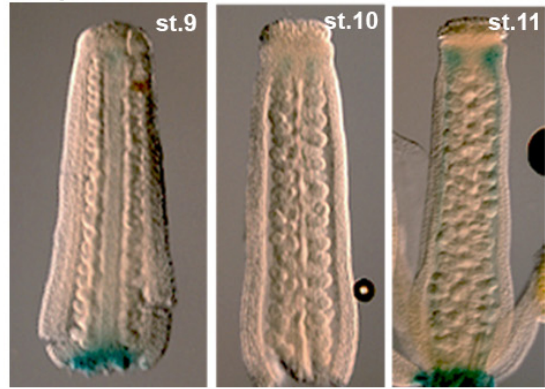
Arabidopsis ETT for Y2H and BiFC	ggggacaagttgtacaaaaagcaggcttcATGGGTGGTTAATCGATCTG GGGGACCACTTTGTACAAGAAAGCTGGGTGCTAGAGAGCAATGTCTAGCA
Arabidopsis RPL for Y2H and BiFC	ggggacaagttgtacaaaaagcaggcttcATGGCTGATGCATACGAGCC GGGGACCACTTTGTACAAGAAAGCTGGGTCTCAACCTACAAAATCATGTAGAAAC
Arabidopsis BP for Y2H and BiFC	ggggacaagttgtacaaaaagcaggcttcATGAAATATAAATCGAGATTAATAG GGGGACCACTTTGTACAAGAAAGCTGGGTGTTATGGACCGAGACGATAAGGTCCATC
Arabidopsis IND for Y2H and BiFC	ggggacaagttgtacaaaaagcaggcttcATGATGGAGCCTCAGCCTCACC GGGGACCACTTTGTACAAGAAAGCTGGGTGTCAGGGTTGGGAGTTGTGGT
Arabidopsis SEU for Y2H and BiFC	ggggacaagttgtacaaaaagcaggcttcATGGTACCATCAGAGCCGCCTAATCC GGGGACCACTTTGTACAAGAAAGCTGGGTGATGGTACCATCAGAGCCGCCTAATCC
<i>B. rapa</i> ETT.a for Y2H	ggggacaagttgtacaaaaagcaggcttcaggggtggttaattgatctgaacg GGGGACCACTTTGTACAAGAAAGCTGGGTGctagagagcaatgtctagcaacatc
<i>B. rapa</i> ETT.b for Y2H	ggggacaagttgtacaaaaagcaggcttcATGGGTGGCTTAATCGATCTG GGGGACCACTTTGTACAAGAAAGCTGGGTCTAGAGAGCAATGTCTAGCAAC
<i>B. rapa</i> RPL.a for Y2H	ggggacaagttgtacaaaaagcaggcttcATGGCCGATGCTTACGAGCC GGGGACCACTTTGTACAAGAAAGCTGGGTCTCAACCTACAAAATCATGTAGAAAC
<i>B. rapa</i> BP for Y2H	ggggacaagttgtacaaaaagcaggcttcATGGAAGAATATCAACATGAAAGC GGGGACCACTTTGTACAAGAAAGCTGGGTGTTATGGTCCAAGACGATAAGGGCC
<i>B. rapa</i> IND for Y2H	ggggacaagttgtacaaaaagcaggcttcATGTCTGGCTCAAAGCAGATGC GGGGACCACTTTGTACAAGAAAGCTGGGTGTCAGACATAGGAGCTCCAAGCTG
<i>B. rapa</i> SEU for Y2H	ggggacaagttgtacaaaaagcaggcttcaggtgccatcagaggcceaattc GGGGACCACTTTGTACAAGAAAGCTGGGTGtcatgcgtccaatcagcgtgaaattg
Arabidopsis UBQ10 for QTRPCR	AGAACTCTTGCTGACTACAATATCCAG ATAGTTTTCCAGTCAACGTCTTAAC
Arabidopsis XTH7 for QTRPCR	ATTGACGGAGGCAGAGCCATTC TCTTCGAAGCAAATCCACATCCTG

S1 Figure.

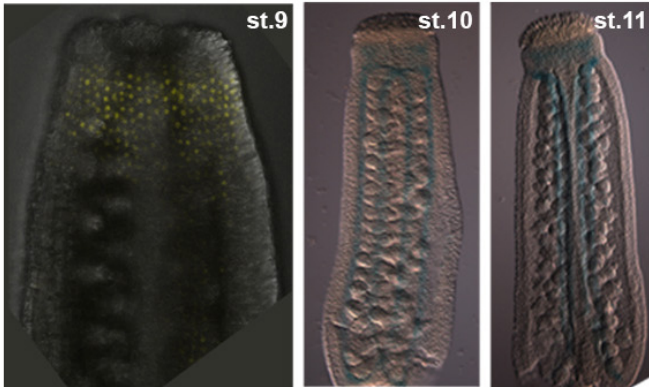
**A** *pETT::GUS*



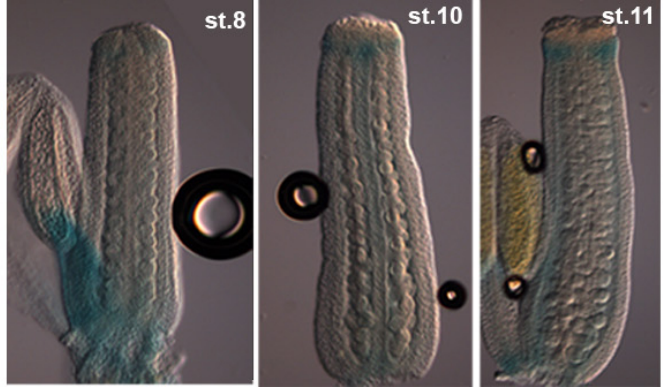
**B** *pBP::GUS*



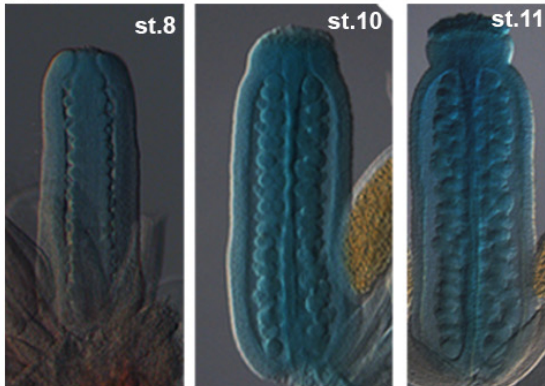
**C** *pIND::IND-YFP*    *pIND::IND-GUS*



**D** *pRPL::RPL-GUS*



**E** *pSEU-GUS*



**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.

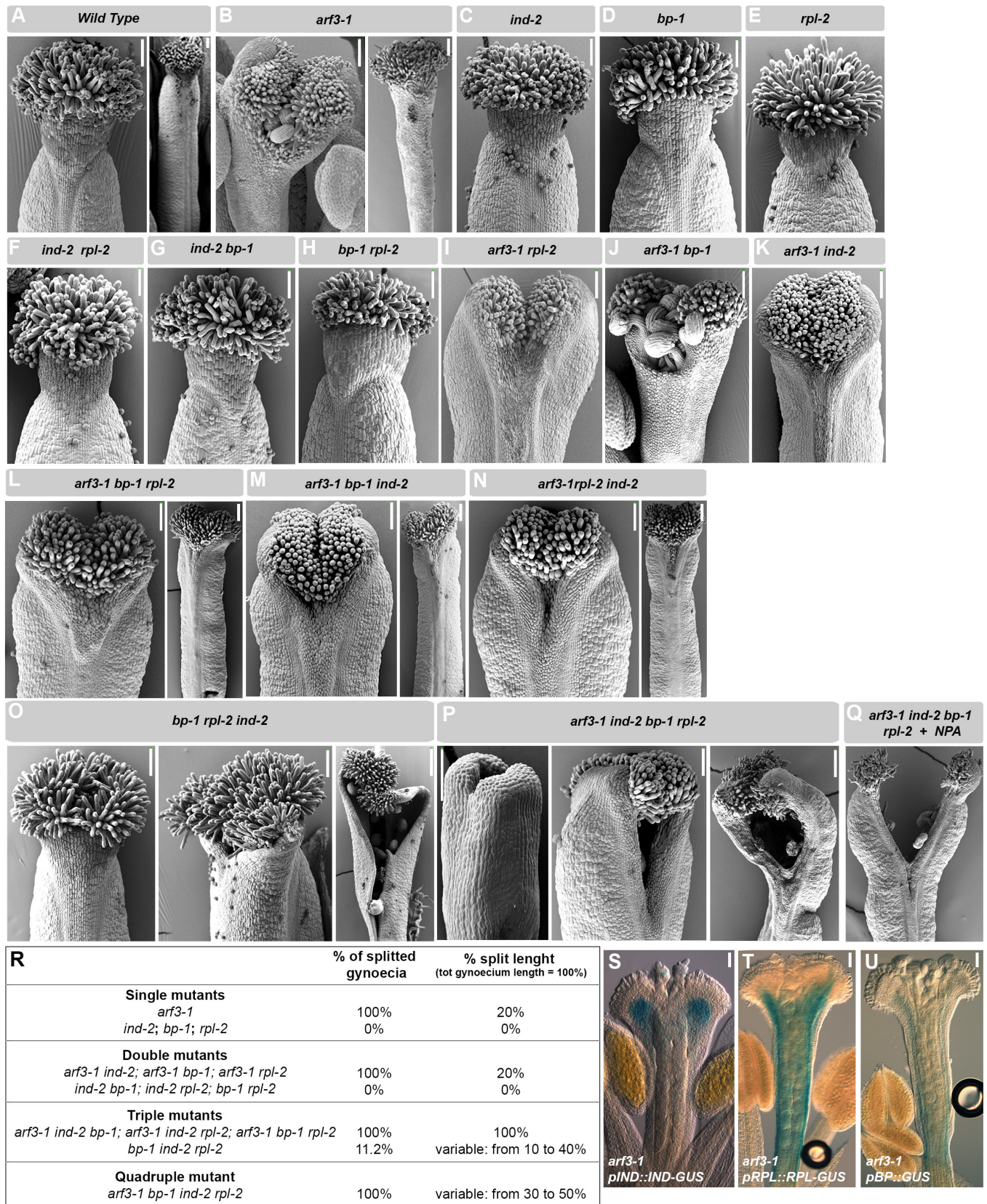
(B) Expression profile of *pBP::GUS* marker line at stages 9, 10 and 11 of gynoecium development..

(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.

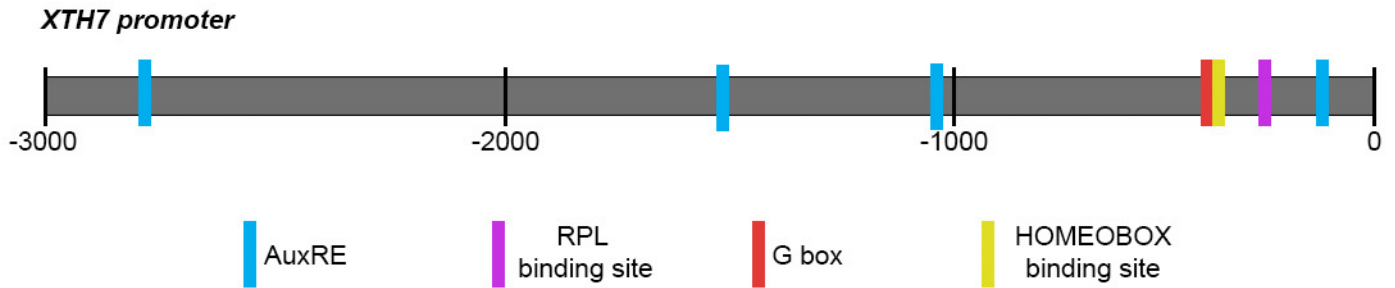
(R) Percentage of splitted gynoecia and split length in the single, double, triple and quadruple mutant combinations.

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

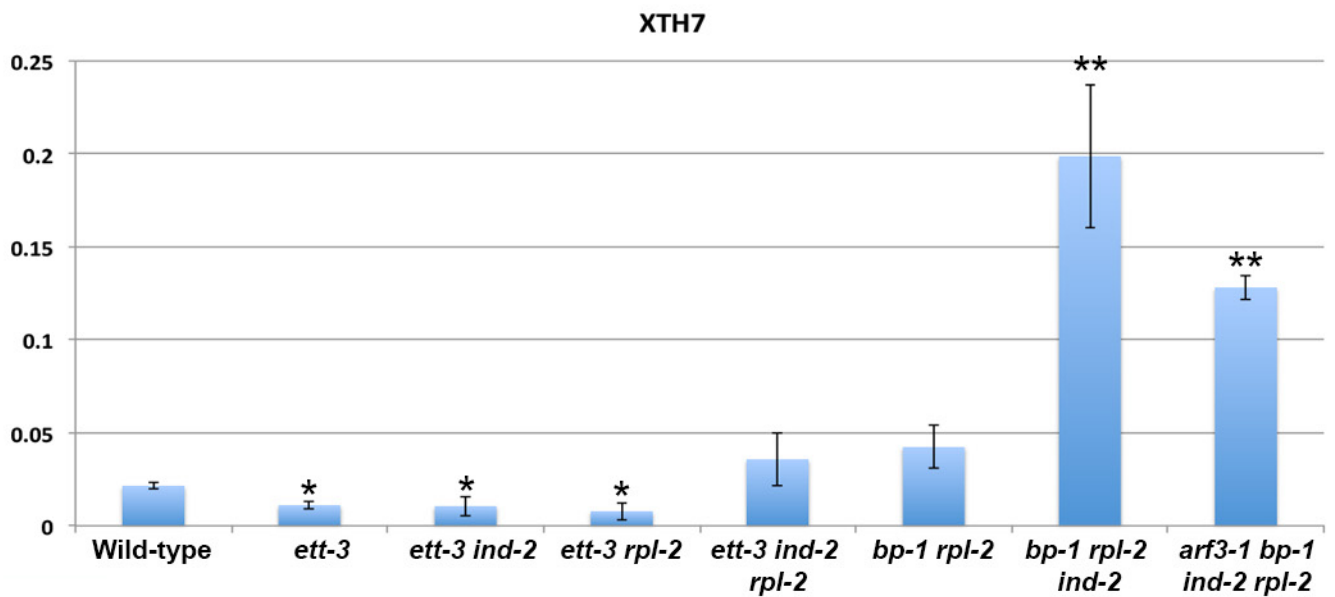
Scale bar: 100µm

### S3 Figure.

A



B



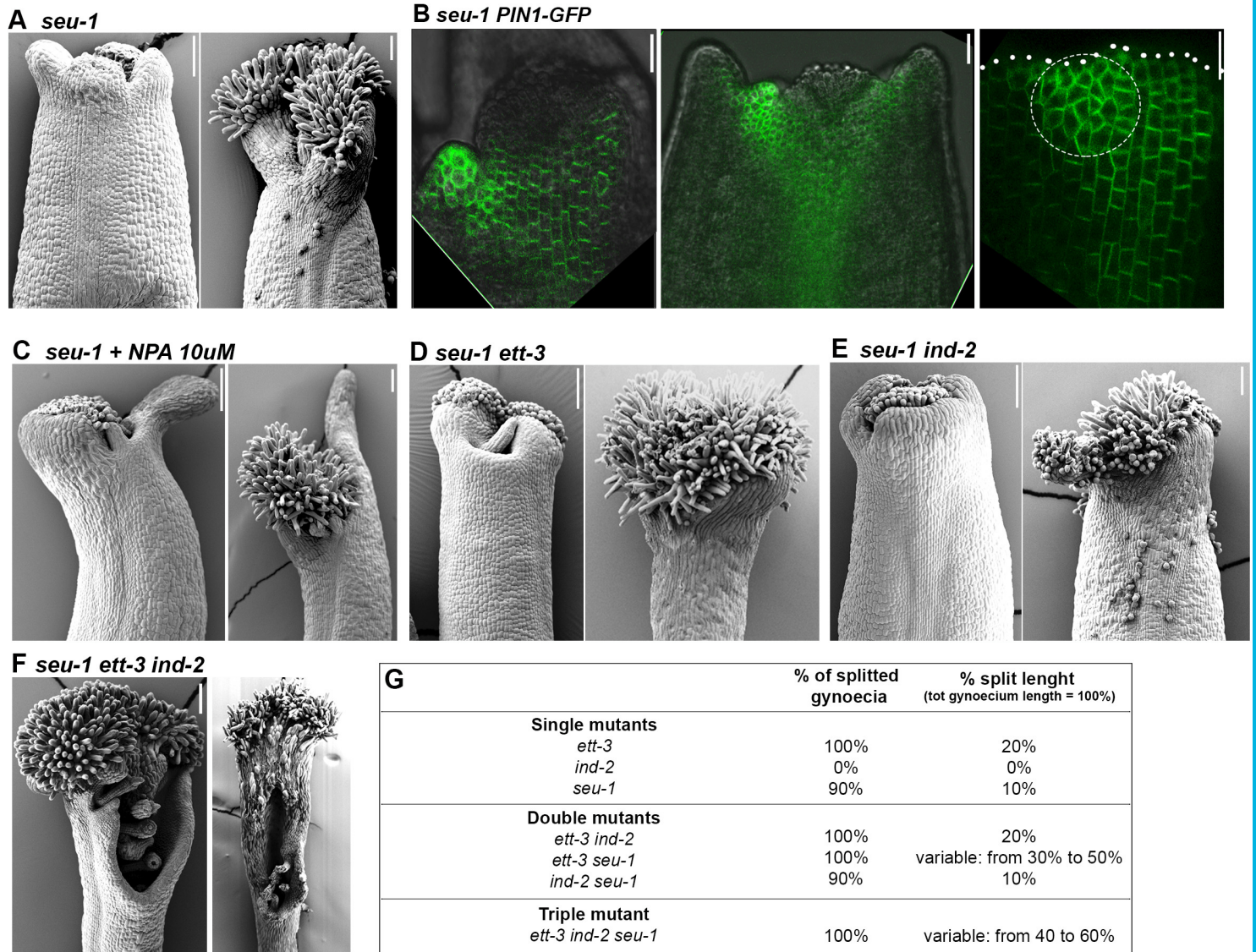
**Figure S3. Expression analysis of *XTH7*.**

(A) Schematic representation of potential binding sites for ARFs (AuxRE; ETT), bHLH (G box; IND), RPL and HOMEBOX (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 length of the split in the single, double and triple mutant combinations.

Scale bar: 100µm

## S5 Figure.

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



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



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



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



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



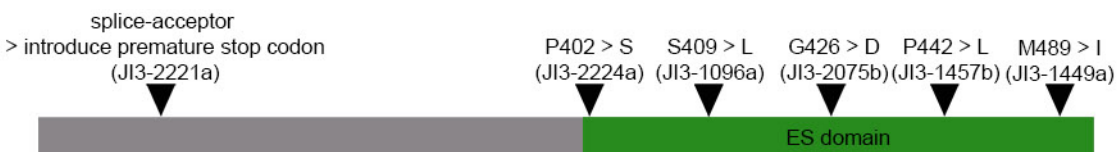
**brSEU (Bra032192), *seu* mutant line - JI3-0822a**



**brETT.a (Bra005465)**

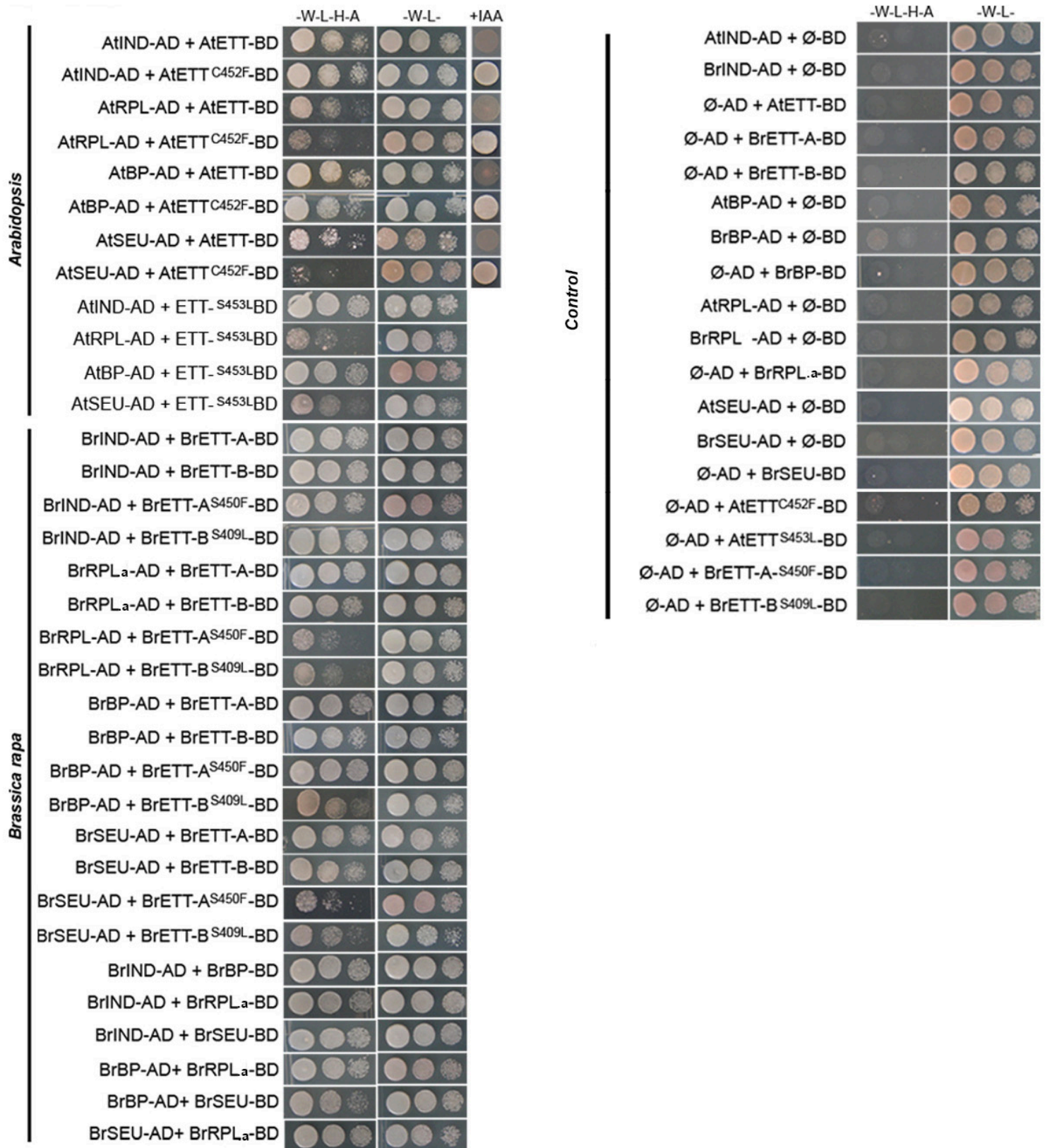


**brETT.b (Bra021885)**



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

S6 Figure.



S6 Figure. Y2H combinations.

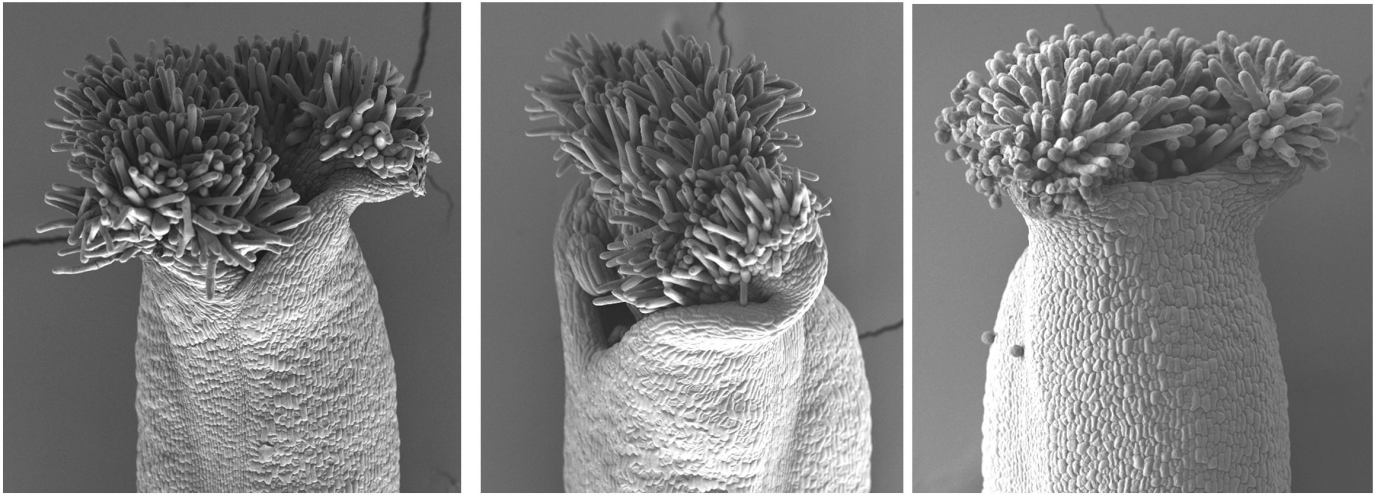
Y2H analyses between IND, ETT, RPL, BP and SEU proteins from *Arabidopsis* and *Brassica rapa* and respective controls.



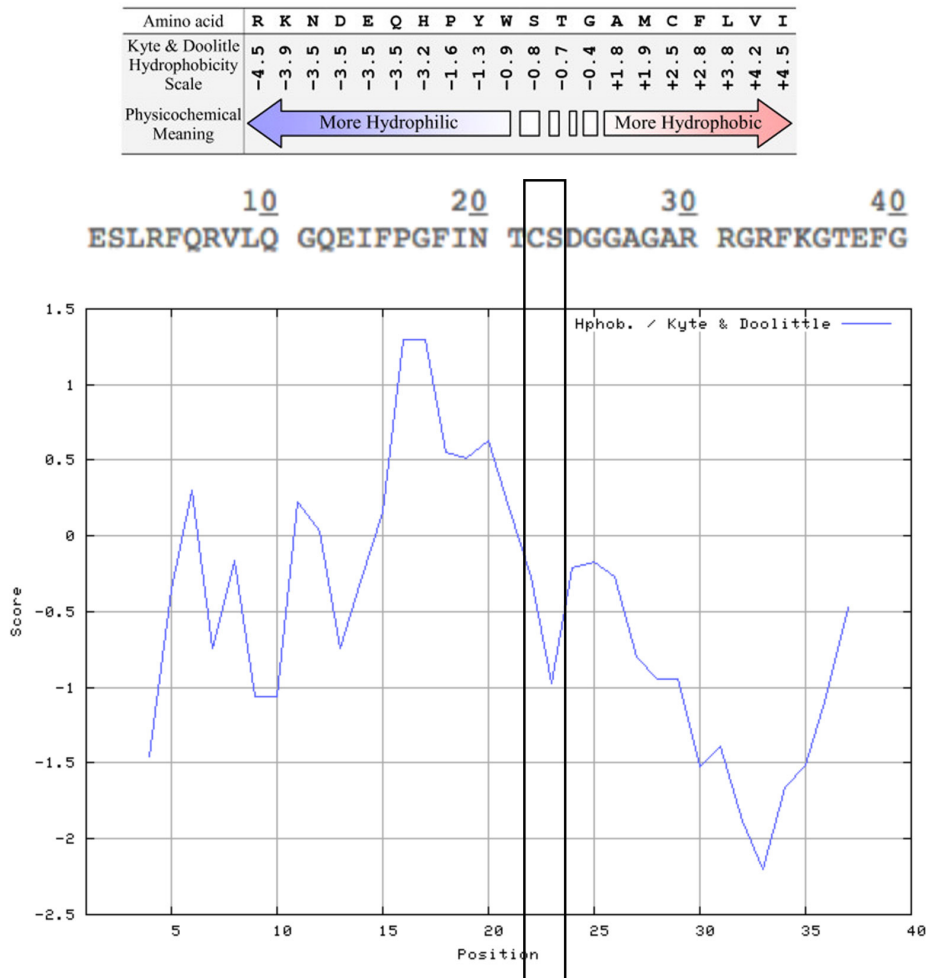


**S8 Figure.**

**A** *ett-3* pETT::ETT-C452F



**B**



**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.