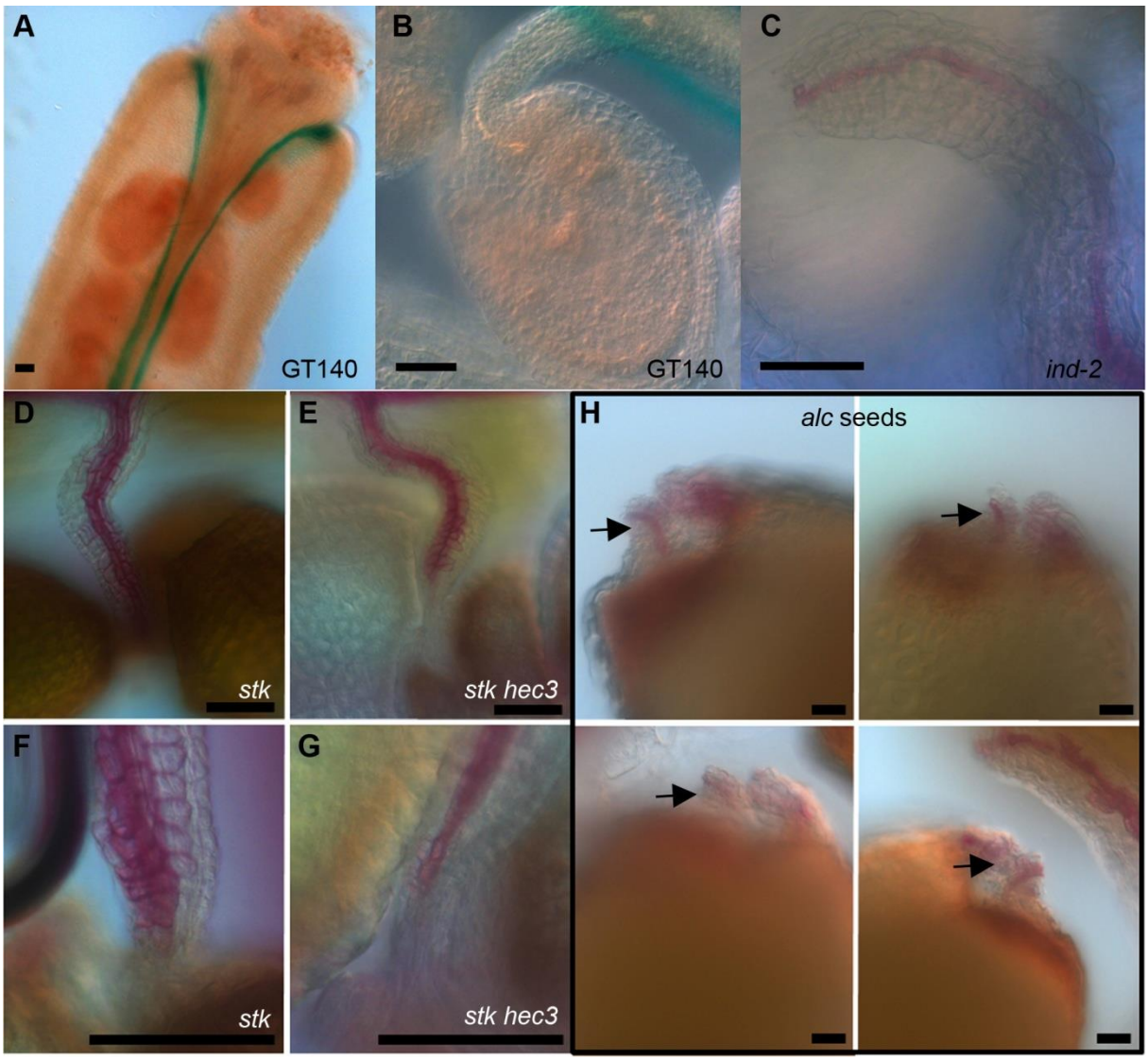
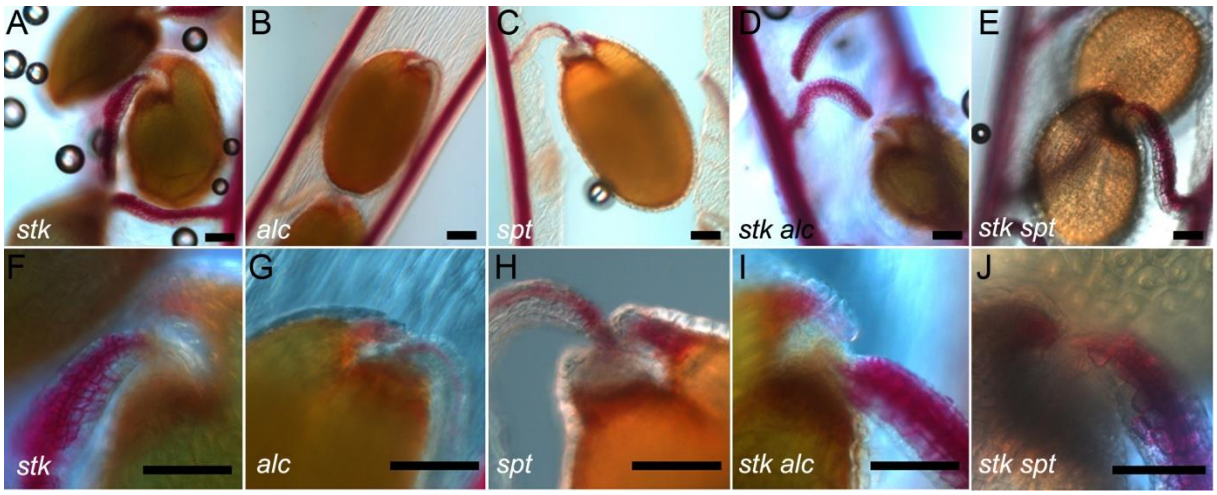
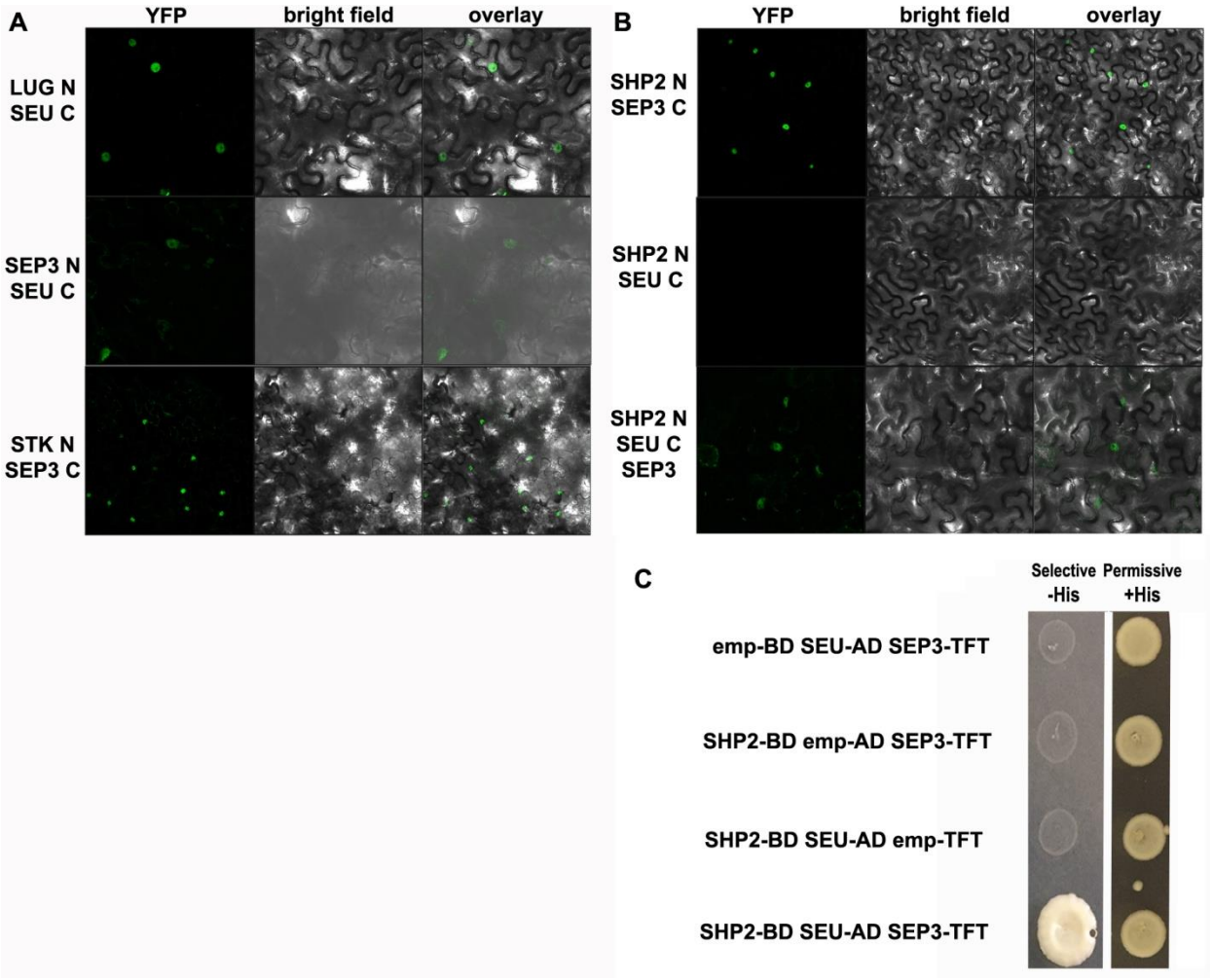



**Supplementary figure 1: GT140 GUS activity and mutant lignin deposition phenotypes in the seed abscission zone**. A-B) GUS staining of the GT140 line (*pIND:GUS*) showing activity at the valve margin of a stage 17 fruit (A). GUS was not detected neither the funiculus nor in the seed abscission zone B). C) Lignification pattern in the *ind-2* mutant was similar to the wild type, with the formation of a lignified ring at the end of the funiculus. D-G) Cleared fruits at stage 17 stained with phloroglucinol of *stk* mutant (D, F) and *stkhec3* double mutant (F-G). Funiculus. (D-E) and abscission zone (E, G) are shown. H) Four different *alc* seeds showing the edge of the funiculus (arrows) still attached to the seed hilum region. Magenta color indicates lignin deposition. Black bars represent 50 µm.




**Supplementary figure 2: Genetic combinations of *stk* with *alc* and *spt*.** Cleared fruits at stage 17 stained with phloroglucinol. Magenta signal corresponds with lignin deposition. Funiculus (A-E) and seed abscission zone (F-J) lignification pattern of *stk* (A,F), *alc-10* (B,G), *spt-12* (C,H), *stk alc-1* (D,I) and *stk spt-12* (E,J). Black bars represent 100 µm.




**Supplementary figure 3: BiFC positive controls and SHP2-SEU interaction**. A,B) BiFC experiment showing the interaction of SEU with LUG (A above) and SEP3 (A center), STK with SEP3 (A below)(positive controls) as well as the SHP2 interaction with SEP3 (B above) and SEU (B center and below). As for STK, SHP2 interacts with SEU through the formation of a heterodimer with SEP3 (B below). Left panels show YFP signal. Central panels show bright field. Right panel show the overlay of YFP and bright field. C) Yeast three hybrid assays showing SHP2-SEP3-SEU interaction, Yeast strains were grown on either selective (without tryptophan, leucine, uracil and histidine) or permissive (without tryptophan, leucine, uracil) medium. Emp- AD, empty vector containing the GAL4 activation domain; emp-BD, empty vector containing the GAL4 binding domain, emp-TFT, empty pTFT.

## **Supplementary Table S1:** Primers used

| SHP2 promoter cloning | |
|---|---|
| **pSHP2 F** | CCGGACGTCATCTCCAACGCATTGTTACG |
| **pSHP2 R** | CCGGACGTCTTCTATAAGCCCTAGCTG |

| STK CDS cloning | |
|---|---|
| **STKgw F** | GGGGACAAGTTTGTACAAAAAAGCAGGCTtcATGGGAAGAGGAAAGATAGAAATAAAG |
| **STKgw R** | GGGGACCACTTTGTACAAGAAAGCTGGGTcTTATCCGAGATGAAGAATTTTCTTG |

| SHP2 CDS cloning | |
|---|---|
| **SHP2gw F** | GGGGACAAGTTTGTACAAAAAAGCAGGCTtcATGGAGGGTGGTGCGAGTAATG |
| **SHP2gw R** | GGGGACCACTTTGTACAAGAAAGCTGGGTcTCAAACAAGTTGCAGAGGTGG |

| qRT-PCR primers | |
|---|---|
| **HEC3 F** | AGCAACCGTCAAGAAACCCA |
| **HEC3 R** | CCTGGCACGAGTCTCTGAAG |
| **ALC F** | GCAGCTTCAACTTCAAGTCCAGAC |
| **ALC R** | GGTGGAACCTGTGGTAATCGCAT |
| **SPT F** | GAAGGACCTGACTTGGAAGAGGGA |
| **SPT R** | TGTGAAAGCGAGGAAGGAGGAGAA |
| **ACT8 F** | CTCAGGTATTGCAGACCGTATGAG |
| **ACT8 R** | CTGGACCTGCTTCATCATACTCTG |

| ChIP primers | |
|---|---|
| **HEC3 I F** | TCACATCACAGTTGCAGAAATG |
| **HEC3 I R** | TGATTCATTTTGGACAGCTAGTTT |
| **HEC3 II F** | AAACCTTTAATCACGTCGCAA |
| **HEC3 II R** | TCTTATCCCGATCAACGGTC |
| **HEC3 III F** | AGAGTGTGGCGGCTAGACAT |
| **HEC3 III R** | GCATTGAAGCCGTATCCATT |
| **VDD F** | GGAAATATGACGCTTGTCTTTTTAG |
| **VDD R** | CAGAAACAGCAATATGCTCGTG |
| **act7 F** | CGTTTCGCTTTCCTTAGTGTTAGCT |
| **act7 R** | AGCGAACGGATCTAGAGACTCACCTTG |

all primers are from 5' to 3'