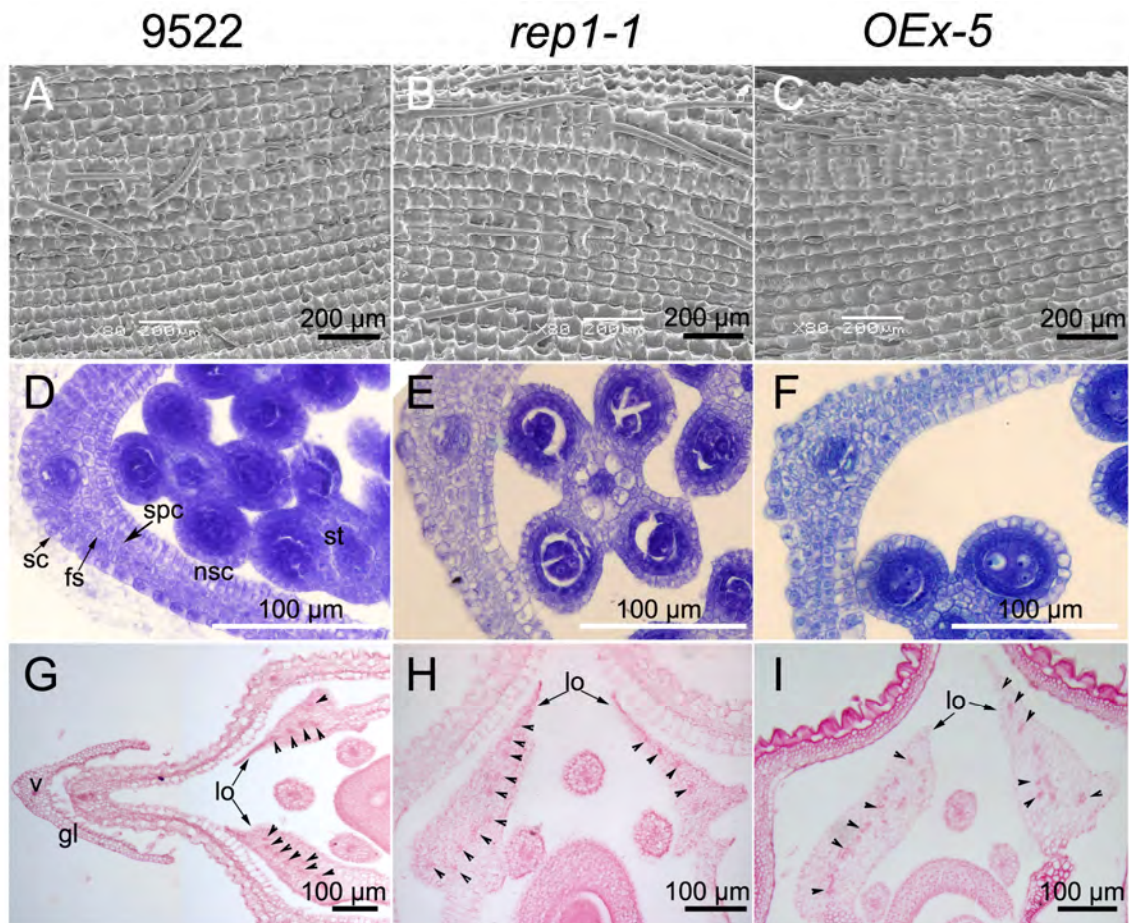
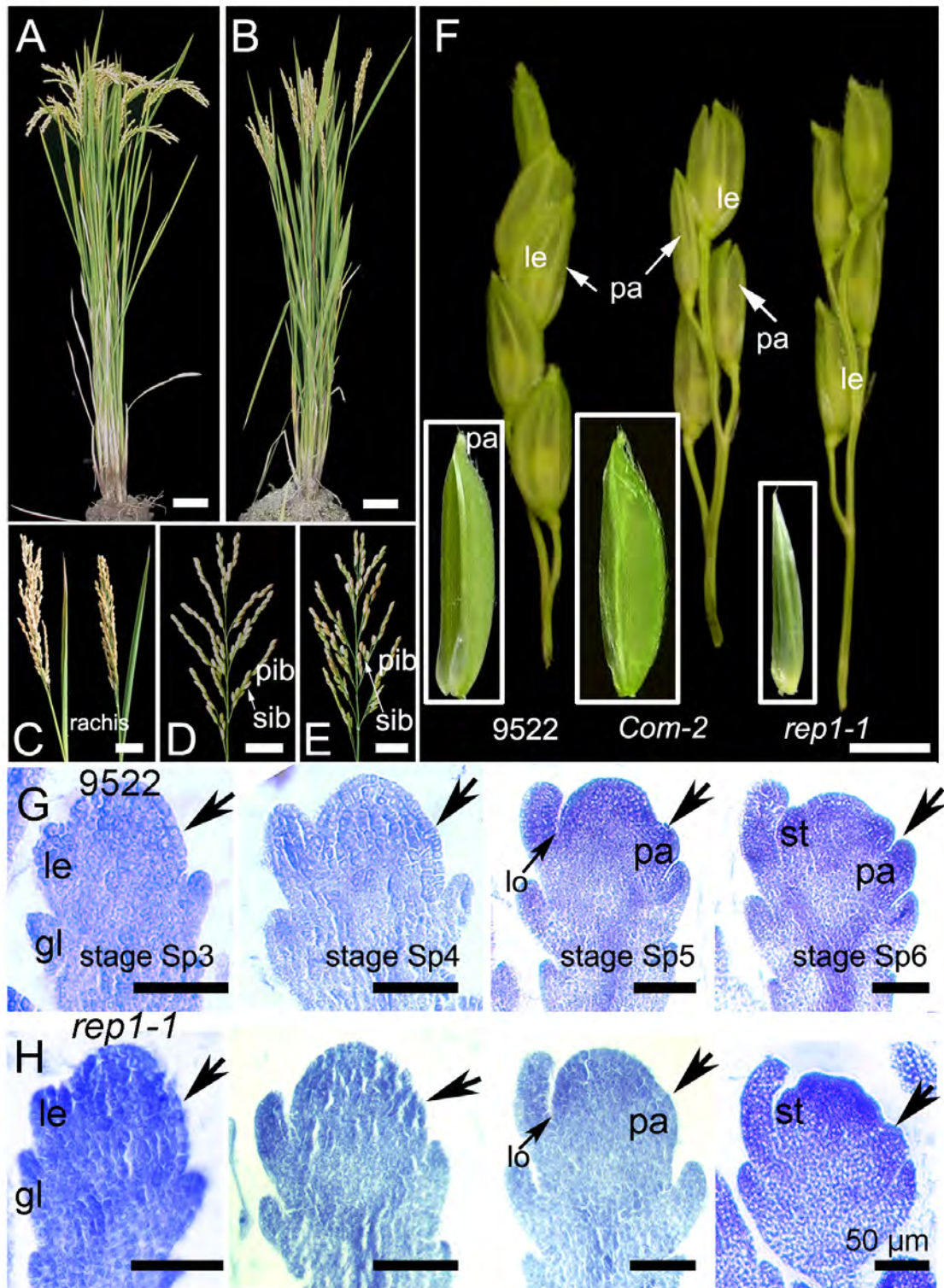


Supplemental Data

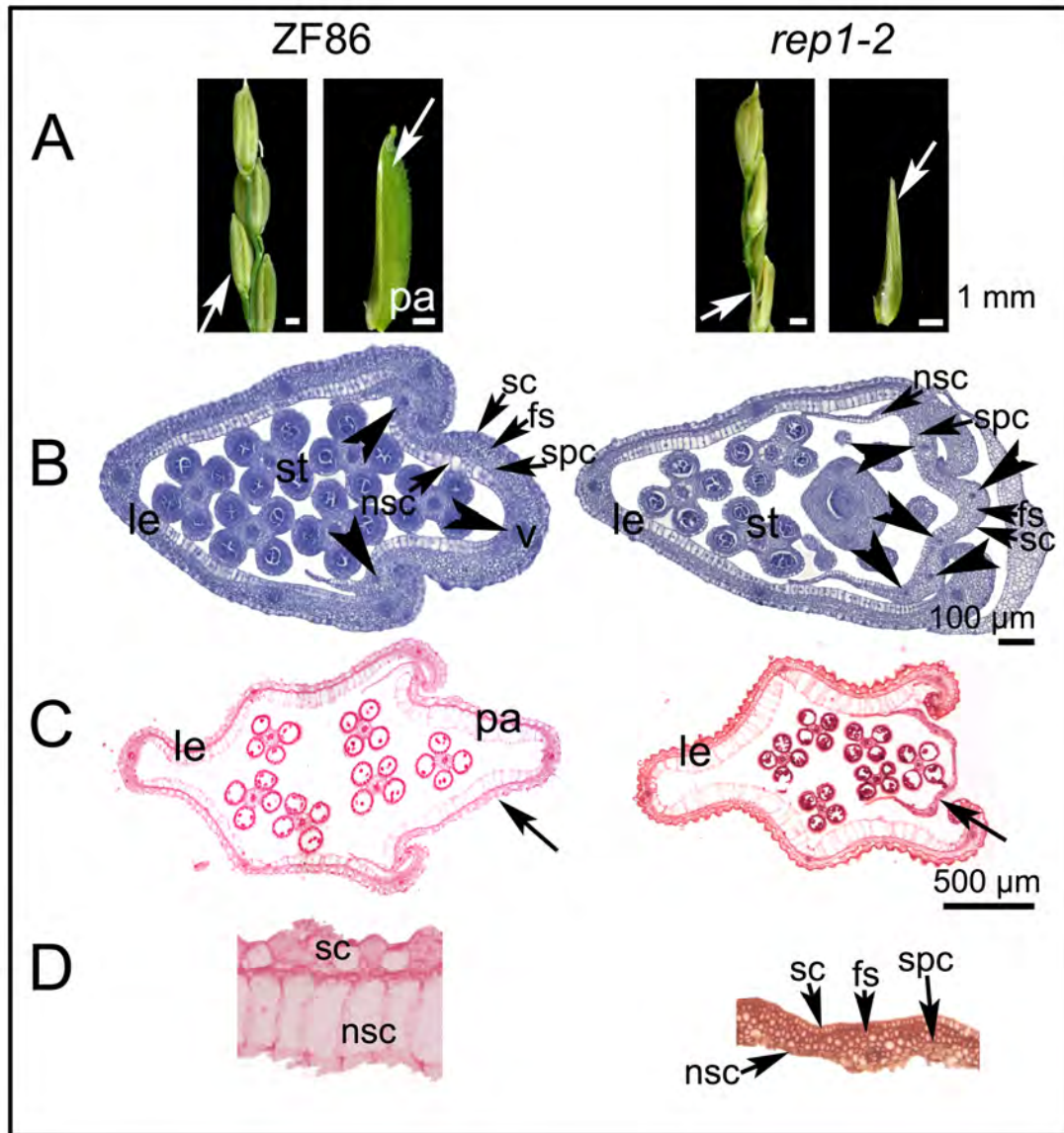


Supplemental Figure 1. Cellular phenotypes of lemma and lodicules in wt, *rep1-1* and *OEx-5* plants. (A-C): SEM (scanning electron microscope) observation of the lemmas of wt, *rep1-1* and *OEx-5*. (D-F): Lemma transverse sections of the wt, *rep1-1* and *OEx-5* transgenic plant at stage Sp 8. (G-I): Flower transverse sections of the wt, *rep1-1* and *OEx-5* transgenic plant around stage In 8. Note that the cell number and cell size have not been changed obviously in the *rep1-1* mutant and the *OEx-5* line compared to that of wt, and the lodicules grew normally in *rep1-1* and *OEx-5* plants with multiple vascular trachea elements dispersed in whole organ (arrowheads). fs: fibrous sclerenchyma. gl: empty glume. lo: lodicules. nsc: non-silicified cell. sc: silicified cell. spc: spongy parenchymatous cell. st: stamen. v: vascular bundle.

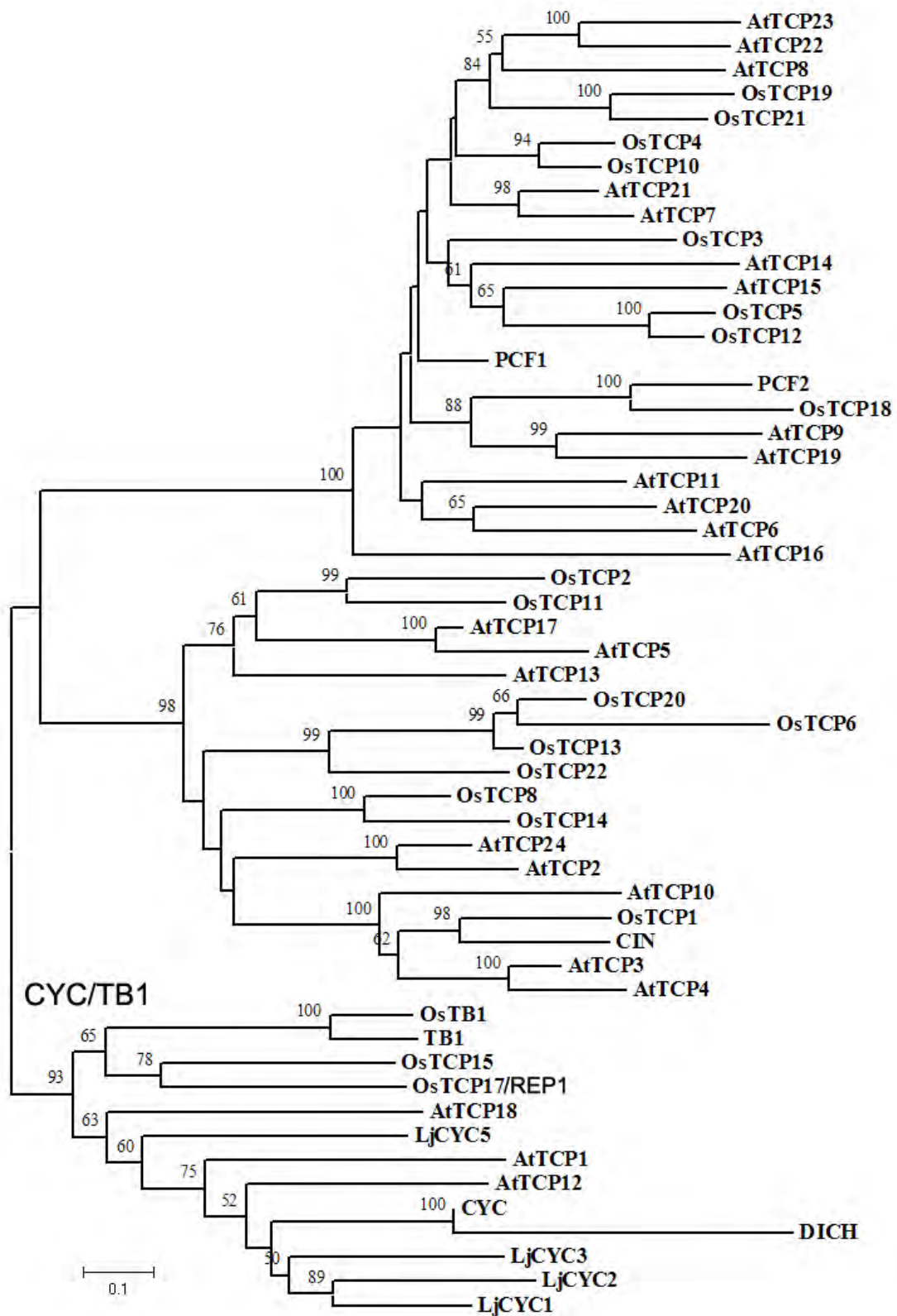


Supplemental Figure 2. Phenotypes of the *rep1-1* mutants and the complementary lines. (A) 9522 wild type plant (wt). (B) The *rep1-1* plant. (C) Inflorescence of wt (left) and *rep1-1* (right) plant. (D) Panicle of wt. (E) Panicle of the *rep1-1* plant. Note that the inflorescence develops normally in the *rep1-1* mutant plant. (F) Inflorescence of wt (left), *Com-2* transgenic plant (*REPI_{com} line-2*, middle) and the *rep1-1* mutant plant (right). Note that the *REPI_{com}* construct could complement the *rep1-1* mutant

phenotypes completely (arrows and insets). (G) Serial transverse sections of wt floret. (H) Serial transverse sections of the *rep1-1* floret. Note the development of *rep1-1* palea primordium was strongly retarded. gl: glume. le: lemma. lo: lodicule. pa: palea. pib: primary inflorescence branch. sib: secondary inflorescence branch. st: stamen. (Scale bar, 2 cm in A and B, 1 cm in C-E, 5 mm in F, 50 μ m in G and H.)

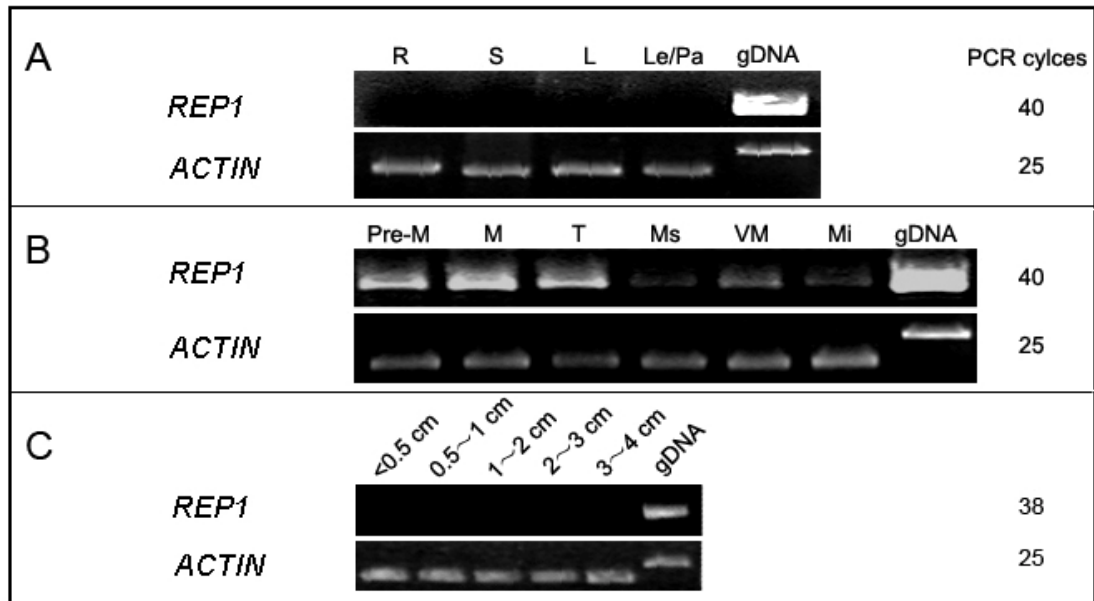


Supplemental Figure 3. Phenotypes of the *rep1-2* mutants. (A) Inflorescence and Close palea pictures of ZF86 and the *rep1-2* mutant plant. Note that development of the *rep1-2* palea was suppressed similarly as in *rep1-1* (arrows). (B) Flower transverse sections of ZF86 and the *rep1-2* plant at stage Sp 8. Note that five vascular bundles form in the *rep1-2* palea instead of three in ZF86 palea (arrowheads). (C) Flower transverse section of ZF86 and the *rep1-2* plant at stage In 8. (D) A close-up of (C) marked by the arrows. Note that the palea cell seemed smaller and under differentiated in *rep1-2* compared to that of ZF86 (arrows). fs: fibrous sclerenchyma. le: lemma. nsc: non-silicified cell. pa: palea. sc: silicified cell. spc: spongy parenchymatous cell. st: stamen. v: vascular bundle. (Scale bar, 1 mm in A, 100 μm in B, 500 μm in C.)

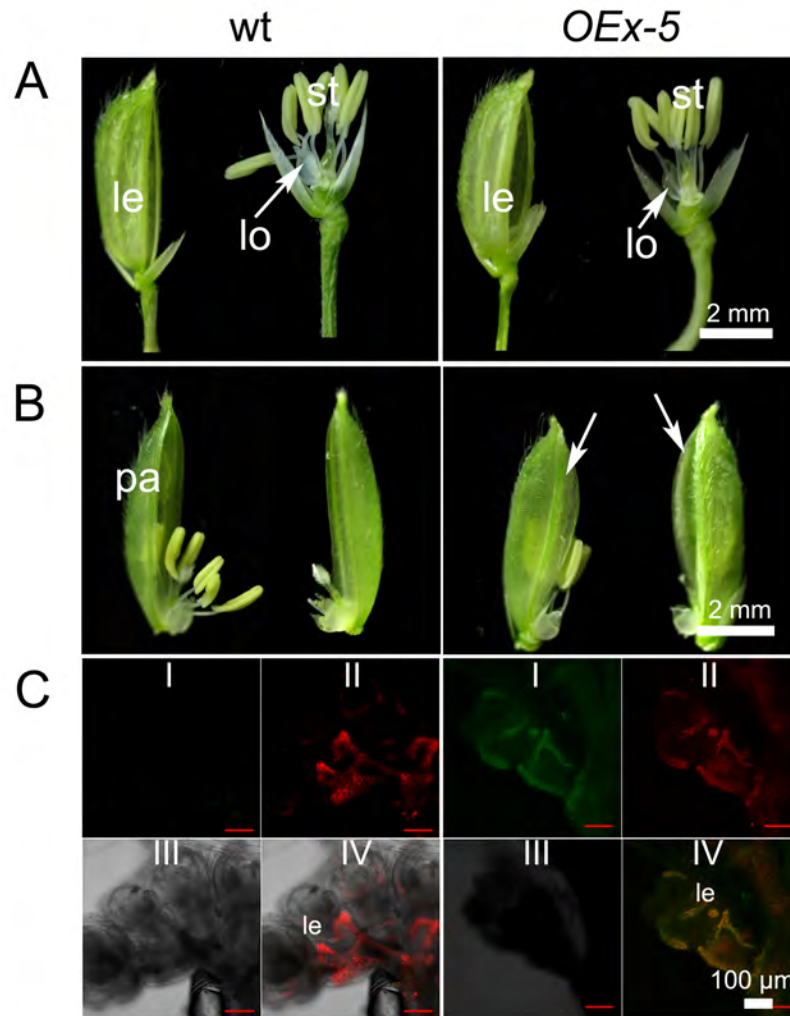


Supplemental Figure 4. Phylogenetic tree visualizing the orthology among REP1 (OsTCP17, arrow) and other TCP proteins. The TCPs are mainly from *Arabidopsis* and rice (Yao et al., 2007); CYC and DICH, *Antirrhinum*; LjCYCs, *L. japonicus* (Feng et al., 2006); PCFs, rice; TB1, maize. The bootstrap values are denoted above the nodes and bootstrap values below 50 are not shown in the phylogenetic tree.

Values denoted below the nodes indicate the bootstrap values, which are built by the maximum parsimony method. The variation rates across the amino acid positions are indicated by the length of the branch as we reported previously (Yao et al., 2007).



Supplemental Figure 5. Expression analysis of *REP1* by RT-PCR. Gene specific primers are REP1-RTF and REP1-RTR. (A) PCR in wt mature floret organs, R: root; S: shoot; L: leaf; Le/Pa: lemma/palea; gDNA: genomic DNA. (B) PCR in wt stamen, Pre-M: pre-meiosis stage stamen; M: meiosis stage stamen; T: tetrad stage stamen; Ms: microspore stage stamen; VM: vacuole stage stamen; Mi: Mitosis stage stamen. (C) PCR in the *repl-2* inflorescence. Note that the *repl-2* mutant is likely a null-allele of *REP1* gene since its expression could not be detected in the *repl-2* mutant. Therefore, the *repl-1* and *repl-2* mutants show similar defects of palea.



Supplemental Figure 6. Phenotypes of the *OEx-5* (*REP_{OEx} line-5*) transgenic plant. (A) Floret of wt and the *OEx-5* transgenic plant showing normal growth of lemma, lodicules and stamen. (B) Palea of wt and the *OEx-5* transgenic plant (same palea in two sides). Note that asymmetric over differentiation was observed in one side the *OEx-5* of palea (arrows). (C) GFP signal (*REP1::sGFP*) could be detected in the inflorescence of the *OEx-5* transgenic plant, whereas no GFP signal in wt. The 488-nm excitation filter showing GFP expression in (I). The 560-nm excitation filter showing chlorophyll autofluorescence in (II). The bright field image in (III) and (IV) is overlay-image. Note that the *REP1* ectopically expressed in lemma and palea tissue during the early stage in the *OEx-5* plant. le: lemma; lo: lodicule; pa: palea; st: stamen. (Scale bar, 2 mm in A and B, 100 μ m in C.)

Primers list:

REP1-CF1: 5-CACCAAAGGTACCCGGTGATGATGAGGCGAAATGACT-3;

REP1-CR1: 5-ATATTGCATACCGTCCAAGAAATCGCCGT-3;

REP1-AF: 5-CACCATGCAGCAGCAGCTGGATCAGCA-3;

REP1IF: 5-GAATTCGACCCCTCCTCCTCCTC-3;

REP1IR: 5-AAGCTTCTAATATTGCATACCGTCCAAGA-3;

E61552: 5-GCTGCTTAGAATTTCCGGTC-3, and

5-AAAGGGCACGGGATGACAAG-3;

CH910: 5-AGTAACGACGTAAATATGTGCG-3, and

5-AATAAAATCGATGGCCTCTAAA-3;

CH911: 5-TTGCTTCCGTCCGCTTCT-3, and 5-CTTCCTTCCCGCCTTCG-3;

5'RACE-A1: 5-ATGCTGCTGCTGCTGCTGC-3;

3'RACE-S1: 5-TTCAACTCCGAGACGCTGG-3;

5'RACE-A2: 5-GGTGGTCGTAGGGTTTGGAG-3;

3'RACE-S2: 5-AGAGGTGGTAGATCGGCG-3;

REP1-RTF: 5-GGATCAGGGAAAGGAGACG-3;

REP1-RTR: 5-GAAATGCTGGGCAGAGTAGC-3;

Supplemental References

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