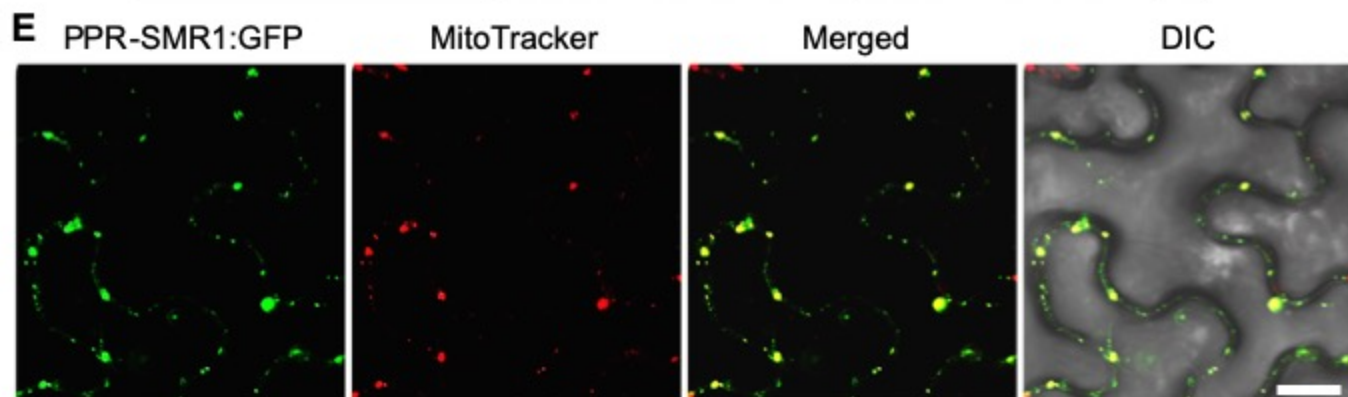
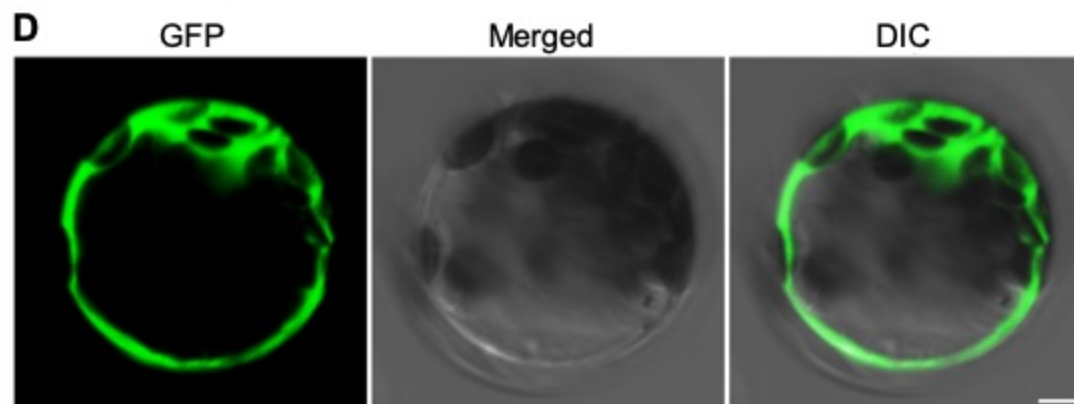
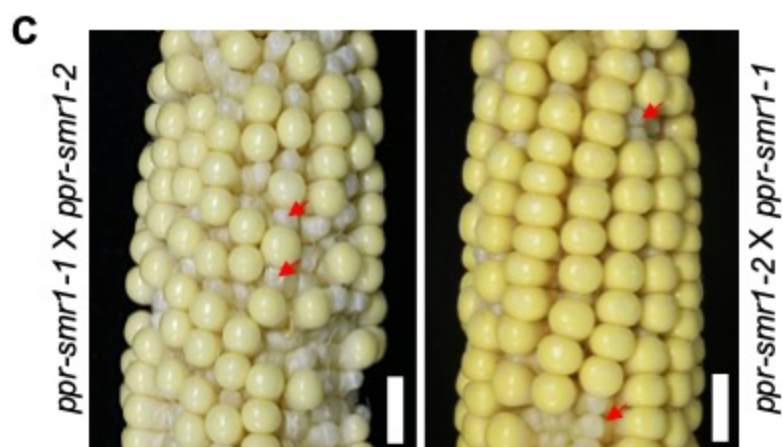
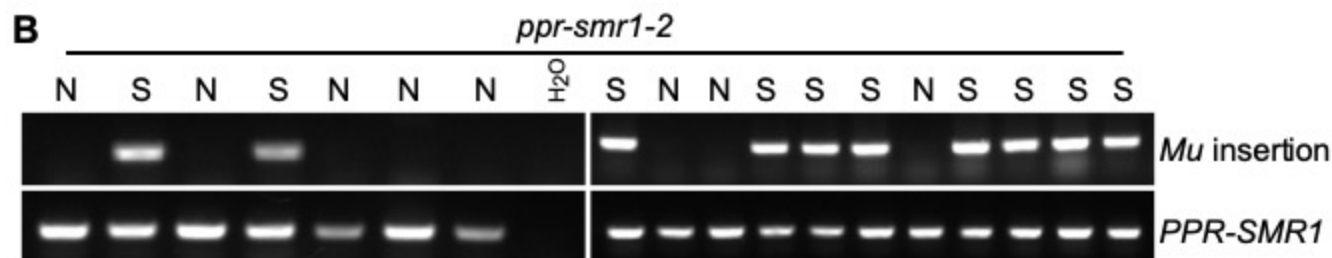
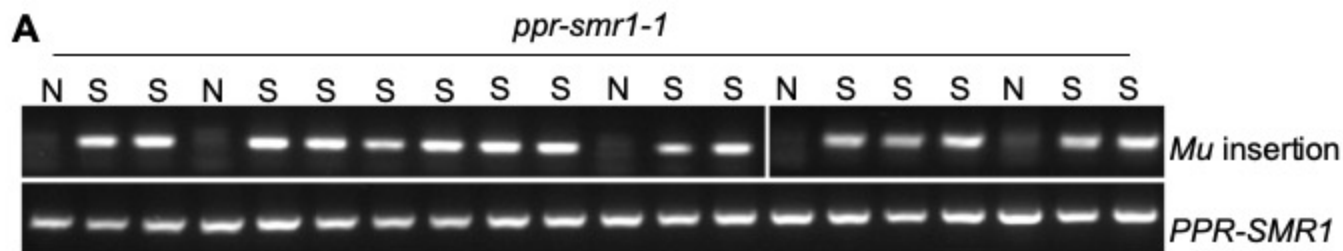
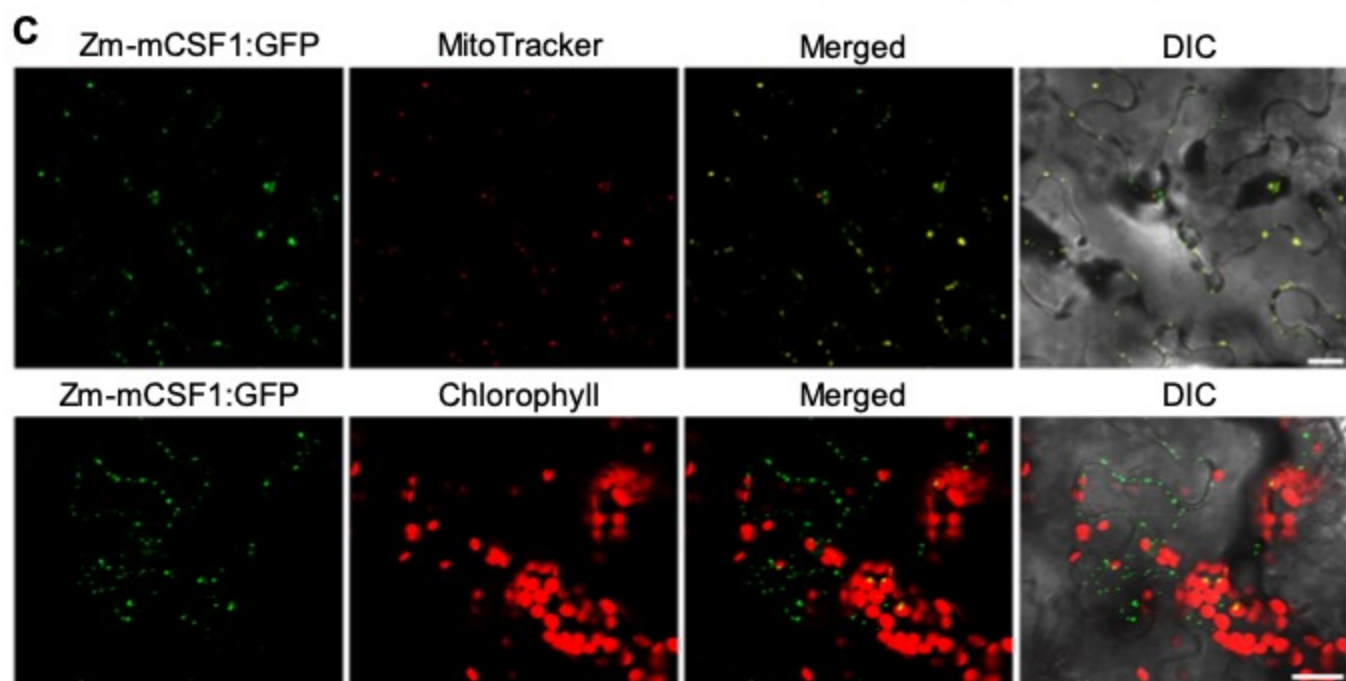
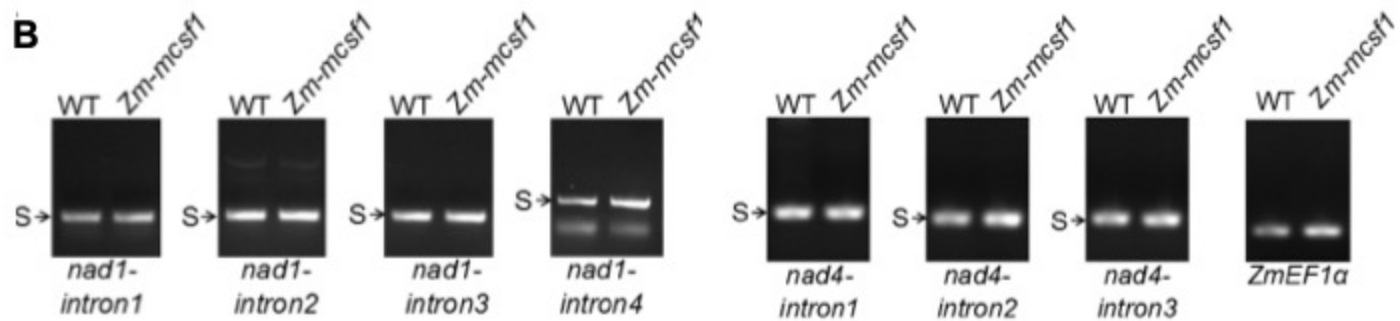
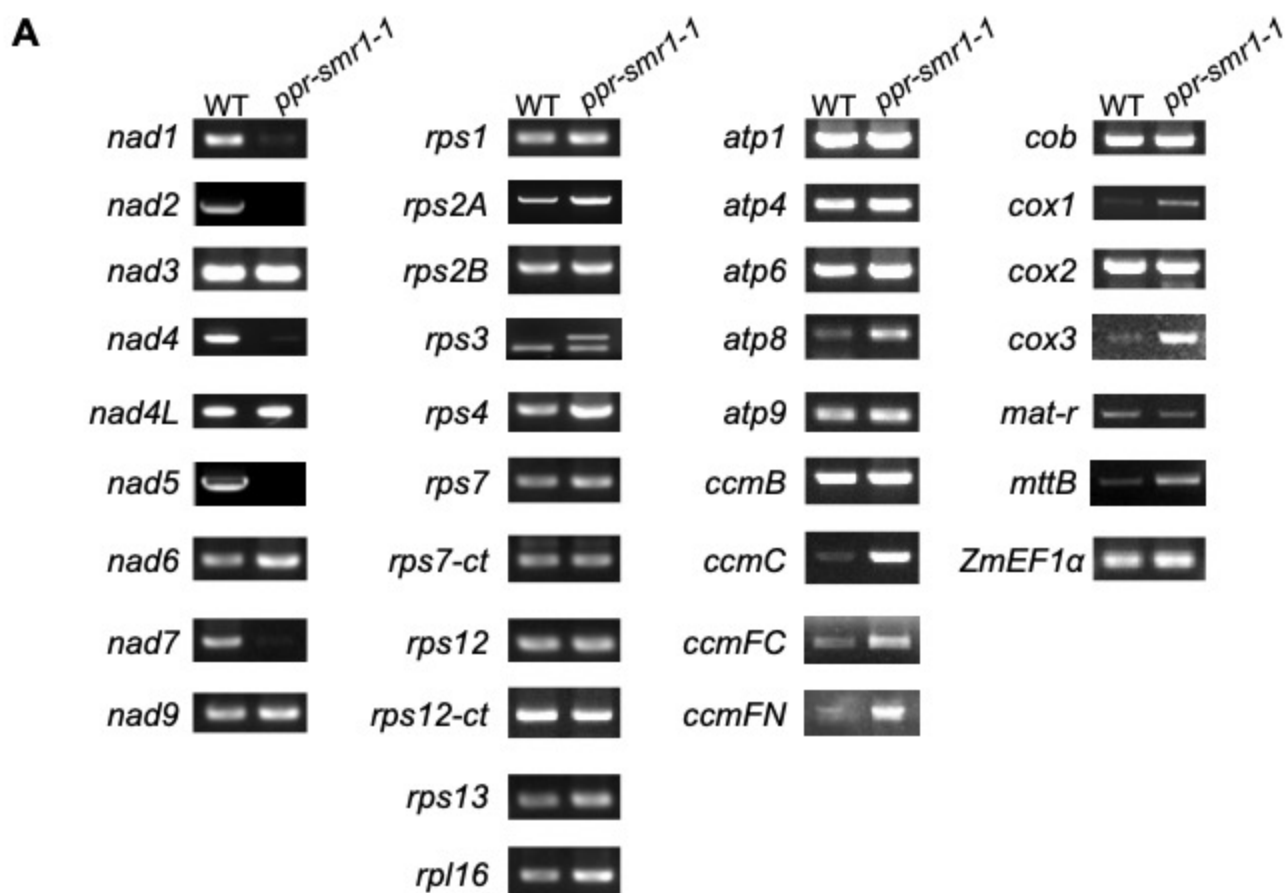


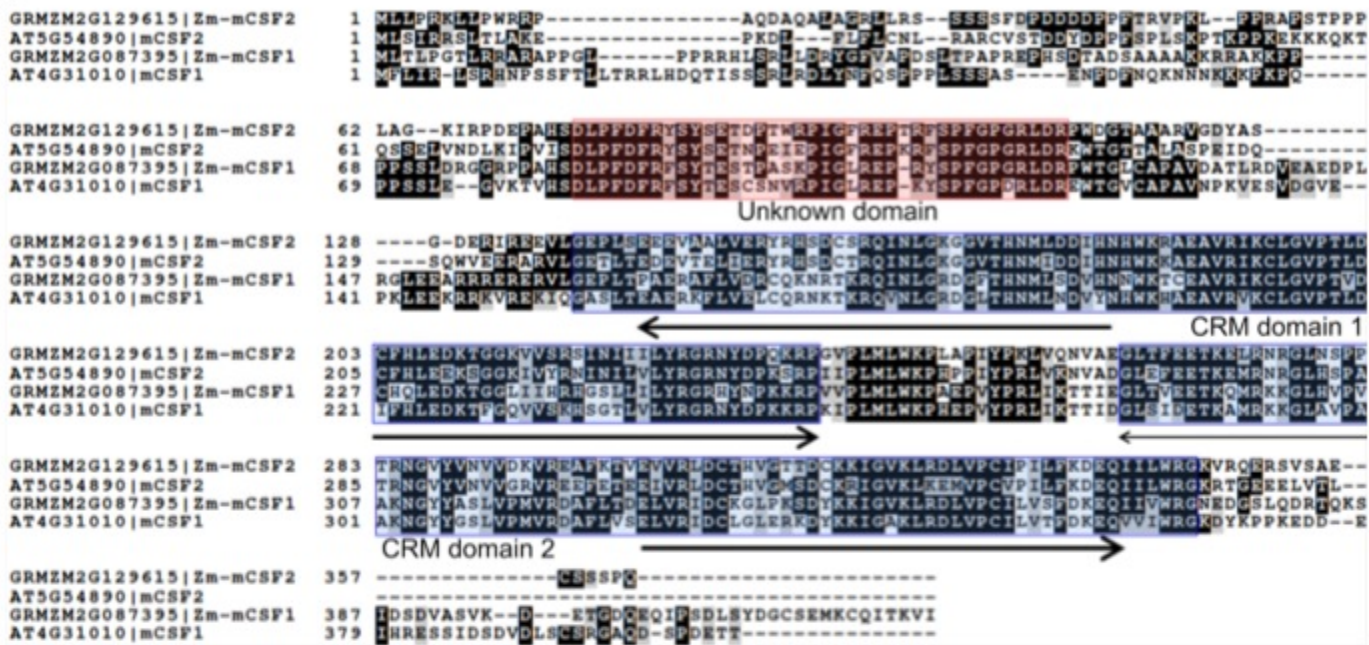
**Figure S1.** PPR-SMR1 and its homologs in Arabidopsis, rice, and sorghum. (A) Phylogenetic analysis of PPR-SMR proteins. (B) Protein sequence alignment of PPR-SMR1 and its Arabidopsis orthologue EMB2217. PPR-SMR1 contains 12 PPR domains and a SMR domain. (C) Multiple sequence alignment of PPR-SMR1 and its homologs in Arabidopsis, rice, and sorghum.



**Figure S2.** Co-segregation and allelism test of *ppr-smr1* alleles and *emp* phenotype. (A) Selfed heterozygous *ppr-smr1-1* ears harbored segregated *emp*. (B) Selfed heterozygous *ppr-smr1-2* ears harbored segregated *emp*. S, segregation; N, non-segregation. (C) reciprocal crosses between *ppr-smr1-1* and *ppr-smr1-2* produced ears segregating empty pericarp kernels (red arrows) at a 1:3 ratio (*emp*:WT). (D) Non-targeted GFP protein signal in mesophyll protoplast of Arabidopsis. (E) Localization of PPR-SMR1 protein. *N. benthamiana* leaves were infiltrated with *Agrobacterium* carrying the PPR-SMR1:GFP construct, mitochondria were stained by MitoTracker. Fluorescence was imaged by confocal microscopy. Bars = 1 cm in (C), 5  $\mu$ m in (D) and 20  $\mu$ m in (E).



**Figure S3.** Altered expressions of mitochondrial transcripts in *ppr-smr1* and *Zm-mcsf1* endosperm. (A) Expression levels of 35 mitochondrial genes in *ppr-smr1-1* endosperm. (B) Normally spliced introns of *nad1* and *nad4* in *Zm-mcsf1* endosperm. (C) Localization of Zm-mCSF1 protein. *N. benthamiana* leaves are infiltrated with *Agrobacterium* carrying the Zm-mCSF1:GFP construct, mitochondria are stained by MitoTracker in the upper panel. In the lower panel, chloroplasts are marked by autofluorescence of chlorophyll. Fluorescence is imaged by confocal microscopy. Fluorescence was imaged by confocal microscopy. Bars = 20  $\mu\text{m}$  in (C).

**A****B****C**

**Figure S4.** mCSF1 and mCSF2 of Arabidopsis and maize and allelism test of *Zm-mcsf1* alleles. (A) Multiple sequence alignment of proteins Zm-mCSF1, Zm-mCSF2, mCSF1, and mCSF2. Blue blocks indicate CRM domains; red block indicates unknown domain. (B) Longitudinal section of mature WT and *Zm-mcsf1-1* kernels. (C) Reciprocal cross between *Zm-mcsf1-1* and *Zm-mcsf1-2* produced ears segregating *empty pericarp* kernels (red arrows) at a 1:3 ratio (*emp*:WT). Bars = 2 mm in (B), and 1 cm in (C).