

Supplementary materials

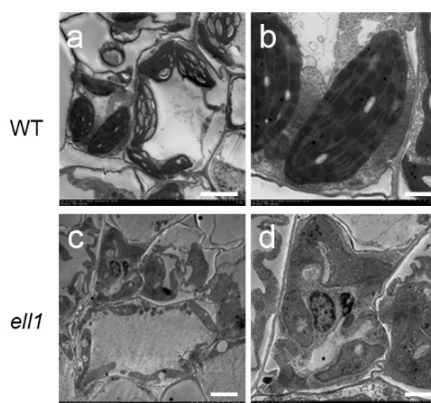


Figure S1. Electron micrographs of chloroplasts from the wild type and *ell1* mutant. Chloroplasts from six-day-old wild-type (WT) and *ell1* plants observed by transmission electron microscopy. Magnified views (for a and d, bars = 5 μ m; for b and e, bars = 1 μ m) are shown on the right.

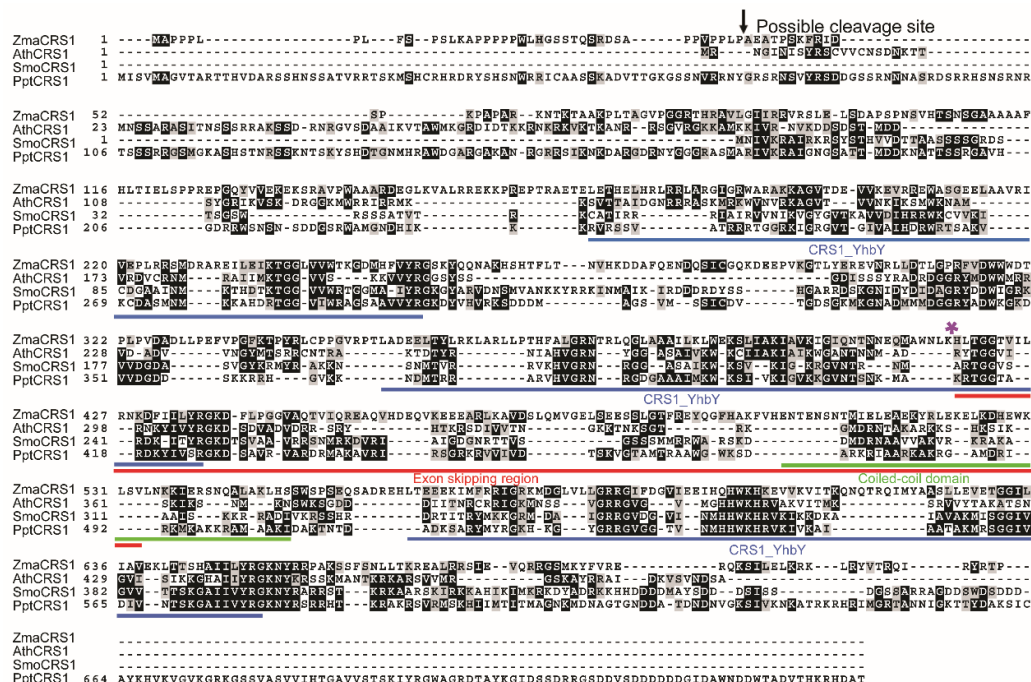


Figure S2. Sequence alignment of CRS1 proteins. Multiple sequence alignment of CRS1 and several homologs. Sequences of CRS1 were obtained from GenBank (<http://www.ncbi.nlm.nih.gov/>) and aligned with ClustalW2. The possible transit peptide cleavage site of CRS1 was predicted with the CBS Prediction Servers (<http://www.cbs.dtu.dk/services/>), which is indicated by a black arrow above the sequence. Identical amino acids are shown with white letters on a black background, and similar amino acids are indicated with black letters on a gray background. The CRS1_YhbY domains are shown with blue lines. The green line indicates the coiled-coil domain. The red line indicates the skipped exon region. Asterisk indicates the predicted alternative cleavage site [16]. ZmaCRS1 (*Zea mays*, NP_001105008.1), AtCRS1 (*Arabidopsis thaliana*, NP_197122.2), SmoCRS1 (*Selaginella moellendorffii*, XP_024545101.1), PptCRS1 (*Physcomitrella patens*, XP_024392253.1).

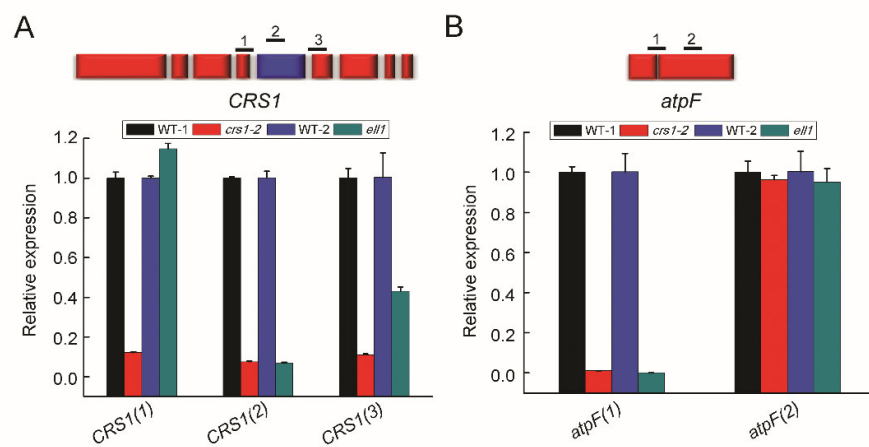


Figure S3. Expression of the incorrectly spliced CRS1 is not affected in *ell1* mutant. Relative expression analysis of *CRS1* and *atpF*. Relative expression of *CRS1* and *atpF* in *crs1-2* and *ell1* mutants was determined by quantitative real-time RT-PCR. Maize ubiquitin was used as control. Means $\pm$ SD (n = 3). Color boxes indicate the exons of *CRS1* or *atpF*, the blue box indicates the skipped exon. Probes used for qRT-PCR are shown above the color boxes.