

Figure S1. Topology and binding site prediction of PPR596 protein. **(A)** The amino acid sequence of the PPR596 protein (At1g80270) is shown. Mitochondrial-targeting peptides are underlined and highlighted in red, with the cleavage site of the mitochondrial-targeted peptide indicated by a red arrow. The PPR motifs (in blue boxes) were predicted using the method described by Yan et al. (2019). Underlined letters within each motif indicate the 5th and 35th positions. **(B)** Predicted PPR codes were used to determine the RNA binding site of PPR596 protein. These results suggest that the PPR codes of PPR596 are not conserved.

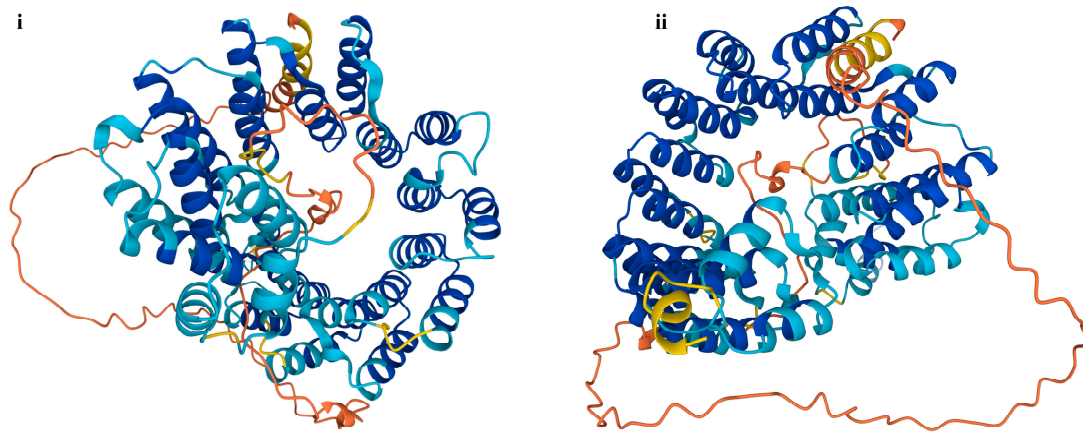
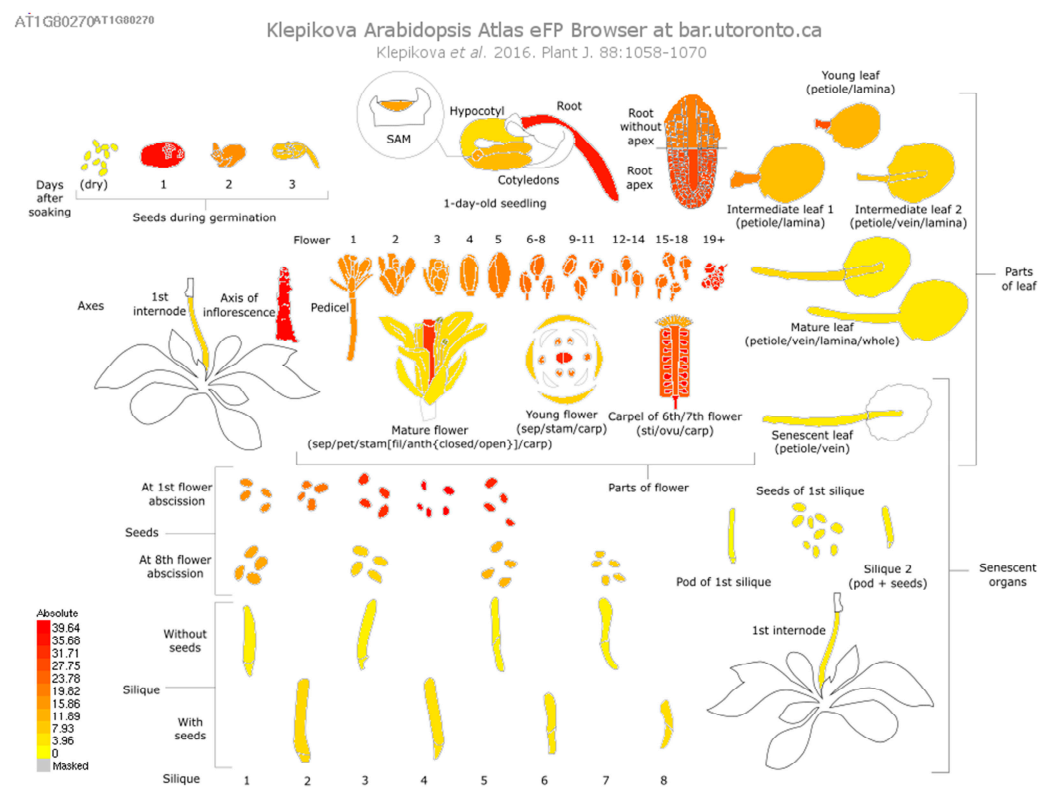


Figure S2. PPR596 protein structure. The ribbon structures (i and ii) of PPR596 were generated using the Alfa Fold server.



Data from A high resolution map of the Arabidopsis thaliana developmental transcriptome based on RNA-seq profiling; Klepikova et al., 2016, Plant J. 88:1058-1070. Total RNA was extracted with RNeasy Plant Kit and Illumina cDNA libraries were generated using the respective manufacturer's protocols. cDNA was then sequenced using Illumina HiSeq2000 with a 50bp read length. The read data are publicly available in NCBI's Sequence Read Archive under the BioProject ID 314076 (accession: PRJNA314076). Reads were aligned to the reference TAIR10 genome (Lamesch et al., 2012) using Tophat (Trapnell et al., 2009). Default Tophat settings and job resource parameters were used, with read groups unspecified. Reads per gene were counted with an in-house Python script using functions from the HTSeq package (Anders et al., 2015). Reads were filtered so that only uninterrupted reads corresponding to a region within exactly one gene were used for RPKM calculation. If a gene's expression level is not displayed, this indicates the reads for this gene did not pass the filtering criteria. RPKM values were compiled using an in-house R script.

Figure S3. Expression pattern of PPR596 during *Arabidopsis* development. The expression pattern of PPR596 was analyzed using the publicly available database 'The Arabidopsis Information Resource' (TAIR; <http://www.arabidopsis.org>).

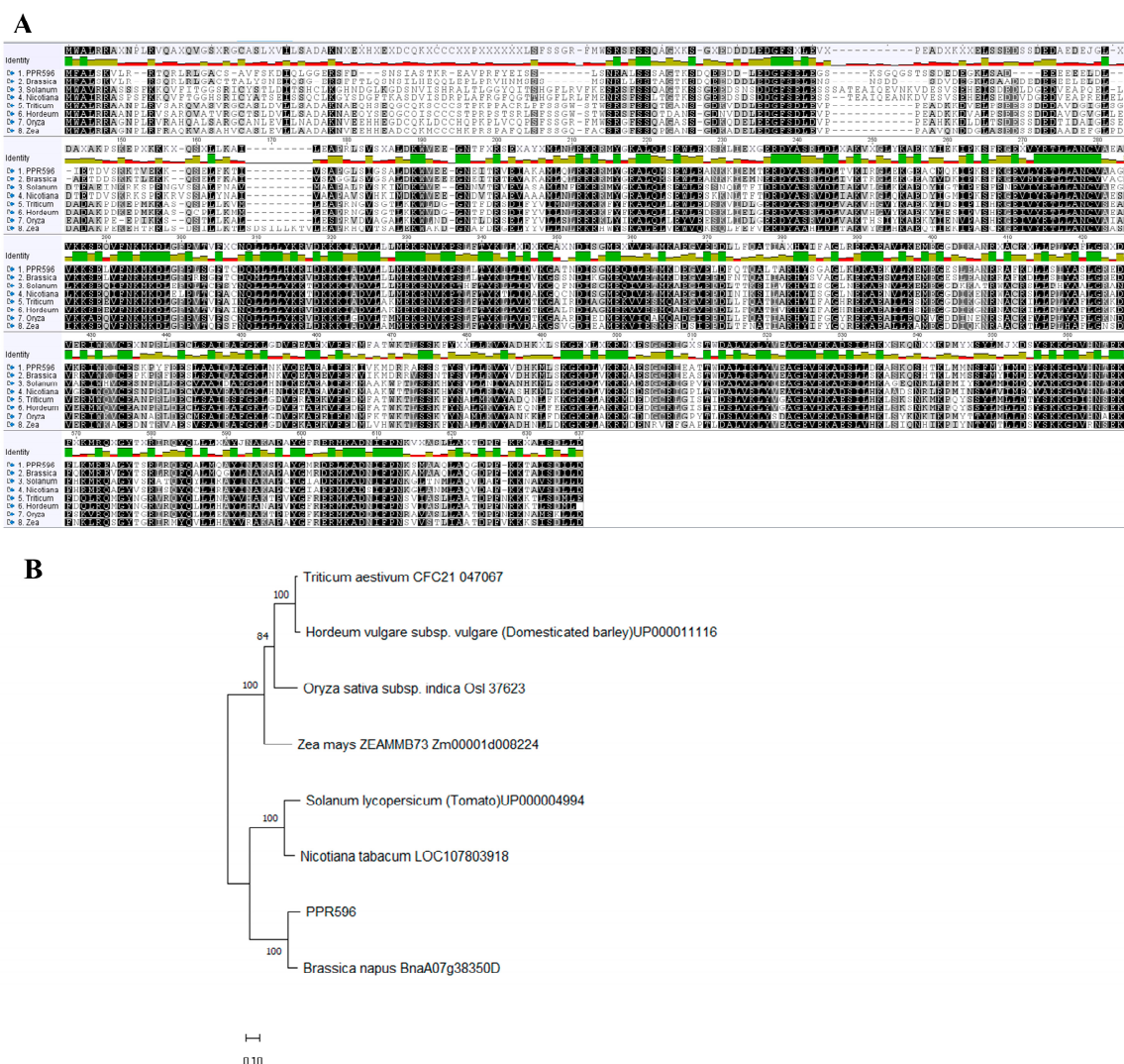


Figure S4. Phylogenetic analysis of PPR596 homologs in plants. Homologous protein sequences of PPR596 were retrieved from the UniProt database using the Basic Local Alignment Search Tool (BLAST). (A) An Alignment of homologous PPR596 proteins from various plant species, including *Arabidopsis thaliana* (At1g80270), *Brassica napus* (BnaA07g38350D), *Nicotiana tabacum* (LOC107803918), *Oryza sativa* subsp. *indica* (OsI_37623), *Zea mays* (ZEAMMB73_Zm00001d008224), *Triticum aestivum* (CFC21_047067), *Hordeum vulgare* subsp. *vulgare* (JUP000011116), and *Solanum lycopersicum* (JUP000004994), was constructed with Geneious 9.2.2 software. Unconserved residues are shaded in the dark. (B) A phylogenetic tree was constructed using MEGA11 with the Maximum Likelihood method and JTT matrix-based model. The analysis was performed using 1000 replicates.