Descriptions of Additional Supplementary Files

Supplementary Data 1. Candidate Proteins with Potential Roles in Chloroplast Lipid Transport or Membrane Contact Sites. Candidate proteins investigated for chloroplast localization and possible involvement in lipid transfer or membrane contact sites. AGI denotes the Arabidopsis Gene Identifier. Name provides a brief description based on TAIR or recent literature. Abbrev. is the abbreviation used to reference the protein throughout the text. Loc. indicates supporting evidence for plastid localization, including: S (SUBA5 prediction), T (TargetP prediction), P (identification in plastid proteomes such as PPDB), and C (prediction from ChloroP). M denotes whether homologs have been identified at membrane contact sites (y = yes). L indicates whether homologs are known to bind or transport lipids (y = yes). References supporting the functional annotations in the M and L columns are cited.

Supplementary Data 2. Statistical Summary of CellProfiler Fluorescence Colocalization Analysis.
Welch's ANOVA with Dunnett's T3 multiple comparisons test results for fluorescent protein signal colocalization across candidate genes. Comparisons include full, partial, and no overlap with chlorophyll autofluorescence.

Supplementary Data 3. Proteins Identified by LC-MS/MS across Chloroplast Membrane Fractions.
List of all proteins detected in the proteomic analysis with corresponding Arabidopsis gene identifiers, peptide counts, sequence coverage, and confidence scores.

Supplementary Data 4. Detected Protein Normalized Abundance Values, Fraction Enrichment, and Subcellular Localization Annotation.
LFQ intensity values for each protein across biological replicates of inner envelope (IE), heavy inner envelope (heavyIE), thylakoid (Thy), and light thylakoid (lightThy) membrane fractions. Proteins showing significant enrichment in comparisons between membrane fractions are indicated, as is direction of abundance when not significant, as "more". Includes fold changes, p-values, and enrichment direction. Subcellular and suborganellar localization of all identified proteins based on curated annotations from SUBA, PPDB, and literature sources.

Supplementary Data 5. Functional Enrichment.
Enrichment analysis was performed using Metascape against the total list of identified proteins. Representative terms from the top enrichment clusters are shown. Gene symbols correspond to the Arabidopsis homologs of the identified pea proteins.

Supplementary Data 6. Proteins with Homology to Membrane Contact Site (MCS) Components.
Proteins enriched in each fraction with sequence similarity to known MCS-associated proteins including name, UniProt ID, and MCS location. MCSdb p-value and MCSdb Bitscore' indicate the statistical significance and quality of the sequence alignment, respectiely, between the *A. thaliana* homolog and the top MCSdb hit.

Supplementary Data 7. Statistical Summary of Maximum Quantum Yield. Statistical significance for maximum quantum yield (F_v/F_m) in wildtype (WT), *tvpfp*, and *pmfp* 21-day-old Arabidopsis rosettes was determined by ordinary one-way ANOVA followed by Dunnett's multiple comparisons test.

Supplementary Data 8. Statistical Summary of Photosynthetic Analysis. Statistical significance for the hyperbolic fits for NPQ and ΦPSII in wildtype (WT), *tvpfp*, and *pmfp* 21-day-old Arabidopsis rosettes was determined by ordinary one-way ANOVA followed by Dunnett's multiple comparisons test.

Supplementary Data 9. Statistical Summary of Pigment Extraction. Statistical significance for pigment extractions in wildtype (WT), *tvpfp*, and *pmfp* 21-day-old Arabidopsis rosettes was determined by ordinary one-way ANOVA followed by Dunnett's multiple comparisons test.

Supplementary Data 10. Perturbation of Chloroplast Ultrastructure by Loss of TVPFP or PMFP. Ultrastructural measurements from transmission electron micrographs of palisade mesophyll chloroplasts in wildtype (WT), *tvpfp*, and *pmfp* seedlings grown under constant light. The number of chloroplasts is summarized by the sample size N. TIES were defined as discrete regions where the thylakoid was continuously less than or equal to 50 nm from the inner envelope membrane. Statistical significance was determined by ordinary one-way ANOVA followed by Dunnett's multiple comparisons test. Chlp, chloroplast; TIES, thylakoid-inner envelope contact site; IMD, intermembrane distance.