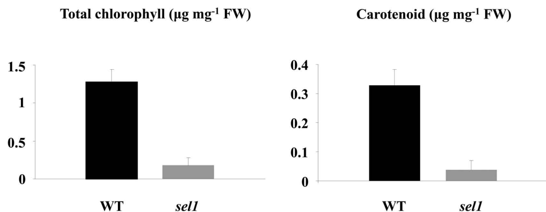
Figure S1

Supplementary Figure 1. Sucrose-dependent growth of *sel1-1*.

14-day-old seedlings on MS agar medium with or without sucrose (1%) under long day condition.

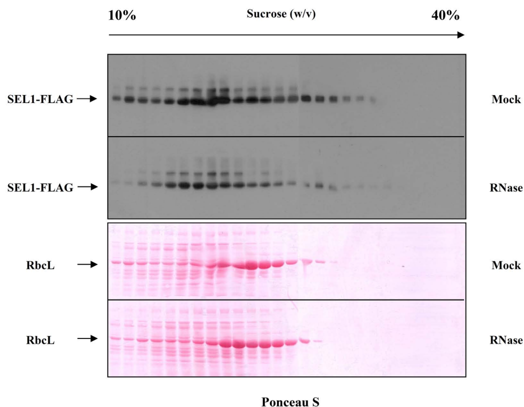
Figure S2



Supplementary Figure 2. The content of pigments in the wild-type (WT) and *sel1* mutant.

Seedlings were grown on MS agar medium for 4 days under long-day conditions. Mean values obtained from three independent experiments (n=30) are based on fresh weight.

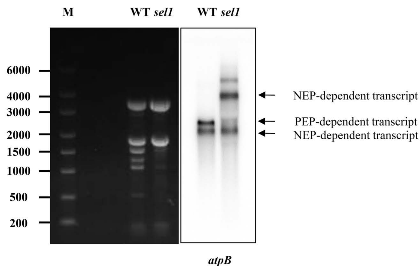
Figure S3



Supplementary Figure 3. Sucrose gradient sedimentation analysis of SEL1-containing particles in chloroplast stroma.

Stromal extract was fractionated by sedimentation through a sucrose gradient as described previously (Williams and Barkan, 2003). An equal volume of each gradient fraction was analyzed by western blot analysis with antibody to FLAG. The same blots stained with Ponceau S show sample loading and the abundance of RbcL.

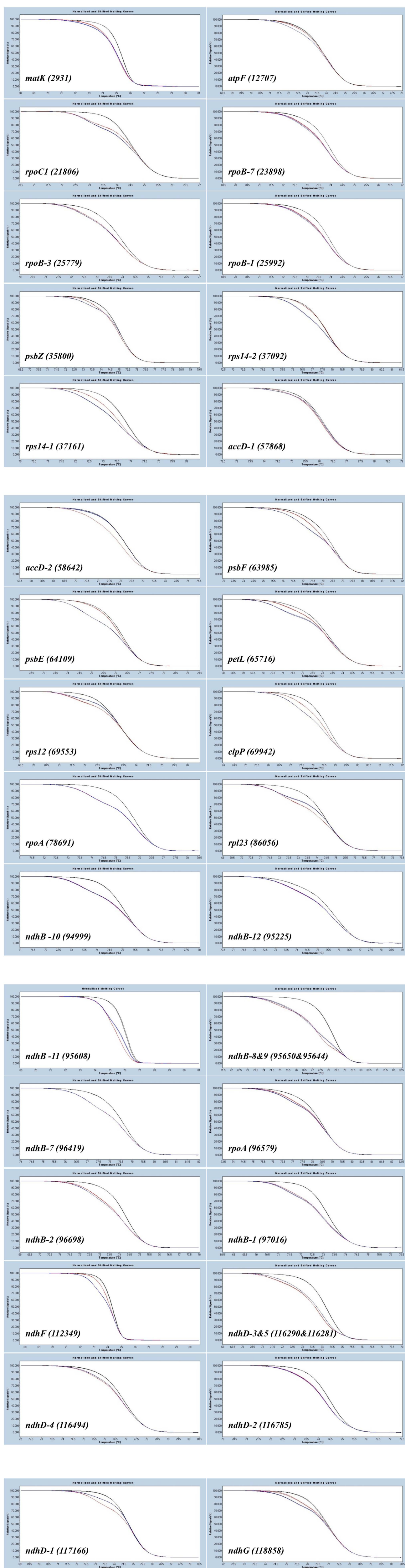
Figure S4



Supplementary Figure 4. Analysis of the *atpB* gene in the *sel1* mutant.

Northern blot analysis for the transcript accumulation and pattern of *atpB* gene in *sel1* mutant. 5 μg of total RNA was isolated from 7-day-old seedlings and analyzed by hybridization to probe for *atpB* gene. The size marker (M) is a RNA ladder and ethidium bromide (EtBr) staining is shown for loading control.

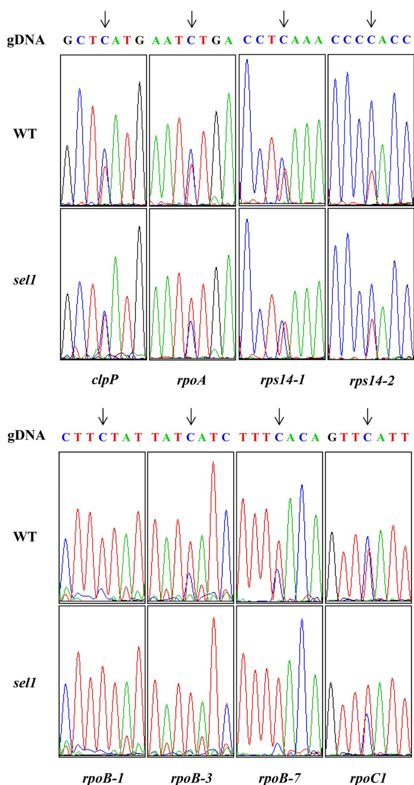
Figure S5



Supplementary Figure 5. High resolution melting (HRM) screening of *sel1* mutant.

High resolution melting analysis was performed as described previously (Chateigner-Boutin and Small, 2007) with the exception that the melting curves of genomic DNA from the wild type was compared to those of cDNA from the wild type and *sel1* mutant. Since RNA editing results in a single nucleotide change between genomic DNA and the corresponding RNA, melting curve of cDNA which contains RNA editing site is different from that of genomic DNA. If RNA editing does not occur in the mutant, the melting curve of cDNA is identical to that of genomic DNA. Black line, genomic DNA of wild type; Red line, cDNA of wild type; Blue line, cDNA of *sel1* mutant.

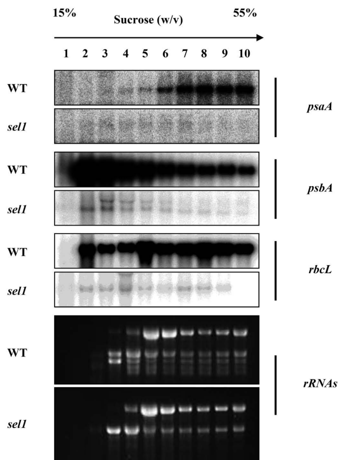
Figure S6



Supplementary Figure 6. *sel1* mutant shows altered RNA editing of plastid transcripts.

Sequence analysis for the plastid transcripts from the wild-type (WT) and *sel1* mutant. Nucleotide sequences including the RNA editing sites are shown as chromatograms. Editing sites are indicated by arrows pointing to the corresponding peaks.

Figure S7

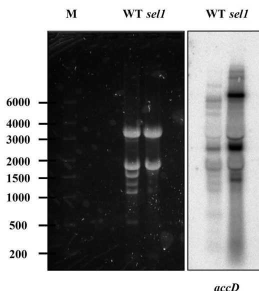


Supplementary Figure 7. Analysis of polysome association of *psaA*, *psbA*, and *rbcL* mRNAs in the wild-type (WT) and *sel1* mutant.

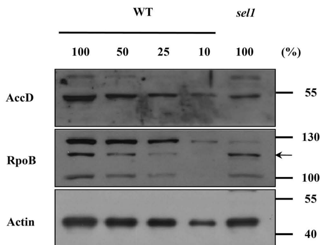
Association of photosynthesis-related RNAs with polysomes in wild-type (WT) and *sel1* mutant. 10 fractions of equal volume were collected from the top to the bottom of the sucrose gradient and equal proportions of RNA purified from each fraction were analyzed by Northern blot analysis. Ethidium bromide (EtBr) stained gel is shown for loading control.

Figure S8

A



B



Supplementary Figure 8. Analysis of *accD* gene in the *sel1* mutant.

(a) Northern blot analysis for the transcript accumulation and pattern of *accD* gene in *sel1* mutant. 5 µg of total RNA was isolated from 7-day-old seedlings and analyzed by hybridization to probe for *accD* gene. The size marker (M) is a RNA ladder and ethidium bromide (EtBr) staining is shown for loading control.

(b) Western blot analysis of the accumulation of AccD and RpoB proteins in *sel1* mutant. Total protein (10 µg or the indicated dilution of the wild-type sample) from 7-day-old-seedlings were loaded per lane. Actin was used as a loading control. Arrow indicates the approximate position of RpoB protein.