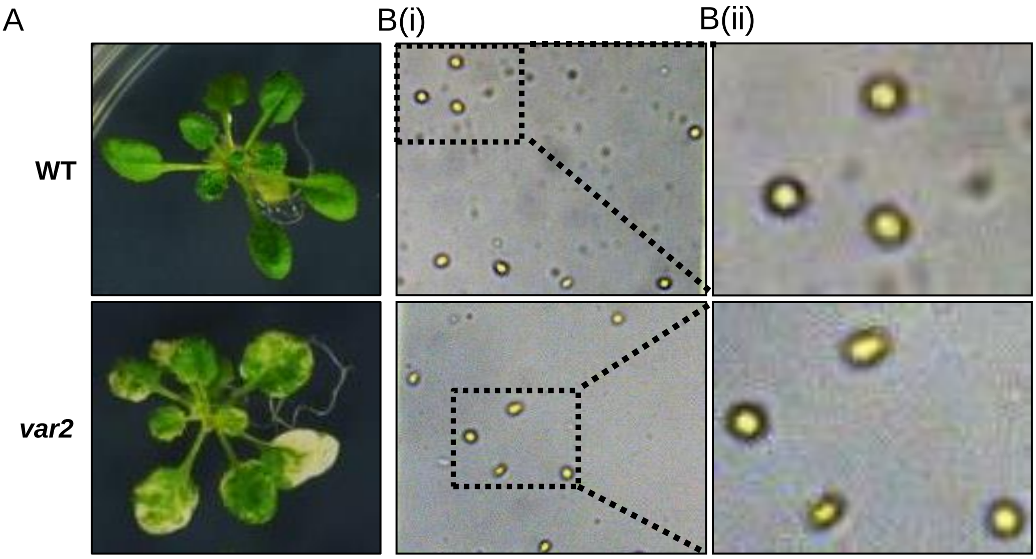
Supplementary Figure S1



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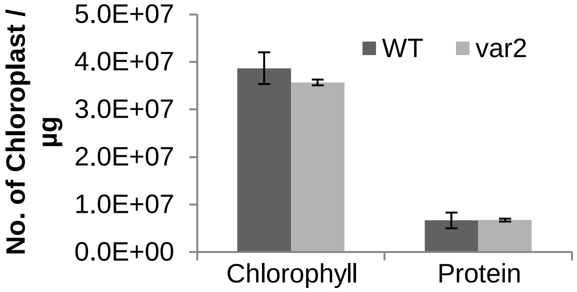
Sample	WT	*var2*
Protein(µg)/ Chlorophyll(µg)	5.8 ± 0.35	5.0 ± 0.2
No. of chloroplast/ Chlorophyll (µg)	3.87×10^7	3.68×10^7
No. of chloroplast/ Protein (µg)	6.67×10^6	6.73×10^6



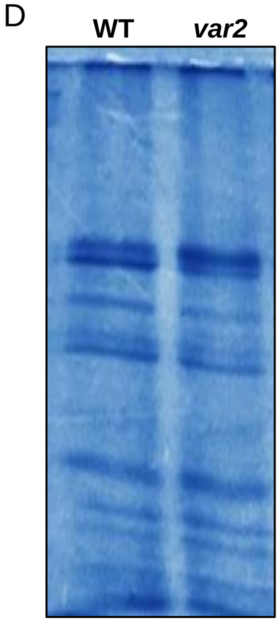


Fig. S1. The green sectors of *var2* are almost similar to WT under low light conditions. (A) Plant phenotype of 3-week-old plants used for chloroplast isolation. (B) Integrity of the isolated chloroplasts. [B(i)] Chloroplasts were observed and counted under Phase Contrast microscope using a 10X optical lens (Leica Microsystems). [B(ii)] Enlarged view. (C) Correlation between amounts of chlorophyll and protein chloroplast number. Chloroplast number with respect to protein amounts were consistent in WT and *var2*. (D) SDS-PAGE analysis of proteins isolated from intact chloroplasts. Similar pattern and abundance of major proteins reconfirmed the consistency between protein amounts in WT and *var2*. Equal amounts (20µg) of total chloroplast proteins were loaded for each genotype.

Supplementary Figure S2

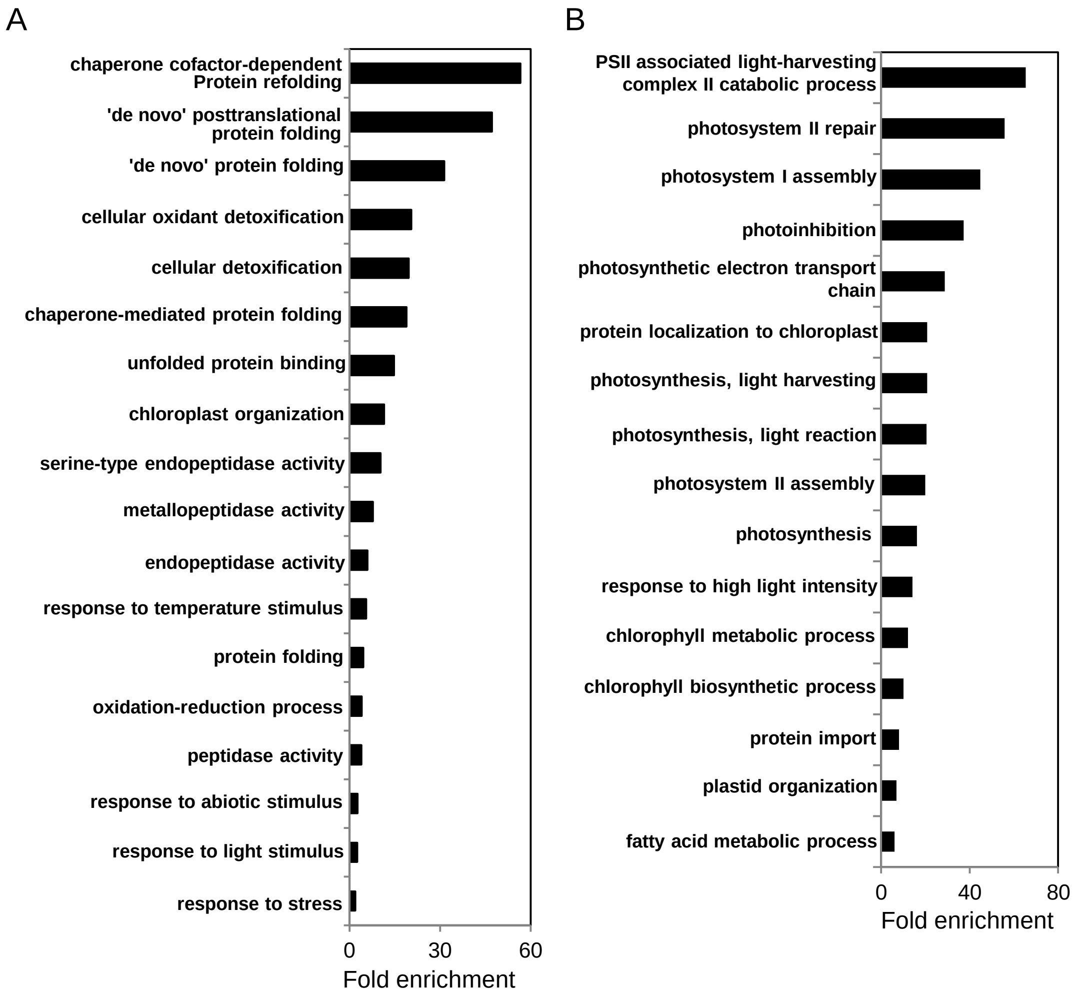


Fig. S2. GO analysis revealed an increased accumulation of PQC-related proteins while reduction in the photosynthesis-related proteins in *var2*. (A) Proteins highly accumulated in *var2* showed a significant enrichment of protein folding, proteolysis, detoxification, and chloroplast organization processes. (B) Downregulated proteins exhibited an significant enrichment of photosynthetic protein import, PSI and PSII assembly, PSII repair, photosynthetic electron transport chain (PETC), and chlorophyll biosynthesis. Bar charts shows the fold enrichment of the top 15 GO terms. Complete GO analysis of proteins up- and down-regulated in *var2* are shown in Supplementary Table S4 and Supplementary Table S6, respectively.

Table S1. List of primers used in the qRT-PCR analysis.

Gene ID	**Gene name**	**Primer sequence (5' to 3')**	**Primer length**	**Product size (bps)**
At1g12410	*CLPR2*	F: GAGCGTGTAATCTTCATTGGAC	22	103
		R: AAATCCTCCTCGAGTCATCAAG	22	
At4g17040	*CLPR4*	F: TTATGATAAAGCAGCCCATTGC	22	175
		R: GTGGGACTAAAATATTTCGGGC	22	
At2g44650	*CPN10*	F: AGGTGGAGTATTGTTGCCTAAA	22	183
		R: CTCTCTTTACAGAAGCAATGCC	22	
At3g23990	*CPN60*	F: AAAAGATGGTGTTACTGTTGCC	22	110
		R: CACCAGCAACATCATTAGTAGC	22	
At4g25100	*FSD1*	F: GAGTTTCACTGGGGAAAACATC	22	187
		R: TCATTGACTCCCAGAAGAACTC	22	
At2g28190	*CSD2*	F: GGTGACCTGGGAAACATAAATG	22	80
		R: CCAGTCAGAGGAATCTGATTGT	22	
At3g62030	*CYP20-3*	F: TCTATGCAGATGGTTCACACTT	22	162
		R: CTTAATGGGTGATGCATAGTGC	22	
At2g26150	*HSFA2*	F: ATGGGTTTGCAGAATGTGAATC	22	116
		R: CATAGCTGCAACTTGACTCTTG	22	
At1g13320	*PP2A*	F: GGACCGGAGCCAACTAGGA	19	80
		R: GCTATCCGAACTTCTGCCTCATT	23	
At4g27670	*HSP21*	F: GAACCAAGGATCAAGTGTC	19	113
		R: CTAACATTTGTCGCATCG	18	
At5g15450	*CLPB3*	CTTGATCATCGGCCGTTC	18	123
		CTCTTTTGCAACATCTGG	18	