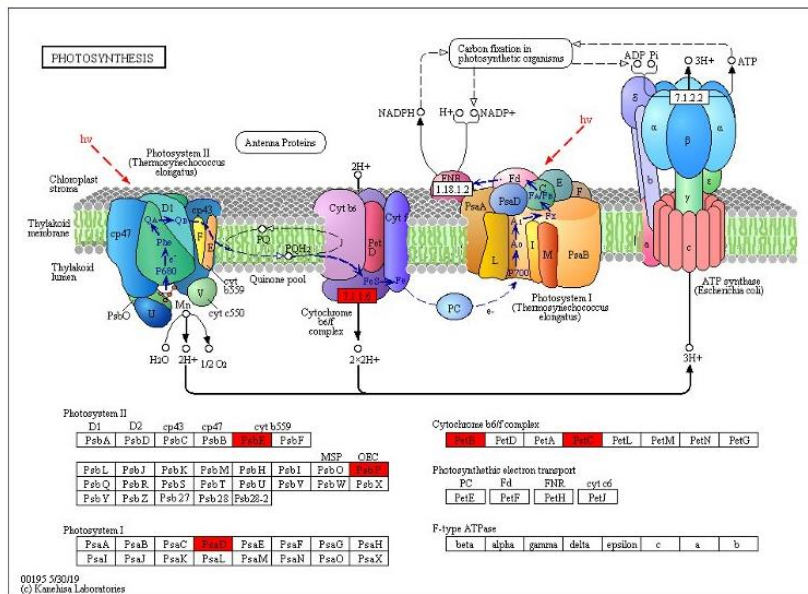


Figure S1. Results of 4D-proteomics, quality control, and differentially abundant proteins (DAPs). (A). Identified spectra after reversed-phase HPLC and LC-MS/MS with 27317 total peptides. Proteins were identified by searching and analyzing *N. benthamiana* protein and UniProt databases. The Y-axis shows the number of spectra, peptides, and proteins. (B). Relationship and of protein mass and coverage. The X-axis represents the protein mass, and the Y-axis shows the sequences coverage of the target protein. (C). Quality control of 4D-proteomics by principal component analysis. The red dots circled refer to the PVX-GFP group, and the cyan dots represent the PVX-P1^{SCSMV} group. (D). Quality control of 4D-proteomics by Pearson's correlation coefficient. (E). Numbers of DAPs among the PVX-GFP and PVX-P1^{SCSMV} groups equal to or greater than 1.5 -fold. Red spot: upregulated proteins. Blue spot: downregulated proteins. Log2 PVX_Pn vs PVX_Pn represents the ratio between PVX-GFP and PVX-P1^{SCSMV} groups taking the natural logarithm. The Y-axis indicates the magnitude of differences in protein levels. (F). Number of DAPs among the PVX-GFP and PVX-P1^{SCSMV} groups equal to or greater than 2-fold.

A.



B.

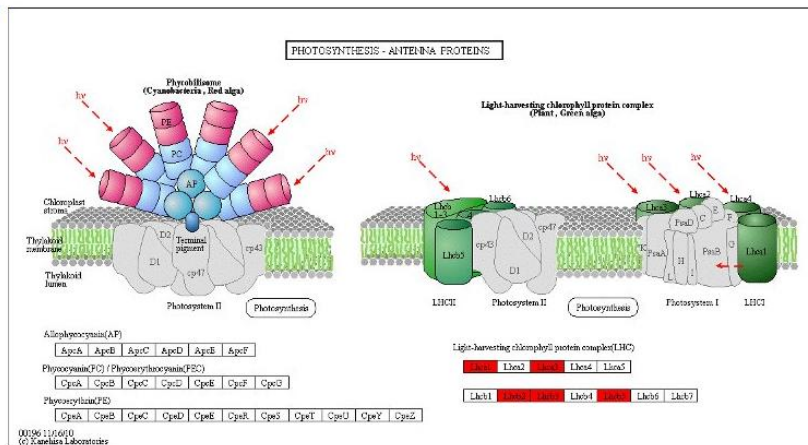


Figure S2. Expression profile of photosynthesis-related proteins by 4D-proteomics. (A). Photosynthesis map illustrating directly related proteins, including photosystem I, photosystem II, cytochrome b6/f complex, photosynthetic electron transport, and F-type ATPase. (B). Photosynthesis map illustrating the photosynthesis related antenna proteins. All the red marked proteins were significantly upregulated by P1^{SCSMV} overexpression.