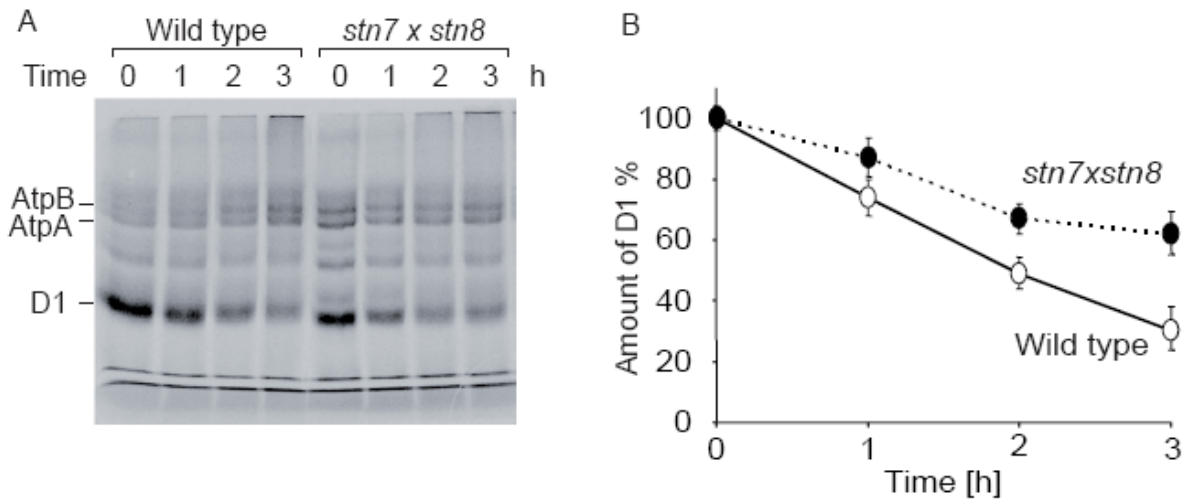


Supplemental Figure 1. Locations of TDNA insertions within STN7 (At1g68830) and STN8 (At5g01920) genes.

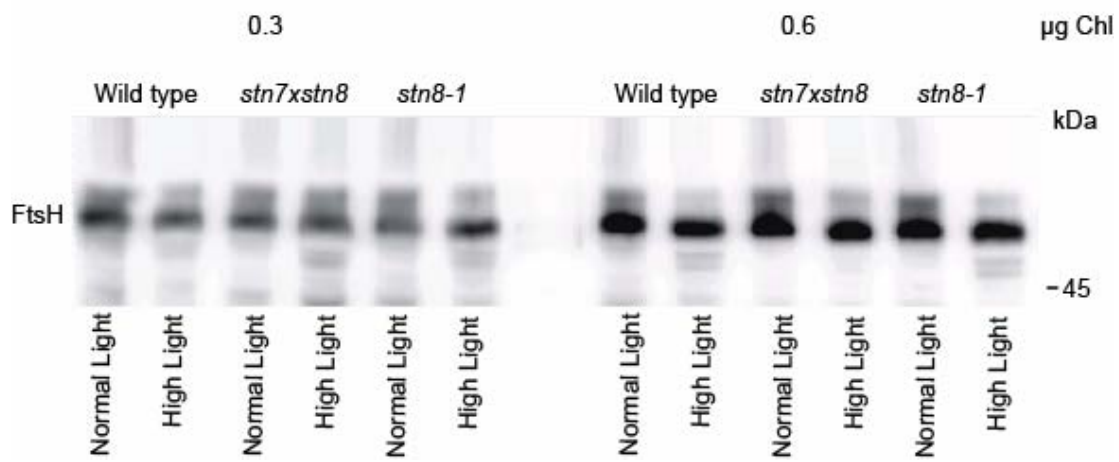
Exons are indicated by black boxes, 5' and 3'UTRs by open boxes and introns by thin lines. PCR was performed on *stn7* and *stn8* in the wild-type (*Col-0*), *stn7* (SALK 073254), *stn8* (SALK 060869, insertion B) and *stn7xstn8* (SALK 073254, SALK 060869). The primers STN7fw (7f), STN7rev (7r), LBb1 (LB), STN8fw (8f), STN8rev (8r) used are indicated. The products of the PCR reactions with 7f and 7r, LB and 7r, 8f and 8r and LB and 8r obtained with the DNAs of the indicated lines were fractionated by agarose gel electrophoresis and detected by fluorescence after ethidium bromide staining. M indicates size markers.



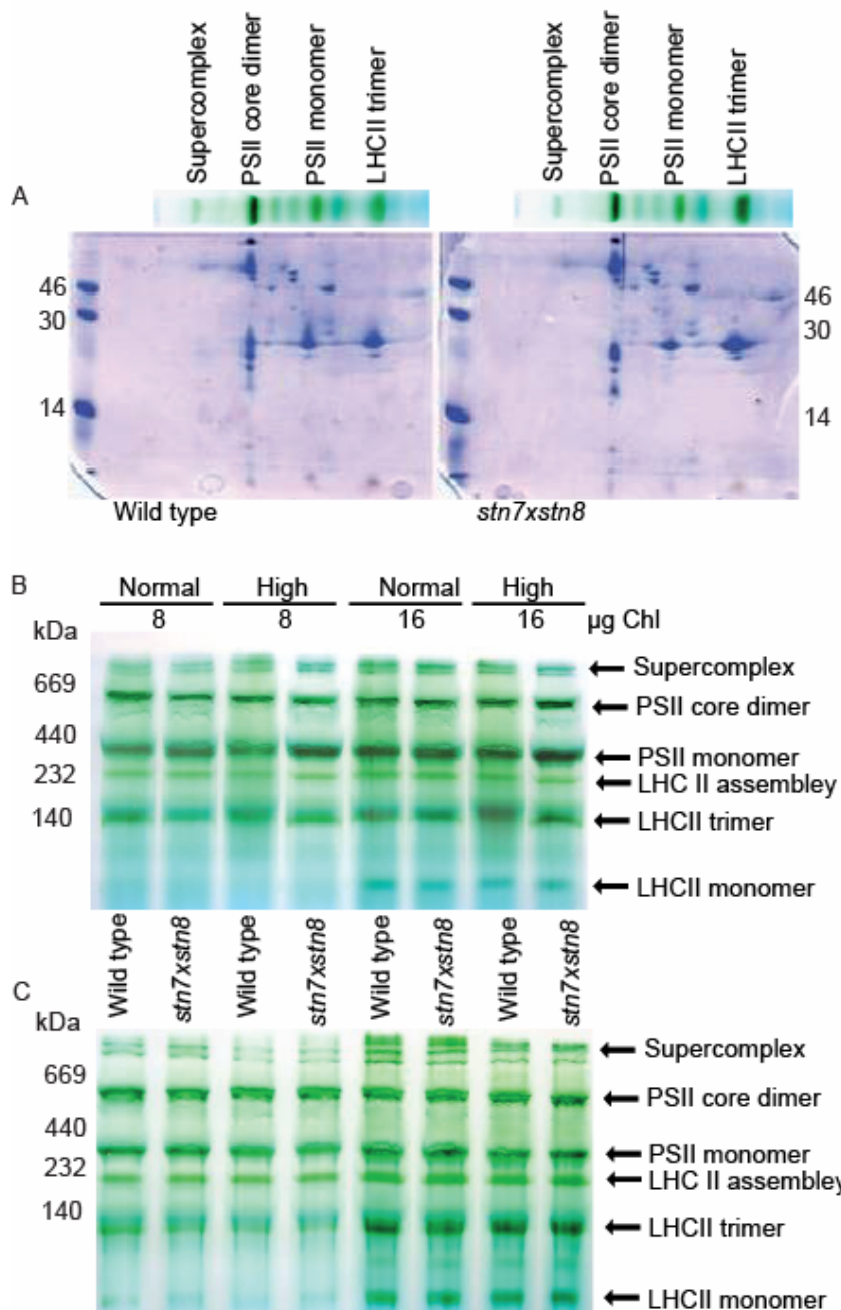
Supplemental Figure 2. *In vivo* pulse-chase experiments with chloroplast proteins of wild-type and *stn7xstn8* plants labeled with [³⁵S] methionine and exposed to high light of 1000 $\mu\text{mol m}^{-2} \text{s}^{-1}$.

(A) 4 week-old wild-type and *stn7xstn8* plants were labeled with [³⁵S] methionine for 2 hours under normal light ($100 \mu\text{mol m}^{-2} \text{s}^{-1}$) in the presence of cycloheximide. After one hour chase period in low light, including 30 min with lincomycin, plants were exposed to high light of $1000 \mu\text{mol m}^{-2} \text{s}^{-1}$ for 1, 2 and 3 h and proteins were analyzed by SDS-PAGE and phosphorimaging. Positions of the labeled AtpA and AtpB subunits of ATP synthase and of the D1 protein are indicated.

(B) Time dependence of the labeled D1 protein degradation in leaves of wild-type and *stn7xstn8* plants subjected to *in vivo* pulse-chase experiments under high light as shown in (A). Amounts of labeled D1 protein were normalized relative to the sum of AtpA and AtpB bands and the CP43 band below. The values are means \pm SEM of three independent experiments for each genotype.



Supplemental Figure 3. Immunoblotting analysis of SDS-PAGE separated thylakoid proteins from wild-type, *stn7xstn8* and *stn8-1* plants exposed to normal light of 120 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ or high light of 900 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ with the FtsH-specific antibody. The thylakoid membranes containing either 0.3 or 0.6 μg chlorophyll were loaded on the gels, as indicated.



Supplemental Figure 4. Blue Native PAGE and Blue Native PAGE/SDS-PAGE gel separations of thylakoid protein complexes from wild-type and the *stn7xstn8* plants exposed to normal light of $120 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ or high light of $900 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ for 3 h.

Thylakoid membranes were solubilized with 0.75% (w/v) n-dodecyl β -D-maltoside (DM), and the mixture was incubated on ice for 5 min. After centrifugation BN-PAGE with a gradient of 5-

13.5% acrylamide in the separation gel was performed. For separation of proteins in the second dimension, lanes were cut out and incubated with 5% β -mercaptoethanol for 30 min at room temperature and then subjected to SDS-PAGE with 15% acrylamide in the separation gel.

(A) Two dimensional gel analyses of thylakoid protein complexes from wild type and *stn7xstn8* plants exposed to normal light ($120 \mu\text{mol photons m}^{-2} \text{s}^{-1}$).

(B) Blue Native PAGE of thylakoid membranes from wild type and *stn7xstn8* plants exposed to either normal light or high light ($900 \mu\text{mol photons m}^{-2} \text{s}^{-1}$) for 3 h and solubilized with 0.75 % DM, with different chlorophyll loading, as indicated.

(C) Replication of Blue Native gel like in **B** from a different experimental preparation.

Supplemental Table 1. Electron microscope measurements of thylakoid membranes in wild-type (*Col-0*), *stn7*, *stn8-1*, *stn8-2* and *stn7xstn8* plant leaves.

	<i>Col-0</i>	<i>stn7x stn8</i>	<i>stn7</i>	<i>stn8-1</i>	<i>stn8-2</i>
Average grana size, nm	439 ± 155 (70)	667 ± 223 (40)	487 ± 138 (23)	623 ± 234 (30)	551 ± 212 (78)
Average number of grana layers	3.7 ± 1.8	3.9 ± 1.2	5.0 ± 1.7	3.9 ± 1.2	3.0 ± 1.2

The length of thylakoid membranes was measured for grana regions (means ± SEM). Appressed membranes were counted twice. Numbers in parenthesis indicate numbers of grana measured.