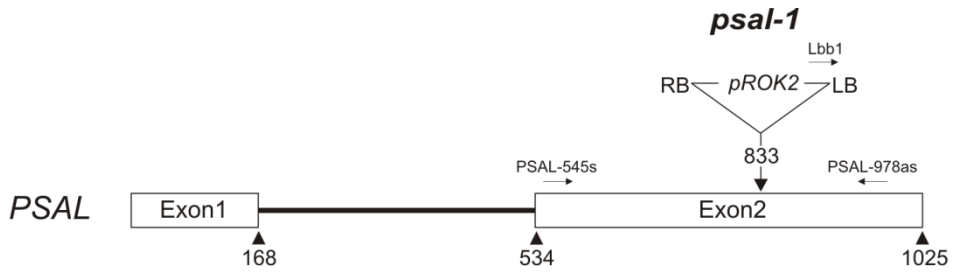
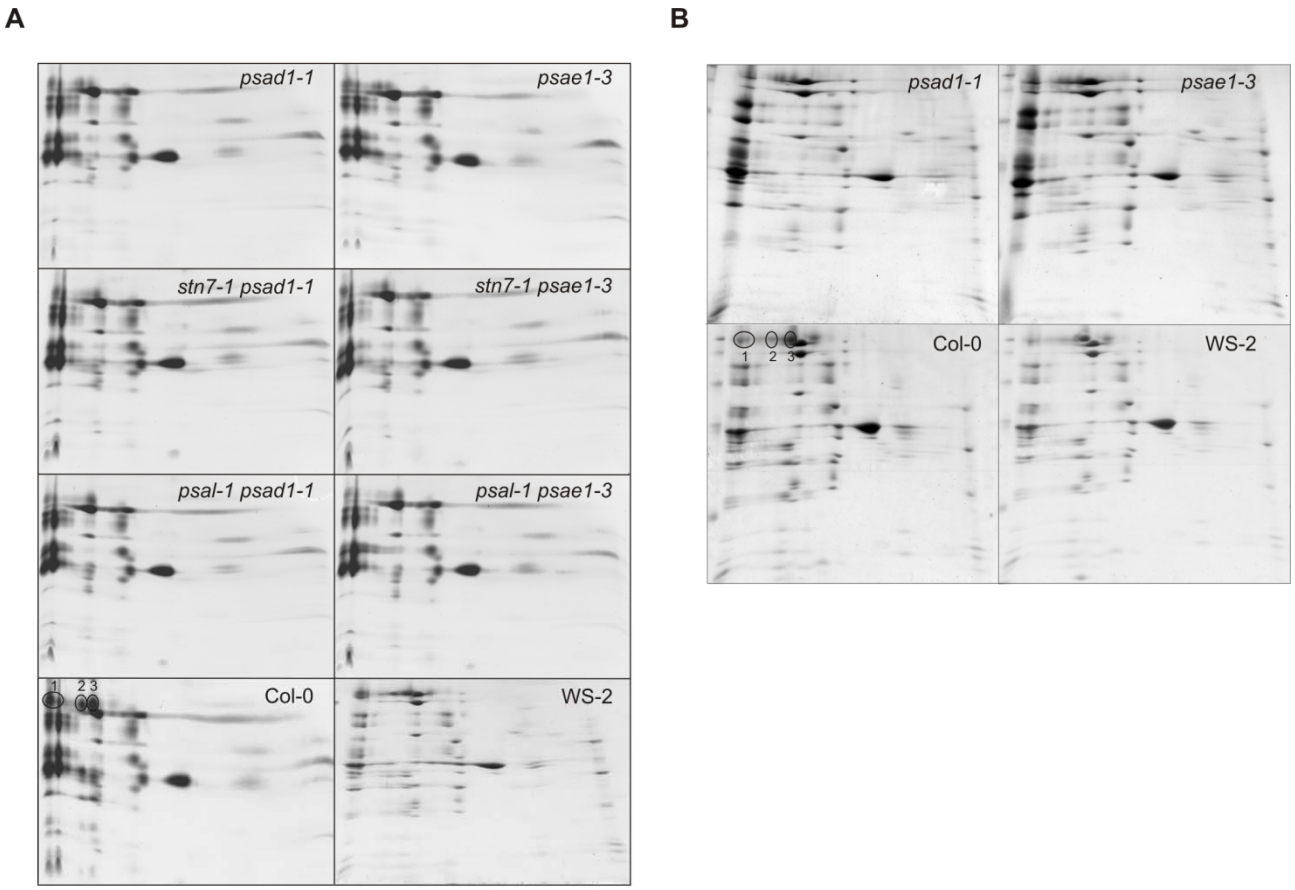
Supplemental Data. Pesaresi et al. (2009). *Arabidopsis* STN7 Kinase Provides a Link Between Short- and Long-Term Photosynthetic Acclimation.

Additional, extensive Supplemental Tables can be found in a second Supplemental Data file entitled "Supplemental Tables 3_4_5_6_7_9"



Supplemental Figure 1. Tagging of the *PSAL* gene (*At4g12800*) coding for the PSI subunit L.
In *psal-1*, the *PSAL* gene is disrupted by an insertion of the pROK2 T-DNA in the second exon. The orientation of primers used for PCR-based genotyping and segregation analysis (LBb1: 5'-GCGTGGACCGCTTGCTGCAACTC-3'; PSAL-545s: 5'-AGTAGTTCAAC CAATCAACGGTG-3'; PSAL-978as: 5'-AGAACGTAGAGAAGGAAGTAAGC-3') is indicated. The LBb1/PSAL-978as and PSAL-545s/PSAL-978as primer combinations were used to amplify the mutant and WT alleles, respectively. Note that the T-DNA insertion and the arrows indicating the primers are not drawn to scale.



Supplemental Figure 2. Quantification of the PSI-LHCI-LHCII complex in WT (Col-0 and WS-2) and mutant plants adapted to state 2 (low light) or state 1 (high light) conditions.
(**A**) 2D-PAGEs, as in Figure 2, of thylakoid membranes isolated from Col-0, WS-2 and mutant (*psad1-1*, *stn7-1 psad1-1*, *psal-1 psad1*, *psae1-3*, *stn7-1 psae1-3*, *psal-1 psae1-3*) leaves adapted to state 2, stained with Coomassie.
(**B**) The BN-gel high-light (state 1) lanes from Col-0, WS-2, *psad1-1* and *psae1-3* in Figure 4B were subjected to denaturing PAGE, and the 2-D gels were stained with Coomassie.

Supplemental Table 1. List of proteins identified within the 670 kDa pigment protein complex (observable in BN-PAGE; see also Figures 2 and 3) by mass-spectrometry (see Methods). Note that only proteins identified by at least 4 peptides are reported.

Gene	Description
psaA	PSI P700 apoprotein A1
psaB	PSI P700 apoprotein A2
psaC	PSI C protein
psaJ	PSI J protein
AT1G03130	PSI reaction center subunit II (PsaD1)
AT1G31330	PSI subunit III (PsaF)
AT1G52230	PSI subunit VI (PsaH2)
AT1G55670	PSI subunit V (PsaG)
AT1G61520	Chlorophyll a/b binding protein (LHCA3)
AT2G20260	PSI reaction center subunit IV (PsaE2)
AT3G16140	PSI subunit VI (PsaH1)
AT3G47470	Chlorophyll a/b binding protein (LHCA4)
AT3G54890	Chlorophyll a/b binding protein (LHCA1)
AT3G61470	Chlorophyll a/b binding protein (LHCA2)
AT4G12800	PSI subunit XI (PsaL)
AT4G28750	PSI subunit IV (PsaE1)
AT5G64040	PSI subunit (PsaN)
AT1G29910	Chlorophyll a/b binding protein (LHCB1.2)
AT1G29930	Chlorophyll a/b binding protein (LHCB1.3)
AT2G05070	Chlorophyll a/b binding protein (LHCB2.2)
AT2G34420	Chlorophyll a/b binding protein (LHCB1.5)
AT2G34430	Chlorophyll a/b binding protein (LHCB1.4)

Supplemental Table 2. Parameters of photosynthetic electron flow based on chlorophyll fluorescence measurements of mutant and wild-type plants.

	F_V/F_M	Φ_{II}	1-qP	J_F
Col-0	0.82 ± 0.01	0.76 ± 0.01	0.04 ± 0.01	14.06 ± 0.3
WS	0.82 ± 0.01	0.76 ± 0.01	0.04 ± 0.01	14.06 ± 0.2
TSP9 RNAi	0.81 ± 0.02	0.75 ± 0.02	0.05 ± 0.01	13.87 ± 0.3
chaos	0.82 ± 0.02	0.77 ± 0.03	0.03 ± 0.00	10.68 ± 0.4
as*Lhcb2.1*	0.80 ± 0.01	0.77 ± 0.02	0.03 ± 0.00	11.39 ± 0.3
stn7-1	0.82 ± 0.01	0.75 ± 0.01	0.07 ± 0.01	13.87 ± 0.4
stn8-1	0.82 ± 0.01	0.76 ± 0.01	0.04 ± 0.00	14.06 ± 0.2
psal-1	0.83 ± 0.01	0.72 ± 0.01	0.10 ± 0.01	13.32 ± 0.2
pete2-1	0.82 ± 0.01	0.68 ± 0.01	0.11 ± 0.02	12.58 ± 0.3
psae1-3	0.79 ± 0.00	0.49 ± 0.02	0.39 ± 0.03	9.06 ± 0.2
psad1-1	0.78 ± 0.01	0.46 ± 0.03	0.42 ± 0.02	8.51 ± 0.3
stn7-1 pete2-1.1	0.81 ± 0.00	0.51 ± 0.01	0.27 ± 0.03	9.43 ± 0.2
stn7-1 psad1-1	0.78 ± 0.00	0.31 ± 0.01	0.57 ± 0.05	5.73 ± 0.3
stn7-1 psae1-3	0.78 ± 0.01	0.32 ± 0.01	0.59 ± 0.02	5.92 ± 0.1
psal-1 pete2-1.1	0.82 ± 0.01	0.62 ± 0.02	0.18 ± 0.01	11.47 ± 0.4
psal-1 psad1-1	0.77 ± 0.00	0.35 ± 0.01	0.55 ± 0.02	6.47 ± 0.3
psal-1 psae1-3	0.78 ± 0.01	0.39 ± 0.02	0.48 ± 0.05	7.21 ± 0.2
stn8-1 pete2-1.1	0.82 ± 0.00	0.68 ± 0.01	0.10 ± 0.01	12.58 ± 0.3
stn8-1 psad1-1	0.78 ± 0.01	0.47 ± 0.02	0.39 ± 0.03	7.21 ± 0.2
stn8-1 psae1-3	0.79 ± 0.00	0.48 ± 0.02	0.38 ± 0.03	8.88 ± 0.3

Measurements were performed as described in the Methods section. Mean values for five plants (±SD) are shown. The *in vivo* electron transport rate (J_F, µmol electrons m^{-2} s^{-1}) was derived from chlorophyll fluorescence measurements at an actinic light intensity of 37 µmol photons m^{-2} s^{-1}.

Supplemental Table 8. Real-time PCR analysis of exemplary genes differentially regulated in the *stn7-1*, *psad1-1*, *stn7-1 psad1-1*, *psae1-3* and *stn7-1 psae1-3* mutants.

Gene	*stn7-1*	*psad1-1*	*psae1-3*	*stn7-1 psad1-1*	*stn7-1 psae1-3*
At3g12580	0.25±0.010 (0.29)	0.12±0.001 (0.06)	0.35±0.026 (0.33)	0.22±0.013 (0.07)	0.52±0.028 (0.36)
At3g16360	0.35±0.003 (0.18)	0.05±0.006 (0.05)	0.17±0.028 (0.25)	0.01±0.001 (0.05)	0.01±0.003 (0.53)
At5g54060	0.15±0.010 (0.20)	0.24±0.003 (0.25)	0.43±0.090 (0.32)	0.25±0.040 (0.30)	0.25±0.036 (0.25)
At3g62950	1.55±0.164 (2.23)	4.49±0.060 (15.20)	4.17±0.435 (6.09)	2.31±0.240 (9.42)	6.49±0.481 (4.17)
At1g17745	0.73±0.085 (0.40)	0.10±0.027 (0.23)	0.29±0.126 (0.28)	0.15±0.011 (0.14)	0.06±0.013 (0.43)

Wild type (Col-O and WS-2) and the different mutant plants were grown for 4 weeks in white light (100 µmol quanta m^{-2} s^{-1}) in a 12 h / 12 h light / dark cycle. Expression values of *HSP70* (*At3g12580*), *HP4* (*At3g16360*), *UF3GT* (*At5g54060*), *GRXC11* (*At3g62950*) and *PGDH* (*At1g17745*) genes are reported as fold changes ± SD in mutants with respect to the corresponding WT plants. Gene expression values obtained by Affymetrix GeneChip analysis are reported in parenthesis.