Supplemental Data. Peng et al. (2009). Efficient operation of NAD(P)H dehydrogenase requires supercomplex formation with photosystem I via minor LHCI in *Arabidopsis*.



Supplemental Figure 1. Amino Acid Sequence Alignment of NDH18.

Protein sequences were aligned using the ClustalW program with default settings (<u>http://clustalw.ddbj.nig.ac.jp/top-e.html</u>). Black boxes indicate strictly conserved amino acids, and gray boxes indicate closely related amino acids. The bar above the sequences indicates the transmembrane domain in At NDH18. The arrow indicates the predicted cleavage site for the plastid-targeting signal. The sequences are named for each organism as follows: At NDH18, *Arabidopsis thaliana* (At5g43750); Gm NDH18, *Glycine max* (accession number CD394214); Nt NDH18, *Nicotiana tabacum* (EB679832); Os NDH18, *Oryza sativa* (Os01g0929100); Zm NDH18, *Zea mays* (DV514173).



Supplemental Figure 2. NDH-PSI Supercomplex Content in the *ndh18* and *fkbp16-2* RNAi lines.

Thylakoids isolated from the wild type (WT), *ndh18* and *fkbp16-2* RNAi lines were subjected to BN-PAGE analysis. After electrophoresis, the high-molecular-weight region corresponding to Bands I and II was excised from the BN gel, and the proteins were denatured in the gel with SDS sample buffer. The proteins were further separated by 12.5% SDS-PAGE and immunodetected with specific antibodies against PsaA, NdhH and NdhL.



Supplemental Figure 3. Localization Analysis of NDH Subunits in Chloroplasts of the Wild Type (WT), *ndhl*, *ppl2*, *crr4-3* and *ndh18* Mutants.

Isolated chloroplasts were osmotically ruptured in a buffer containing 20 mM HEPES/KOH (pH 7.6), 5 mM MgCl₂, and 2.5 mM EDTA. Thylakoid membranes were pelleted by centrifugation (17,600 × g for 20 min) and resuspended in the same buffer. The concentration of the stroma protein was determined with a Bio-Rad Protein Assay Kit (cat. No. 500-0006). Immunoblotting was performed with antibodies against NdhL, NDF1, NDF2, NDH18, FKBP16-2, and RbcL proteins. Thylakoid proteins were loaded on an equal chlorophyll basis and 2µg stroma protein was loaded on each well.



Supplemental Figure 4. Visible Phenotype of *lhca6* Mutant.

Seedlings were cultured at 50 μ mol photons m⁻² s⁻¹ for 4 weeks after germination. The leaves labeled 1–2 and 3–6 were used as immature and mature leaves, respectively, in Figures 4, 5, 7, and 8.



Supplemental Figure 5. NDH-PSI Supercomplex Content in *lhca5* and *lhca6*.

Thylakoids isolated from wild type (WT), *lhca5* and *lhca6* mutants were subjected to BN-PAGE analysis. After electrophoresis, the high-molecular-weight region corresponding to Band I was excised from the BN gel, and the proteins were denatured in the gel with SDS sample buffer. The proteins were further separated by 12.5% SDS-PAGE and immunodetected with specific antibodies against PsaA, NdhH and NdhL.



Supplemental Figure 6. Analysis of Thylakoid protein complexes from Wild-type (WT) and *lhca6* mature leaves.

Thylakoid membrane complexes separated by BN-PAGE were further subjected to 12.5% 2D SDS-PAGE, and the proteins were immunodetected with specific antibodies against Lhca3, NDH18 and NDF1. Positions of NDH-PSI supercomplex and putative smaller NDH-PSI supercomplex are indicated by red and black arrows respectively.

		¥ ——
AtLhca6	1	MAFAIASALTSTLTLSTSRVQNPTQRRHVASTSSTGGRLMRERLVVVRAGK-EVSSVCE
NtLhca6	1	FSMALAIHSTAFSSIPIRELHTKKIPGKVSTCLISRKSRLNAGK-EVSSVCE
GmLhca6	1	MALALSSTALSSIPNREIRQKGFPERTPTCLSLTRRTIANATK-GVSAVCE
ZmLhca6	1	FTRTPQRRANATKGGVSTVCE
OsLhca6	1	WALPSGSFAACSTOPRVRAALRAPTLPSONAAVARMAGHRAGATKGGVSAVCE
AtLhca2	1	MASSLCASSATAAISSPSFLGGKKLRLKKKLTVPAVSRPDASVRAV
OsLhca2	1	MALVSASSSTTAVAALPGAARASSFLGGAGRSGRLLLRQAESSSARASFAVR
		-
AtLhca6	60	PLPPDRPLWFPGSSPPEWLDGSLPGDFGFDPLGLGSDP <mark>DT</mark> LKWFAQAEL <mark>I</mark> HSRWAMLAV <mark>T</mark>
NtLhca6	52	PLPPDRPLWFPGS <mark>P</mark> PPEWLDGSLPGDFGFDPLGLGSDPE <mark>T</mark> LKWFAQAELMHSRWAMLAVA
GmLhca6	51	PLPPDRPLWFPGSSPPEWLDGSLPGDFGFDPLGLGSDPELLKWFAQAELMHSRWAMLAV <mark>F</mark>
ZmLhca6	36	PL <mark>C</mark> PDRP H WFPGSSPP P WLDGSLPGDFGFDPLGLGSEPELL <mark>R</mark> WFAQAELMH <mark>G</mark> RWAMLA <mark>A</mark> A
OsLhca6	54	PLGPDRPLWFPGSSPPPWLDGSLPGDFGFDPLGLGSDPELLRWFAQAELMHSRWAMLAVA
AtLhca2	47	AADPDRPIWFPGSTPPEWLDGSLPGDFGFDPLGL <mark>S</mark> SDPDSLKW <mark>NVQAEIV</mark> HCRWAMLGAA
OsLhca2	53	AAAPDRPIWFPGSTPPPWLDGSLPGDFGFDPLGLGSDPE <mark>SLRWNVQAEL</mark> WHCRWAMLGAA
AtLhca6	120	GIIIPECLERLGFIEN-FSWYDAGSREYFADSTTLFVAQMVLMGWAEGRRWADLIKPGSV
NtLhca6	112	GILIPEWLESIGFIDN-FSWYDAGEREYFADSTTLFVVQLVLMGWAEGRRWADIMNPGCV
GmLhca6	111	GILVPELLERIGVIEN-FSWYDAGTREYFVDPTTLFVVQMGLMGWVEGRRWADIVNPGSV
ZmLhca6	96	GILVPDLLARWGFIDAGFSWFDAGSREYFADPWTLFVSQMALMGWAEGRRWADYLRPGCV
OsLhca6	114	GILVPEVLEKWGFMED-YSWIDAGARDYFADPWTLFVSQMALMGWAEGRRWADYLNPGCV
AtLhca2	107	GIFIPEFLTKIGILNT-PSWYTAGEQEYFTDKTTLFVVELILIGWAEGRRWADIIKPGSV
OsLhca2	113	GIFIPEFLTKIGILNT-PSWYTAGEQQYFTDTTTLFIIELILIGWAEGRRWADIIKPGCV
AtLhca6	179	diepkwphkvnpkpdvgypgglwfdfmmwgrgspepvmvlrtkeikngrlamlafmgfcf
NtLhca6	171	diepkvphkkkpksdvgypgglwfdpfmwgrgspepvmvlrtkeikngrlamlafvgfcf
GmLhca6	170	DIEPKVPHVTNPKPDVGYPGGLWFDPMMWGRGSPEPVMVLRTKEIKNGRLAMLAFVGFWF
ZmLhca6	156	DIEPRFPNRKNPVPDVGYPGGLWFDWANWGRGSPEPVMVLRTKEIKNGRLAMLAFVGFWF
OsLhca6	173	AMEPREPNERNPVPDVGYPGGLWFDWGNWGRGSPEPVMVLETKEIKNGELAMLAFVGFWF
AtLhca2	166	NTDPVFPNNKLTGTDVGYPGGLWFDPLGWGSGSPAKLKELRTKEIKNGRLAMLAVMGAWF
OsLhca2	172	NTDPIFPNNKLTGTDVGYPGGLWFDPLGWGTGSPEKIKELKNGRLAMLAVMGAWF
N hTheof	220	
ACLICA6	239	
Cmlbcaf	231	
GmLnca6	230	
2mLnca6	222	
Atthan?	233	
AcLineaz	220	
Oslnca2	232	QABITGIGFIDNLFAHLADPGHATIFQAFTPK

Supplemental Figure 7. Amino Acid Sequence Alignments of Lhca6 and Lhca2.

The sequences of At Lhca6 (At1g19150, Arabidopsis), Nt Lhca6 (DW000027, *Nicotiana tabacum*), Gm Lhca6 (EH258354, *Glycine max*), Zm Lhca6 (DV507315, *Zea mays*), Os Lhca6 (AK067780, *Oryza sativa*), At Lhca2 (At3g61470, Arabidopsis), and Os Lhca2 (AK104651, *Oryza sativa*) were aligned with CLUSTALW. Black boxes indicate strictly conserved amino acids, and gray boxes indicate closely related amino acids. The predicted cleavage sites for the plastid-targeting signal in At Lhca6 and At Lhca2 are indicated by black and clear arrows, respectively. The additional conserved N-terminal extension of the mature Lhca6 protein compared to Lhca2 is indicated as a bar above the sequences.



Supplemental Figure 8. State 1-State 2 transitions in Wild-type (WT), *stn7* and *lhca6* plants.

State transitions were investigated by measuring chlorophyll fluorescence as previous reports (Jensen et al., 2000; Bellafiore et al., 2005). The leaf was kept in the dark for 30 min and the maximal fluorescence yield (Fm) was measured with a saturating 0.8-s flash. Then the leaf was illuminated for 20 min with 80 μ mol m⁻² s⁻¹ blue light (which favors PSII) from high intensity light source equipped with a BLF-460B filter. The maximal fluorescence yield (Fm2) was then measured in this state (state 2). Subsequently the far-red light (which favors PSI) was switched on. After 15 min of illumination, the maximum fluorescence yield (Fm1) was measured in state 1.

Locus	Lhca6	At4g39710	At5g43750
At1g70760: NdhL	0.91	0.86	0.88
At5g58260: NdhN	0.92	0.87	0.85
At1g74880: NdhO	0.85	0.83	0.82
At1g15980: NDF1/NDH48	0.90	0.82	0.91
At1g64770: NDF2/NDH45	0.84	0.81	0.79
At3g16250: NDF4	0.93	0.90	0.89
At1g18730: NDF6	0.85	0.80	0.87
At2g39470: PPL2	0.93	0.89	0.87
At5g52100: CRR1	0.86	0.88	0.8
At2g01590: CRR3	0.88	0.83	0.81
At1g19150: Lhca6	-	0.89	0.88
At4g39710: FKBP16-2	0.89	-	0.83
At5g43750: NDH18	0.88	0.83	-

Supplemental Table 1. r-Value between NDH Complex-Related Genes with *Lhca6*, *FKBP16-2* and *NDH18*.

r-values were obtained from the ATTED-II database when *Lhca6*, *At4g39710*, *At5g43750* served as a query gene, respectively.

Supplemental Table 2. Primer List and Sequence

The following primers used for RNAi vectors construction:

Lhca6-Sence1:	5' AGTTCTAGACAATCAAAGATGACACTAGC 3'
Lhca6-Sence2:	5' AGTCTCGAGCAATCAAAGATGACACTAGC 3'
Lhca6-Antisence1:	5' CAGGGATCCATAAAGGACGGTCCGG 3'
Lhca6-Antisence2:	5' CAGGGTACCATAAAGGACGGTCCGG 3'
FKBP16-2-Sence1:	5' TACTCTAGATCAGGACTTGGATTTTGC 3'
FKBP16-2-Sence2:	5' TACCTCGAGTCAGGACTTGGATTTTGC 3'
FKBP16-2-Antisence1:	5' GGAGGATCCTTCATCTTGTATTACTTCCTG 3'
FKBP16-2-Antisence2:	5' GGAGGTACCTTCATCTTGTATTACTTCCTG 3'
NDH18-Sence1:	5' CGATTCTAGAAAAACTCTGAGACAGAGCAAG 3'
NDH18-Sence2:	5' CGATGAATTCAAAACTCTGAGACAGAGCAAG 3'
NDH18-Antisence1:	5' TACGGATCCTTATCGTGTGGCGATATCATC 3'

NDH18-Antisence2: 5' TCCGGTACCTTATCGTGTGGCGATATCATC 3'

The following primers used for RT-PCR:

Lhca6RT-LP:	5' AGAGAAGACCACATGTAGCGTCCAC 3'			
Lhca6RT-RP:	5' GCAGAAGTTGTAACAACGGCGAGTG 3'			
OsLhca6RT-LP:	5' TCACTCTAGACCATGGCTCTGCCCTC 3'			
OsLhca6RT-RP:	5' AATCTCGAGAATGGGACGTGAATGCCGAG 3'			
Lhca2RT-LP:	5' AGGTCAACAACGTCGAGAATAATGG 3'			
Lhca2RT-RP:	5' GGAACCTTAATTTGCATTCGACCAC 3'			
NDH18RT-LP:	5' ATGGCTCCAAAACTCTGAGACAGAG 3'			
NDH18RT-RP:	5' GTCATGATTATAACGAGATCACAATCC 3'			
FKBP16-2RT-LP:	5' AAGGAGCTCGTTTTCGGAGTGGGTTTAG 3'			
FKBP16-2RT-RP:	5' TTGCTCGAGTCTTGTATTACTTCCTGGG 3'.			
FKBP13RT-LP:	5' ATGAGCTCCTTGGGGGTTTTCAGTTG 3'			
FKBP13RT-RP:	5' GCTCTCTCAAGCTTTACCTATGTACTC 3'			
ACT-LP:	5' GAGAGATTCAGGTGCCCAG 3'			
ACT-RP:	5' AGAGCGAGAGCGGGTTTTCA 3'			
The following primers used for protein expression vectors construction:				
NDH18antibody-LP1:	5' GGCGAATTCTTGAAGTTAGCGAAGCTG 3'			
NDH18antibody-RP1:	5' ATCAAGCTTCATCCCAAGAGCTATAGC 3'			
NDH18antibody-LP2:	5' TGTAAGCTTGAGATGGATAAACCTGACC 3'			

NDH18antibody-RP2: 5' ATTCTCGAGTCGTGTGGCGATATCATC 3'

FKBP16-2antibody-LP: 5'- AAGGAGCTCGTTTTCGGAGTGGGTTTAG -3'

FKBP16-2antibody-RP: 5'- TTGCTCGAGTCTTGTATTACTTCCTGGG -3'

REFERENCES ADDED FOR SUPPLEMENTAL INFORMATION

Bellafiore, S., Barneche, F., Peltier, G., and Rochaix, J.-D. (2005). State transitions and light adaptation require chloroplast thylakoid protein kinase STN7. Nature **433**: 892-895.

Jensen, P.E., Gilpin, M., Knoetzel, J., and Scheller, H.V. (2000). The PSI-K subunit of photosystem I is involved in the interaction between light-harvesting complex I and the photosystem I reaction center core. J. Biol. Chem. **275**: 24701–24708.