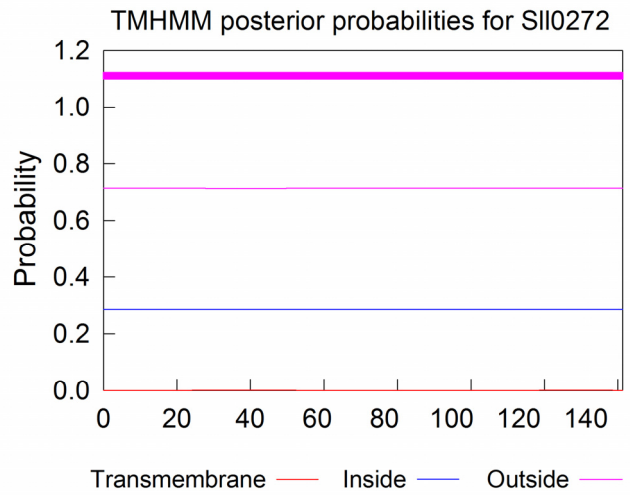
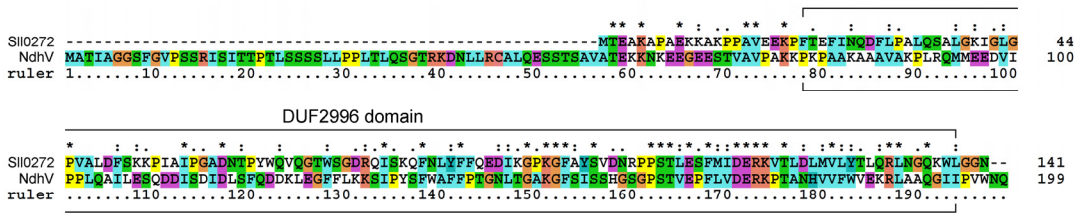
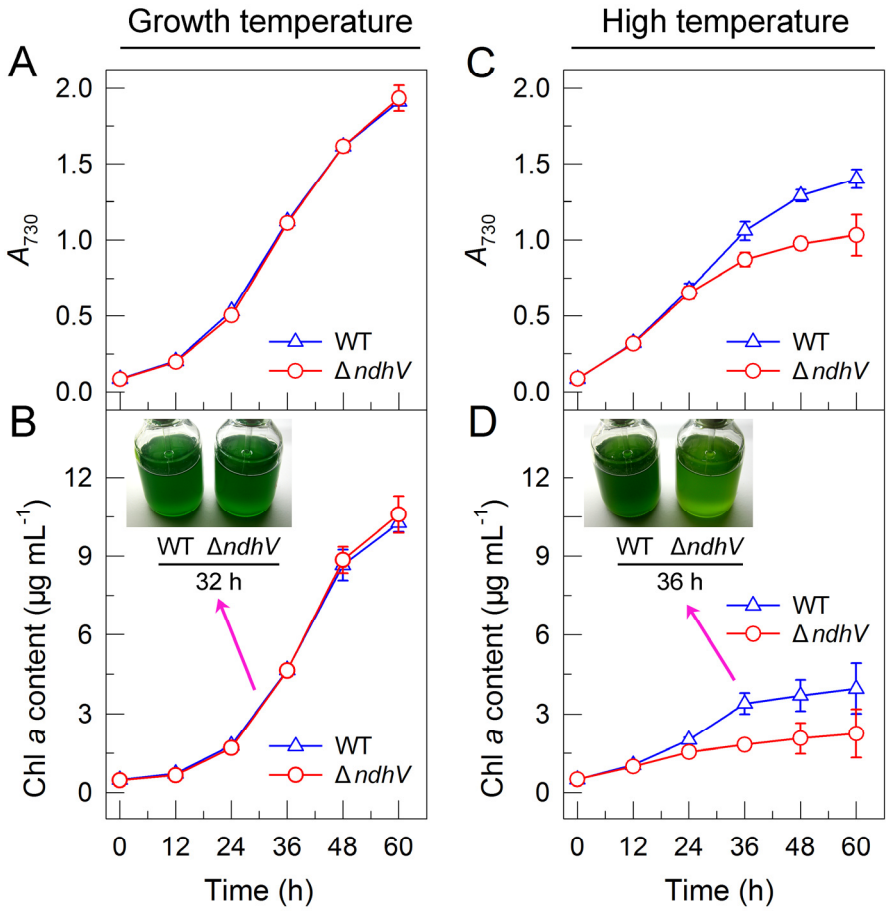
Supplemental Data



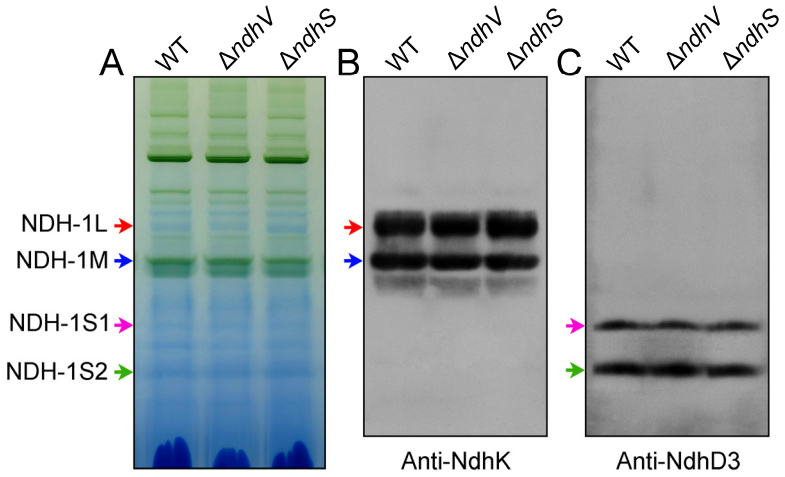
Supplemental Figure S1. Prediction of transmembrane region for Sll0272. The translated amino acid sequence of Sll0272 was used to predict transmembrane region with TMHMM (http://www.cbs.dtu.dk/services/TMHMM/). The pink bar indicates that Sll0272 does not contain any transmembrane region.



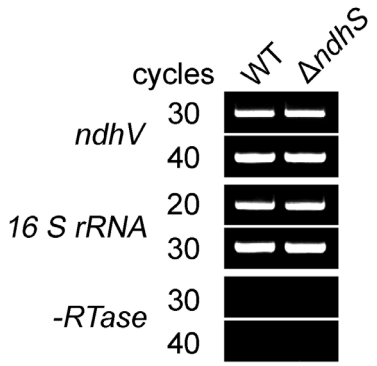
Supplemental Figure S2. Sequence comparison between Sll0272 (*Synechocystis* sp. strain PCC 6803) and NdhV (*Arabidopsis thaliana*) (At2g04039). The sequences were aligned using ClustalX 1.83. Asterisks indicate identical amino acids; colons and dots indicate conserved amino acid substitutions. The position of putative domain DUF2996 was indicated.



Supplemental Figure S3. Growth of WT and Δ*ndhV* cells under different temperature conditions. Cell density (A) and Chl *a* content (B) were monitored under growth temperature (30°C). Cell density (C) and Chl *a* content (D) were monitored under high temperature (42°C). Values are means ± SD (n = 5).



Supplemental Figure S4. Western analyses of NDH-1 complexes from the air-grown WT, Δ*ndhV* and Δ*ndhS* cells. A, Thylakoid protein complexes isolated from the air-grown WT, Δ*ndhV* and Δ*ndhS* cells were separated by BN-PAGE. Thylakoid membrane extract corresponding to 7 µg Chl *a* was loaded onto each lane. Red, blue, pink and green arrows indicate the positions of NDH-1L, NDH-1M, NDH-1S1 and NDH-1S2 complexes, respectively. B and C, Protein complexes were electroblotted to a polyvinylidene difluoride membrane, and the membrane was cross-reacted with anti-NdhK and NdhD3 to probe the assembly of NDH-1 complexes.



Supplemental Figure S5. RT-PCR analysis of *ndhV* in the WT and Δ*ndhS* strains. The transcript level of *16 S rRNA* in each sample is shown as a control. The absence of contamination of DNA was confirmed by PCR without reverse transcriptase.

Supplemental Table S1. Primers used in this study.

Primers used for identifying the sites of transposon insertion.

Name	Primer sequence (5'–3')	Purpose
Transprimer-FP	ACCTACAACAAAGCTCTCATCAACC	Identifying the transposon insertion sites
Transprimer-RP	GCAATGTAACATCAGAGATTTTGAG	

Primers used to construct the *pEASY*-Blunt Zero-Δ*ndhV* vector.

Name	Primer sequence (5'–3')	Purpose
ndhV-A	GAGCAGATAAAGCAAGGGATAAATG	Amplification of *ndhV* gene and its flanking sequences
ndhV-B	CAGAGTAAGAACAAATAAGCACG	
ndhV-C	CGGAATTCAAAATAAAAAAGGGG	Amplification of spectinomycin gene
ndhV-D	GCTCTAGAAAAATAAAAAAGGGGACC	
ndhV-E	GAGCAGATAAAGCAAGGGATAAATG	Segregation analysis
ndhV-F	CAGAGTAAGAACAAATAAGCACG	

Primers used to construct vectors to express NdhV protein to raise antibody.

Name	Primer sequence (5'–3')	Purpose
ndhV-FP	CGGGATCCATGACAGAAGCCAAAGC	NdhV antibody
ndhV-RP	CGAGCTCTTAGTTGCCCCCTAGCC	

Primers used to construct the yeast two-hybrid vector.

Name	Primer sequence (5'–3')	Purpose
ndhV-FP	CCTCGAGATGACAGAAGCCAAAGCC	NdhV bait
ndhV-RP	CCTCGAGTTAGTTGCCCCCTAGCCA	
ndhO-FP	CGGAATTCATGGCCGCTAAAATGAAAAAGG	NdhO bait
ndhO-RP	CCCCTCGAGCTAAGCCAGGGCTTCGATTTGG	

ndhS-FP	CGGAATTCATGATTTTTCCCGG	NdhS prey
ndhS-RP	CCCTCGAGCTAGATGGGTTTGACTG	
ndhI-FP	CCCCTCGAGATGTTTAACAACATTCTCAAACAG	NdhI prey
ndhI-RP	CCCCTCGAGCTATTCTGCTTTCACCAAATCTTC	
ndhB-FP	CCCCTCGAGATGGACTTTTCTAGTAACGTTGCA	NdhB prey
ndhB-RP	CCCCTCGAGCTAGGGTAAATCATGGGAAATGGC	

Primers used to construct the fusion protein expression vector.

Name	Primer sequence (5'–3')	Purpose
ndhV-A	CGGGATCCATGACAGAAGCCAAAGC	Purifying NdhV using His-tag
ndhV-B	CGAGCTCTTAGTTGCCCCCTAGCC	
ndhV-C	CCTCGAGATGACAGAAGCCAAAGCC	Purifying NdhV using GST-tag
ndhV-D	CCTCGAGTTAGTTGCCCCCTAGCCA	
ndhS-A	CGGGATCCATGATTTTTCCCGG	Purifying NdhS using His-tag
ndhS-B	CGGAATTCCTAGATGGGTTTGACTG	
ndhS-C	CGGAATTCATGATTTTTCCCGG	Purifying NdhS using GST-tag
ndhS-D	CCCTCGAGCTAGATGGGTTTGACTG	

Primers used for RT-PCR.

Name	Primer sequence (5'–3')	Purpose
ndhV-FP	CGCAGTGGAAGAGAAGCCCTTCACC	*ndhV* transcript
ndhV-RP	GTTGCAGGGTGTAGAGCACCATCAG	
16 S rRNA-FP	CGACTGCTAATACCCAATGTGC	*16 S rRNA* transcript
16 S rRNA-RP	GTCCCTCAGTGTCAGTTTCAGC	