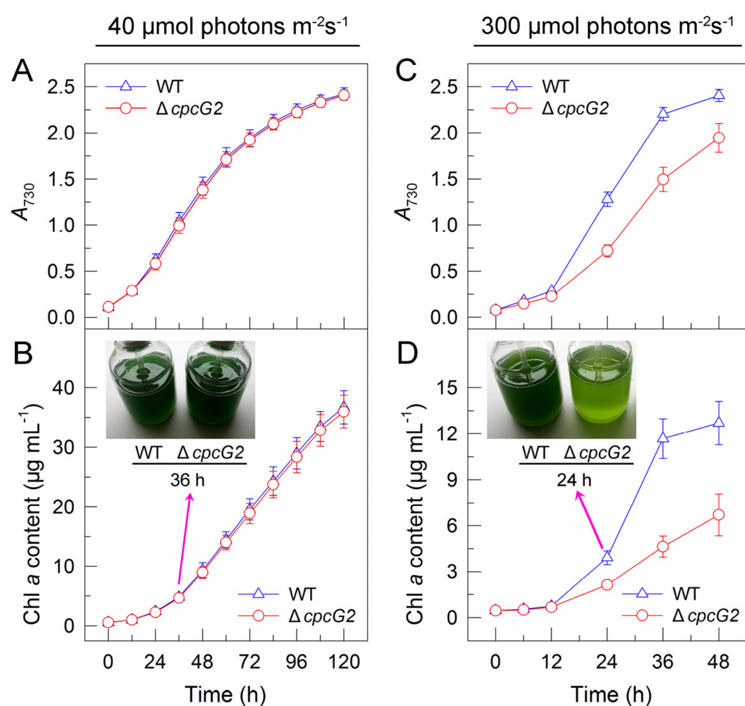
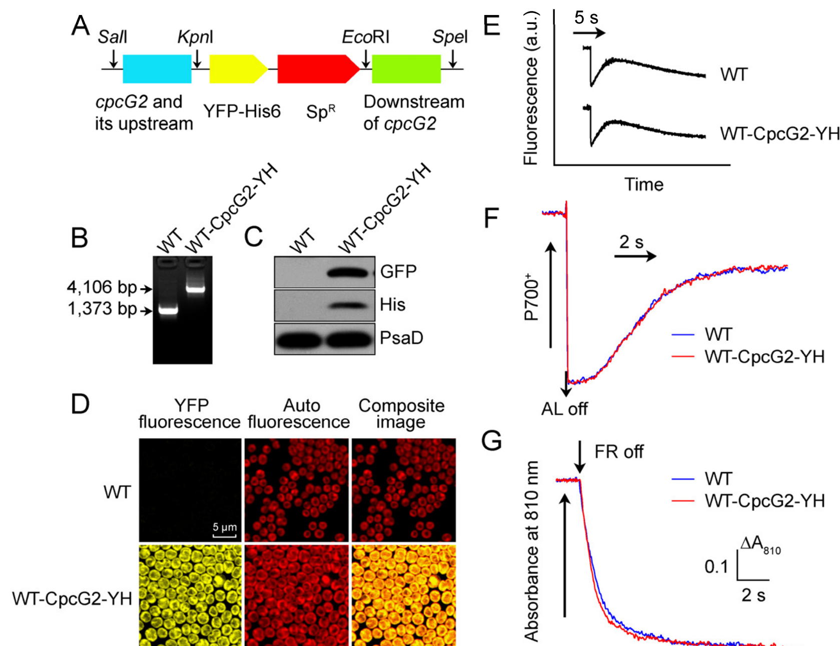
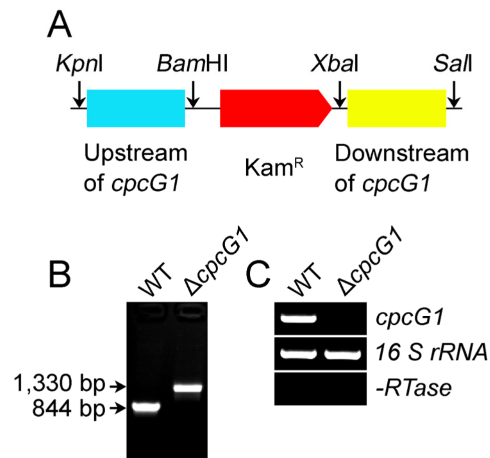
Supplemental Data



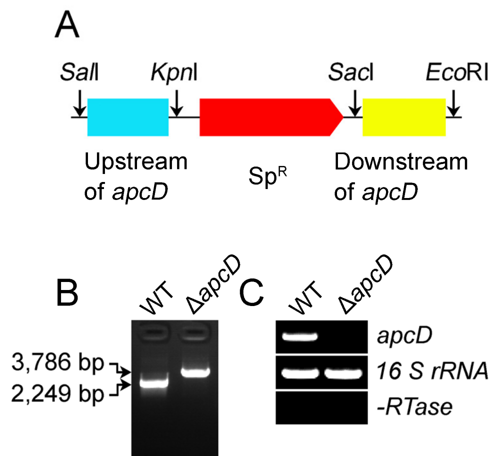
Supplemental Figure S1. Growth curve of WT and Δ*cpcG2* cells under different intensities. Cell density (A) and Chl *a* content (B) were monitored under normal light (40 μmol photons $m^{-2}s^{-1}$). Cell density (C) and Chl *a* content (D) were monitored under high light (300 μmol photons $m^{-2}s^{-1}$). Values are means ± SD (n = 5).



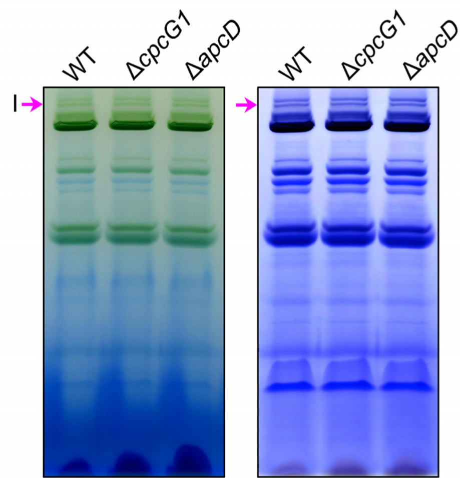
Supplemental Figure S2. Construction and characterization of WT-CpcG2-YH strain. A, Construction of plasmid to generate WT-CpcG2-YH mutant. DNA fragment containing *cpcG2* and its upstream region amplified by PCR was ligated between *Sal*I and *Kpn*I sites of the pEYFP-His6-Sp^R plasmid and a fragment downstream of *cpcG2* was ligated between *Eco*RI and *Spe*I sites. The plasmid thus constructed was used to transform WT cells to generate the tagged mutant. B, PCR segregation analysis of the WT-CpcG2-YH mutant using the *cpcG2-yfp-his6*-E and -F primer sequences (Supplemental Table S1). C, Western analysis of proteins from the WT and WT-CpcG2-YH strains using GFP and His antibodies. Total protein corresponding to 1 µg Chl *a* was loaded onto each lane. PsaD was detected as a loading control. D, Confocal microscopy analysis of WT and WT-CpcG2-YH cells. The scale bar indicates 5 µm. E, Monitoring of NDH-CET activity by Chl fluorescence. F, Redox kinetics of P700 after termination of actinic light (AL) illumination (800 µmol photons $m^{-2}s^{-1}$ for 30 s) under a background of far-red light (FR). G, Kinetics of $P700^+$ re-reduction in darkness after turning off FR with a maximum at 720 nm in the presence of 10 µM DCMU. The Chl *a* concentration was adjusted to 20 µg/mL and curves are normalized to the maximal signal. See Experimental Procedures for details.



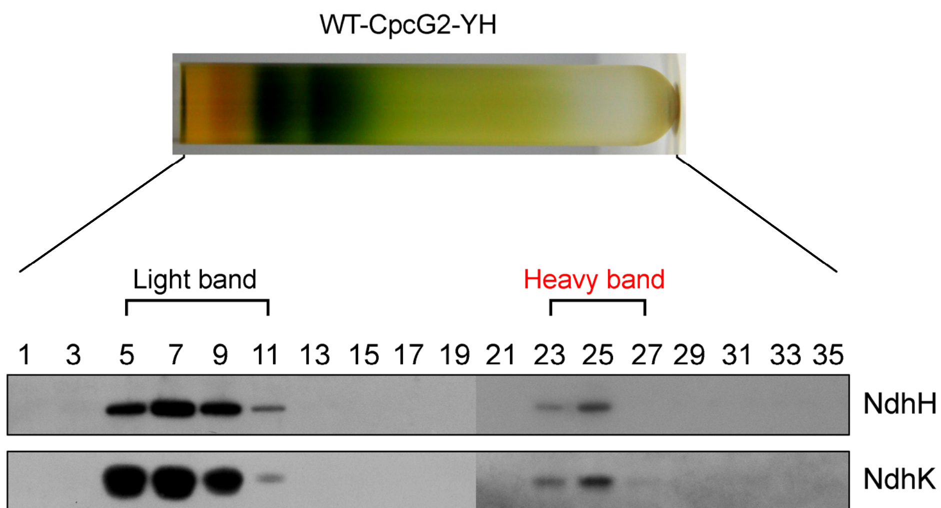
Supplemental Figure S3. Construction and analysis of *cpcG1* deletion mutant. A, Plasmid constructed to generate the *cpcG1* deletion mutant (Δ*cpcG1*). B, PCR segregation analysis of the Δ*cpcG1* mutant using the *cpcG1*-G and *cpcG1*-H primer sequences (Supplemental Table S1). C, Transcript levels of *cpcG1* in the WT and Δ*cpcG1* 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.



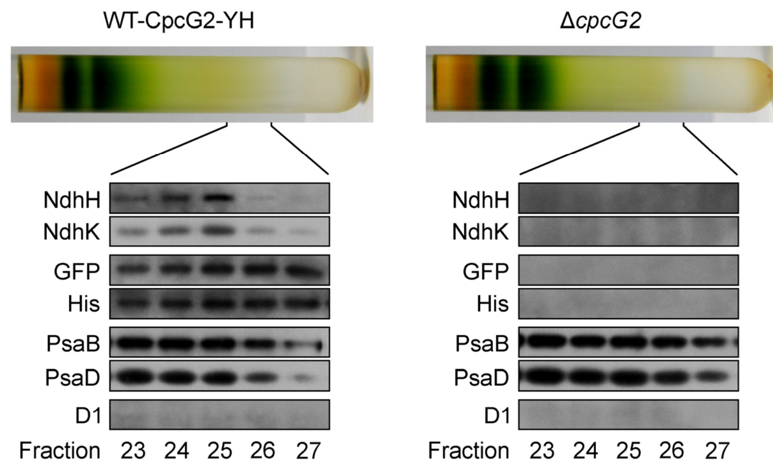
Supplemental Figure S4. Construction and analysis of *apcD* deletion mutant. A, Plasmid constructed to generate the *apcD* deletion mutant (Δ*apcD*). B, PCR segregation analysis of the Δ*apcD* mutant using the *apcD*-G and *apcD*-H primer sequences (Supplemental Table S1). C, Transcript levels of *apcD* in the WT and Δ*apcD* 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.



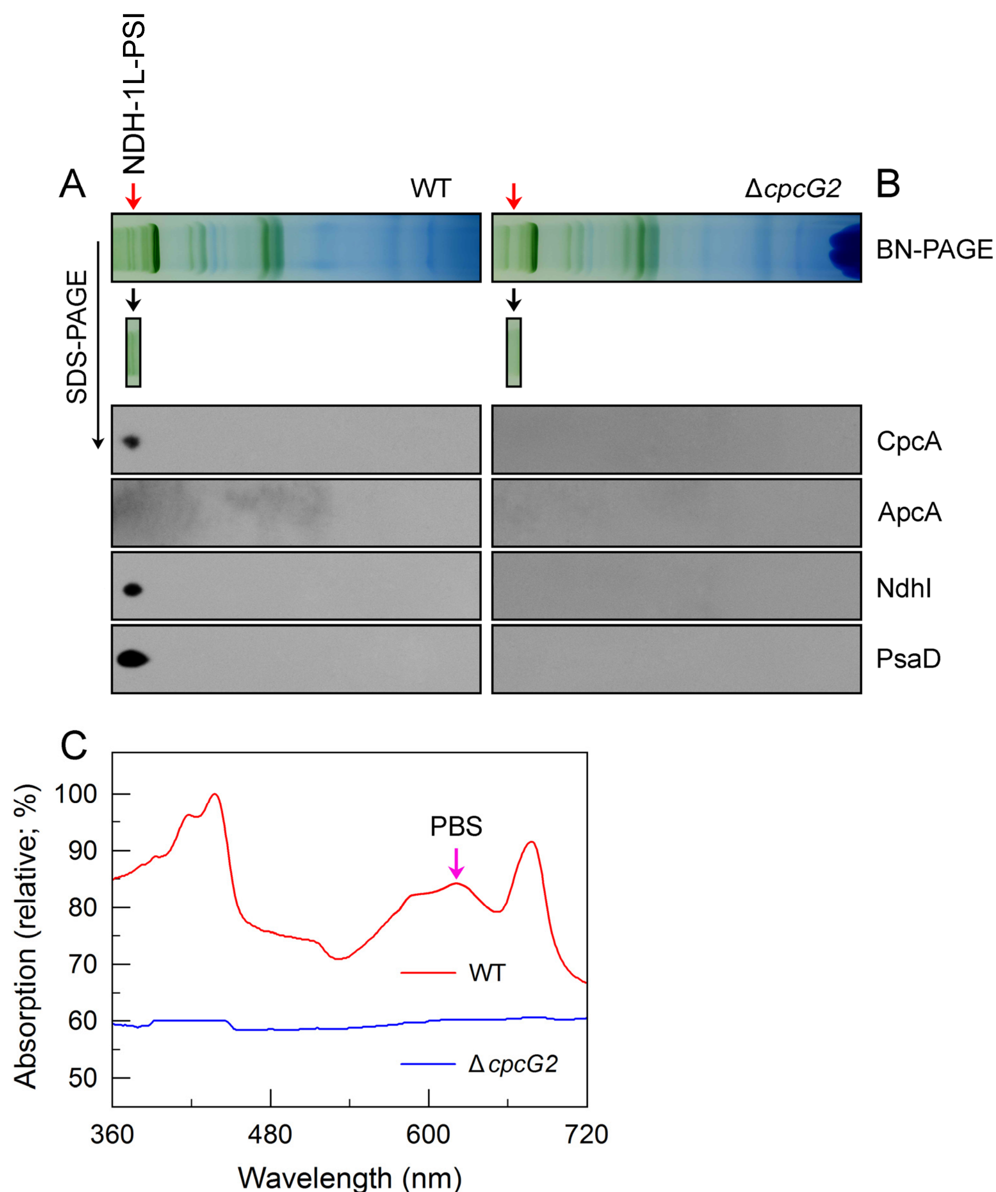
Supplemental Figure S5. Analysis of band I in the WT, Δ*cpcG1* and Δ*apcD* strains. Thylakoid membrane complexes isolated from the WT, Δ*cpcG1* and Δ*apcD* mutants were solubilized and separated by BN-PAGE (left side) and stained with CBB (right side). Band I is shown by pink arrows.



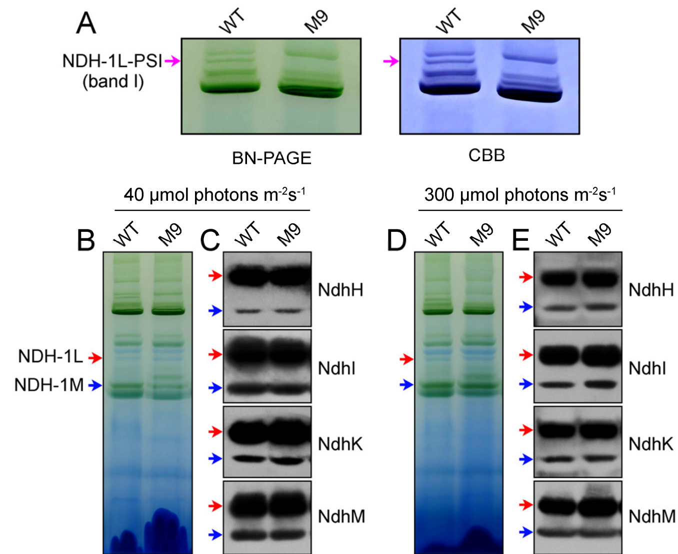
Supplemental Figure S6. Sucrose density gradient analysis of NDH-1 complexes isolated from the WT-CpcG2-YH strain. Thylakoid membranes were solubilized and separated in a linear 5-40% sucrose gradient. After centrifugation, 36 equal fractions were divided and alternate fractions were immunoblotted with antibodies against NdhH and NdhK.



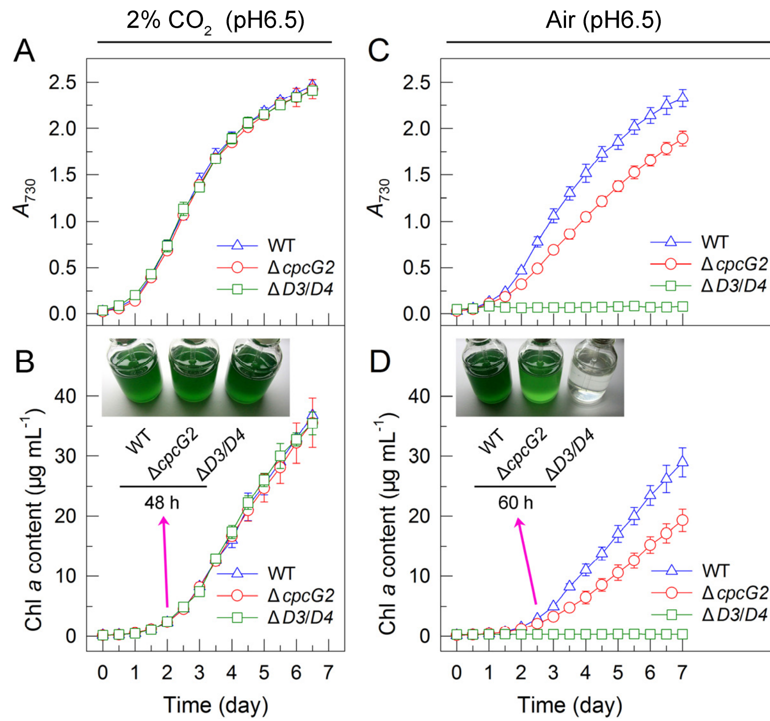
Supplemental Figure S7. Sucrose density gradient analysis of thylakoid membrane protein complexes isolated from the WT-CpcG2-YH and Δ*cpcG2* strains. Thylakoid membranes were solubilized and separated in a linear 5-40% sucrose gradient. After centrifugation, 36 equal fractions were divided and fractions 23 to 27 were immunoblotted with antibodies against the subunits of the major photosynthetic complexes.



Supplemental Figure S8. Identification of phycobilisome components in the NDH-1L-PSI supercomplex. A, Immunodetection showed the presence of peripheral rods of PBS but not its core in NDH-1L-PSI supercomplex. The supercomplex separated by BN-PAGE was cut out and was analyzed by western blot with specific antibodies, as indicated on the left. B, Measurement of the absorption spectrum indicated the presence of peak of PBS (see pink arrow) in NDH-1L-PSI supercomplex. The supercomplex strips cut out from BN-PAGE (A) were positioned into a cuvette and were analyzed by a spectrophotometer (UV3000; Shimadzu).



Supplemental Figure S9. Analysis of NDH-1L-PSI, NDH-1L and NDH-1M in WT and M9 strains. A, Analysis of NDH-1L-PSI (band I) in the WT and M9 strains. B and D, Profiles of BN-PAGE on the thylakoid membranes isolated from the WT and M9 strains. Thylakoid membrane extract corresponding to 9 µg Chl *a* was loaded onto each lane. Red and blue arrows indicate the positions of NDH-1L and NDH-1M complexes, respectively. C and E, Protein complexes were electroblotted to a polyvinylidene difluoride membrane and were cross-reacted with anti-NdhH, NdhI, NdhK, and NdhM.



Supplemental Figure S10. Growth curve of WT, Δ*cpcG2* and Δ*D3/D4* cells under different CO_2 concentrations at pH 6.5. Cell density (A) and Chl *a* content (B) were monitored under 2% CO_2 at pH 6.5. Cell density (C) and Chl *a* content (D) were monitored under air level of CO_2 at pH 6.5. Values are means ± SD (*n* = 5).

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 pUC-Δ*cpcG2* vector.

Name	Primer sequence (5’–3’)	Purpose
cpcG2-A	CGGAATTCTTCATCGGAAAAGGTCC	Amplification of upstream region
cpcG2-B	GGGGTACCTTTTTTTGACGGTAAAGC	
cpcG2-C	GGGGTACCGGGGGGGGGGGAAAG	Amplification of kanamycin gene
cpcG2-D	GCTCTAGAGGGGGGGGGGGCG	
cpcG2-E	GCTCTAGAAGATAAAGTTAGTAATTAAAC	Amplification of downstream region
cpcG2-F	GCTGCAGAAGGGGCGTGAACGAGTG	
cpcG2-G	TTAAACCGCCTAAGTCCCCCAGG	Segregation analysis
cpcG2-H	GTTATTGGCTGGACATTAAACAAC	

Primers used to construct pUC-Δ*cpcG1* vector.

Name	Primer sequence (5’–3’)	Purpose
cpcG1-A	GGGGTACCCGAAGCTGTTTGGGTTT	Amplification of upstream region
cpcG1-B	CGGGATCCGTGTAAACCTCCGTGATC	
cpcG1-C	CGGGATCCGGGGGGGGGGGAAAG	Amplification of kanamycin gene
cpcG1-D	GCTCTAGAGGGGGGGGGGGCG	
cpcG1-E	CTCTAGAGCACTAAGGTCAGAGG	Amplification of downstream region
cpcG1-F	GCGTCGACGATTCCGTGGTGTTCTG	
cpcG1-G	CTTCTTTAAGATCACGGAGGTTTAC	Segregation analysis
cpcG1-H	CAGTAACTATCCACGCTAGGAATGC	

Primers used to construct pUC-Δ*apcD* vector.

Name	Primer sequence (5'–3')	Purpose
apcD-A	GCGTCGACCTGAAGCAATGATGAAG	Amplification of upstream region
apcD-B	GGGGTACCCCCTATTTTGATTACAT	
apcD-C	GGGGTACCAAAATAAAAAAGGGGACCTC	Amplification of Spectinomycin gene
apcD-D	CGAGCTCAAAATAAAAAAGGGGACCTCTA GGGTC	
apcD-E	CGAGCTCGGCTTGCAAAATAACTTG	Amplification of downstream region
apcD-F	CGGAATTCTCGGAAGTACGTAAATC	
apcD-G	GCGTCGACCTGAAGCAATGATGAAG	Segregation analysis
apcD-H	CGGAATTCTCGGAAGTACGTAAATC	

Primers used for the pEYFP-CpcG2-YFP-His6 plasmid construction.

Name	Primer sequence (5'–3')	Purpose
cpcG2-yfp-his6-A	GCGTCGACTTCTCTATCAACCTCAG	Amplification of *cpcG2* and its upstream region
cpcG2-yfp-his6-B	GGGGTACCTTCAACCCAATAATGCC	
cpcG2-yfp-his6-C	CCGGAATTCTTTTTTTGACGGTAAA GCC	Amplification of downstream region
cpcG2-yfp-his6-D	GGACTAGTTAGGCTTGATGGTATTC	
cpcG2-yfp-his6-E	GGTTACCTGGCTTCATCAACGAACT	Segregation analysis
cpcG2-yfp-his6-F	GGACTAGTTAGGCTTGATGGTATTC	

Primers used for RT-PCR.

Name	Primer sequence (5'–3')	Purpose
cpcG2-FP	GGTTACCTGGCTTCATCAACGAACT	*cpcG2* transcript
cpcG2-RP	ACTAAGGGCAACGGCAATTATCCCT	
cpcG1-FP	CTTCCCCTATTGAACTACG	*cpcG1* transcript
cpcG1-RP	TTGAGGTACTCGTCGCTGTT	
apcD-FP	CAAGTTATTTTGCAAGCCGACGATC	*apcD* transcript
apcD-RP	AATAGGGAGCTGTCTCATTGGCATC	
16 S rRNA-FP	CGACTGCTAATACCCAATGTGC	*16 S rRNA* transcript
16 S rRNA-RP	GTCCCTCAGTGTCAGTTTCAGC	

Primers used to construct vectors to express proteins to raise antibodies.

Name	Primer sequence (5'–3')	Purpose
ndhA-FP	CGGAATTCATGAAGATTTCCGCCGCCG	NdhA antibody
ndhA-RP	CCCTCGAGCTTGGCGGGTACTACATC	
ndhN-FP	CGGGATCCATGTTGCCATTGCCA	NdhN antibody
ndhN-RP	CGGAATTCCTAGGCCGCCTGCAAG	