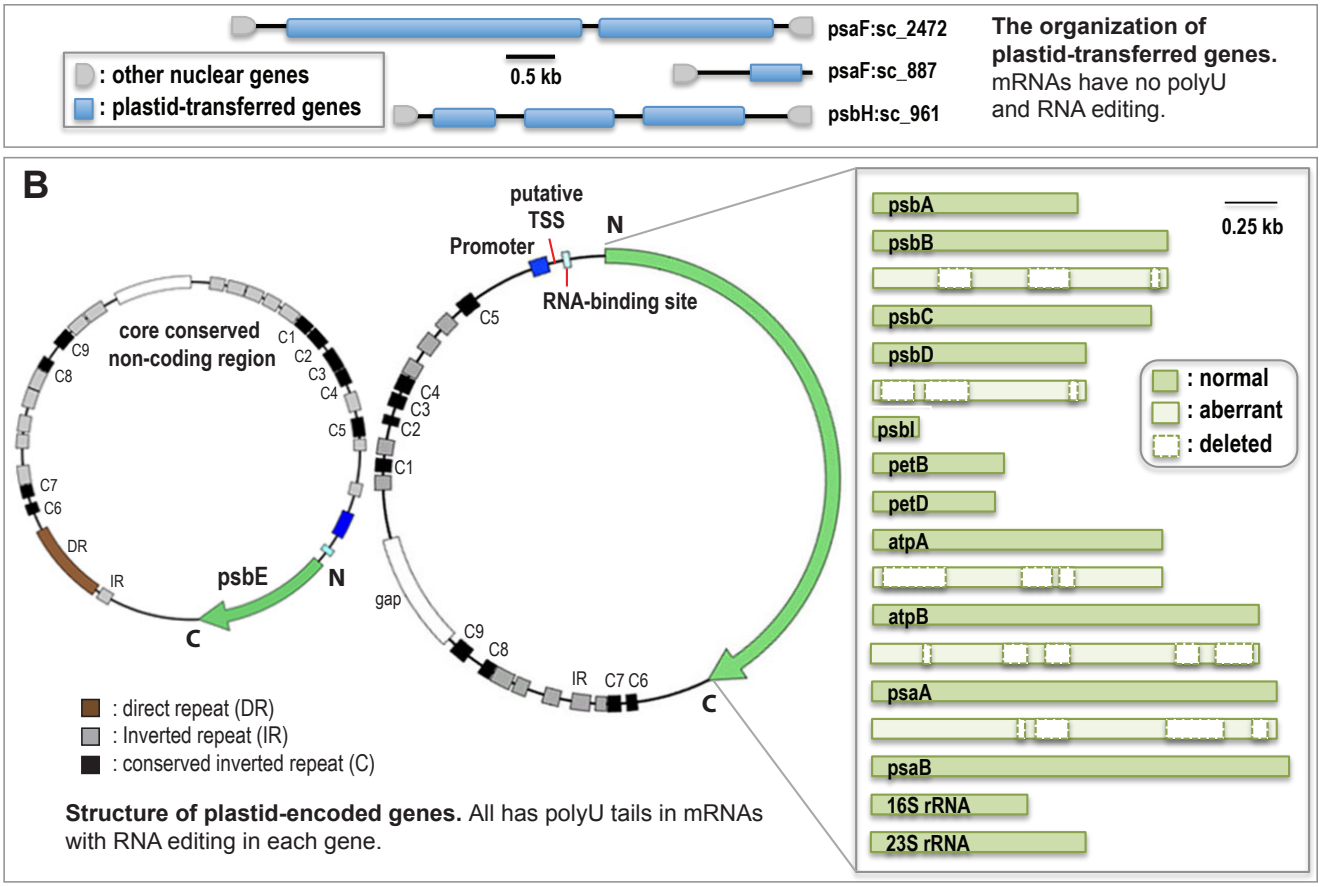
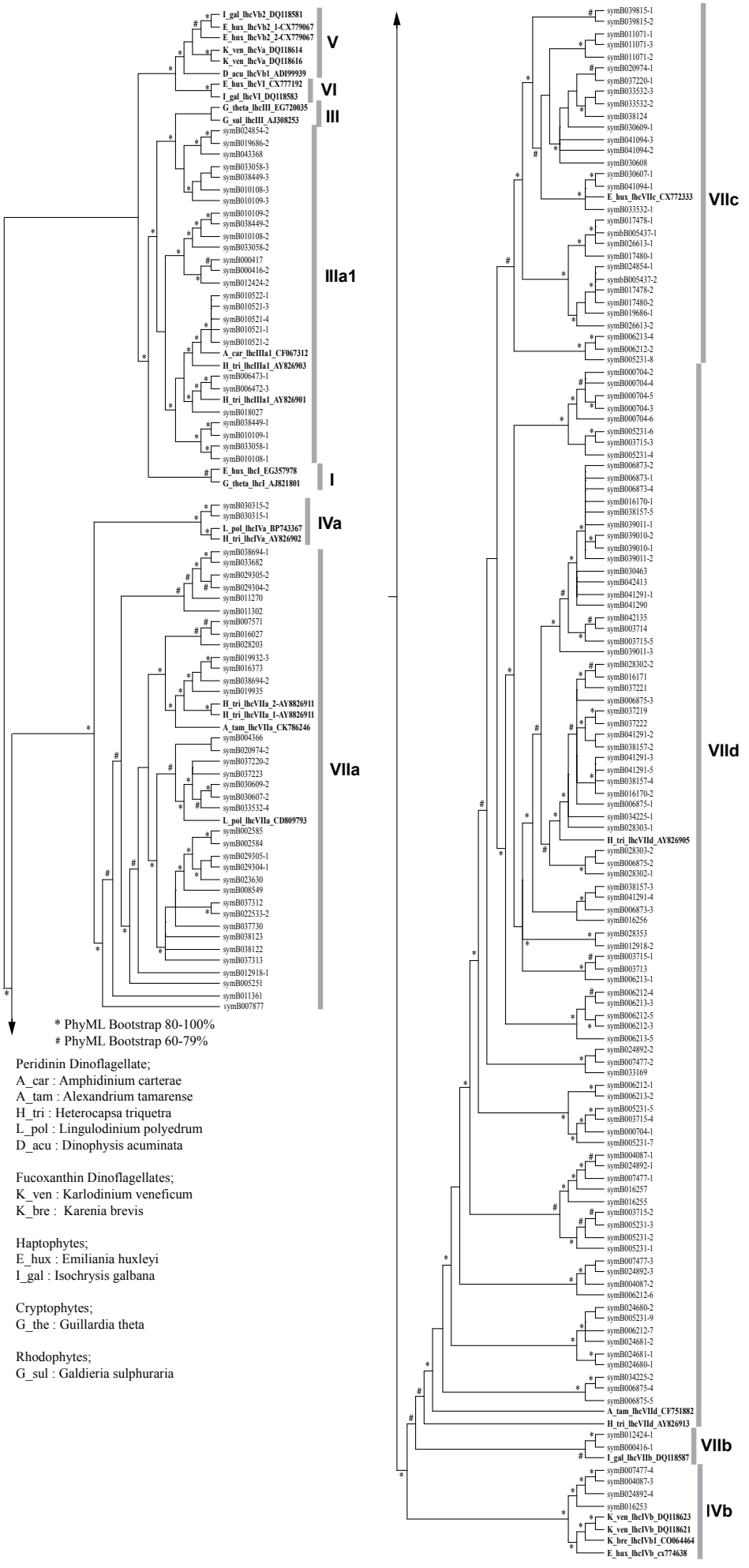
SUPPLEMENTARY FIGURES



Supplementary Figure S1: Structure of plastid-transferred genes and plastid-encoded genes (DNA minicircles) of *Symbiodinium minutum*. (**A**) Two examples of plastid-transferred genes. Two genes show duplications, often adjacent, on the same scaffold, and only rarely on different scaffolds. (**B**) Fourteen plastid-encoded genes organized in minicircles. The most common minicircle structure contains a coding region, plus a non-coding region containing a high density of inverted repeats (IR) (gray) and a minimum of nine conserved regions (black). The number of IRs varies from 10-16. In coding regions, aberrant forms were found in *psbB*, *psbD*, *atpA*, *atpB* and *psaA* with 3-5 deletions of ~50-300 bp. The *psbE* mincircle contains a direct repeat (brown) of 35 bp (GCAATCCTGCAGCATA**GCA**TATGCTGCAACCTGCT) in 4 copies. Each repeat is inverted. Therefore, *psbE* has the highest density of IRs (29) observed in *Symbiodinium*. A "GAP box" (white) represents incomplete sequences that were estimated from PCR products. A comparison of (A) and (B) above, demonstrates that nuclear-encoded genes have a completely different structure from plastid-encoded genes.



* PhyML Bootstrap 80-100%
\# PhyML Bootstrap 60-79%

Peridinin Dinoflagellate;
A_car : Amphidinium carterae
A_tam : Alexandrium tamarense
H_tri : Heterocapsa triquetra
L_pol : Lingulodinium polyedrum
D_acu : Dinophysis acuminata

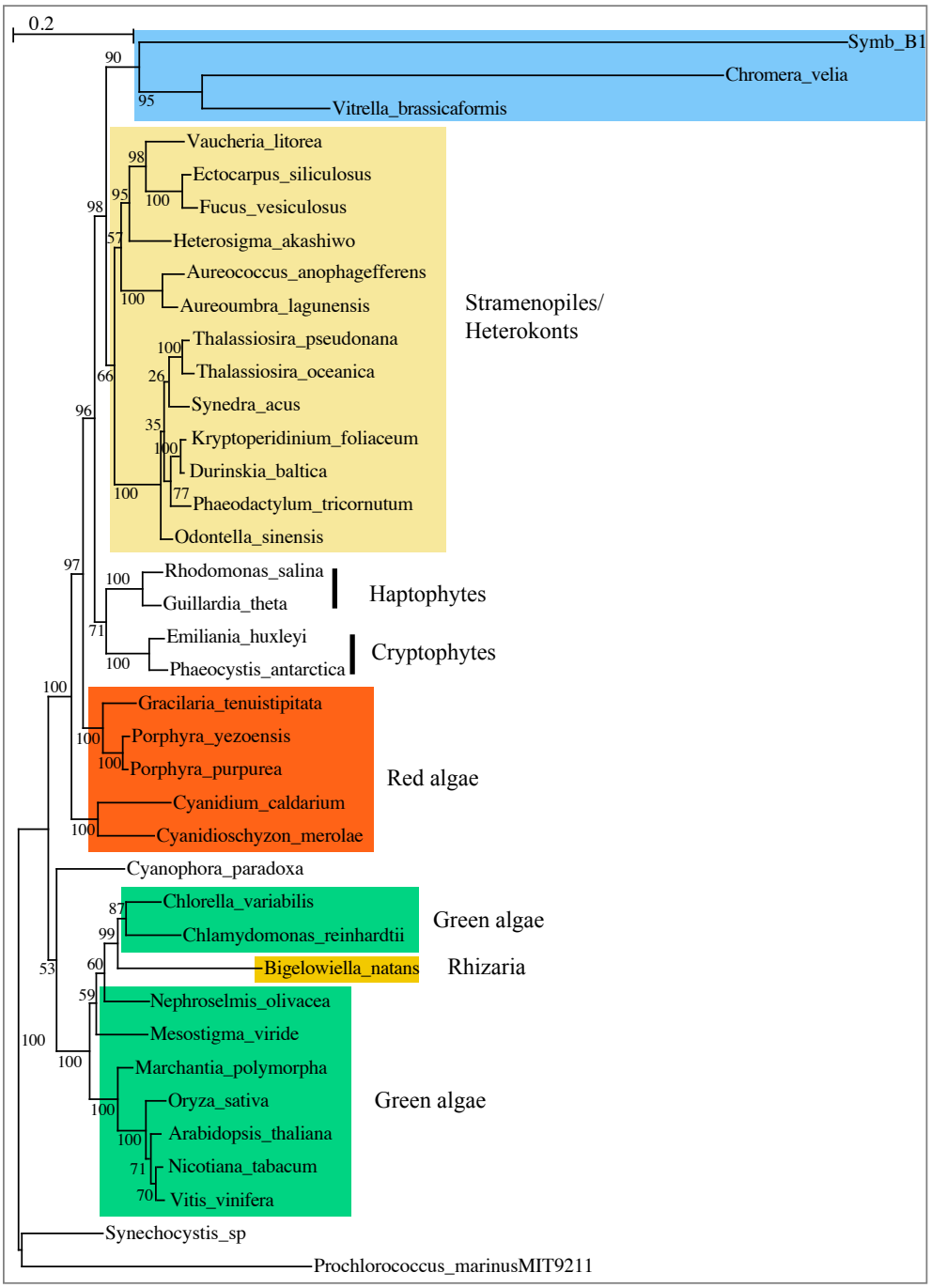
Fucoxanthin Dinoflagellates;
K_ven : Karlodinium veneficum
K_bre : Karenia brevis

Haptophytes;
E_hux : Emiliania huxleyi
I_gal : Isochrysis galbana

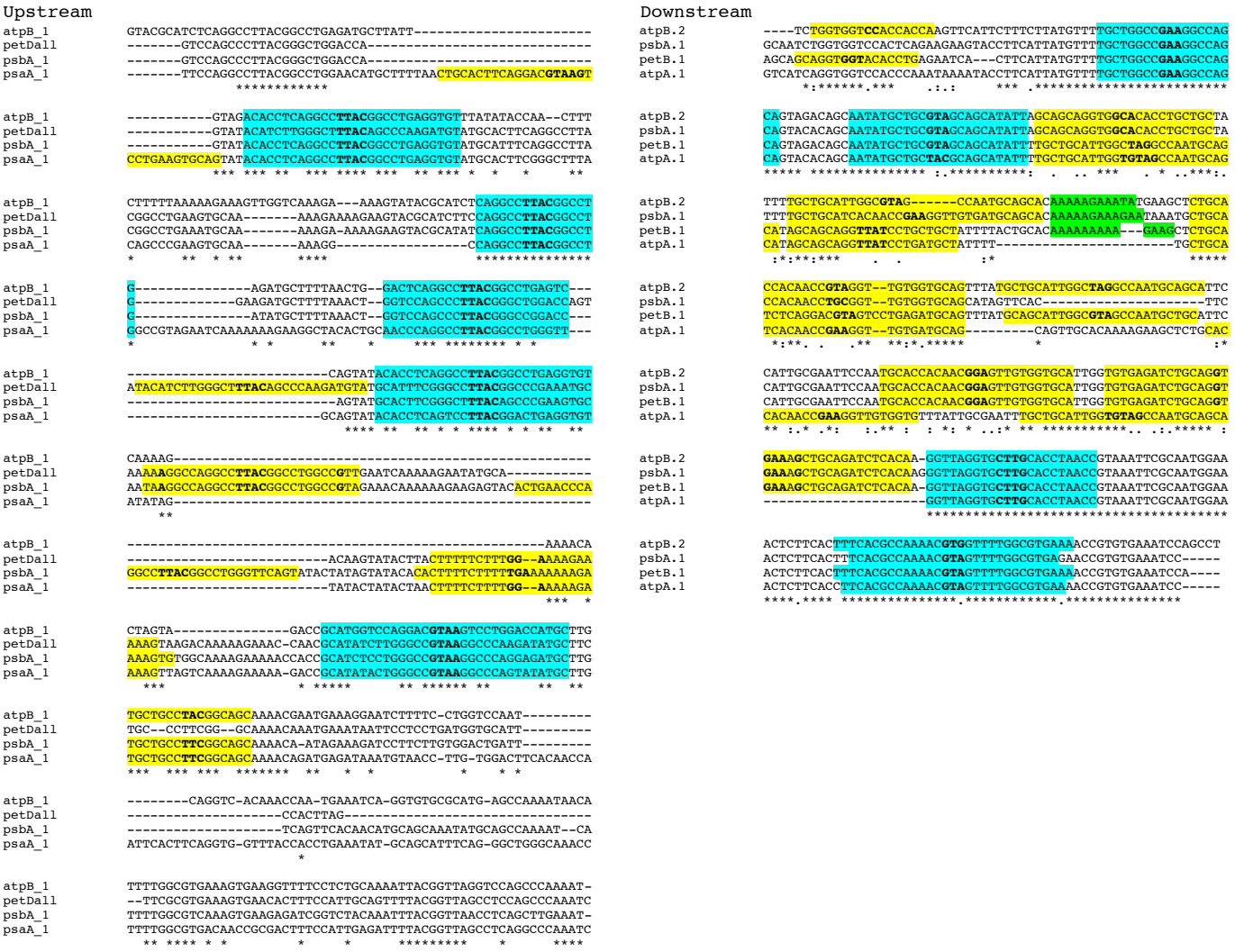
Cryptophytes;
G_the : Guillardia theta

Rhodophytes;
G_sul : Galdieria sulphuraria

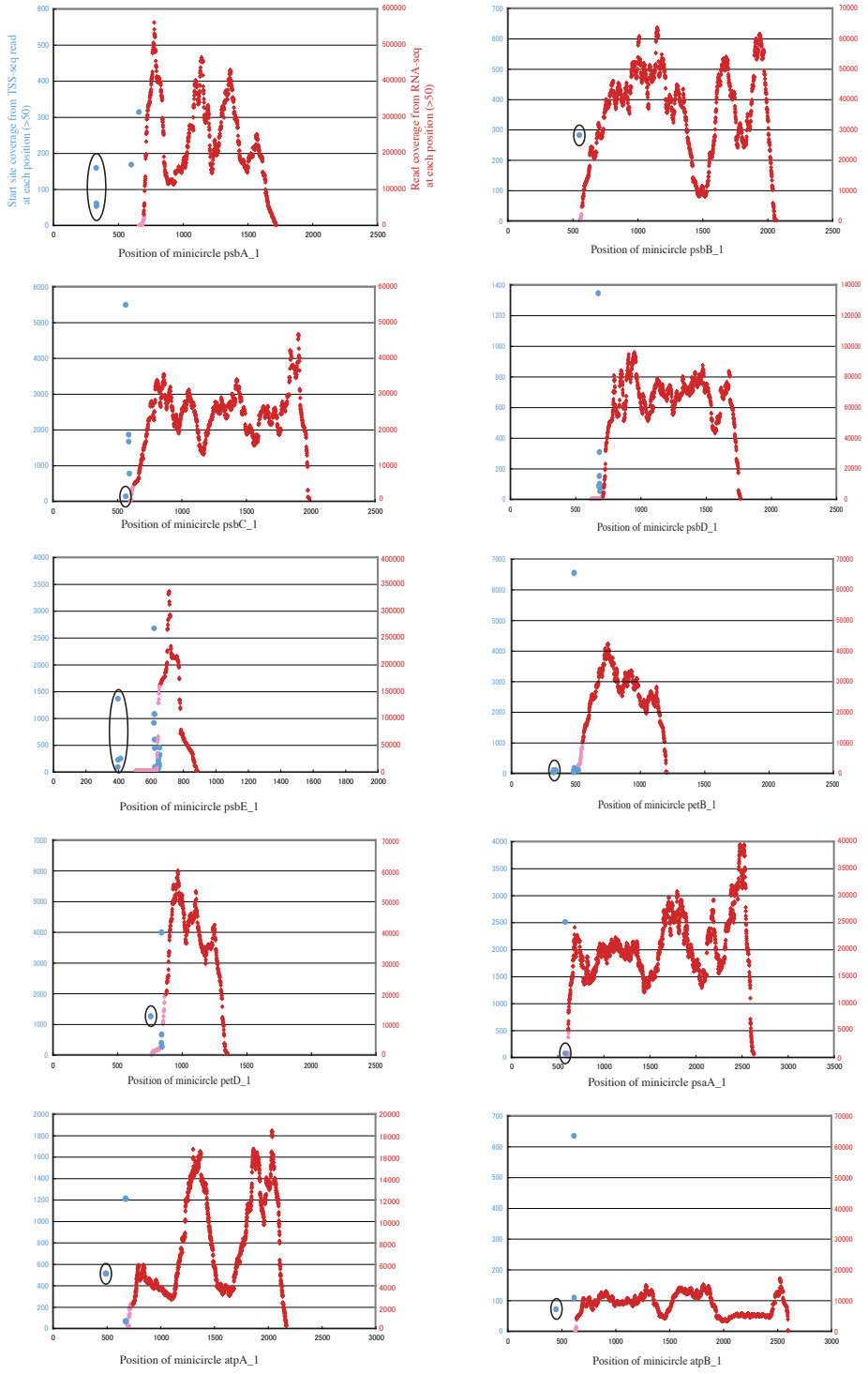
Supplementary Figure S2: Phylogenetic tree analysis of light-harvesting complexe proteins (LHCs) of *Symbodinium minutum*. Maximum likelihood analysis based on amino acid sequences of 101 *lhcb* genes. Polyprotein LHC sequences are treated as separate sequences with specific ID numbers. LHC sequences classified by Hoffman *et al*. (bold) were used as references to define *Symbiodinum* LHCs into subfamilies. By their share number, it can be seen that proteins in subfamily VIId have undergone extensive duplication in *Symbiodinium*.



Supplementary Figure S3: Genome-wide molecular phylogenetics of *Symbodinium minutum* based on proteins encoded by plastid DNA minicircles. Maximum-likelihood analysis based on alignment of 3,789 amino acid residues from proteins encoded by 11 core photosystem genes. *psbI* was excluded because it has been lost from the *Chromera* plastid genome. The clade of phylum Chromalveolata/red algae is supported by a 100% bootstrap value, whereas the Group Rhizaria is associated with green algae, forming an independent clade. The scale bar represents 0.2 expected substitutions per site in the aligned regions. The dinoflagellates and apicomplexans (blue) form a clade with the red algae (red) and the stramenopiles (yellow).

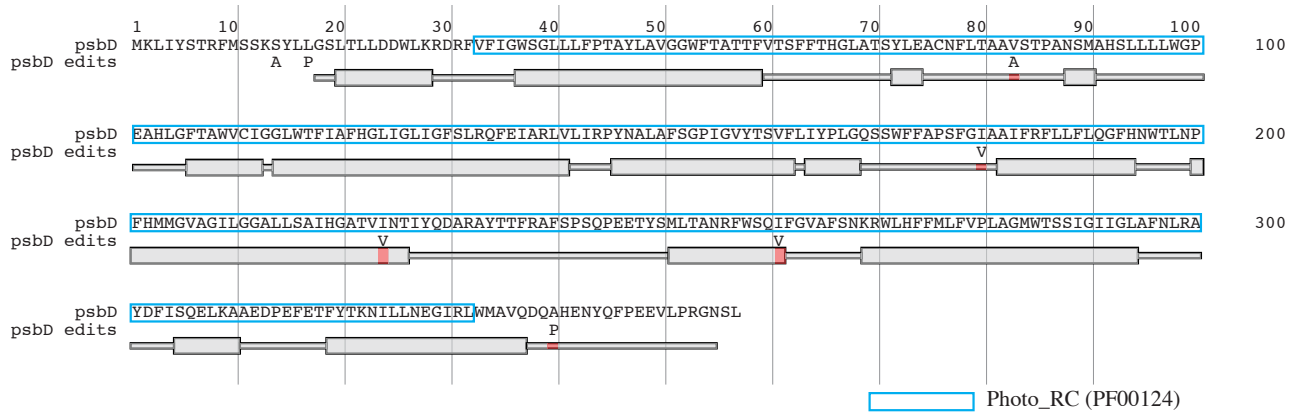


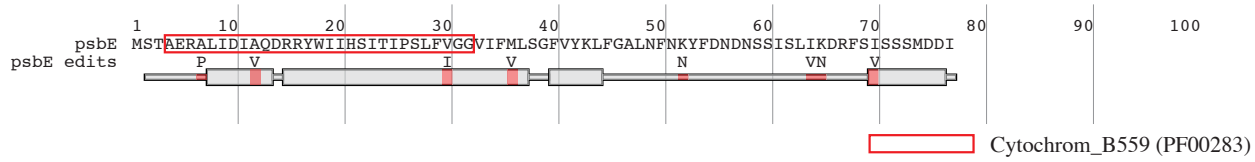
Supplementary Figure S4: Alignment of non-coding sequences of *Symbiodinium minutum* minicircles. Since the sequence of the non-coding region was incomplete, the upstream sequence beyond the start codon and the downstream sequence after the stop codon were used for the alignment. Inverted repeats (IRs) contain conserved regions (blue) and variable regions (yellow). Conserved regions are embedded in variable regions, which contain insertions and deletions. These variable regions also contain many IRs. Bold bases are intra-IR spacers. The number of IRs varies in the variable region. A region of high AT-content (green), is surrounded by an IR region. All *Symbiodinium* minicircles contain large numbers of IRs, the function of which is presently unknown. However, it has been suggested that the region bracketed by these sequences may contain the origin of replication.

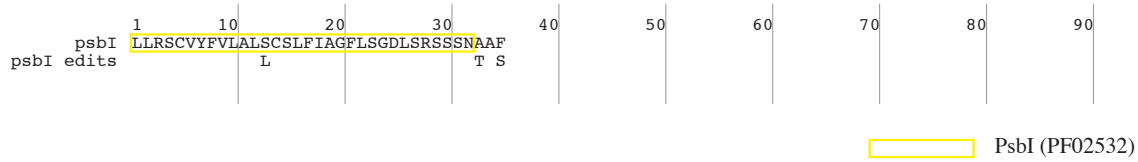


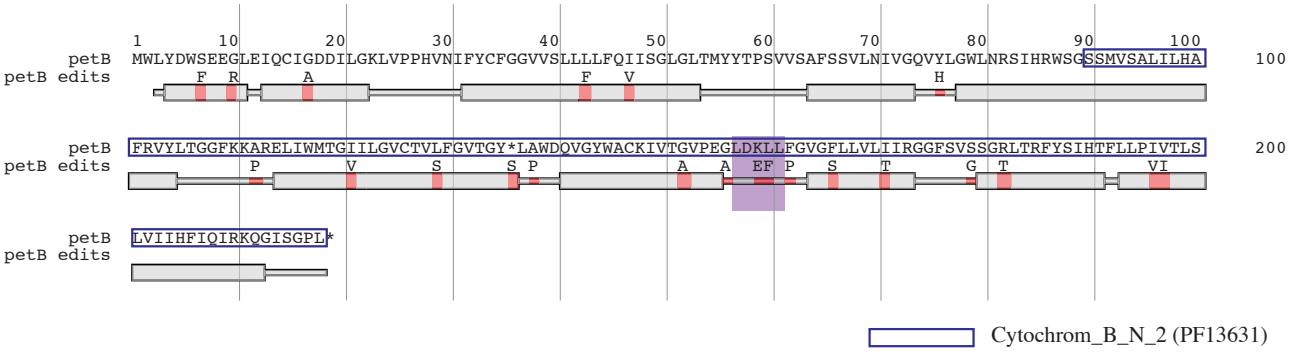
Supplementary Figure S5: TSS analysis of protein-coding genes of *Symbiodinium minutum* DNA minicircles. Blue dots show start site coverage (left Y axis) of reads from the TSS-library. Start site coverage of ORFs is omitted. In contrast, pink dots on UTRs and red dots on ORFs indicate read coverage (right Y axis) from RNA-seq without enzyme treatments. Most 5' dots removed from ORFs are surrounded by black line, corresponding to putative TSS sites (fig. 2). For psbD-containing minicircle, RNA-seq reads without enzyme treatments are mapped on most 5' region for that upstream of ORF.

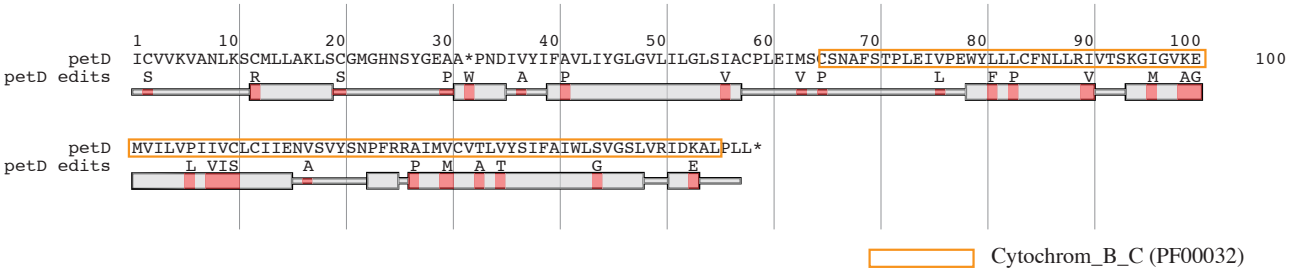

A
psbA
psbA edits
MKNRSYYQLNLLGNVIGFVLSTTNRLYIGCFGILMFPLLTLATIAYITAFILAPAVDIDGIREPVAGSLLYGNNIITGAVIPSSNAIGVHFYPVWESNHF
DECLYNGGTYQFVVLHFMLGVACWMGREWEFSFRLGMRPWIFVAFSAPVIAAFAVFVVYPIGQASFSDGMPLGISGTFNFMLVFQAEHNILMHPFHILGV
AGVFGGSLFSAMHGSLVTSSLLAESAGDISLNVGYKFGQEDETYSISAAHGYFGRLIFQYASFNNSRSLHFFLAAWPVIGIWFTALGVSTMAFNLNGLNF
NQSILDSSGHLILSWADIVNRADLGMEVMHERNAHNFPLDLA*
Photo_RC (PF00124)
psbB
psbB edits
MQITDALPWFRVHIVILNDPGRLISSHIMHTALVAGWSALMLLYELITIDPTDPVYNPIWRQAAYTLPFISRIGVIRSLFSWSLGIDPTSNLIWTYETMN
IAHILLSGLLILASFWHWAYWDLDLFFTSTLTLDLNQILSIHLTLASSLCLGFGLAHLTGFLGPGMWTSDSLNLVGSIRFVKASFNILSYARLAYGVISS
HHIISGLLGTSIGLWHITLRPLAYLYNLLSMGKVESILSSSITAVFFTAFLISALMWYGSAHTTQELFGPTRYSWDNAYYSLDIRTSCSNAWNTLPDKLV
LYDYIGSNPAKGGLFRSGPMLKADGLVQNWLGHACFSMGTLSLSIRRMPAFFETFPVILIDQTSTVRADIAFRRSTSTYSMEESQIQVYFSGGCLNGTEY
STPSLVKAYARKAQFGQIFTFDKKTSRLTDGVFRTSSRGWYSFSHIGLAFLFFFGHLWHASRAIFKDIWTGVTFESQAKQEYGRNEKLGDKTSSTKSIV*
PSII (PF00421)
psbC
psbC edits
MPLIYSLKRRTLVGSKYAWWSGNARFIELSGKFLGAHLVHTALILVWAGRMSLFELSHFIPEKPLYEQGFILLPHLFELGGNLYSHFIISILHLISAGIL
ALGGIYHAIVGGERLEETSYSSLFAYGLQDRFRITAILGSHLLTLGIGAGLLFAKAVYLGGLYDTWACGGGDMRLIERVELGLNPYLLAQYLLRAPFGSS
GWIISINNMEDLIGGHYWVSFYLILGSCWHIQTRALTITTRAFTWSAEAYLSYTLSAVTLCGSITSLFSWYNNTAYPSEFYGPTGAEASQAQSFTFLIRD
WKLGIKISSSEGPTALGKYLMRSPTGEIIFGGESMRFWSMQAHWLEALRTSFGLDLSKIQSDIQTWQERRAAEYMTHAPLGSLNSVGGVATEINSVNYVS
PRSWLTSSHWFLAFFILVGHWWHGARSRAAALSSETGLSRVYEPVLYMRPID*
PSII (PF00421)

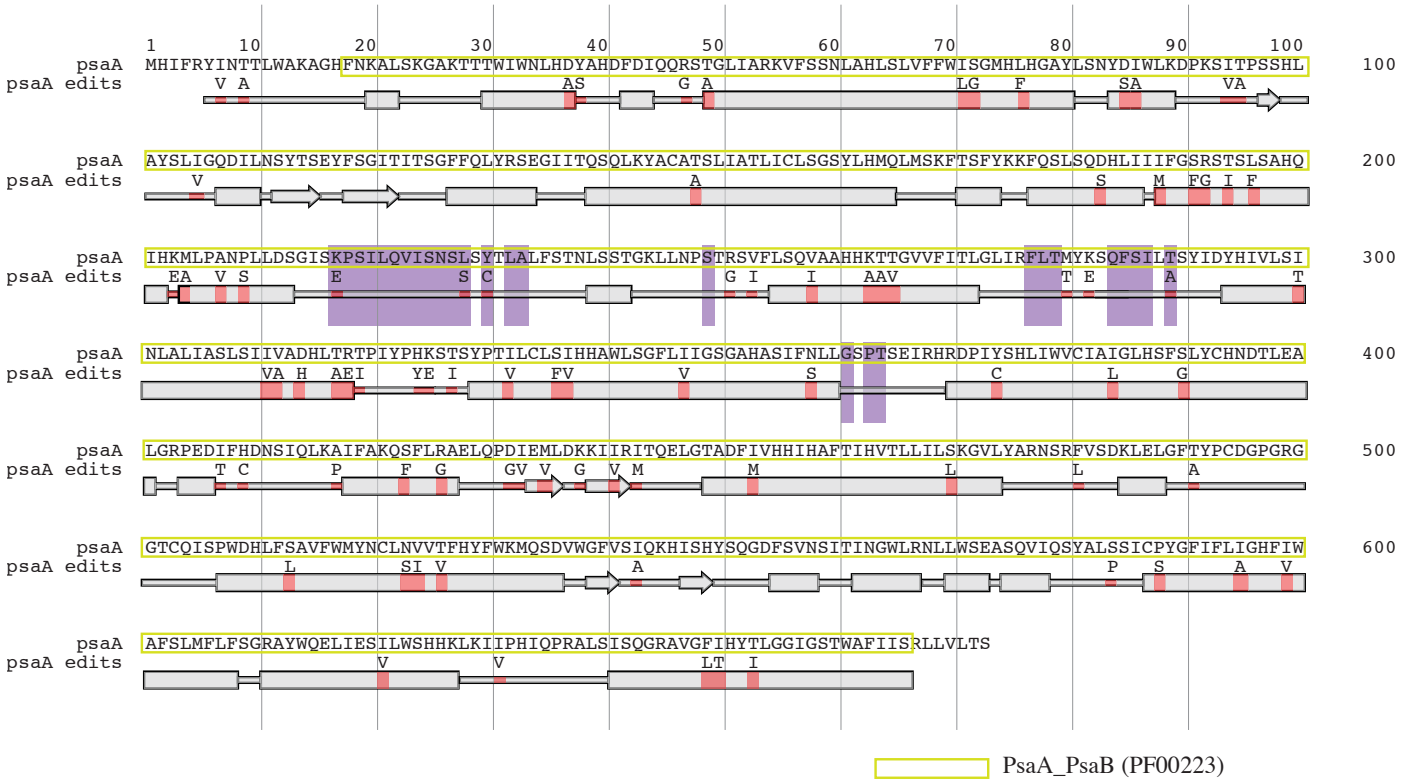

psbD MKLIYSTRFMSSKSYLLGSLTLLDDWLKRDRFVFIGWSGLLLFPTAYLAVGGWFTATTFVTSFFTHGLATSYLEACNFLTAAVSTPANSMAHSLLLLWGP 100
psbD edits A P A
psbD EAHLGFTAWVCIGGLWTFIAFHGLIGLIGFSLRQFEIARLVLIRPYNALAFSGPIGVYTSVFLIYPLGQSSWFFAPSFGIAAIFRFLLFLQGFHNWTLNP 200
psbD edits V
psbD FHMMGVAGILGGALLSAIHGATVINTIYQDARAYTTFRAFSPSQPEETYSMLTANRFWSQIFGVAFSNKRWLHFFMLFVPLAGMWTSSIGIIGLAFNLRA 300
psbD edits V V
psbD YDFISQELKAAEDPEFETFYTKNILLNEGIRLWMAVQDQAHENYQFPEEVLPRGNSL
psbD edits P
Photo_RC (PF00124)

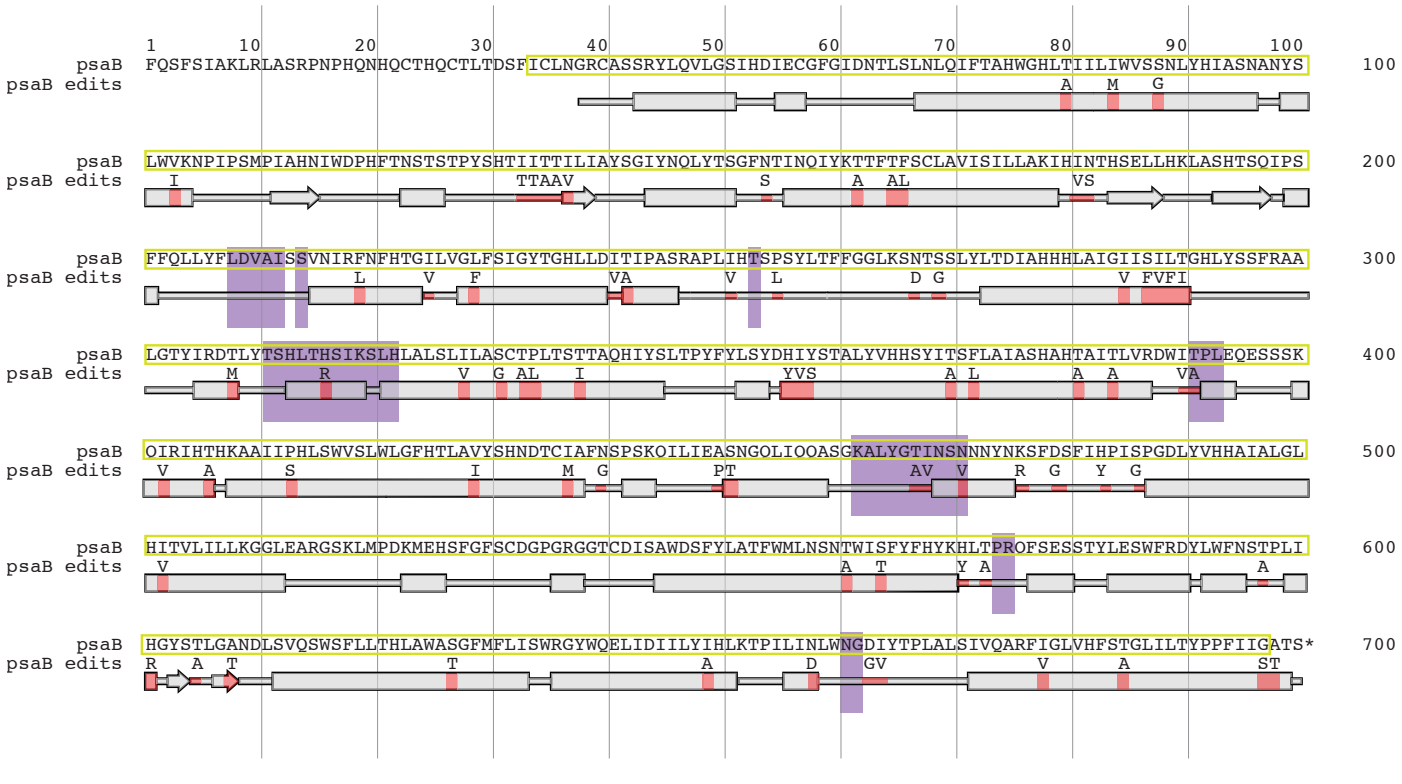

psbE MSTAERALIDIAQDRRYWIIHSITIPSLFVGGVIFMLSGFVYKLFGALNFNKYFDNDNSSISLIKDRFSISSSMDDI
psbE edits P V I V N VN V
Cytochrom_B559 (PF00283)

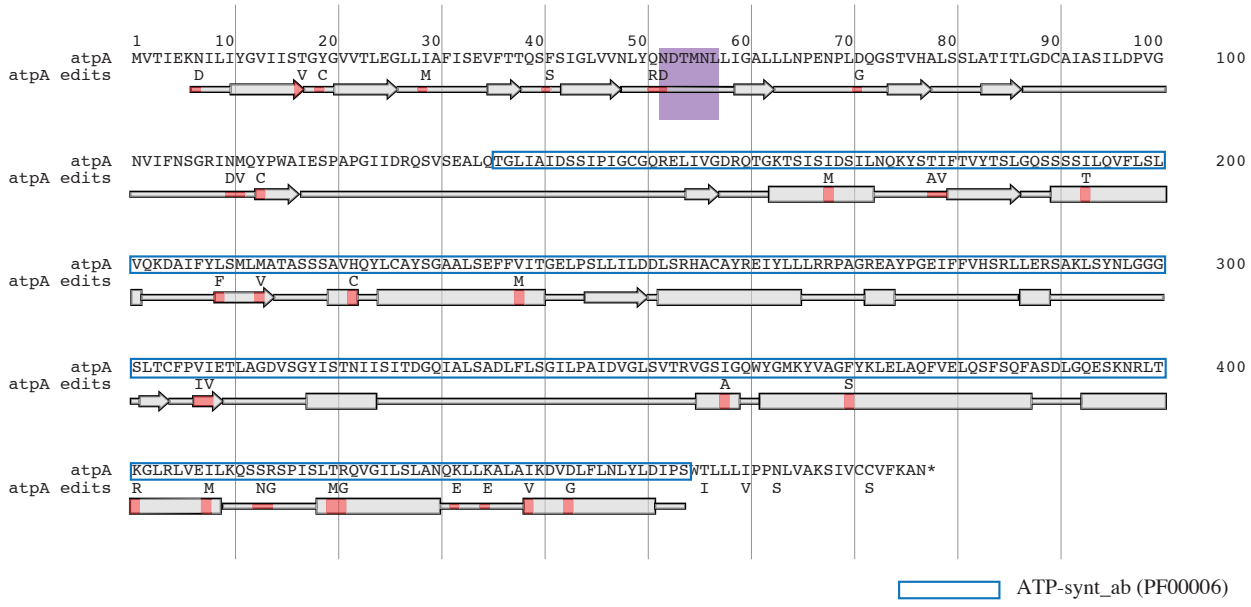

psbI LLRSCVYFVLALSCSLFIAGFLSGDLSRSSSNAAF
psbI edits L T S
PsbI (PF02532)

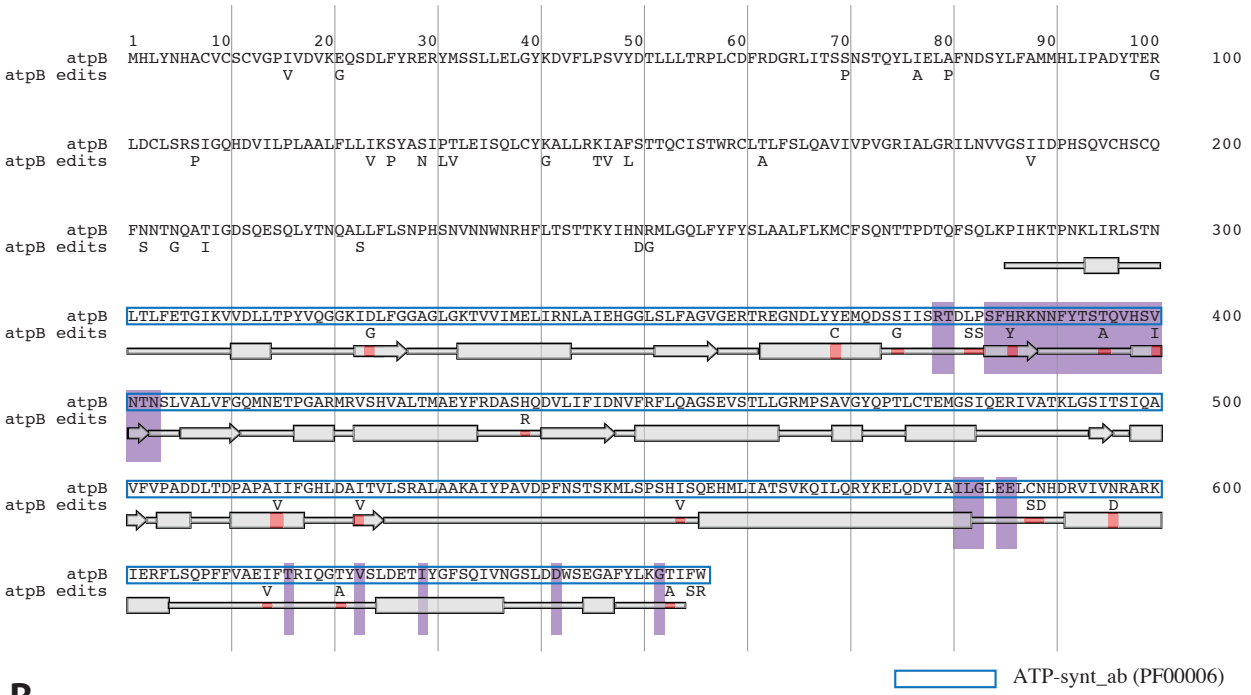

petB MWLYDWSEEGLEIQCIGDDILGKLVPPHVNIFYCFGGVVSLLLLFQIISGLGLTMYYTPSVVSAFSSVLNIVGQVYLGWLNRSIHRWSGSSMVSALILHA 100
petB edits F R A F V H
petB FRVYLTGGFKKARELIWMTGIILGVCTVLFGVTGY*LAWDQVGYWACKIVTGVPEGLDKLLFGVGFLLVLIIRGGFSVSSGRLTRFYSIHTFLLPIVTLS 200
petB edits P V S S P A A EF P S T G T VI
petB LVIIHFIQIRKQGISGPL*
petB edits
Cytochrom_B_N_2 (PF13631)


petD ICVVKVANLKSCMLLAKLSCGMGHNSYGEAA*PNDIVYIFAVLIYGLGVLILGLSIACPLEIMSCSNAFSTPLEIVPEWYLLLCFNLLRIVTSKGIGVKE 100
petD edits S R S P W A P V V P L F P V M AG
petD MVILVPIIVCLCIIENVSVYSNPFRRAIMVCVTLVYSIFAIWLSVGSLVRIDKALPLL*
petD edits L VIS A P M A T G E
Cytochrom_B_C (PF00032)

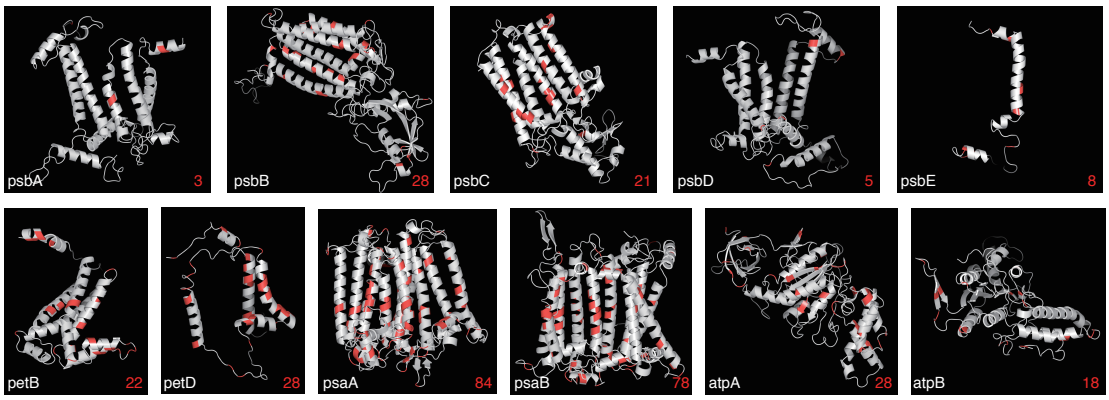

psaA
psaA edits
PsaA_PsaB (PF00223)


psaB
psaB edits
PsaA_PsaB (PF00223)


atpA
atpA edits
ATP-synt_ab (PF00006)


atpB
atpB edits
ATP-synt_ab (PF00006)

B


psbA 3
psbB 28
psbC 21
psbD 5
psbE 8
petB 22
petD 28
psaA 84
psaB 78
atpA 28
atpB 18

Supplementary Figure S6: Distribution of amino acid residues converted by RNA editing in plastid-encoded genes of *Symbiodinium minutum* and predicted secondary structures. (A) Lower case letters show edited amino acid residues. Conserved structures found by a pfam domain search are colored. Predicted secondary structures, helix (gray boxes), β-sheet (arrow boxes) and others (lines) are shown. Edited sites are marked in red. Regions showing significant conformational changes are highlighted in purple. **(B)** Secondary structures of plastid-encoded genes are also shown in 3D models. Residue numbers of amino acids converted by RNA editing are shown in red.