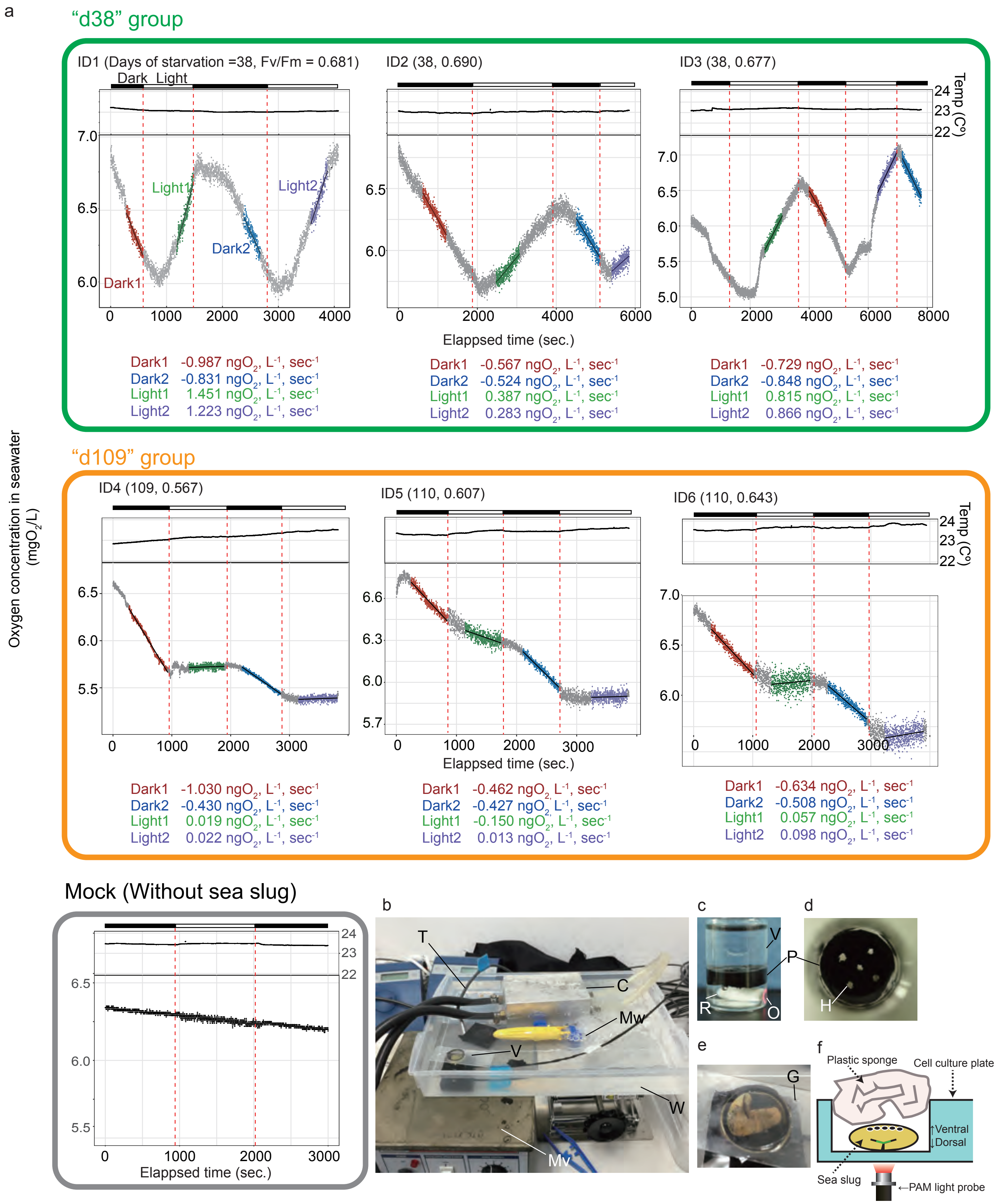
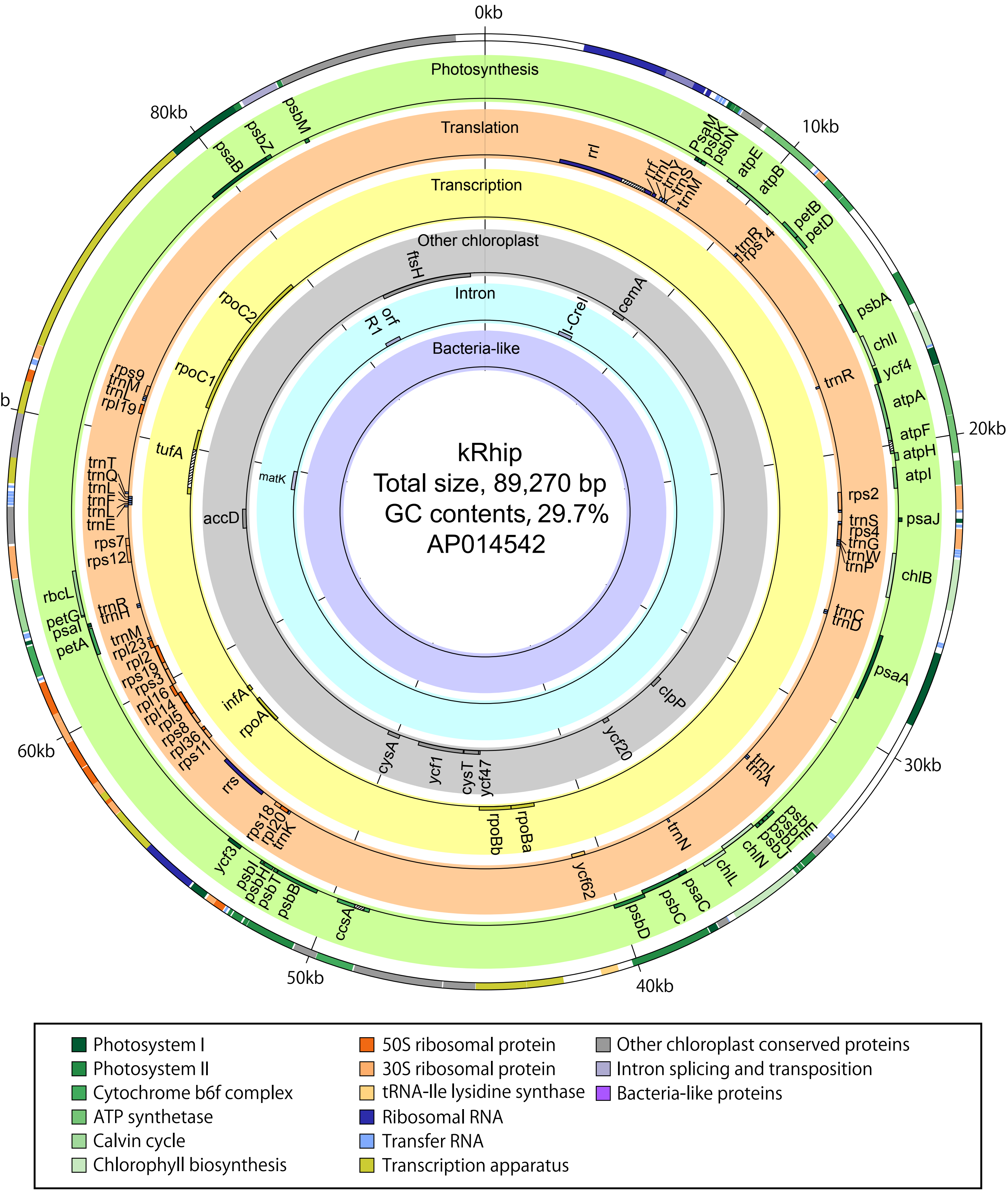


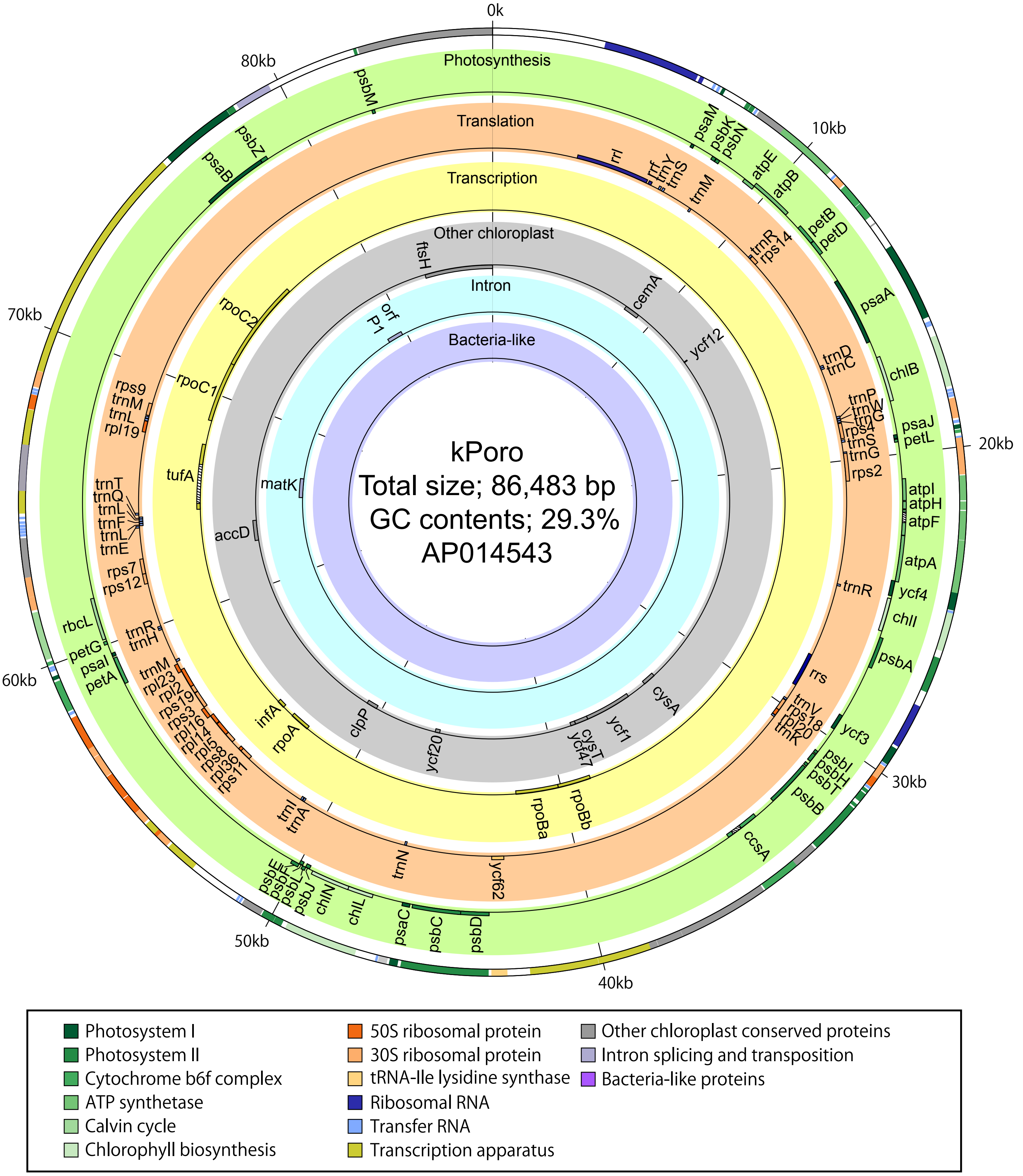
Supplementary Figure 1 Light-dependent oxygen generation by *P. ocellatus.*

a Oxygen concentration time-course of sample-rearing seawater. Each plot means a result from a single PoB individual in a vial filled with seawater. Raw data, DOI 10.6084/m9.figshare.12301865. **b-e** Oxygen measurement system. **b** Overview of the applied oxygen measurement system. C, Iron chilling block; Mw, Mixer for lagging water; Mv, Mixer for sea slug rearing seawater; V, Glass vial caging a sea slug; W, Plastic tray filled with lagging water for the vial. **c** Horizontal view of glass vial. O, Oxygen sensitive optode; P, Rubber-made partition plate to separate sea slug from optode and rotor; R, Rotor for seawater agitation. **d** Top view of the vial. H, Hole for water ventilation. **e** Top vial view with a sea slug. G, glass plate sealing the top of the vial. **f** Diagram of PAM measurement method. Horizontal view of the sea slug in a well of the cell culture plate and positions of a sponge and a light probe.

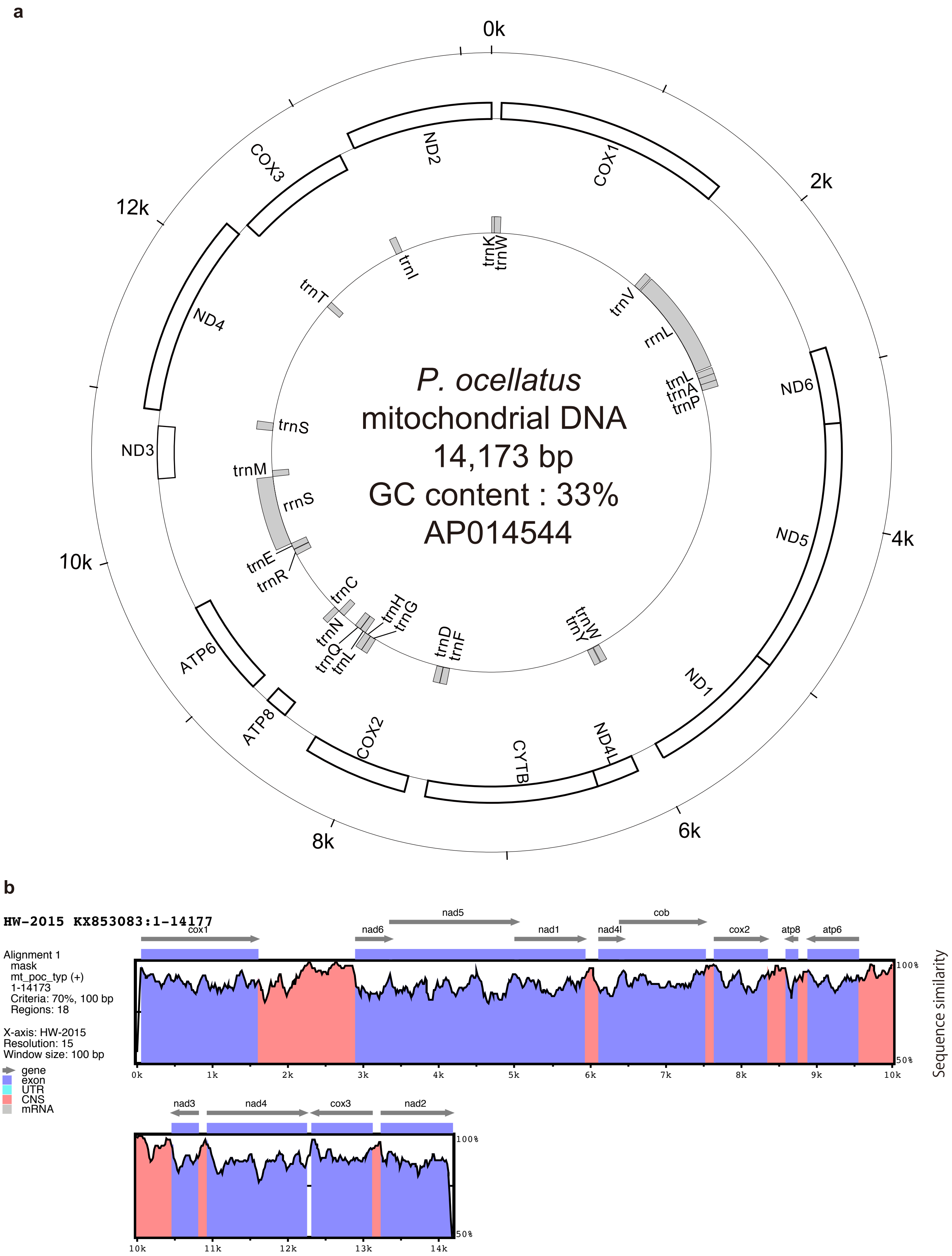


Supplementary Figure 2 Gene map of a *P. ocellatus* kleptoplast DNA sequestered from *Rhipidosiphon lewmanomontiae*

The outer circle shows the distribution of all genes on kpDNA. Colors show functional categories of the genes (the corresponding between the color and the category was presented in the boxed legend). Inner circles show the names and positions of genes related to photosynthesis (2nd circle), translation (3rd) and transcription (4th), other conserved chloroplast genes (5th), genes relating intron-splicing and transposition (6th) and bacteria-like genes (7th). Genes on the outside of each circle are transcribed in the clockwise direction; genes on the inside are transcribed in the anticlockwise direction. Hatched boxes on the inner circles show introns.

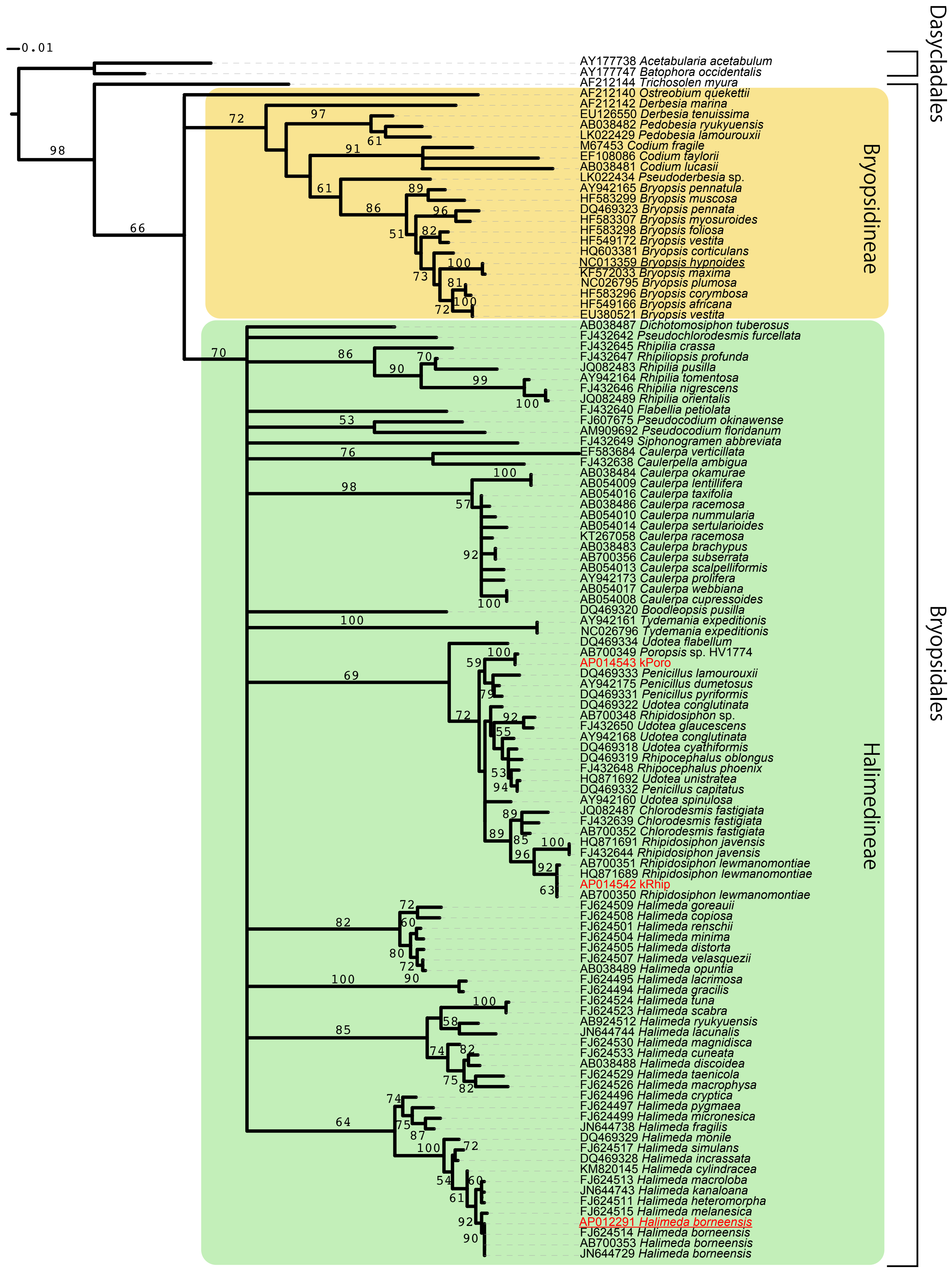


Supplementary Figure 3 Gene map of a *P. ocellatus* kleptoplast DNA sequestered from *Poropsis* spp. Circles and colors are as in Supplementary Figure 2.

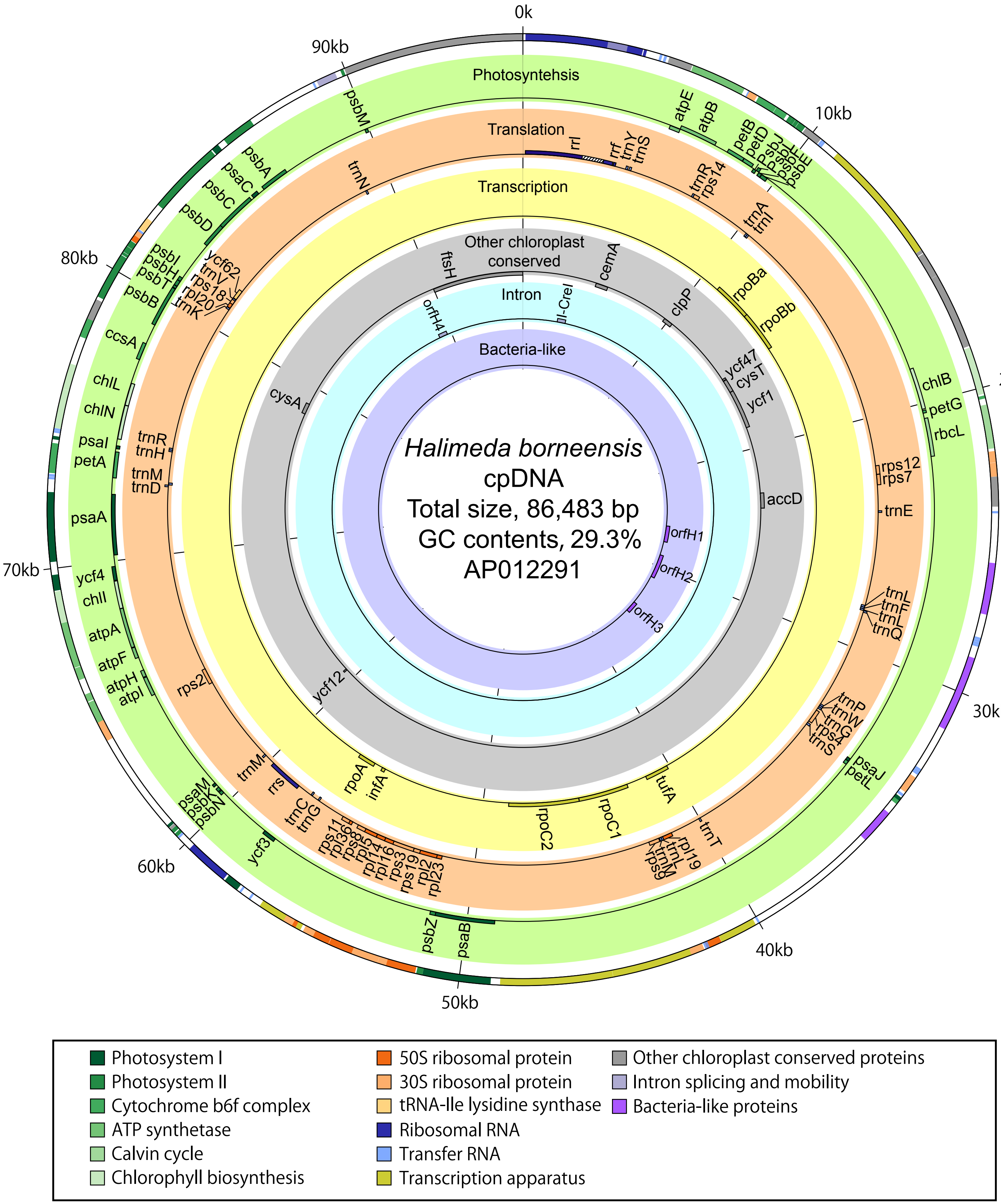


Supplementary Figure 4 Gene map of a *P. ocellatus* type black mitochondrial DNA.

a The outer circle gives the scale in base pairs. Inner circles show the names and positions of protein-encoding genes (2nd circle) and structure RNA encoding genes (3rd). **b** Sequence similarity between our *P. ocellatus* type black mitochondrial DNA and previously sequenced ones from *P.* cf. *ocellatus* HW-2015 (KX853083). Data were visualized with mVISTA software.

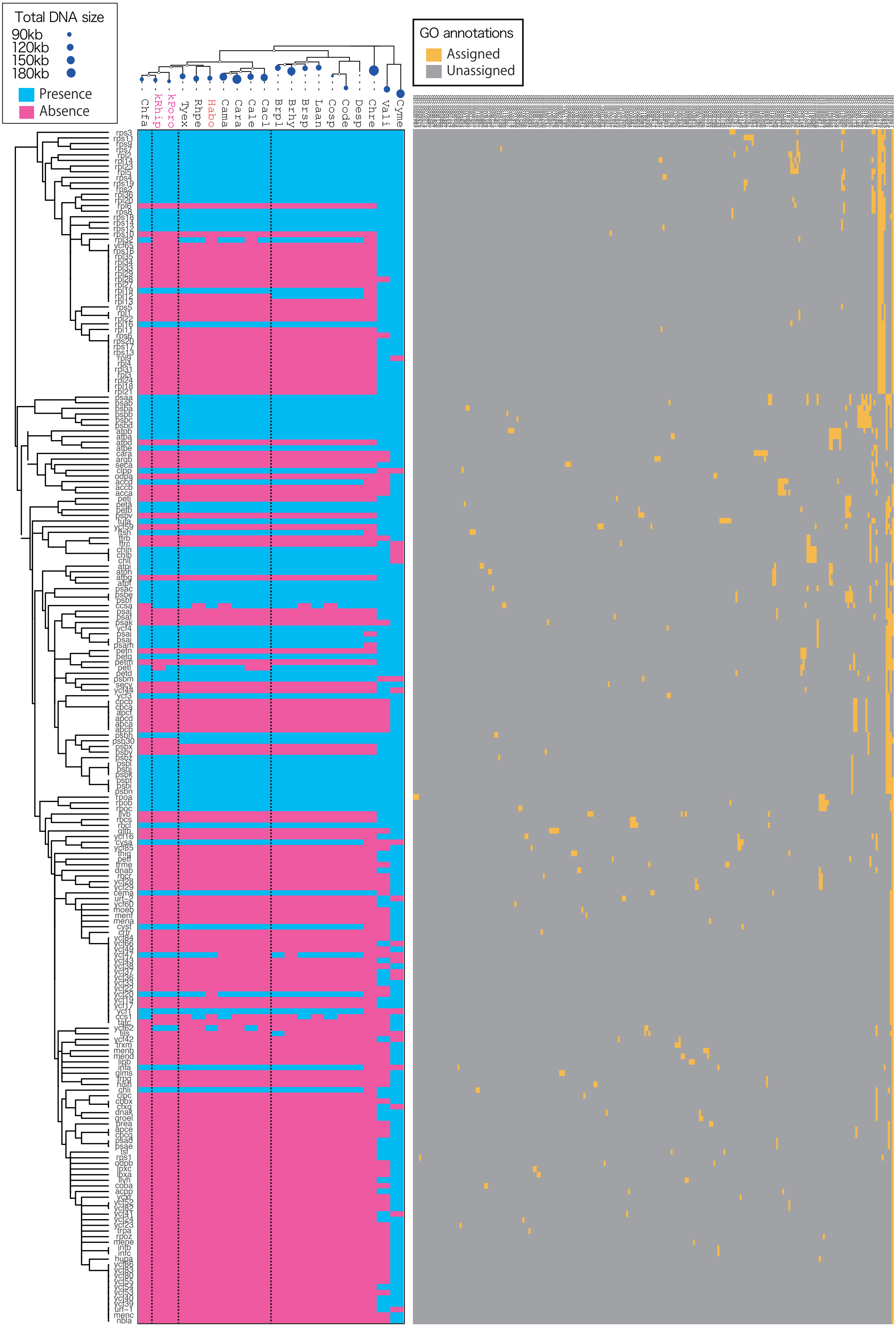


Supplementary Figure 5 Bryopsidales ML tree made by RAxML (a -x 12345 -p 12345 -# 300 -m GTRGAMMAI) based on 457 positions of *rbcL* genes. Bootstrap values are described at each node. We omitted the node with <50 bootstrap values. Scale bar represents the branch length. The color and underlines at the OTUs have the same meanings as in Fig. 3b.



Supplementary Figure 6 Gene map of the *H. borneensis* chloroplast DNA.

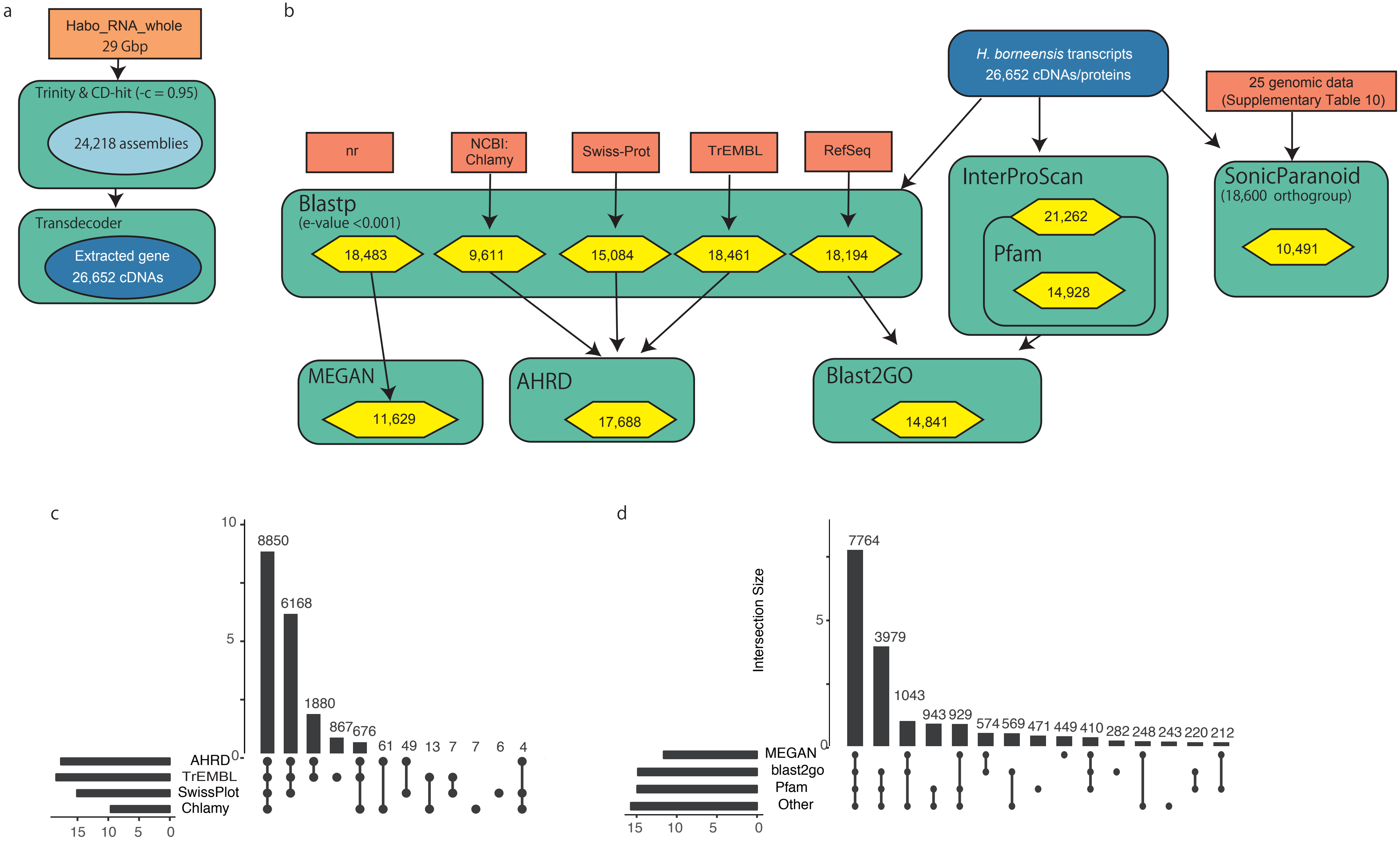
Circles and colors are as in Supplementary Figure 2.


Total DNA size
90kb
120kb
150kb
180kb
Presence
Absence
GO annotations
Assigned
Unassigned
Chfa
kRhip
kPoro
Tyex
Rhpe
Habo
Cama
Cara
Cale
Cacl
Brpl
Brhy
Brsp
Laan
Cosp
Code
Desp
Chre
Vali
Cyme
rps3
rps11
rps9
rps7
rpl2
rpl14
rpl23
rpl5
rps4
rps19
rps2
rpl36
rpl20
rpl6
rps8
rps18
rps14
rps12
rps10
rpl32
ycf65
rps16
rpl35
rpl34
rpl33
rpl29
rpl28
rpl27
rpl19
rpl12
rpl13
rps5
rpl1
rpl22
rpl16
rpl11
rps6
rps20
rps17
rps13
rpl9
rpl4
rpl31
rpl3
rpl24
rpl18
rpl21
psaa
psab
psba
psbb
psbc
psbd
atpb
atpa
atpd
atpe
cara
argb
seca
clpp
odpa
accd
accb
acca
petj
peta
petb
psbv
tufa
ycf59
ftsh
ftrb
ftrc
chln
chlb
chll
atpi
atph
atpg
atpf
psac
psbe
psbf
ccsa
psaj
psaf
psak
ycf4
psai
psal
psam
petn
petg
petm
petl
petd
psbm
secy
ycf44
ycf3
cpcb
cpca
apcf
apcd
abca
abcb
psbh
psb30
psbx
psby
psbz
psbl
psbj
psbk
psbt
psbi
psbn
rpoa
rpob
rpoc
ilvb
rbcs
rbcl
gltb
ycf16
cysa
ycf85
thig
petf
trme
dnab
rbcr
ycf28
ycf29
cema
urf-2
ycf60
moeb
menf
mena
cyst
crtr
ycf84
ycf66
ycf49
ycf47
ycf43
ycf38
ycf37
ycf36
ycf33
ycf22
ycf20
ycf19
ycf17
ycf1
ccs1
tatc
ycf62
tils
ycf42
trxm
menb
mend
lipb
infa
glms
trpg
hish
chli
clpc
cbbx
cfxq
dnak
groel
prea
apce
cbcq
psad
psae
tsf
rps1
odpb
lpxc
lpxa
ilvh
coba
acpp
ycf21
ycf52
ycf82
ycf41
ycf24
ycf23
trpa
rpoz
mene
infb
infc
hupa
ycf86
ycf83
ycf80
ycf55
ycf54
ycf53
ycf40
ycf39
urf-1
menc
nbla

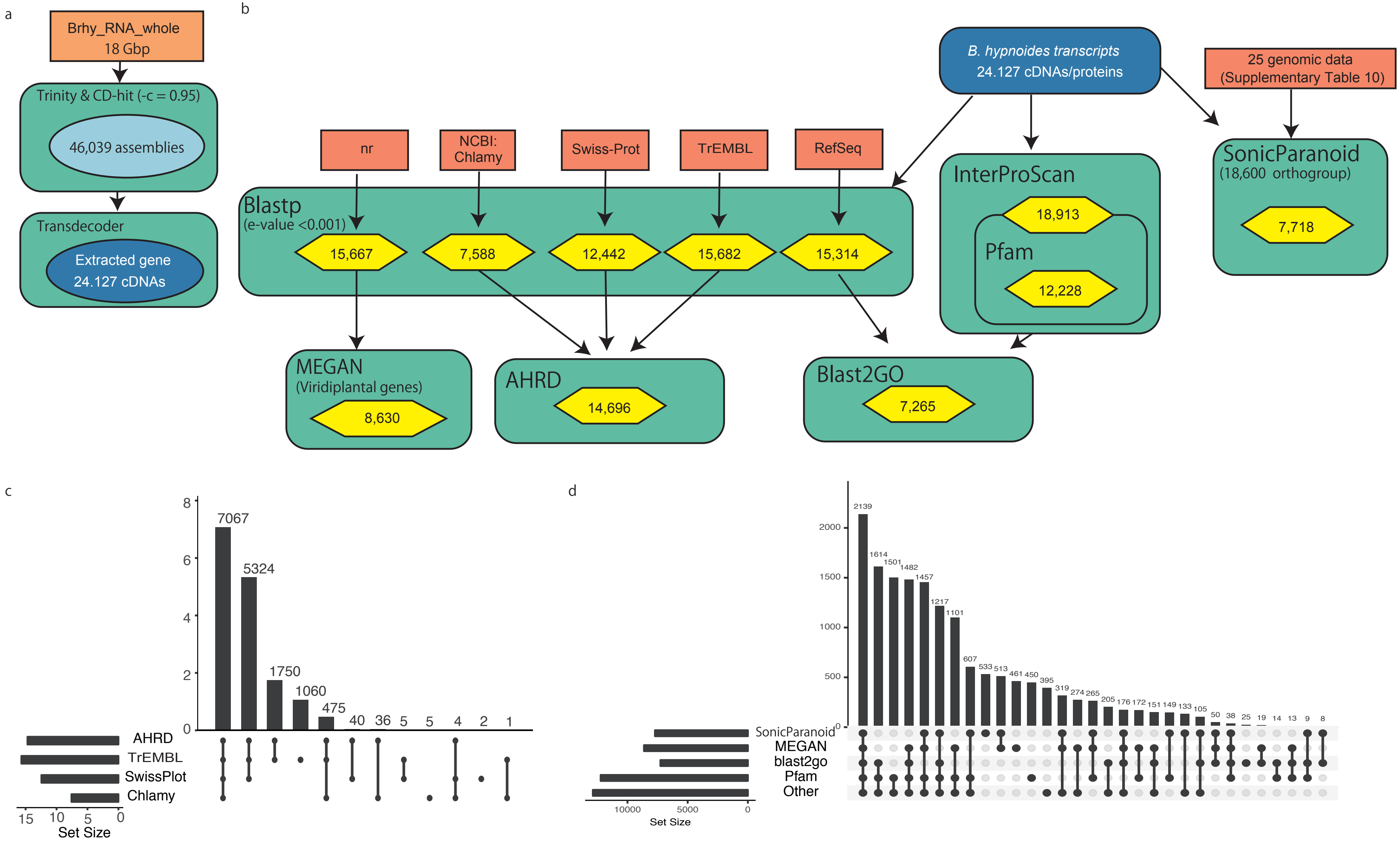
Supplementary Figure 7 Gene compositions of 18 algal cpDNAs and *P. ocellatus* kpDNAs.

Presence (cyan) and Absence (Magenta) of the genes were visualized with the color tiles. The X-axis shows the species, and Y-axis shows the gene. Top tree shows the ML tree made by IQ-tree based on 51 conserved plastid genes (*ycf4, ycf3, tufa, rps9, rps8, rps7, rps4, rps3, rps2, rps19, rps18, rps14, rps12, rps11, rpoa, rpl5, rpl36, rpl23, rpl20, rpl2, rpl16, rpl14, rbcL, psbZ, psbT, psbN, psbL, psbK, psbJ, psbI, psbH, psbF, psbE, psbD, psbC, psbB, psbA, psaJ, psaC, psaB, psaA, petG, petD, petB, petA, atpI, atpH, atpF, atpE, atpB, atpA*, 9882 amino acid positions). Left side genes were clustered base on the GO annotation of each gene. GO annotations were described on the right-side boxes.

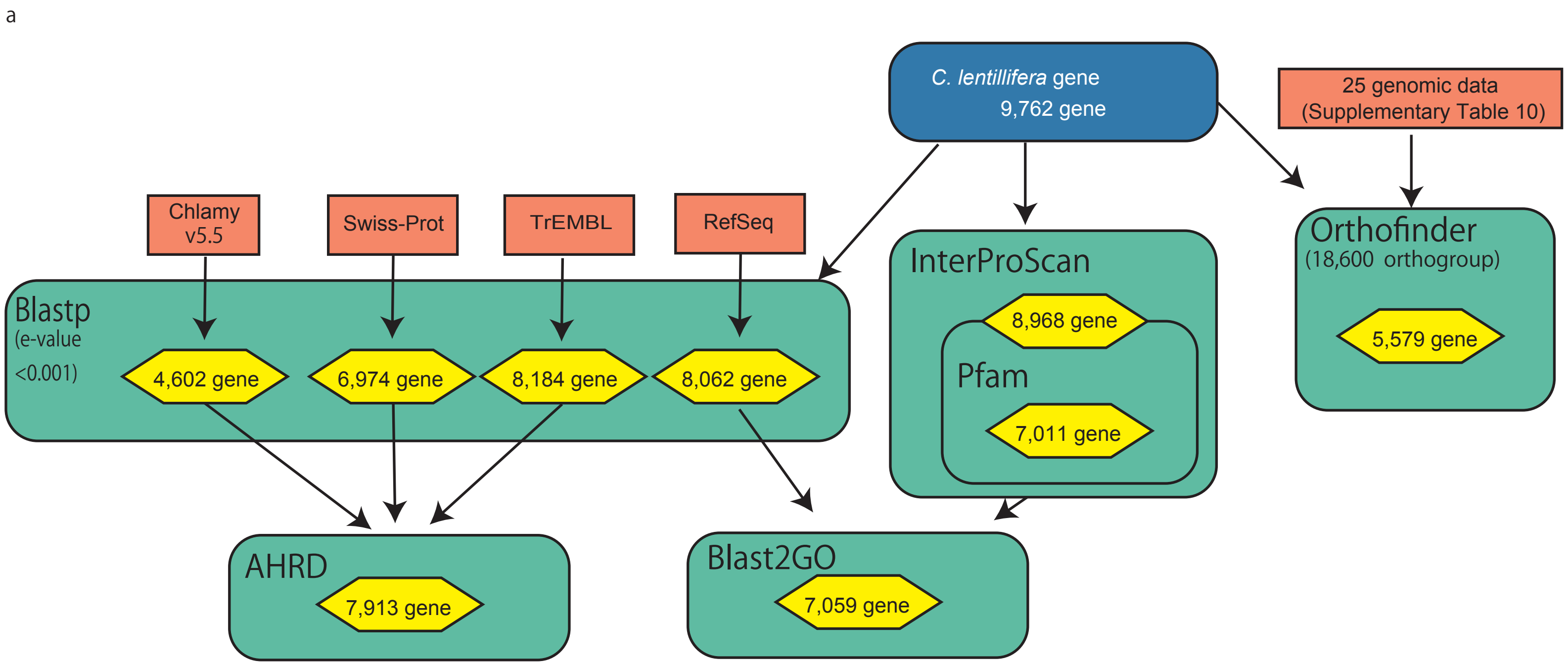
Raw data, 10.6084/m9.figshare.12311990.



Supplementary Figure 8 Annotation procedure of *H. borneensis* transcripts
a *De novo* transcripts assembling procedure. **b** Annotation procedure of the constructed transcripts. Dark blue = Submitted *H. borneensis* transcripts for DDBJ. Light red = Reference data. Aquamarine = annotation method (for detail, see material and methods). Yellow = annotated gene number for each step. **c-b** Upset plot of annotated gene number for each annotation step.
We deposited detailed annotation data about the kleptopalst/chloroplast-encoded genes and *H. borneensis* transcripts (DOI 10.6084/m9.figshare.12316163, 10.6084/m9.figshare.12316283) in FigShare.

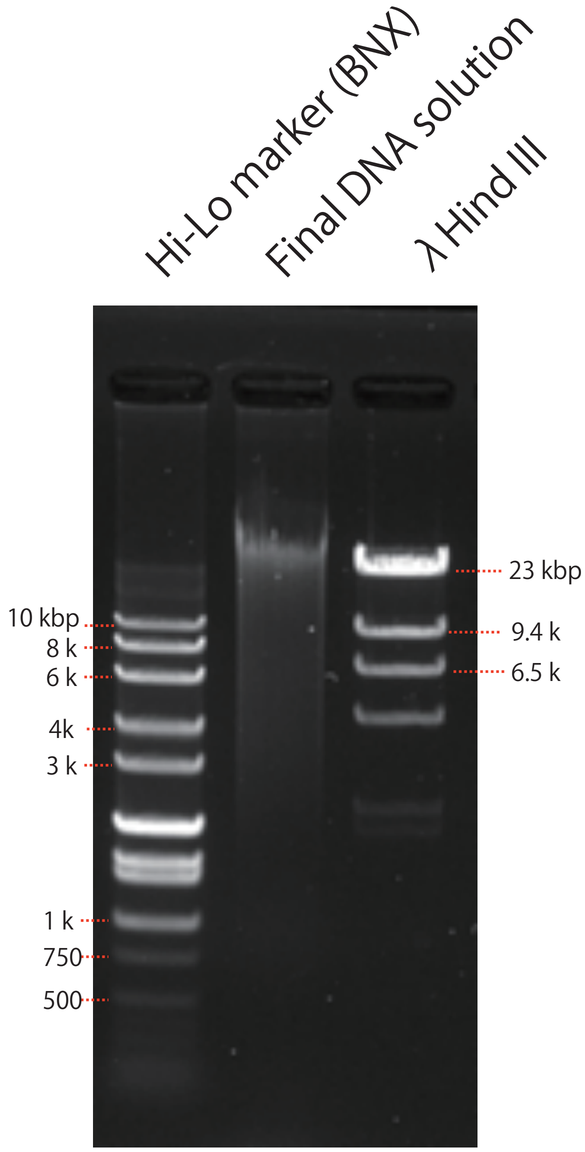


Supplementary Figure 9 Annotation procedure of *B. hypnoides* transcripts.
Colors and boxes are as in Supplementary Figure 8. Annotations of the obtained genes, DOI 10.6084/m9.figshare.12316868.



Supplementary Figure 10 Annotation procedure of *C. lentillifera.*

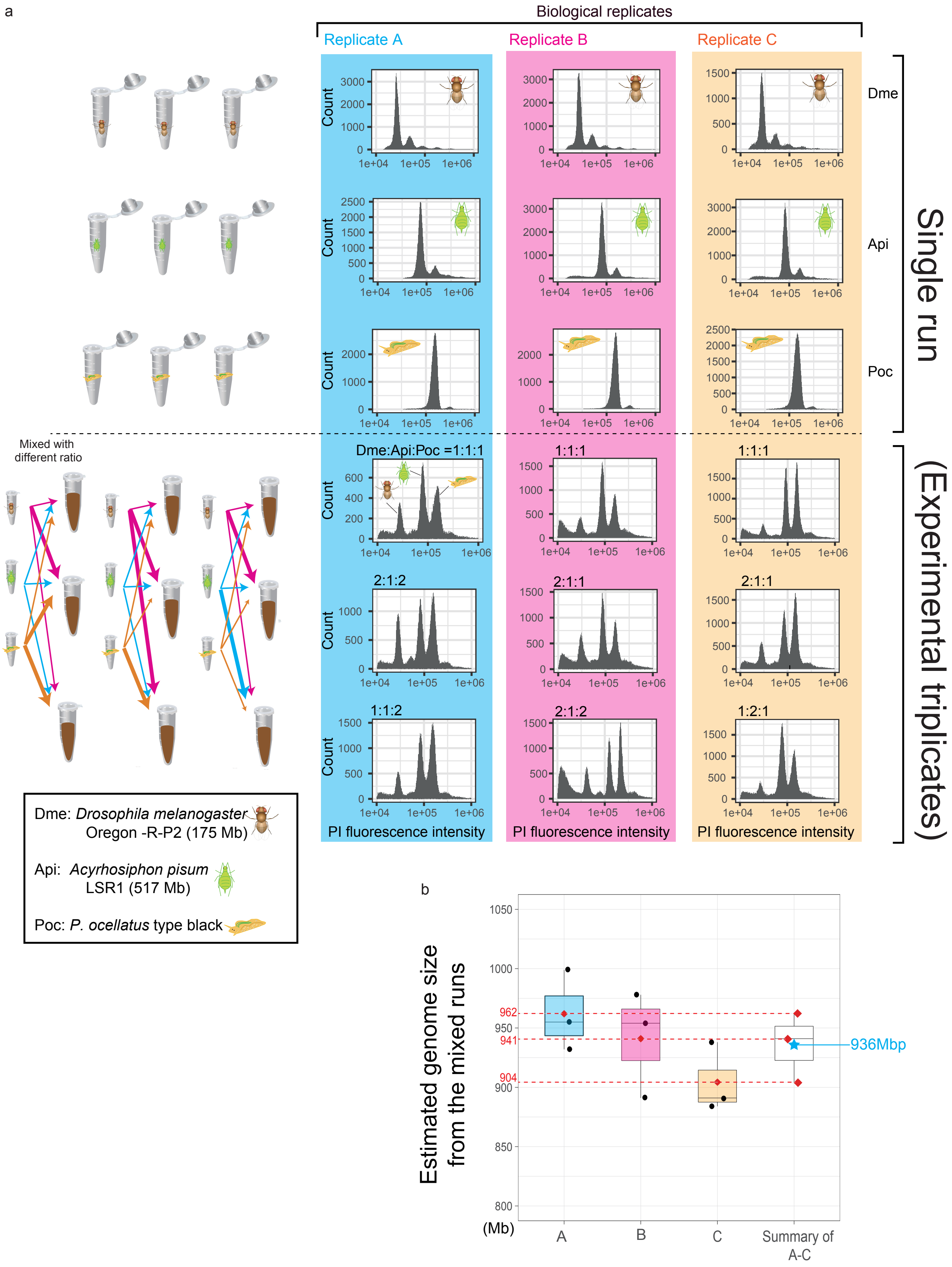
Colors and boxes are as in Supplementary Figure 8. Annotations of the obtained genes, DOI 10.6084_m9.figshare.12316895.



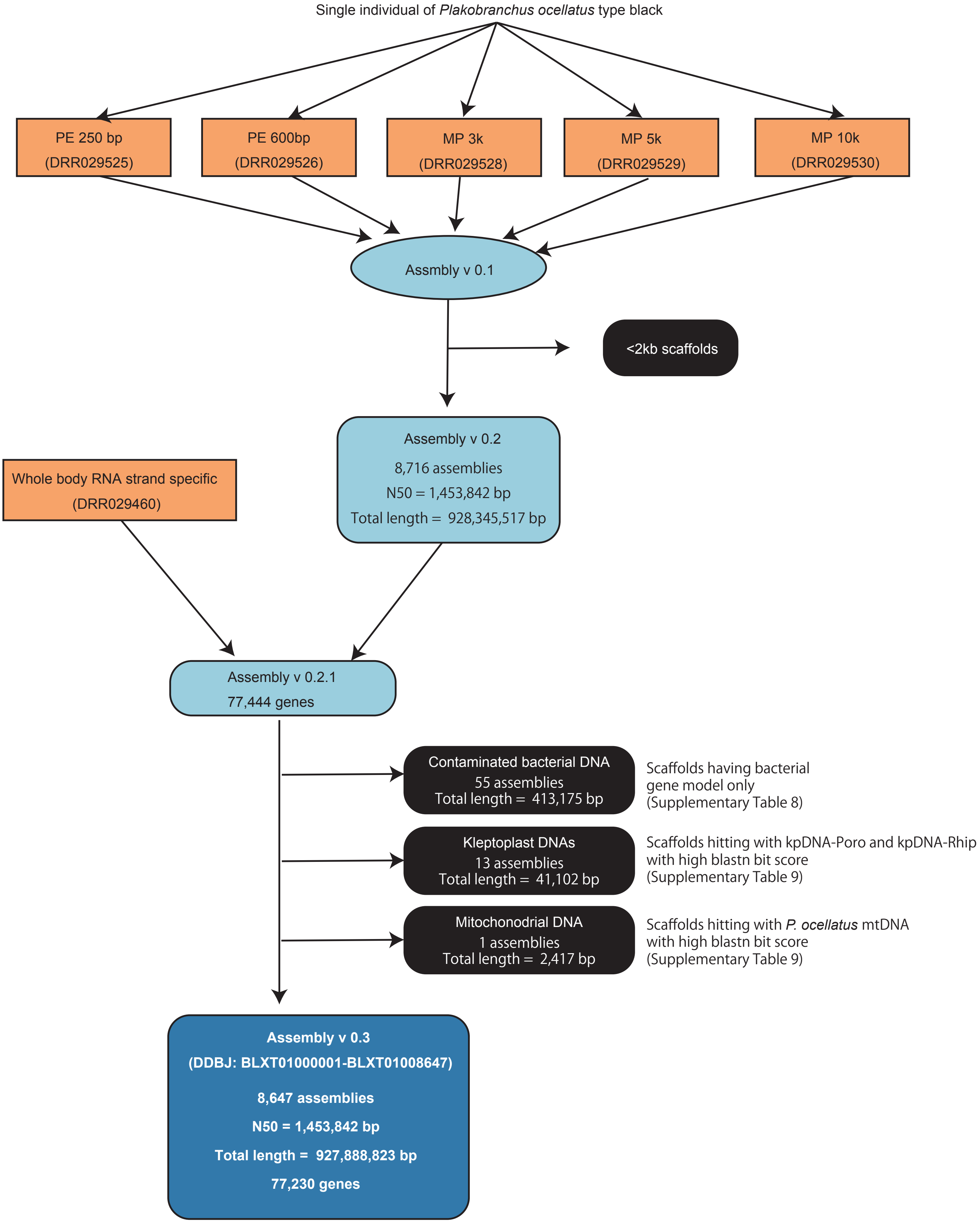
0.7% Agarose gel
50 V 60 min.

stained by SYBR safe
(Thermo)

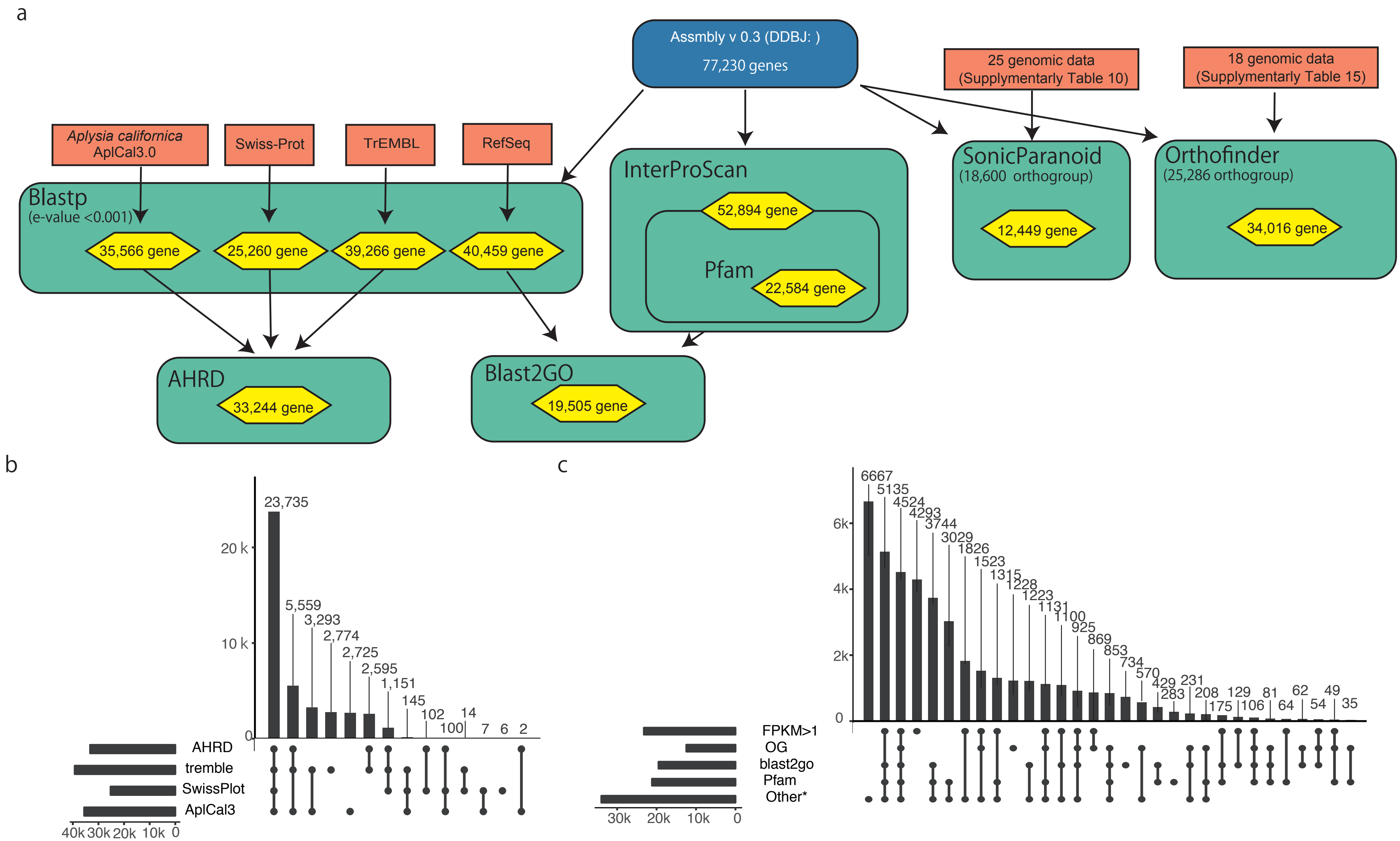
Supplementary Figure 11 Agarose gel image displaying extracted *P. ocellatus* DNA for the nuclear genome sequencing and two kinds of fragment size markers.



Supplementary Figure 12 *P. ocellatus* genome size estimation with flow cytometry.
a Histograms showing the fluorescence peaks of the analyzed nuclei (x-axis) and count of the nuclei (y-axis). Analyzed species were represented with pictograms and abbreviations as in the left bottom box. Each nuclei suspension was analyzed for each species to confirms that the noiseless peaks (particle) are given. Then, three suspensions from different species were mixed with the ratio described on the left shoulder of each histogram to distinct the peak derived from each species. **b** box-plot of predicted genomic size from the mixed runs of *P. ocellatus* with other genome size standards. Black dot = Predicted PoB genome size from each experimental triplicate. Red diamond shows an averagedv genome size of the experimental triplicates (estimated genome size for each biological triplicate). A blue star means an averaged genome size of the biological triplicate.

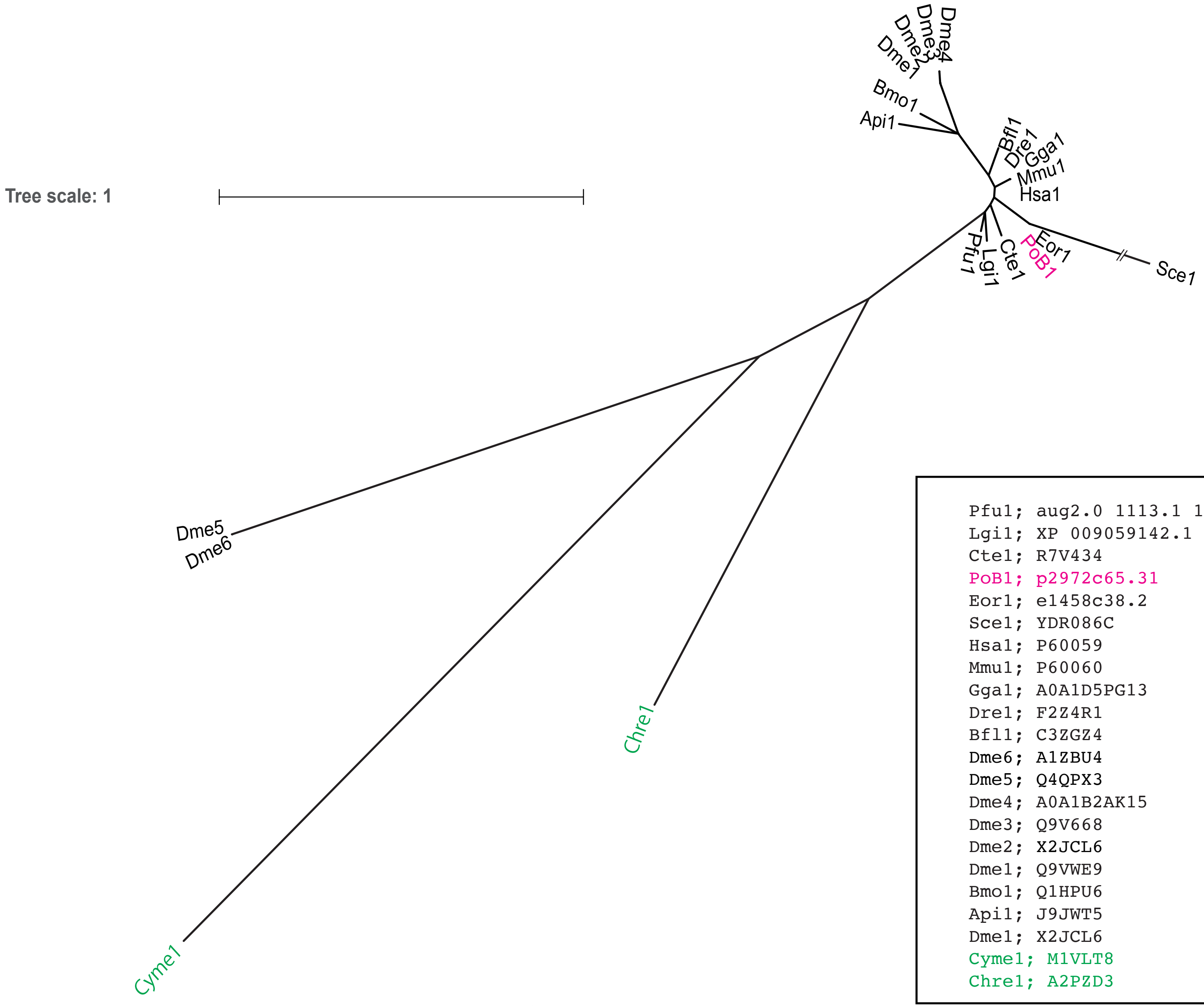


Supplementary Figure 13 Genome assembling and gene modeling approach for the *P. ocellatus* genome analysis. Light orange = raw read data (for detail, see DOI 10.6084/m9.figshare.12301277). Light blue = intermediate assembly data. Dark blue = a final assembly for DDBJ submission. Black = eliminated assemblies.



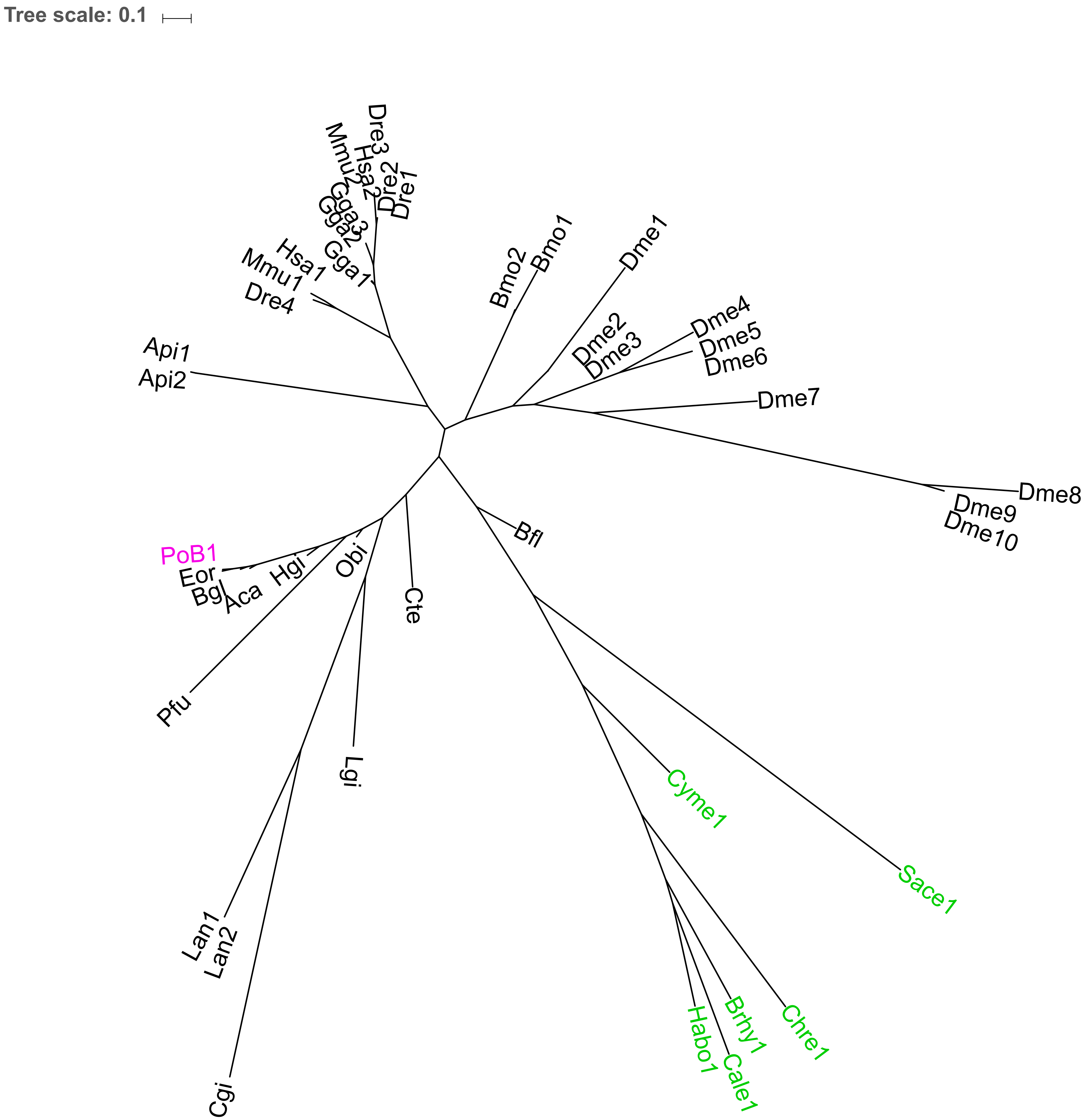
Supplementary Figure 14 Annotation procedure for the genomic gene models of *P. ocellatus* type black.

Dark blue; *P. ocellatus* genome assembly for DDBJ submission. Light red; Reference data. Aquamarine; annotation method (for detail, see material and methods). Yellow; annotated *P. ocellatus* gene number.Other colors and boxes are as in Supplementary Figure 8.



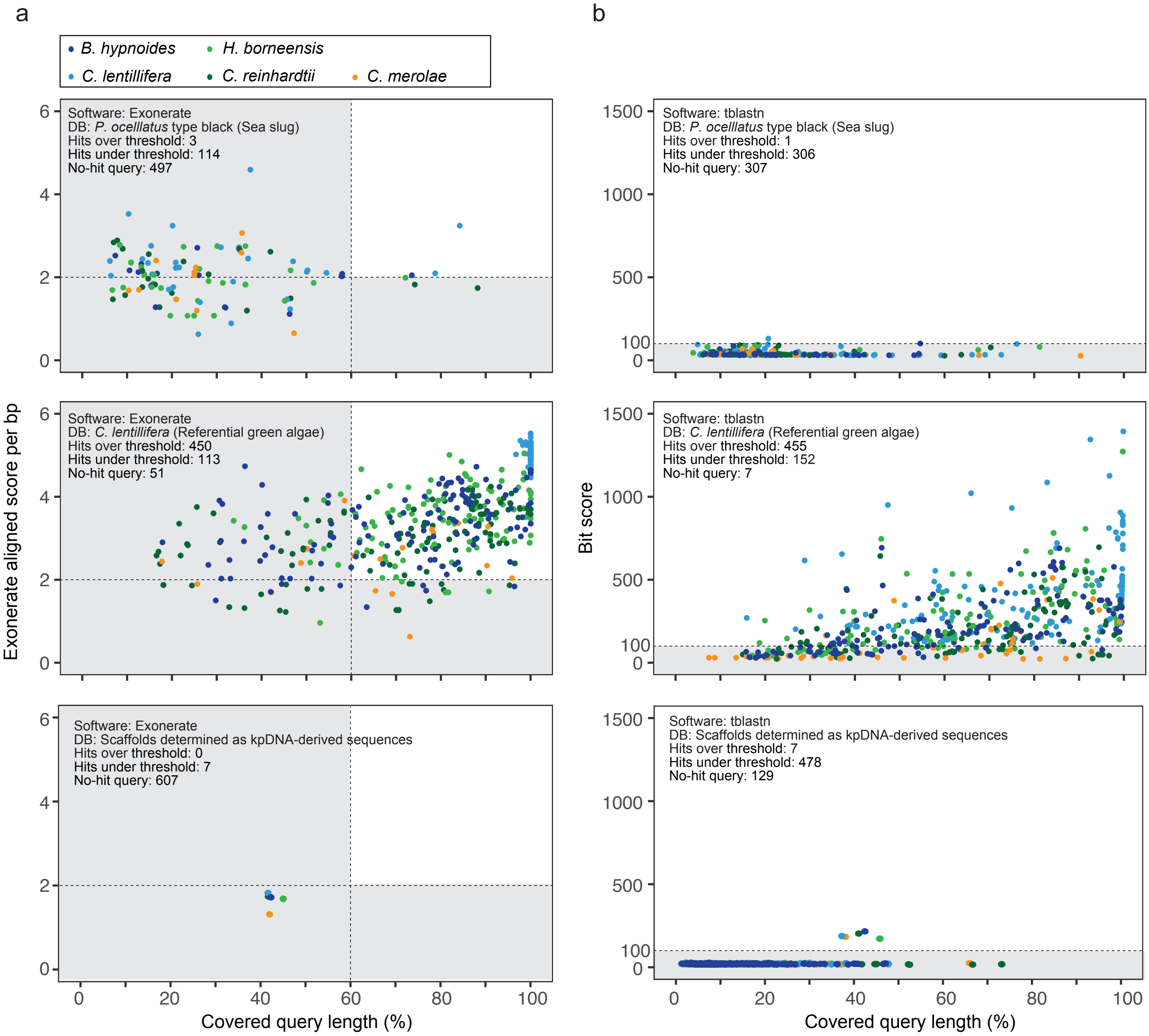
Pfu1; aug2.0 1113.1 11445.t1
Lgi1; XP 009059142.1
Cte1; R7V434
PoB1; p2972c65.31
Eor1; e1458c38.2
Sce1; YDR086C
Hsa1; P60059
Mmu1; P60060
Gga1; A0A1D5PG13
Dre1; F2Z4R1
Bfl1; C3ZGZ4
Dme6; A1ZBU4
Dme5; Q4QPX3
Dme4; A0A1B2AK15
Dme3; Q9V668
Dme2; X2JCL6
Dme1; Q9VWE9
Bmo1; Q1HPU6
Api1; J9JWT5
Dme1; X2JCL6
Cyme1; M1VLT8
Chre1; A2PZD3

Supplementary Figure 15 ML tree for the orthologous group “4058” by SonicParanoid.
Green; algal gene. Magenta; *P. ocellatus* gene. Gene ID (INSDC ID, OIST Marine Genomics Unit database [https://marinegenomics.oist.jp], or our annotation ID) were descrived in a box. A PoB gene model, p2972c65.31, was annotated as “Chloroplast envelope” (GO0009941). However, the PoB gene formed a monophyletic clade with molluscan orthologs rather than algal gene, indicating this gene is molluscan origin (no HGT). Raw data, 10.6084/m9.figshare.12319001 and 10.6084/m9.figshare.12319424. Four genes (gene ID: p197c68.18, p234c64.89, p45387c41.1, and p466c59.83) annotated as “Chloroplast” (Fig. 4a and 10.6084/m9.figshare.12319532) showed no orthologous relationships with algal genes.

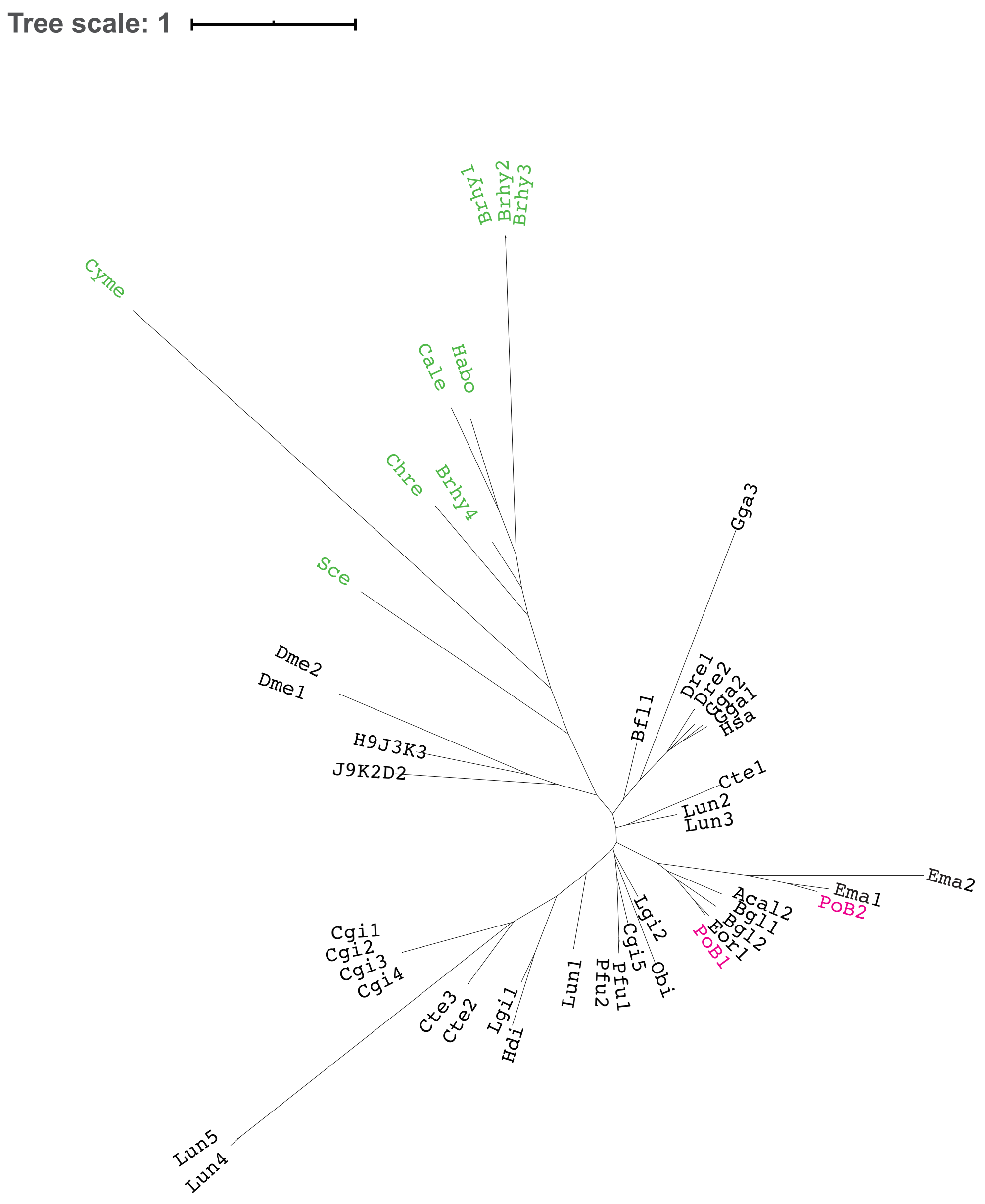


Aca1; XP 012941103.1
Api1; C4WT07
Api2; J9JQB3
Bgl1; XP 013088345.1
Bmo1; H9IY82
Bmo2; A1YM12
Cgi1; XP 011427766.1
Cte1; R7TKE3
Dme1; Q6NMV8
Dme2; E8NH43
Dme3; Q7PLT4
Dme4; Q9VJP1
Dme5; Q8T903
Dme6; Q9VRF6
Dme7; Q9VNA0
Dme8; Q9VN97
Dme9; Q9VGA2
Dme10; A0A0B4LH92
Dre1; Q6NZZ0
Dre2; F6NU65
Dre3; A0A0R4ILL9
Dre4; A8WHN3
Eor1; evm.model.scaffold181 cov40.1
Gga1; Q5ZJF5
Gga2; A0A1D5PQM6
Gga3; F1NM85Bfl; C3YLR4
Hgi1; HDSC00251CG00080
Hsa1; O60830
Hsa2; Q99595
Lan1; A0A1S3HSB6
Lan2; A0A1S3I2S5
Lgi1; XP 009053591.1
Mmu1; Q9Z0V7
Mmu2; Q9Z0V8
Obi1; XP 014770271.1
Pfu1; aug2.0 5.1 16677.t1
PoB1; p503c65.126
Brhy1; TRINITY DN11295 c1 g1 i1 m.23045
Cale1; g1915.t1
Chre1; A8I032
Cyme1; tr M1VM69 M1VM69 CYAM1
Habo1; c10815 g1 i1 m.18878
Sace1; YJL143W

Supplementary Figure 16 ML tree for the orthologous group “2017” by SonicParanoid.
Colors are as in Supplementary Figure 15.
A PoB gene model, p503c65.126, was annotated as “Chloroplast envelope” (GO0009941). However, the PoB gene formed a monophyletic clade with molluscan orthologs rather than algal gene, indicating this gene is molluscan origin (no HGT).



Supplementary Figure 17 Summary of Exonerate and tblastn results.
a Scatter plot of Exonerate results. DB = *P. ocellatus* genome (Top plate), *C. lentillifera* genome (Middle plate), or kpDNA-derived scaffolds (see Supplementary Table 9) (Bottom plate). Query = algal A614 gene set. The top box shows the source algae of each query. Dashed lines are thresholds for the credible query hit (Covering over 60% of the query sequence, and over two normalized aligned scores for aligned length). Query hit statistics were described on the left shoulder of each plate. All seven hit queries on kpDNAs were algal chlD gene (encoding Magnesium-chelatase subunit ChlD) resembling the kleptoplast-encoded chlL gene. **b** Scatter plot of tblastn results. DB = *P. ocellatus* genome (Top plate) , *C. lentillifera* genome (Middle plate), or kpDNA-derived scaffolds (see, Supplementary Table 9). Query = algal A614 gene set. Dashed lines are thresholds (bit score = 100) for the credible query hit. All seven significant hit queries on the kpDNA-derived scaffolds were algal *chlD* gene (encoding Magnesium-chelatase subunit chlD) resembling the kleptoplast-encoded chlL gene (see Supplementary Table 20 and 10.6084/m9.figshare.12628709).
Raw data, DOI 10.6084/m9.figshare.12318920.

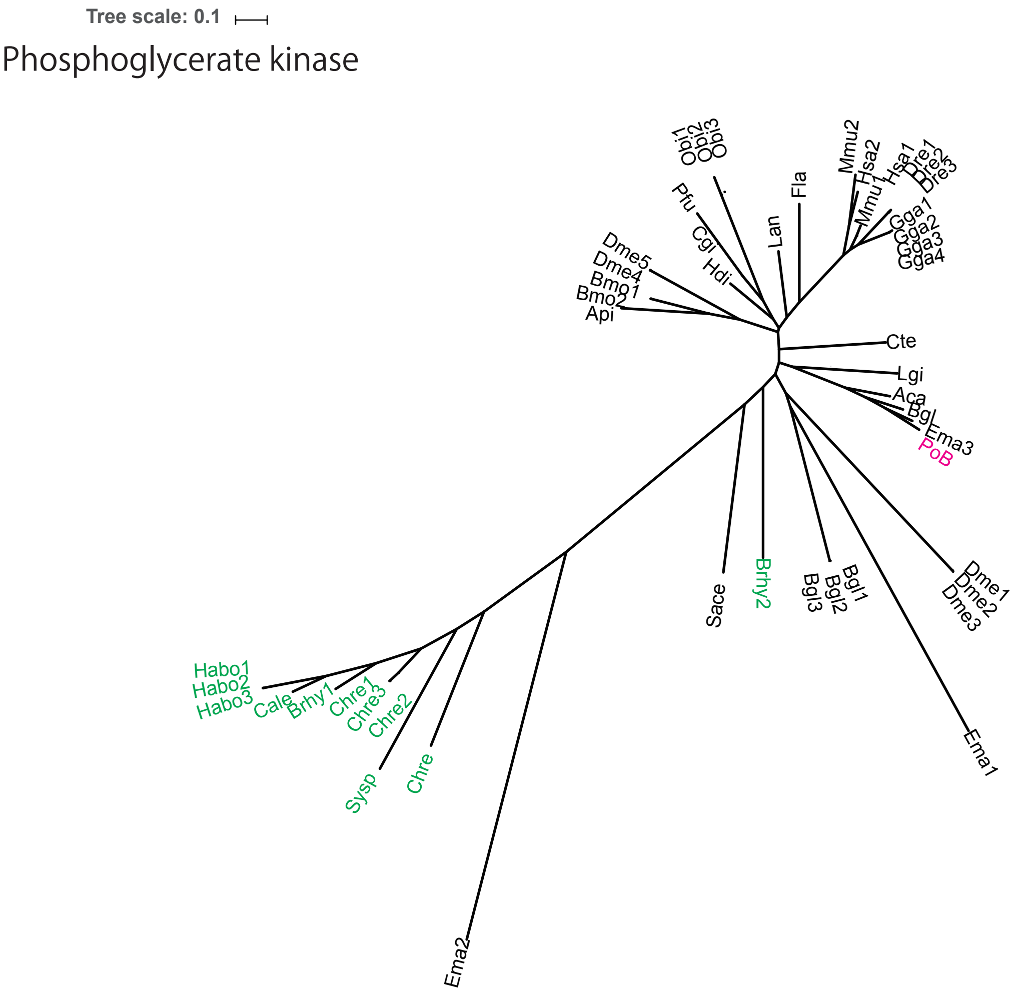


Supplementary Figure 18 ML tree for the orthologous group 65 by SonicParanoid.

Colors are as in Supplementary Figure 15.

Raw data, DOI 10.6084/m9.figshare.12318977 and 10.6084/m9.figshare.12319532.

Api1; J9K2D2
Acal1; XP_005099547.2
Acal2; XP_012941160.1
Bfl1; C3YX59
Bgl1; XP_013086066.1
Bgl2; XP_013086068.1
Bmo; H9J3K3
Brhy1; TRINITY_DN15712_c0_g2_i1_m.25540
Brhy2; TRINITY_DN15712_c0_g2_i2_m.25550
Brhy3; TRINITY_DN15712_c0_g2_i2_m.25551
Brhy4; TRINITY_DN15712_c0_g3_i1_m.25561
Cte1; R7TC54
Cte2; R7VEA1
Cte3; R7TRQ8
Cale; g2233.t1
Chre; A8IFY3
Cgi1; XP_011433686.1
Cgi2; XP_019924656.1
Cgi3; XP_019924657.1
Cgi4; XP_019924658.1
Cgi5; XP_019929326.1
Cyme; tr_M1V583_M1V583_CYAM1
Dme1; Q95TG7
Dme2; A8DYB0
Ema1; e4271c37.7
Ema2; e4271c37.1
Habo; c12624_g1_i1_m.52286
Hdi; HDSC49952CG00010
Lun1; A0A1S3H4V0
Lun2; A0A1S3H6C9
Lun3; A0A1S3IXZ2
Lun4; A0A1S3H7D6
Lun5; A0A1S3H4I4
Lgi1; XP_009045458.1
Lgi2; XP_009045461.1
Obi; XP_014789895.1
PoB1; p258757c71.61
PoB2; p258757c71.57
Sce; YLR106C
Dre1; E7F4D6
Dre2; F1QMM1
Gga1; E1C4X6
Gga2; A0A1D5P4E1
Gga3; A0A1D5PNK8
Hsa; Q9NU22
Pfu1; aug2.0_176.1_20367.t1
Pfu2; aug2.0_10247.1_26360.t1



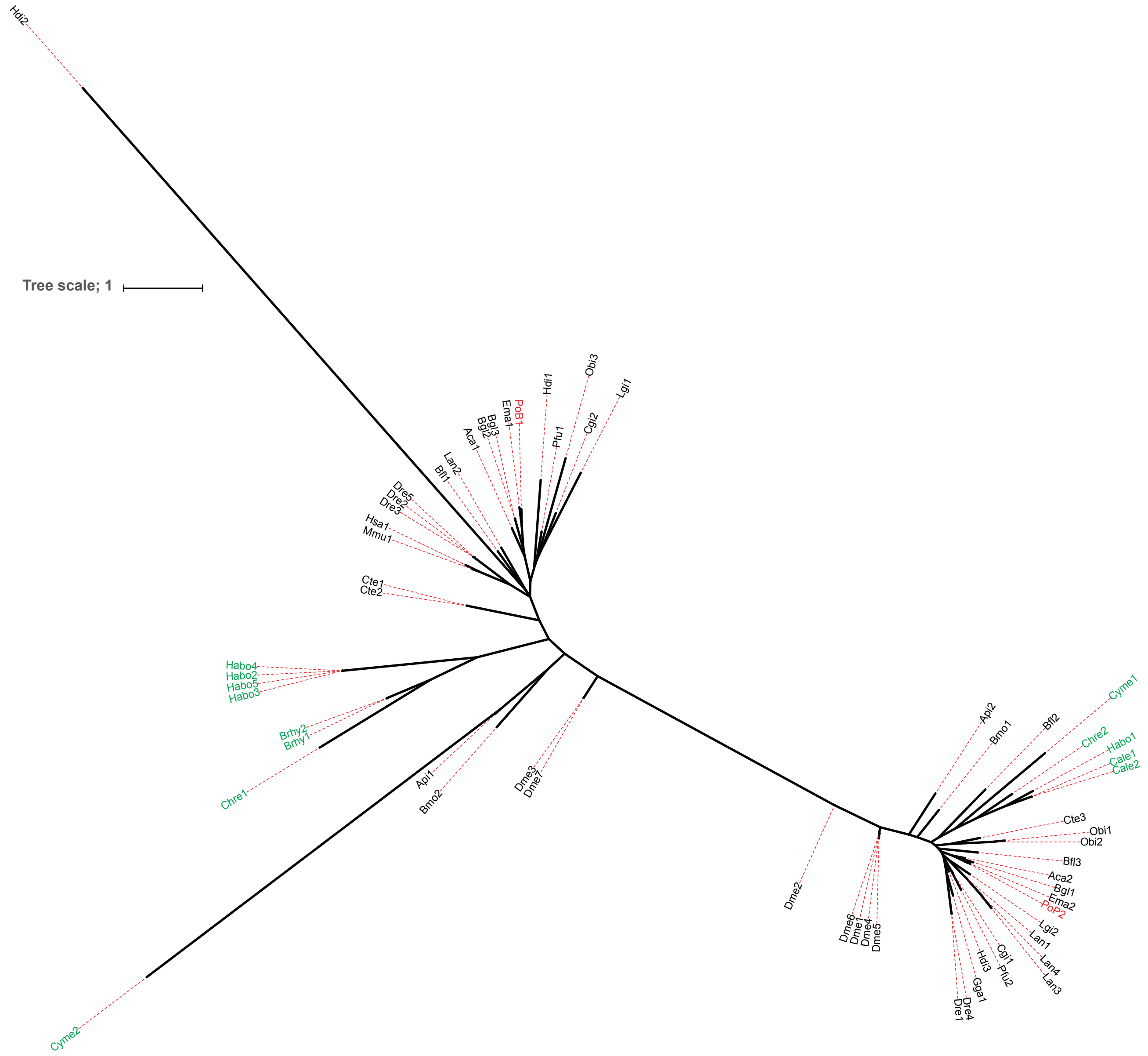
Aca; XP 012936693.1
Api; J9K4W4
Bgl; XP 013066033.1
Bgl1; XP 013061476.1
Bgl2; XP 013061475.1
Bgl3; XP 013061477.1
Bmo1; H9JDT4
Bmo2; E5EVW6
Cgi; XP 011419255.1
Cte; R7TJM0
Dme1; Q8T447
Dme2; B5RJA1
Dme3; Q9VQF4
Dme4; Q01604
Dme5; M9PCE0
Dre1; F1QXV8
Dre3; Q6P003
Dre2; Q7ZV29
Ema1; evm.model.scaffold44.20
Ema2; evm.model.scaffold69.33
Ema3; evm.model.scaffold3214 cov43.1
Fla; C3XW30
Gga1; P51903
Gga2; A0A1L1RXH1
Gga3; A0A1D5NZW9
Gga4; F1NU17
Hdi; HDSC00324CG00210
Hsa1; P00558
Hsa2; P07205
Lan; A0A1S3HH77
Lgi; XP 009047142.1
Mmu1; P09411
Mmu2; P09041
Obi1; XP 014774198.1
Obi2; XP 014774182.1
Obi3; XP 014774190.1
Pfu; aug2.0 329.1 30622.t1
PoB; p105c62.89

Brhy1; TRINITY DN35033 c0 g1 i1 m.48831
Brhy2; TRINITY DN36447 c0 g1 i1 m.33737
Chre; tr A0A125YSW1 A0A125YSW1 CYAM1
Chre1; Q548U3
Chre2; P41758
Chre3; A8JC04
Cale; g2055.t1
Habo1; c11923 g1 i3 m.33221
Habo2; c11923 g1 i1 m.33202
Habo3; c11923 g1 i2 m.33212
Sace; YCR012W
Sysp; P74421 PGK SYNY3

Supplementary Figure 19 ML tree for the orthologous group 501 by SonicParanoid.

Colors are as in Supplementary Figure 15.

Raw data, DOI 10.6084/m9.figshare.12318977 and 10.6084/m9.figshare.12319532.

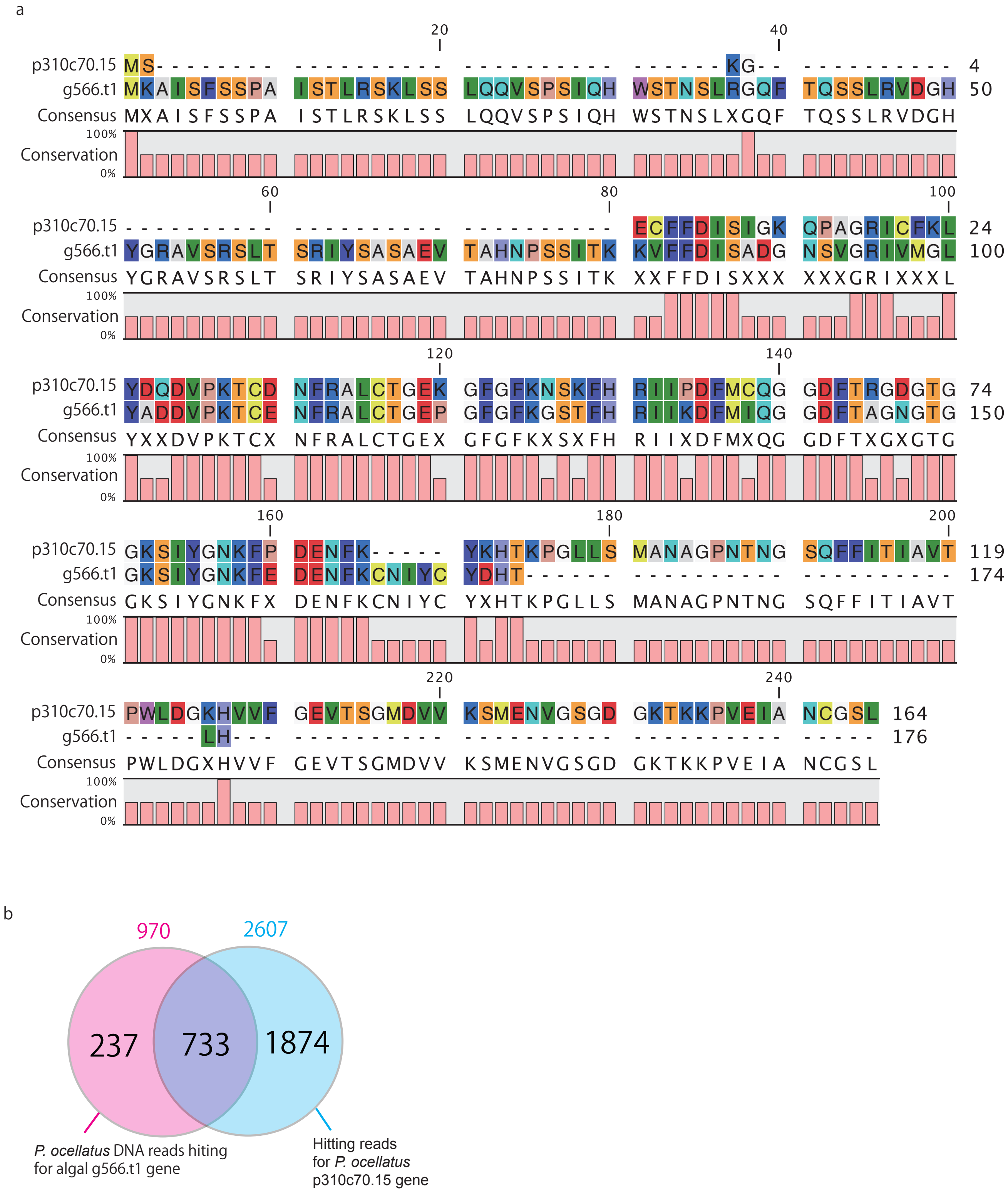


Dre1; A0A0R4IS22
Lan1; A0A1S3H867
Lan2; A0A1S3HV36
Lan3; A0A1S3K7R9
Lan4; A0A2R2MN91
Dme1; A1Z757
Dme2; A1Z758
Dme3; A1Z759
Chre1; A8JAN4
Pfu1; aug2.0_4854.1_16038.t1
Pfu2; aug2.0_680.1_01048.t1
Bfl1; C3Y1S2
Bfl2; C3ZD92
Bfl3; C3ZWY3
Ema1; e2072c39.23
PoB1; p440c72.239
PoB2; p855c67.9
Eor2; evm.model.scaffold9727_cov36.9
Gga1; F1NSZ2
Dre2; F1Q8W7
Bmo1; H9J281
Bmo2; H9JWI3
Hdi1; HDSC00027CG00110
Hdi2; HDSC04373CG00010
Hdi3; HDSC07471CG00010
Api1; J9JT18
Api2; J9K3D6

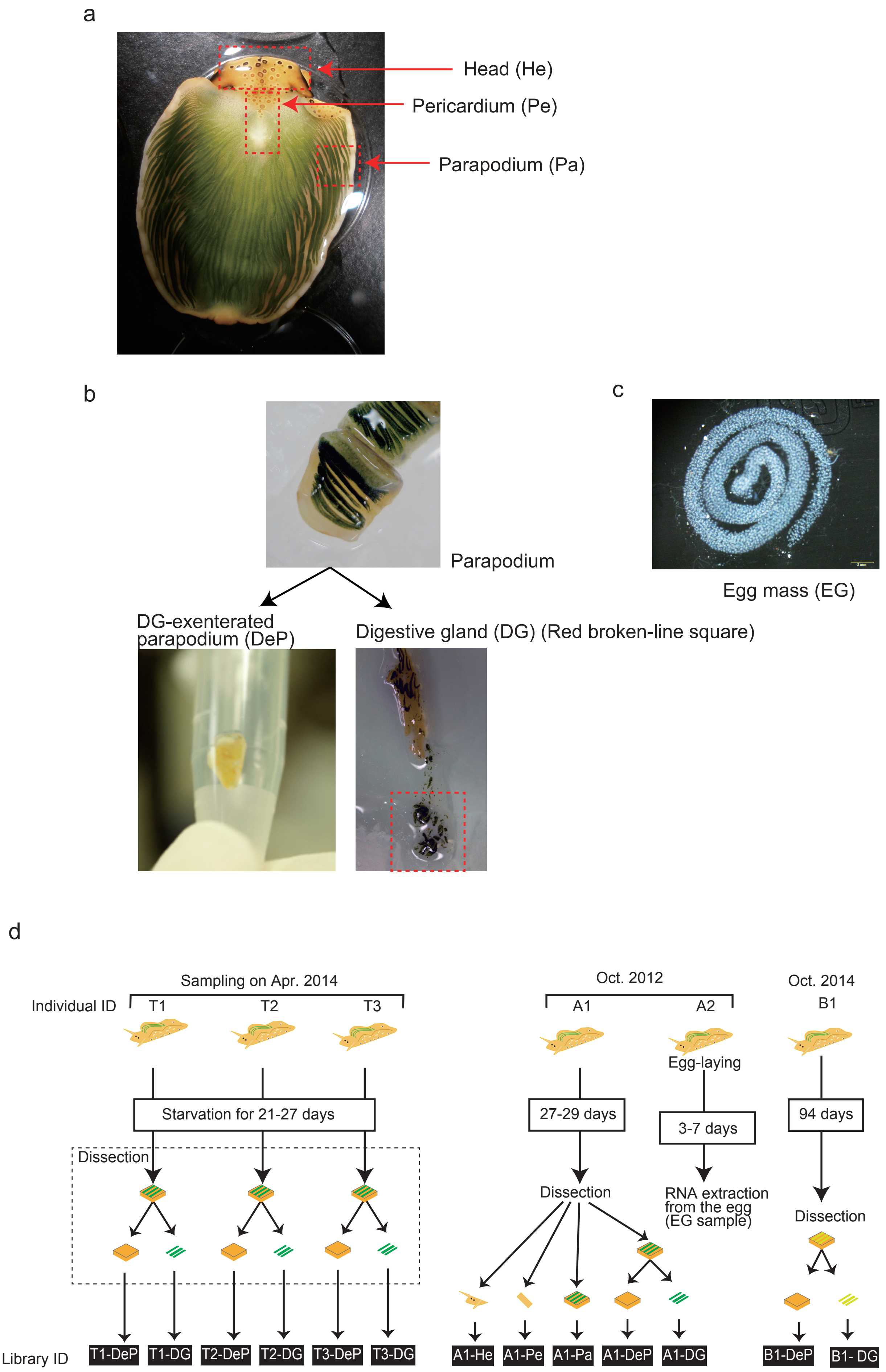
Dme4; Q24443
Dme5; Q26373
Dre3; Q3B7R6
Mmu1; Q562D6
Dme6; Q7JY97
Dre4; Q7SYI9
Dme7; Q8MR50
Hsa1; Q9BU70
Chre2; Q9XHE2
Dre5; R4GEK9
Cte1; R7T6M9
Cte2; R7THN0
Cte3; R7TV65
Aca1; XP_005089019.1
Lgi1; XP_009048710.1
Lgi2; XP_009060728.1
Cgi1; XP_011422754.2
Cgi2; XP_011442441.2
Aca2; XP_012935158.1
Bgl1; XP_013068586.1
Bgl2; XP_013073365.1
Bgl3; XP_013073366.1
Obi1; XP_014780460.1
Obi2; XP_014780461.1
Obi3; XP_014781937.1

Habo1; c11176_g1_i1_m.22572
Habo2; c11217_g2_i1_m.23039
Habo3; c11217_g2_i2_m.23046
Habo4; c11217_g2_i3_m.23050
Habo5; c11217_g2_i4_m.23056
Cale1; g7280.t1
Cale2; g7280.t2
Cyme1; tr_M1V506_M1V506_CYAM1
Cyme2; tr_M1VLH0_M1VLH0_CYAM1
Brhy1; TRINITY_DN11446_c0_g1_i1_m.26666
Brhy2; TRINITY_DN11446_c0_g2_i1_m.26667

Supplementary Figure 20 ML tree for the orthologous group 456 by SonicParanoid.
Colors are as in Supplementary Figure 15.
Raw data, DOI 10.6084/m9.figshare.12318977 and 10.6084/m9.figshare.12319532.

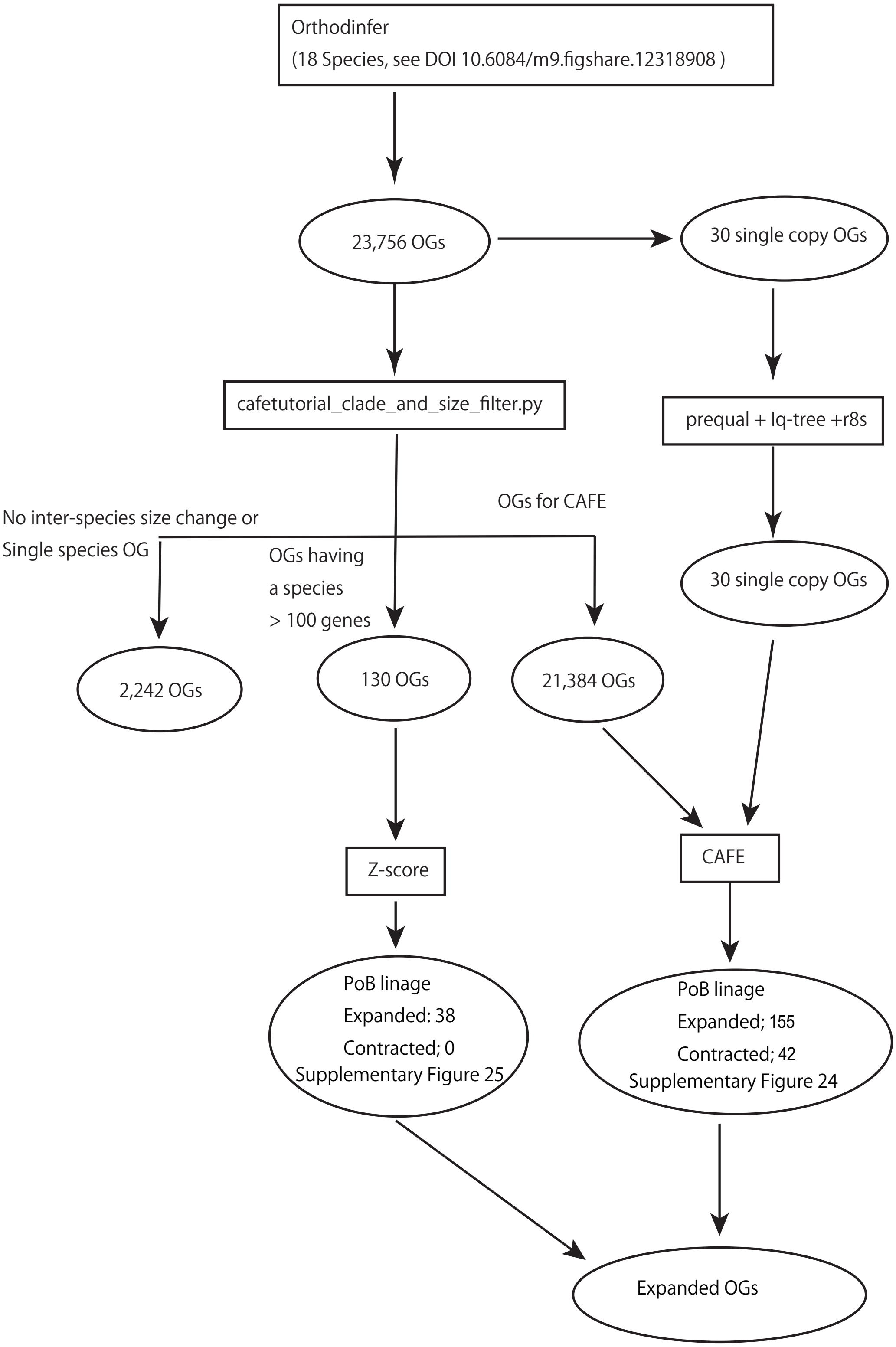


Supplementary Figure 21 Sequence comparison between g566.t1 (*C. lentillifera*) and p310c70.15 (*P. ocellatus*). **a** Sequence alignment and similarity **b** Venn' s plot of hit read number from MMseq2 analysis. DB = pre-assembling Illumina DNA sequencing read (DRR029525 and DRR029526, also see 10.6084/m9.figshare.12301277)



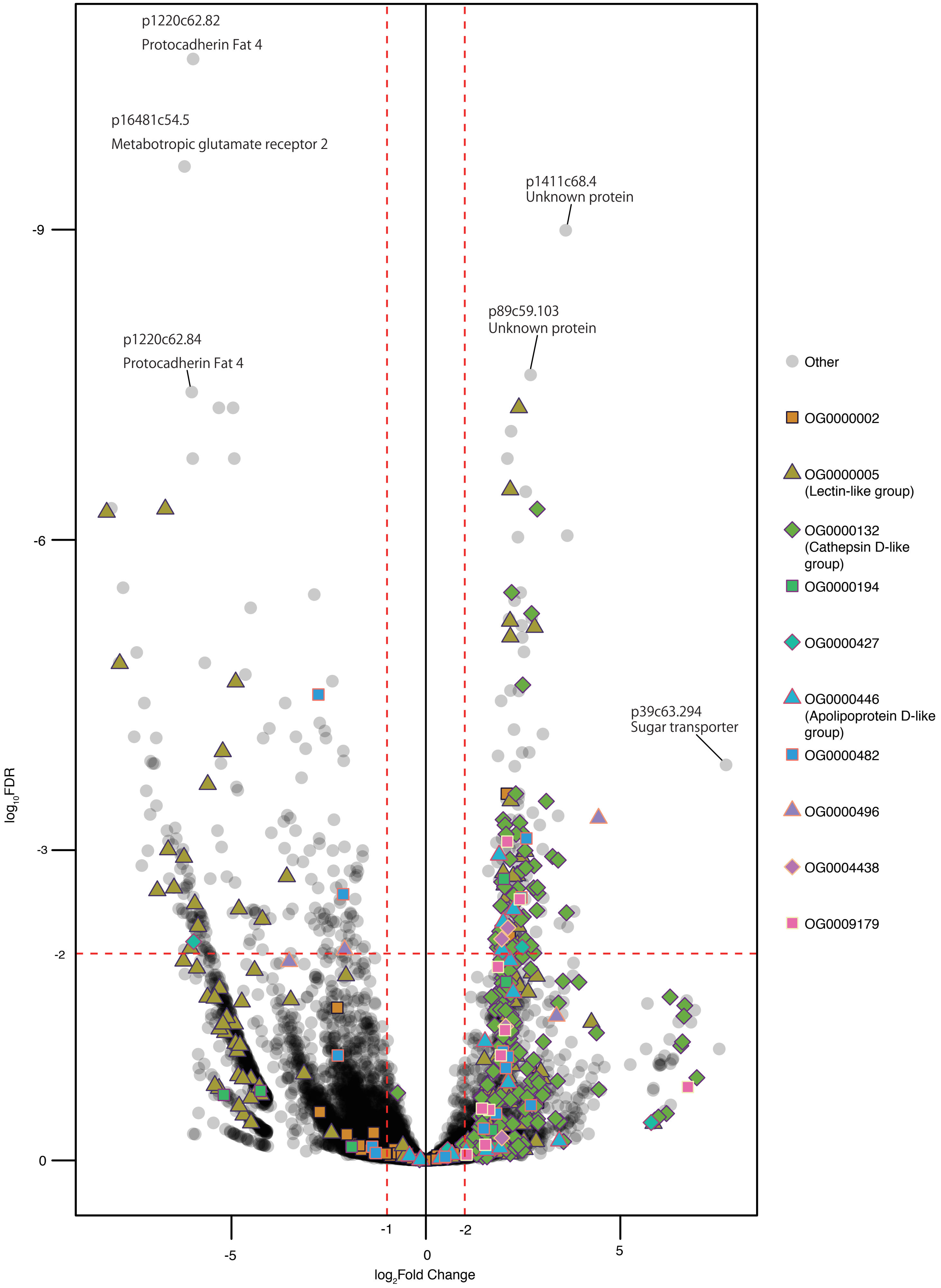
Supplementary Figure 22

a Overview of the *P. ocellatus* dissection and the positions of each sample tissue. **b** Pictures of dissected parapodium, digestive gland, and parapodium without digestive gland. Digestive glands were obtained from parapodium using a razor by hand. **c** Egg mass of PoB. **d** Incubation states of the dissected sea slug and interaction among the samples.

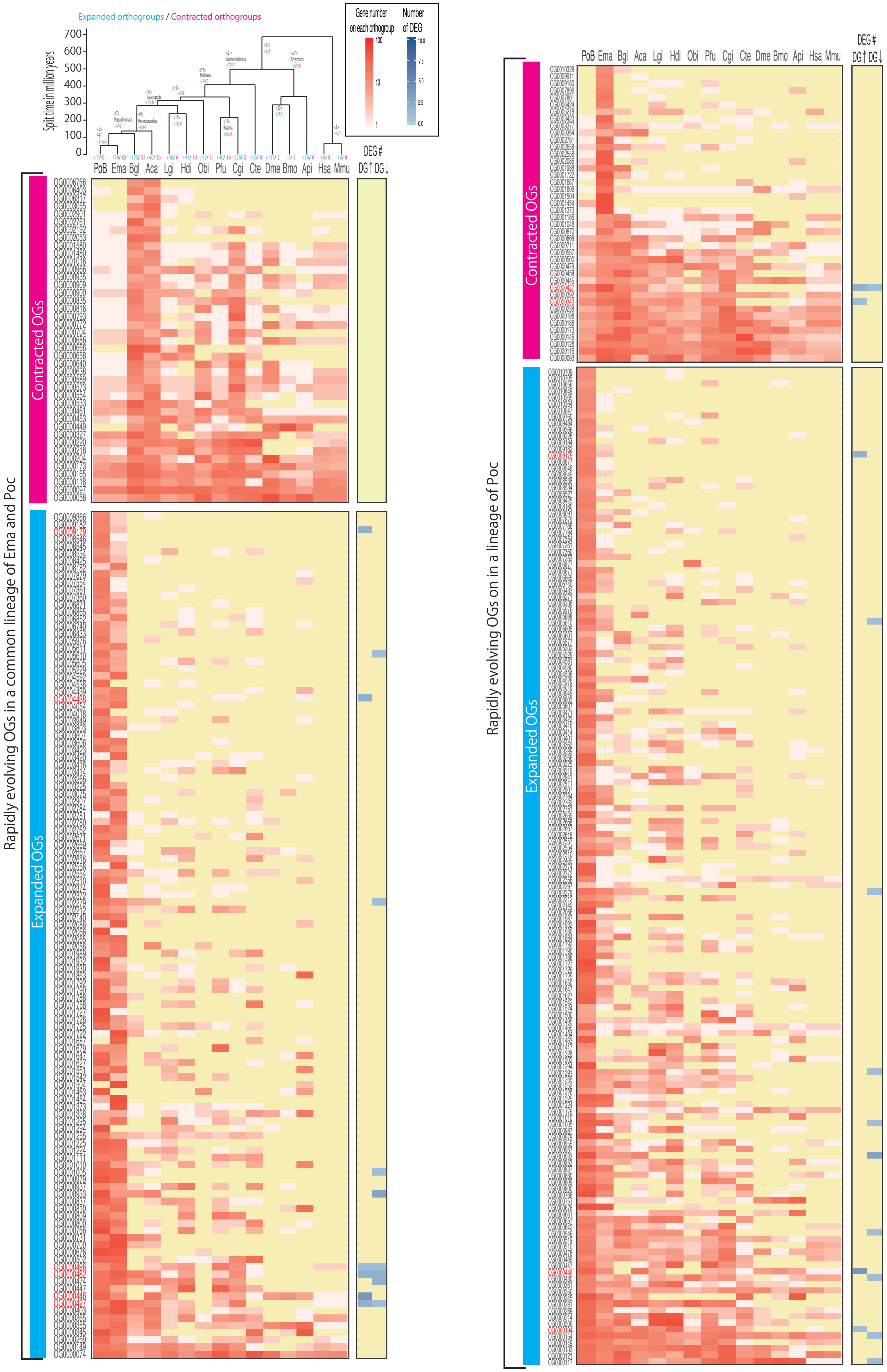


Supplementary Figure 23 Procedure of gene family history analyses.
Circle means the adapted analysis and square boxes mean obtained orthogroup (OG) dataset.

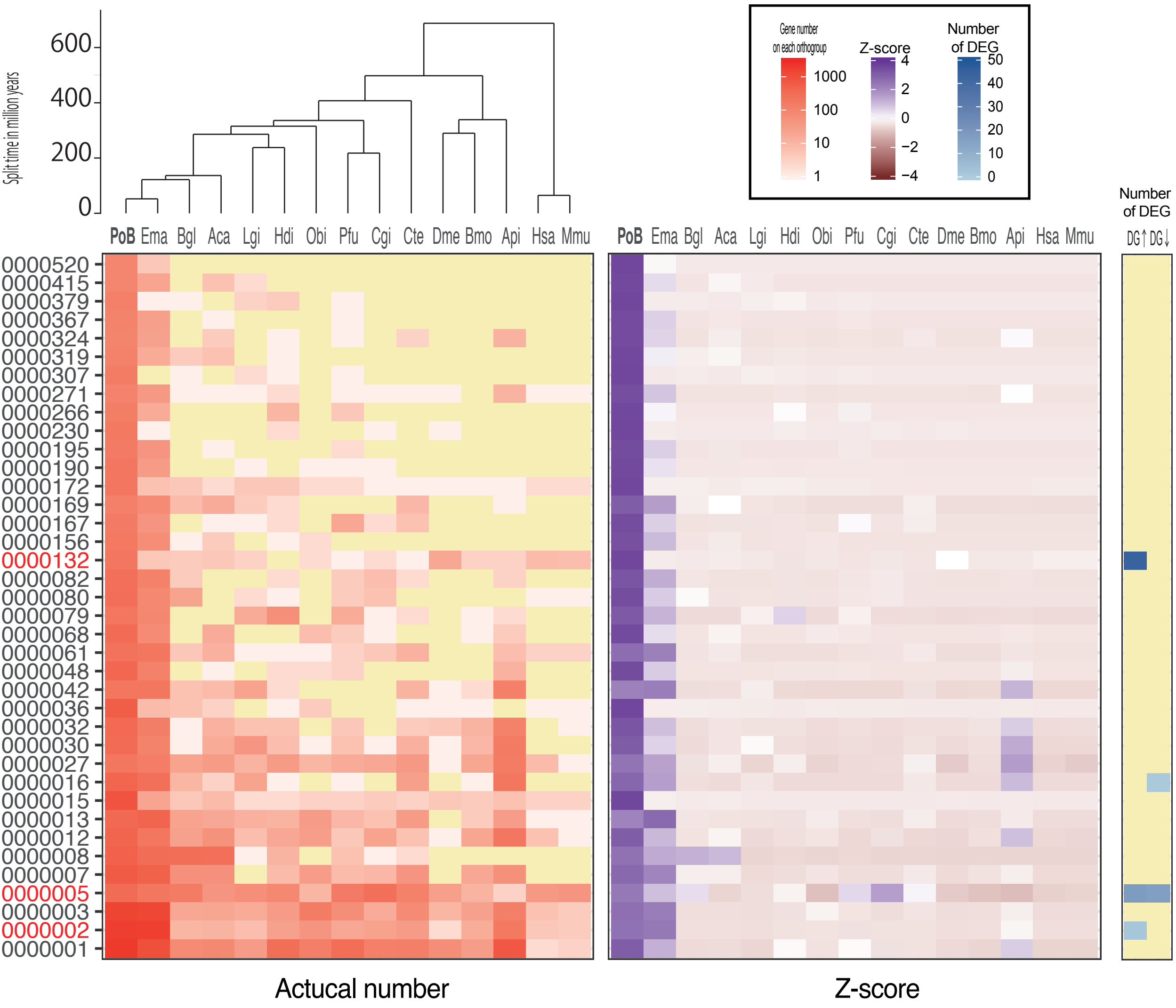
Supplementary Figure 24 DG-upregulated genes by the RNA-Seq comparison.
Raw data, DOI 10.6084/m9.figshare.12319826.



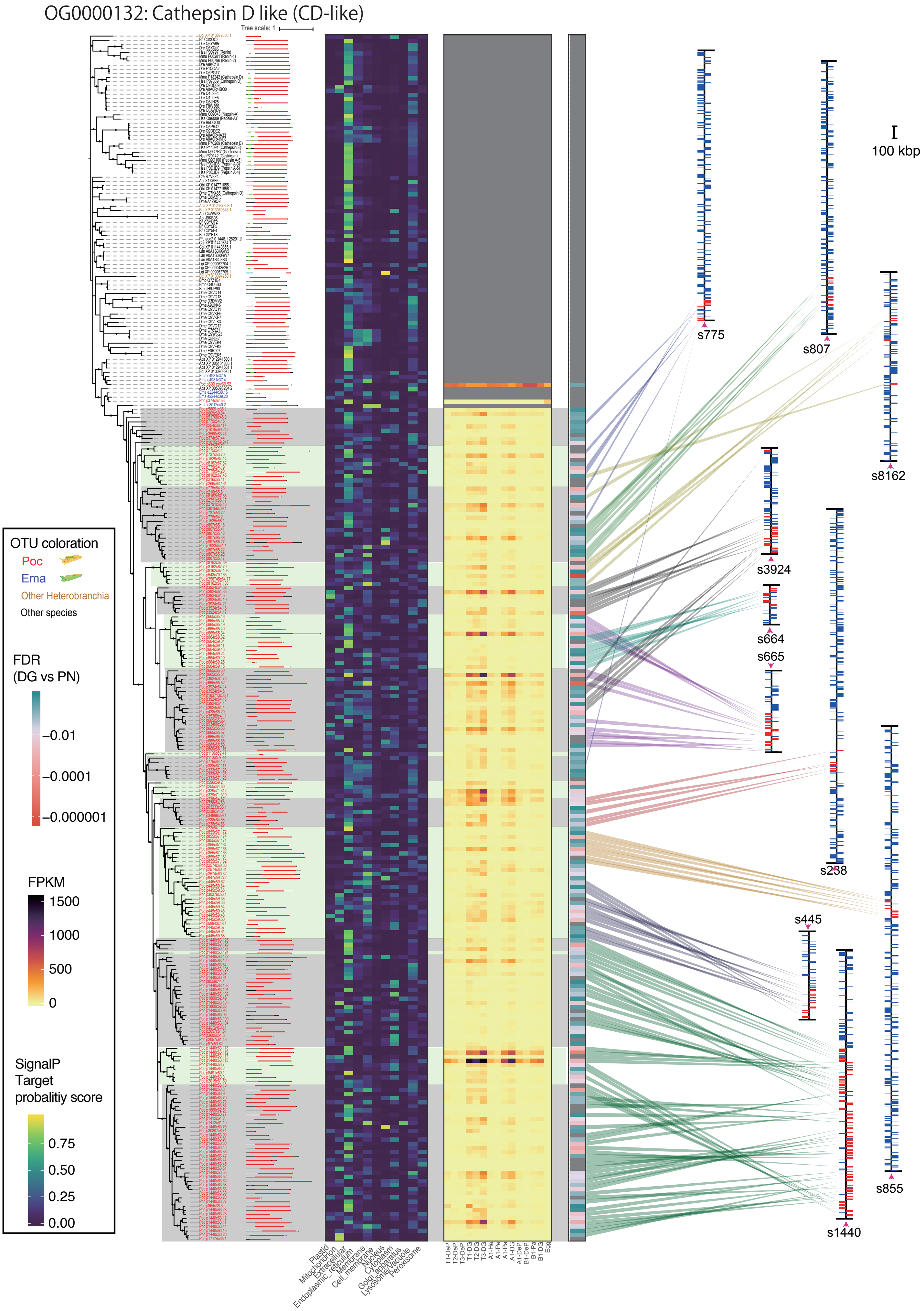
Supplementary Figure 25 Volcano plot of the cross-tissue comparison between DG and DeP. Each dot represents a gene. Colors and dot shapes mean the belonging orthogroups of each gene. Raw data, DOI 10.6084/m9.figshare.12319826



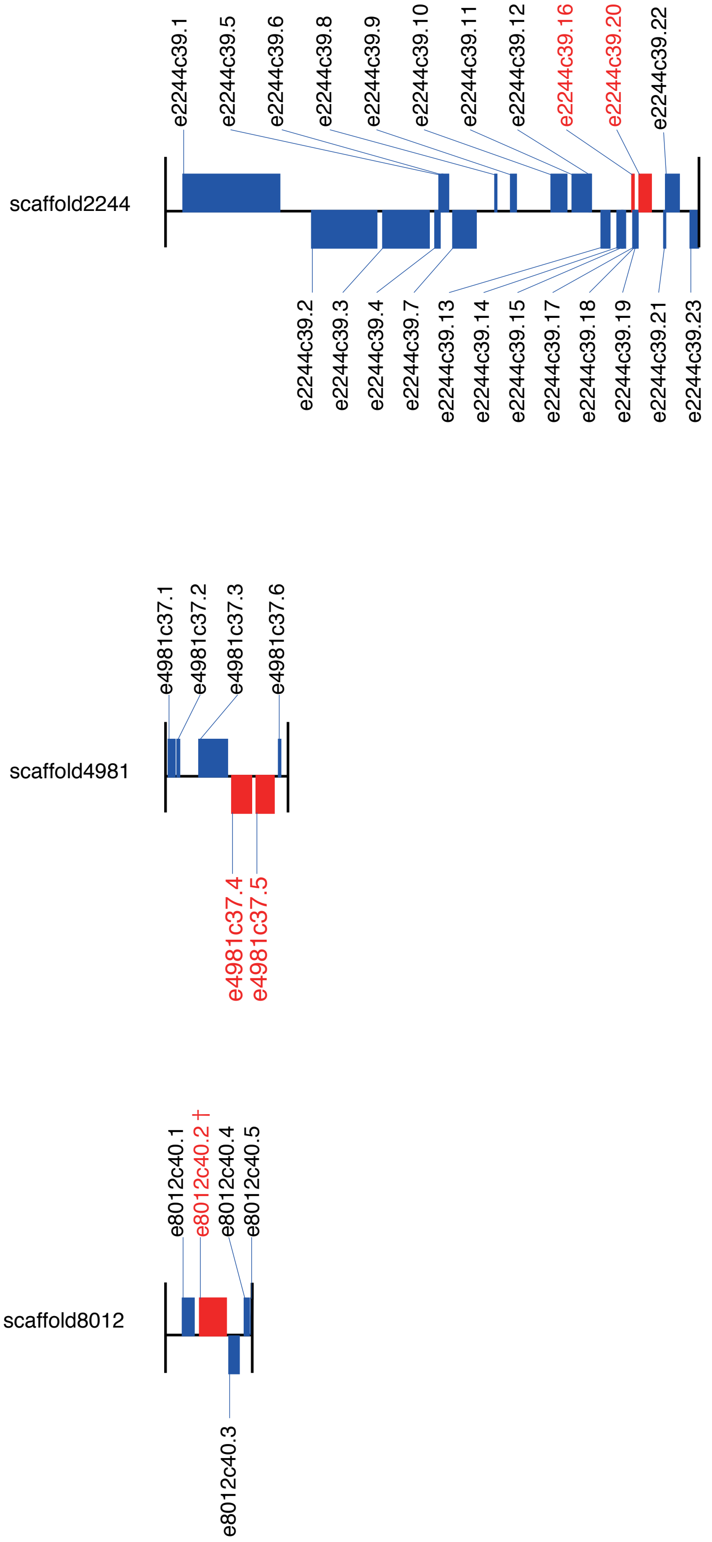
Supplementary Figure 26 CAFE-based all rapidly evolving genes on the sacoglossan linage. The gene count of all rapidly evolving orthogroups on *P. ocellatus* (left side) and the common node between *P. ocellatus* and *E. marginata* (right side) were plotted with a heat map. The red color means the number of genes. The blue color indicates the number of differentially expressed genes between DG and DeP tissue.



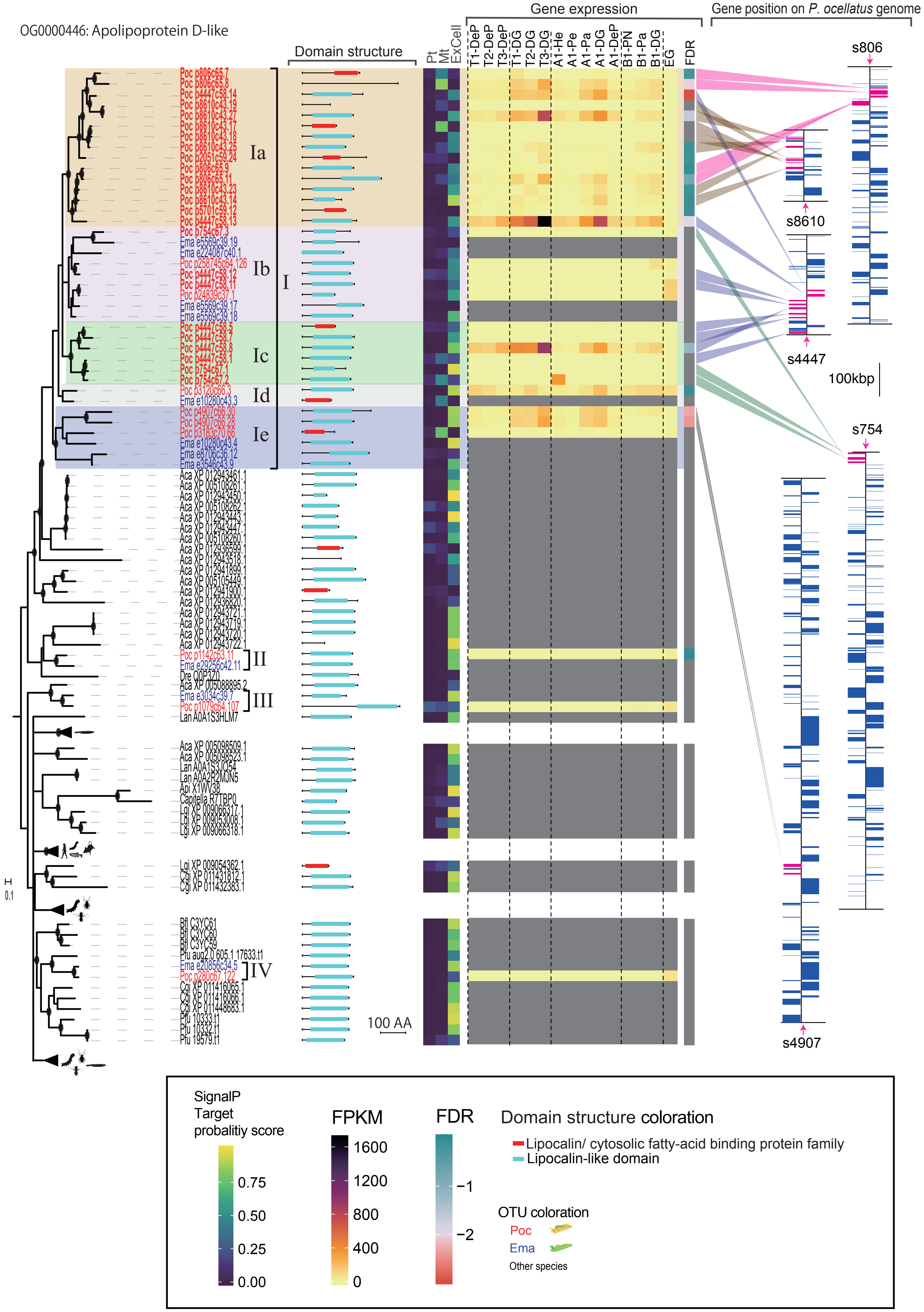
Supplementary Figure 27 Z-score-based rapidly evolving genes on the *P. ocellatus* linage. Color legends were described on the top right box.



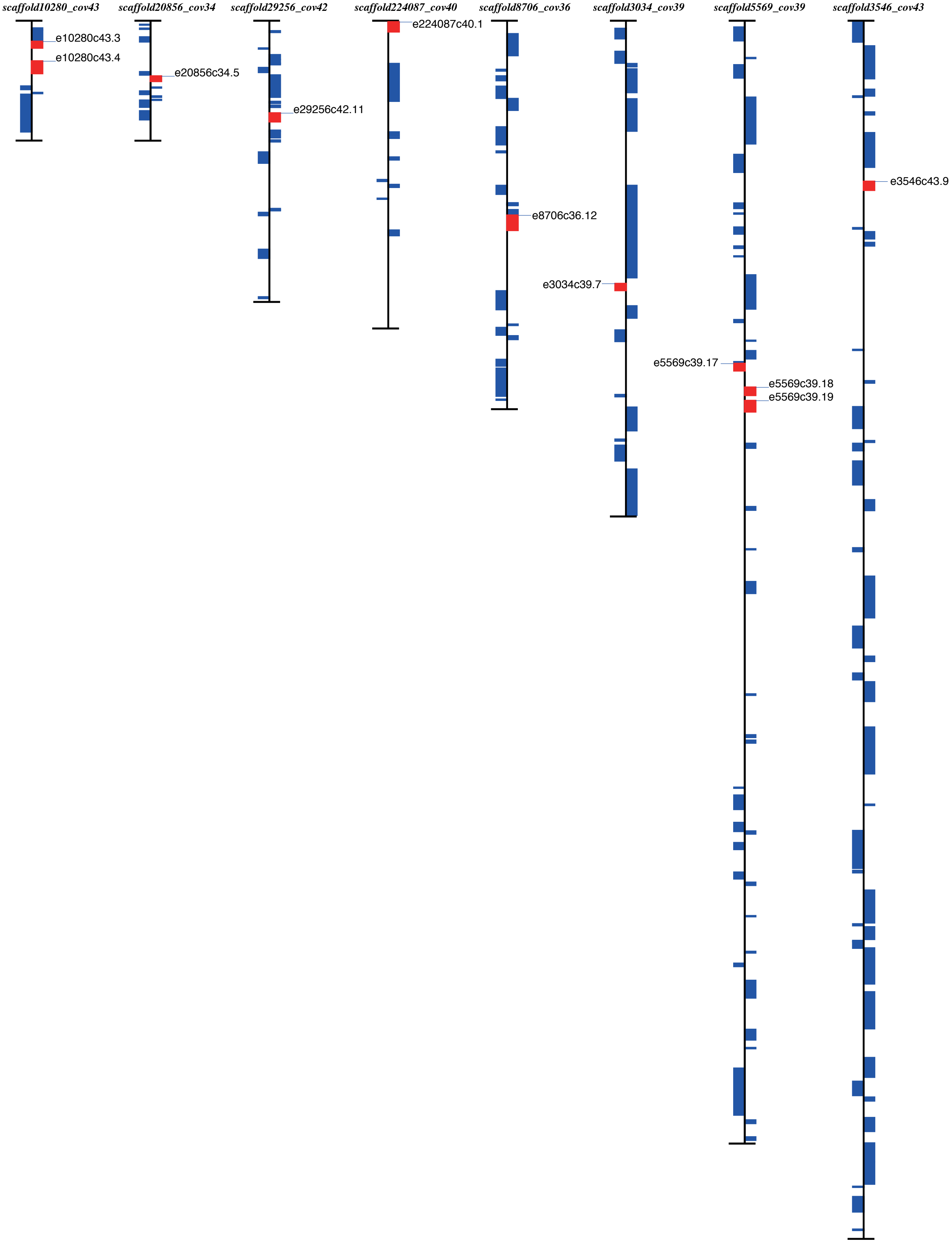
Supplementary Figure 28 Gene tree for the all member of OG0000132 (Cathepsin D like), predicted intracellular location with SignalP, expression profiles in cross-tissue RNA-Seq, and the gene position on *P. ocellatus* genome. Color legends were described on the left box.



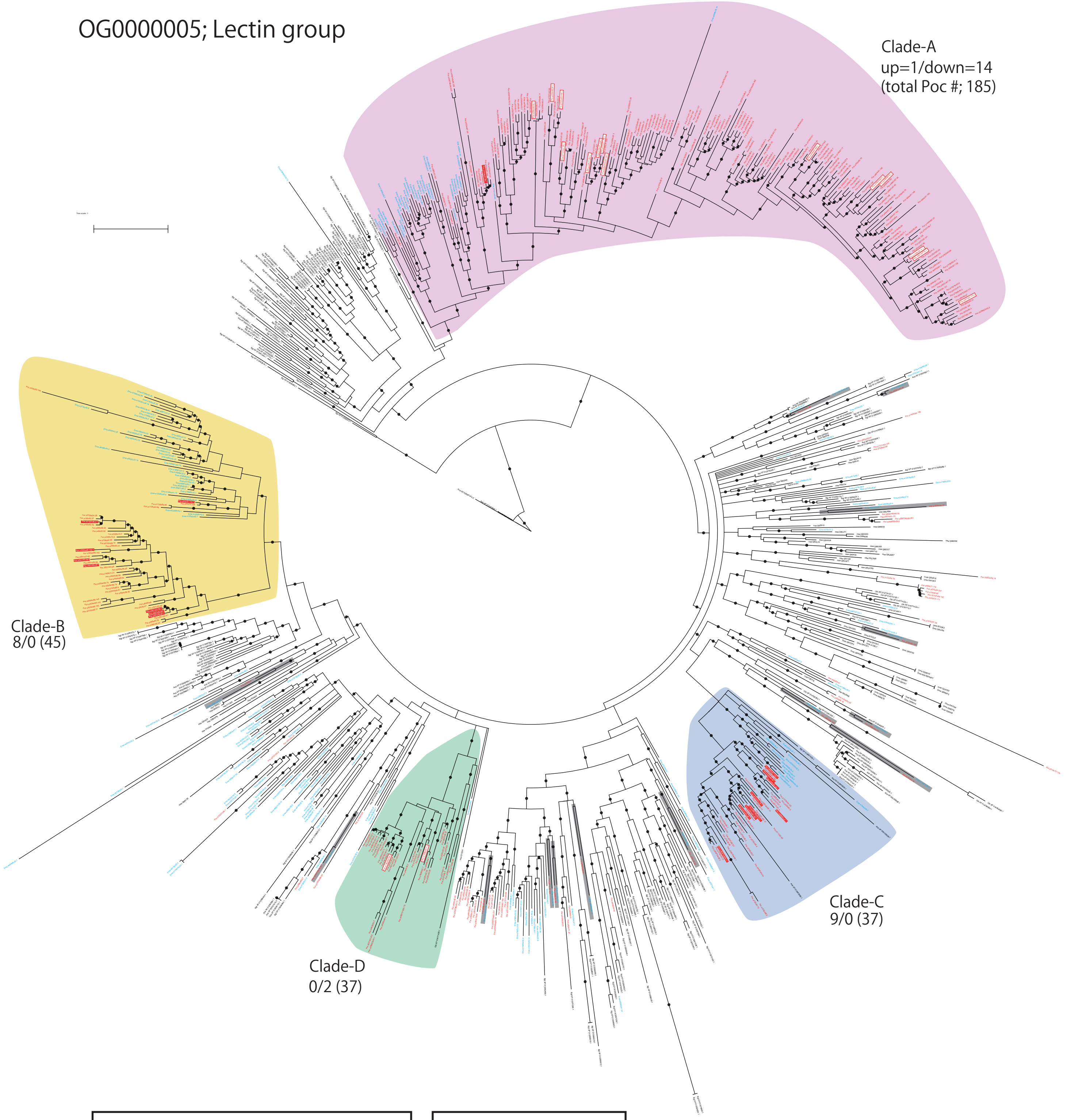
Supplementary Figure 29 Gene positions of OG0000132 on *E. marginata* genome. Red; OG0000132 genes. Blue; other genes. †Clade-γ gene



Supplementary Figure 30 Gene tree for the member of OG0000446 (Apolipoprotein D-like), predicted intracellular location with SignalP, expression profiles in cross-tissue RNA-Seq, and the gene position on *P. ocellatus* genome. Color legends were described on the bottom box.



Supplementary Figure 31 Gene positions of OG0000446 on *E. marginata* genome. Red; OG0000446 genes, Blue; other genes.

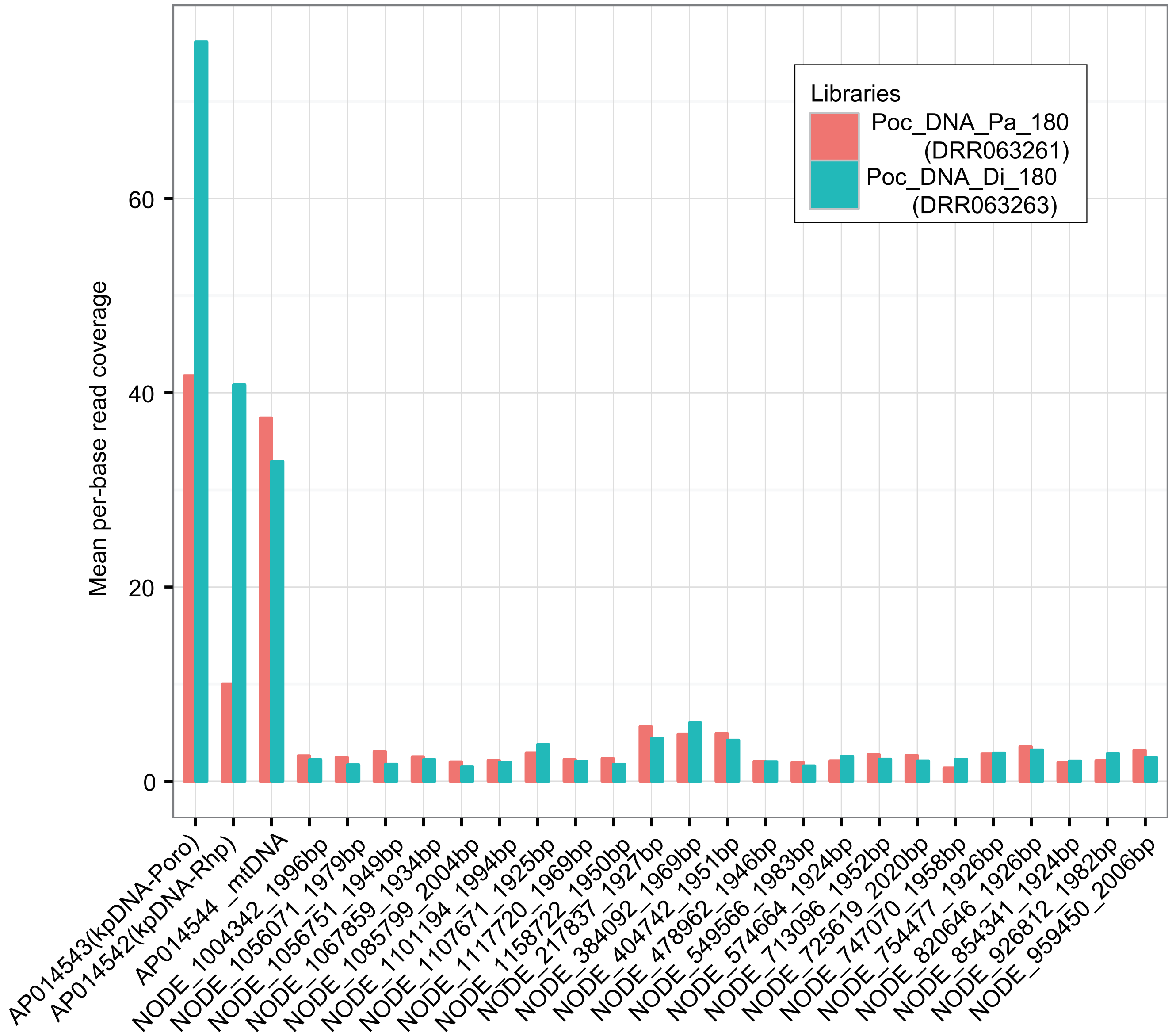


DG-downregulated
p339c68.52
p1147c61.57
p335c60.39
p1352c59.54
p6313c71.6
p124c71.259
p227c62.170
p339c68.166
p1857c64.5
p1209c50.1
p258753c65.149
p1121c63.100
p124c71.261
p124c71.266
p256c68.16
p1529c64.11

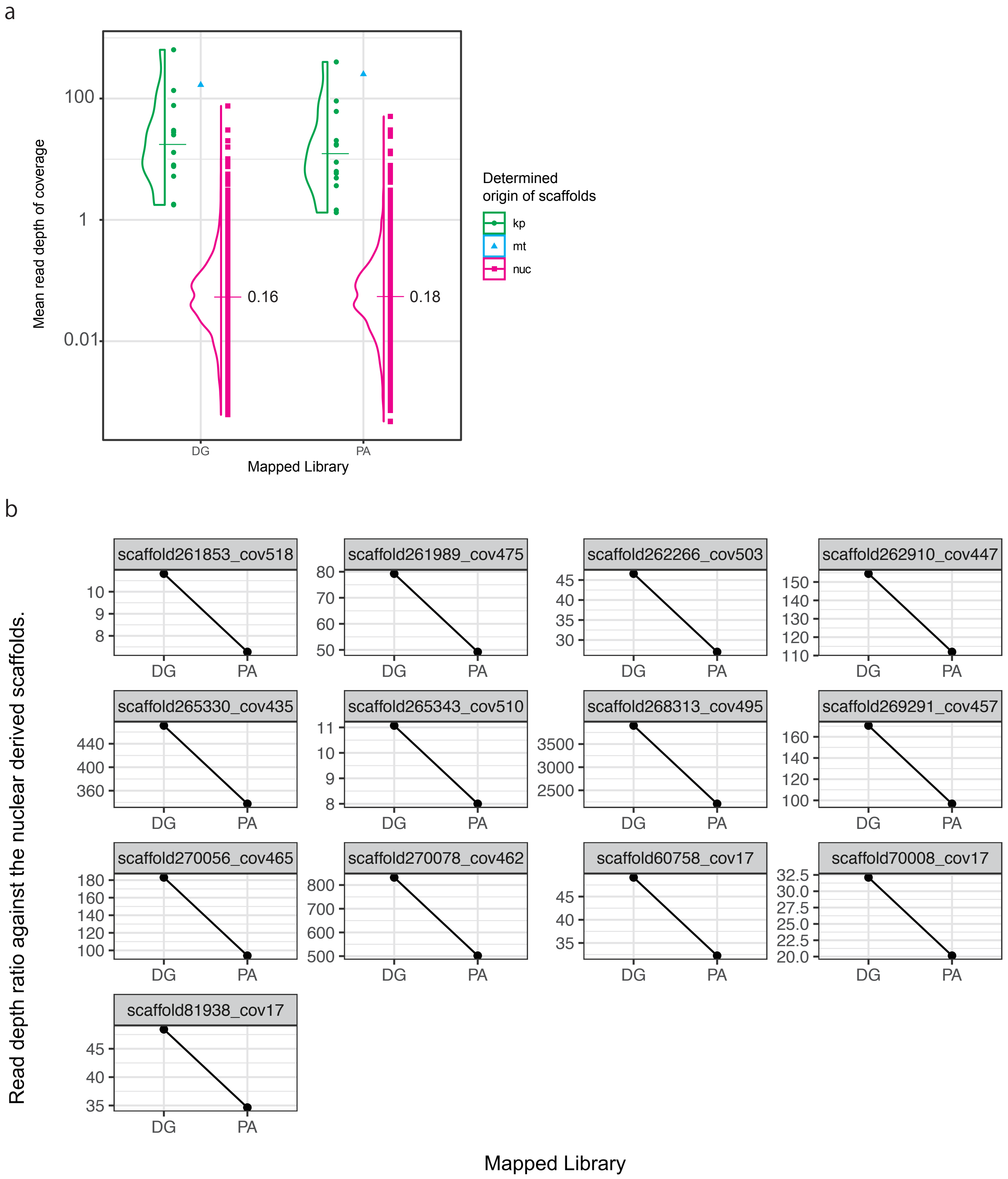
DG-upregulated
p3334c67.98
p3054c66.152
p501c63.67
p501c63.64
p501c63.56
p4334c64.28
p47c72.174
p501c63.63
p4334c64.26
p501c63.50
p7187c46.2
p4334c64.30
p855c67.129
p335c60.28
p258754c68.4
p258746c66.63
p958c60.27
p335c60.25

OTU coloration
Poc
Ema
Other species
DG-upregulated Poc gene
DG-downregulated Poc gene

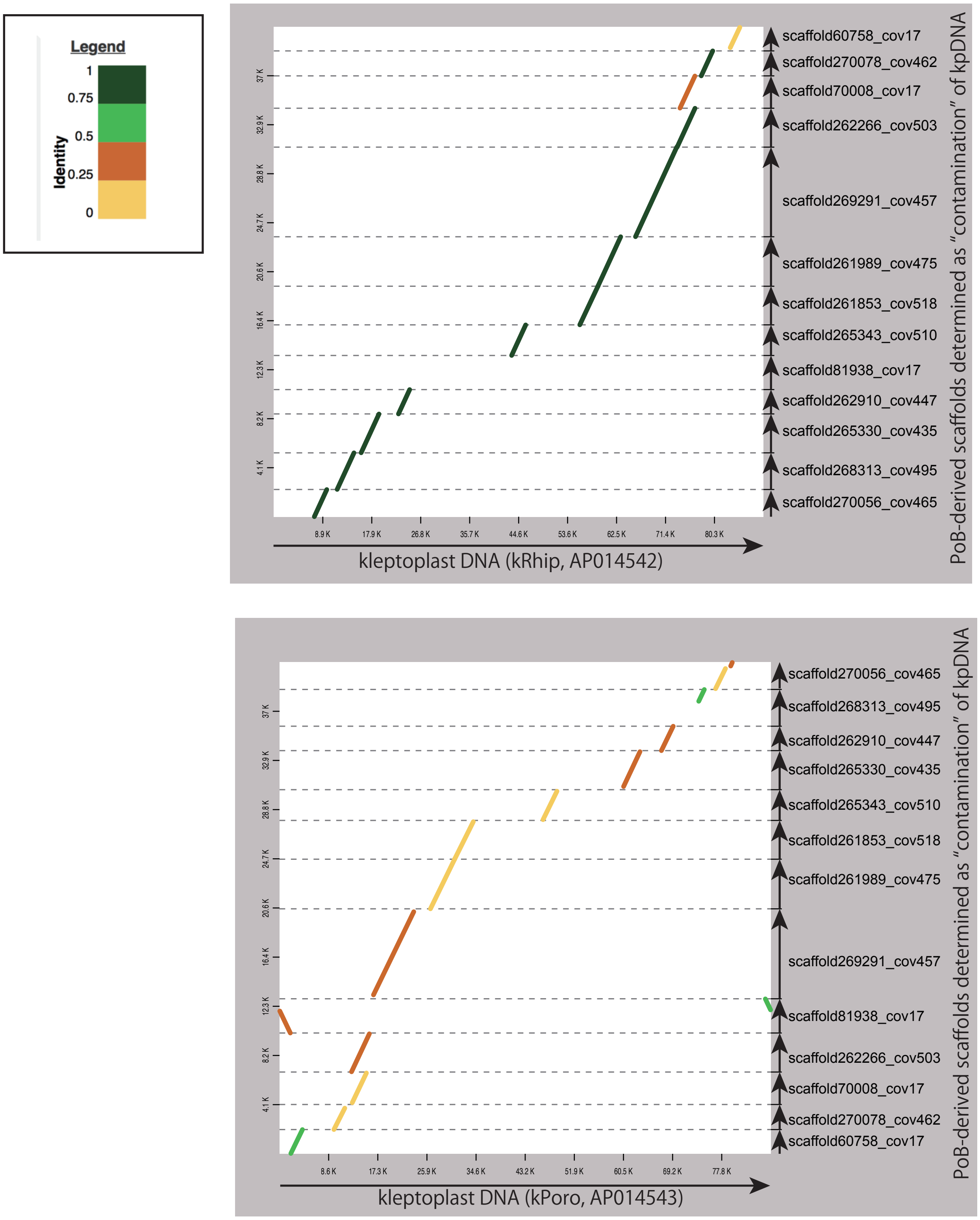
Supplementary Figure 32 Gene tree for the member of OG0000005 (Lectin-like). The black dot on the node indicates the Bootstrap support over 80. One-by-one ortholog pairs were masked with gray color.



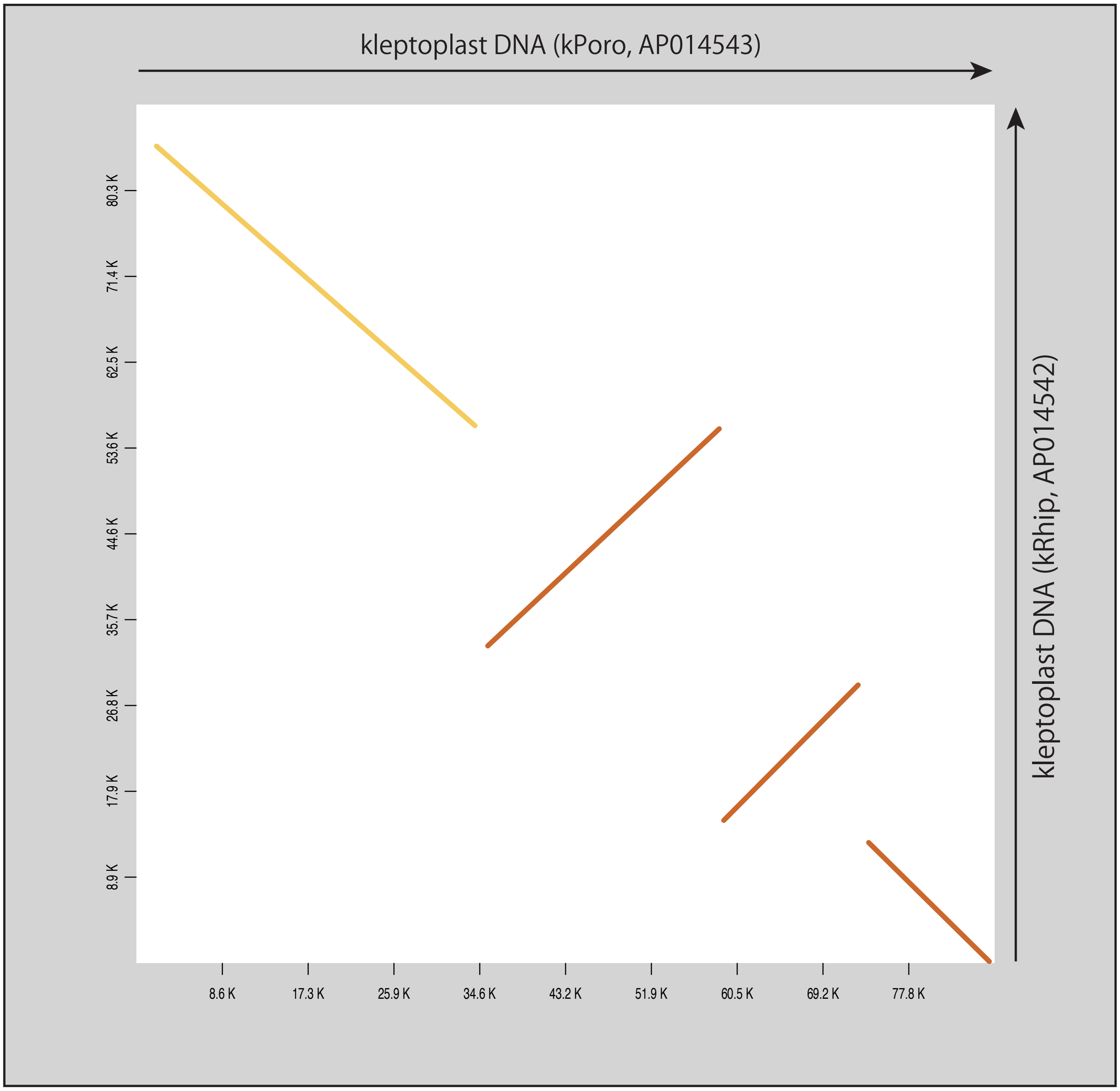
Supplementary Figure 33 Read coverage depth of the constructed *P. ocellatus* genomic assemblies.
We mapped the two libraries to the constructed assemblies to determine the origin of each assemblies. The "Poc_DNA_Pa_180" is a kleptoplast-poor sample and "Poc_DNA_Di_180" is a kleptoplast-enriched sample. Considerable change of depth on AP014543 and AP014542 reflects the different origin (kleptoplast) of the assemblies from the rest data.



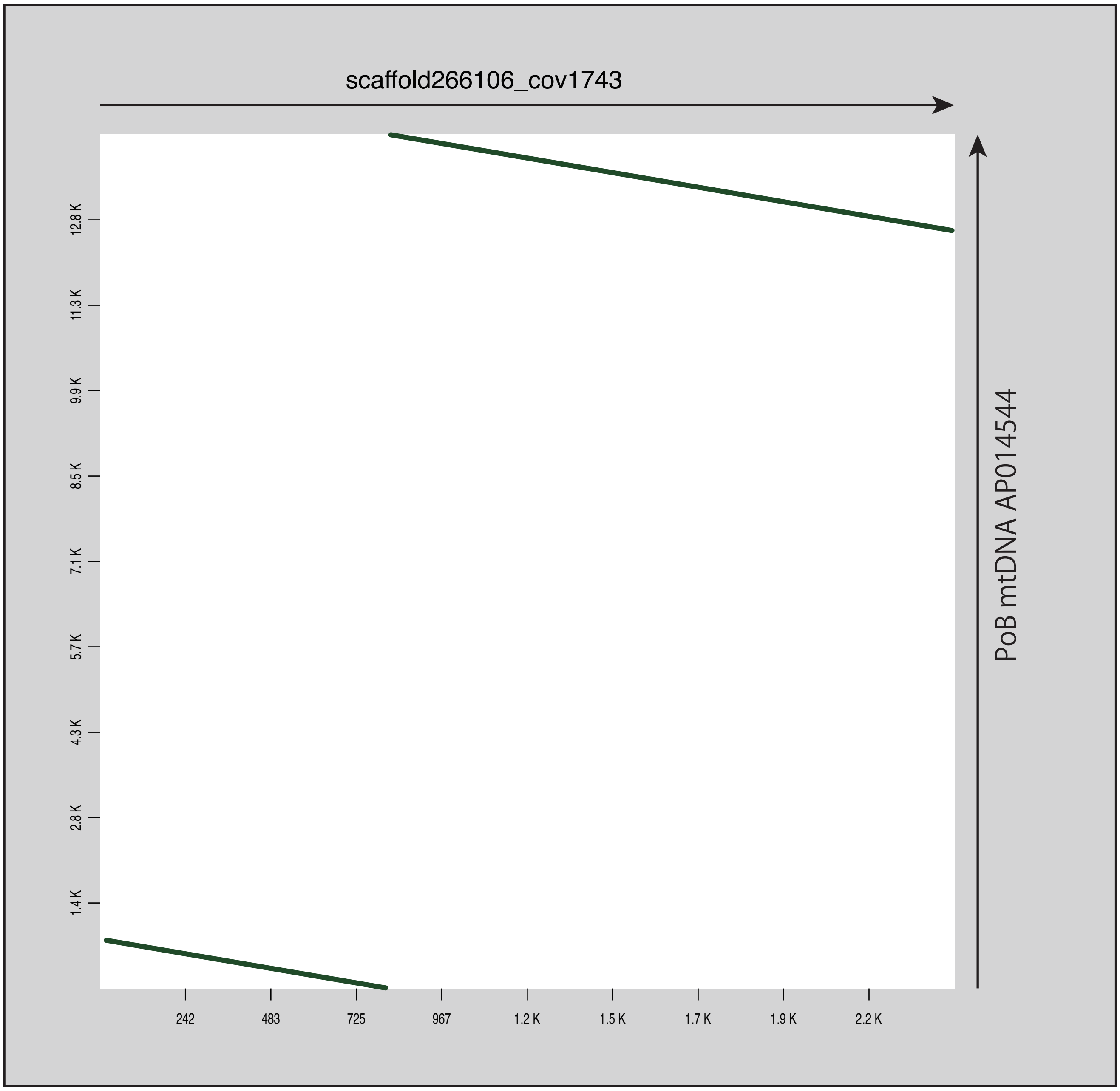
Supplementary Figure 34 Read depth of the PoB genome assemblies. Two types of the Illumina library form PoB DNA (DG = digestive gland , PA = parapodium) were mapped to the 13 kleptoplastic (kp), 1 mitochondrial (mt), and 8647 nuclear (nuc) scaffolds. **a** Violin and scatter plot of the mapped read depth. Each dot means a scaffold, the average of depth values was indicated as a horizontal bar. The legend of coloration are indicated in the right box. **b** Line graph of the relative value of the read depth of the kleptoplastic scaffolds against the averaged depth of all nuclear scaffolds in each library. Kleptopalstic scaffold IDs were descrived on the top of each graph.



Supplementary Figure 35 Dot plot of the referential kleptoplast DNAs and PoB genomic scaffolds determined as the kleptoplast DNA (kpDNA). X-axis, referential kleptoplast DNAs (kPoro and kRhip). Y-axis, 13 scaffolds that were determined as kpDNA sequences. The diagonals indicate matching contiguously aligned regions. The coloration indicates the identity of the aligned regions. The legend of similarity coloration are indicated in the top left box. Arrows indicate the aligned sequences and direction. We used D-GENIES software to make the dot-plots. Althogh the "scaffold81938_cov17" and "scaffold268313_cov495" were aligned to only one of the two referential kpDNAs, this discrepancy may be due to the fact that PoB retain chloroplasts derived from multiple algal species simultaneously, and the sequence of chloroplast DNA varies considerably between algal species (see Supplementary Figure 36). The reason for the differences from the reference maybe because those scaffolds are derived from miner kleptoplasts whose genomes have not yet been sequenced. Overall, these results support that the the sequence of 13 scaffolds are not derived from anything other than chloroplasts/kleptoplast.



Supplementary Figure 36 Dot plot of the two referential kleptoplast DNAs. Arrows and colors are as in Supplementary Figure 35



Supplementary Figure 37 Dot plot of the referential mtDNAs and one scaffold determined as mtDNA sequence. Arrows and colors are as in Supplementary Figure 35.

Supplementary Table 1 Fv/Fm and oxygen generation activity of *P. ocellatus* type black

Raw data were submitted to FigShare (DOI 10.6084/m9.figshare.12301865). ND, no data.

Individual ID	Species	Days of starvation	Fv/Fm	Oxygen generation rate (pgO_2/hour/individual)		
				Dark	Light	Gross photosynthesis
ID1	*P. ocellatus* type black	38	0.681	-44.2	65.0	109.2
ID2	*P. ocellatus* type black	38	0.690	-26.5	16.3	42.8
ID3	*P. ocellatus* type black	38	0.677	-38.3	40.8	79.2
ID4	*P. ocellatus* type black	109	0.567	-35.5	1.0	36.5
ID5	*P. ocellatus* type black	110	0.607	-21.6	-3.3	18.3
ID6	*P. ocellatus* type black	110	0.643	-27.8	3.8	31.5
Habo1	*H. borneensis*	ND	0.756	ND	ND	ND
Habo2	*H. borneensis*	ND	0.744	ND	ND	ND
Habo2	*H. borneensis*	ND	0.734	ND	ND	ND

Supplementary Table 2 The longevity of starved *Plakobranchus ocellatus* type black.

Sample ID	Incubation condition	Longevity (Days)
D1	Dark	145
D2	Dark	150
D3	Dark	150
D4	Dark	165
D5	Dark	165
LD1	Light/Dark	165
LD2	Light/Dark	173
LD3	Light/Dark	204
LD4	Light/Dark	204
LD5	Light/Dark	237

Supplementary Table 3 Plastidial DNAs for the kpDNA gene composition comparison.

Taxon. V, Viridiplantae; R, Rhodophyta; H, Heterokonta; U, Ulvophyceae; C, Chlorophyceae; B, Bryopsidles

Summary of the sequenced raw data was submitted to FigShare (DOI 10.6084/m9.figshare.12301277)

Species name	Abbreviation in figures	Taxon			Plastid genome (RefSeq ID)	cpDNA size (bp)	Chloroplast recipients
Bryopsis hypnoides	Brhy	V	U	B	NC_013359.1	153,429	*Elysia marginata*
Bryopsis plumosa	Brpl	V	U	B	NC_026795.1	106,859	
Bryopsis sp. HV04063	Brsp	V	U	B	NC_037363.1	100,655	
Halimeda borneensis	Habo	V	U	B	AP_012291.1	86,483	*Plakobranchus ocellatus*
Caulerpa cliftonii	Cacl	V	U	B	NC_031368.1	131,135	
Caulerpa manorensis	Cama	V	U	B	NC_037367.1	140,597	
Caulerpa racemosa	Cara	V	U	B	NC_032042.1	176,522	
Caulerpa lentillifera	Cale	V	U	B	NC_039377.1	119,402	
Chlorodesmis fastigiata	Chfa	V	U	B	NC_037364.1	88,592	
Codium decorticatum	Code	V	U	B	NC_032043.1	91,509	
Codium sp. 'arenicola'	Cosp	V	U	B	NC_037366.1	83,933	
Derbesia sp. WEST4838	Desp	V	U	B	NC_031367.1	115,765	
Lambia antarctica	Laan	V	U	B	NC_032284.1	104,098	
Rhipilia penicilloides	Rhpe	V	U	B	NC_037365.1	105,774	
Tydemania expeditionis	Tyex	V	U	B	NC_026796.1	105,200	
Chlamydomonas reinhardtii	Chre	V	C		NC_005353.1	203,828	
Cyanidioschyzon merolae	Cyme	R			NC_004799.1	149,987	
Vaucheria litorea	Vali	H			NC_011600.1	115,341	*Elysia chlorotica*

Supplementary Table 4 Structural RNA gene composition of analyzed plastid DNA.

Species abbreviations are defined in Supplementary Table 3.

		Chf	kPoro	kRhip	Tye	Rhp	Hab	Cam	Car	Cal	Cac	Cod	Cos	Des	Laa	Brp	Brs	Brh	Chr	Cym	Val
16SrRNA		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
23SrRNA		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Ala	AGC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	CGC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	TGC	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Arg	ACG	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	CCG	+	+	+	-	+	-	+	+	+	+	-	-	-	-	-	-	-	-	-	+
	CCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	TCG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	TCT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
Asn	GTT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Asp	GTC	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Cys	GCA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Gln	CTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	TTG	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Glu	CTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	TTC	+	+	-	+	+	+	+	+	+	+	-	-	-	-	-	-	-	+	+	+
Gly	GCC	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	TCC	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
His	GTG	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Ile	AAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	GAT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	TAT	-	-	-	+	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
Leu	CAA	+	+	+	-	+	-	-	-	+	-	-	-	-	-	-	-	+	-	+	-
	GAG	+	-	+	+	+	+	-	-	+	+	-	-	-	-	-	-	-	-	+	-
	TAA	-	-	+	-	-	+	+	+	+	-	-	-	+	-	-	-	+	+	+	+
	TAG	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lys	CTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	TTT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Met	CAT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Phe	GAA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Pro	AGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	TGG	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Ser	GCT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
	TGA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Thr	AGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	GGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
	TGT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Trp	CCA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Tyr	GTA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Val	AAC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	CAC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
	GAC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
	TAC	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

Supplementary Table 5 Assembly statistics of *de novo* RNA-seq of donor algae

Trinity assemblies, *de novo* RNA assemblies clustered by CD-Hit (c=0.95). All models, constructed gene models from Trinity assemblies by Transdecoder. Viridiplantal, Viridiplantal genes identified by MEGAN analysis. NA, not analyzed. Summary of the sequenced raw data was submitted to FigShare (DOI, 10.6084/m9.figshare.12301277).

	Number of models	Averaged length (bp)	Hit models with BUSCO (total BUSCO = 303)									
			Complete		Complete single-copy		Complete duplicated		Fragmented BUSCOs		Missing BUSCOs	
			#	%	#	%	#	%	#	%	#	%
Halimeda borneensis												
Trinity assemblies	24,218	1717	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
All models	26,652	1042	262	86%	130	43%	132	44%	16	5%	25	8%
Viridiplantal	11,629	NA	214	71%	106	35%	108	36%	17	6%	72	24%
Bryopsis hypnoides												
Trinity assemblies	46,039	875	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
All models	24,127	1002	281	93%	247	82%	34	11%	10	3%	12	4%
Viridiplantal	8630	NA	226	75%	209	69%	17	6%	13	4%	64	21%

Supplementary Table 6 Algal genes used for referential query (A614 dataset)

Raw data were submitted to FigShare (DOI 10.6084/m9.figshare.12318947)

Species	Gene model ID	Product name
Halimeda borneensis	c10130_g1_i1|m.13140	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c10130_g1_i2|m.13155	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c10139_g1_i1|m.13200	Photosystem II manganese
Halimeda borneensis	c10139_g1_i3|m.13209	Photosystem II manganese
Halimeda borneensis	c10202_g1_i1|m.13618	PsbP domain-OEC23 like protein
Halimeda borneensis	c10202_g1_i2|m.13631	PsbP domain-OEC23 like protein
Halimeda borneensis	c10202_g1_i3|m.13644	PsbP domain-OEC23 like protein
Halimeda borneensis	c10359_g1_i1|m.14901	Low PSII Accumulation 3
Halimeda borneensis	c10360_g1_i1|m.14907	Photosystem II reaction center PsbP family protein
Halimeda borneensis	c10604_g1_i1|m.16759	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c10621_g1_i1|m.16844	Photosystem I reaction center subunit XI
Halimeda borneensis	c10633_g1_i1|m.16952	Photosyst
Halimeda borneensis	c10633_g1_i2|m.16956	Photosystem II D1 processing protein PSB27-H2, chloroplastic
Halimeda borneensis	c10633_g1_i3|m.16958	Photosystem II D1 processing protein PSB27-H2, chloroplastic
Halimeda borneensis	c10644_g1_i1|m.17084	Ferredoxin-thioredoxin reductase, variable chain
Halimeda borneensis	c10644_g1_i2|m.17095	Ferredoxin-thioredoxin reductase, variable chain
Halimeda borneensis	c10644_g1_i5|m.17106	Ferredoxin-thioredoxin reductase, variable chain
Halimeda borneensis	c10644_g1_i7|m.17117	Ferredoxin-thioredoxin reductase, variable chain
Halimeda borneensis	c10806_g1_i1|m.18764	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c10867_g1_i1|m.19289	PsaO
Halimeda borneensis	c10867_g1_i2|m.19309	PsaO
Halimeda borneensis	c10967_g1_i1|m.20274	Protein Thf1
Halimeda borneensis	c11000_g1_i1|m.20583	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c11000_g1_i2|m.20597	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c11000_g1_i3|m.20612	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c11000_g1_i4|m.20625	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c11205_g1_i1|m.22907	Mg-protoporphyrin IX chelatase
Halimeda borneensis	c11205_g1_i3|m.22926	Mg-protoporphyrin IX chelatase
Halimeda borneensis	c11205_g1_i5|m.22942	Mg-protoporphyrin IX chelatase
Halimeda borneensis	c11556_g1_i1|m.27176	Photosystem II reaction center W protein
Halimeda borneensis	c11750_g1_i1|m.30081	Geranylgeranyl reductase
Halimeda borneensis	c11812_g2_i1|m.31052	Photosystem II reaction center PsbP family protein
Halimeda borneensis	c11838_g6_i1|m.31607	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c11923_g1_i1|m.33202	Phosphoglycerate kinase
Halimeda borneensis	c11923_g1_i2|m.33212	Phosphoglycerate kinase
Halimeda borneensis	c11923_g1_i3|m.33221	Phosphoglycerate kinase
Halimeda borneensis	c11992_g1_i1|m.34555	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c11992_g1_i2|m.34572	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c12019_g3_i1|m.35190	Photosystem II reaction center PsbP family protein
Halimeda borneensis	c12058_g4_i1|m.36211	Photosystem II 10 kDa polypeptide, chloroplastic
Halimeda borneensis	c12063_g1_i2|m.36272	Proline--tRNA ligase
Halimeda borneensis	c12213_g1_i1|m.39684	Solanesyl diphosphate synthase
Halimeda borneensis	c12285_g1_i1|m.41562	Photosystem II core complex proteins psbY
Halimeda borneensis	c12285_g1_i2|m.41582	Photosystem II core complex proteins psbY
Halimeda borneensis	c12285_g1_i3|m.41600	Photosystem II core complex proteins psbY
Halimeda borneensis	c12285_g1_i4|m.41620	Photosystem II core complex proteins psbY
Halimeda borneensis	c12285_g1_i8|m.41640	Photosystem II core complex proteins psbY
Halimeda borneensis	c12485_g2_i2|m.47159	Photosystem I reaction center subunit N
Halimeda borneensis	c12485_g2_i4|m.47173	Photosystem I reaction center subunit N
Halimeda borneensis	c13873_g1_i1|m.53546	NmrA-like
Halimeda borneensis	c14836_g1_i1|m.53851	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c14923_g1_i1|m.53994	Proton gradient regulation 5
Halimeda borneensis	c15972_g1_i1|m.54474	Oxygen-evolving enhancer protein 3
Halimeda borneensis	c17102_g1_i1|m.54887	Photosystem I reaction center subunit II
Halimeda borneensis	c17135_g1_i1|m.55002	Photosystem I reaction center subunit III
Halimeda borneensis	c17137_g1_i1|m.55006	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c18279_g1_i1|m.55485	Photosystem II oxygen-evolving enhancer protein 2
Halimeda borneensis	c2011_g1_i1|m.979	Photosystem I reaction center subunit V
Halimeda borneensis	c2516_g1_i1|m.1178	Thylakoid lumen protein

Species	Gene model ID	Product name
Halimeda borneensis	c2516_g1_i2|m.1181	Thylakoid lumen protein
Halimeda borneensis	c5655_g1_i2|m.2421	Photosystem II lipoprotein Psb27
Halimeda borneensis	c5754_g1_i1|m.2541	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c6345_g1_i1|m.3131	PsbP-like protein 1
Halimeda borneensis	c6345_g1_i2|m.3134	PsbP-like protein 1
Halimeda borneensis	c6657_g1_i1|m.3594	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c6657_g1_i2|m.3603	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c6847_g1_i1|m.3868	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c7852_g1_i1|m.5043	Photosystem I reaction center subunit VI
Halimeda borneensis	c7901_g1_i1|m.5169	Glyceraldehyde-3-phosphate dehydrogenase
Halimeda borneensis	c8046_g1_i1|m.5446	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c8430_g1_i2|m.6720	PsbP domain-containing protein 1
Halimeda borneensis	c8430_g1_i3|m.6726	PsbP domain-containing protein 1
Halimeda borneensis	c8430_g1_i5|m.6732	PsbP domain-containing protein 1
Halimeda borneensis	c8767_g1_i1|m.7731	Phosphoribulokinase
Halimeda borneensis	c8767_g1_i2|m.7752	Phosphoribulokinase
Halimeda borneensis	c9307_g2_i1|m.9349	Photosystem I reaction center subunit psaK
Halimeda borneensis	c9585_g1_i1|m.10690	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c11454_g1_i2|m.25690	Protein LOW PSII ACCUMULATION 3, chloroplastic
Halimeda borneensis	c11503_g2_i1|m.26337	Cytochrome c6
Halimeda borneensis	c11974_g1_i1|m.34152	Cytochrome b6-f complex iron-sulfur subunit
Halimeda borneensis	c11974_g1_i2|m.34176	Cytochrome b6-f complex iron-sulfur subunit
Halimeda borneensis	c11974_g1_i4|m.34199	Cytochrome b6-f complex iron-sulfur subunit
Halimeda borneensis	c12063_g1_i1|m.36256	Proline--tRNA ligase
Halimeda borneensis	c12387_g1_i2|m.44368	Serine/threonine protein kinase
Halimeda borneensis	c12387_g1_i3|m.44382	Serine/threonine protein kinase
Halimeda borneensis	c12387_g1_i4|m.44396	Serine/threonine protein kinase
Halimeda borneensis	c12387_g1_i5|m.44409	Serine/threonine protein kinase
Halimeda borneensis	c12387_g1_i6|m.44423	Serine/threonine protein kinase
Halimeda borneensis	c12387_g1_i7|m.44437	Serine/threonine protein kinase
Halimeda borneensis	c12482_g1_i1|m.47079	Photosystem II reaction center PsbP family protein
Halimeda borneensis	c18307_g1_i1|m.55531	Beta-propeller domain-containing protein
Halimeda borneensis	c6105_g1_i1|m.2865	Tetratricopeptide repeat
Halimeda borneensis	c9439_g1_i1|m.10060	Ribulose bisphosphate carboxylase small chain
Halimeda borneensis	c9439_g1_i2|m.10069	Ribulose bisphosphate carboxylase small chain
Halimeda borneensis	c10309_g1_i3|m.14470	Peptidyl-prolyl cis-trans isomerase
Halimeda borneensis	c11984_g1_i1|m.34368	NA
Halimeda borneensis	c11984_g1_i2|m.34379	NA
Halimeda borneensis	c11984_g1_i4|m.34390	NA
Halimeda borneensis	c11984_g1_i5|m.34401	NA
Halimeda borneensis	c11984_g1_i6|m.34411	NA
Halimeda borneensis	c11984_g1_i7|m.34423	NA
Halimeda borneensis	c12550_g1_i1|m.49400	Peptidase M50 family protein
Halimeda borneensis	c12550_g1_i11|m.49438	Peptidase M50 family protein
Halimeda borneensis	c12550_g1_i3|m.49410	Peptidase M50 family protein
Halimeda borneensis	c12550_g1_i4|m.49420	Peptidase M50 family protein
Halimeda borneensis	c12550_g1_i7|m.49429	Peptidase M50 family protein
Halimeda borneensis	c1596_g1_i1|m.730	Photosystem II manganese
Halimeda borneensis	c5758_g1_i1|m.2549	Ultraviolet-B-repressible protein
Halimeda borneensis	c5758_g1_i2|m.2555	Ultraviolet-B-repressible protein
Halimeda borneensis	c6451_g1_i1|m.3322	Expressed protein
Halimeda borneensis	c8027_g1_i1|m.5432	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c8289_g1_i1|m.6257	Photosystem II reaction center PsbP family protein
Halimeda borneensis	c8289_g1_i2|m.6265	Photosystem II reaction center PsbP family protein
Halimeda borneensis	c8782_g1_i1|m.7817	Chlorophyll a-b binding protein, chloroplastic
Halimeda borneensis	c10309_g1_i2|m.14469	Peptidyl-prolyl cis-trans isomerase
Halimeda borneensis	c10611_g1_i1|m.16776	VKOR-domain-containing protein
Halimeda borneensis	c10611_g1_i2|m.16777	Vitamin K epoxide reductase
Halimeda borneensis	c10632_g1_i1|m.16945	Protein CHLOROPLAST ENHANCING STRESS TOLERANCE
Halimeda borneensis	c11124_g1_i1|m.22046	Protein low psii accumulation 2, chloroplastic
Halimeda borneensis	c11503_g2_i1|m.26335	Cytochrome c6
Halimeda borneensis	c11580_g1_i2|m.27450	FAN protein

Species	Gene model ID	Product name
Halimeda borneensis	c11580_g1_i5|m.27457	FAN protein
Halimeda borneensis	c11580_g1_i6|m.27466	FAN protein
Halimeda borneensis	c12063_g1_i2|m.36277	Proline--tRNA ligase
Halimeda borneensis	c12073_g1_i1|m.36486	Acetylglucosaminyltransferase
Halimeda borneensis	c12354_g1_i2|m.43524	Phenylalanine-trna alpha subunit
Halimeda borneensis	c12405_g1_i2|m.44746	LGP2
Halimeda borneensis	c12563_g1_i1|m.49896	{ECO:0000313|EMBL:BAD31802.1};
Halimeda borneensis	c12563_g1_i2|m.49907	{ECO:0000313|EMBL:BAD31802.1};
Halimeda borneensis	c12563_g1_i3|m.49920	{ECO:0000313|EMBL:BAD31802.1};
Halimeda borneensis	c12563_g1_i5|m.49932	{ECO:0000313|EMBL:BAD31802.1};
Halimeda borneensis	c12563_g1_i7|m.49946	{ECO:0000313|EMBL:BAD31802.1};
Halimeda borneensis	c13752_g1_i1|m.53423	Expressed protein
Halimeda borneensis	c1506_g1_i1|m.633	Photosystem II reaction center PsbP family protein
Halimeda borneensis	c6424_g1_i1|m.3282	Carbohydrate kinase-like protein
Halimeda borneensis	c7971_g1_i1|m.5294	Ran-binding protein
Halimeda borneensis	c8355_g1_i1|m.6553	Photosystem I reaction centre subunit N
Halimeda borneensis	c8355_g1_i2|m.6560	Photosystem I reaction centre subunit N
Halimeda borneensis	c9173_g3_i1|m.8728	Calmodulin-binding protein, putative, expressed
Halimeda borneensis	c11016_g1_i1|m.20733	BnaA06g31770D protein
Halimeda borneensis	c11016_g1_i2|m.20745	BnaA06g31770D protein
Halimeda borneensis	c11485_g1_i1|m.26071	Protein translocase subunit SecA
Halimeda borneensis	c11485_g1_i2|m.26080	Protein translocase subunit SecA
Halimeda borneensis	c11051_g1_i1|m.21180	DnaJ-like protein
Halimeda borneensis	c11051_g1_i2|m.21188	DnaJ-like protein
Halimeda borneensis	c11051_g1_i3|m.21196	DnaJ-like protein
Halimeda borneensis	c11074_g1_i2|m.21498	Chloroplast precursor;
Halimeda borneensis	c11074_g1_i3|m.21508	Chloroplast precursor;
Halimeda borneensis	c11129_g3_i1|m.22090	Rna binding protein
Halimeda borneensis	c11459_g1_i1|m.25719	Kinase-like protein
Halimeda borneensis	c11683_g1_i10|m.28986	ABC1 family protein
Halimeda borneensis	c11683_g1_i2|m.28884	ABC1 family protein
Halimeda borneensis	c11683_g1_i3|m.28898	ABC1 family protein
Halimeda borneensis	c11683_g1_i6|m.28938	ABC1 family protein
Halimeda borneensis	c11683_g1_i7|m.28949	ABC1 family protein
Halimeda borneensis	c11683_g1_i8|m.28961	ABC1 family protein
Halimeda borneensis	c11683_g1_i9|m.28972	ABC1 family protein
Halimeda borneensis	c11782_g1_i1|m.30630	Fructose-1,6-bisphosphatase class 1
Halimeda borneensis	c11919_g1_i1|m.33132	Rubredoxin
Halimeda borneensis	c11919_g1_i2|m.33137	Rubredoxin
Halimeda borneensis	c12485_g2_i2|m.47156	Fructose-1,6-bisphosphatase class 1
Halimeda borneensis	c12485_g2_i4|m.47171	Fructose-1,6-bisphosphatase class 1
Halimeda borneensis	c12581_g2_i1|m.50422	BnaA04g03770D protein
Halimeda borneensis	c12581_g2_i2|m.50429	BnaA04g03770D protein
Halimeda borneensis	c12581_g2_i3|m.50443	BnaA04g03770D protein
Halimeda borneensis	c12581_g2_i4|m.50463	BnaA04g03770D protein
Halimeda borneensis	c12581_g2_i5|m.50506	BnaA04g03770D protein
Halimeda borneensis	c18274_g1_i1|m.55476	Ferredoxin--NADP reductase
Halimeda borneensis	c2353_g1_i1|m.1136	Rieske
Halimeda borneensis	c7052_g1_i1|m.4120	Gdt1-like protein chloroplastic-like
Halimeda borneensis	c7288_g1_i1|m.4372	Thylakoid lumenal protein
Halimeda borneensis	c7288_g1_i2|m.4374	Thylakoid lumenal 16.5 kDa protein
Halimeda borneensis	c7288_g1_i3|m.4376	Thylakoid lumenal protein
Halimeda borneensis	c7288_g1_i3|m.4375	Thylakoid lumenal protein
Halimeda borneensis	c9535_g1_i1|m.10380	Retinol dehydrogenase 12
Halimeda borneensis	c9596_g1_i1|m.10738	Fatty-acid desaturase
Bryopsis hypnoides	TRINITY_DN10574_c0_g1_i1|m.43562	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN10651_c0_g1_i1|m.35752	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN11783_c0_g1_i1|m.53042	Photosystem II lipoprotein Psb27
Bryopsis hypnoides	TRINITY_DN12481_c0_g2_i1|m.11453	Thylakoid lumen protein
Bryopsis hypnoides	TRINITY_DN13502_c0_g2_i1|m.39188	Photosystem II reaction center PsbP family protein
Bryopsis hypnoides	TRINITY_DN13612_c0_g1_i1|m.40084	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN13612_c0_g1_i2|m.40089	Chlorophyll a-b binding protein, chloroplastic

Species	Gene model ID	Product name
Bryopsis hypnoides	TRINITY_DN13742_c1_g1_i3|m.46210	Photosystem II reaction center PsbP family protein
Bryopsis hypnoides	TRINITY_DN13742_c1_g1_i6|m.46216	Photosystem II reaction center PsbP family protein
Bryopsis hypnoides	TRINITY_DN14368_c0_g2_i1|m.13752	Photosystem II reaction center PsbP family protein
Bryopsis hypnoides	TRINITY_DN14730_c2_g1_i1|m.30859	Lumenal PsbP-like protein
Bryopsis hypnoides	TRINITY_DN15063_c0_g1_i1|m.27665	Photosystem II repair protein PSB27-H1, chloroplastic
Bryopsis hypnoides	TRINITY_DN15063_c0_g1_i2|m.27668	Photosystem II repair protein PSB27-H1, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c2_g3_i1|m.12096	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c2_g3_i2|m.12100	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c2_g3_i3|m.12102	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c2_g4_i1|m.12103	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c2_g4_i4|m.12104	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c2_g4_i5|m.12106	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN16093_c0_g1_i1|m.54248	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase
Bryopsis hypnoides	TRINITY_DN16153_c0_g1_i1|m.33391	Photosystem I reaction center subunit V
Bryopsis hypnoides	TRINITY_DN16170_c0_g1_i1|m.33317	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN16179_c0_g1_i1|m.33383	Protein Thf1
Bryopsis hypnoides	TRINITY_DN16266_c0_g1_i1|m.18608	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN16357_c0_g1_i1|m.1070	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN20081_c0_g1_i1|m.33879	Photosystem II reaction center W protein
Bryopsis hypnoides	TRINITY_DN20083_c0_g1_i1|m.33830	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN20147_c0_g1_i1|m.5646	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN20187_c0_g1_i1|m.5577	Photosystem I reaction center subunit III
Bryopsis hypnoides	TRINITY_DN20330_c0_g1_i1|m.9442	Photosystem II PsbY protein
Bryopsis hypnoides	TRINITY_DN20330_c0_g2_i1|m.9443	Photosystem II PsbY protein
Bryopsis hypnoides	TRINITY_DN20330_c0_g3_i1|m.9446	Photosystem II PsbY protein
Bryopsis hypnoides	TRINITY_DN20336_c0_g1_i1|m.9554	PsbP family protein, expressed
Bryopsis hypnoides	TRINITY_DN20517_c0_g1_i1|m.51608	NmrA family protein
Bryopsis hypnoides	TRINITY_DN2379_c0_g1_i1|m.49472	Photosystem II PsbP protein
Bryopsis hypnoides	TRINITY_DN2379_c0_g2_i1|m.49474	Photosystem II PsbP protein
Bryopsis hypnoides	TRINITY_DN23826_c0_g1_i1|m.10436	Oxygen-evolving enhancer protein 3
Bryopsis hypnoides	TRINITY_DN23833_c0_g1_i1|m.10470	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN23994_c0_g1_i1|m.3984	Photosystem II oxygen-evolving enhancer protein 2
Bryopsis hypnoides	TRINITY_DN24082_c0_g1_i1|m.43185	Photosystem I reaction center subunit N
Bryopsis hypnoides	TRINITY_DN2631_c0_g1_i1|m.41720	Photosystem I subunit VI
Bryopsis hypnoides	TRINITY_DN27976_c0_g1_i1|m.61072	Photosystem II oxygen-evolving enhancer protein 2
Bryopsis hypnoides	TRINITY_DN31326_c0_g1_i1|m.12617	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN31408_c0_g1_i1|m.38740	Photosystem I reaction center subunit II
Bryopsis hypnoides	TRINITY_DN32025_c0_g1_i1|m.57757	Photosystem II 10 kDa polypeptide, chloroplastic
Bryopsis hypnoides	TRINITY_DN35043_c0_g1_i1|m.48937	Photosystem II reaction center Psb28 protein
Bryopsis hypnoides	TRINITY_DN35053_c0_g1_i1|m.48782	Geranylgeranyl reductase
Bryopsis hypnoides	TRINITY_DN35055_c0_g1_i1|m.48902	Photosystem II 10 kDa polypeptide, chloroplastic
Bryopsis hypnoides	TRINITY_DN35100_c0_g1_i1|m.17347	Photosystem I reaction center subunit XI
Bryopsis hypnoides	TRINITY_DN35130_c1_g1_i1|m.17373	Photosystem II manganese
Bryopsis hypnoides	TRINITY_DN35653_c0_g1_i1|m.44671	Photosystem II protein
Bryopsis hypnoides	TRINITY_DN35724_c0_g1_i1|m.33570	Ferredoxin-thioredoxin reductase, variable chain
Bryopsis hypnoides	TRINITY_DN4505_c0_g1_i1|m.29343	Photosystem II reaction center PsbP family protein
Bryopsis hypnoides	TRINITY_DN4617_c0_g1_i1|m.51949	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN6205_c0_g2_i1|m.45850	Solanesyl diphosphate synthase
Bryopsis hypnoides	TRINITY_DN6620_c0_g1_i1|m.2960	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN8468_c0_g1_i1|m.48129	PsbP-like protein
Bryopsis hypnoides	TRINITY_DN31415_c0_g1_i1|m.38867	PsaO
Bryopsis hypnoides	TRINITY_DN11416_c0_g1_i1|m.26546	Photosystem I reaction center subunit II
Bryopsis hypnoides	TRINITY_DN11493_c0_g1_i1|m.26677	Photosystem I reaction center subunit II
Bryopsis hypnoides	TRINITY_DN11864_c0_g1_i1|m.30228	Ultraviolet-B-repressible protein
Bryopsis hypnoides	TRINITY_DN14114_c1_g1_i1|m.1835	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN14715_c0_g2_i1|m.30729	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c0_g1_i1|m.12095	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c2_g5_i1|m.12108	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c5_g1_i1|m.12109	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN15534_c6_g1_i1|m.12112	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN1758_c0_g1_i1|m.7636	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN214_c1_g1_i1|m.18173	Fibrillin

Species	Gene model ID	Product name
Bryopsis hypnoides	TRINITY_DN22385_c0_g1_i1|m.8367	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN24336_c0_g1_i1|m.35884	Expressed protein
Bryopsis hypnoides	TRINITY_DN24660_c0_g1_i1|m.27815	Oxygen-evolving enhancer protein 1
Bryopsis hypnoides	TRINITY_DN27886_c0_g1_i1|m.60741	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN31290_c0_g1_i1|m.823	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN35106_c0_g1_i1|m.17297	Oxygen-evolving enhancer protein 3
Bryopsis hypnoides	TRINITY_DN35373_c0_g1_i1|m.36129	NA
Bryopsis hypnoides	TRINITY_DN407_c0_g2_i1|m.38613	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN4257_c0_g1_i1|m.50760	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN4496_c0_g1_i1|m.53876	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN4811_c0_g1_i1|m.35461	{ECO:0000313|EMBL:BAD31802.1};
Bryopsis hypnoides	TRINITY_DN6480_c0_g2_i1|m.4826	Peptidyl-prolyl cis-trans isomerase
Bryopsis hypnoides	TRINITY_DN8948_c0_g1_i1|m.24854	Chlorophyll a-b binding protein, chloroplastic
Bryopsis hypnoides	TRINITY_DN16338_c0_g1_i1|m.1033	Photosystem II reaction center PsbP family protein
Bryopsis hypnoides	TRINITY_DN2551_c0_g1_i1|m.19119	Photosystem I reaction centre subunit N
Bryopsis hypnoides	TRINITY_DN2551_c0_g2_i1|m.19121	Photosystem I reaction centre subunit N
Bryopsis hypnoides	TRINITY_DN31766_c0_g1_i1|m.38192	PRC-barrel domain-containing protein
Bryopsis hypnoides	TRINITY_DN5199_c0_g1_i1|m.16122	RNA-binding S4 domain-containing protein
Bryopsis hypnoides	TRINITY_DN5199_c0_g2_i1|m.16125	RNA-binding S4 domain-containing protein
Bryopsis hypnoides	TRINITY_DN10061_c0_g1_i1|m.5314	Kinase-like protein
Bryopsis hypnoides	TRINITY_DN10291_c1_g2_i1|m.39405	BnaCnng33260D protein
Bryopsis hypnoides	TRINITY_DN10923_c0_g1_i1|m.44456	Ribulose bisphosphate carboxylase small chain
Bryopsis hypnoides	TRINITY_DN11001_c0_g1_i1|m.16529	Beta-propeller domain-containing protein, methanol dehydrogenase
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i1|m.22685	NA
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i1|m.22686	Calcium homeostasis regulater-like protein CHoR1
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i2|m.22687	BnaC08g26090D protein
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i3|m.22688	NA
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i4|m.22689	BnaC08g26090D protein
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i5|m.22690	BnaC08g26090D protein
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i6|m.22692	Calcium homeostasis regulater-like protein CHoR1
Bryopsis hypnoides	TRINITY_DN12147_c0_g1_i6|m.22691	NA
Bryopsis hypnoides	TRINITY_DN12378_c0_g1_i1|m.15485	ABC1 family protein
Bryopsis hypnoides	TRINITY_DN13362_c0_g1_i1|m.31548	Tetratricopeptide repeat
Bryopsis hypnoides	TRINITY_DN13570_c0_g1_i1|m.38915	Phosphoribulokinase
Bryopsis hypnoides	TRINITY_DN14030_c0_g1_i1|m.9923	Serine/threonine protein kinase
Bryopsis hypnoides	TRINITY_DN14077_c0_g1_i2|m.9836	Rna binding protein
Bryopsis hypnoides	TRINITY_DN14101_c1_g1_i1|m.1958	Glyceraldehyde-3-phosphate dehydrogenase
Bryopsis hypnoides	TRINITY_DN14101_c1_g1_i2|m.1964	Glyceraldehyde-3-phosphate dehydrogenase
Bryopsis hypnoides	TRINITY_DN14101_c1_g1_i3|m.1970	Glyceraldehyde-3-phosphate dehydrogenase
Bryopsis hypnoides	TRINITY_DN14450_c0_g1_i1|m.3591	Thylakoid lumenal 16.5 kDa protein
Bryopsis hypnoides	TRINITY_DN14711_c0_g1_i1|m.30440	DnaJ-like protein
Bryopsis hypnoides	TRINITY_DN15663_c0_g1_i1|m.49965	Serine protease
Bryopsis hypnoides	TRINITY_DN15786_c0_g1_i1|m.25788	Protein translocase subunit SecA
Bryopsis hypnoides	TRINITY_DN16109_c0_g1_i1|m.33463	Fructose-1,6-bisphosphatase
Bryopsis hypnoides	TRINITY_DN16114_c0_g1_i1|m.33466	Fructose-1,6-bisphosphatase class 1
Bryopsis hypnoides	TRINITY_DN16641_c1_g2_i1|m.37990	Protochlorophyllide reductase
Bryopsis hypnoides	TRINITY_DN20085_c0_g1_i1|m.33814	Cytochrome b6-f complex subunit petO, chloroplastic
Bryopsis hypnoides	TRINITY_DN20328_c0_g1_i1|m.9504	Cytochrome b6-f complex iron-sulfur subunit
Bryopsis hypnoides	TRINITY_DN230_c0_g1_i1|m.18060	Rieske
Bryopsis hypnoides	TRINITY_DN2322_c0_g1_i1|m.49283	BnaC07g26740D protein
Bryopsis hypnoides	TRINITY_DN23884_c0_g1_i1|m.10360	Ferredoxin--NADP reductase
Bryopsis hypnoides	TRINITY_DN24330_c0_g1_i1|m.35853	Rubredoxin
Bryopsis hypnoides	TRINITY_DN2524_c0_g1_i1|m.19259	Ribulose bisphosphate carboxylase small chain
Bryopsis hypnoides	TRINITY_DN27786_c0_g1_i1|m.16489	Mg-protoporphyrin IX chelatase
Bryopsis hypnoides	TRINITY_DN29007_c0_g1_i1|m.23619	Gdt1-like protein chloroplastic-like
Bryopsis hypnoides	TRINITY_DN31298_c0_g1_i1|m.789	Cytochrome c6
Bryopsis hypnoides	TRINITY_DN35033_c0_g1_i1|m.48831	Phosphoglycerate kinase
Bryopsis hypnoides	TRINITY_DN6424_c0_g1_i1|m.4839	Fatty-acid desaturase
Bryopsis hypnoides	TRINITY_DN9341_c0_g1_i1|m.58406	Proline--tRNA ligase
Bryopsis hypnoides	TRINITY_DN9539_c0_g3_i1|m.24606	Low PSII Accumulation 3
Caulerpa lentillifera	g1080.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g1190.t1	10 kDa photosystem II polypeptide

Species	Gene model ID	Product name
Caulerpa lentillifera	g1253.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g1265.t1	TRIGALACTOSYLDIACYLGLYCEROL chloroplastic
Caulerpa lentillifera	g1281.t1	Protein translocase subunit SecA
Caulerpa lentillifera	g1286.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g142.t1	PsbP family protein
Caulerpa lentillifera	g1568.t1	Photosystem II PsbY protein
Caulerpa lentillifera	g1660.t1	Protein containing PDZ domain, a K-box domain, and a TPR
Caulerpa lentillifera	g1724.t1	Beta-propeller domain-containing protein, methanol dehydrogenase
Caulerpa lentillifera	g1771.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g1772.t1	Fatty-acid desaturase
Caulerpa lentillifera	g1846.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g1916.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g2014.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g2055.t1	Phosphoglycerate kinase
Caulerpa lentillifera	g2084.t1	ATP synthase delta-subunit
Caulerpa lentillifera	g210.t1	Photosystem I reaction center subunit III
Caulerpa lentillifera	g2205.t1	Oxygen-evolving enhancer protein 3
Caulerpa lentillifera	g2246.t1	Phototropin-like, blue light receptor
Caulerpa lentillifera	g2253.t1	Solanesyl diphosphate synthase
Caulerpa lentillifera	g2269.t1	Phosphoribulokinase
Caulerpa lentillifera	g2337.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g2388.t1	PsaB RNA binding protein
Caulerpa lentillifera	g2559.t1	Adenosine kinase
Caulerpa lentillifera	g263.t1	Proton gradient regulation 5
Caulerpa lentillifera	g2606.t1	Glyceraldehyde-3-phosphate dehydrogenase
Caulerpa lentillifera	g2659.t1	Protein thf1
Caulerpa lentillifera	g2659.t2	Protein thf1
Caulerpa lentillifera	g278.t1	Peptidase M50 family protein
Caulerpa lentillifera	g2776.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g2899.t1	Photosystem I reaction center subunit XI
Caulerpa lentillifera	g3011.t1	Alpha/beta hydrolase
Caulerpa lentillifera	g3098.t1	Photosystem I subunit O
Caulerpa lentillifera	g3247.t1	Photosystem I reaction center subunit N, chloroplastic
Caulerpa lentillifera	g3398.t1	2-alkenal reductase
Caulerpa lentillifera	g3749.t1	Rieske
Caulerpa lentillifera	g3875.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g3887.t1	PsbP family protein, expressed
Caulerpa lentillifera	g4139.t1	protein LOW PSII ACCUMULATION 3, chloroplastic
Caulerpa lentillifera	g4288.t1	Calvin cycle protein CP12
Caulerpa lentillifera	g4299.t1	Gdt1-like protein chloroplastic-like
Caulerpa lentillifera	g4382.t1	Phosphoribulokinase
Caulerpa lentillifera	g4641.t1	Glyceraldehyde-3-phosphate dehydrogenase
Caulerpa lentillifera	g4647.t1	Photosystem I reaction center subunit psaK like
Caulerpa lentillifera	g4687.t1	Protein thf1
Caulerpa lentillifera	g4748.t1	Ferredoxin--NADP reductase, chloroplastic
Caulerpa lentillifera	g4759.t1	Cytochrome b6-f complex, subunit 8
Caulerpa lentillifera	g4845.t1	Cryptochrome DASH
Caulerpa lentillifera	g4868.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g4899.t1	Thylakoid lumenal 16.5 kDa protein, chloroplastic
Caulerpa lentillifera	g4915.t1	Calvin cycle protein CP12
Caulerpa lentillifera	g4980.t1	Cytochrome b6-f complex iron-sulfur subunit
Caulerpa lentillifera	g5017.t1	Protein phosphatase 2C-like protein
Caulerpa lentillifera	g515.t1	Oxygen evolving enhancer protein 3
Caulerpa lentillifera	g5197.t1	Fructose-1,6-bisphosphatase
Caulerpa lentillifera	g5265.t1	Cytochrome c6
Caulerpa lentillifera	g5266.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g5300.t1	3-beta hydroxysteroid dehydrogenase
Caulerpa lentillifera	g5362.t1	protein LOW PSII ACCUMULATION 3, chloroplastic
Caulerpa lentillifera	g5370.t1	protein LOW PSII ACCUMULATION 3, chloroplastic
Caulerpa lentillifera	g5414.t1	Ferredoxin-thioredoxin reductase, variable chain
Caulerpa lentillifera	g5430.t1	Mg-protoporphyrin IX chelatase
Caulerpa lentillifera	g5505.t1	Chlorophyll a-b binding protein, chloroplastic

Species	Gene model ID	Product name
Caulerpa lentillifera	g5519.t1	GTP pyrophosphokinase, (P)ppGpp synthetase I
Caulerpa lentillifera	g566.t1	Peptidyl-prolyl cis-trans isomerase
Caulerpa lentillifera	g5705.t1	protein EMBRYO SAC DEVELOPMENT ARREST 3, chloroplastic
Caulerpa lentillifera	g5711.t1	Geranylgeranyl reductase
Caulerpa lentillifera	g5801.t1	Photosystem II oxygen-evolving enhancer protein 1
Caulerpa lentillifera	g5830.t1	Photosystem I reaction center subunit II like
Caulerpa lentillifera	g5970.t1	Photosystem II reaction center Psb28 protein
Caulerpa lentillifera	g5990.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g6009.t1	Photosystem I reaction center subunit V, chloroplastic
Caulerpa lentillifera	g609.t1	PsbP family protein
Caulerpa lentillifera	g618.t1	ATP synthase delta-subunit
Caulerpa lentillifera	g6308.t1	Tetratricopeptide repeat
Caulerpa lentillifera	g6445.t2	Ultraviolet-B-repressible protein
Caulerpa lentillifera	g6472.t1	Photosystem II D1 processing PSB27-chloroplastic isoform X1
Caulerpa lentillifera	g650.t1	Bifunctional sensory photoreceptor isoform A
Caulerpa lentillifera	g6490.t1	Photosystem I reaction center subunit VI, chloroplastic
Caulerpa lentillifera	g6520.t1	Fatty-acid desaturase
Caulerpa lentillifera	g6521.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g6576.t1	Kinase-like protein
Caulerpa lentillifera	g6718.t1	Photosystem II PsbY protein
Caulerpa lentillifera	g6795.t1	Sn1-specific diacylglycerol lipase beta
Caulerpa lentillifera	g6827.t1	ABC-1 domain-containing protein
Caulerpa lentillifera	g6963.t1	Photosystem I reaction center subunit II protein
Caulerpa lentillifera	g6963.t2	Photosystem I reaction center subunit II protein
Caulerpa lentillifera	g7003.t1	Ribulose bisphosphate carboxylase small chain
Caulerpa lentillifera	g7120.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g7280.t1	Deoxyribodipyrimidine photo-lyase
Caulerpa lentillifera	g7280.t2	Deoxyribodipyrimidine photo-lyase
Caulerpa lentillifera	g7370.t1	Proline--tRNA ligase
Caulerpa lentillifera	g752.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g7488.t1	Fructose-1,6-bisphosphatase
Caulerpa lentillifera	g7554.t1	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase
Caulerpa lentillifera	g7662.t1	Fructose-1,6-bisphosphatase
Caulerpa lentillifera	g7909.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g7934.t1	Photosystem II oxygen-evolving enhancer protein 2
Caulerpa lentillifera	g8052.t1	Deoxyribodipyrimidine photolyase/cryptochrome
Caulerpa lentillifera	g8114.t1	2-alkenal reductase
Caulerpa lentillifera	g8114.t2	2-alkenal reductase
Caulerpa lentillifera	g8157.t1	Ferritin
Caulerpa lentillifera	g8216.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g8258.t1	Thylakoid lumenal 19 kDa chloroplastic
Caulerpa lentillifera	g8423.t1	PsbP family protein
Caulerpa lentillifera	g8497.t1	Photosystem I reaction center subunit VI, chloroplastic
Caulerpa lentillifera	g82.t1	Photosystem II reaction center W protein, chloroplastic
Caulerpa lentillifera	g894.t1	Photosystem II S4 domain protein
Caulerpa lentillifera	g898.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g8880.t1	Ferredoxin--NADP reductase, chloroplastic
Caulerpa lentillifera	g8997.t1	Serine/threonine protein kinase
Caulerpa lentillifera	g9015.t1	Chlorophyll a-b binding protein, chloroplastic
Caulerpa lentillifera	g9107.t1	Photosystem II oxygen evolving complex
Caulerpa lentillifera	g9205.t1	Cytochrome b6-f complex, subunit 8
Caulerpa lentillifera	g9217.t1	Ribulose bisphosphate carboxylase small chain
Chlamydomonas reinhardtii	A8HNE8	Geranylgeranyl reductase (EC 1.3.1.-)
Chlamydomonas reinhardtii	A8HRQ4	Solanesyl diphosphate synthase (EC 2.5.1.-)
Chlamydomonas reinhardtii	A8HTY7	Ser/thr kinase, ABC1 family
Chlamydomonas reinhardtii	A8I547	Thylakoid membrane protein
Chlamydomonas reinhardtii	A8IAE5	Predicted protein
Chlamydomonas reinhardtii	A8ISE8	Predicted protein (Fragment)
Chlamydomonas reinhardtii	A8IXV0	Thylakoid lumen protein
Chlamydomonas reinhardtii	A8J9W8	Predicted protein (Fragment)
Chlamydomonas reinhardtii	A8JA70	Ferredoxin thioredoxin reductase, variable chain
Chlamydomonas reinhardtii	A8JDK2	Predicted protein

Species	Gene model ID	Product name
Chlamydomonas reinhardtii	A8JGP5	Ribulose bisphosphate carboxylase small chain (EC 4.1.1.39)
Chlamydomonas reinhardtii	A8JH83	Predicted protein
Chlamydomonas reinhardtii	A8JHT4	Serine/threonine protein kinase
Chlamydomonas reinhardtii	P41758	Phosphoglycerate kinase, chloroplastic (EC 2.7.2.3)
Chlamydomonas reinhardtii	Q547G1	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q8S567	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q9S8U0	Chlorophyll a-b binding protein, chloroplastic (Fragment)
Chlamydomonas reinhardtii	Q9S8U1	Chlorophyll a-b binding protein, chloroplastic (Fragment)
Chlamydomonas reinhardtii	Q9S8U2	Chlorophyll a-b binding protein, chloroplastic (Fragment)
Chlamydomonas reinhardtii	Q9S8U3	Chlorophyll a-b binding protein, chloroplastic (Fragment)
Chlamydomonas reinhardtii	Q9S9B5	Photosystem I light-harvesting complex chlorophyll A/B protein
Chlamydomonas reinhardtii	Q9FVE3	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q7DM26	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	P14273	Chlorophyll a-b binding protein of LHCII type I, chloroplastic
Chlamydomonas reinhardtii	Q9AXF6	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8IXU9	Predicted protein
Chlamydomonas reinhardtii	A8J9V2	Predicted protein
Chlamydomonas reinhardtii	A8I9T6	Predicted protein
Chlamydomonas reinhardtii	A8J5N6	Predicted protein
Chlamydomonas reinhardtii	A8I8C6	Predicted protein
Chlamydomonas reinhardtii	A8HZ72	Predicted protein
Chlamydomonas reinhardtii	A8I531	Mg-protoporphyrin IX chelatase (EC 6.6.1.1)
Chlamydomonas reinhardtii	A6Q0K5	Calvin cycle protein CP12, chloroplastic (CP12 domain-containing protein)
Chlamydomonas reinhardtii	A8IRG9	Predicted protein
Chlamydomonas reinhardtii	A8I5A0	Predicted protein
Chlamydomonas reinhardtii	A8ITX0	Copper response defect 1 protein
Chlamydomonas reinhardtii	Q9LD46	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase 1
Chlamydomonas reinhardtii	P46284	Sedoheptulose-1,7-bisphosphatase, chloroplastic
Chlamydomonas reinhardtii	Q9AR22	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase 2
Chlamydomonas reinhardtii	A8IKK7	Copper target 1 protein
Chlamydomonas reinhardtii	A8IC93	Heavy metal transporting ATPase
Chlamydomonas reinhardtii	A8I8X2	DegP-type protease
Chlamydomonas reinhardtii	A8JH35	DegP-type protease
Chlamydomonas reinhardtii	A8HQB3	DegP-type protease (EC 3.4.21.-)
Chlamydomonas reinhardtii	O48663	Chloroplast w6 desaturase (Omega-6-FAD, chloroplast isoform)
Chlamydomonas reinhardtii	A8IKQ0	Fructose-1,6-bisphosphatase (EC 3.1.3.11)
Chlamydomonas reinhardtii	P50362	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic
Chlamydomonas reinhardtii	Q84Y02	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8J249	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q05093	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8IKC8	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8JF10	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8I000	Chlorophyll a-b binding protein, chloroplastic (Fragment)
Chlamydomonas reinhardtii	A8ISG0	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8ITV3	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q9ZSJ5	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q9ZSJ4	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8J6D1	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q93WD2	Chlorophyll a-b binding protein CP29 (Lhcbm4)
Chlamydomonas reinhardtii	Q9FEK6	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8JCU4	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q8S3U0	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8J264	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8J287	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q8S3T8	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8J270	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q8S3T9	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8I3C6	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q75VZ0	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q75VY9	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q75VY8	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q75VY7	Chlorophyll a-b binding protein, chloroplastic

Species	Gene model ID	Product name
Chlamydomonas reinhardtii	Q75VY6	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q75VY4	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q93WL4	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q93WE0	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	Q93VE0	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8I0C6	Chlorophyll a-b binding protein, chloroplastic (Fragment)
Chlamydomonas reinhardtii	A8J431	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	P93663	Chlorophyll a-b binding protein, chloroplastic (Fragment)
Chlamydomonas reinhardtii	P93664	Chlorophyll a-b binding protein, chloroplastic
Chlamydomonas reinhardtii	A8J9Y1	Cytochrome b6-f complex iron-sulfur subunit (EC 1.10.9.1)
Chlamydomonas reinhardtii	B2XYG6	Rieske iron-sulfur protein of cytochrome B6/F complex (Fragment)
Chlamydomonas reinhardtii	P49728	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic
Chlamydomonas reinhardtii	P53991	Ferredoxin--NADP reductase, chloroplastic (FNR) (EC 1.18.1.2)
Chlamydomonas reinhardtii	P08197	Cytochrome c6, chloroplastic
Chlamydomonas reinhardtii	P50369	Cytochrome b6-f complex subunit 6
Chlamydomonas reinhardtii	P0C1D4	Cytochrome b6-f complex subunit 8, chloroplastic
Chlamydomonas reinhardtii	Q9LLC6	Cytochrome b6-f complex subunit petO, chloroplastic
Chlamydomonas reinhardtii	A8HPJ2	NADPH-protochlorophyllide oxidoreductase (EC 1.3.1.33)
Chlamydomonas reinhardtii	Q39617	Protochlorophyllide reductase, chloroplastic (PCR)
Chlamydomonas reinhardtii	P19824	Phosphoribulokinase, chloroplastic (PRK) (PRKase)
Chlamydomonas reinhardtii	A8J827	Organellar class II aminoacyl tRNA synthetase
Chlamydomonas reinhardtii	Q39615	Photosystem I reaction center subunit II, chloroplastic
Chlamydomonas reinhardtii	Q5NKW4	Photosystem I reaction center subunit II, 20 kDa
Chlamydomonas reinhardtii	A8ICV4	Photosystem I 8.1 kDa reaction center subunit IV
Chlamydomonas reinhardtii	P12352	Photosystem I reaction center subunit IV, chloroplastic
Chlamydomonas reinhardtii	A8J4S1	Photosystem I reaction center subunit III
Chlamydomonas reinhardtii	P12356	Photosystem I reaction center subunit III, chloroplastic
Chlamydomonas reinhardtii	A8JHN9	Photosystem I reaction center subunit V (Fragment)
Chlamydomonas reinhardtii	P14224	Photosystem I reaction center subunit V, chloroplastic
Chlamydomonas reinhardtii	A8IH77	Subunit H of photosystem I
Chlamydomonas reinhardtii	P13352	Photosystem I reaction center subunit VI, chloroplastic
Chlamydomonas reinhardtii	A8J6K8	Photosystem I reaction center subunit psaK
Chlamydomonas reinhardtii	P14225	Photosystem I reaction center subunit psaK, chloroplastic
Chlamydomonas reinhardtii	A8IL32	Photosystem I reaction center subunit XI
Chlamydomonas reinhardtii	A8I835	Photosystem I reaction center subunit N
Chlamydomonas reinhardtii	Q9AXJ2	PsaN
Chlamydomonas reinhardtii	A8JCL6	Photosystem I subunit O
Chlamydomonas reinhardtii	A8III5	Photosystem II reaction center Psb28 protein
Chlamydomonas reinhardtii	A8J0E4	Oxygen-evolving enhancer protein 1 of photosystem II
Chlamydomonas reinhardtii	P12853	Oxygen-evolving enhancer protein 1, chloroplastic (OEE1)
Chlamydomonas reinhardtii	P11471	Oxygen-evolving enhancer protein 2, chloroplastic (OEE2)
Chlamydomonas reinhardtii	A8IYH9	Oxygen-evolving enhancer protein 2 of photosystem II
Chlamydomonas reinhardtii	A8J3S9	PsbP-like protein
Chlamydomonas reinhardtii	A8IKE6	OEE2-like protein of thylakoid lumen
Chlamydomonas reinhardtii	A8J4E8	Lumenal PsbP-like protein
Chlamydomonas reinhardtii	A8J170	Thylakoid-anchored PsbP-like protein
Chlamydomonas reinhardtii	A8IHH9	Lumen targeted protein
Chlamydomonas reinhardtii	A8J1Z8	PsbP-like protein
Chlamydomonas reinhardtii	A8JEV1	Oxygen evolving enhancer protein 3
Chlamydomonas reinhardtii	P12852	Oxygen-evolving enhancer protein 3, chloroplastic (OEE3)
Chlamydomonas reinhardtii	A8HXG5	10 kDa photosystem II polypeptide (Fragment)
Chlamydomonas reinhardtii	A8HPM2	Chloroplast photosystem II-associated 22 kDa protein
Chlamydomonas reinhardtii	A8HPM5	Chloroplast photosystem II-associated 22 kDa protein
Chlamydomonas reinhardtii	A8JFQ7	Photosystem II reaction center W protein
Chlamydomonas reinhardtii	Q9SPI9	Photosystem II reaction center W protein, chloroplastic (PSII 6.1 kDa protein)
Chlamydomonas reinhardtii	A8I846	4.1 kDa photosystem II subunit
Chlamydomonas reinhardtii	A8I003	Ycf32-related subunit of photosystem II
Chlamydomonas reinhardtii	A8JKA1	Ycf32-related polyprotein of photosystem II (Fragment)
Chlamydomonas reinhardtii	P00873	Ribulose bisphosphate carboxylase small chain 1, chloroplastic
Chlamydomonas reinhardtii	P08475	Ribulose bisphosphate carboxylase small chain 2, chloroplastic
Chlamydomonas reinhardtii	A8JGP8	Ribulose bisphosphate carboxylase small chain (EC 4.1.1.39)
Chlamydomonas reinhardtii	A8I686	Rubredoxin

Species	Gene model ID	Product name
Chlamydomonas reinhardtii	A8J682	Protein translocase subunit SecA
Chlamydomonas reinhardtii	A8J680	Chloroplast-associated SecA protein (Fragment)
Chlamydomonas reinhardtii	Q84V17	Protein kinase
Chlamydomonas reinhardtii	Q84V18	Serine/threonine-protein kinase stt7, chloroplastic (EC 2.7.11.1)
Chlamydomonas reinhardtii	Q7X8Y6	PsaB RNA binding protein (Tab2 protein)
Chlamydomonas reinhardtii	A8HY43	Thylakoid lumenal protein
Chlamydomonas reinhardtii	A8J4Q7	Rieske [2Fe-2S] protein
Chlamydomonas reinhardtii	A8JH60	Predicted protein
Chlamydomonas reinhardtii	A8HR79	Inositol phosphatase-like protein
Chlamydomonas reinhardtii	P50370	Photosystem II reaction center protein Ycf12
Chlamydomonas reinhardtii	A8JFP5	DnaJ-like zinc-finger protein
Cyanidioschyzon merolae	Q85FX6	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase
Cyanidioschyzon merolae	Q85FW7	Allophycocyanin alpha chain
Cyanidioschyzon merolae	Q85FW6	Allophycocyanin beta chain
Cyanidioschyzon merolae	Q85FS6	Allophycocyanin alpha-B chain
Cyanidioschyzon merolae	Q85FW8	Phycobilisome linker polypeptide
Cyanidioschyzon merolae	Q85G58	Allophycocyanin B18 chain
Cyanidioschyzon merolae	Q85G43	Phycocyanin alpha chain
Cyanidioschyzon merolae	Q85G42	Phycocyanin beta chain
Cyanidioschyzon merolae	Q85G55	Phycobilisome rod-core linker polypeptide
Cyanidioschyzon merolae	M1VEV9	Similar to oxygen-evolving complex component psbQ
Cyanidioschyzon merolae	M1VAS6	Photosystem II biogenesis protein Psb29
Cyanidioschyzon merolae	M1V7V9	Photosystem II 12 kD extrinsic protein
Cyanidioschyzon merolae	M1V7X1	Cytochrome b6-f complex iron-sulfur subunit (EC 1.10.9.1)
Cyanidioschyzon merolae	A0A125YL28	Manganese-stabilzing protein
Cyanidioschyzon merolae	M1URM8	Geranylgeranyl hydrogenase
Cyanidioschyzon merolae	M1V8D6	Photosystem II protein Psb27
Cyanidioschyzon merolae	M1USG1	Probable potassium transporter
Cyanidioschyzon merolae	M1V5Q9	Mg-protoporphyrin IX chelatase (EC 6.6.1.1)
Cyanidioschyzon merolae	M1V926	Uncharacterized protein
Cyanidioschyzon merolae	M1UU36	Similar to chlorophyll a/b-binding protein, CP24
Cyanidioschyzon merolae	M1V9B8	Photosystem II oxygen-evolving complex 23K protein
Cyanidioschyzon merolae	M1VET8	Cytochrome b6-f complex iron-sulfur subunit (EC 1.10.9.1)
Cyanidioschyzon merolae	M1UUN3	Fructose-1,6-bisphosphatase
Cyanidioschyzon merolae	M1UUN7	Phycocyanin-associated rod linker protein
Cyanidioschyzon merolae	M1VFH7	Similar to ferredoxin-thioredoxin reductase, variable chain
Cyanidioschyzon merolae	M1V643	Fructose-1,6-bisphosphatase
Cyanidioschyzon merolae	M1VFP4	Phycocyanin-associated rod linker protein
Cyanidioschyzon merolae	M1VKK5	Similar to light harvesting protein
Cyanidioschyzon merolae	M1UVM3	Cytochrome b6-f complex iron-sulfur subunit (EC 1.10.9.1)
Cyanidioschyzon merolae	M1VGG3	Protein translocase subunit SecA
Cyanidioschyzon merolae	M1UWW8	Uncharacterized protein
Cyanidioschyzon merolae	M1VCA0	DegP protease
Cyanidioschyzon merolae	M1V7K1	Photosystem II protein M
Cyanidioschyzon merolae	M1VIA2	PGR5
Cyanidioschyzon merolae	M1VML8	Similar to oxygen-evolving complex component psbP
Cyanidioschyzon merolae	Q85FS2	Cytochrome c6 (Cytochrome c-553) (Cytochrome c553)
Cyanidioschyzon merolae	Q85FX8	Cytochrome b6-f complex subunit 7
Cyanidioschyzon merolae	Q85FX7	Cytochrome b6-f complex subunit 8
Cyanidioschyzon merolae	Q85FX3	Prenyl transferase
Cyanidioschyzon merolae	Q85FZ1	Photosystem I iron-sulfur center subunit VII
Cyanidioschyzon merolae	Q85FS9	Photosystem I reaction center subunit II
Cyanidioschyzon merolae	Q85G51	Photosystem I reaction center subunit X
Cyanidioschyzon merolae	Q85FP8	Photosystem I reaction center subunit XI (PSI subunit V) (PSI-L)
Cyanidioschyzon merolae	Q85FS3	Cytochrome c-550 (Cytochrome c550)
Cyanidioschyzon merolae	Q85FS5	Photosystem II reaction center X protein
Cyanidioschyzon merolae	Q85G61	Photosystem II protein Y
Cyanidioschyzon merolae	O22024	Ribulose bisphosphate carboxylase small chain
Cyanidioschyzon merolae	Q85G86	Photosystem II reaction center protein Ycf12

Supplementary Table 7 Assembly statistics of *Plakobranchus ocellatus* & *Elysia marginata* genome

Summary of the sequenced raw data was submitted to FigShare (DOI, 10.6084/m9.figshare.12301277)

	Plakobranchus ocellatus type black	*Elysia marginata*	*Elysia chlorotica* by Cai *et al* (for comparison)
Predicted genome size	936 Mb	900 Mb	575 Mb
Total length of scaffolds (bases)	927,888,823	790,322,091	557,479,671 bases
% of estimated genome size	99%	88%	97%
# scaffolds	8,647	14,149	9,987
# N bases	78,653,622	82,443,809	16,928,330
Longest scaffold (bp)	6,058,556	1,540,588	2,353,793
Scaffold N50 (bases)	1,453,842	225,654	441,954
L50	191	967	386
GC %	35.85	36.56	37.65
# of predicted genes	77,230	70,752	23,871
BUSCO (eukaryota_odb9)	93.4% (283/303)	89.5% (271/303)	96.0% (291/303)
Complete single copy	92.1% (279/303)	87.8% (266/303)	95.0% (288/303)
Complete duplicated	1.3% (4/303)	1.7% (5/303)	1.0% (3/303)
Fragmented	5.9% (18/303)	9.2% (28/303)	1.7% (5/303)
Missing	0.7% (2/303)	1.3% (4/303)	2.3% (7/303)
BUSCO (metazoa_odb9)	95.0% (929/978)	91.1% (891/978)	94.7% (926/978)
Complete single copy	93.1% (911/978)	89.6% (876/978)	93.3% (912/978)
Complete duplicated	1.8% (18/978)	1.5% (15/978)	1.4% (14/978)
Fragmented	3.6% (35/978)	6.7% (66/978)	2.5% (24/978)
Missing	1.4% (14/978)	2.2% (21/978)	2.8% (28/978)

Supplementary Table 8 *P. ocellatus* scaffolds determined as bacterial contaminants.

These scaffolds were removed from the final assemblies. The mean depth of the read coverage was obtained from qualimap software. The mean coverage of reliable scaffolds = 31 (SD = 7)

	Number of assigned genes to each taxon						
Scaffold ID	Bacteria	Lophotrochozoa	Number of assigned genes	Bacterial gene (%)	Lophotrochozoan gene (%)	Length of scaffold	Mean depth of read coverage (DRR029525)
scaffold14744_cov19	15	0	15	100%	0%	10435	14
scaffold23411_cov18	15	0	15	100%	0%	20458	10
scaffold29205_cov16	12	0	12	100%	0%	17359	5
scaffold36956_cov17	11	0	11	100%	0%	19423	5
scaffold9181_cov18	11	0	11	100%	0%	19699	5
scaffold6787_cov20	7	0	7	100%	0%	68528	18
scaffold2938_cov18	6	0	6	100%	0%	5117	11
scaffold41017_cov16	5	0	5	100%	0%	3853	6
scaffold10524_cov18	5	0	5	100%	0%	7455	5
scaffold14201_cov20	5	0	5	100%	0%	8425	11
scaffold38777_cov18	4	0	4	100%	0%	5337	6
scaffold43224_cov17	4	0	4	100%	0%	5427	5
scaffold76888_cov19	3	0	3	100%	0%	2009	8
scaffold91525_cov17	3	0	3	100%	0%	2018	6
scaffold47273_cov19	3	0	3	100%	0%	2185	8
scaffold104155_cov18	3	0	3	100%	0%	2295	5
scaffold101317_cov17	3	0	3	100%	0%	2361	7
scaffold63294_cov18	3	0	3	100%	0%	2378	8
scaffold68812_cov17	3	0	3	100%	0%	2444	6
scaffold94243_cov18	3	0	3	100%	0%	2477	5
scaffold139099_cov17	3	0	3	100%	0%	2947	7
scaffold2019_cov18	3	0	3	100%	0%	2995	7
scaffold29460_cov16	3	0	3	100%	0%	3206	7
scaffold36584_cov18	3	0	3	100%	0%	3906	6
scaffold14112_cov18	3	0	3	100%	0%	4069	5
scaffold14975_cov17	3	0	3	100%	0%	4502	5
scaffold38649_cov18	3	0	3	100%	0%	4625	5
scaffold133004_cov14	2	0	2	100%	0%	2170	8
scaffold102852_cov17	2	0	2	100%	0%	2181	8
scaffold133690_cov15	2	0	2	100%	0%	2189	7

Supplementary Table 8 (continue)

Scaffold ID	Number of assigned genes to each taxon		Number of assigned genes	Bacterial gene (%)	Lophotrochozoan gene (%)	Length of scaffold	Mean depth of read coverage (DRR029525)
	Bacteria	Lophotrochozoa					
scaffold70567_cov16	2	0	2	100%	0%	2238	6
scaffold7044_cov15	2	0	2	100%	0%	2252	6
scaffold132820_cov15	2	0	2	100%	0%	2360	9
scaffold51863_cov16	2	0	2	100%	0%	2374	6
scaffold20986_cov16	2	0	2	100%	0%	2415	6
scaffold24966_cov16	2	0	2	100%	0%	2430	8
scaffold2495_cov21	2	0	2	100%	0%	2616	8
scaffold42664_cov15	2	0	2	100%	0%	2740	5
scaffold34283_cov13	2	0	2	100%	0%	2771	9
scaffold47213_cov18	2	0	2	100%	0%	2803	7
scaffold75651_cov17	2	0	2	100%	0%	3318	5
scaffold38162_cov16	2	0	2	100%	0%	3368	6
scaffold91118_cov47	2	0	2	100%	0%	3713	23
scaffold56142_cov17	2	0	2	100%	0%	3860	5
scaffold28252_cov17	2	0	2	100%	0%	3901	4
scaffold5516_cov17	2	0	2	100%	0%	4165	3
scaffold59092_cov17	2	0	2	100%	0%	4973	3
scaffold4312_cov15	2	0	2	100%	0%	5982	3
scaffold40129_cov20	2	0	2	100%	0%	7301	17
scaffold4993_cov50	2	0	2	100%	0%	8072	328
scaffold14367_cov18	2	0	2	100%	0%	11542	11
scaffold5373_cov18	2	0	2	100%	0%	12943	20
scaffold24205_cov20	2	0	2	100%	0%	17847	18
scaffold383_cov20	2	0	2	100%	0%	18449	14
scaffold2812_cov22	2	0	2	100%	0%	36269	15

Supplementary Table 9 Scaffolds of PoB determined as kleptoplast/mitochondrion sequences

	Blastn Bits score against...						
Scaffold ID	kpDNA-Poro (AP014542)	kpDNA-Rhip (AP014543)	*Bryopsis hypnoides*	mtDNA of *P. ocellatus* (AP014544)	Length of scaffold	Mean depth of read coverage	Contaminant
scaffold261989_cov475	4130	7661	-	-	4148	1957	Kp
scaffold265330_cov435	3616	6024	-	-	3265	3673	Kp
scaffold269291_cov457	2878	13854	-	-	7520	1546	Kp
scaffold262266_cov503	2839	6026	-	-	3263	1963	Kp
scaffold262910_cov447	1965	3770	-	-	2041	1574	Kp
scaffold81938_cov17	1755	-	-	-	2861	4876	Kp
scaffold60758_cov17	1568	-	-	-	2026	5143	Kp
scaffold265343_cov510	1543	4747	-	-	2570	1678	Kp
scaffold268313_cov495	1496	5677	-	-	3074	2306	Kp
scaffold270056_cov465	1447	3880	-	-	2284	631	Kp
scaffold270078_cov462	1066	3869	-	-	2095	1624	Kp
scaffold70008_cov17	1002	1077	-	-	2714	953	Kp
scaffold261853_cov518	955	5836	-	-	3241	537	Kp
scaffold266106_cov1743	-	-	-	2939	2417	1284	Mt

Supplementary Table 10 Analyzed protein sequences by SonicParanoid analysis

Four PoB genes (gene ID: p197c68.18, p234c64.89, p45387c41.1, and p466c59.83) annotated as "Chloroplast" (Fig. 4a) showed no orthologous relationships with algal genes. Detailed data was submitted to FigShare (DOI 10.6084/m9.figshare.12301277)

ID	Species (genome version)	Number of sequences	Source
Mmu	*Mus musculus*	16,998	Uniprot; 10090 (Reviewed genes only)
Hsa	*Homo sapiens*	*20,350*	Uniprot; 9606 (Reviewed genes only)
Gga	*Gallus gallus*	36,539	Uniprot; 9031
Dre	*Danio rerio*	59,676	Uniprot; 7739
Bfl	*Branchiostoma floridae*	29,302	Uniprot; 7955
Dme	*Drosophila melanogaster*	*42,467*	Uniprot; 7227
Bmo	*Bombyx mori*	*18,381*	Uniprot; 7091
Api	Acyrthosiphon pisum	*37,406*	Uniprot; 7029
Cte	*Capitella teleta*	*32,114*	Uniprot; 283909
Lan	*Lingula anatina* (synonym *unguis*)	*34,469*	Uniprot; 7574
Obi	*Octopus bimaculoides*	*23,994*	INSDC; PRJNA270931 (Octopus_bimaculoides_v2_0)
Cgi	*Crassostrea gigas (oyster_v9)*	*46,748*	INSDC; PRJNA276446
Pfu	*Pinctada fucata (v2.0)*	*31,477*	http://marinegenomics.oist.jp/pearl/viewer/info?project_id=36
Hdi	*Haliotis discus*	*29,449*	http://gigadb.org/dataset/100281
Lgi	*Lottia gigantea*	*23,822*	INSDC; PRJNA259762
Bgl	*Biomphalaria glabrata (ASM45736v1)*	*36,675*	INSDC: PRJNA290623
Aca	*Aplysia californica (*AplCal3.0)	*27,591*	INSDC; PRJNA209509
Eor	*Elysia ornata*	70,752	Present data
Poc	*Plakobranchus ocellatus*	77,230	Present data
Cale	*Caulerpa lentillifera*	9,762	https://marinegenomics.oist.jp/umibudo/viewer/info?project_id=55
Brhy	*Bryopsis hypnoides*	24,127	Present data
Habo	*Halimeda borneensis*	26,652	Present data
Sysp	*Synechocystis* sp. (strain PCC 6803 / Kazusa)	3,507	Uniprot; 1111708
Cyme	*Cyanidioschyzon merolae* (strain 10D)	4,997	Uniprot; 280699
Chre	*Chlamydomonas reinhardtii*	15,245	Uniprot; 3055
Sace	Saccharomyces cerevisiae (strain S288C)	5,917	The Saccharomyces Genome Database

Supplementary Table 11 *P. ocellatus* gene models matching with algal A614 gene set (bit score > 100), and the difference of the top-hit bit score against the RefSeq database. We checked the potential HGT with A614 which contain sequences closer to the potential gene donor (e.g. transcriptomic data of *H. borneensis*) than RefSeq. If PoB genes contains the genes derived from the candidate gene donors, a blast analysis using A625 is expected to show a higher similarity score than using RefSeq. A blastp search of the gene models against the A614 dataset, however, obtained no hits with bit scores (measure of similarity) exceeding the values against the RefSeq database. Predicted taxonomical origin of the genes was described as "MEGAN annotation". Raw data were deposited to FigShare (DOI, 10.6084/m9.figshare.12318977 and 10.6084/m9.figshare.12318989)

Query ID	blastp serch for A614 (Tophit)		blastp serch for RefSeq		MEGAN annotation
	Hit ID	bitscore	Hit ID	bitscore	
p1001c63.45	g2246.t1	184	XP_012946173	1538	*Aplysia californica*
p1039c62.98	c11580_g1_i6|m.27466	253	XP_012943102	2108	*Aplysia californica*
p105c62.89	g2055.t1	369	XP_013066033	724	Euthyneura
p1126c66.54	g2246.t1	102	XP_005112692	468	Euthyneura
p1129c66.3	g2246.t1	145	XP_013086043	1535	Biomphalaria
p1194c63.185	A8HTY7	126	XP_005101564	720	*Aplysia californica*
p12c69.84	A8HPJ2	112	XP_005097012	420	Eumetazoa
p128c64.119	g2246.t1	105	XP_005105193	845	Euthyneura
p128c64.123	A8IC93	108	XP_005093402	425	Euthyneura
p128c64.124	A8IC93	212	XP_005093402	1262	Euthyneura
p1410c65.71	c11580_g1_i6|m.27466	309	XP_005106574	1159	Bilateria
p1415c66.5	g2246.t1	113	XP_005101959	486	Bilateria
p143c69.19	c7971_g1_i1|m.5294	109	XP_012942374	268	*Aplysia californica*
p1579c67.15	g2246.t1	196	XP_013079086	1268	Euthyneura
p1662c68.113	g2253.t1	214	XP_005111077	425	Mollusca
p172c64.28	P41758	159	XP_012938921	715	*Aplysia californica*
p1740c61.62	g6827.t1	110	XP_013080012	1171	Euthyneura
p1749c74.6	g566.t1	114	XP_013074513	269	Euthyneura
p177c64.95	g566.t1	116	XP_013082106	597	Biomphalaria
p178c62.99	c7901_g1_i1|m.5169	288	NP_001267755	551	cellular organisms
p1866c63.114	g2246.t1	156	NP_001191516	1026	Euthyneura
p1874c66.18	TRINITY_DN16641_c1_g2_i1|m.37990	115	XP_005103964	655	Euthyneura
p195c62.4	g566.t1	104	XP_013071140	325	Protostomia
p197c68.61	P41758	126	XP_009047142	264	Bilateria
p197c68.62	TRINITY_DN35033_c0_g1_i1|m.48831	162	XP_029167923	244	Opisthokonta
p197c68.63	g2055.t1	160	XP_029826656	293	Opisthokonta
p2c67.70	M1V643	358	XP_005094525	554	Mollusca
p2036c63.14	g2246.t1	156	XP_013067755	512	Biomphalaria

Supplementary Table 11 (continue)

Query ID	blastp serch for A614 (Tophit)		blastp serch for RefSeq (Tophit)		MEGAN annotation
	Hit ID	bitscore	Hit ID	bitscore	
p2150c71.16	c7971_g1_i1|m.5294	104	XP_012936649	982	*Aplysia californica*
p22c64.33	g8157.t1	147	XP_025087870	242	Bilateria
p22c64.91	g2246.t1	199	XP_013084647	710	Gastropoda
p220c72.103	A8HPJ2	115	XP_005108304	473	*Aplysia californica*
p233c60.101	g2246.t1	182	XP_012939135	1226	*Aplysia californica*
p234c64.107	TRINITY_DN12378_c0_g1_i1|m.15485	105	XP_005094813	510	Bilateria
p240c62.223	c7901_g1_i1|m.5169	234	XP_013095144	399	Opisthokonta
p258745c64.57	g2246.t1	174	XP_025109728	889	Mollusca
p258747c66.26	c7901_g1_i1|m.5169	252	XP_021882283	442	Opisthokonta
p258753c65.32	g2246.t1	119	XP_005096925	934	*Aplysia californica*
p258757c71.5	g2246.t1	135	XP_013063533	770	*Biomphalaria glabrata*
p258767c72.8	c12405_g1_i2|m.44746	110	XP_013074851	510	Euthyneura
p258785c70.94	g2246.t1	112	XP_005089392	576	*Aplysia californica*
p258855c56.6	g4845.t1	193	XP_005098341	809	Euthyneura
p2590c71.26	c11580_g1_i6|m.27466	288	XP_012936084	2115	*Lingula anatina*
p286c65.86	g2246.t1	119	XP_005106460	668	Euthyneura
p288c60.11	g566.t1	119	XP_005108744	524	Bilateria
p288c60.152	g2246.t1	191	XP_012945723	755	Mollusca
p2897c68.9	TRINITY_DN16641_c1_g2_i1|m.37990	126	XP_005108305	407	Metazoa
p310c70.15	g566.t1	132	XP_005706153	254	cellular organisms
p310c70.19	g566.t1	127	XP_017281256	268	Deuterostomia
p400c61.2	TRINITY_DN9341_c0_g1_i1|m.58406	375	XP_013406588	1973	Bilateria
p431c71.1	c11580_g1_i6|m.27466	404	XP_012940404	928	*Aplysia californica*
p47c72.89	g2246.t1	171	XP_013092315	751	Euthyneura
p477c68.21	TRINITY_DN6205_c0_g2_i1|m.45850	115	XP_005110593	552	*Aplysia californica*
p4907c66.39	g2246.t1	213	XP_013094545	1404	Euthyneura
p4907c66.70	g8157.t1	158	NP_001191661	310	Mollusca
p59c63.135	g2246.t1	169	XP_013063765	830	Euthyneura

Supplementary Table 11 (continue)

Query ID	blastp serch for A614 (Tophit)		blastp serch for RefSeq (Tophit)		MEGAN annotation
	Hit ID	bitscore	Hit ID	bitscore	
p6c66.218	g2246.t1	174	XP_013077719	903	Gastropoda
p63c64.1	TRINITY_DN6424_c0_g1_i1|m.4839	106	XP_013078984	417	Euthyneura
p63c64.15	TRINITY_DN6424_c0_g1_i1|m.4839	112	XP_013078984	462	Euthyneura
p638c73.235	g5017.t1	103	XP_013069446	726	Euthyneura
p698c62.15	g2246.t1	127	XP_013068187	2881	*Biomphalaria glabrata*
p761c66.63	g2246.t1	118	NP_001191420	647	Bilateria
p763c69.146	g3398.t1	117	XP_013081789	579	Euthyneura
p768c75.40	g2246.t1	195	NP_001191633	818	*Aplysia californica*
p770c72.37	g4845.t1	156	XP_005098341	548	Euthyneura
p800c68.13	g2246.t1	169	XP_012945411	1051	Euthyneura
p8162c67.56	g2246.t1	110	XP_005105833	547	*Aplysia californica*
p855c67.9	g7280.t1	424	XP_012935158	834	Bilateria
p928c68.104	g2246.t1	178	XP_012938859	832	Euthyneura
p943c68.38	g2246.t1	176	XP_005103277	3090	*Aplysia californica*

Supplementary Table 12 Applied species for HGT index analysis

Data name	Contained taxon	Number of sequence	Source*
Algae_DB	Chlorophyta	288,246	Uniprot; 3041 (2018/10/19）
	Cyanobacteria	13,705	Uniprot; 1117 (reviewed protein only: 2018/10/19）
	Rhodophyta	94,537	Uniprot; 2763 (2018/10/19）
	PX clade	29,453	Uniprot; 569578 (2018/10/19）
	Bryopsis hypnoides	24,127	Present data (transcriptome)
	Halimeda borneensis	26,652	Present data (transcriptome)
	Caulerpa lentillifera	9,762	https://marinegenomics.oist.jp/umibudo/viewer/info?project_id=55
Loph_DB	Lophotrochozoa	314,718	taxonomy:"Lophotrochozoa [1206795]" - "Heterobranchia [216305]"
Prokaryote__DB	Bacteria	333,708	Uniprot; 2 (reviewed protein only: 2018/11/1）
	Archaea	19,544	Uniprot; 2157 (reviewed protein only:2018/11/1）
Eukaryote_DB	Eukaryota	188,529	Uniprot; 2759 (reviewed protein only:2018/11/1）
Referential query			
Aca query	*Aplysia californica*	27,591	INSDC; PRJNA209509 (AplCal3.0)
Bgl query	*Biomphalaria glabrata*	36,675	INSDC: PRJNA290623 (ASM45736v1)

Supplementary table 13 Enriched GOs of the significantly upregulated genes on the digestive gland of *P. ocellatus* type black (PoB)

GO term description	Over represented p-value	DEG number from PoB	Total gene number in PoB	DG-upregulated gene belong the GO
GO:0004190 aspartic-type endopeptidase activity	2.56E-71	45	288	p1440c63.113, p664c69.11, p855c67.174, p807c65.17, p1440c63.126, p3924c64.18, p1440c63.80, p543c70.163, p1440c63.23, p1440c63.36, p1440c63.12, p3924c64.17, p1440c63.63, p775c64.19, p3924c64.1, p665c65.51, p664c69.19, p428c65.20, p1440c63.105, p665c65.34, p445c59.46, p1440c63.3, p1412c61.10, p1440c63.11, p1440c63.8, p855c67.163, p1440c63.84, p1015c69.247, p665c65.52, p596c69.2, p329c71.312, p855c67.168, p775c64.23, p2791c66.18, p1440c63.43, p3924c64.35, p238c64.67, p445c59.50, p8162c67.79, p737c53.70, p3924c64.16, p775c64.20, p1440c63.115, p1440c63.119, p665c65.58,
GO:0006508 proteolysis	1.65E-60	49	684	p1440c63.113, p664c69.11, p855c67.174, p807c65.17, p1440c63.126, p3924c64.18, p1440c63.80, p543c70.163, p1440c63.23, p1440c63.36, p1440c63.12, p3924c64.17, p1440c63.63, p775c64.19, p3924c64.1, p665c65.51, p664c69.19, p428c65.20, p1440c63.105, p665c65.34, p445c59.46, p1440c63.3, p1412c61.10, p1440c63.11, p1440c63.8, p855c67.163, p1440c63.84, p1015c69.247, p665c65.52, p596c69.2, p329c71.312, p855c67.168, p775c64.23, p2791c66.18, p1440c63.43, p3924c64.35, p238c64.67, p445c59.50, p8162c67.79, p737c53.70, p3924c64.16, p775c64.20, p1440c63.115, p1440c63.119, p1510c68.4, p89c59.118, p22c64.145, p665c65.58, p258731c69.52,
GO:0004869 cysteine-type endopeptidase inhibitor activity	6.52E-05	2	6	p34c66.53, p34c66.54,
GO:0006952 defense response	1.95E-04	2	10	p4035c66.3, p606c64.1,
GO:0043169 cation binding	2.38E-04	2	11	p128c64.183, p1548c63.54,
GO:0006885 regulation of pH	3.36E-04	2	13	p11c67.36, p1947c65.69,
GO:0006730 one-carbon metabolic process	4.51E-04	2	15	p1053c67.29, p1947c65.69,
GO:0005975 carbohydrate metabolic process	4.67E-04	4	169	p590c70.27, p128c64.183, p105c62.18, p1548c63.54,
GO:0048856 anatomical structure development	9.83E-04	2	22	p1440c63.115, p1440c63.119,

Supplementary table 14 Applied species for the comparative genomic analysis

Detailed data was deposited for FigShare (DOI 10.6084/m9.figshare.12318908)

Abbreviation in Fig. 5	Pictogram	Scientific name	Data source
Mmu		*Mus musculus*	Uniprot; 10090 ("Reviewed" genes only)
Hsa		*Homo sapiens*	Uniprot; 9606 ("Reviewed" genes only)
Dre		*Danio rerio*	Uniprot;7739
Bfl		*Branchiostoma floridae*	Uniprot;7955
Dme		*Drosophila melanogaster*	Uniprot; 7227
Bmo		*Bombyx mori*	Uniprot; 7091
Api		Acyrthosiphon pisum	Uniprot; 7029
Cte		*Capitella teleta*	Uniprot;283909
Lan		*Lingula anatina* (synonym *unguis*)	Uniprot; 7574
Obi		*Octopus bimaculoides*	INSDC; PRJNA270931
Cgi		*Crassostrea gigas (oyster_v9)*	INSDC; PRJNA276446
Pfu		*Pinctada fucata (v2.0)*	http://marinegenomics.oist.jp/pearl/viewer/info?project_id=36
Hdi		*Haliotis discus*	http://gigadb.org/dataset/100281
Lgi		*Lottia gigantea*	INSDC; PRJNA259762
Bgl		*Biomphalaria glabrata (ASM45736v1)*	INSDC: PRJNA290623
Aca		*Aplysia californica* (AplCal3.0)	INSDC; PRJNA209509
PoB		*Plakobranchus ocellatus* type black	Present study
Ema		*Elysia marginata*	Present study

Supplementary Table 15 Cross-tabulation table for the significant enrichment analysis of DG-upregulated gene number on the PoB-expanded orthogroup.

Orthogroup by Orthofinder		DG-upregulated		P-value	q-value by Benjamini-Hochberg method
		YES	NO		
OG0000132	YES	45	158	8.16E-79	5.E-78
	NO	117	76910		
OG0000005	YES	18	349	1.87E-19	6.E-19
	NO	144	76719		
OG0000446	YES	4	29	0.0000007	0.0000015
	NO	158	77039		
OG0000002	YES	2	1848	0.5998108	0.5998108
	NO	160	75220		
OG0009179	YES	2	12	0.0003914	0.0005871
	NO	160	77056		
OG0000194	YES	1	24	0.0511495	0.0613794
	NO	161	77044		

Supplementary Table 16 *E. marginata* scaffolds determined as bacterial contaminants.

The mean depth of read-coverage was obtained from qualimap. The mean coverage of reliable sea-slug scaffolds = 12 (SD = 2.7)

	# Assigned gene to each taxon							
Scaffold name	Bacteria	Lophotrochozoan	# all assigned genes	%Bacteria	% Lophotrochozoan	Length of scaffold	Mean depth of read coverage	Contaminant
scaffold23590_cov9	20	0	0	100%	0%	40162	3	Y
scaffold39866_cov8	12	0	0	100%	0%	10506	2	Y
scaffold51037_cov8	9	0	0	100%	0%	7322	2	Y
scaffold9184_cov10	9	0	0	100%	0%	12665	3	Y
scaffold17697_cov9	8	0	0	100%	0%	7808	3	Y
scaffold11600_cov9	7	0	0	100%	0%	18938	2	Y
scaffold34081_cov9	7	0	0	100%	0%	10089	2	Y
scaffold13134_cov9	7	0	0	100%	0%	8506	3	Y
scaffold39263_cov9	7	0	0	100%	0%	11387	3	Y
scaffold31936_cov25	7	0	0	100%	0%	17157	6	Y
scaffold14781_cov8	6	0	0	100%	0%	10946	2	Y
scaffold41731_cov8	6	0	0	100%	0%	8371	2	Y
scaffold35011_cov8	6	0	0	100%	0%	12920	2	Y
scaffold93349_cov10	6	0	0	100%	0%	12781	2	Y
scaffold38871_cov8	6	0	0	100%	0%	4726	2	Y
scaffold92553_cov8	6	0	0	100%	0%	7722	3	Y
scaffold42214_cov8	5	0	0	100%	0%	5442	2	Y
scaffold63069_cov8	5	0	0	100%	0%	3474	3	Y
scaffold21396_cov9	5	0	0	100%	0%	5378	3	Y
scaffold48418_cov9	5	0	0	100%	0%	6054	3	Y
scaffold26067_cov9	5	0	0	100%	0%	3822	3	Y
scaffold3896_cov9	4	0	0	100%	0%	7642	2	Y
scaffold5429_cov8	4	0	0	100%	0%	8932	2	Y
scaffold48374_cov9	4	0	0	100%	0%	4921	2	Y
scaffold65911_cov9	4	0	0	100%	0%	5318	2	Y
scaffold11877_cov9	4	0	0	100%	0%	8275	3	Y
scaffold31476_cov8	4	0	0	100%	0%	5287	3	Y
scaffold40886_cov10	4	0	0	100%	0%	2666	3	Y
scaffold7979_cov8	4	0	0	100%	0%	2732	3	Y
scaffold23464_cov9	3	0	0	100%	0%	14253	1	Y
scaffold73315_cov8	3	0	0	100%	0%	4286	2	Y

Supplementary Table 16 (continue)

	# Assigned gene to each taxon							
Scaffold name	Bacteria	Lophotrochozoan	# all assigned genes	%Bacteria	% Lophotrochozoan	Length of scaffold	Mean depth of read coverage	Contaminant
scaffold157565_cov8	3	0	0	100%	0%	5013	2	Y
scaffold77011_cov8	3	0	0	100%	0%	8007	2	Y
scaffold34019_cov9	3	0	0	100%	0%	8123	2	Y
scaffold83306_cov9	3	0	0	100%	0%	4099	2	Y
scaffold129716_cov8	3	0	0	100%	0%	2759	2	Y
scaffold32111_cov8	3	0	0	100%	0%	5348	2	Y
scaffold32000_cov9	3	0	0	100%	0%	9779	2	Y
scaffold35097_cov9	3	0	0	100%	0%	11436	2	Y
scaffold82518_cov9	3	0	0	100%	0%	8213	2	Y
scaffold55489_cov8	3	0	0	100%	0%	2739	2	Y
scaffold21071_cov7	3	0	0	100%	0%	2613	2	Y
scaffold100012_cov10	3	0	0	100%	0%	6095	2	Y
scaffold199_cov8	3	0	0	100%	0%	5988	2	Y
scaffold111304_cov9	3	0	0	100%	0%	3973	2	Y
scaffold35599_cov9	3	0	0	100%	0%	2714	2	Y
scaffold114815_cov7	3	0	0	100%	0%	2772	3	Y
scaffold91979_cov9	3	0	0	100%	0%	2272	3	Y
scaffold118630_cov7	3	0	0	100%	0%	2962	3	Y
scaffold20629_cov8	3	0	0	100%	0%	3842	3	Y
scaffold27965_cov10	3	0	0	100%	0%	2232	3	Y
scaffold6368_cov9	3	0	0	100%	0%	4506	3	Y
scaffold14877_cov8	3	0	0	100%	0%	5181	3	Y
scaffold9742_cov10	3	0	0	100%	0%	4534	3	Y
scaffold84644_cov7	3	0	0	100%	0%	2016	3	Y
scaffold28513_cov8	3	0	0	100%	0%	4439	3	Y
scaffold4272_cov8	3	0	0	100%	0%	2659	3	Y
scaffold134952_cov9	3	0	0	100%	0%	2037	3	Y
scaffold95757_cov8	3	0	0	100%	0%	2707	3	Y
scaffold36125_cov9	3	0	0	100%	0%	2946	3	Y
scaffold81605_cov10	3	0	0	100%	0%	2203	3	Y
scaffold109203_cov9	3	0	0	100%	0%	4044	3	Y

Supplementary Table 16 (continue)

	# Assigned gene to each taxon							
Scaffold name	Bacteria	Lophotrochozoan	# all assigned genes	%Bacteria	% Lophotrochozoan	Length of scaffold	Mean depth of read coverage	Contaminant
scaffold60887_cov9	2	0	0	100%	0%	5707	2	Y
scaffold89507_cov8	2	0	0	100%	0%	2694	2	Y
scaffold171847_cov8	2	0	0	100%	0%	2399	2	Y
scaffold82519_cov9	2	0	0	100%	0%	4591	2	Y
scaffold68312_cov8	2	0	0	100%	0%	2015	2	Y
scaffold50258_cov9	2	0	0	100%	0%	8070	2	Y
scaffold122550_cov7	2	0	0	100%	0%	2347	2	Y
scaffold83650_cov8	2	0	0	100%	0%	6499	2	Y
scaffold32242_cov8	2	0	0	100%	0%	3866	2	Y
scaffold67918_cov8	2	0	0	100%	0%	2095	2	Y
scaffold72779_cov9	2	0	0	100%	0%	2268	2	Y
scaffold154054_cov8	2	0	0	100%	0%	2095	2	Y
scaffold45258_cov7	2	0	0	100%	0%	2314	2	Y
scaffold46247_cov6	2	0	0	100%	0%	2136	2	Y
scaffold122674_cov7	2	0	0	100%	0%	2601	2	Y
scaffold98356_cov8	2	0	0	100%	0%	2538	2	Y
scaffold72280_cov8	2	0	0	100%	0%	5647	2	Y
scaffold64373_cov7	2	0	0	100%	0%	2139	2	Y
scaffold59031_cov7	2	0	0	100%	0%	2173	2	Y
scaffold37748_cov8	2	0	0	100%	0%	3106	2	Y
scaffold27682_cov8	2	0	0	100%	0%	5920	2	Y
scaffold33277_cov8	2	0	0	100%	0%	2430	2	Y
scaffold63561_cov8	2	0	0	100%	0%	5671	2	Y
scaffold57482_cov7	2	0	0	100%	0%	2227	3	Y
scaffold58575_cov9	2	0	0	100%	0%	2743	3	Y
scaffold44101_cov9	2	0	0	100%	0%	2003	3	Y
scaffold12309_cov8	2	0	0	100%	0%	2715	3	Y
scaffold61678_cov9	2	0	0	100%	0%	2513	3	Y
scaffold7531_cov9	2	0	0	100%	0%	3787	3	Y
scaffold39421_cov7	2	0	0	100%	0%	2139	3	Y
scaffold66144_cov9	2	0	0	100%	0%	4130	3	Y

Supplementary Table 16 (continue)

	# Assigned gene to each taxon							
Scaffold name	Bacteria	Lophotrochozoan	# all assigned genes	%Bacteria	% Lophotrochozoan	Length of scaffold	Mean depth of read coverage	Contaminant
scaffold91578_cov8	2	0	0	100%	0%	2021	3	Y
scaffold5033_cov8	2	0	0	100%	0%	2948	3	Y
scaffold86910_cov8	2	0	0	100%	0%	3134	3	Y
scaffold38224_cov7	2	0	0	100%	0%	2232	3	Y
scaffold98184_cov8	2	0	0	100%	0%	2352	3	Y
scaffold150251_cov7	2	0	0	100%	0%	2527	3	Y
scaffold32703_cov9	2	0	0	100%	0%	3846	3	Y
scaffold96059_cov8	2	0	0	100%	0%	2135	3	Y
scaffold110604_cov10	2	0	0	100%	0%	4361	3	Y
scaffold143394_cov7	2	0	0	100%	0%	2104	3	Y
scaffold57862_cov7	2	0	0	100%	0%	2106	3	Y
scaffold116596_cov11	2	0	0	100%	0%	3475	3	Y
scaffold83170_cov10	2	0	0	100%	0%	7084	3	Y
scaffold166938_cov10	2	0	0	100%	0%	2546	3	Y
scaffold6277_cov8	2	0	0	100%	0%	2015	3	Y
scaffold23621_cov8	2	0	0	100%	0%	2169	3	Y
scaffold50970_cov15	2	0	0	100%	0%	2288	4	Y
scaffold200571_cov70	3	0	0	100%	0%	5335	17	N
scaffold66964_cov62	4	0	0	100%	0%	7570	18	N
scaffold56391_cov74	6	0	0	100%	0%	10556	19	N
scaffold212257_cov72	5	0	0	100%	0%	8763	19	N
scaffold214892_cov71	17	0	0	100%	0%	52790	19	N
scaffold21315_cov69	56	0	0	100%	0%	117125	19	N
scaffold25863_cov72	31	0	0	100%	0%	85382	20	N
scaffold35214_cov28	2	0	0	100%	0%	2296	20	N
scaffold62180_cov71	6	0	0	100%	0%	25437	20	N
scaffold12740_cov69	13	0	0	100%	0%	36389	20	N
scaffold93141_cov74	5	0	0	100%	0%	18595	21	N
scaffold12646_cov69	15	0	0	100%	0%	39111	21	N
scaffold229251_cov77	2	0	0	100%	0%	3578	21	N
scaffold230446_cov77	2	0	0	100%	0%	5601	21	N

Supplementary Table 16 (continue)

Scaffold name	# Assigned gene to each taxon		# all assigned genes	%Bacteria	% Lophotrochozoan	Length of scaffold	Mean depth of read coverage	Contaminant
	Bacteria	Lophotrochozoan						
scaffold72533_cov71	3	0	0	100%	0%	5740	21	N
scaffold45687_cov70	3	0	0	100%	0%	3300	21	N
scaffold230466_cov77	2	0	0	100%	0%	2863	21	N
scaffold199637_cov69	2	0	0	100%	0%	3300	21	N
scaffold93143_cov73	7	0	0	100%	0%	21492	22	N
scaffold227732_cov77	6	0	0	100%	0%	14063	22	N
scaffold102818_cov73	11	0	0	100%	0%	24962	22	N
scaffold97498_cov70	6	0	0	100%	0%	12816	22	N
scaffold231090_cov78	2	0	0	100%	0%	4748	22	N
scaffold227021_cov78	3	0	0	100%	0%	4012	22	N
scaffold230855_cov77	2	0	0	100%	0%	4406	22	N
scaffold224935_cov77	3	0	0	100%	0%	3310	22	N
scaffold228045_cov77	6	0	0	100%	0%	11778	22	N
scaffold230030_cov78	3	0	0	100%	0%	5970	22	N
scaffold228658_cov78	2	0	0	100%	0%	9631	22	N
scaffold229924_cov80	2	0	0	100%	0%	3921	22	N
scaffold78637_cov71	8	0	0	100%	0%	11055	23	N
scaffold228295_cov78	3	0	0	100%	0%	8155	23	N
scaffold224632_cov77	2	0	0	100%	0%	4617	23	N
scaffold225617_cov78	2	0	0	100%	0%	2638	23	N
scaffold228972_cov80	2	0	0	100%	0%	7002	23	N
scaffold228172_cov78	3	0	0	100%	0%	5707	23	N
scaffold225641_cov80	3	0	0	100%	0%	5947	24	N
scaffold230027_cov78	3	0	0	100%	0%	5277	24	N
scaffold225951_cov82	3	0	0	100%	0%	5099	25	N
scaffold230955_cov77	2	0	0	100%	0%	4045	25	N

Supplementary Table 17 *E. marginata* scaffolds determined as kleptoplast/mitochondrial DNA

Kp, kleptoplast DNA. Mt, mitochondorial DNA.

Scaffold ID	Blastn Bits score		Length of scaffold	Mean depth of read coverage	Contaminant
	Query: *Bryopsis hypnoides* (NC_013359.1)	Query: PoB mitochondria			
scaffold225599_cov800	11103	-	6426	211	Kp
scaffold226864_cov1102	9751	-	6439	324	Kp
scaffold226859_cov908	9690	-	5339	267	Kp
scaffold226412_cov833	9631	-	5265	229	Kp
scaffold227624_cov983	9081	-	5164	302	Kp
scaffold227068_cov1079	8386	-	4605	294	Kp
scaffold226732_cov826	8072	-	4407	224	Kp
scaffold224802_cov999	7880	-	4325	289	Kp
scaffold226090_cov853	7315	-	4036	244	Kp
scaffold229670_cov1043	6191	-	3640	303	Kp
scaffold227707_cov845	5463	-	3006	249	Kp
scaffold231044_cov864	5121	-	2791	226	Kp
scaffold227481_cov1024	4979	-	2699	301	Kp
scaffold230536_cov963	4953	-	2726	250	Kp
scaffold228103_cov969	4466	-	2446	267	Kp
scaffold231292_cov925	4333	-	2408	243	Kp
scaffold230892_cov944	4292	-	2854	258	Kp
scaffold225945_cov1033	4067	-	2244	291	Kp
scaffold227228_cov1106	3973	-	2218	318	Kp
scaffold230563_cov1102	3930	-	2149	307	Kp
scaffold229916_cov877	3722	-	2055	253	Kp
scaffold229771_cov921	3531	-	2020	251	Kp
scaffold228521_cov891	3125	-	2181	250	Kp
scaffold224398_cov872	2001	-	2918	242	Kp
scaffold228088_cov814	1980	-	3692	224	Kp
scaffold227279_cov3491	-	8222	14136	965	Mt

Supplementary table 18 OrthoFinder result with additional data from *E. chlorotica* (Ecl) gene set (gene counts)

Group name	Ema	PoB	Ecl	Api	Aca	Bfl	Bgl	Bmo	Cte	Cgi	Dme	Hdi	Lan	Lgi	Mus	Obi	Dre	Has	Pfu
Cathepsin D-like	5[A]	203[B]	4[C]	3	5	5	4	3	1	2	19	0	3	3	7	2	17	8	1
Lectin-like	214[D]	410[E]	72[F]	3	46	398	126	11	128	275	28	96	133	62	44	10	105	37	166
Apolipoprotein D-like	8[G]	36[H]	3[I]	85	1	0	0	14	11	54	7	22	8	15	4	5	8	4	1

A: e2244c39.16, e2244c39.20, e4981c37.4, e4981c37.5, e8012c40.2

B: p1015c69.245, p1015c69.247, p1106c69.41, p1106c69.44, p1412c61.10, p1412c61.2, p1440c63.10, p1440c63.100, p1440c63.101, p1440c63.102, p1440c63.103, p1440c63.104, p1440c63.105, p1440c63.106, p1440c63.11, p1440c63.113, p1440c63.115, p1440c63.117, p1440c63.119, p1440c63.12, p1440c63.120, p1440c63.122, p1440c63.124, p1440c63.125, p1440c63.126, p1440c63.127, p1440c63.14, p1440c63.15, p1440c63.2, p1440c63.20, p1440c63.23, p1440c63.26, p1440c63.27, p1440c63.28, p1440c63.3, p1440c63.30, p1440c63.36, p1440c63.42, p1440c63.43, p1440c63.44, p1440c63.45, p1440c63.51, p1440c63.52, p1440c63.55, p1440c63.58, p1440c63.63, p1440c63.69, p1440c63.7, p1440c63.73, p1440c63.76, p1440c63.77, p1440c63.79, p1440c63.8, p1440c63.80, p1440c63.81, p1440c63.83, p1440c63.84, p1440c63.89, p1440c63.9, p1440c63.90, p1440c63.91, p1440c63.96, p1440c63.98, p1525c58.1, p1529c64.14, p17174c35.1, p183713c35.1, p1860c62.49, p1860c62.50, p1860c62.51, p19234c41.1, p2015c61.59, p2057c61.46, p2057c61.51, p216c65.11, p216c65.8, p22c64.171, p238c64.56, p238c64.58, p238c64.60, p238c64.61, p238c64.67, p254c66.117, p255c64.80, p2574c60.31, p2574c60.32, p2574c60.35, p258745c64.77, p266c63.161, p2791c66.17, p2791c66.18, p30156c39.1, p30376c56.1, p30807c69.1, p329c71.310, p329c71.312, p333c67.117, p333c67.123, p333c67.126, p333c67.128, p34996c59.1, p35389c41.1, p3560c63.43, p35754c38.1, p3605c51.5, p374c67.44, p374c67.53, p3924c64.1, p3924c64.14, p3924c64.16, p3924c64.17, p3924c64.18, p3924c64.19, p3924c64.21, p3924c64.32, p3924c64.35, p3924c64.4, p3924c64.5, p3924c64.6, p3924c64.78, p428c65.20, p445c59.36, p445c59.38, p445c59.43, p445c59.46, p445c59.50, p445c59.54, p445c59.57, p445c59.58, p445c59.61, p445c59.62, p445c59.64, p445c59.66, p51766c46.3, p543c70.163, p56091c35.1, p596c69.2, p59943c48.1, p609c69.52, p609c69.84, p63233c38.1, p664c69.11, p664c69.13, p664c69.15, p664c69.19, p664c69.24, p664c69.25, p664c69.32, p664c69.34, p665c65.34, p665c65.40, p665c65.47, p665c65.48, p665c65.49, p665c65.50, p665c65.51, p665c65.52, p665c65.53, p665c65.57, p665c65.58, p665c65.59, p665c65.62, p665c65.65, p737c53.70, p737c53.71, p737c53.72, p775c64.1, p775c64.15, p775c64.16, p775c64.19, p775c64.2, p775c64.20, p775c64.23, p800c68.116, p807c65.16, p807c65.17, p807c65.22, p807c65.25, p807c65.27, p807c65.38, p807c65.41, p807c65.42, p8162c67.103, p8162c67.108, p8162c67.48, p8162c67.79, p8162c67.82, p8162c67.88, p8162c67.89, p8491c59.1, p8558c44.1, p855c67.161, p855c67.162, p855c67.163, p855c67.164, p855c67.168, p855c67.171, p855c67.172, p855c67.174, p864c38.3, p93400c36.1, p947c59.272, p97c59.82

C: RUS74941.1, RUS87636.1, RUS87637.1, RUS89981.1

D: e10094c43.1, e10094c43.2, e101c35.8, e10327c38.3, e103301c44.16, e10462c41.1, e10655c37.1, e10666c38.1, e10764c35.2, e10764c35.3, e1113c45.25, e1116c29.10, e1121c45.40, e1131c43.70, e11361c34.21, e11595c36.1, e1164c44.4, e1164c44.9, e11668c37.2, e11880c35.1, e11969c36.4, e12295c25.4, e12486c38.7, e12518c40.3, e12518c40.5, e12595c42.5, e12595c42.6, e12595c42.7, e12651c38.5, e12682c48.9, e1275c33.6, e128757c48.1, e13123c30.5, e1318c44.48, e13376c36.12, e14309c38.2, e14600c41.2, e1496c33.3, e1516c38.8, e15522c35.1, e15573c33.1, e15859c36.9, e1598c45.65, e16001c30.2, e16112c35.14, e1652c45.28, e1653c43.13, e16666c32.1, e16666c32.2, e16666c32.5, e16777c31.1, e17217c35.4, e17234c30.2, e1732c40.7, e1733c40.17, e174475c32.1, e1770c40.1, e18174c38.12, e18174c38.9, e1895c40.21, e19587c27.2, e19625c44.21, e19625c44.24, e1967c35.2, e1967c35.4, e1994c41.12, e20336c40.1, e20336c40.2, e210547c19.2, e212284c41.7, e212290c37.5, e212290c37.7, e2125c39.2, e2125c39.5, e214759c45.7, e216082c42.8, e2177c43.3, e224005c42.2, e224005c42.3, e224005c42.4, e224099c35.1, e22489c36.2, e2330c38.9, e23356c42.1, e2366c41.32, e2366c41.33, e2366c41.34, e2391c33.8, e24512c39.1, e2538c33.7, e2632c42.1, e2640c39.3, e27845c35.3, e280c43.52, e280c43.54, e28258c37.9, e2891c46.44, e2924c47.1, e2936c41.16, e2951c42.3, e3030c36.12, e30461c43.16, e308c40.33, e3309c35.4, e3349c37.4, e3489c45.48, e3573c41.1, e3702c38.31, e3733c45.9, e374c43.6, e3770c38.30, e37732c19.1, e379c31.2, e3909c35.9, e3950c37.4, e3991c44.11, e4013c42.2, e4139c37.5, e413c40.1, e4195c32.3, e4278c41.3, e4409c43.1, e4409c43.5, e4497c33.9, e4517c36.4, e4572c33.2, e463c36.10, e46448c25.1, e4674c39.16, e4674c39.27, e46971c29.1, e4740c32.8, e47886c33.1, e4788c40.4, e4810c33.3, e4897c45.38, e499c42.5, e502c47.6, e502c47.7, e5202c34.8, e5323c35.2, e54608c41.1, e5559c41.2, e5626c39.2, e5661c36.2, e5716c37.7, e5744c33.1, e5786c35.2, e5869c35.14, e588c41.23, e588c41.27, e588c41.30, e588c41.33, e588c41.35, e5c41.4, e6009c34.4, e603c38.41, e6182c43.13, e6444c46.9, e6489c44.4, e6611c34.4, e6621c41.8, e6631c31.3, e66797c25.1, e6837c39.10, e6837c39.8, e6863c45.35, e6889c38.3, e6922c33.3, e6924c35.6, e6926c34.11, e6926c34.3, e6926c34.5, e7085c37.9, e7329c41.8, e7333c41.4, e7372c37.4, e7390c42.26, e7390c42.30, e7487c37.10, e7487c37.13, e7487c37.8, e7488c35.1, e75968c25.1, e76442c41.1, e7786c30.1, e7837c39.12, e7856c39.22, e785c40.4, e7944c38.7, e8025c35.21, e8068c38.1, e8350c35.4, e83820c30.1, e8532c37.3, e8598c31.1, e8728c35.1, e8901c40.1, e8901c40.4, e9032c37.14, e934c37.40, e946c31.2, e954c34.13, e954c34.33, e955c43.19, e955c43.22, e955c43.23, e955c43.24, e955c43.25, e955c43.27, e955c43.29, e955c43.30, e955c43.31, e9716c25.5

E: p1013c63.45, p1015c69.241, p1015c69.5, p10278c41.2, p1039c62.2, p108080c46.1, p110c62.105, p1121c63.100, p1121c63.130, p1121c63.97, p1121c63.98, p1147c61.57, p1147c61.59, p114c62.106, p114c62.114, p114c62.97, p114c62.99, p115899c41.1, p118c63.26, p118c63.39, p118c63.42, p118c63.50, p118c63.51, p118c63.59, p118c63.61, p118c63.73, p1194c63.105, p1209c50.1, p1215c59.122, p12237c46.1, p12294c64.10, p123c64.16, p124c71.257, p124c71.259, p124c71.261, p124c71.262, p124c71.264, p124c71.266, p12763c48.1, p1321c62.95, p1352c59.54, p14216c54.2, p1425c64.196, p1425c64.197, p1425c64.198, p1425c64.92, p1427c68.91, p143c69.9, p145c61.17, p1464c63.83, p1511c63.56, p1511c63.58, p1516c67.88, p1529c64.11, p1529c64.37, p1531c64.13, p1531c64.9, p1581c68.1, p1581c68.2, p16742c40.7, p1686c67.2, p1686c67.3, p16c66.82, p170c62.58, p170c62.59, p170c62.62, p171c61.137, p171c61.192, p171c61.196, p1739c63.85, p1739c63.86, p174c61.58, p1753c40.21, p1819c60.9, p1846c62.20, p1857c64.5, p1866c63.111, p1874c66.27, 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F: RUS68616.1, RUS68633.1, RUS68647.1, RUS68662.1, RUS69163.1, RUS69541.1, RUS69648.1, RUS69842.1, RUS70124.1, RUS70475.1, RUS70726.1, RUS71236.1, RUS71340.1, RUS71551.1, RUS72059.1, RUS72139.1, RUS72211.1, RUS73268.1, RUS73297.1, RUS74009.1, RUS74083.1, RUS75111.1, RUS75504.1, RUS75505.1, RUS76015.1, RUS76722.1, RUS76779.1, RUS77171.1, RUS77679.1, RUS80279.1, RUS80935.1, RUS81139.1, RUS81800.1, RUS82192.1, RUS82307.1, RUS82887.1, RUS83253.1, RUS83536.1, RUS83755.1, RUS83907.1, RUS83908.1, RUS84090.1, RUS84091.1, RUS84408.1, RUS84451.1, RUS85257.1, RUS85260.1, RUS85335.1, RUS86035.1, RUS86039.1, RUS86136.1, RUS86160.1, RUS86267.1, RUS86568.1, RUS86702.1, RUS87571.1, RUS87572.1, RUS87614.1, RUS87724.1, RUS87725.1, RUS87726.1, RUS88118.1, RUS88255.1, RUS88257.1, RUS88258.1, RUS88638.1, RUS88639.1, RUS89920.1, RUS90178.1, RUS90265.1, RUS90584.1, RUS91679.1

G: e12398c37.5, e15279c22.1, e19340c38.16, e2950c42.1, e358c35.6, e358c35.7, e42367c51.1, e4695c40.1

H: p1001c63.5, p11751c81.2, p12498c72.2, p126c77.126, p126c77.67, p1425c64.85, p1662c68.129, p17146c62.2, p189c72.53, p189c72.54, p2081c70.47, p221c62.44, p238c64.62, p2538c67.15, p2550c65.67, p258670c68.31, p258755c69.28, p282c66.68, p329c71.111, p339c68.7, p385c65.19, p38c58.15, p40759c49.1, p4154c75.33, p440c72.42, p473c72.110, p474c68.27, p474c68.28, p509c73.151, p589c77.14, p59c63.60, p6257c70.26, p6430c70.39, p735c63.50, p754c67.20, p838c70.295
I RUS69394.1, RUS74332.1, RUS74836.1

Supplementary Table 19 Composition information of DNA extraction solutions for *P. ocellatus* genomic DNA

	2X CTAB buffer (50 ml)	10% CTAB solution (50 ml)	CTAB precipitation buffer (50 ml)	High salt TE buffer (50 ml)
CTAB	1 g	5 g	0.5 g	-
NaCl (1.4M)	4.1 g	4.1 g	-	3 g
1M Tris-CHl ph 8.0 (100mM)	5 ml	5 ml	2.5 ml	0.5ml
0.5M EDTA pH 8.0 (20mM)	2 ml	2 ml	1 ml	100 µl

Supplementary Table 20 Result of the Exonerate search (database = the 13 scaffolds determined as kpDNA, query = algal photosynthetic genes [A614])

Query				Target				score
ID	start	end	strand	ID	start	end	strand	
A8I531	77	397	.	scaffold265330_cov435	253	1216	+	557
M1V5Q9	70	380	.	scaffold265330_cov435	256	1222	+	407
TRINITY_DN27786_c0_g1_i1|m.16489	67	387	.	scaffold265330_cov435	253	1216	+	550
c11205_g1_i1|m.22907	1	302	.	scaffold265330_cov435	310	1216	+	507
c11205_g1_i3|m.22926	1	302	.	scaffold265330_cov435	310	1216	+	507
c11205_g1_i5|m.22942	1	302	.	scaffold265330_cov435	310	1216	+	507
g5430.t1	74	386	.	scaffold265330_cov435	277	1216	+	568