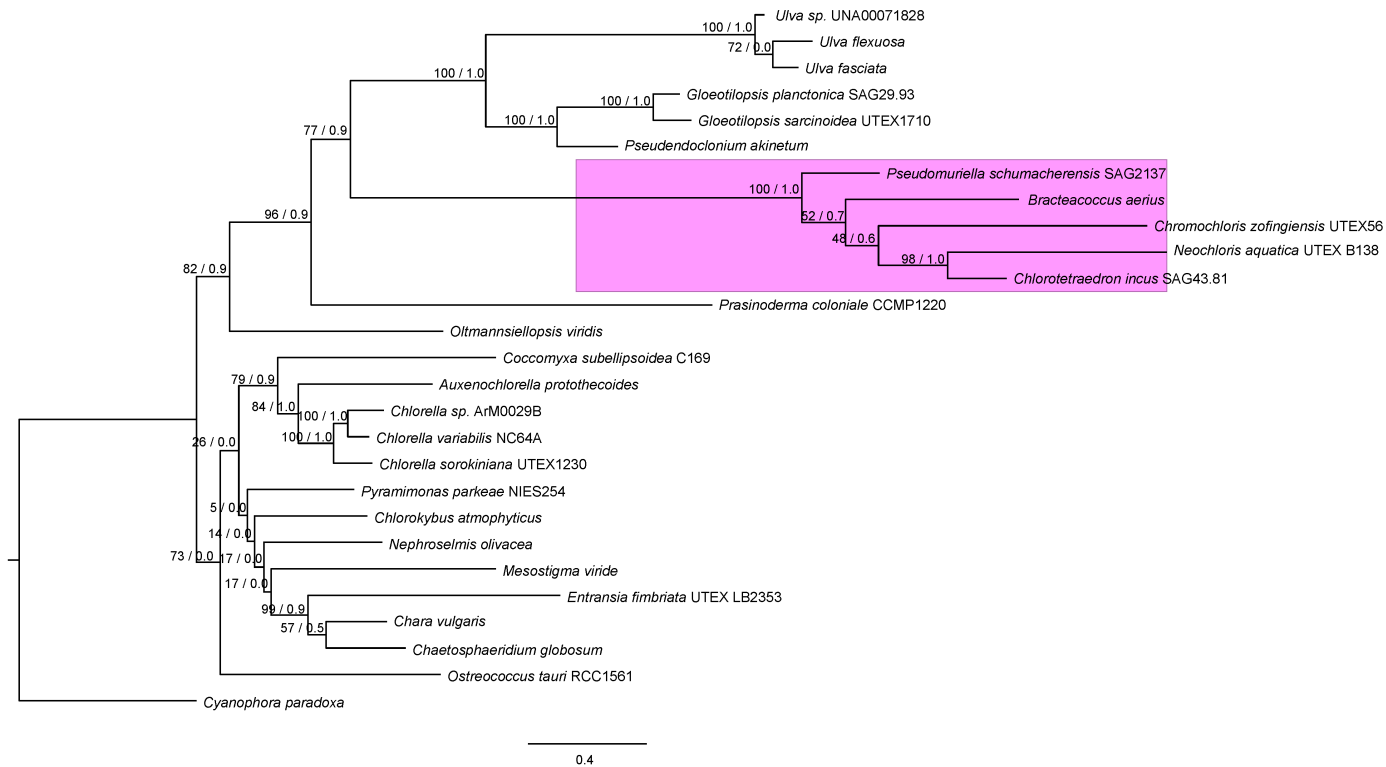


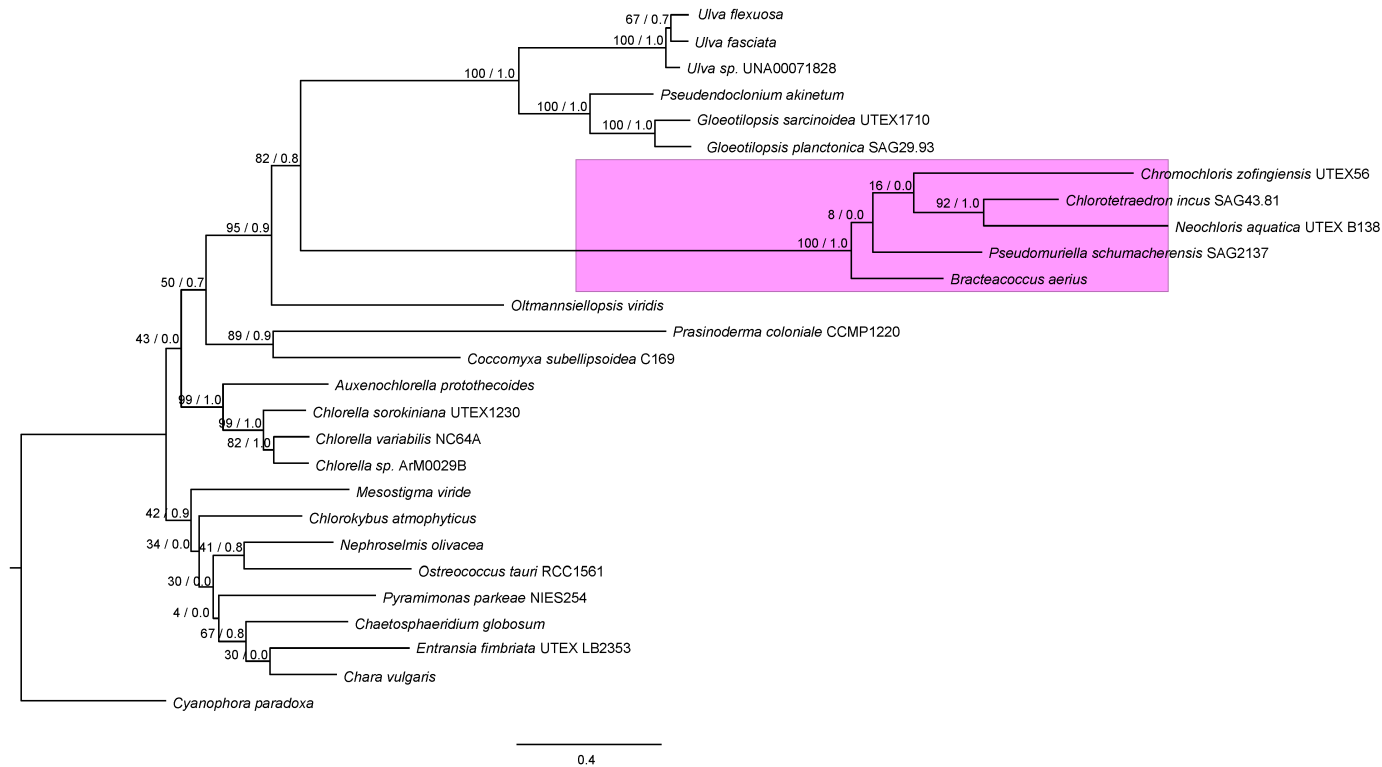
**S3 Fig. A.** Maximum-Likelihood tree inferred from mitochondrial *nad1* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



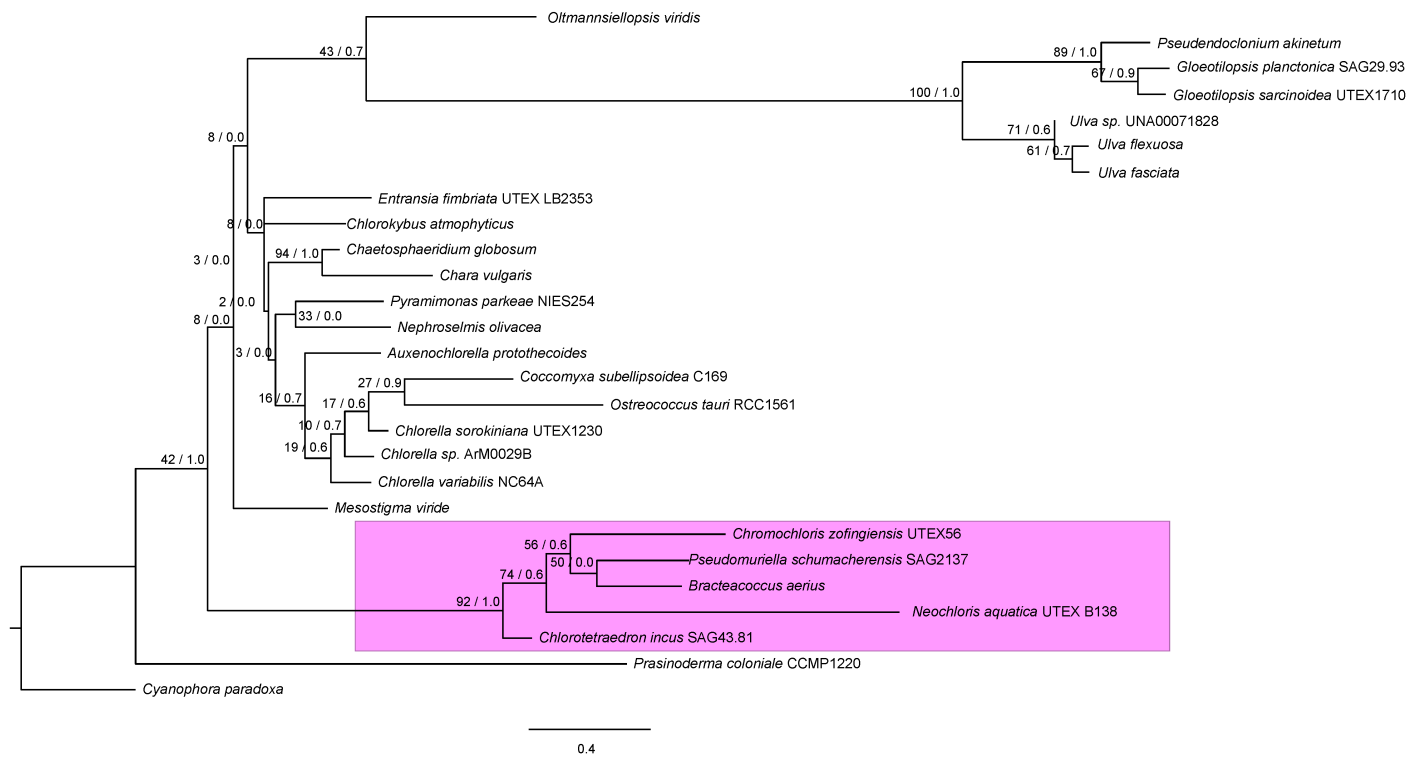
**S3 Fig. B. Maximum-Likelihood tree inferred from mitochondrial *nad2* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



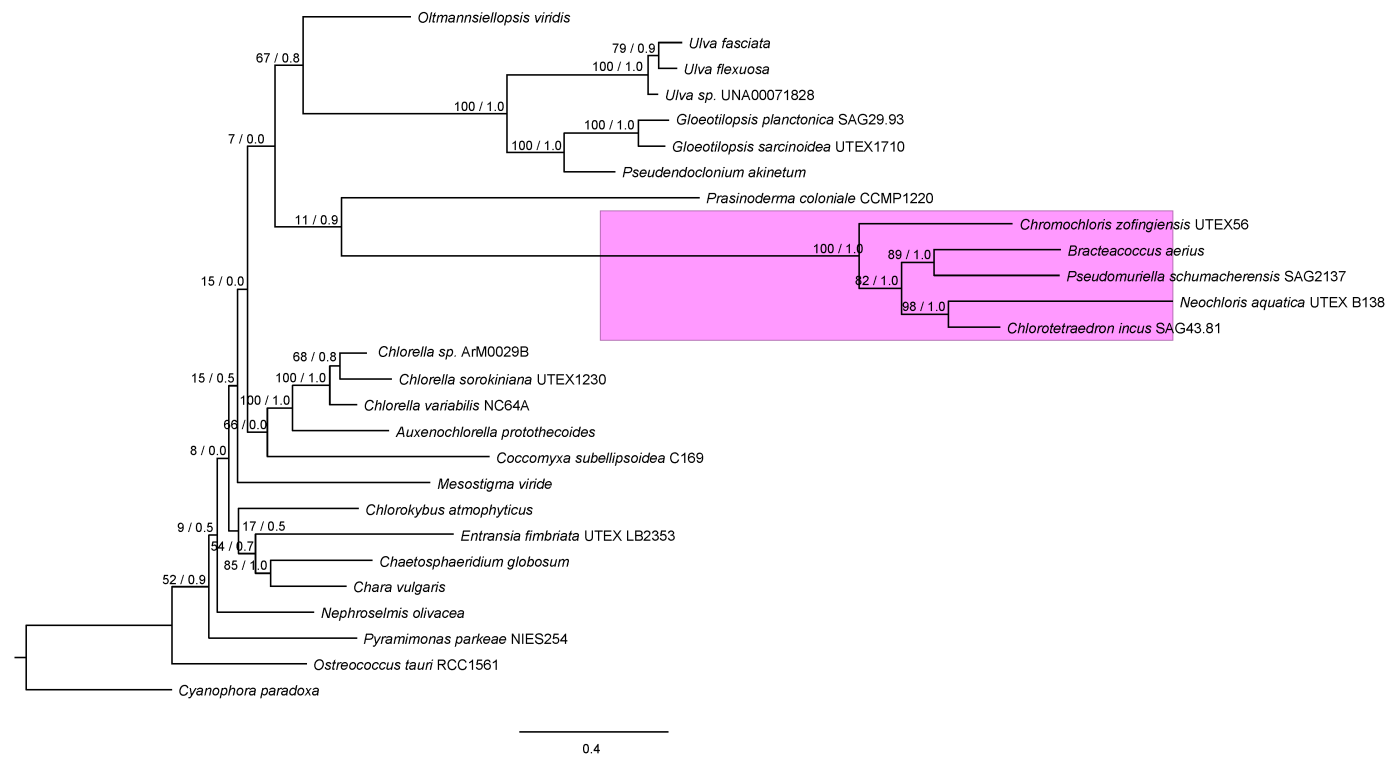
**S3 Fig. C. Maximum-Likelihood tree inferred from mitochondrial *nad3* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



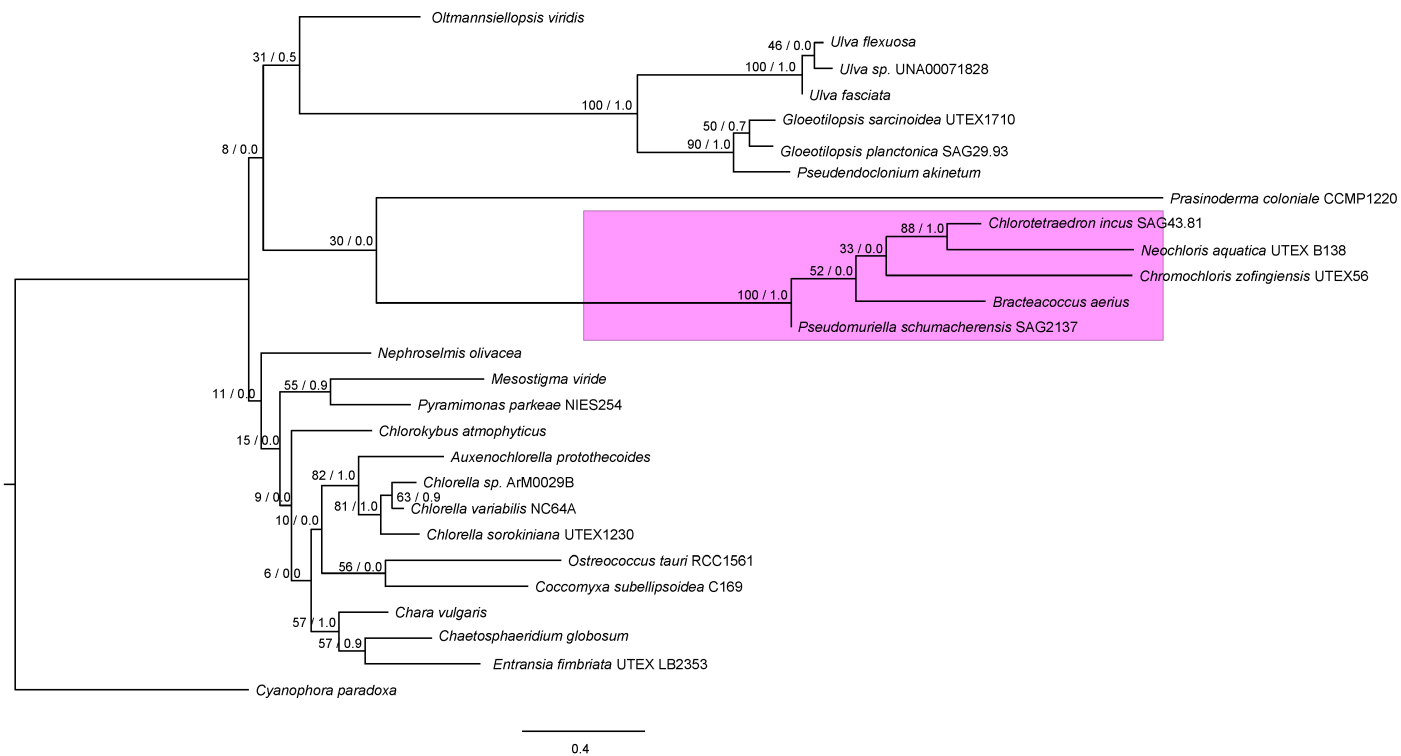
**S3 Fig. D. Maximum-Likelihood tree inferred from mitochondrial *nad4* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



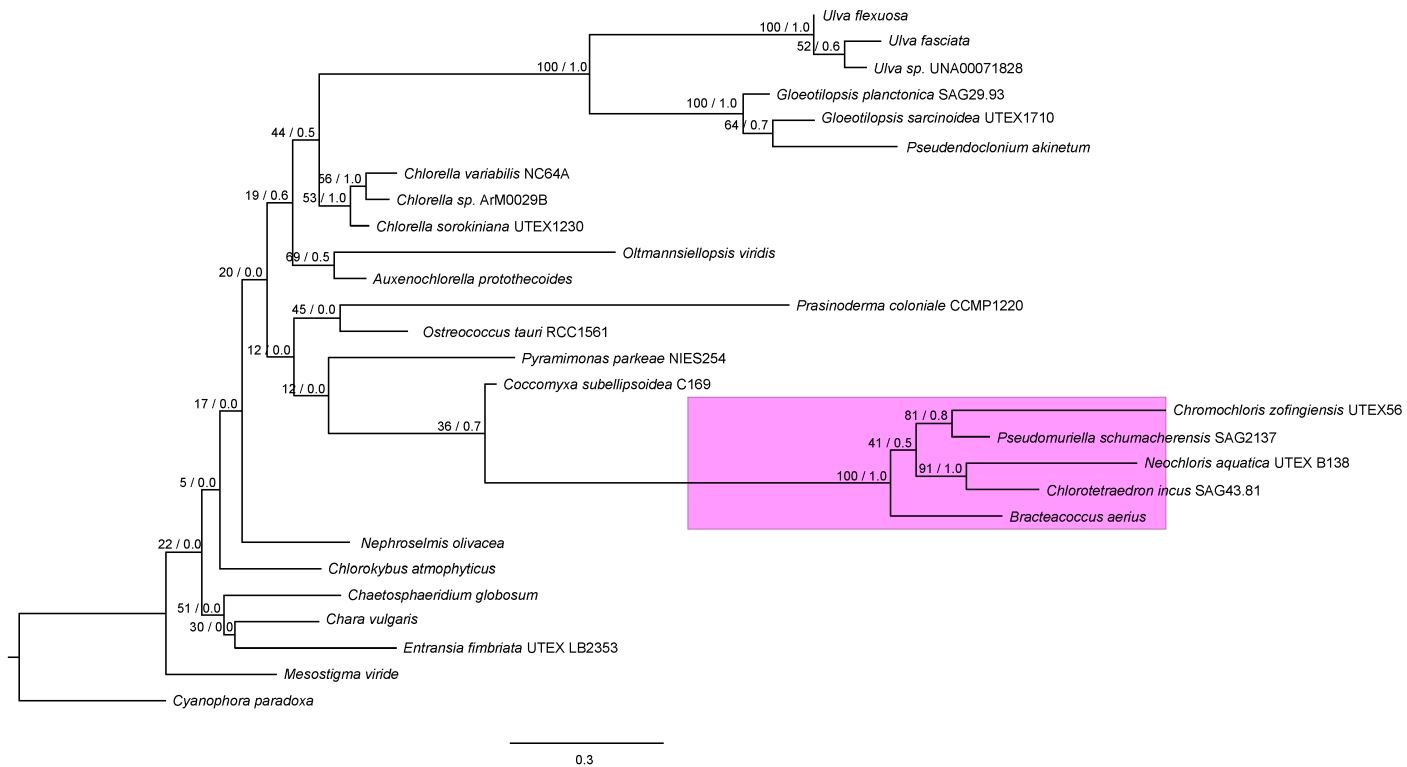
**S3 Fig. E. Maximum-Likelihood tree inferred from mitochondrial *nad4L* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. F. Maximum-Likelihood tree inferred from mitochondrial *nad5* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

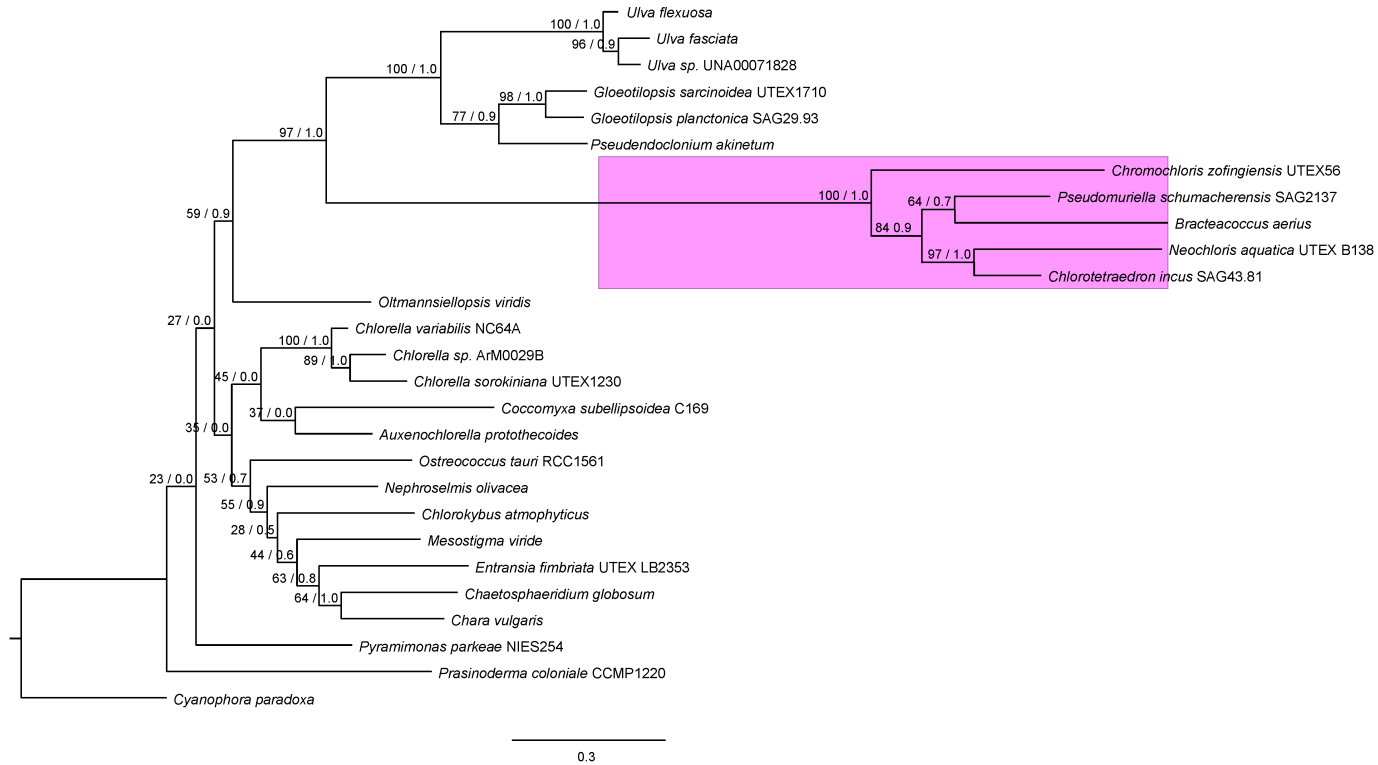


**S3 Fig. G. Maximum-Likelihood tree inferred from mitochondrial *nad6* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

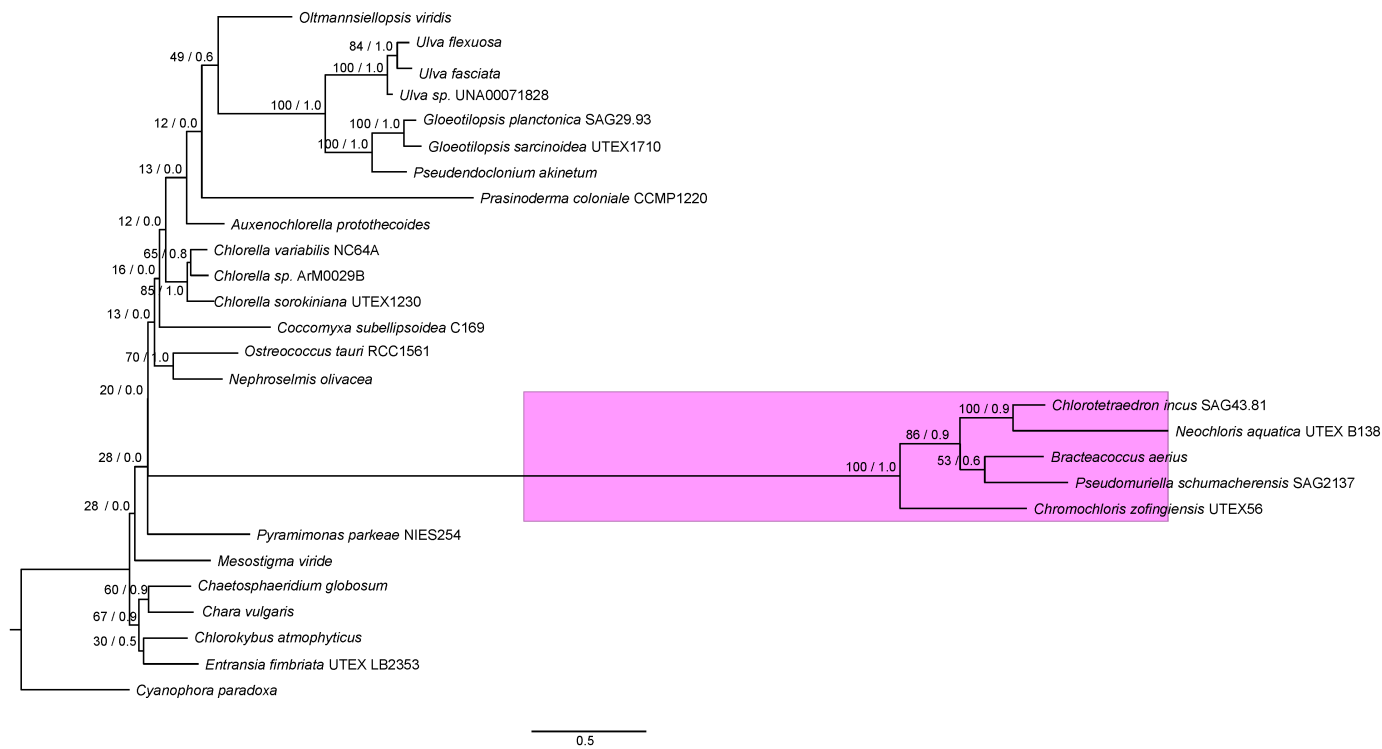


**S3 Fig. H. Maximum-Likelihood tree inferred from mitochondrial *cox2* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

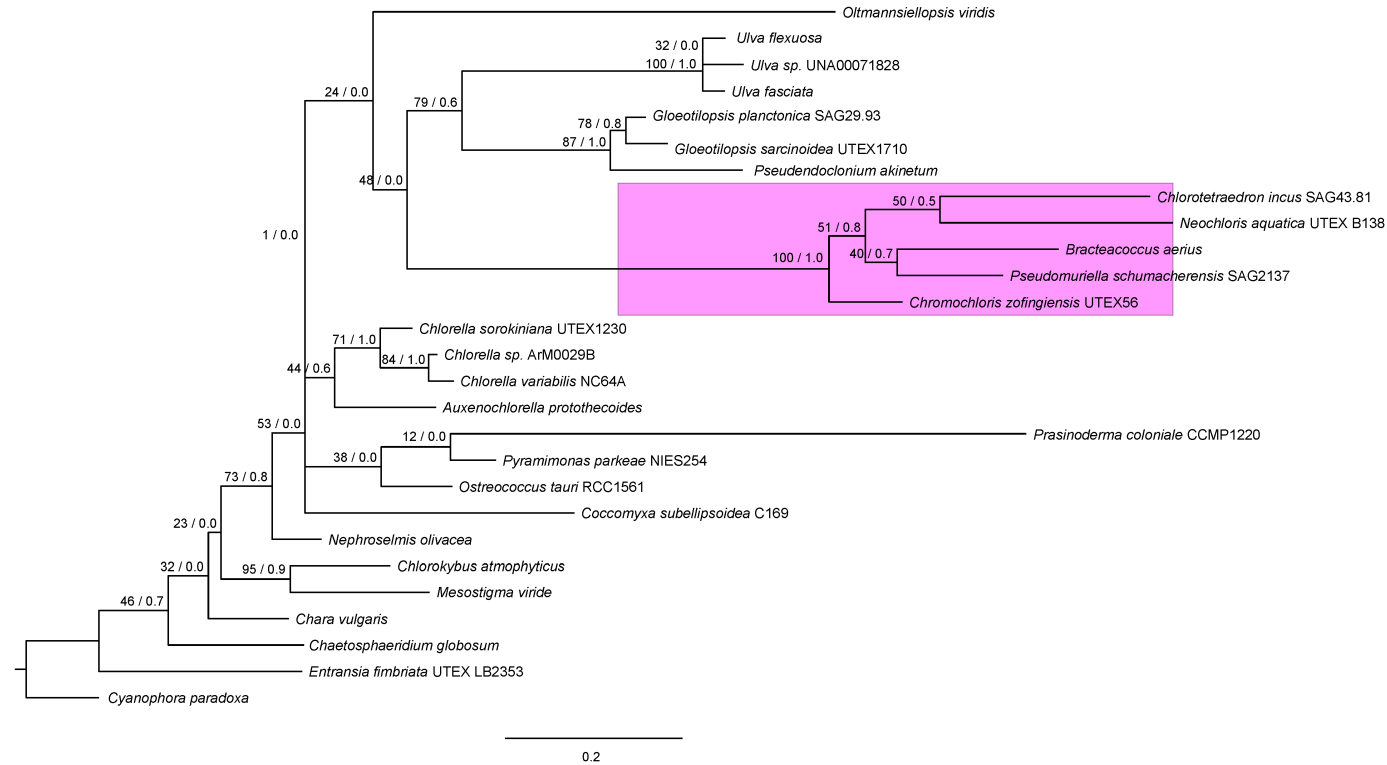




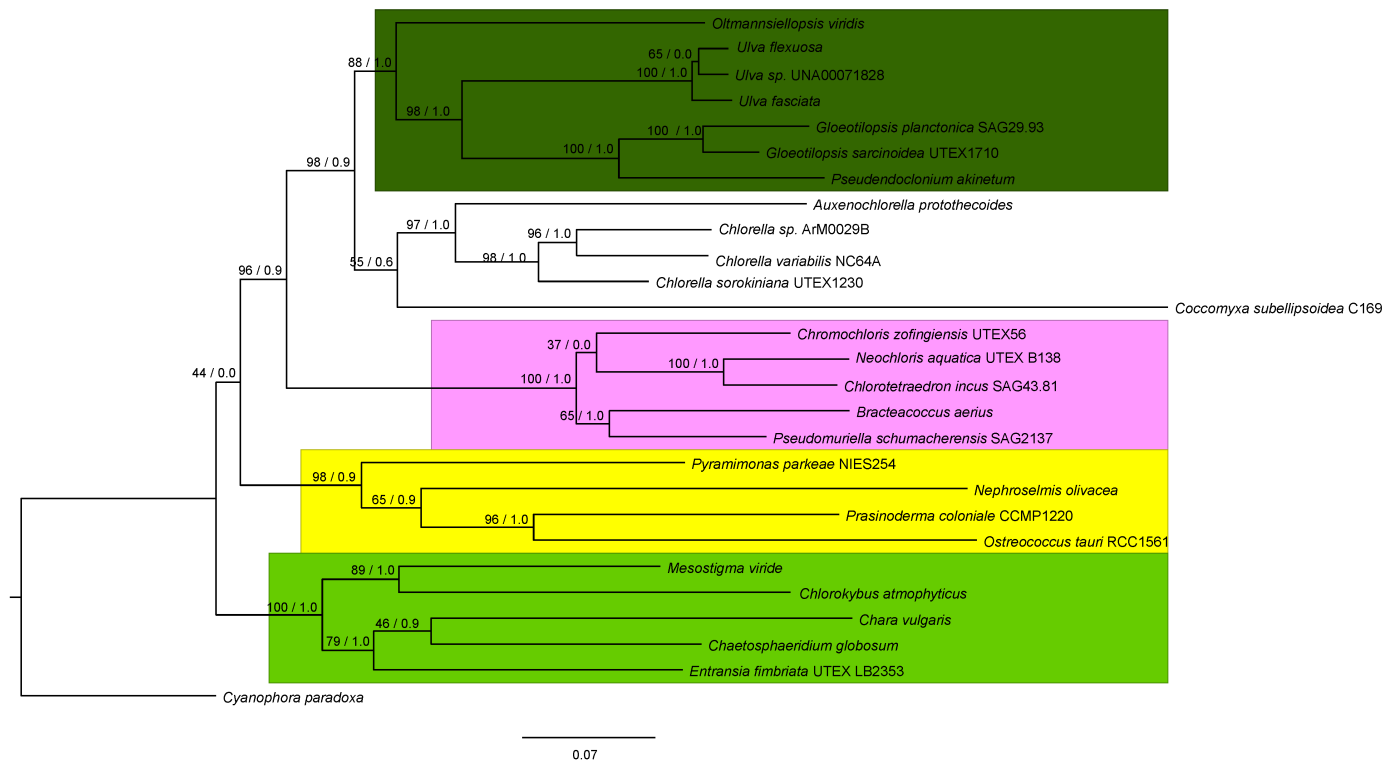
**S3 Fig. I. Maximum-Likelihood tree inferred from mitochondrial *cox3* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



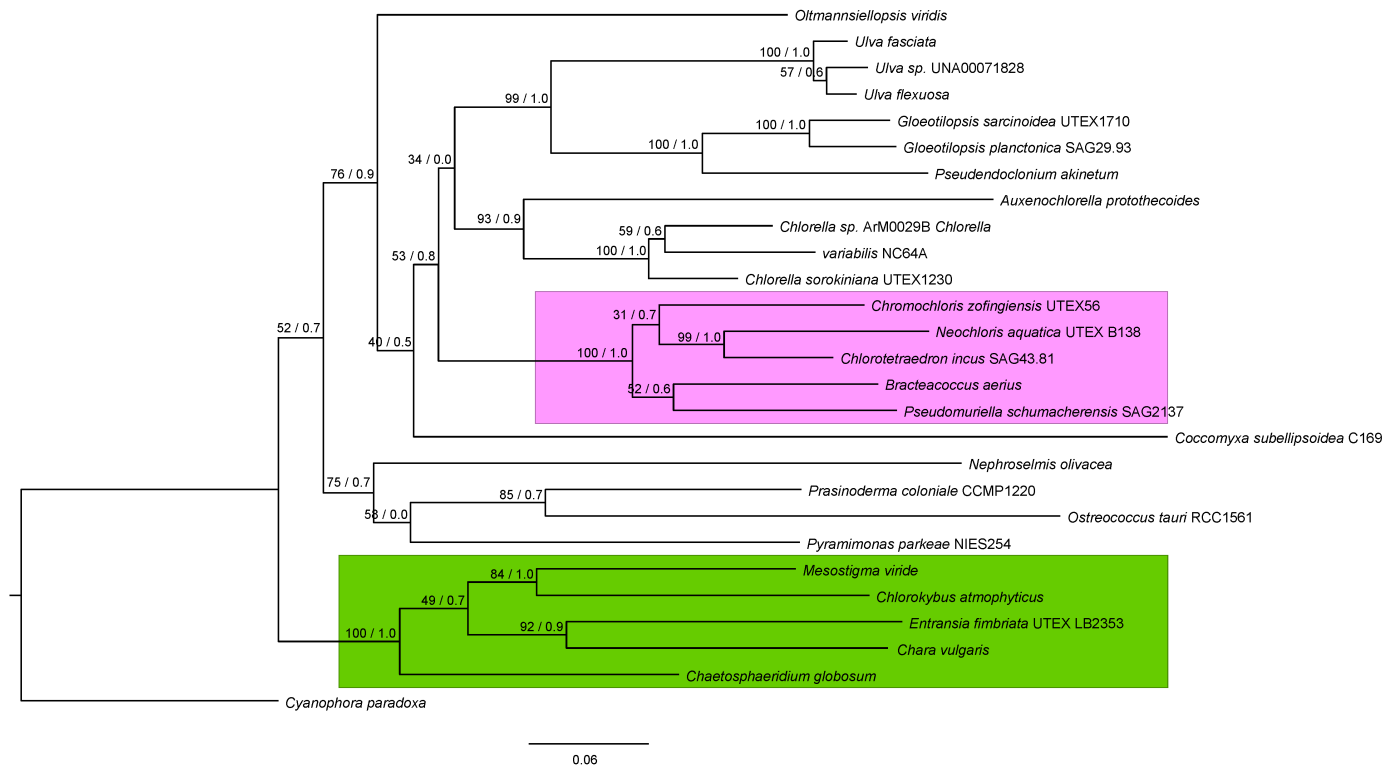
**S3 Fig. J. Maximum-Likelihood tree inferred from mitochondrial *atp6* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



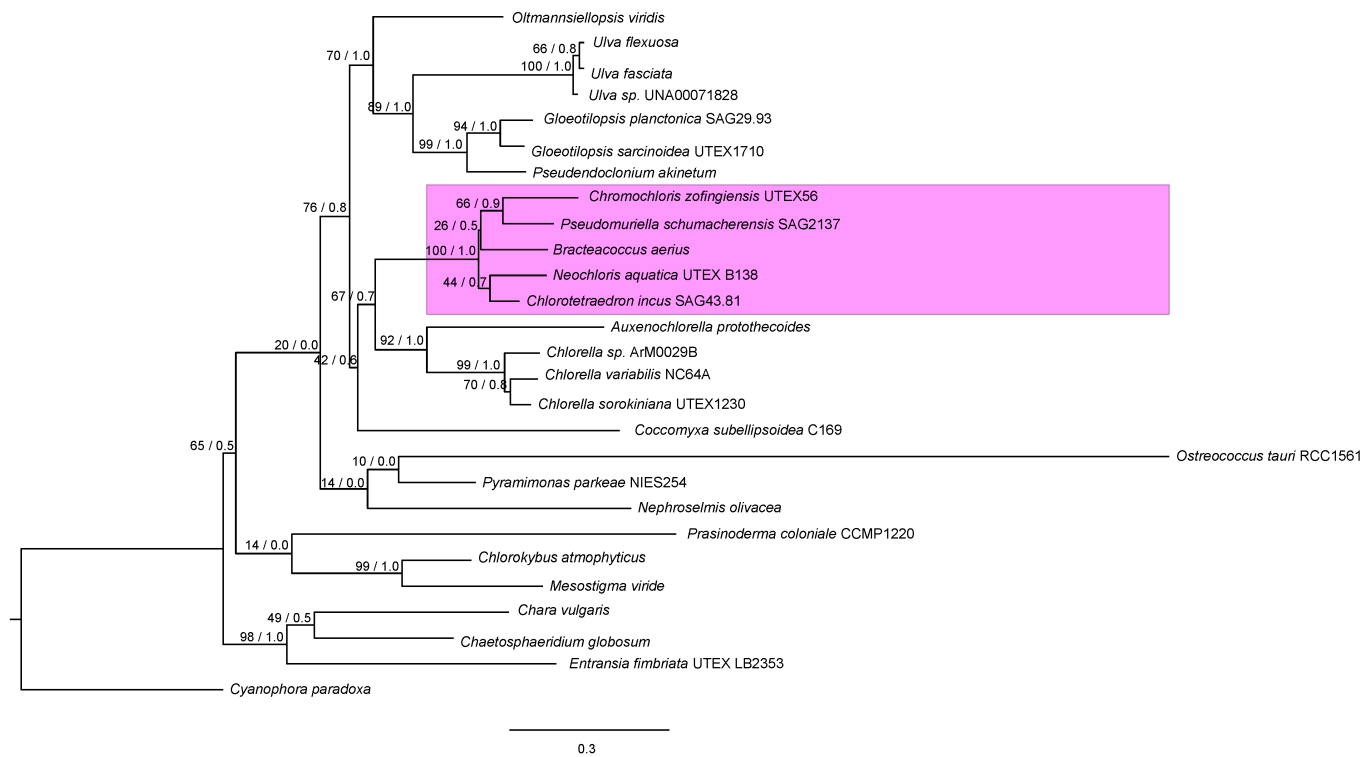
**S3 Fig. K. Maximum-Likelihood tree inferred from mitochondrial *atp9* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



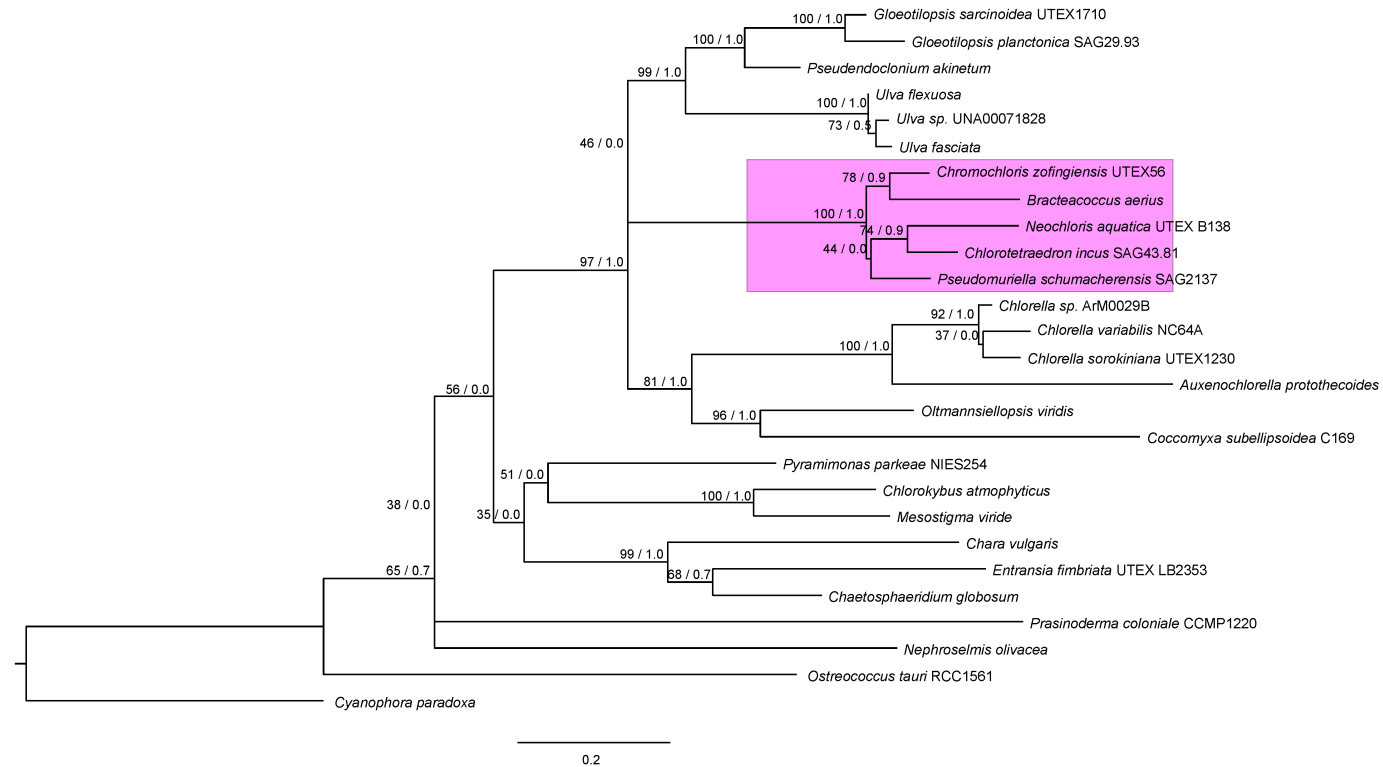
**S3 Fig. L. Maximum-Likelihood tree inferred from plastid *atpA* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



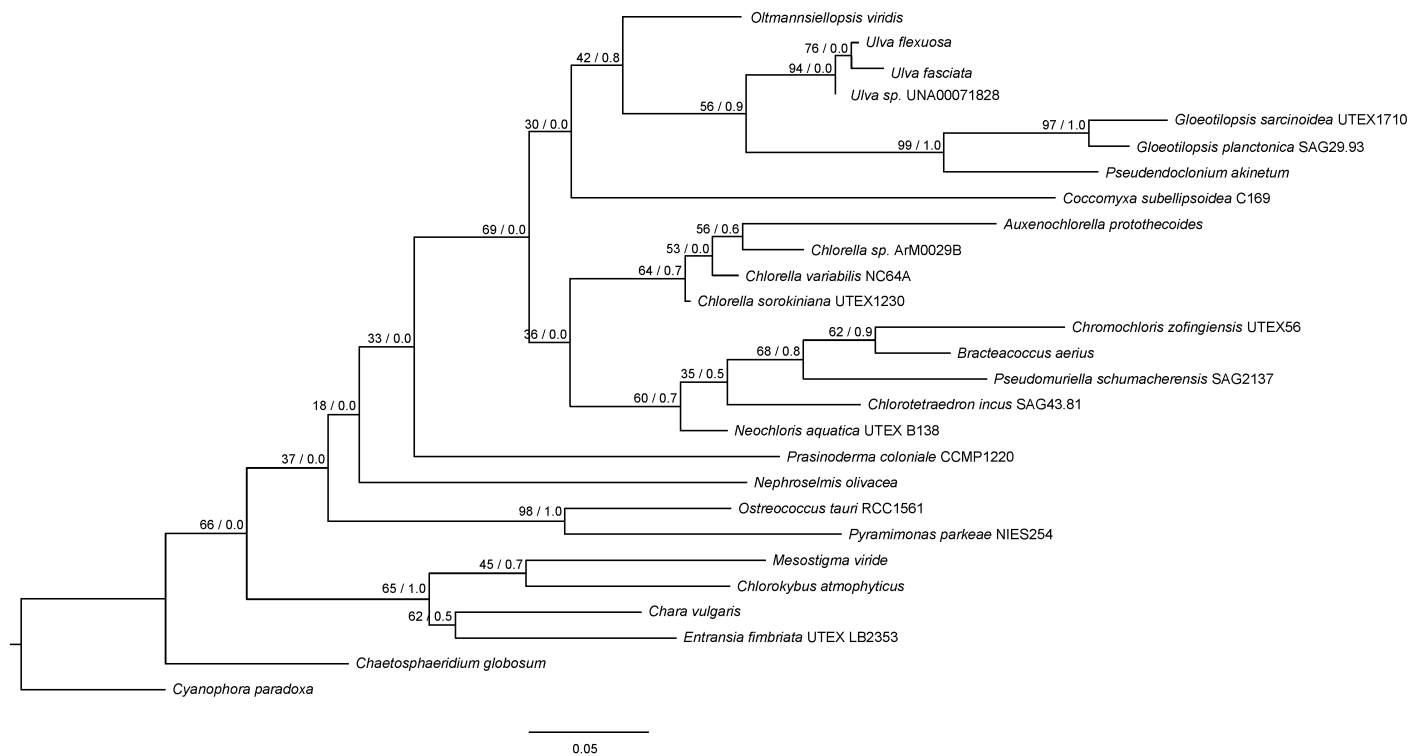
**S3 Fig. M. Maximum-Likelihood tree inferred from plastid *atpB* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. N.** Maximum-Likelihood tree inferred from plastid *atpE* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

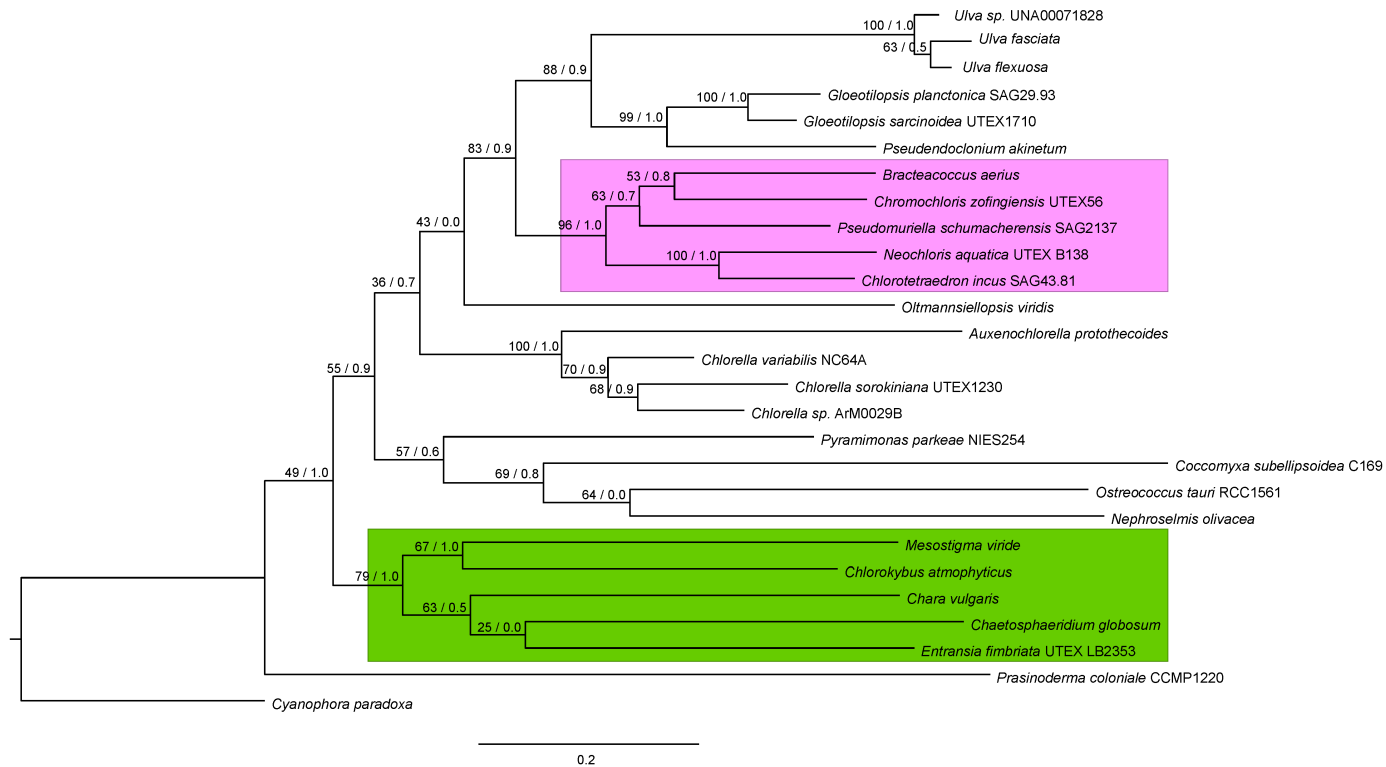


**S3 Fig. O.** Maximum-Likelihood tree inferred from plastid *atpF* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

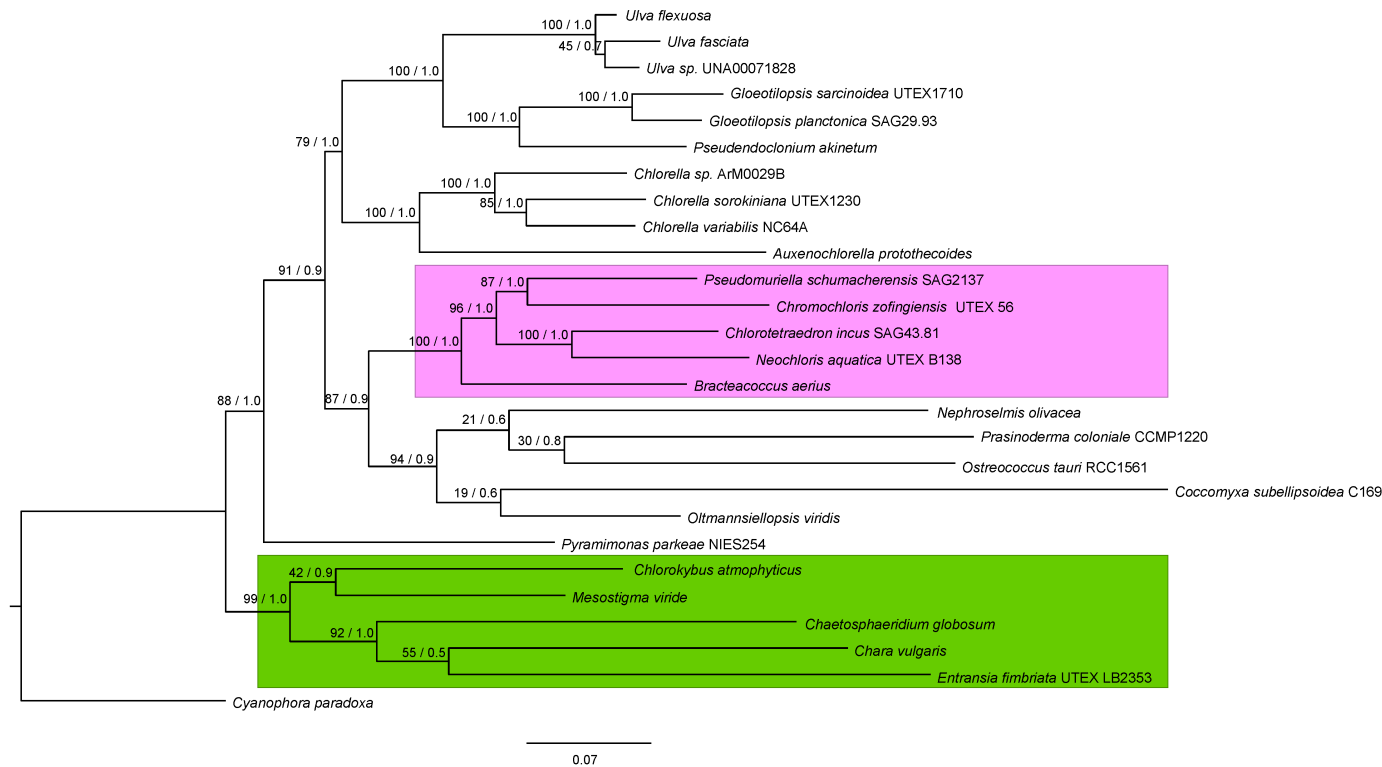


**S3 Fig. P.** Maximum-Likelihood tree inferred from plastid *atpH* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

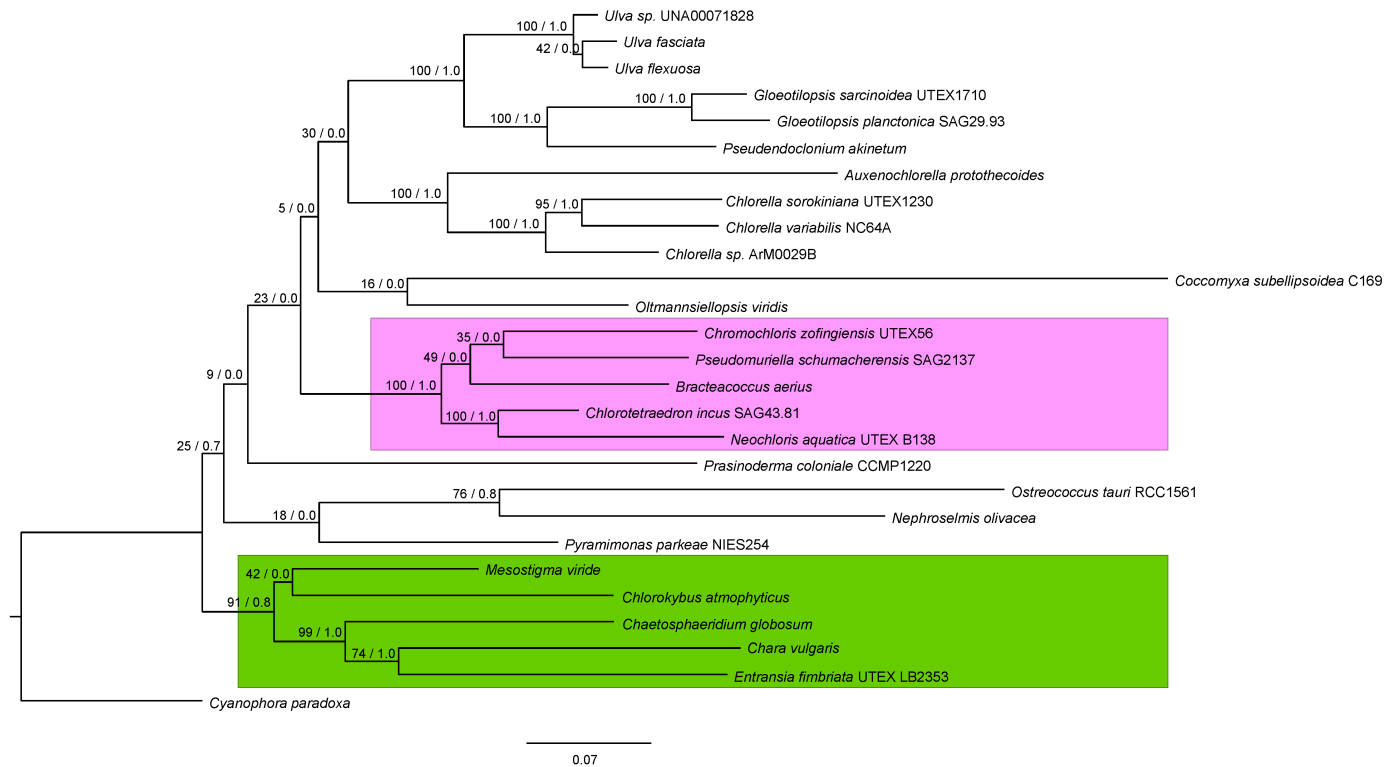




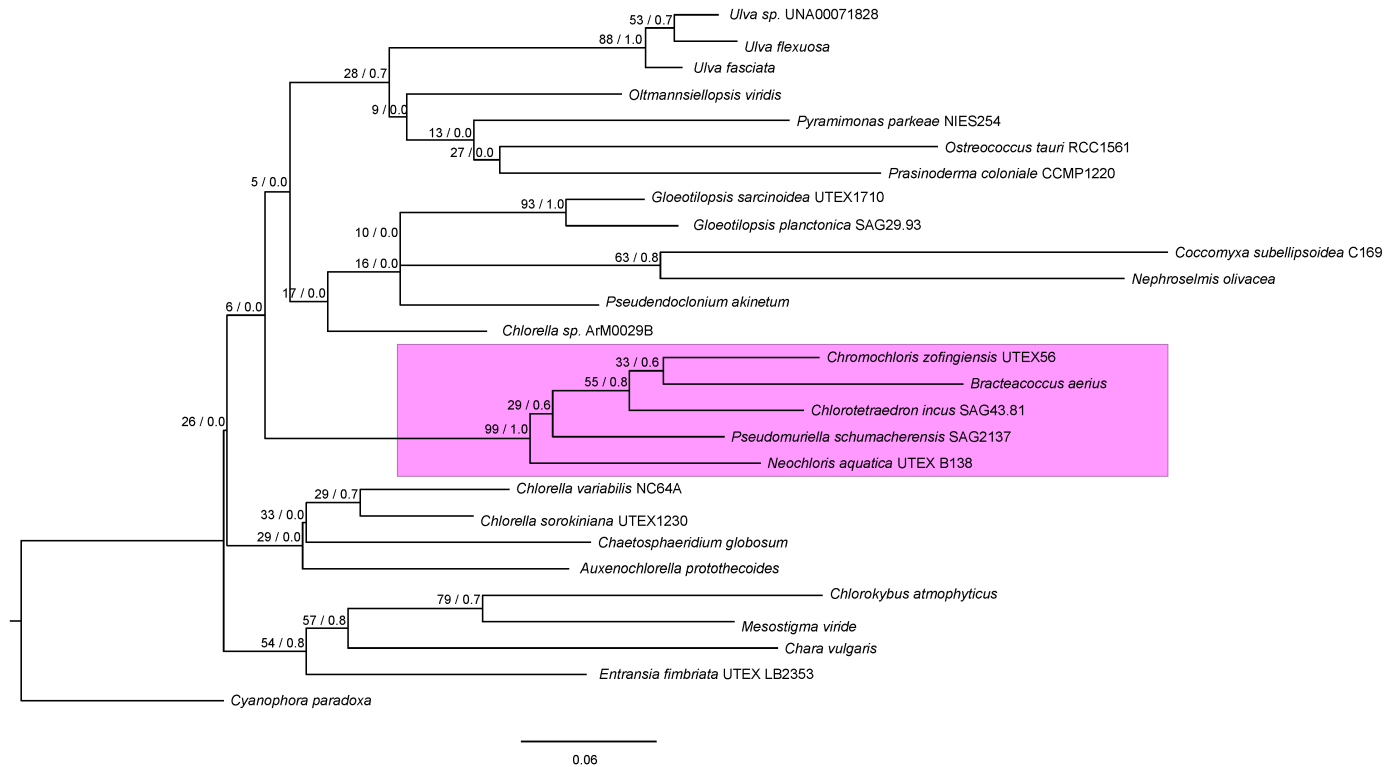
**S3 Fig. Q.** Maximum-Likelihood tree inferred from plastid *petA* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



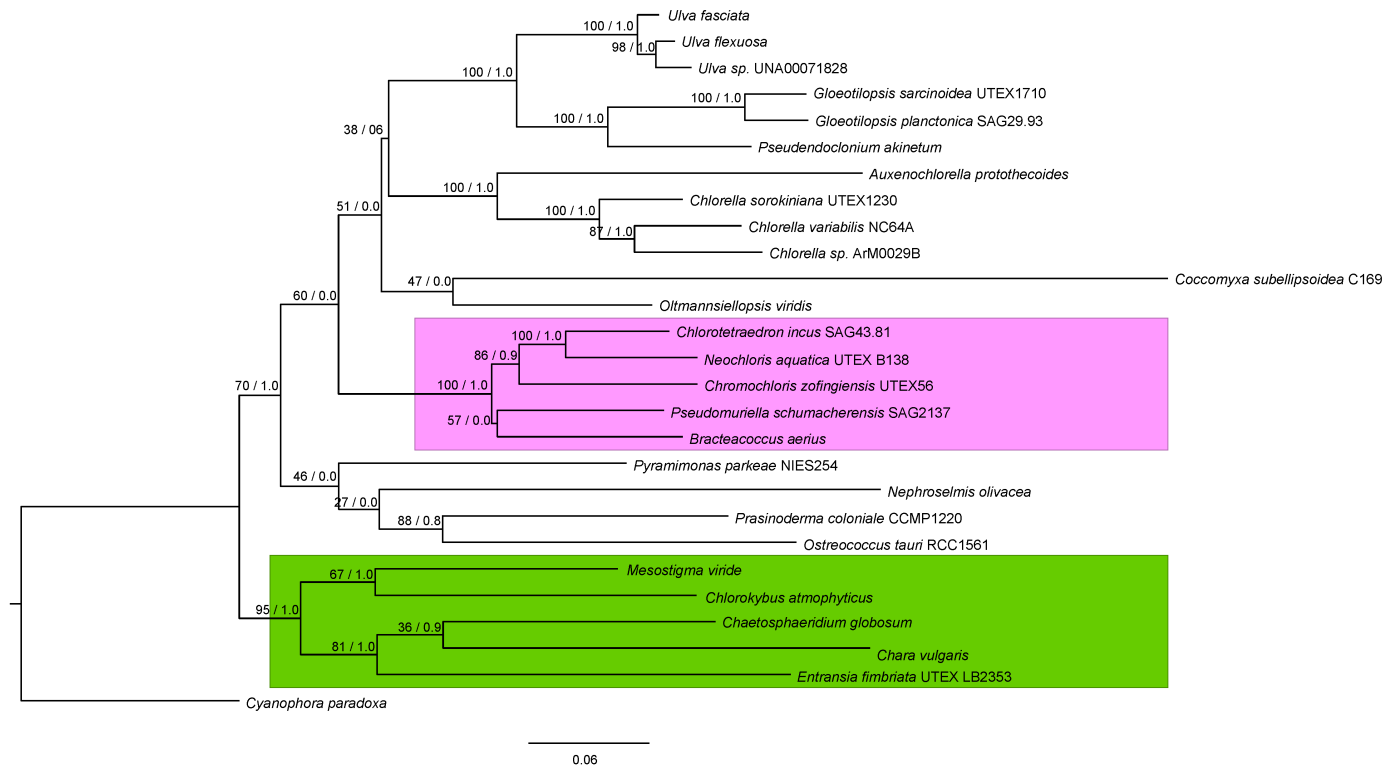
**S3 Fig. R Maximum-Likelihood tree inferred from plastid *psaA* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



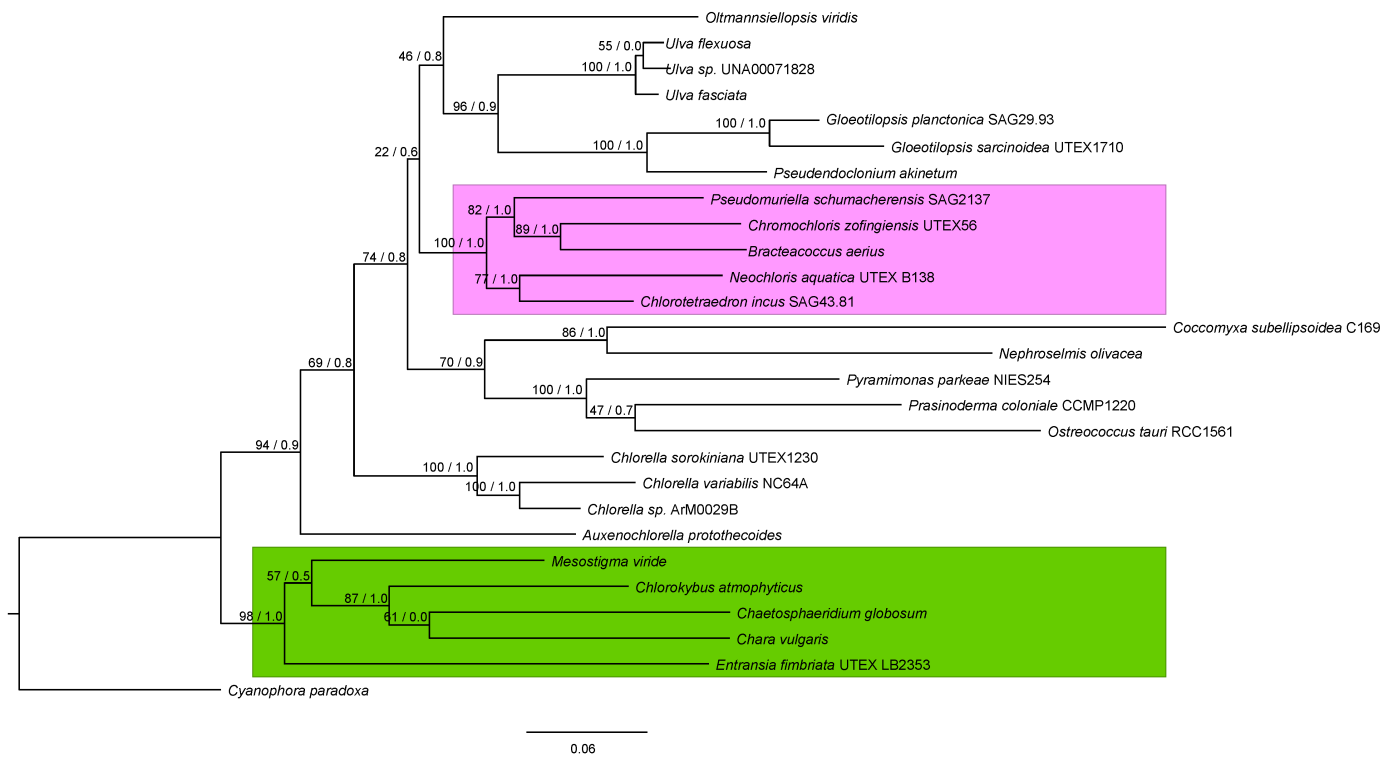
**S3 Fig. S.** Maximum-Likelihood tree inferred from plastid *psaB* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



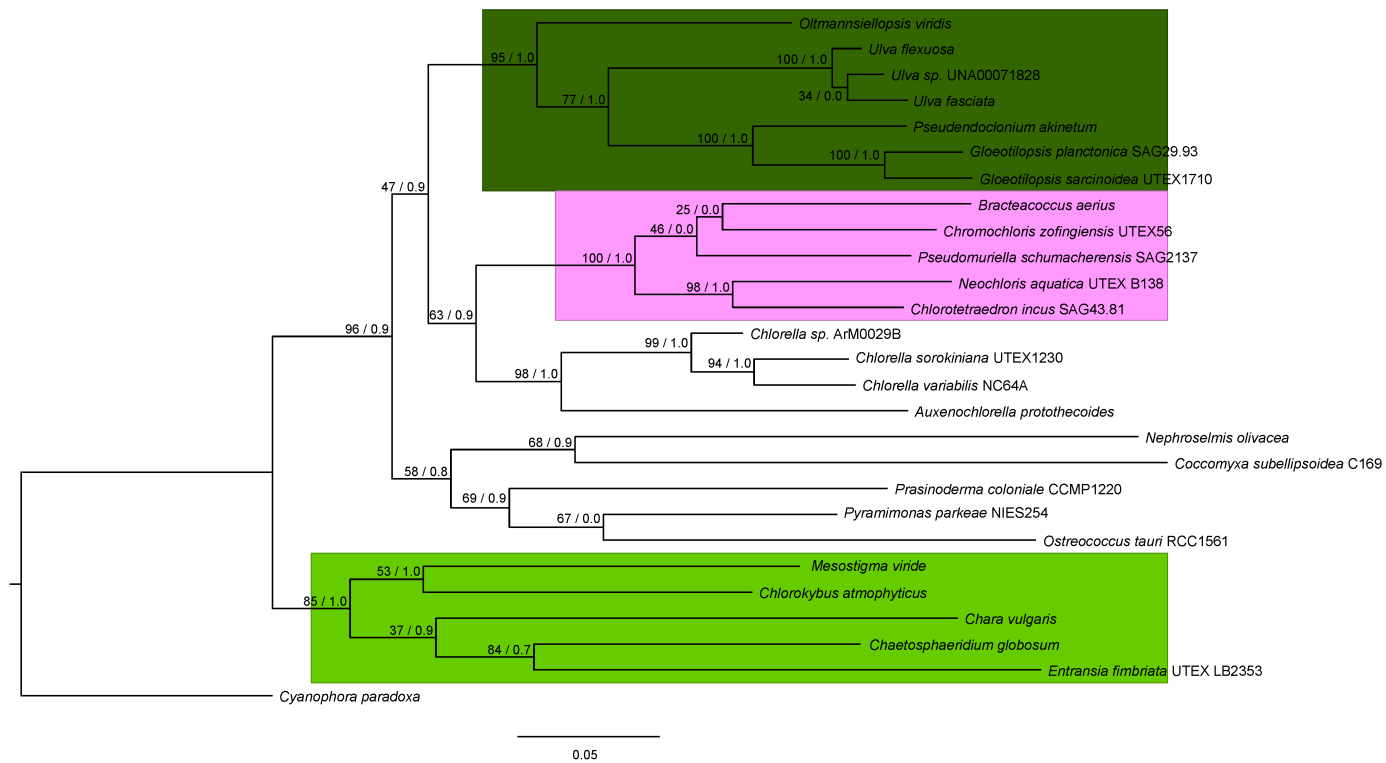
**S3 Fig. T. Maximum-Likelihood tree inferred from plastid *psaC* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



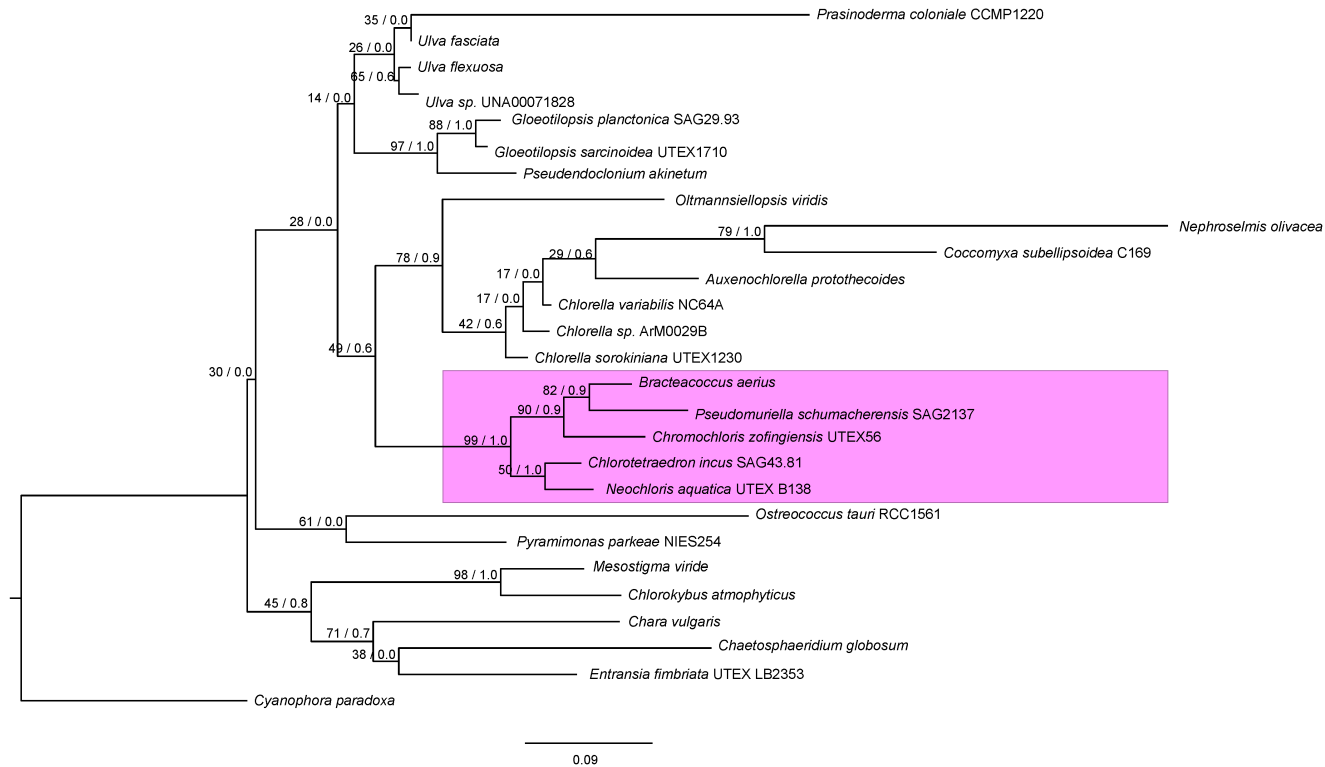
**S3 Fig. U.** Maximum-Likelihood tree inferred from plastid *psbB* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. V.** Maximum-Likelihood tree inferred from plastid *psbC* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

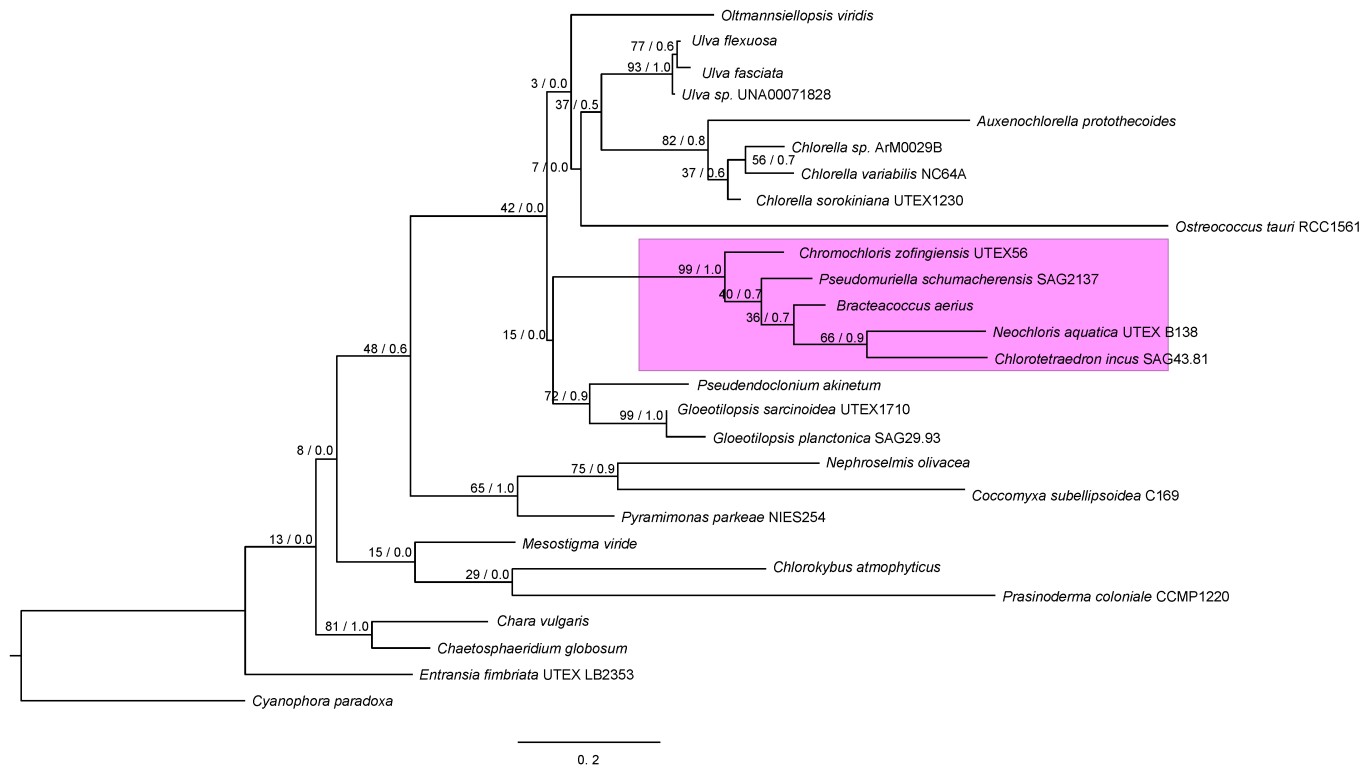


**S3 Fig. W.** Maximum-Likelihood tree inferred from plastid *psbD* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

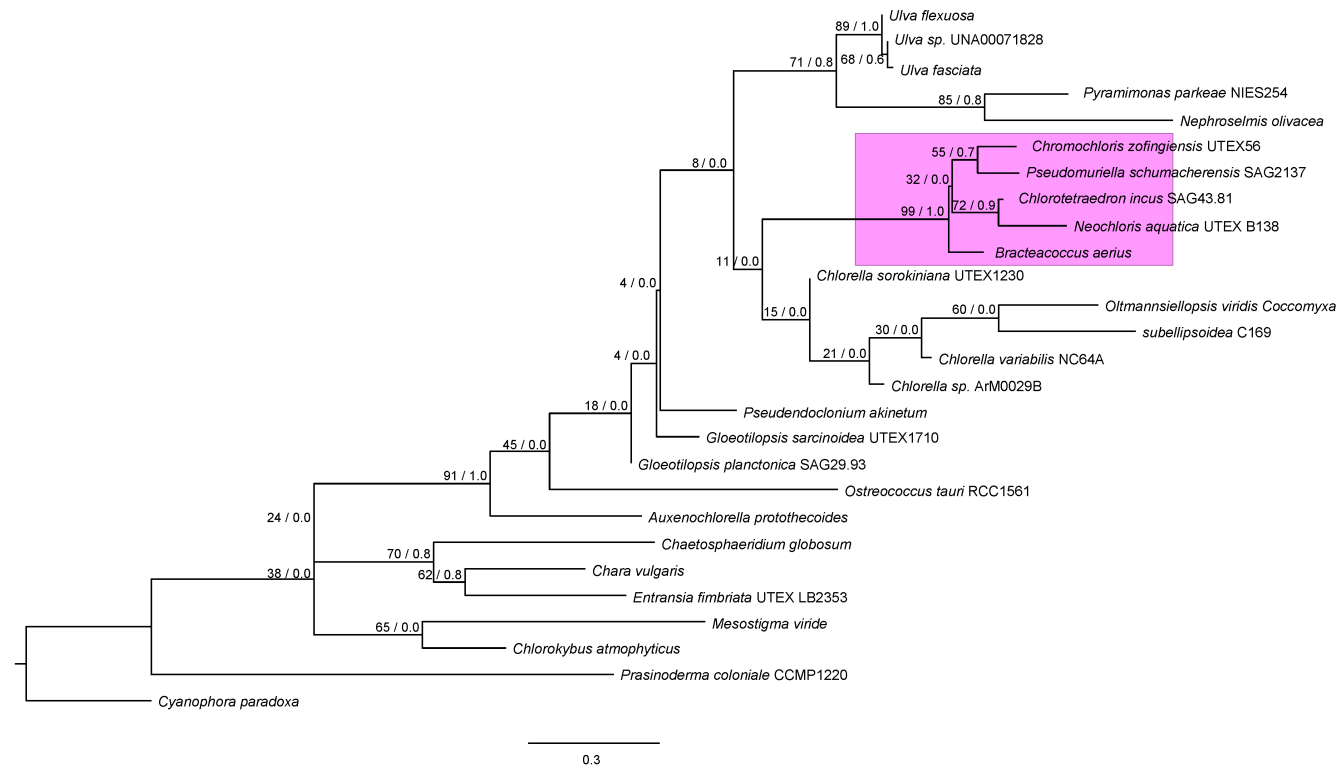


**S3 Fig. X.** Maximum-Likelihood tree inferred from plastid *psbE* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

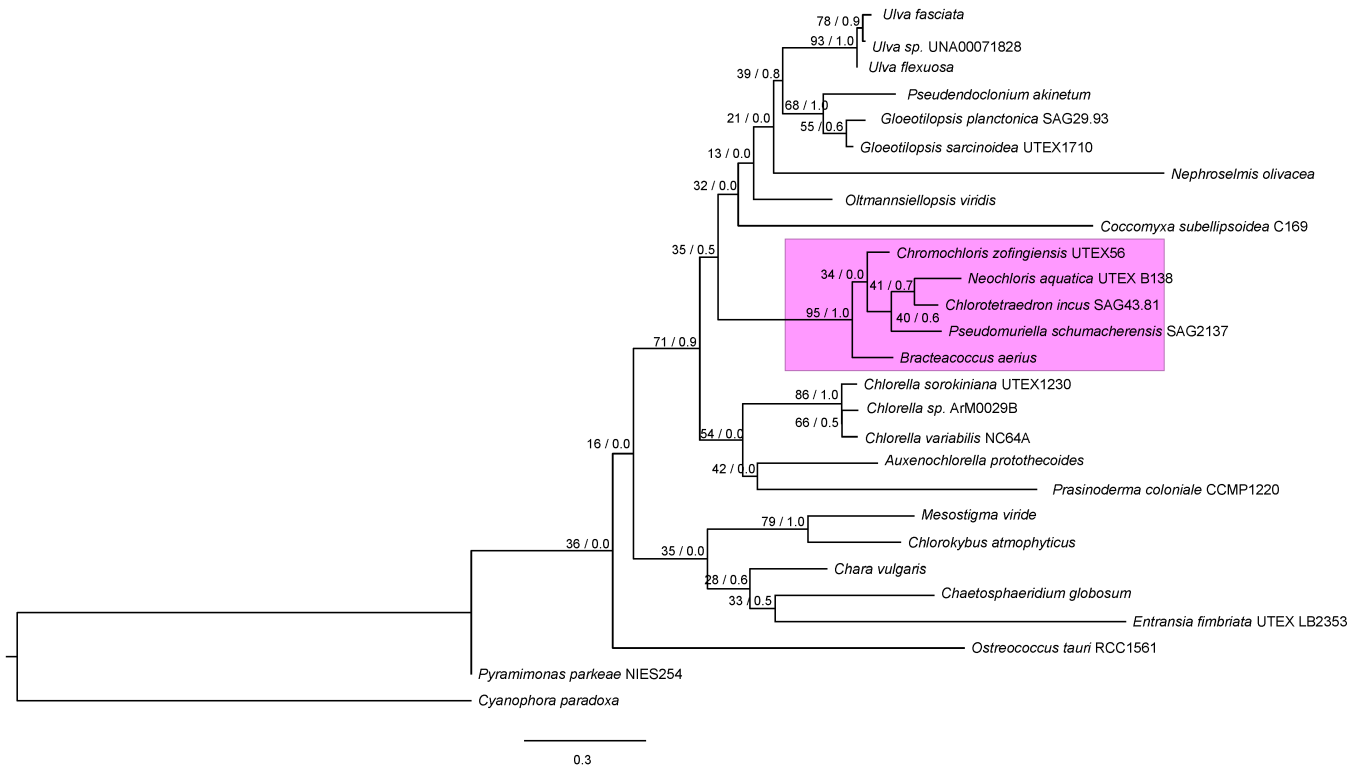




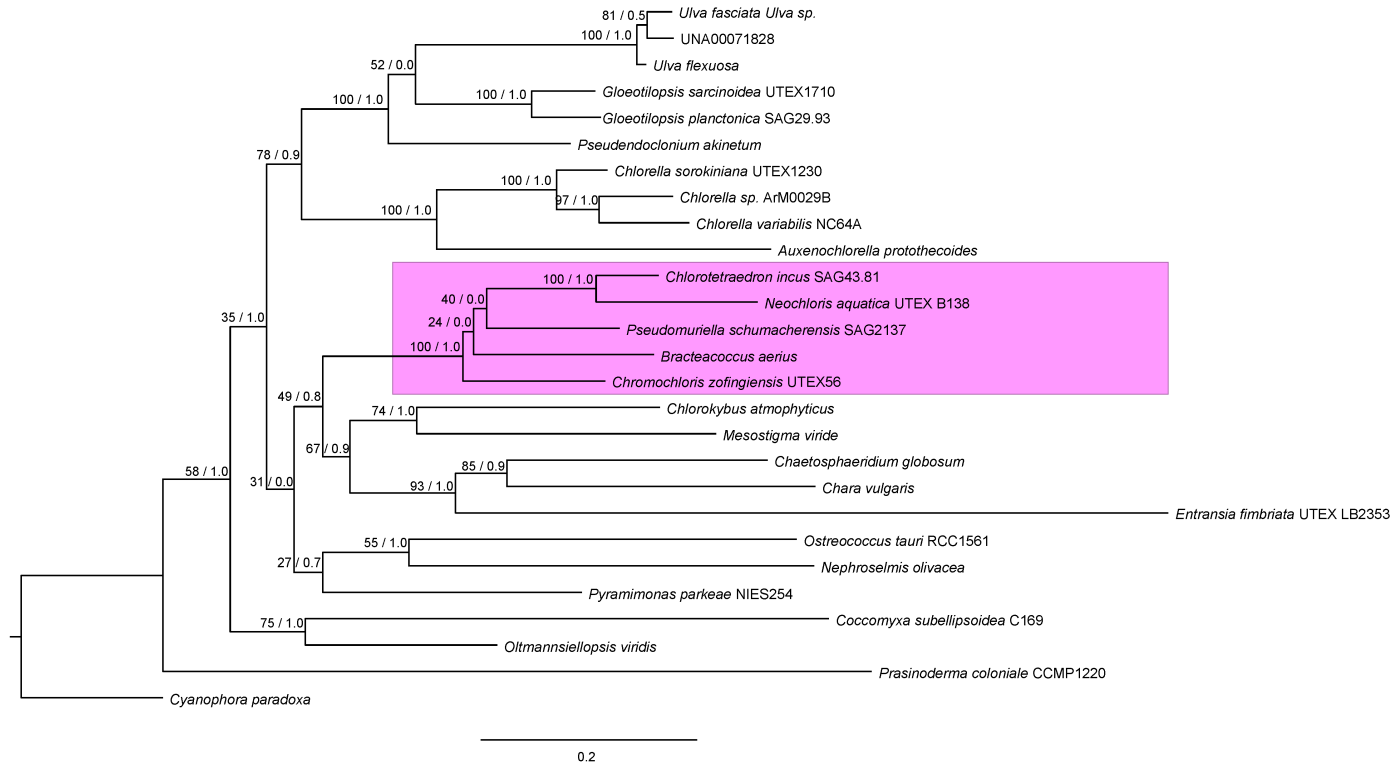
**S3 Fig. Y.** Maximum-Likelihood tree inferred from plastid *psbH* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



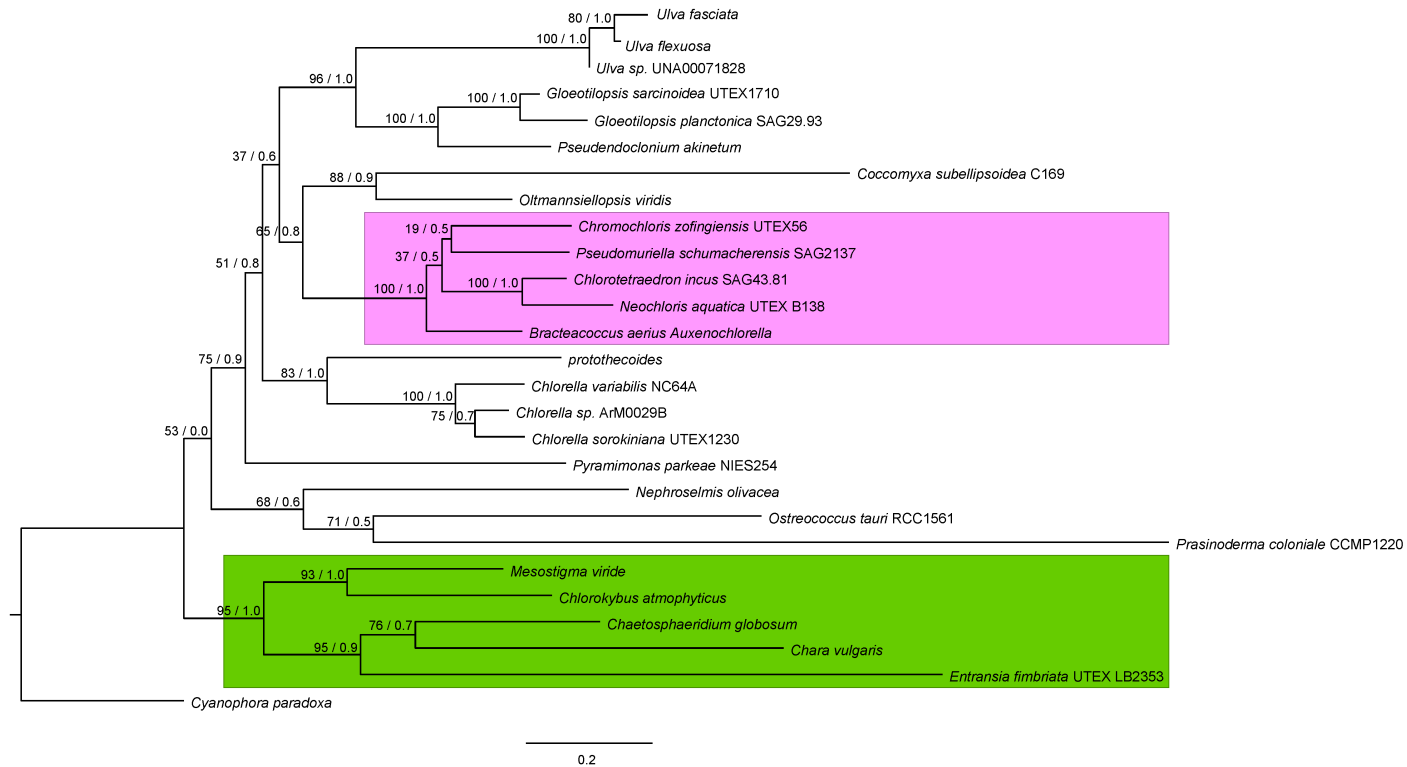
**S3 Fig. Z.** Maximum-Likelihood tree inferred from plastid *psbN* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



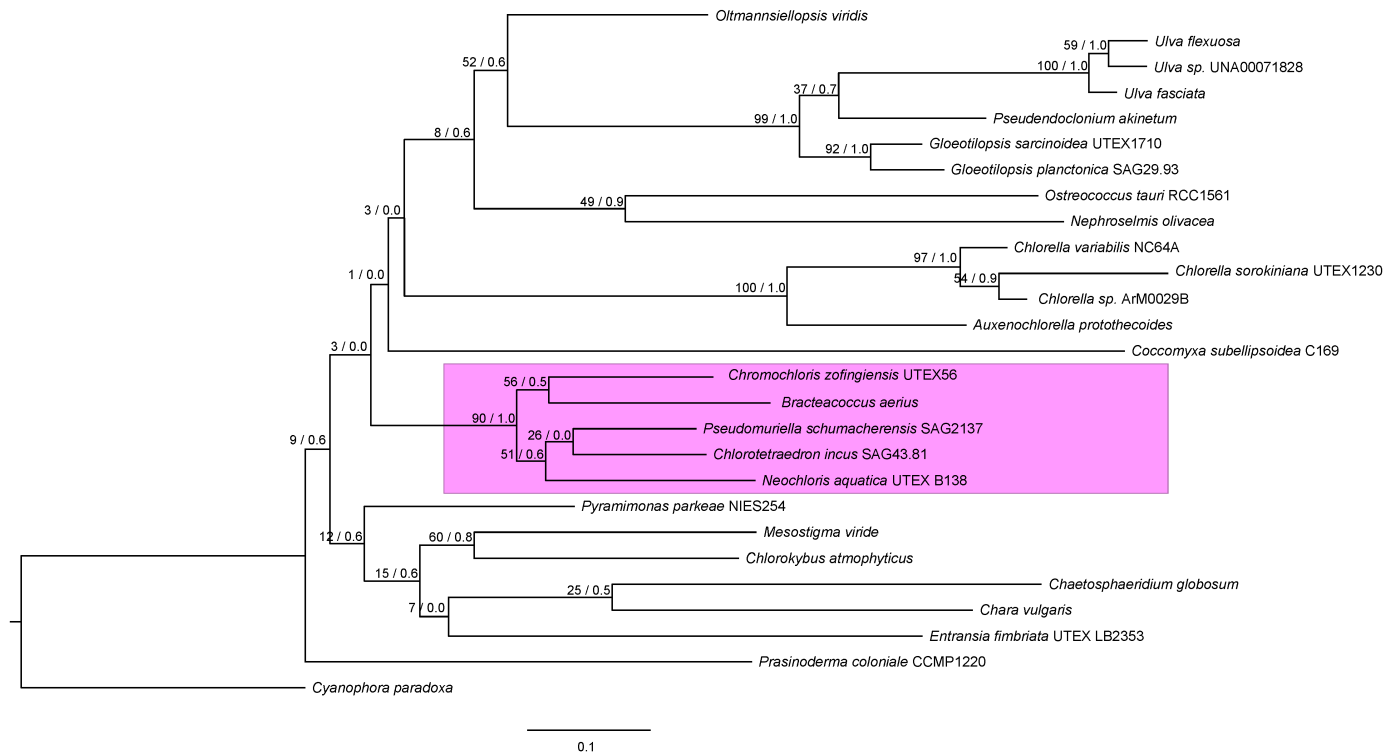
**S3 Fig. AA.** Maximum-Likelihood tree inferred from plastid *psbZ* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



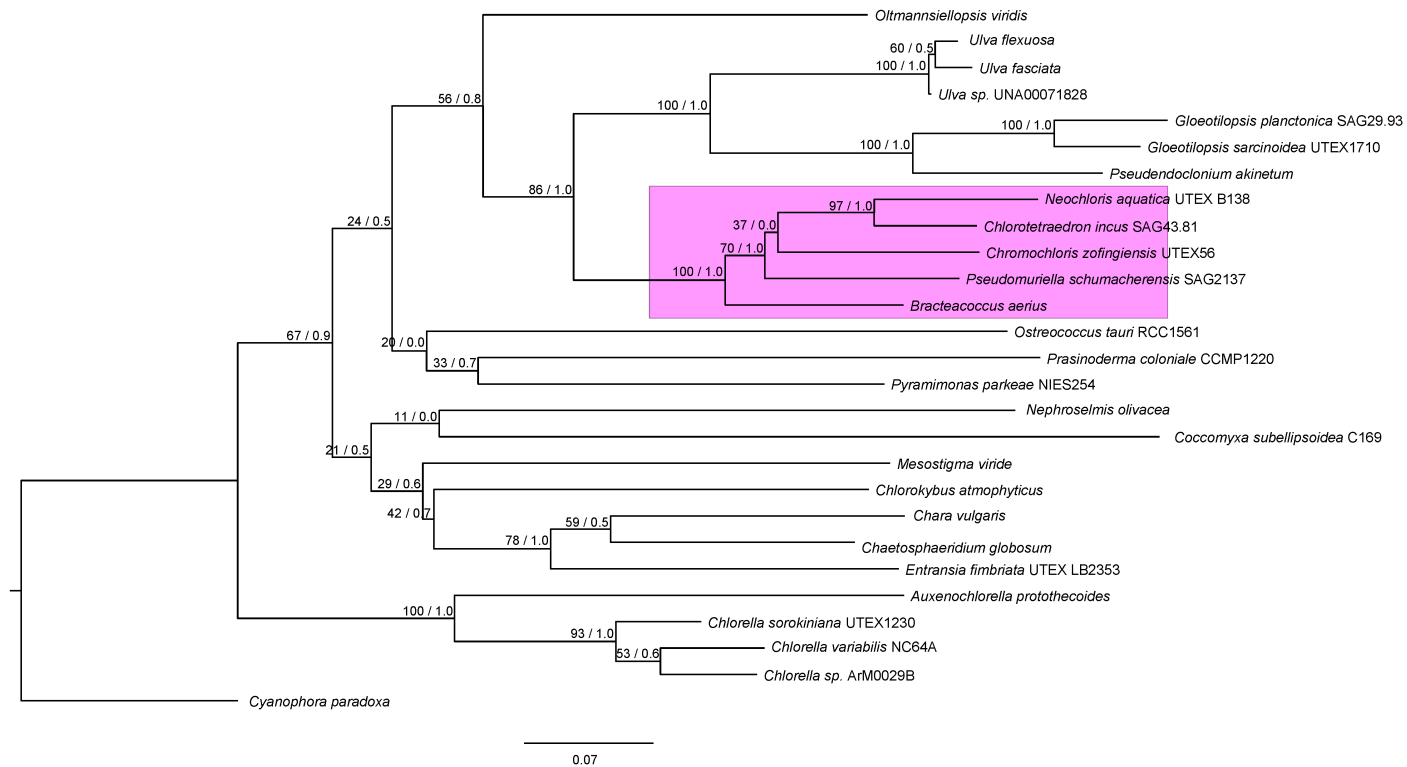
**S3 Fig. AB.** Maximum-Likelihood tree inferred from plastid *rpl2* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



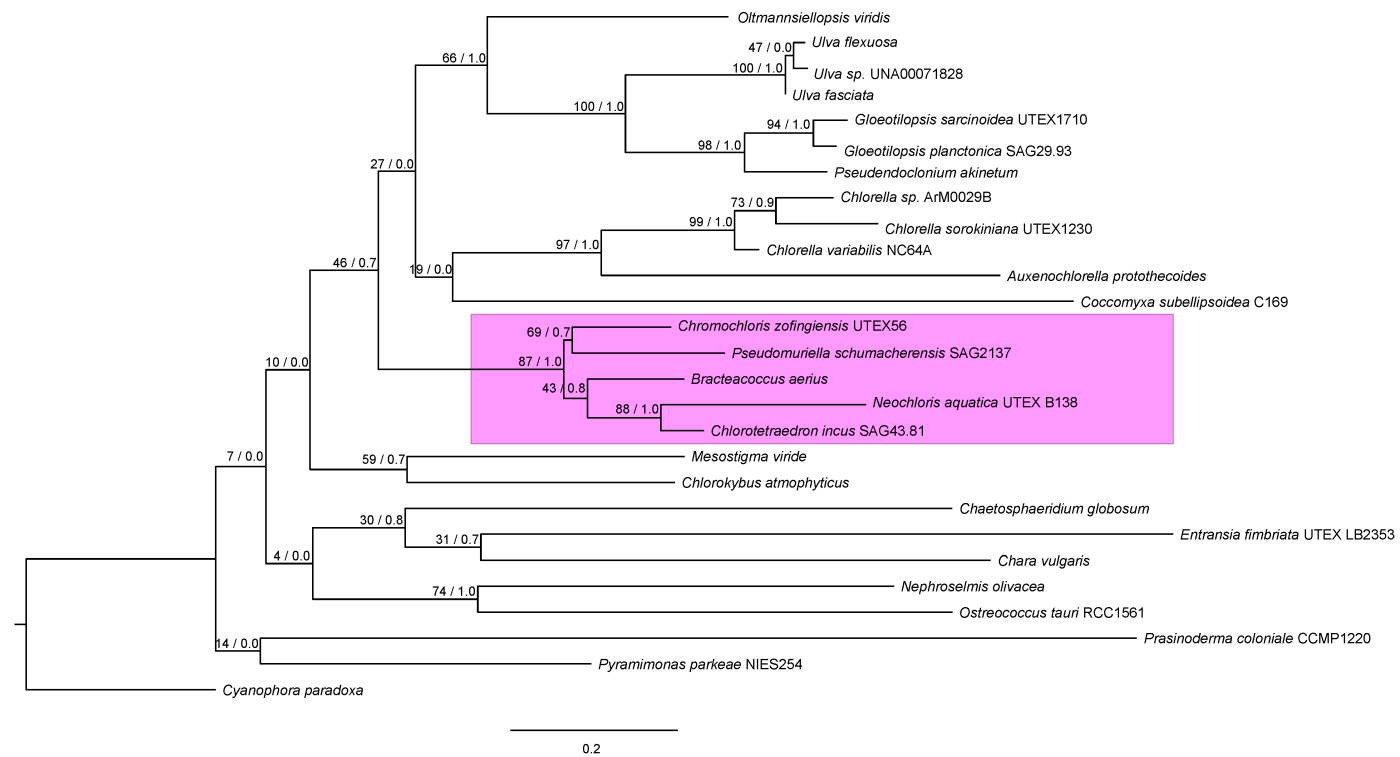
**S3 Fig. AC.** Maximum-Likelihood tree inferred from plastid *rpl5* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. AD.** Maximum-Likelihood tree inferred from plastid *rpl14* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

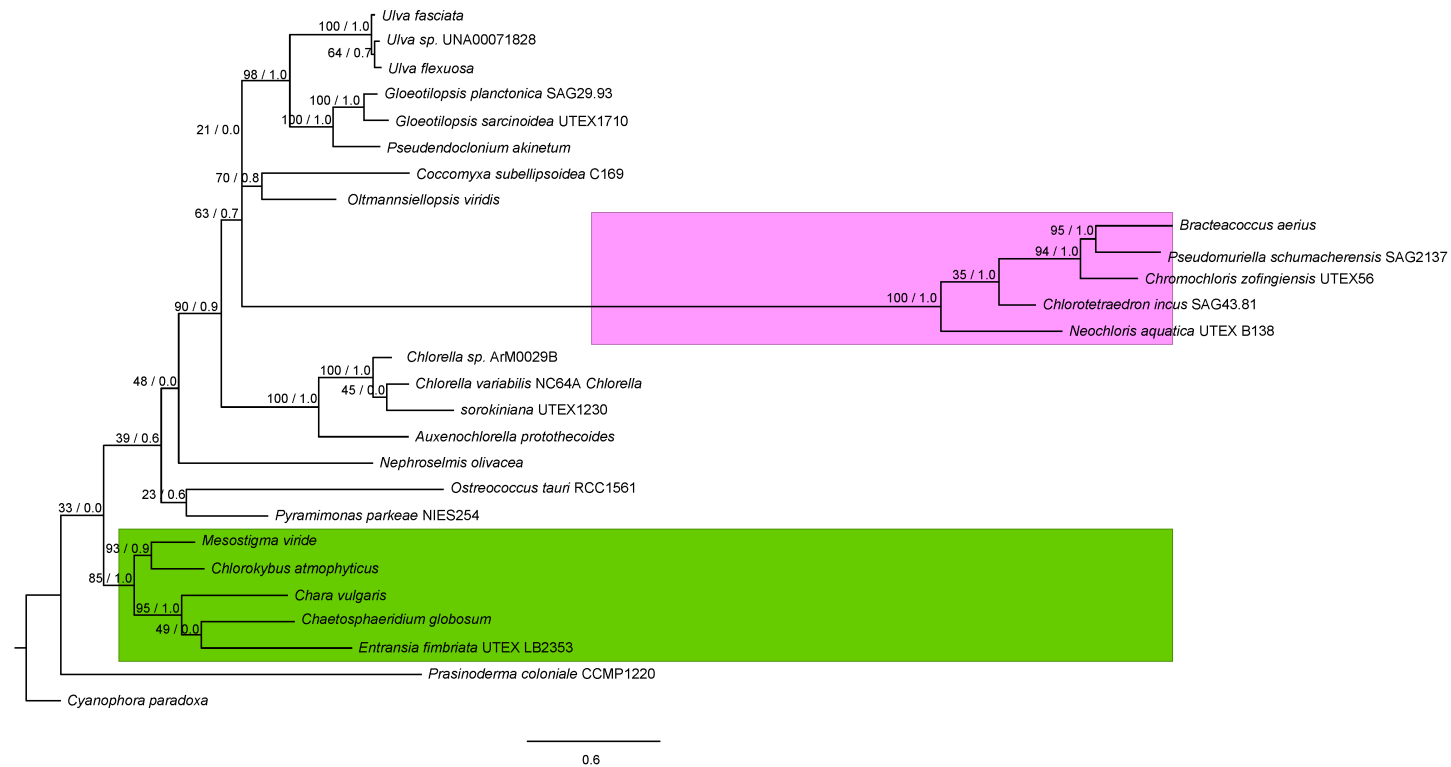


**S3 Fig. AE.** Maximum-Likelihood tree inferred from plastid *rpl16* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

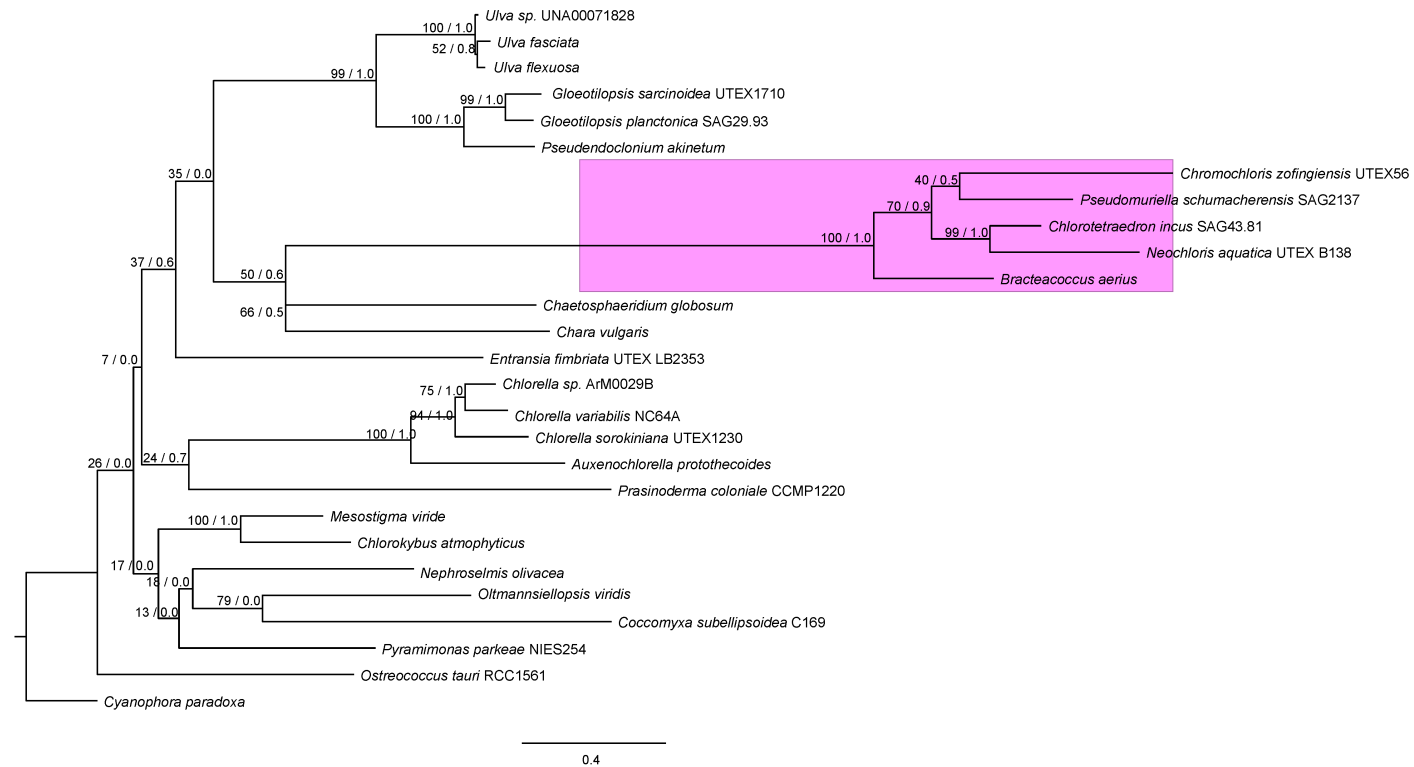


**S3 Fig. AF.** Maximum-Likelihood tree inferred from plastid *rpl20* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

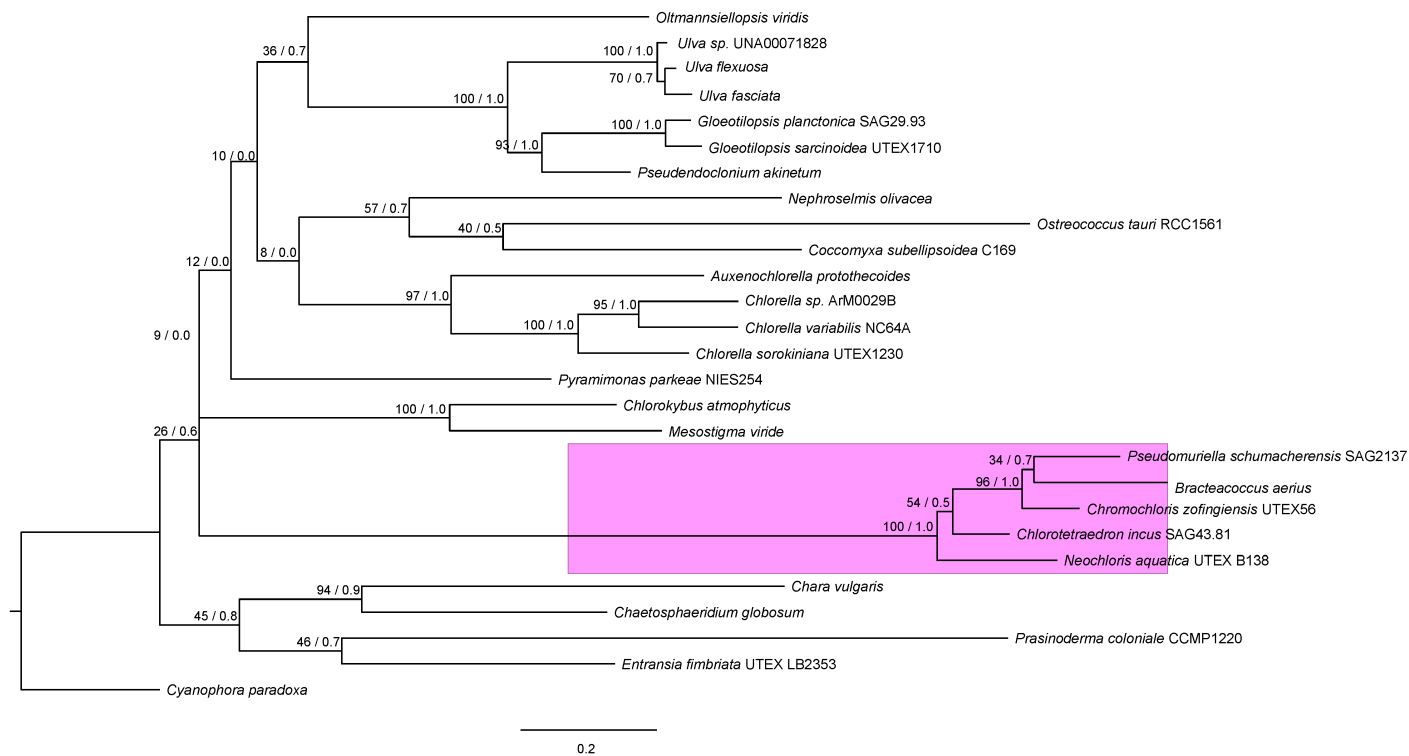




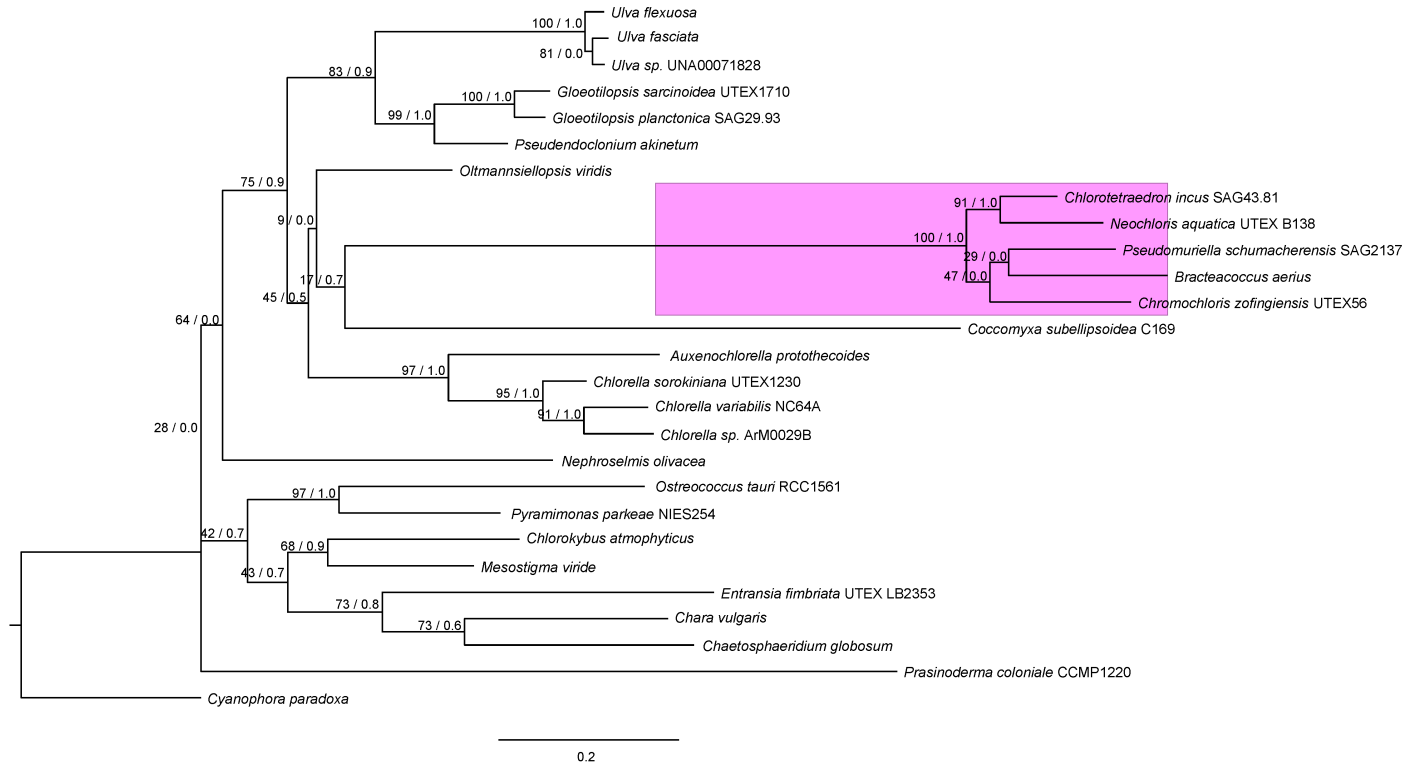
**S3 Fig. AG.** Maximum-Likelihood tree inferred from plastid *rps2* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



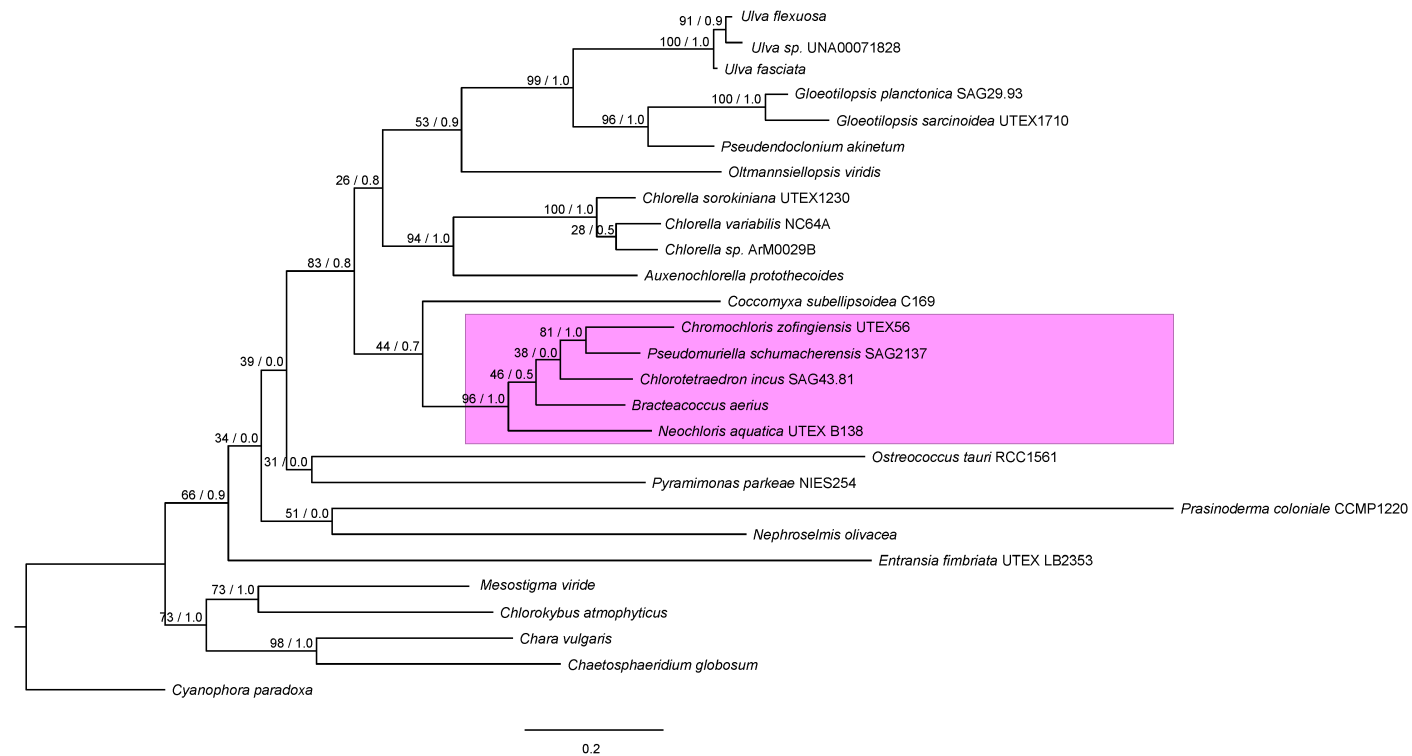
**S3 Fig. AH. Maximum-Likelihood tree inferred from plastid *rps3* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.**



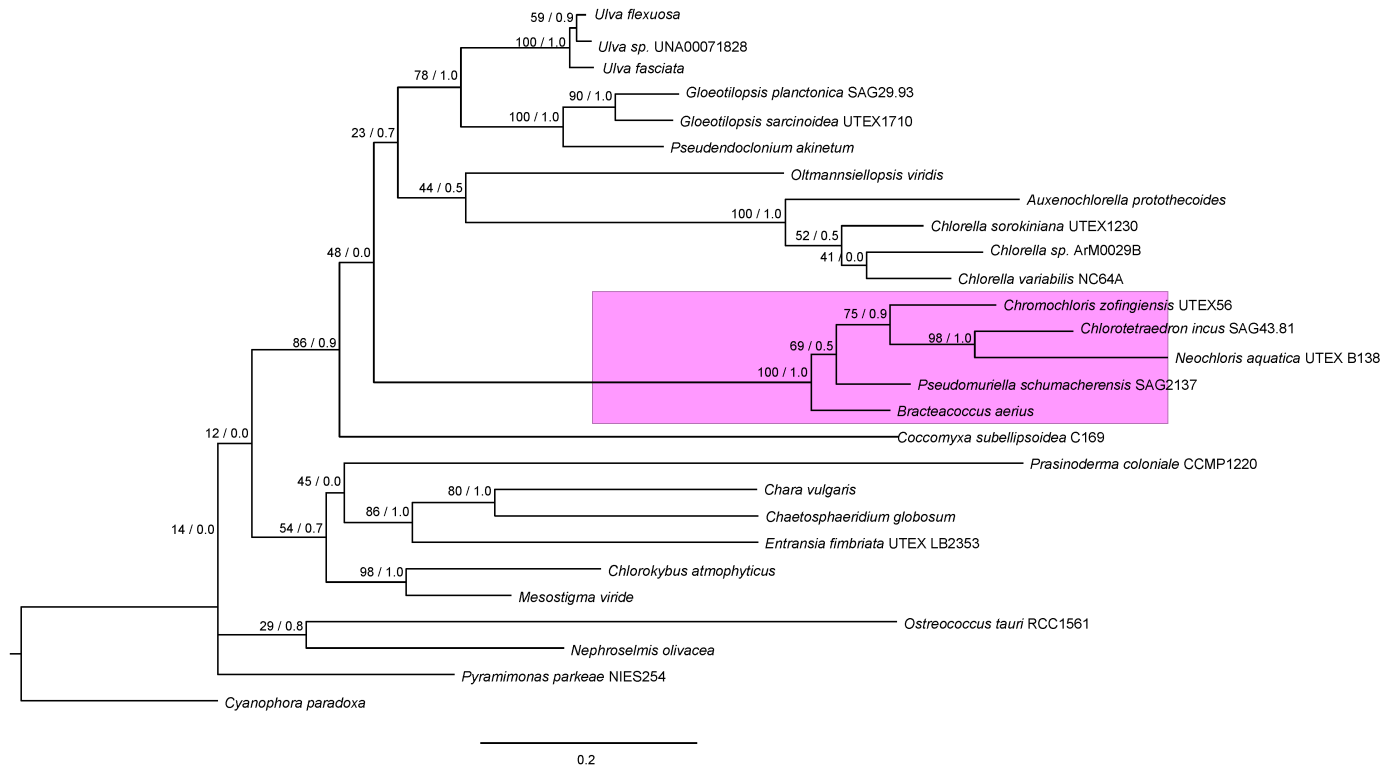
**S3 Fig. AI. Maximum-Likelihood tree inferred from plastid *rps4* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



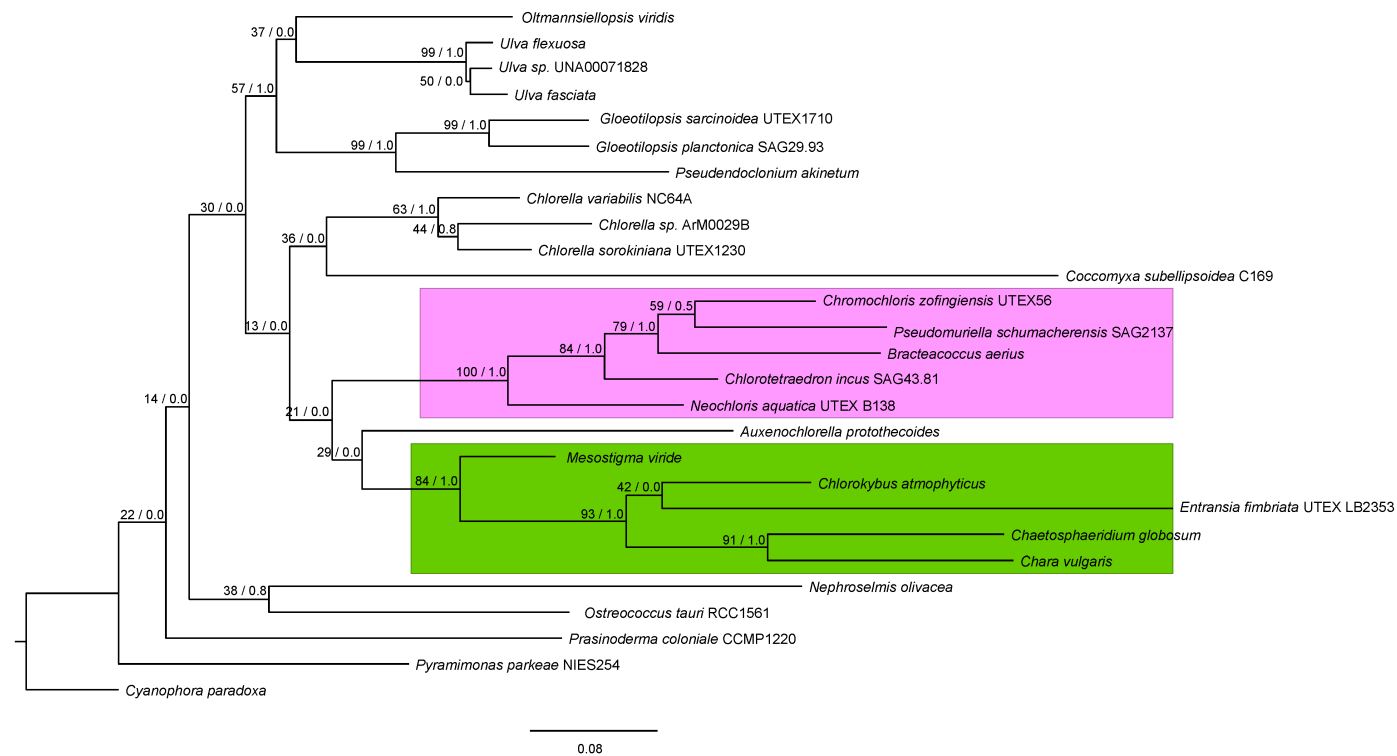
**S3 Fig. AJ. Maximum-Likelihood tree inferred from plastid *rps7* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



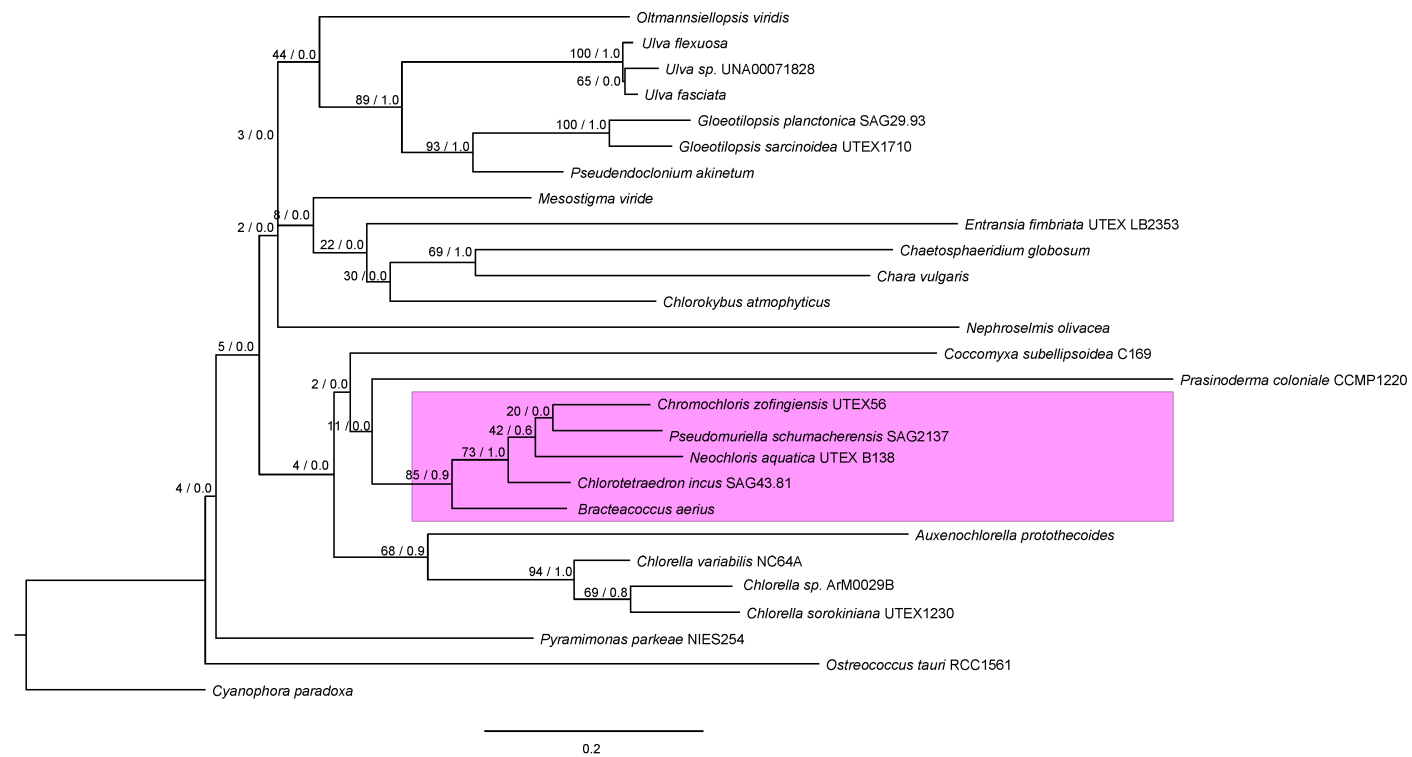
**S3 Fig. AK.** Maximum-Likelihood tree inferred from plastid *rps8* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. AL. Maximum-Likelihood tree inferred from plastid *rps11* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

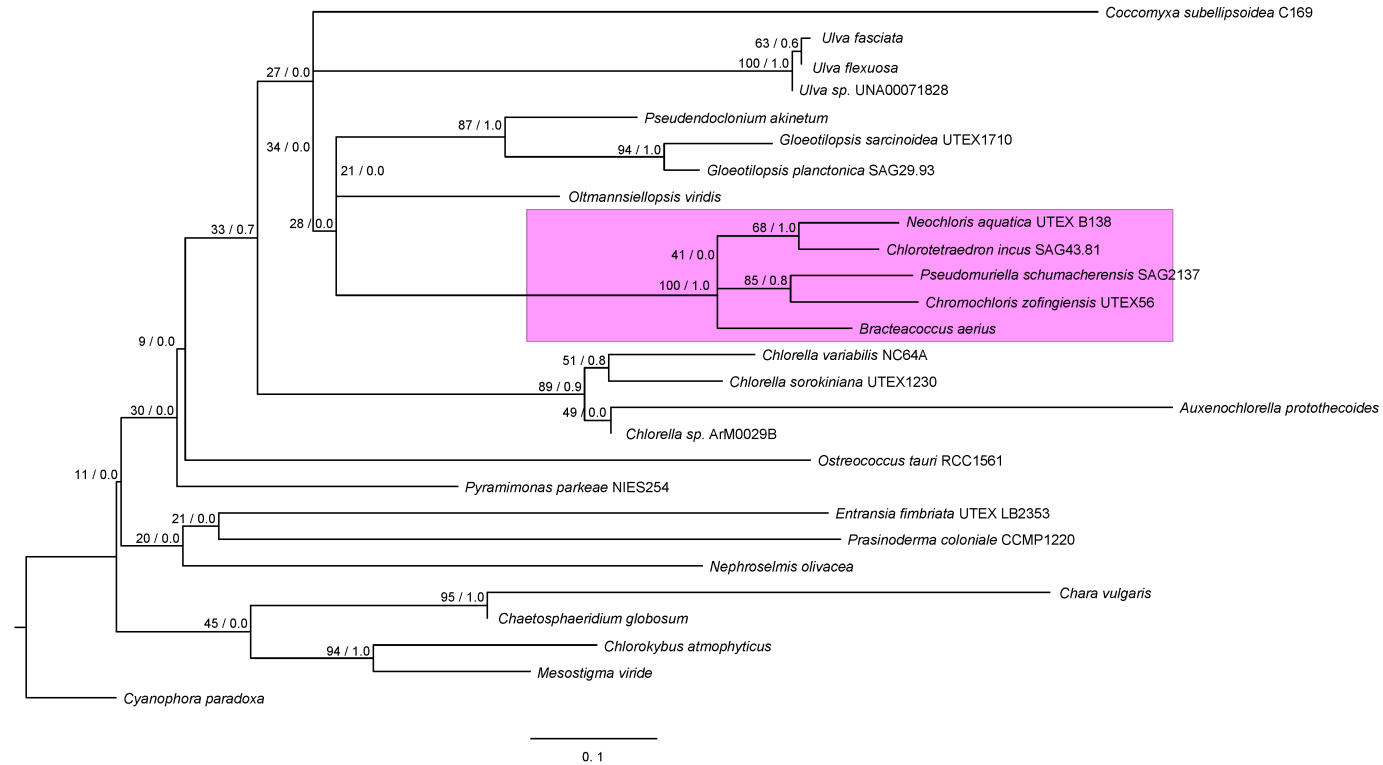


**S3 Fig. AM. Maximum-Likelihood tree inferred from plastid *rps12* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

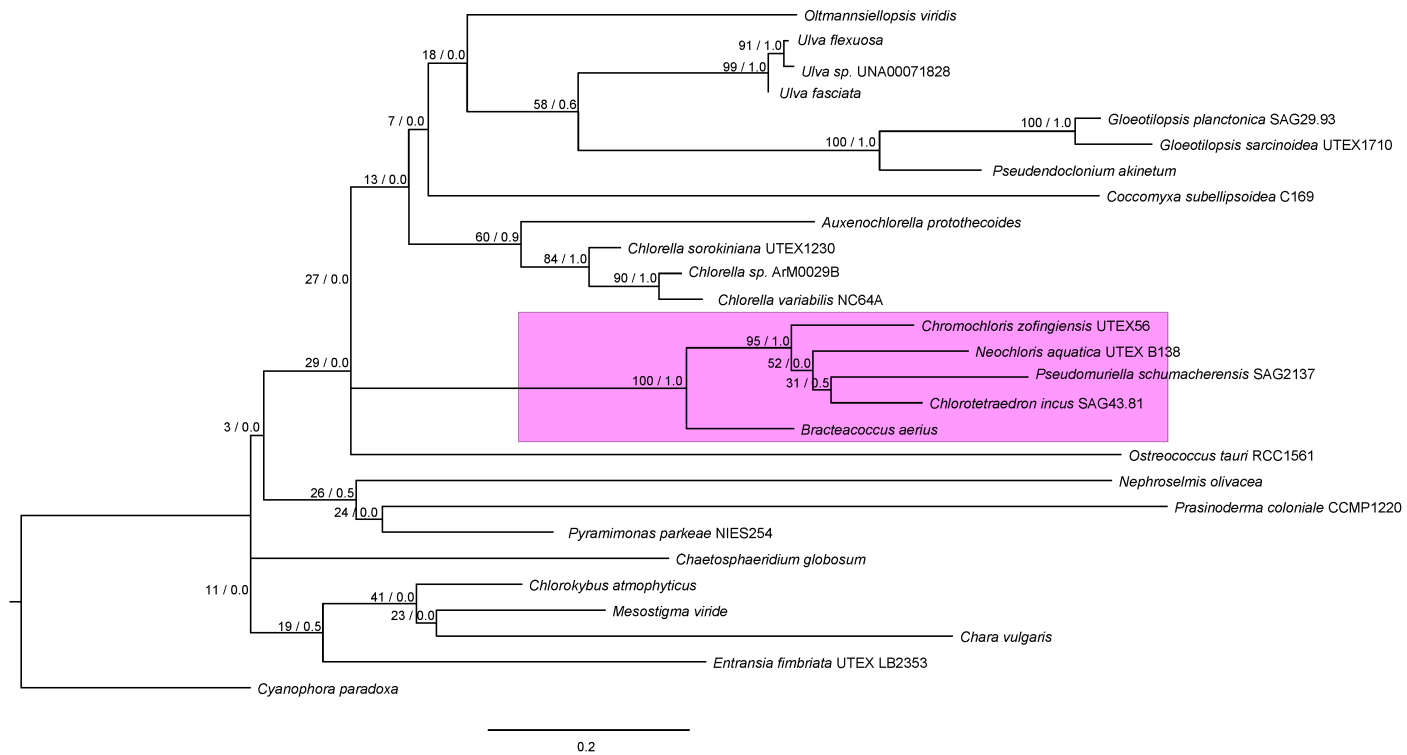


**S3 Fig. AN.** Maximum-Likelihood tree inferred from plastid *rps14* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

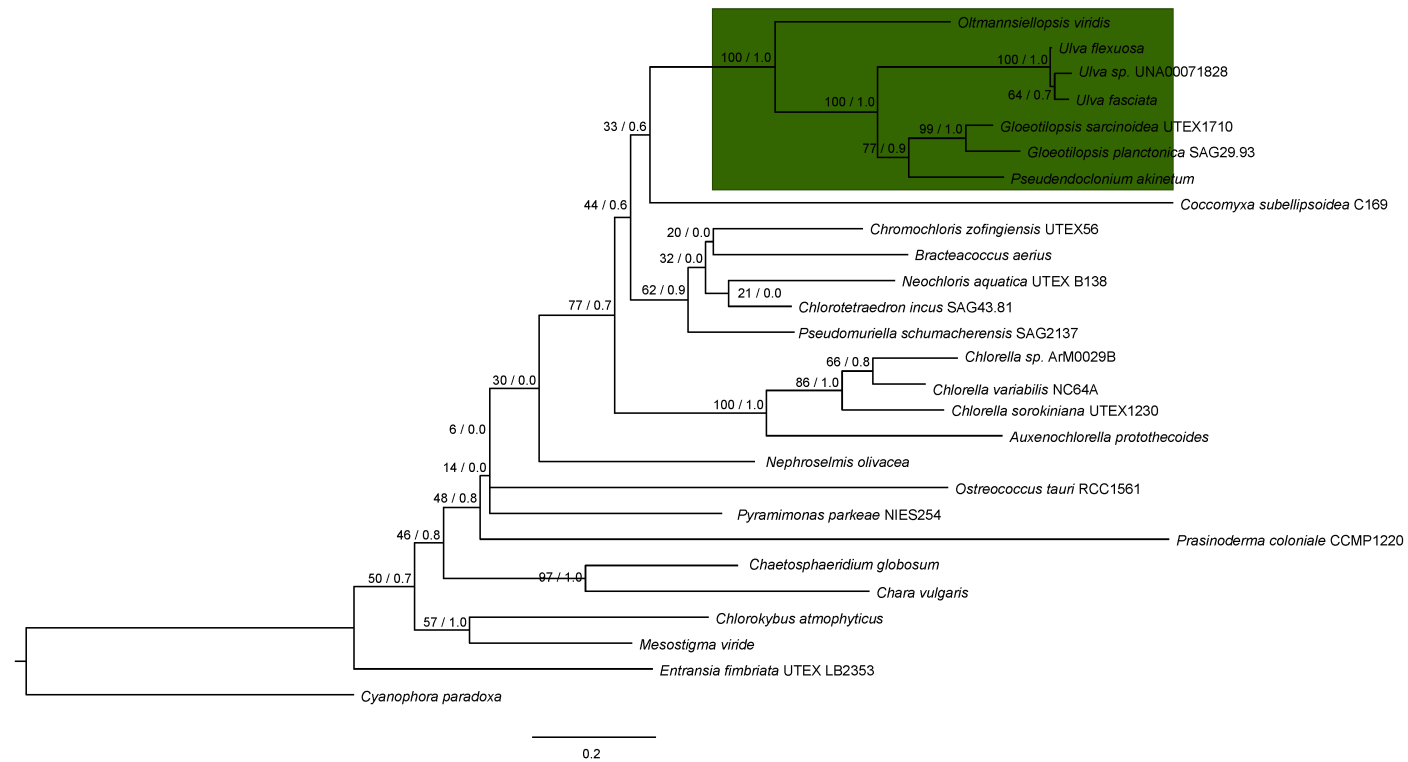




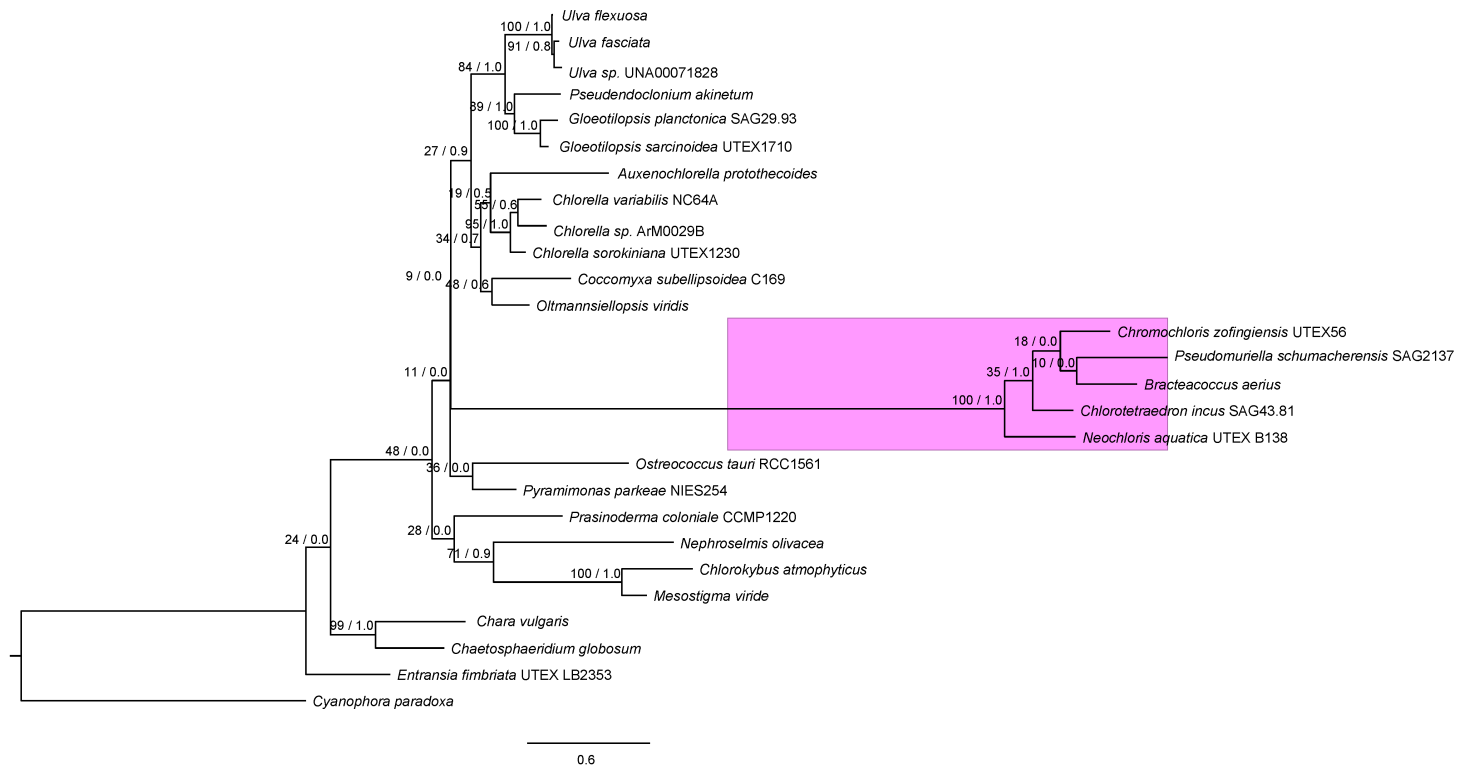
**S3 Fig. AO.** Maximum-Likelihood tree inferred from plastid *rps18* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



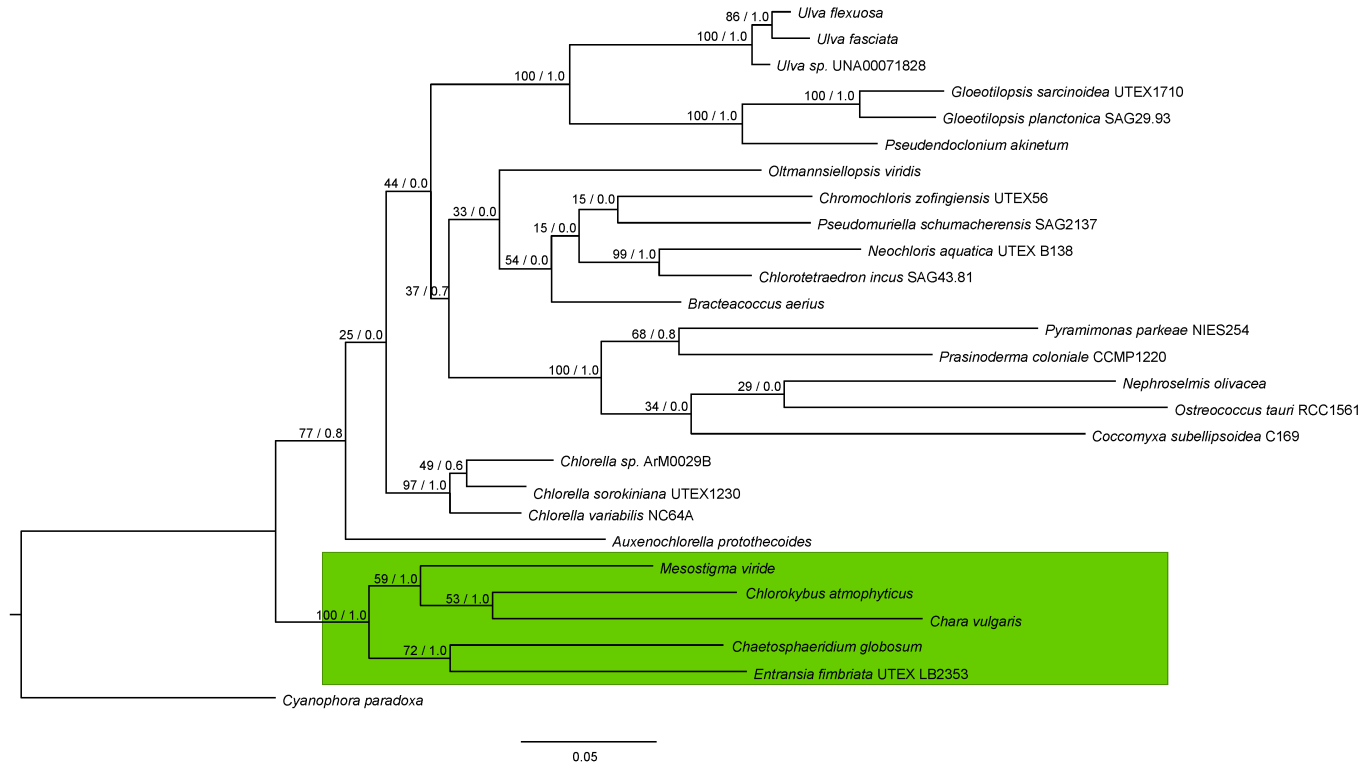
**S3 Fig. AP. Maximum-Likelihood tree inferred from plastid *rps19* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



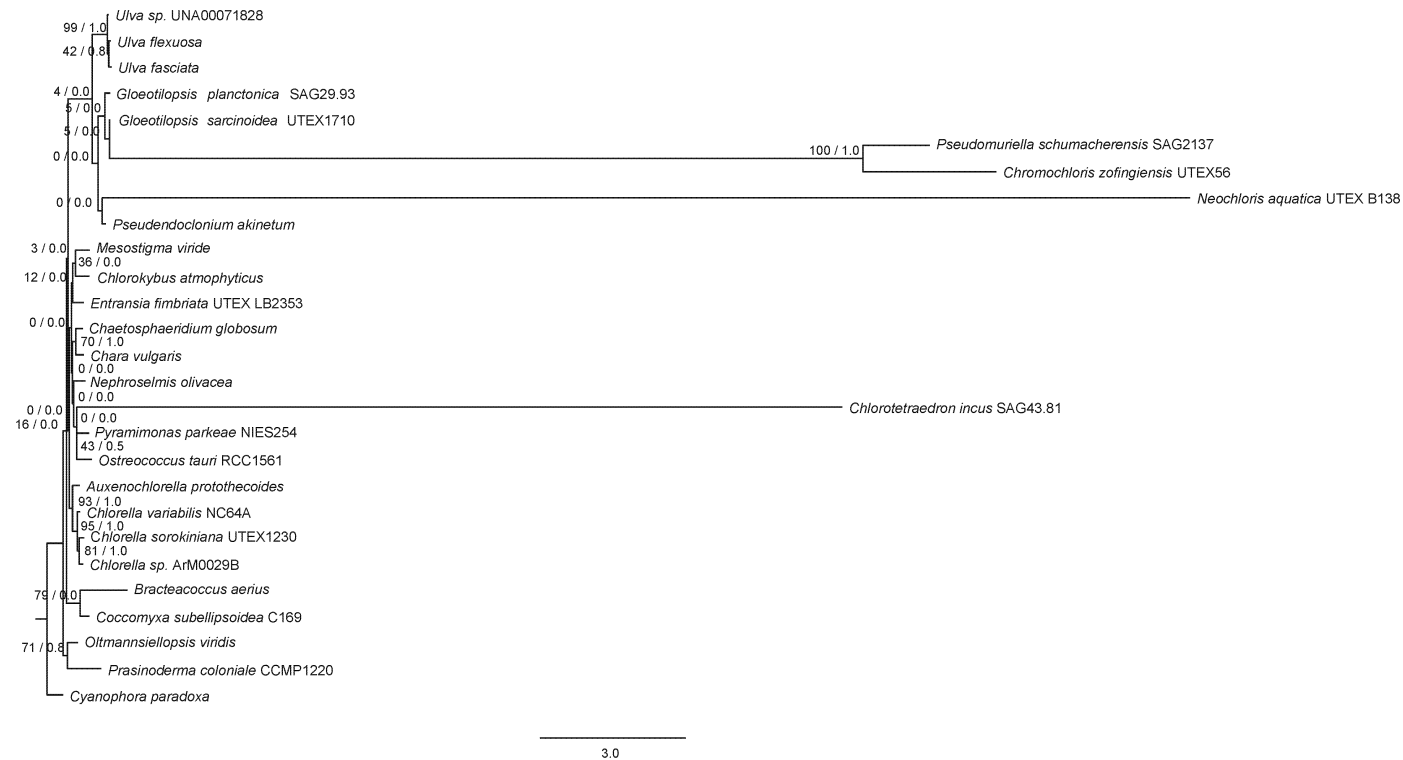
**S3 Fig. AQ.** Maximum-Likelihood tree inferred from plastid *ycf3* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



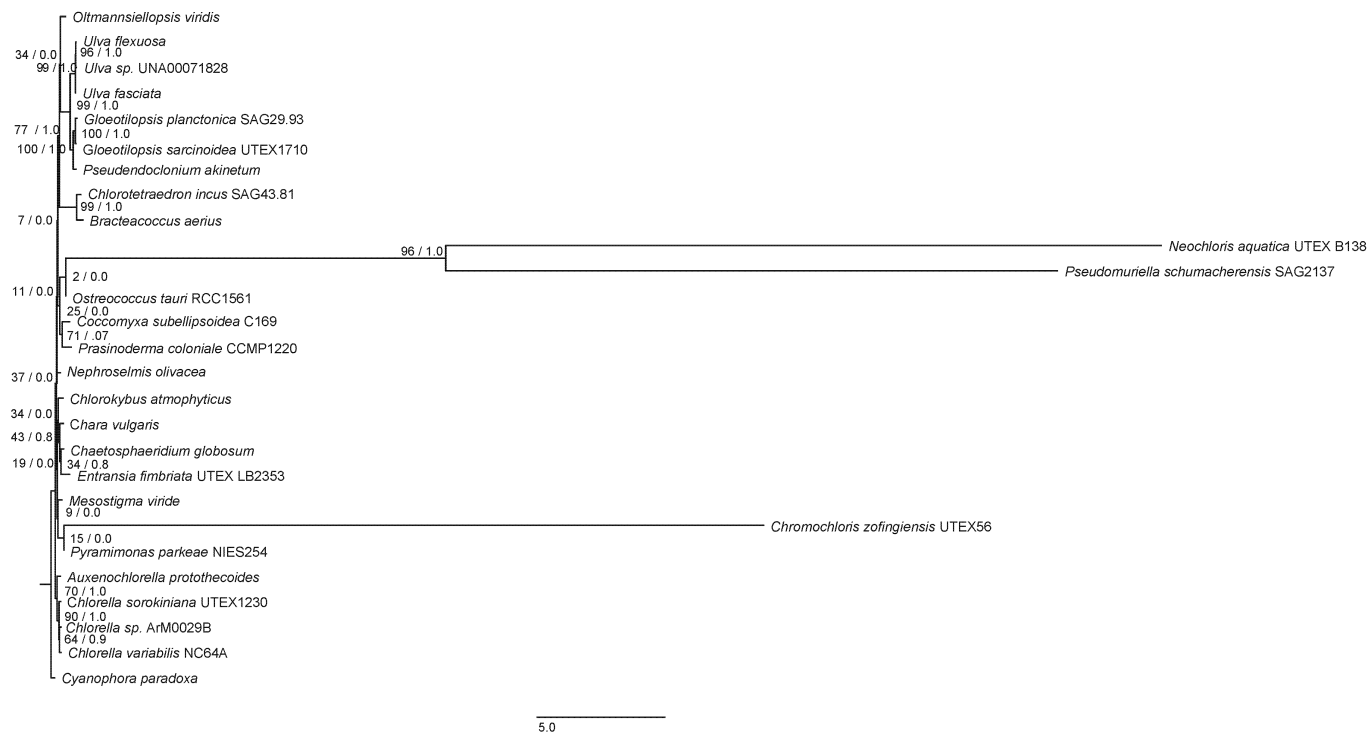
**S3 Fig. AR.** Maximum-Likelihood tree inferred from plastid *clpP* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



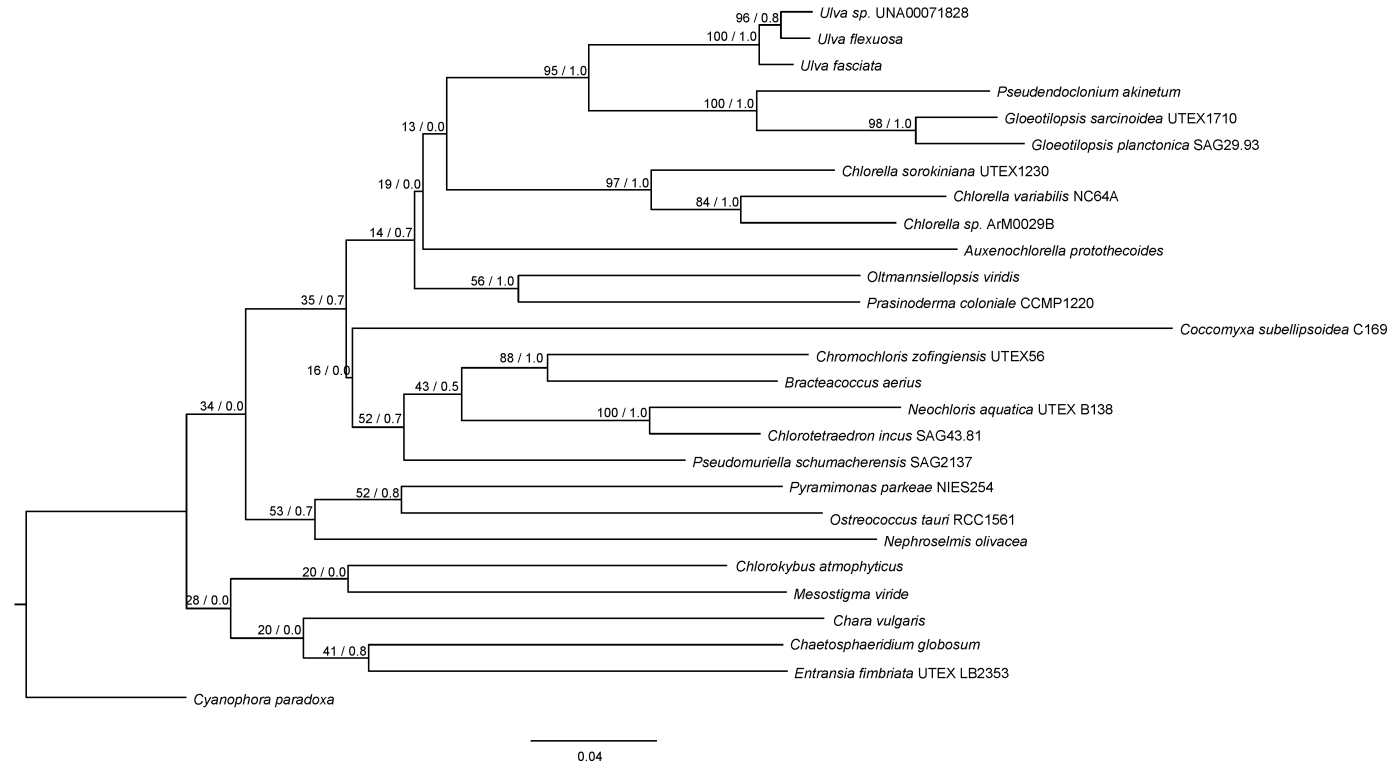
**S3 Fig. AS. Maximum-Likelihood tree inferred from plastid *rbcL* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. AT. Maximum-Likelihood tree inferred from mitochondrial *cob* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

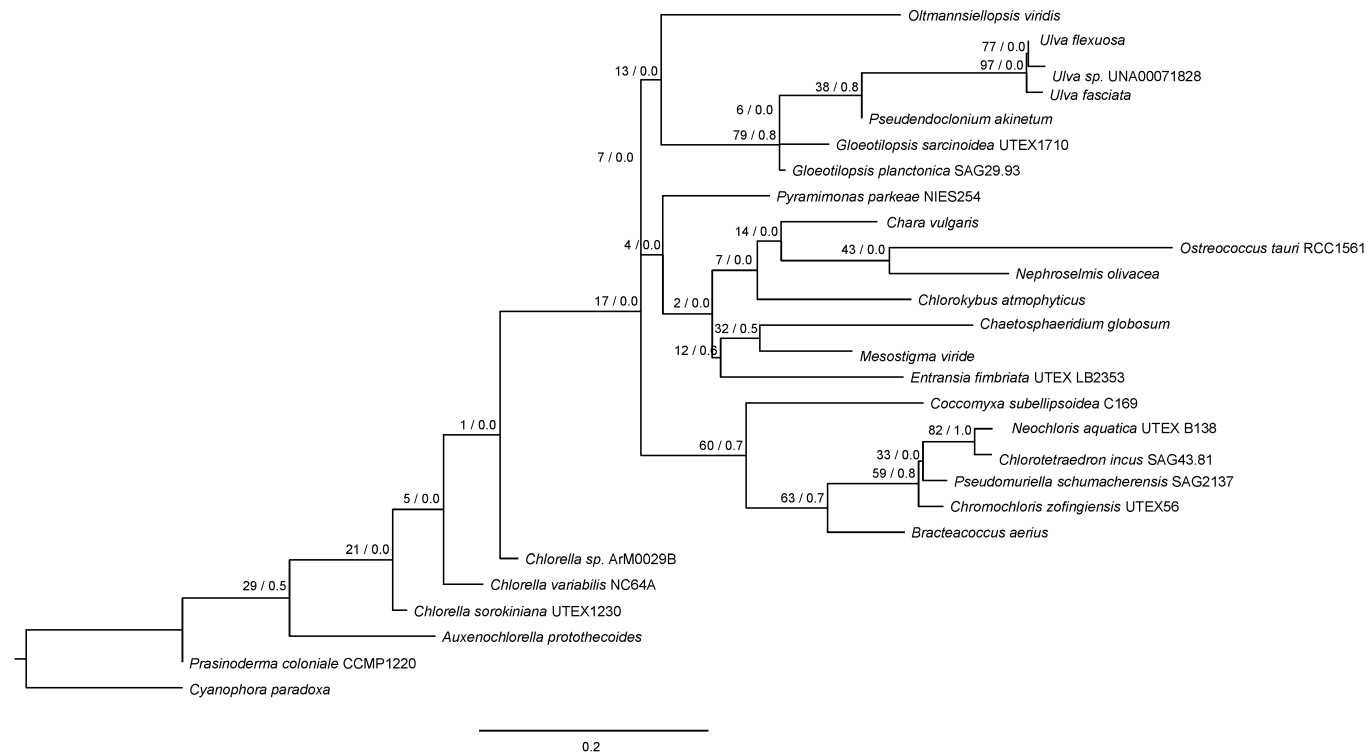


**S3 Fig. AU. Maximum-Likelihood tree inferred from mitochondrial *cox1* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.**

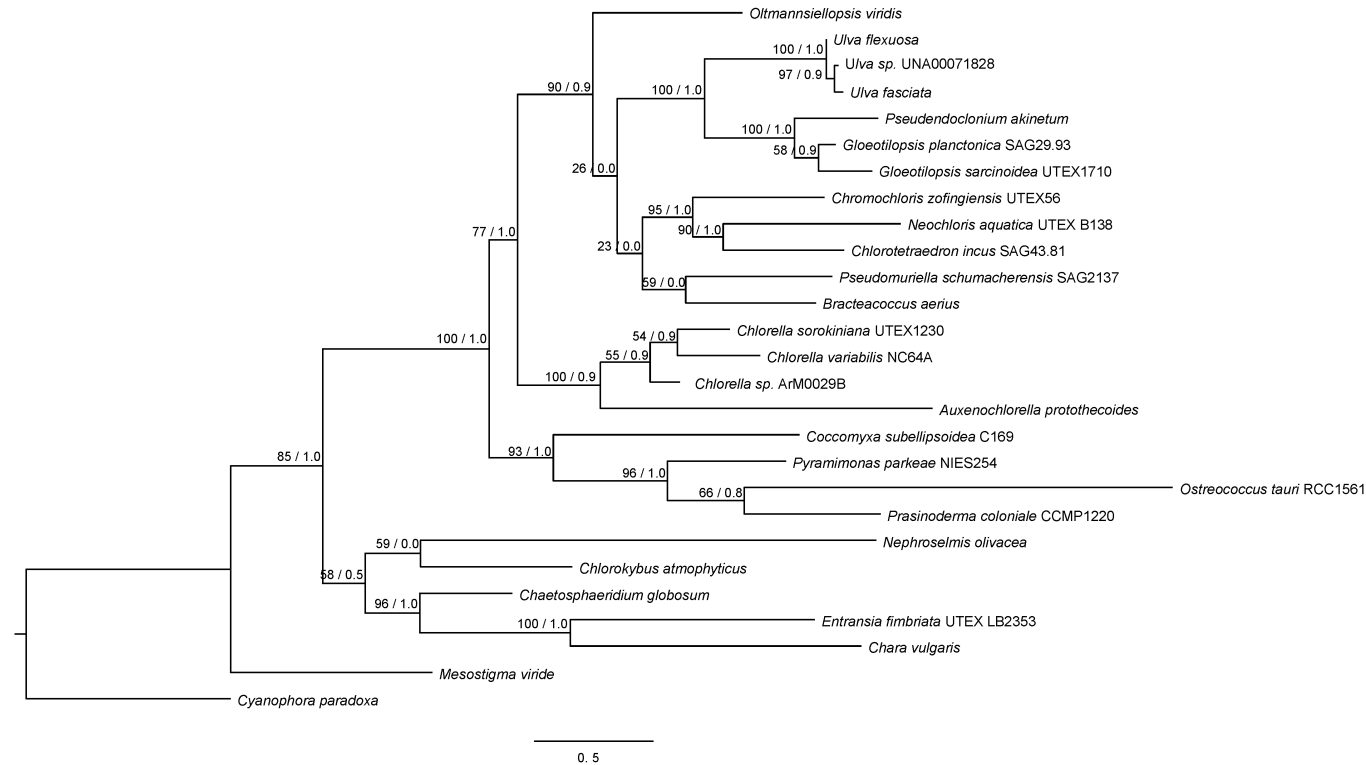


**S3 Fig. AV.** Maximum-Likelihood tree inferred from plastid *petB* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

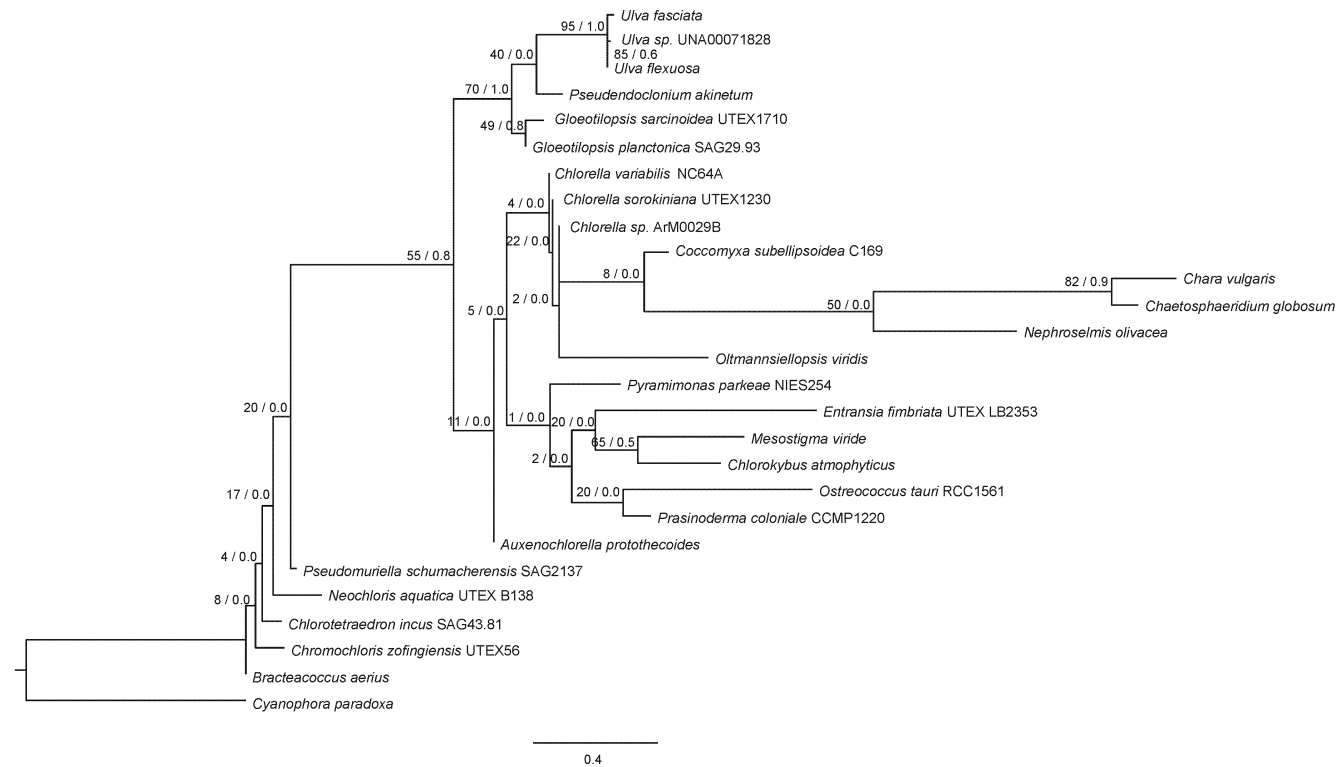




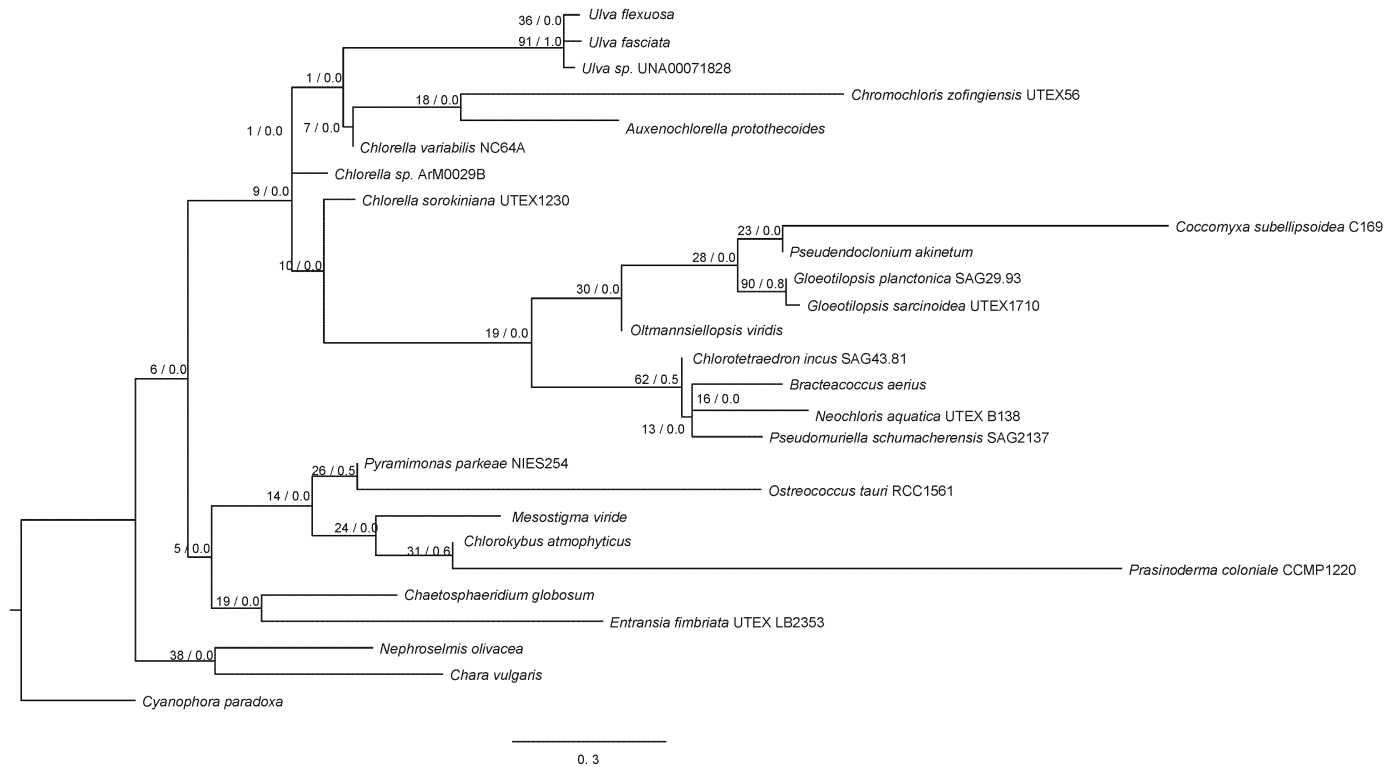
**S3 Fig. AW.** Maximum-Likelihood tree inferred from plastid *petG* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



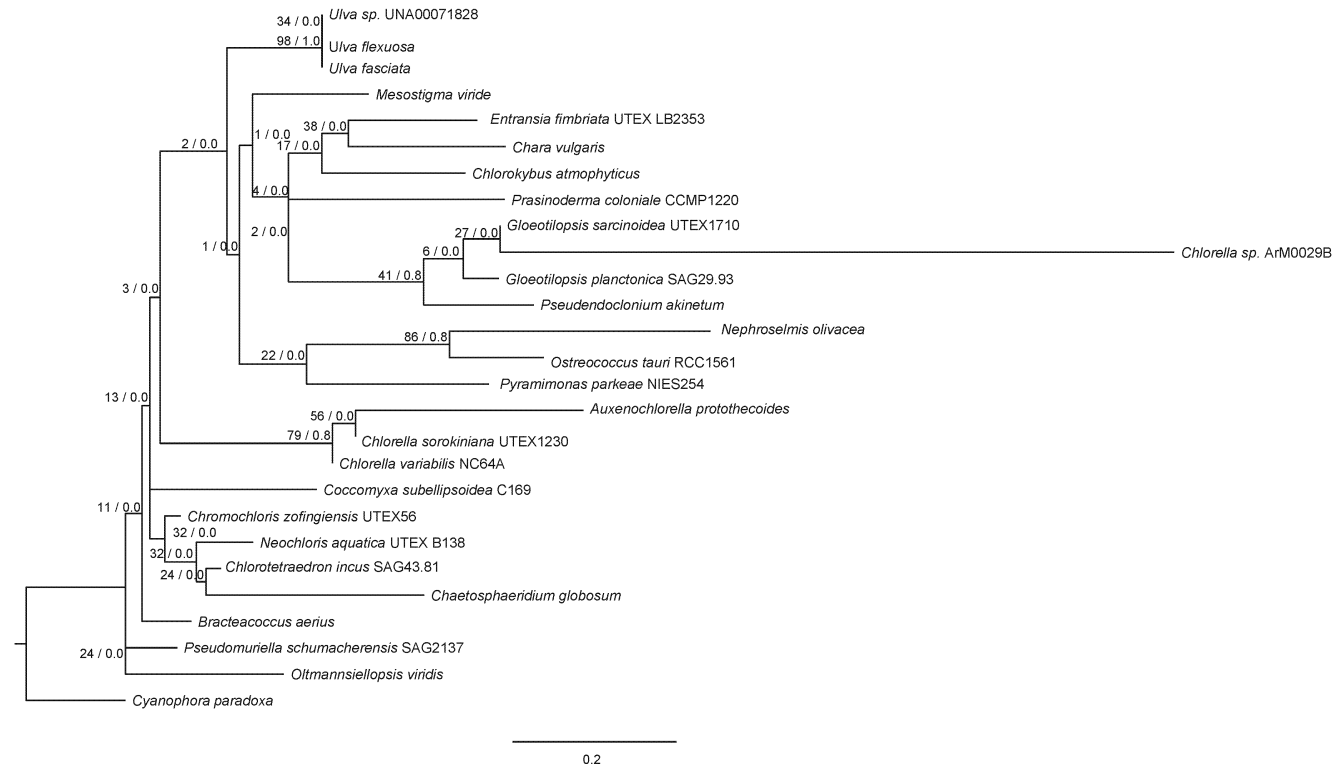
**S3 Fig. AX.** Maximum-Likelihood tree inferred from plastid *psbA* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



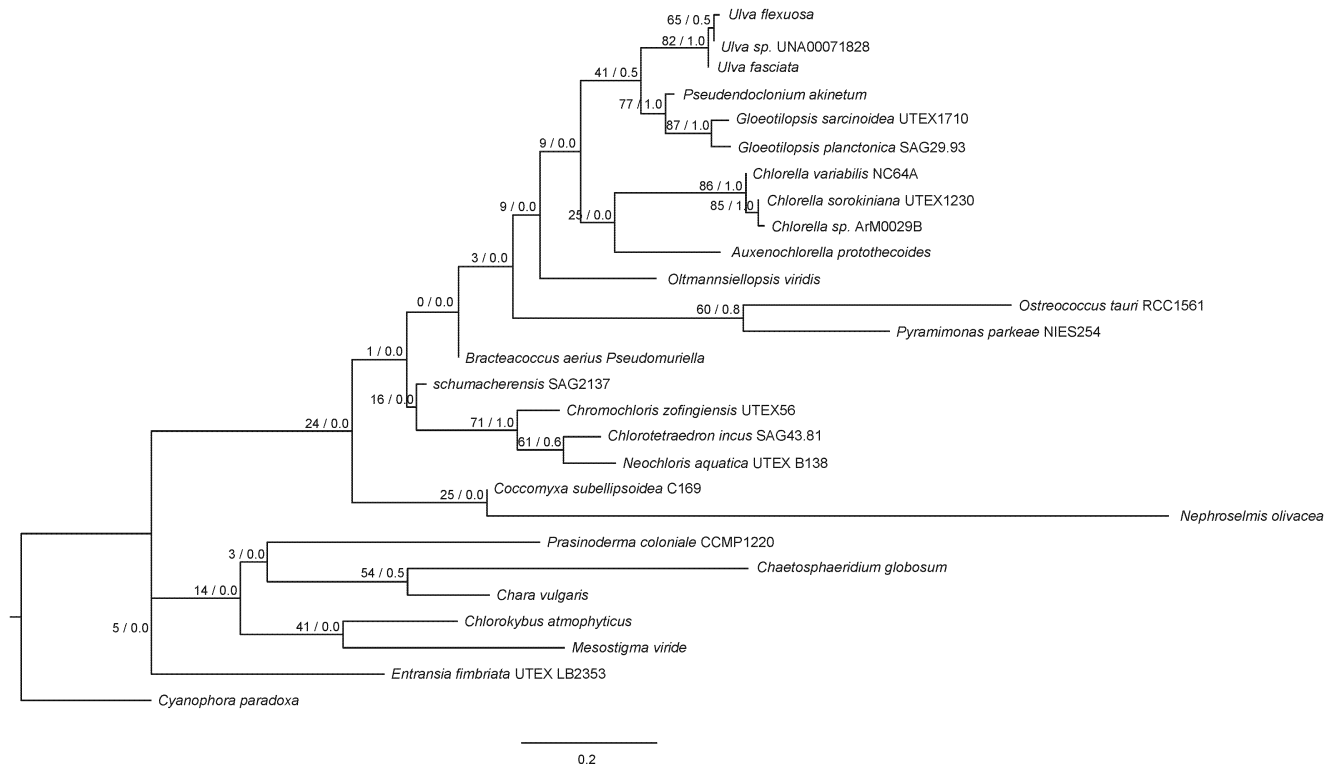
**S3 Fig. AY.** Maximum-Likelihood tree inferred from plastid *psbF* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



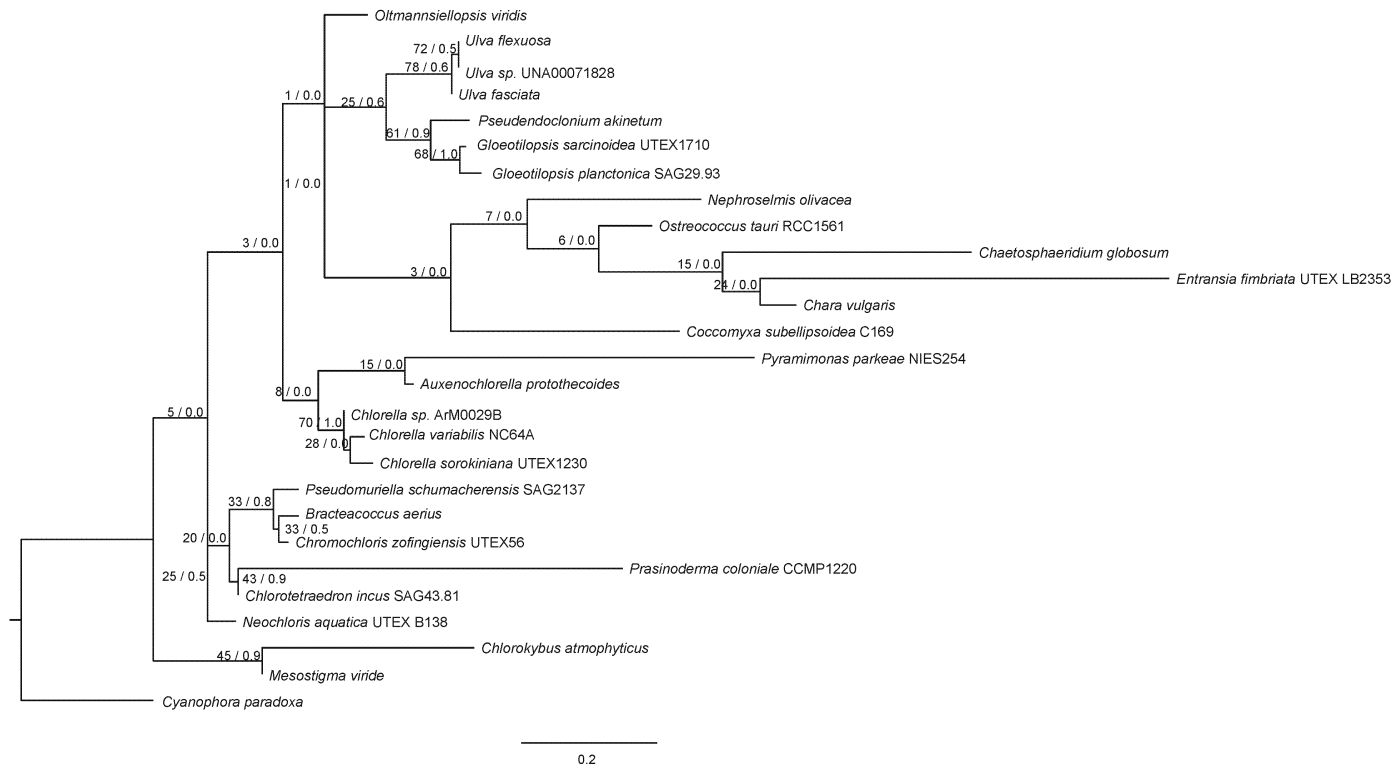
**S3 Fig. AZ.** Maximum-Likelihood tree inferred from plastid *psbI* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



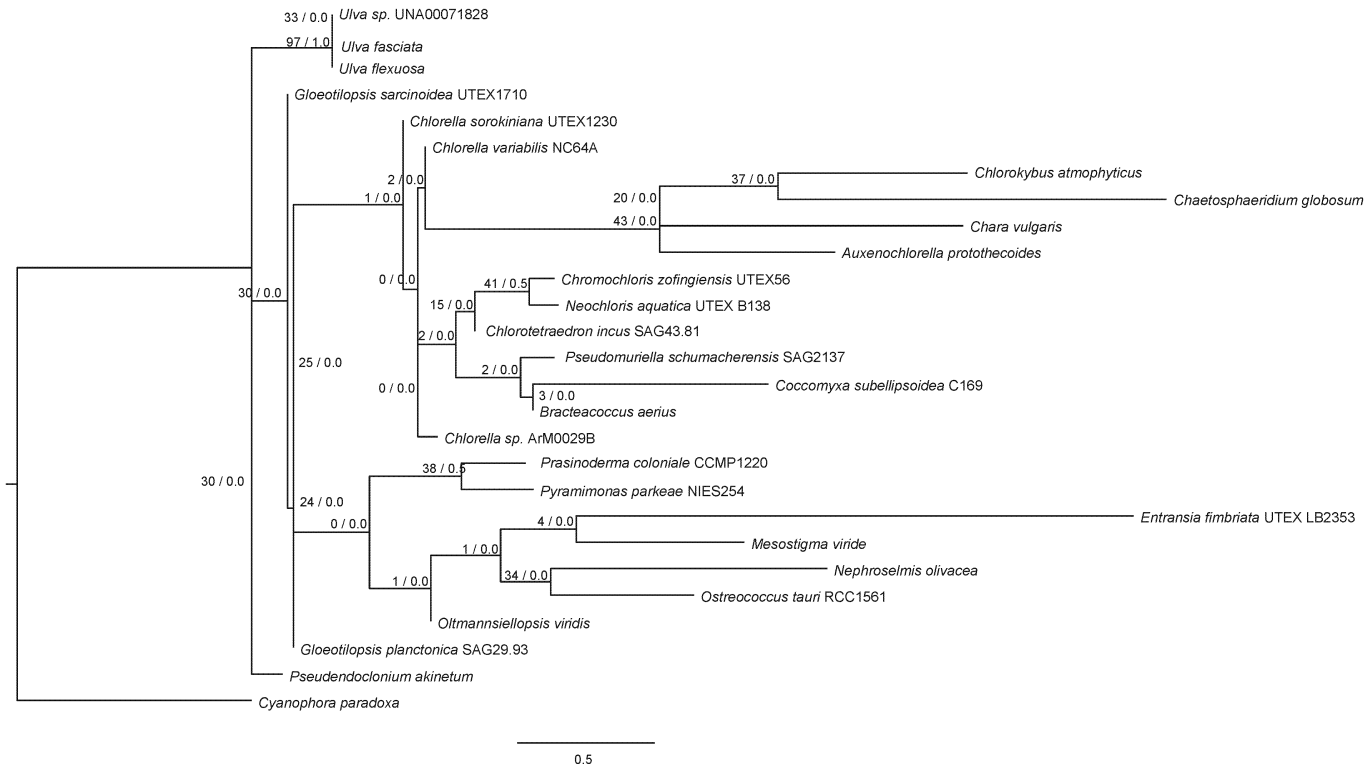
**S3 Fig. BA. Maximum-Likelihood tree inferred from plastid *psbJ* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.**



**S3 Fig. BB. Maximum-Likelihood tree inferred from plastid *psbK* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

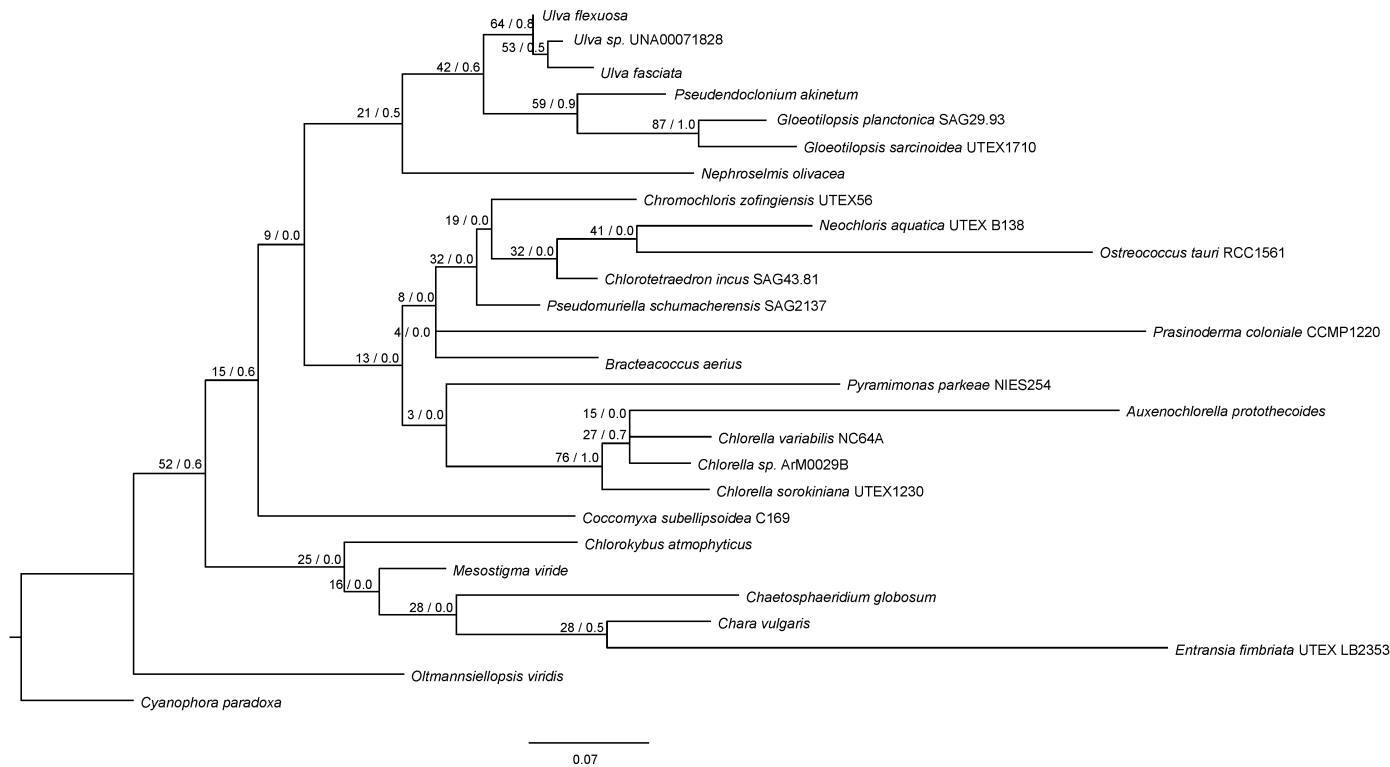


**S3 Fig. BC. Maximum-Likelihood tree inferred from plastid *psbL* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

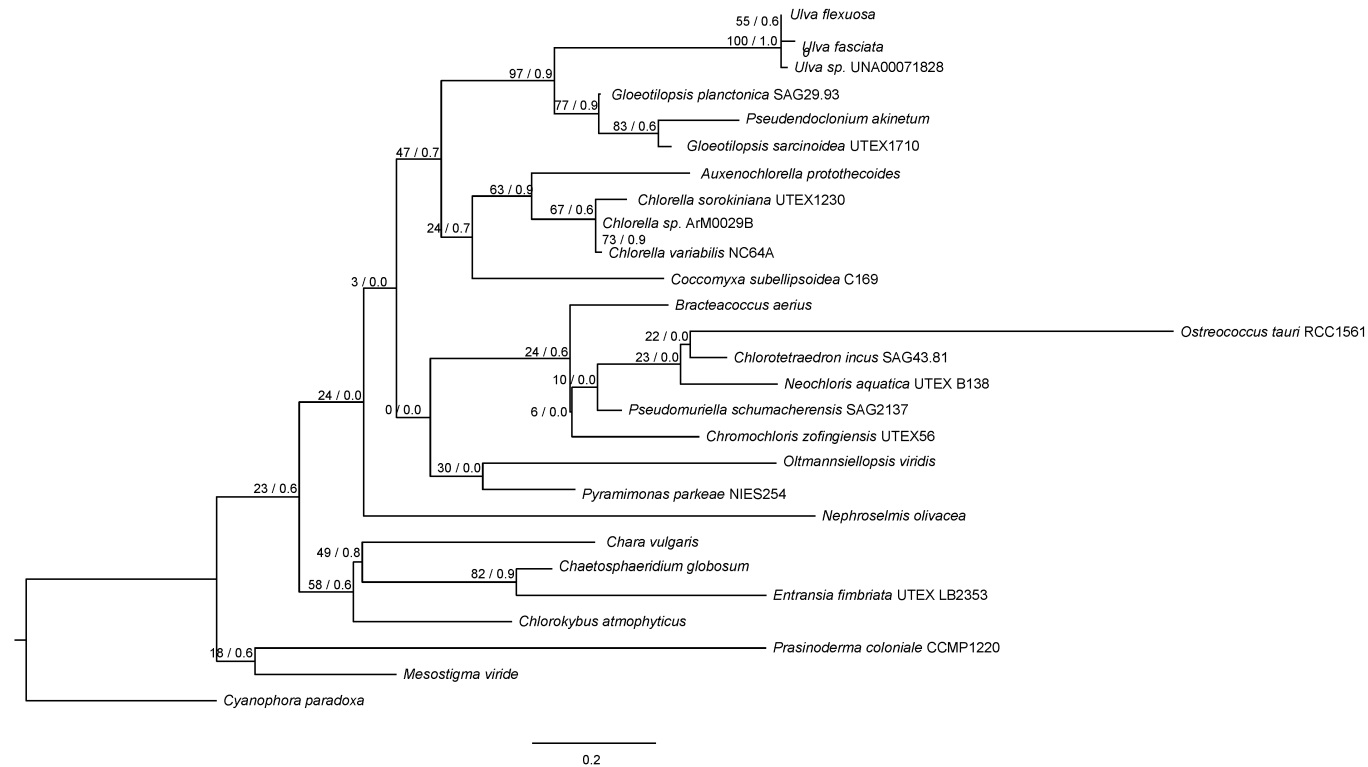


**S3 Fig. BD. Maximum-Likelihood tree inferred from plastid *psbT* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.

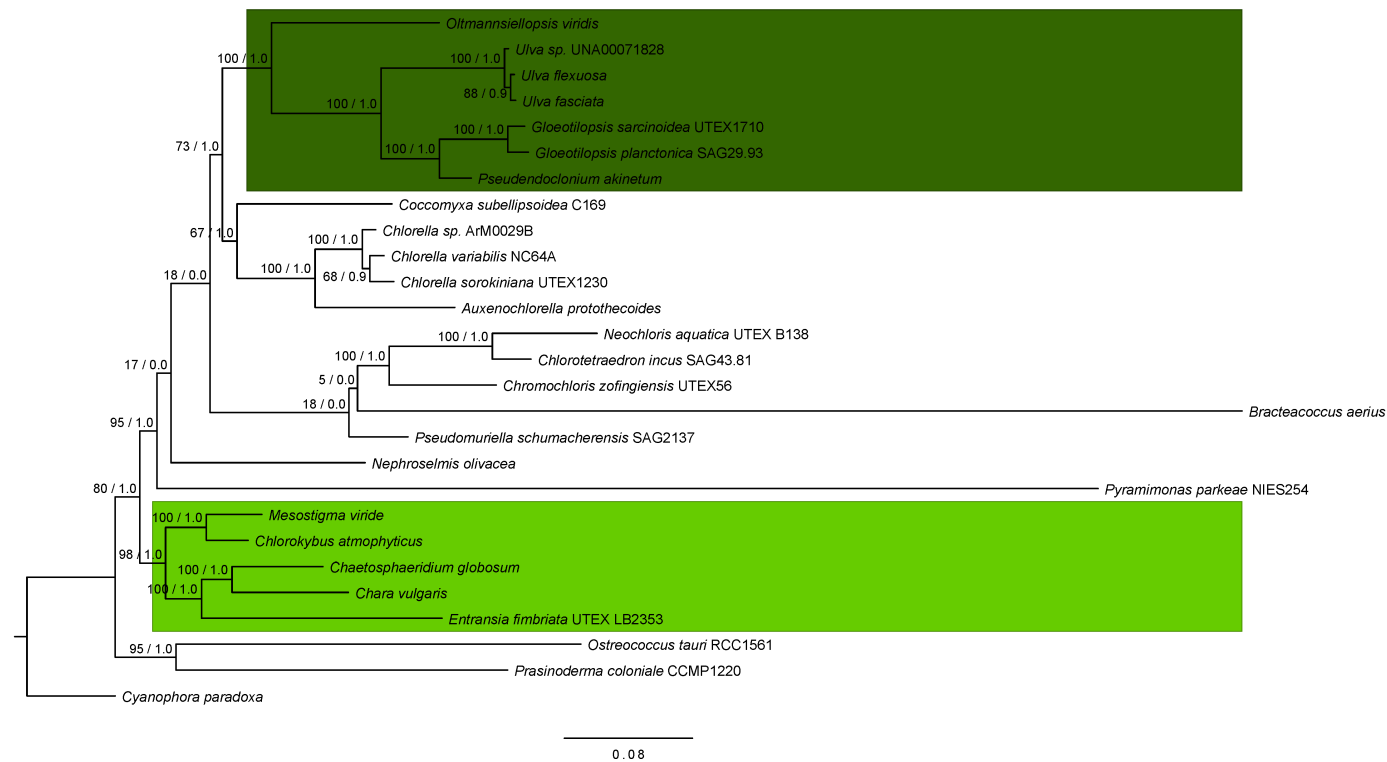




**S3 Fig. BE. Maximum-Likelihood tree inferred from plastid *rpl36* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. BF. Maximum-Likelihood tree inferred from plastid *ycf12* of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model.** Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.



**S3 Fig. BG.** Maximum-Likelihood tree inferred from 2 rDNA sequences (*rrnL* and *rrs*) of algal taxa in Table 1 using a GTR+ $\Gamma$ +I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.