Additional File

Title: Supporting materials for the study.

Sequences used in this study.

Protein	Taxon	Sequence Accession Number
WECE	*Seculamonas ecuadoriensis*	EC816654; EC816654
	Jakoba bahamiensis	EC686674, EC685007, EC684822
	Sawyeria marylandensis	EC826207
MVIM	*Karlodinium micrum*	EC160173
	Jakoba bahamiensis	EC687464, EC685628
	Sawyeria marylandensis	EC825128
Epimerase	*Phytophthora ramorum*	jgi|Phyra1_1|73107|fgenesh1_pg.C_scaffold_2000172*
	Thalassiosira pseudonana	jgi|Thaps3|35046|e_gw1.6.331.1*
	Giardia lamblia	XP_769114, AAO39053
	Spironucleus barkhanus	ABI15605
CAS -like	*Karlodinium micrum*	EC156868, EC158513, EC148099, EC160669
	Alexandrium tamarense	CK784871
	Emiliania huxleyi	CF753752
	Isochrysis galbana	EC140831
	Chlamydomonas reinhardtii	jgi|Chlre3|127464|estExt_gwp_1H.C_20095*
	Ostreococcus lucimarinus	jgi|Ostta4|35883|1200010181*
	Ostreococcus tauri	jgi|Ost9901_3|26795|eugene.1200010140*
MQO-DH	*Karlodinium micrum*	EC161113, EC156079, EC151820
	Alexandrium tamarense	CF948531, CV554334
	Heterocapsa triquetra	DT382779
	Emiliania huxleyi	CX779033
MQO-A	*Plasmodium yoelii*	EAA17232
	Plasmodium berghei	CAH94470
	Plasmodium chabaudi	XP_742339
	Plasmodium falciparum	CAG25406
	Toxoplasma gondii	ABE76504
	Eimeria tenella	CAK51433
mtMDH	*Karlodinium micrum*	EC154776
	Alexandrium tamarense	CK784465
	Isochrysis galbana	EC147060, EC147055
cytMDH	*Isochrysis galbana*	EC143180, EC146073
	Pavlova lutheri	EC176556, EC176389, EC176299
NADP-IDH	*Karlodinium micrum*	EC155818, EC150415
	Alexandrium tamarense	CK433031, CK784788, CK783806
	Amphidinium carterae	CF065460, CF064816
	Heterocapsa triquetra	DT385947, DT385631

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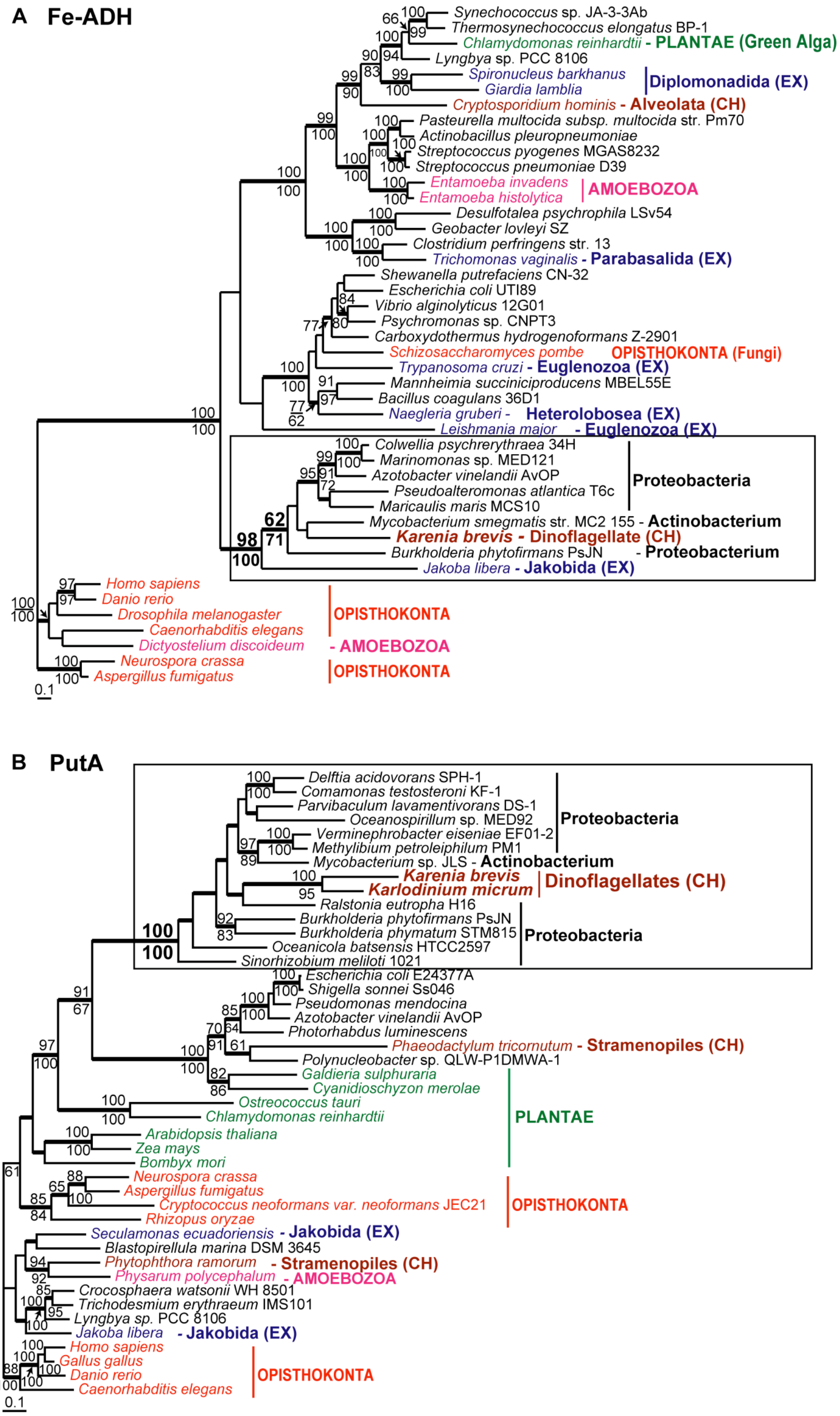
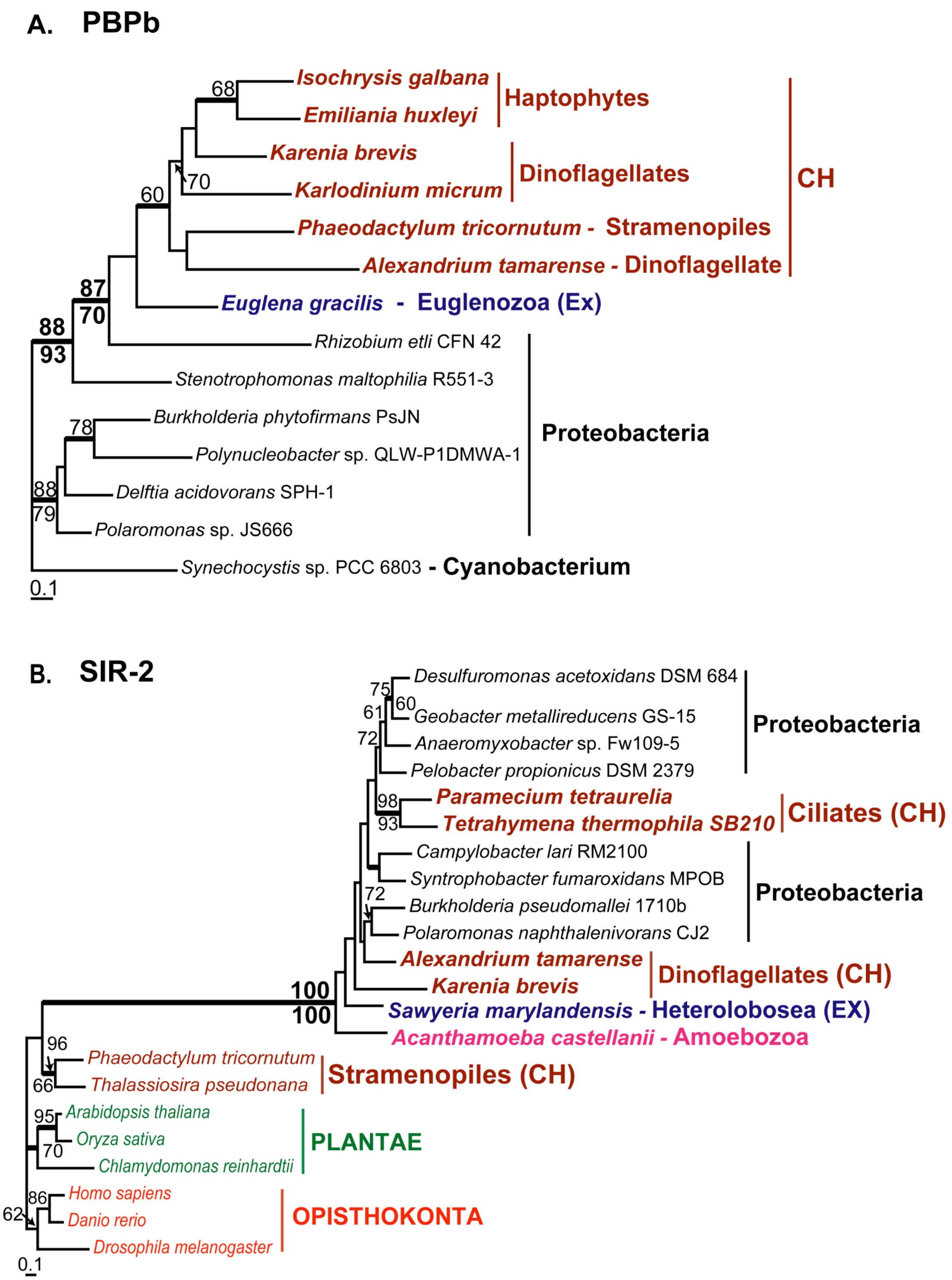
	Pavlova lutheri	EC177146, EC177552, EC176343
	Phytophthora ramorum	jgi|Phyra1_1|71206|fgenesh1_pm.C_scaffold_8000012*
	Phytophthora sojae	jgi|Physo1_1|109259|estExt_fgenesh1_pm.C_810006*
	Thalassiosira pseudonana	jgi|Thaps3|269148|estExt_thaps1_ua_kg.C_chr_60290*
	Jakoba libera	EC692709, EC692770, EC690987
	Cyanophora paradoxa	EC660009, EG946313, EG944985, EG946356
	Glaucocystis nostochinearum	EC124674

Note: All sequences except for the sequences labeled with "*" and "**" are available from the GenBank nonredundant data base and dbEST (http://www.ncbi.nlm.nih.gov/). Sequences labeled with "*"are available from the DOE Joint Genome Institute (JGI) (http://www.jgi.doe.gov/); "**" – from the *Cyanidioschyzon merolae* Genome Project database (http://merolae.biol.s.u-tokyo.ac.jp/



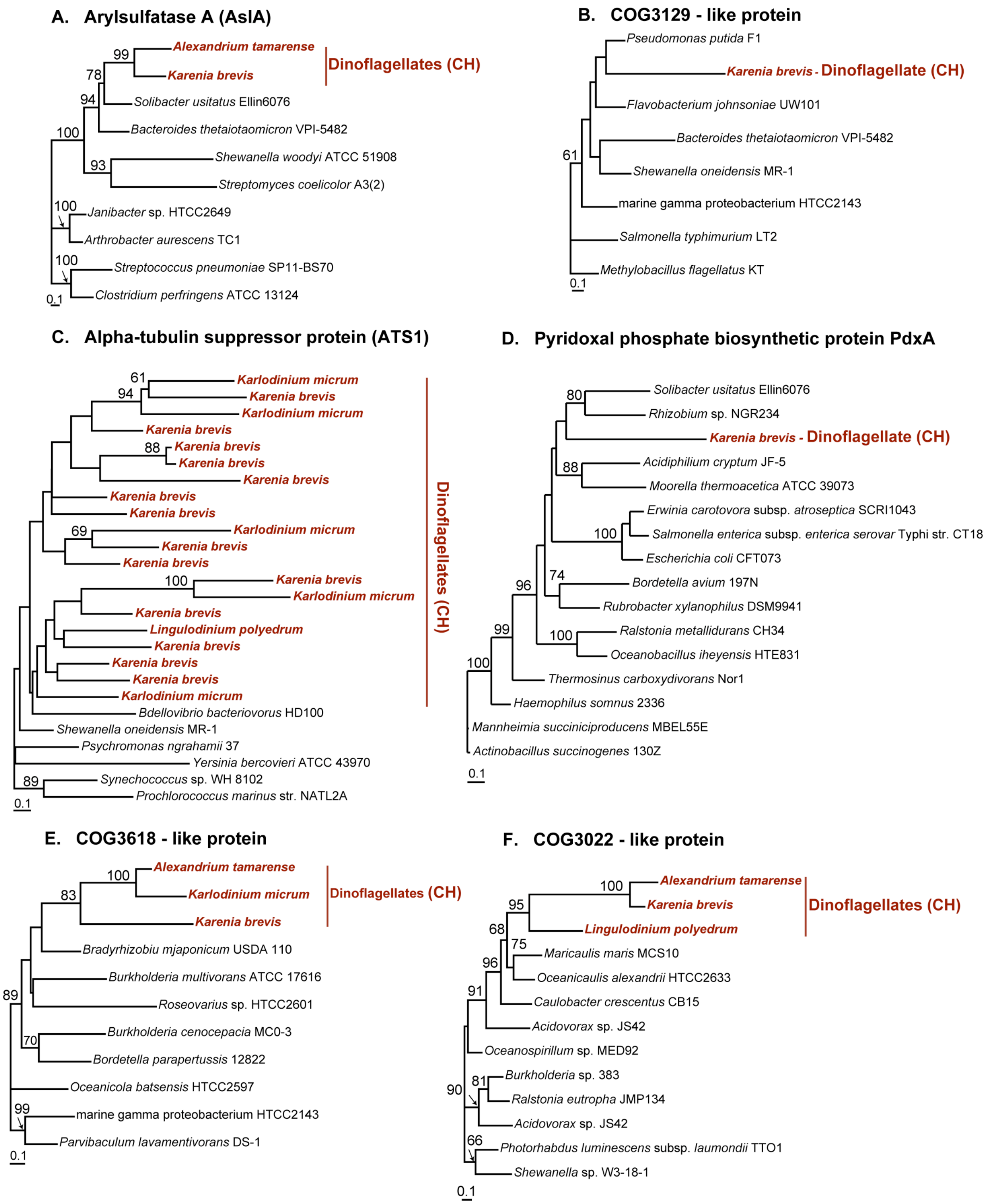
Origins of iron-containing alcohol dehydrogenase (Fe-ADH) and NAD-dependent aldehyde dehydrogenase (PutA) in eukaryotes by multiple HGTs

A. ML tree of Fe-ADH. **B.** ML tree of PutA. The numbers above and below the branches are the results of ML and NJ bootstrap analyses, respectively. Only bootstrap values ≥ 60% are shown. The thick branches indicate ≥ 0.96 posterior probability from Bayesian inference. Branch lengths are proportional to the number of substitutions per site (see scale bars). CH and brawn color indicate a supergroup Chromalveolata; EX and blue color indicate a supergroup Excavata. Red color indicates Opisthokonta, pink – Amoebozoa, green – Plantae.



Origins of substrate-bound periplasmic binding protein (PBPb) and silent information regulator 2 (SIR2) in protists

A. ML tree of PBPb. **B.** ML tree of SIR2. The numbers above and below the branches are the results of ML and NJ bootstrap analyses, respectively. Only bootstrap values ≥ 60% are shown. The thick branches indicate ≥ 0.96 posterior probability from Bayesian inference. Branch lengths are proportional to the number of substitutions per site (see scale bars). Short abbreviations and the color scheme are as above.



Horizontal gene transfer from bacteria to dinoflagellates
ML trees of: **A.** Arylsulfatase A (AslA). **B.** COG3129-like protein. **C.** Alpha-tubulin suppressor protein (ATS1). **D.** Pyridoxal phosphate biosynthetic protein PdxA. **E.** COG3618-like protein. **F.** COG3022-like protein. The numbers above the branches are the results of ML bootstrap analyses. Only bootstrap values ≥ 60% are shown. Branch lengths are proportional to the number of substitutions per site (see scale bars). Short abbreviations and the color scheme are as above.