

Supplementary Table 1. List of databases, sequence identifiers and accessions used in the work.

Supplementary Figure 1. Phylogeny of EF1A with ciliates. The tree was reconstructed using Bayesian inference (PhyloBayes) under CAT profile mixture model with 4 discrete gamma categories and the exchange rates fixed by the LG model (maxdiff=0.217; loglik effsize=58). Node support values are given for two types of tree inference methods – Bayesian posterior probability (left) and maximum likelihood bootstrap support value (right); bootstrap support was generated on the basis of 1000 replicates using RAxML and LG+G+I model. Support values for nodes with Bayesian posterior probabilities <0.95 and ML bootstrap support <50% are omitted. Nodes with Bayesian posterior probabilities ≥ 0.95 and ML bootstrap support $\geq 50\%$ are given with thick lines. The branch leading to diplomonads, marked with a hatch, is artificially shortened.

Supplementary Figure 2. Bayesian tree of EFL (PhyloBayes under CAT profile mixture model with 4 discrete gamma categories and the exchange rates fixed by the LG model) calculated after excluding the most variable 18.6% positions from the alignment.

Supplementary Figure 3. Bayesian tree of EF1A (PhyloBayes under CAT profile mixture model with 4 discrete gamma categories and the exchange rates fixed by the LG model) calculated after excluding the most variable 16.2% positions from the alignment.

Supplementary Figure 3. Bayesian tree of the alveolates SSU rDNA. Alternative positions of Colpodellida-1/Chomerida clade were tested with the approximately unbiased test, and the calculated *p*-values are indicated.

EF1A

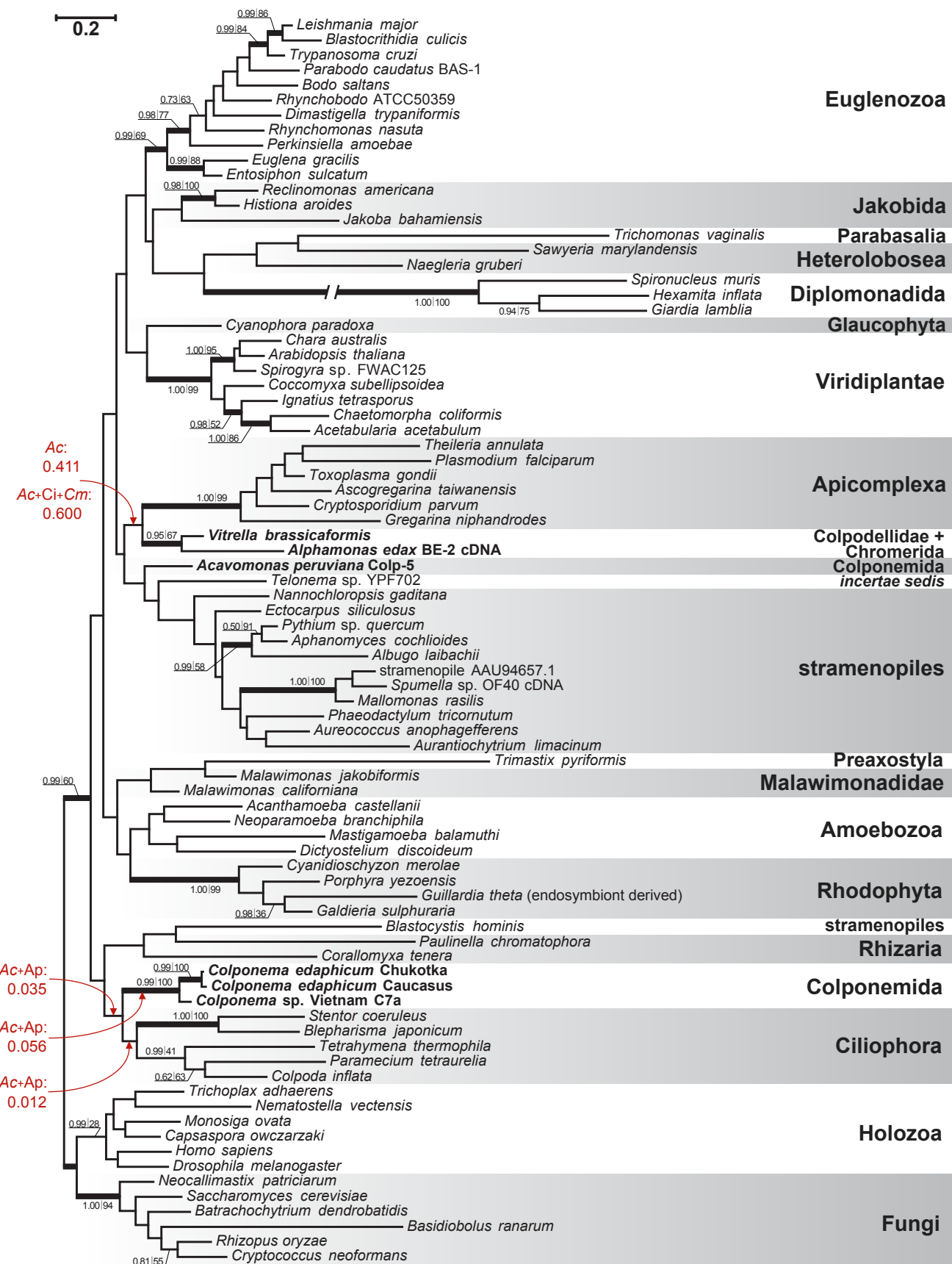
Name	Database	Accession
<i>Acanthamoeba castellanii</i>	TBestDB	ACL00002409
<i>Acetabularia acetabulum</i>	GenBank	EF551321.1
<i>Albugo laibachii</i>	GenBank	CCA22726.1
<i>Aphanomyces cochlioides</i>	GenBank	ABN54676.1
<i>Arabidopsis thaliana</i>	GenBank	AAL57653.1
<i>Ascogregarina taiwanensis</i>	GenBank	ABJQ01004964.1
<i>Aurantiochytrium limacinum</i>	DOE Joint Genome Institute	gjilAurli1 105065 estExt_Genew ise1Plus.C_7_t10466
<i>Aureococcus anophagefferens</i>	DOE Joint Genome Institute	gjilAuran1 36932
<i>Basidiobolus ranarum</i>	GenBank	DQ282610.1
<i>Batrachochytrium dendrobatidis</i>	DOE Joint Genome Institute	gjilBatde5 19314 estExt_Genew ise1Plus.C_40375
<i>Blastocrithidia culicis</i>	GenBank	ACO50122.1
<i>Blastocystis hominis</i>	GenBank	AAC36746.2
<i>Blepharisma japonicum</i>	GenBank	AAD03251.1
<i>Bodo saltans</i>	GenBank	ACO50123.1
<i>Capsaspora owczarzaki</i>	Broad Institute, Origins of Multicellularity Sequencing Project	CAOG_07807
<i>Chaetomorpha coliformis</i>	GenBank	ACL97368.1
<i>Chara australis</i>	GenBank	ABQ81936.1
<i>Coccomyxa subellipsoidea</i>	DOE Joint Genome Institute	gjilChlvu1 35848 estExt_Genew ise1.C_30373
<i>Colpoda inflata</i>	GenBank	AAD03253.1
<i>Corallomyxa tenera</i>	GenBank	ADK90072.1
<i>Cryptococcus neoformans</i>	GenBank	XM_767104.1
<i>Cryptosporidium parvum</i>	GenBank	XM_001388307.1
<i>Cyanidioschyzon merolae</i>	GenBank	BAC67667.1
<i>Cyanophora paradoxa</i>	GenBank	AF092951.1
<i>Dictyostelium discoideum</i>	GenBank	XP_645839.1
<i>Dimastigella trypaniformis</i>	GenBank	ACO50124.1
<i>Drosophila melanogaster</i>	GenBank	NP_477375.1
<i>Ectocarpus siliculosus</i>	GenBank	CBJ32893.1
<i>Entosiphon sulcatum</i>	GenBank	ACO50125.1
<i>Euglena gracilis</i>	GenBank	ACO50110.1
<i>Galdieria sulphuraria</i>	Michigan State University Galdieria Database	GS01080
<i>Giardia lamblia</i>	GenBank	XP_001704529.1
<i>Gregarina niphandrodes</i>	GenBank	AFNH01001746.1
<i>Guillardia theta</i>	DOE Joint Genome Institute	gjilGuith1 84077 estExt_Genew ise1Plus.C_30325
<i>Hexamita inflata</i>	GenBank	U37081.1
<i>Histiona aroides</i>	TBestDB	HAL00000058
<i>Homo sapiens</i>	GenBank	NP_001949.1
<i>Ignatius tetrasporus</i>	GenBank	ACL97363.1
<i>Jakoba bahamiensis</i>	TBestDB	JBL00000183
<i>Leishmania major</i>	GenBank	XP_001682258.1
<i>Malawimonas californiana</i>	TBestDB	MCL00000750
<i>Malawimonas jakobiformis</i>	TBestDB, GenBank	MJL00000647, DQ295227.1
<i>Mallomonas rasilis</i>	GenBank	AAX09601.1
<i>Mastigamoeba balamuthi</i>	TBestDB	MBL00000044
<i>Monosiga ovata</i>	TBestDB	MNL00000153
<i>Naegleria gruberi</i>	DOE Joint Genome Institute	gjilNaegr1 56672 estExt_fgenesHS_pg.C_20241
<i>Nannochloropsis gaditana</i>	Nannochloropsis Genome Project	Nga02886
<i>Nematostella vectensis</i>	GenBank	AB126336.1
<i>Neocallimastix patriciarum</i>	GenBank	EH432084.1, EH432103.1, EH432107.1, EH432109.1, EH432097.1, EH432118.1, EH432108.1, EH431334.1, EH432079.1, EH431347.1, EH431566.1, EH432018.1, EH431651.1, EH431466.1, EH431201.1, EH432044.1, EH432035.1, EH432076.1, EH432048.1, EH431583.1, EH431639.1, EH431436.1, EH431602.1
<i>Neoparamoeba branchiphila</i>	GenBank	ACO50132.1
<i>Paramecium tetraurelia</i>	GenBank	XM_001426894.1
<i>Paulinella chromatophora</i>	GenBank	BAJ14650.1
<i>Perkinsiella amoebae</i>	GenBank	ACO50133.1
<i>Phaeodactylum tricornutum</i>	DOE Joint Genome Institute	gjilPhatr2 13878 e_gw 1.13.85.1
<i>Plasmodium falciparum</i>	GenBank	XP_001350281.1
<i>Porphyra yezoensis</i>	GenBank	AB098024.1
<i>Pythium sp. quercum</i>	GenBank	ABI83804.1
<i>Reclinomonas americana</i>	TBestDB	RAL00001686
<i>Rhizopus oryzae</i>	Broad Institute, Rhizopus oryzae Database	RO3G_08488
<i>Rhynchobodo ATCC50359</i>	GenBank	ACO50135.1

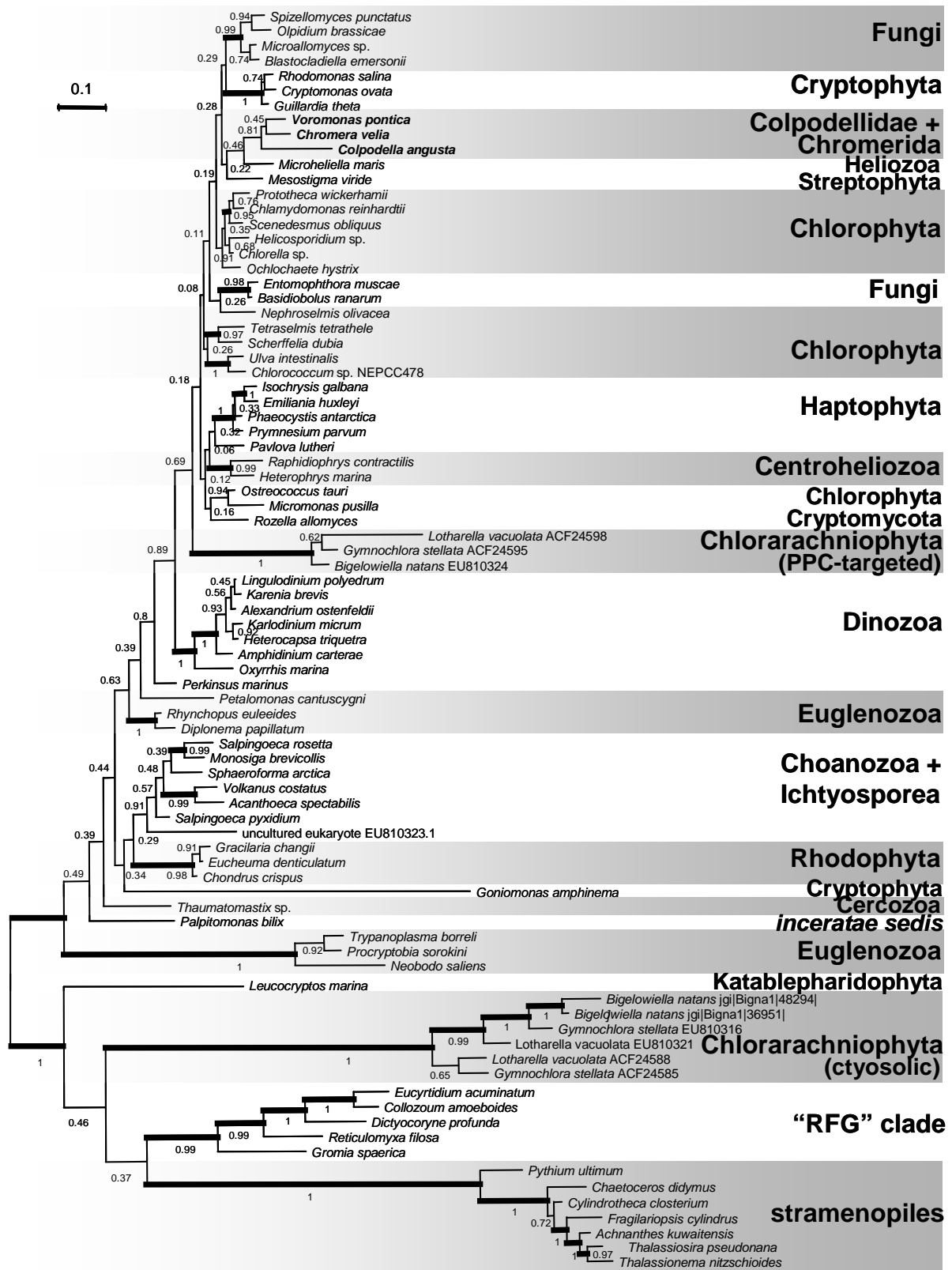
<i>Rhynchomonas nasuta</i>	GenBank	ACO50121.1
<i>Saccharomyces cerevisiae</i>	GenBank	NP_009676.1
<i>Sawyeria marylandensis</i>	TBestDB	SML00000003
<i>Spirogyra</i> sp. FWAC125	GenBank	ABQ81941.1, ABQ81942.1
<i>Spironucleus muris</i>	GenBank	U94405.1
<i>Stentor coeruleus</i>	GenBank	AAD03262.1
stramenopile AAU94657.1	GenBank	AAU94657.1
<i>Telonema</i> sp. YPF702	GenBank	BAL63503.1
<i>Tetrahymena thermophila</i>	GenBank	XM_001032213.2
<i>Theileria annulata</i>	GenBank	NW_001091929.1
<i>Toxoplasma gondii</i>	GenBank	XP_002369268.1
<i>Trichomonas vaginalis</i>	GenBank	XP_001325483.1
<i>Trichoplax adhaerens</i>	DOE Joint Genome Institute	gj Triad1 36635 estExt_Genew ise1.C_210042
<i>Trimastix pyriformis</i>	TBestDB	TPL00002905
<i>Trypanosoma cruzi</i>	GenBank	XP_804709.1
<i>Vitrella brassicaformis</i>	Marine Microbial Eukaryote Transcriptome Sequencing Project	MMETSP0288-20130426 9258

EFL

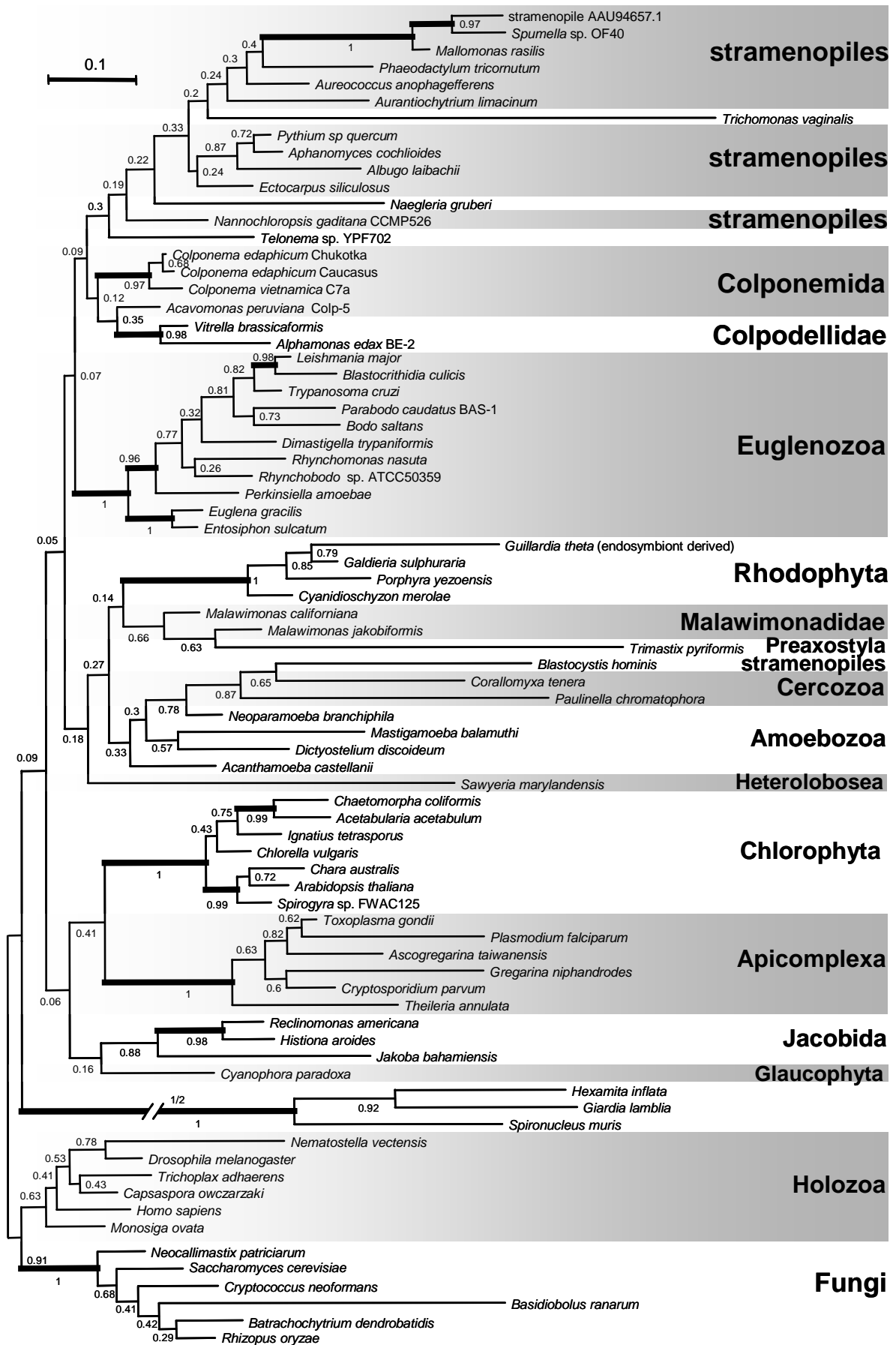
Name	Database	Accession
<i>Acanthoeca spectabilis</i>	GenBank	ACD74791.1
<i>Achnanthes kuwaitensis</i>	GenBank	BAG30802.1
<i>Alexandrium ostenfeldii</i>	GenBank	HO658306.1, HO663348.1, HO659275.1, HO663080.1, HO663249.1, HO660709.1, HO654698.1, HO658436.1, HO657895.1, HO658699.1, HO659289.1, HO653990.1, HO660459.1, HO659554.1, HO653259.1, HO663458.1, HO655795.1, HO662048.1, HO652731.1, HO659833.1, HO661052.1, HO661042.1, HO663148.1, HO660391.1, HO661900.1, HO657998.1, HO655571.1, HO661530.1, HO660939.1
<i>Amphidinium carterae</i>	GenBank	CF064659.1
<i>Basidiobolus ranarum</i>	GenBank	ABB84535.1
<i>Bigeloviella natans</i>	GenBank	EU810324.1
<i>Bigeloviella natans</i> 1	DOE Joint Genome Institute	gj Bigna1 48294 estExt_Genew ise1.C_250046
<i>Bigeloviella natans</i> 2	DOE Joint Genome Institute	gj Bigna1 36951 e_gw 1.17.41.1
<i>Blastocladia emersonii</i>	GenBank	EF064246.1
<i>Chaetoceros didymus</i>	GenBank	BAG30804.1
<i>Chlamydomonas reinhardtii</i>	DOE Joint Genome Institute	gj Chlre3 132905 estExt_gw p_1H.C_780011
<i>Chlorella variabilis</i>	DOE Joint Genome Institute	gj ChINC64A_1 30705 estExt_Genew ise1.C_70295
<i>Chlorococcum</i> NEPCC478	GenBank	EF551323.1
<i>Chondrus crispus</i>	GenBank	CO653259.1, CO649783.1, CO651752.1, CO652990.1, CO651454.1, CO652274.1, CO649837.1, CO650625.1, CO652099.1, CO653172.1, CO652788.1, CO649943.1
<i>Chromera velia</i>	Marine Microbial Eukaryote Transcriptome Sequencing Project	MMETSP0290-20130426 15931
<i>Collozoum amoeboides</i>	GenBank	BAM28641.1
<i>Cryptomonas ovata</i>	GenBank	AB332030.1
<i>Cylindrotheca closterium</i>	GenBank	BAG30805.1
<i>Dictyocoryne profunda</i>	GenBank	BAM28639.1
<i>Diplonema papillatum</i>	TBestDB	DPL00000038
<i>Emiliana huxleyi</i>	GenBank	CV068986.1
<i>Entomophthora muscae</i>	GenBank	ABB84538.1
<i>Eucheuma denticulatum</i>	GenBank	GR427904.1, GR433766.1, GR430211.1, GR430945.1, GR427588.1, GR431549.1, GR433700.1
<i>Eucyrtidium acuminatum</i>	GenBank	BAM28638.1
<i>Fragilariopsis cylindrus</i>	DOE Joint Genome Institute	gj Frac1 269944 estExt_fgenes2_kg.C_90222
<i>Goniomonas amphinema</i>	GenBank	AB332031.1
<i>Gracilaria changii</i>	GenBank	DV965525.1, DV963172.1, DV963090.1, DV968745.1, DV963156.1, DV966484.1, DV967969.1, DV964985.1, DV965095.1, DV964877.1, DV966975.1, DV969684.1, DV964639.1, DV966046.1
<i>Gromia spaerica</i>	GenBank	SRR071237
<i>Guillardia theta</i>	DOE Joint Genome Institute	gj Guith1 149923 fgenes2_kg.2_#_103_#_1003_1_CCFL_CCFN_EXT_A_EXTB
<i>Gymnochlora stellata</i>	GenBank	ACF24595.1
<i>Gymnochlora stellata</i> 1	GenBank	EU810316.1
<i>Gymnochlora stellata</i> 2	GenBank	ACF24585.1
<i>Helicosporidium</i> sp.	GenBank	AY729488.1
<i>Heterocapsa triquetra</i>	GenBank	AY729485.1
<i>Heterophrys marina</i>	GenBank	AFA56270.1
<i>Isochrysis galbana</i>	TBestDB	ISL00000533
<i>Karenia brevis</i>	GenBank	EX876503.1, EX875229.1, EX961328.1, EX961327.1, EX875228.1, EX876502.1, EX972320.1, EX972319.1
<i>Karlodinium micrum</i>	TBestDB	KML00002411

<i>Leucocryptos marina</i>	GenBank	BAJ10903.1
<i>Lingulodinium polyedrum</i>	GenBank	CD809674.1
<i>Lotharella vacuolata</i>	GenBank	ACF24598.1
<i>Lotharella vacuolata 1</i>	GenBank	EU810321.1
<i>Lotharella vacuolata 2</i>	GenBank	ACF24588.1
<i>Mesostigma viride</i>	GenBank	DN254721.1, EC732354.1, EC731514.1, EC731433.1, EC731954.1, EC731134.1, DN254248.1, DN254627.1, DN256785.1, DN256319.1, DN258988.1
<i>Microallomyces</i> sp.	GenBank	ABB84542.1
<i>Microheliella maris</i>	GenBank	AFA56271.1
<i>Micromonas pusilla</i>	DOE Joint Genome Institute	jgijMicpuC2 33445
<i>Monosiga brevicollis</i>	GenBank	AY026073.1
<i>Neobodo saliens</i>	GenBank	ACO50138.1
<i>Nephroselmis olivacea</i>	GenBank	ACN59934.1
<i>Ochlochaete hystrix</i>	GenBank	ACL97364.1
<i>Olpidium brassicae</i>	GenBank	ABB84544.1
<i>Ostreococcus tauri</i>	DOE Joint Genome Institute	jgijOstta4 23014 estExt_fgenes1_pm.C_Ch_13.00010011
<i>Oxyrrhis marina</i>	TBestDB	OML00001433
<i>Palpitomonas bilix</i>	GenBank	BAL63502.1
<i>Pavlova lutheri</i>	TBestDB	PLL00000038
<i>Perkinsus marinus</i>	GenBank	EER13701.1
<i>Petalomonas cantuscygni</i>	GenBank	ACO50134.2
<i>Phaeocystis antarctica</i>	GenBank	gnl ti 2192857123, gnl ti 2192513925
<i>Prototheca wickerhamii</i>	TBestDB	PWL00000297
<i>Prymnesium parvum</i>	GenBank	DV097486.1
<i>Pythium ultimum</i>	Pythium Genome Database	scf1117875581981
<i>Raphidiophrys contractilis</i>	GenBank	AB332032.1
<i>Reticulomyxa filosa</i>	GenBank	ACF24599.1
<i>Rhodomonas salina</i>	GenBank	DQ659244.1
<i>Rhynchopus euleeides</i>	GenBank	ACO50120.1
<i>Rozella allomycis</i>	GenBank	ABB84537.1
<i>Salpingoeca pyxidium</i>	GenBank	ACD74798.1
<i>Salpingoeca rosetta</i>	Broad Institute, Origins of Multicellularity Sequencing Project	PTSG_02256
<i>Scenedesmus obliquus</i>	TBestDB	SOL00000077
<i>Scherffelia dubia</i>	GenBank	AJ919303.1
<i>Sphaeroforma arctica</i>	Broad Institute, Origins of Multicellularity Sequencing Project	SARC_12681
<i>Spizellomyces punctatus</i>	Broad Institute, Origins of Multicellularity Sequencing Project	SPPG_08407
<i>Tetraselmis tetrathele</i>	GenBank	EF551330.1
<i>Thalassionema nitzschioides</i>	GenBank	BAG30809.1
<i>Thalassiosira pseudonana</i>	DOE Joint Genome Institute	jgijThaps3 41829 estExt_gw p_gw 1.C_chr_100079
<i>Thaumatomastix</i> sp.	GenBank	BAJ14652.1
<i>Trypanoplasma borreli</i>	GenBank	ACO50139.1
<i>Ulva intestinalis</i>	GenBank	EF551324.1
uncultured eukaryote EU810323.1	GenBank	EU810323.1
<i>Volkanus costatus</i>	GenBank	ACD74794.1

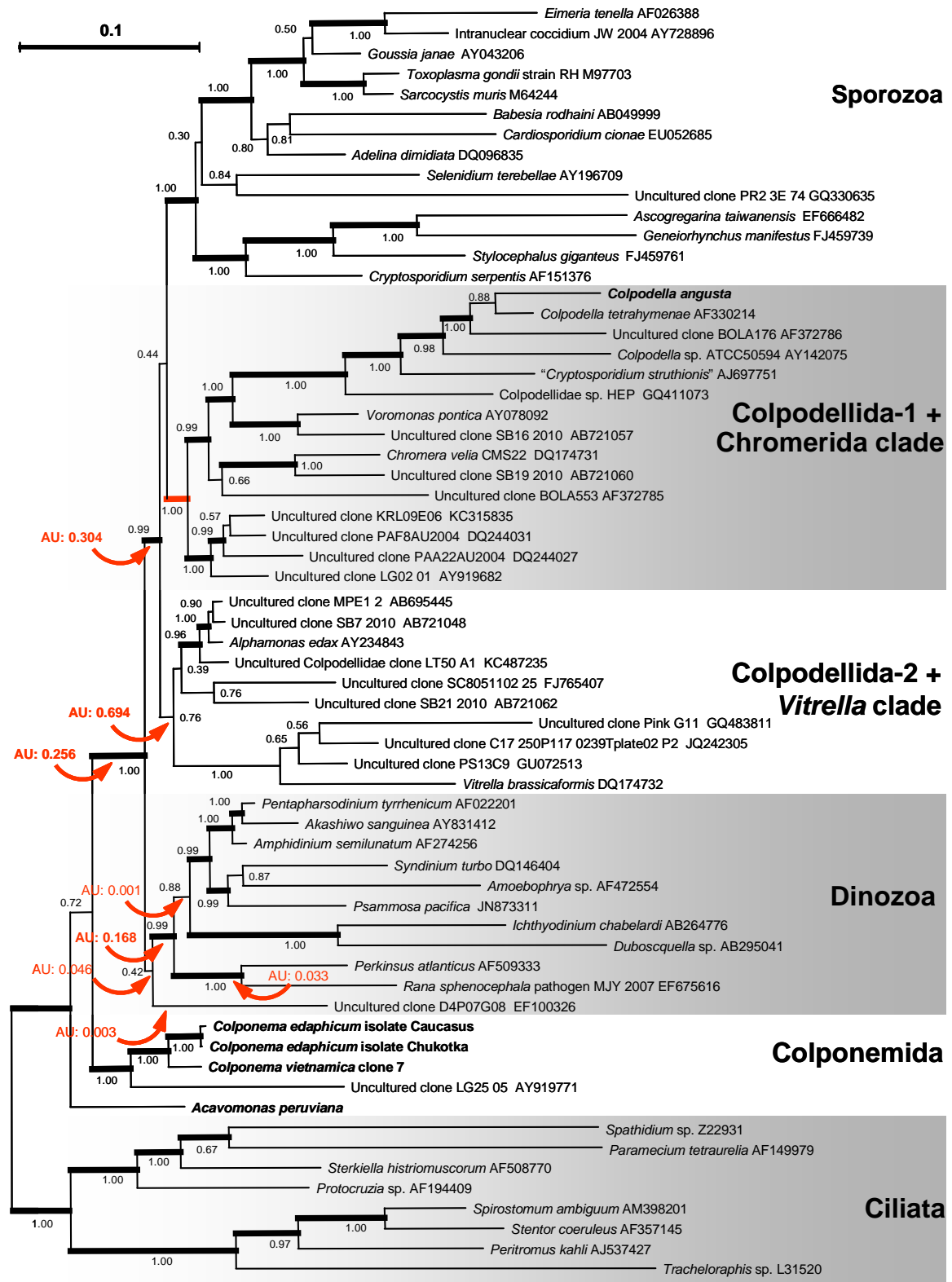




Supplementary Figure S2



Supplementary Figure S3



Supplementary Figure S4