Supporting Information

Kamikawa *et al.* 10.1073/pnas.0711084105

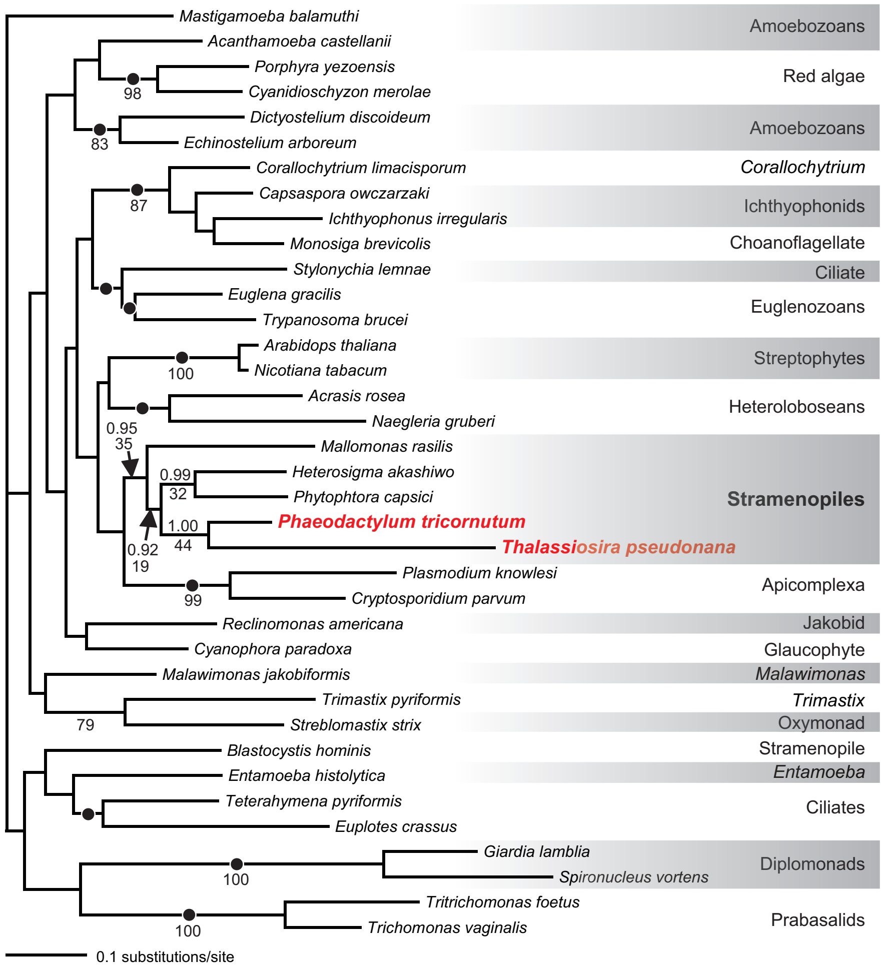

Fig. S1. Maximum-likelihood EF-1α phylogeny estimated by IQPNNI v.3.1. The diatom sequences are highlighted in red. The ML bootstrap values and Bayesian posterior probabilities for the nodes that are significant for the origin of the diatom homologues are shown. For other nodes, only ML bootstrap values ≥70% are indicated. Bayesian posterior probabilities ≥0.95 calculated by MrBayes v. 3.1.1 are also highlighted by dots.

A $^{P}/_{T}$KK motif

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Yeast  EF-1α  KKVGYNPKT-------VPFVP
Thapse EFL    QMIGFKPKK-------VPFIP
Linpol EFL    VKVGWK---KDFVEKCVPILP
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B K indel

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Yeast  EF-1α  LIIAGGVGE
Thapse EFL    LVPAEKGGF
Linpol EFL    MVPAD-GNF
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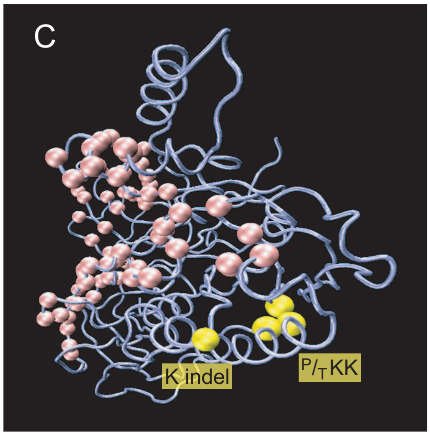

Fig. S2. P/TKK modtif and K indel. (*A* and *B*) $^{P}/_{T}$KK modtif (*A*) and K indel (*B*) in the primary structure. Yeast EF-1α, *Thalassiosira* (Thapse) EFL, and *Ligulodinium* (Linpol) EFL sequences are aligned. The motifs are highlighted in yellow. (*C*) The two motifs in the putative EF-1α/EFL tertiary structure. The EFL motifs are mapped on yeast EF-1α tertiary sturcture (PDB ID code 1IJF). The putative residues that are responsible for elongation factor functions in EF-1α (9) are highlighted in pink. The residues that correspond to the EFL motifs are highlighted in yellow.

Table S1. Clones obtained in the initial RT-PCR survey

Species		EFL	EF-1α	eRF3	HBS1	Others*	Total
Centrales	*Chaetoceras dydimus*	5	0	4	0	4	13
	Detonula confervacea	10	1	0	0	0	11
	Ditylum brightwellii	11	0	0	0	0	11
	Skeletonema costatum	12	0	0	2	0	14
Pennales	*Asterionella glacialis*	4	1	8	0	2	15
	Achnanthes kawaitensis	12	1	0	0	0	13
	Cylindrotheca closterium	7	0	3	0	2	12
	Thalassionema nitzschioides	8	1	0	0	0	9

eRF3, eukaryotic release factor 3; HBS1, hsp70 subfamily B suppressor 1.

*Sequences that do not belong to eukaryotic EF-1α superfamily.

Table S2. Primers used for the RT real-time PCR assay

Gene	Target species	Primers		Annealing temp., deg. C
		Direction	Sequence	
EF-1α	*Tp*	Forward	5′-CCACCACAACTGGGCATCTA-3′	55
		Reverse	5′-ACTACTGTGAAATCATACTTTGG-3′	
	Pt	Forward	5′-CACTACTGGTCATTTGATC-3′	52
		Reverse	5′-ATGACGGTAAAGGAGTATTTGG-3′	
EFL	*Tp*	Forward	5′-GGACACTTGATCTTCAAGC-3′	55
		Reverse	5′-GACAATGGTGTAGTGGTACTTTTC-3′	
α-tubulin	*Tp*	Forward	5′-CAAGTGTGATCCTCGTCACGG-3′	60
		Reverse	5′-GCAACCATGCACACGGCACG-3′	
	Pt	Forward	5′-CAAGTGTGATCCTCGTCACGG-3′	60
		Reverse	5′-GCAACCATGCACACGGCACG-3′	

Tp, *Thalassiosila psuedonana*; *Pt*, *Phaeodactylum tricornutum*.