

**Table S1.**—Presence/absence of 154 genes in the plastid genomes of diverse primary and secondary plastid-containing organisms, as well as a representative cyanobacterium. The column designated "Tree" indicates whether the *Cryptomonas paramecium* homolog branches with the cryptomonads *Rhodomonas salina* and *Guillardia theta* in a phylogenetic tree (T) or does not branch with sequences from these two species (F) (see main text). "+" = gene present, "-" = gene absent, "y" = pseudogene, "#" means the *C. paramecium* protein could not be analyzed in a phylogenetic tree. Abbreviations: orf; open reading frame, C.p; *Cryptomonas paramecium*, R.s; *Rhodomonas salina*, G.t; *Guillardia theta*, E.h; *Emiliania huxleyi*, O.s; *Odontella sinensis*, P.t; *Phaeodactylum tricornutum*, T.p; *Thalassiosira pseudonana*, P.p; *Porphyra purpurea*, Gr.t; *Gracilaria tenuistipitata*, C.c; *Cyanidium caldarium*, C.m; *Cyanidioschyzon merolae*, C.pa; *Cyanophora paradoxa*, C.r; *Chlamydomonas reinhardtii*, E.g; *Euglena gracilis*, B.n; *Bigelowiella natans*, A.m; *Aneura mirabilis*, E.l; *Euglena longa*, E.v; *Epifagus virginiana*, H.s; *Helicosporidium* sp., T.g; *Toxoplasma gondii*, P.f; *Plasmodium falciparum*, Syn; *Synechocystis* sp. PCC6803. Cp vs. Rs; pair-wise distances between *Cryptomonas paramecium* and *Rhodomonas salina* protein homologs, Cp vs. Gt; pair-wise distance between *Cryptomonas paramecium* and *Guillardia theta* protein homologs, Rs vs. Gt; pair-wise distance between *Rhodomonas salina* and *Guillardia theta* protein homologs.

Gene	C.p	R.s	G.t	E.h	O.s	T.p	P.t	P.p	Gr.t	C.c	C.m	Cy.p	C.r	E.g	B.n	A.m	E.l	E.v	H.s	T.g	P.f	Syn	Tree	Cp vs. Rs	Cp vs. Gt	Rs vs. Gt
rps4	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	T	0.131	0.176	0.038
orf335	+	+	+	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	F	1.166	1.403	0.749
rbcL	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	T	0.095	0.081	0.056
rbcS	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	T	0.157	0.220	0.107
cbbX	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	T	0.270	0.274	0.108
ilvH	+	+	+	-	-	-	-	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	F	0.298	0.339	0.238
cemA	+	+	+	-	-	-	-	+	+	+	+	-	+	-	-	+	-	-	-	-	-	-	T	0.249	0.242	0.099
sufB	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	+	+	+	T	0.305	0.352	0.251
sufC	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	T	0.435	0.529	0.391
atpA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	T	0.388	0.395	0.094
atpD	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	T	1.378	1.345	0.605
atpF	y	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	#			
atpG	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	F	1.221	1.207	0.207
atpH	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	F	0.140	0.140	0.000
atpI	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	-	-	-	-	-	-	F	0.552	0.553	0.095
tsf	+	+	+	-	-	-	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	F	0.553	0.524	0.320
rps2	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	F	0.514	0.524	0.199
rpoC2	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	-	+	-	-	+	T	0.621	0.643	0.270
rpoC1	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	T	0.395	0.411	0.121
rpoB	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	T	0.403	0.394	0.114
rps20	+	+	+	-	-	-	+	+	+	-	+	+	-	-	-	-	-	-	-	-	-	-	T	0.619	0.658	0.454
rpl33	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	+	-	+	-	-	-	+	F	0.286	0.306	0.234
rps18	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	+	F	0.864	0.889	0.272
infB	+	+	+	-	-	-	-	+	+	-	+	-	-	-	-	-	-	-	-	-	-	-	F	1.116	1.197	0.695
atpB	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	T	0.265	0.270	0.093
atpE	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	-	-	-	F	1.562	1.581	0.148
tatC	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	T	0.955	1.017	0.317
rpl20	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	T	0.420	0.355	0.335
rpl35	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	T	0.829	0.893	0.549
pbsA	+	+	+	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	T	0.769	0.786	0.486
rps14	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	F	0.572	0.535	0.410
acpP	+	+	+	-	+	-	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	F	0.131	0.176	0.038
dnaK	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	T	0.203	0.196	0.130

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rpl3	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.561	0.612	0.477
rpl4	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.856	1.137	0.880
rpl23	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	-	+	F	0.632	0.888	0.504
rpl2	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	T	0.460	0.494	0.249
rps19	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	F	0.433	0.433	0.258
rpl22	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	+	-	-	-	-	+	T	0.530	0.564	0.367
rps3	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	T	0.653	0.671	0.271
rpl16	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	T	0.306	0.284	0.183
rpl29	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.907	0.979	0.691
rps17	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	+	+	+	F	0.424	0.457	0.287
rpl14	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	F	0.245	0.267	0.048
rpl24	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.801	0.782	0.558
rpl5	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	-	-	+	T	0.404	0.370	0.299
rps8	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	F	0.369	0.365	0.142
rpl6	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	+	+	+	T	0.635	0.710	0.588
rpl18	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.429	0.565	0.448
rps5	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	+	+	+	T	0.508	0.570	0.222
secY	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.784	0.833	0.222
rpl36	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	F	0.110	0.110	0.055
rps13	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.386	0.350	0.294
rps11	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	T	0.431	0.431	0.157
rpoA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	-	-	+	+	F	0.738	0.794	0.400
rpl13	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.788	0.841	0.531
rps9	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	-	-	-	-	+	T	0.383	0.511	0.271
rpl31	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.487	0.481	0.200
rps12	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	F	0.142	0.113	0.067
rps7	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	F	0.402	0.446	0.182
tufA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	+	+	+	T	0.090	0.096	0.068
rps10	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.578	0.611	0.518
petF	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.275	0.276	0.112
ilvB	+	+	+	-	-	-	-	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.272	0.279	0.252
rpl19	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	-	-	-	-	-	+	F	0.653	0.705	0.336
clpC	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	+	+	+	T	0.225	0.226	0.029
rpl11	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	+	-	T	0.263	0.293	0.225
rpl1	+	+	+	-	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.345	0.389	0.203
rpl12	+	+	+	-	+	+	+	+	+	+	+	+	-	+	-	-	+	-	+	-	-	+	T	0.354	0.432	0.232
ycf20	+	-	+	+	-	-	-	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F		0.808	
orf91	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	#			
secA	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.632	0.645	0.302
rpl34	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	+	F	0.477	0.354	0.347
orf555	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	#			
rps16	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.519	0.383	0.333
ycf19	+	+	+	+	-	-	-	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.970	0.911	0.112
orf147	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	#			
groEL	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	T	0.194	0.195	0.132
ycf29/tctD	+	+	+	-	-	-	-	+	+	+	+	-	-	-	-	-	-	-	-	-	-	+	F	1.746	2.088	1.478
orf164	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	#			
rpl27	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	F	0.595	0.558	0.229
rpl21	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	+	-	-	-	-	+	F	0.888	0.929	0.243
chlI	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	-	-	-	-	+	F	0.811	0.794	0.168



