Supplemental Table 2. General Features of Chara Mitochondrial Introns and of their ORFs

Intron				Intron ORF			
Designation	Site[a]	Size (nt)	Subgroup[b]	Size (a.a.)	Location[c]	Frame	Domains[d]
atp9.i1	148	2315	IIA	576	DIV	Free	RT(YADD), X
atp9.i2	246	998	IIA	_	_	_	_
cob.i1	262	742	IIA	_	_	_	_
cob.i2	525	2014	IIB	448	DIV	Free	RT(YADD), X
cob.i3	676	642	IIA	_	_	_	_
coxI.i1	214	1692	IIA	389	DIV	Free	RT(YEKD), X
coxI.i2	732	671	IB	_	_	_	_
cox1.i3	743	377	IB	_	_	_	_
cox1.i4	838	2019	IIA	550	DIV	Free	RT(YADD), X
cox1.i5	879	276	IB2	_	_	_	_
cox1.i6	912	339	IB2	_	_	_	_
cox2.i1	131	1123	IIA	_	_	_	_
nad3.i1	152	2554	IIA	713[e]	DIV	Fused	RT(FADD), X
nad3.i2	223	2397	IIA	558	DIV	Free	RT(YADD), X
nad4.i1	973	1693	IIA	_	_	_	_
rnl.i1	779	455	IA3	_	_	_	_
rnl.i2	1923	261	IB4	_	_	_	_
rnl.i3	1931	449	IB4	_	_	_	_
rnl.i4	1943	263	IB	_	_	_	_
rnl.i5	2262	297	IB	_	_	_	_
rnl.i6	2500	382	IB4	_	_	_	_
rnl.i7	2533	444	IA3	_	_	_	_
rnl.i8	2571	535	IB	_	_	_	_
rnl.i9	2584	321	IB	_	_	_	_
rns.i1	793	1013	IA3	259	L8	Free	LAGLIDADG
rps3.i1	74	1231	IIA	_	_	_	_
trnN(guu).i1	38	605	IIA	_	_	_	_

[a] For protein-coding and tRNA genes, insertion sites are given relative to the corresponding genes in *Reclinomonas americana*; for rRNA genes, they are given relative to the corresponding genes in *Escherichia coli*. For each site, the position corresponding to the nucleotide immediately preceding the intron is reported.

[b] Six IB introns could not be unambiguously assigned to any of the four subcategories described by Michel and Westhof (1990).

[c] D refers to a domain of group II intron secondary structure; L followed by a number refers to the loop extending the base-paired region identified by the number.

[d] RT, reverse transcriptase domain, with the catalytic motif in subdomain 5 indicated in parentheses; X, domain X (putative splicing function).

[e] Size was determined based on the first amino acid fully coded within the intron.