

Supplementary Table S2 – Amount of nuclear DNA in *Chlamydomonas reinhardtii* that maps to the mitochondrial and plastid genomes.

		# of similarity regions ^a	Avg. length of similarity region (nt)	Max similarity length (nt)	Cumulative lengths of similarity regions (nt)	Fraction of nuclear genome
Amount of nucDNA mapping to the mitochondrial genome (by mtDNA subcategory ^b)	Protein-coding genes ^c	34	61	333	2075	2.0 x 10 ⁻⁵
	Structural-RNA genes ^d	7	40	57	281	0.3 x 10 ⁻⁵
	Intronic ORFs ^e	13	32	43	413	0.4 x 10 ⁻⁵
	Intergenic and non-ORF intronic regions ^f	16	50	206	751	0.7 x 10 ⁻⁵
	Subtotal	70	55	333	3520	3.4 x 10 ⁻⁵
Amount of nucDNA mapping to the plastid genome (by ptDNA subcategory ^b)	Protein-coding genes ^c	34	44	129	1528	1.5 x 10 ⁻⁵
	Structural-RNA genes ^d	12	50	94	596	0.6 x 10 ⁻⁵
	Intronic ORFs ^e	---	---	---	---	---
	Intergenic and non-ORF intronic regions ^f	11	64	1093	1496	1.5 x 10 ⁻⁵
	Subtotal	57	63	1093	3620	3.6 x 10 ⁻⁵
Total amount of nucDNA that maps to organelle DNA		137	60	1093	7140	7.0 x 10 ⁻⁵

Note: Nuclear DNA analyses are based on the *C. reinhardtii* draft nuclear genome sequence (version 3.1) at the DOE JGI [52]. Only the first 75 scaffolds of the nuclear-genome assembly were analyzed; approximately 84% of the *C. reinhardtii* nucDNA is contained in these 75 scaffolds and their cumulative length is 101.2 Mb.

^a The number of distinct regions in the *C. reinhardtii* nucDNA that show >90% sequence identity and at least 25 nt of aligned length to organelle DNA.

^b Refers to the region of the organelle genome to which the nucDNA maps.

^c Includes all of the identified protein-coding genes.

^d Includes all of the identified tRNA- and rRNA-coding genes.

^e Includes all of the identified group I and II intronic-ORFs. Note, there are no intronic ORFs in the *C. reinhardtii* ptDNA.

^f Includes all of the identified intergenic and non-ORF intronic regions.