

Table 1. Comparison of *Chlamydomonas* genome statistics to those of selected sequenced genomes. nd, Not determined. [Source for all but *Chlamydomonas (1)*]

	<i>Chlamydomonas</i>	<i>Ostreococcus tauri</i>	<i>Cyanidioschyzon</i>	<i>Arabidopsis</i>	Human
Assembly length (Mb)	121	12.6	16.5	140.1	2,851
Coverage	13×	6.7×	11×	nd	~8×
Chromosomes	17	20	20	5	23
G+C (%)	64	58	55	36	41
G+C (%) coding sequence	68	59	57	44	52
Gene number	15,143	8,166	5,331	26,341	~23,000
Genes with EST support (%)	63	36	86	60	nd
Gene density (per kb)	0.125	0.648	0.323	0.190	~0.0008
Average bp per gene	4312	nd	1553	2232	27,000
Average bp per transcript	1580	1257	1552	nd	nd
Average number of amino acids per polypeptide	444	387	518	413	491
Average number of exons per gene	8.33	1.57	1.005	5.2	8.8
Average exon length	190	750	1540	251	282*
Genes with introns (%)	92	39	0.5	79	85†
Mean length of intron	373	103	248	164	3,365
Coding sequence (%)	16.7	81.6	44.9	33.0	~1
Number of rDNA units (28S/18S/5.8S + 5S)	3 + 3	4 + 4	3 + 3‡	12 + 700	5 + nd
Number tRNAs	259§	nd	30	589	497
Selenocysteine (Sec) tRNAs	1	nd	nd	0	1

*National Center for Biotechnology Information (NIH) NCBI 36 from Ensembl build 38. †[Source (56)]. ‡Three regions contain 5S rDNA exclusively, and three regions contain 28S-18S-5.8S rDNAs exclusively. §65 tRNAs that were included in SINE elements were removed from the tRNA-scanSE predictions.