Supplementary Table 1. A set of gene-specific primers designed for *E. gracilis* organellar fractions and used for qPCR. **M**, mitochondrial; **N**, nuclear; **C**, chloroplast

	***Euglena gracilis* genes**		
primers	**M gene** ***cox1***	**N gene** ***psbO***	**C gene** ***psbA***
forward primer sequence	cttgggcttcaggtagaggtt	gtcatgagccgcgttaactt	tgttgctggtgtttttggtg
reverse primer sequence	ccggtaaatccaccaaaaca	ttgttggaggcagtctggta	cagtcgtttcacgaagcaaa
product size	91	98	83
gene accession number	Y07965.1	GQ925710.1	X00929.1
gene description	cytochrome *c* oxidase subunit 1, respiratory chain	subunit O, photosystem II	CP47, photosystem II

Supplementary Table 2. Genomic and transcriptomic sequencing libraries and their parameters.

Sequencing parameters	**genomic**		**transcriptomic**
library	paired-end	mate pair	paired-end
sequencing platform	Illumina MiSeq	Illumina HiSeq	Illumina HiSeq
insert size, bp	280 – 980	1300 – 4300	120 – 300
read length, nt	250	100	100
number of reads	25,073,026	27,168,328	44,988,890
sequencing facility	GeneCore, Germany http://genecore3.genecore.embl.de /genecore3/index.cfm		Macrogen, Korea http://dna.macrogen.com/eng/

Supplementary Table 3. Identification of *Euglena gracilis* mitochondrial genes. *Euglena* contigs were searched with tBLASTx against mitochondrial genomes of excavates *Malawimonas jakobiformis*, accession number NC_002553; *Jakoba libera*, KC353355 and *J. bahamiensis* KC353354.1 and *Reclinomonas americana*, NC_001823.1. *E. gracilis* mitochondrial genes (*cob*, *cox1*, *cox2*, *nad1*, *nad4*, *nad5*) highlighted in red belonged to high-coverage contigs, as compared to putative nucleus-encoded genes marked in blue (*atp1*, *atp6*, *rpl6*, *rpl7*, *rpl12 rpl18*, *rpl20*, *rpoB*, *tufA*) located on low-coverage contigs.

Gene	Species	E - value	Contig length	Average coverage
atp1	*Reclinomonas americana*	7.23×10^{-12}	331	3.00
atp9	*Jakoba libera*	1.37×10^{-11}	509	3.60
cob	*Jakoba bahamiensis*	1.43×10^{-66}	1333	87.70
cox1	*Reclinomonas americana*	2.56×10^{-78}	964	317.20
cox2	*Jakoba libera*	5.82×10^{-28}	1203	81.00
nad1	*Reclinomonas americana*	8.06×10^{-25}	1396	59.60
nad4	*Reclinomonas americana*	5.06×10^{-16}	1491	69.80
nad5	*Malawimonas jakobiformis*	7.45×10^{-25}	591	96.80
rpl6	*Reclinomonas americana*	3.29×10^{-13}	289	2.80
rps7	*Reclinomonas americana*	1.76×10^{-29}	211	3.30
rps12	*Reclinomonas americana*	8.50×10^{-45}	211	3.30
rpl18	*Reclinomonas americana*	3.29×10^{-13}	289	2.80
rpl20	*Jakoba libera*	2.55×10^{-09}	211	3.30
rpoB	*Jakoba bahamiensis*	2.63×10^{-09}	211	3.30
tufA	*Jakoba bahamiensis*	5.69×10^{-145}	211	3.30