

	Genome Size (Mbp)	Scaffolds	N50 (L50) (Kbp)	Contigs	Gene Models	CEGMA C P %	BUSCO C D F M %
<i>Pythium aphanidermatum</i>	35.9	1,774	37.38 (0.27)	5,487	● 12,312	89 95	80 14 4.8 14
<i>Phytophthora sojae</i>	82.6	83	7609 (0.004)	863	● 26,584	90 95	84 13 2.5 12
<i>Saprolegnia parasitica</i>	53.09	1,442	280.94 (0.04)	4,125	● 20,113	91 95	75 10 9.5 15
<i>Hyphochytrium catenoides</i>	65.7*	4,758	35.57 (0.39)	8,490	● 15,388	89 93	52 5 11.0 35
<i>Thalassiosira pseudonana</i>	31	27	1992 (0.007)	45	● 11,390	89 91	72 10 4.6 22
<i>Nannochloropsis gaditana</i>	28.4	1,844	38.08 (0.25)	4,045	● 9,053	73 80	60 17 9.0 30
<i>Ectocarpus siliculosus</i>	195.8	1,561	497.38 (0.11)	13,304	● 16,788	71 87	43 2.5 22 34

Numbers in italics are inferrd from scaffold data.

CEGMA: C = Complete, P = Partial

BUSCO: C = Complete, D = Duplicated, F = Fragmented, M= Missing

* K-mer estimation

All numbers are gathered from the genome portlas of each taxa.