Table S2. Primer used in the study.

Used primer	Sequence 5’-3’	Target marker region	References
Cob 1f	ATG GYT TTT YTC WAC WAA TCA	COI	Peterson et al. (2006)
Gaz 2R	ACT TCT GGA TGT CCA AAA AAY CA	COI	Saunder (2005)
ITS 1420f	CAG GTC TGT GAT GCC C	ITS1-5.8S-ITS2	Rogers et al. (2006)
ITS 4r	TCC TCC GCT TAT TGA TAT GC	ITS1-5.8S-ITS2	White et al. (1990)
Sogin2f	AGG GTTCGA TTC CGG	18S	Modified after Gunderson et al. (1986)
Proto5r	GACCGGGCGGTGTGTAC	18S	Medinger et al. (2010)
82F	GAA ACT GCG AAT GGC TC	18S	López-García et al. (2003)
LEUK2	ACCCGCTGAACTTAAGCATATCACT	LSU	Liu et al. (2010)
LSU-740DR	ACCCTATTCAGGCATAGTT	LSU	Veselá et al. (2012)

Table S3. Estimates of average evolutionary divergence over sequence pairs within groups for selected gene markers. All positions containing gaps and missing data were eliminated. Analyses were conducted using the Kimura 2-parameter model. Evolutionary analyses were conducted in MEGA5 (Tamura et al. 2011). The number of base substitutions per site from averaging over all sequence pairs within each group are shown. (n=number of analyzed sequences for the respective marker; n.a.=not analyzed)

	18S	V4	5.8S	LSU	COI
Ochromonadales	0.01693	0.04083	0.05654	0.07495	0.22006
Synurales (18S n=24, V4 n=24, 5.8S n=13, LSU n=27, COI n=10)	0.02162	0.06189	0.02183	0.09134	0.20718
Paraphysomonas (18S n=15, V4 n=16, 5.8S n= 7, LSU n=12, COI n=14)	0.03375	0.10162	0.03267	0.06999	0.22295
Apoikiida (18S n=3, V4 n=3, 5.8S n= 2, LSU n= 4, COI n=3)	0.03087	0.07250	0.0100	0.02243	0.21266
Chromulinales (18S n=3, V4 n=4, 5.8S n=1, LSU n=4, COI n=2)	0.03733	0.10502	n.a.	0.10820	0.28381

Table S4.Estimates of average evolutionary divergence between groups for selected gene markers. All ambiguous positions were removed for each sequence pair. Analyses were conducted using the Kimura 2-parameter model. Evolutionary analyses were conducted in MEGA5 (Tamura et al. 2011).

Analyzed groups and marker regions (18S, V4, 5.8S, LSU, COI)	Ochromonadales	Synurales	Paraophysomonadida	Apoikiida
Synurales (18S n=24, V4 n=24, 5.8S n=13, LSU n=27, COI n=10)	0.04638 0.12165 0.09461 0.18123 0.24974			
Paraphysomonas (18S n=15, V4 n=16, 5.8S n= 7, LSU n=12, COI n=14)	0.06084 0.15426 0.08930 0.15874 0.29907	0.06148 0.15583 0.09508 0.17760 0.28881		
Apoikiida (18S n=3, V4 n=3, 5.8S n= 2, LSU n= 4, COI n=3)	0.04556 0.13074 0.06918 0.14417 0.25302	0.04852 0.12750 0.07309 0.18873 0.22532	0.06191 0.15382 0.07315 0.16436 0.27931	
Chromulinales (18S n=3, V4 n=4, 5.8S n=1, LSU n=4, COI n=2)	0.04914 0.11600 0.08893 0.17081 0.27071	0.05546 0.13200 0.08560 0.20327 0.27262	0.06847 0.16487 0.10924 0.18059 0.29395	0.05767 0.14638 0.07460 0.17229 0.26483

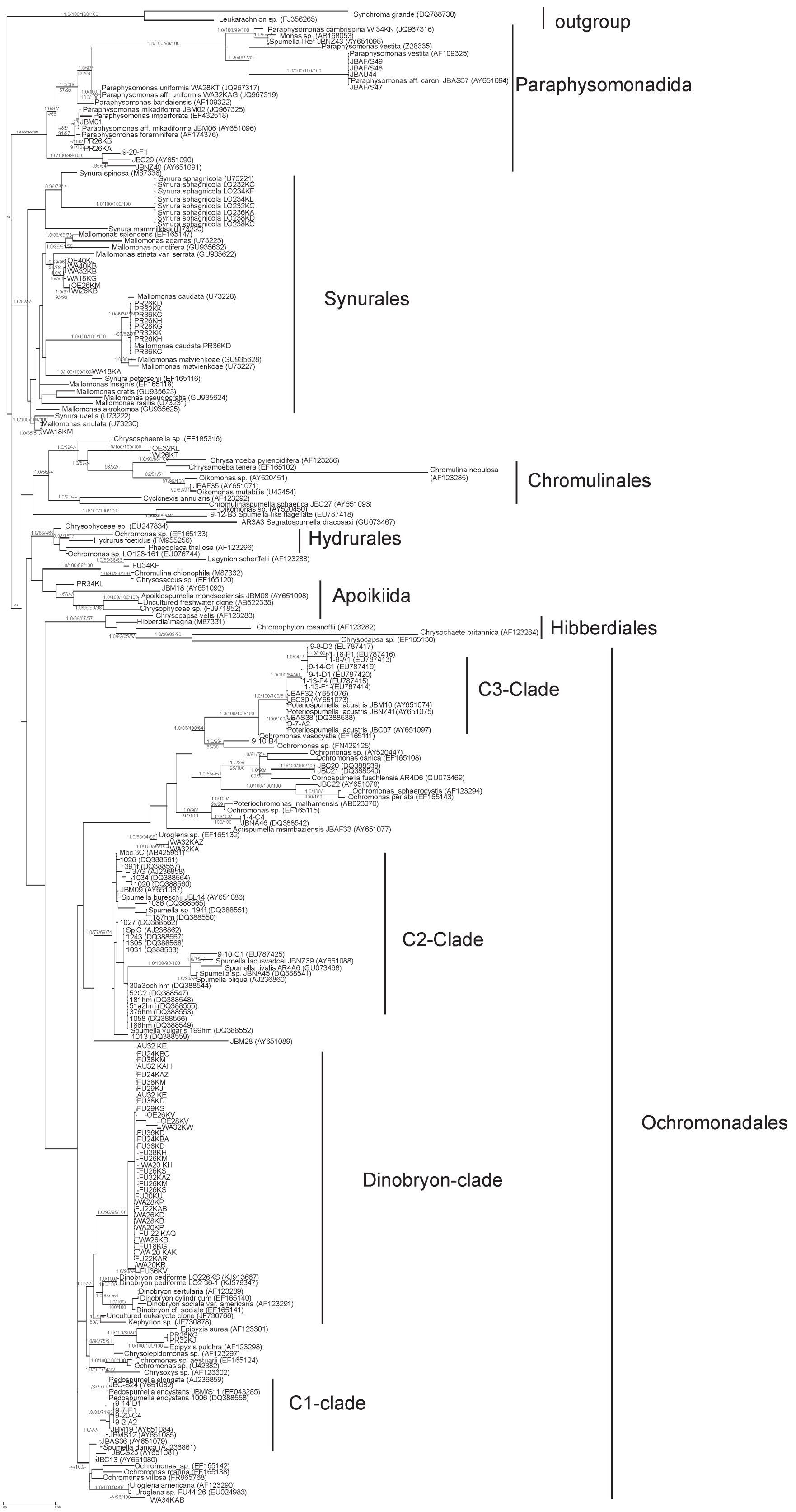

Figure S1. Complete phylogeny of the chrysophytes obtained by maximum likelihood inference of the SSU rDNA dataset. Values at the nodes indicate statistical support estimated by four methods—Bayesian inference (MB), maximum likelihood (ML), maximum parsimony (MP), distance (neighbor joining; NJ). Hyphens indicate support below 50% for ML,MP, NJ and below 0.95 for MB. Scale bar represents the expected number of substitutions per site.

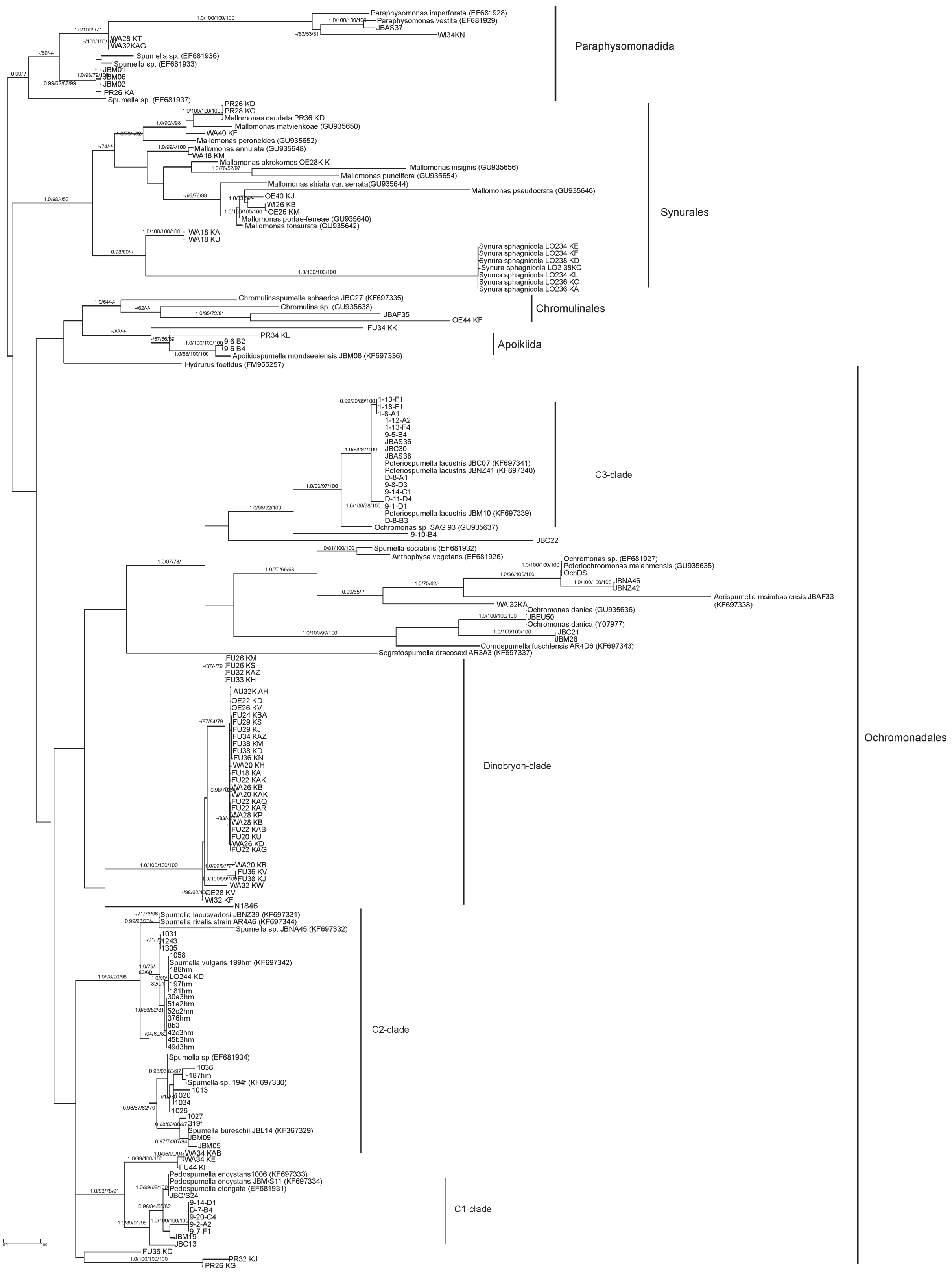

Figure S2. Complete phylogeny of the chrysophytes obtained by maximum likelihood inference of the LSU D1-D2 rDNA dataset. Values at the nodes indicate statistical support estimated by four methods—Bayesian inference (MB), maximum likelihood (ML), maximum parsimony (MP), distance (neighbor joining; NJ). Hyphens indicate support below 50% for ML,MP, NJ and below 0.95 for MB Scale bar represents the expected number of substitutions per site.

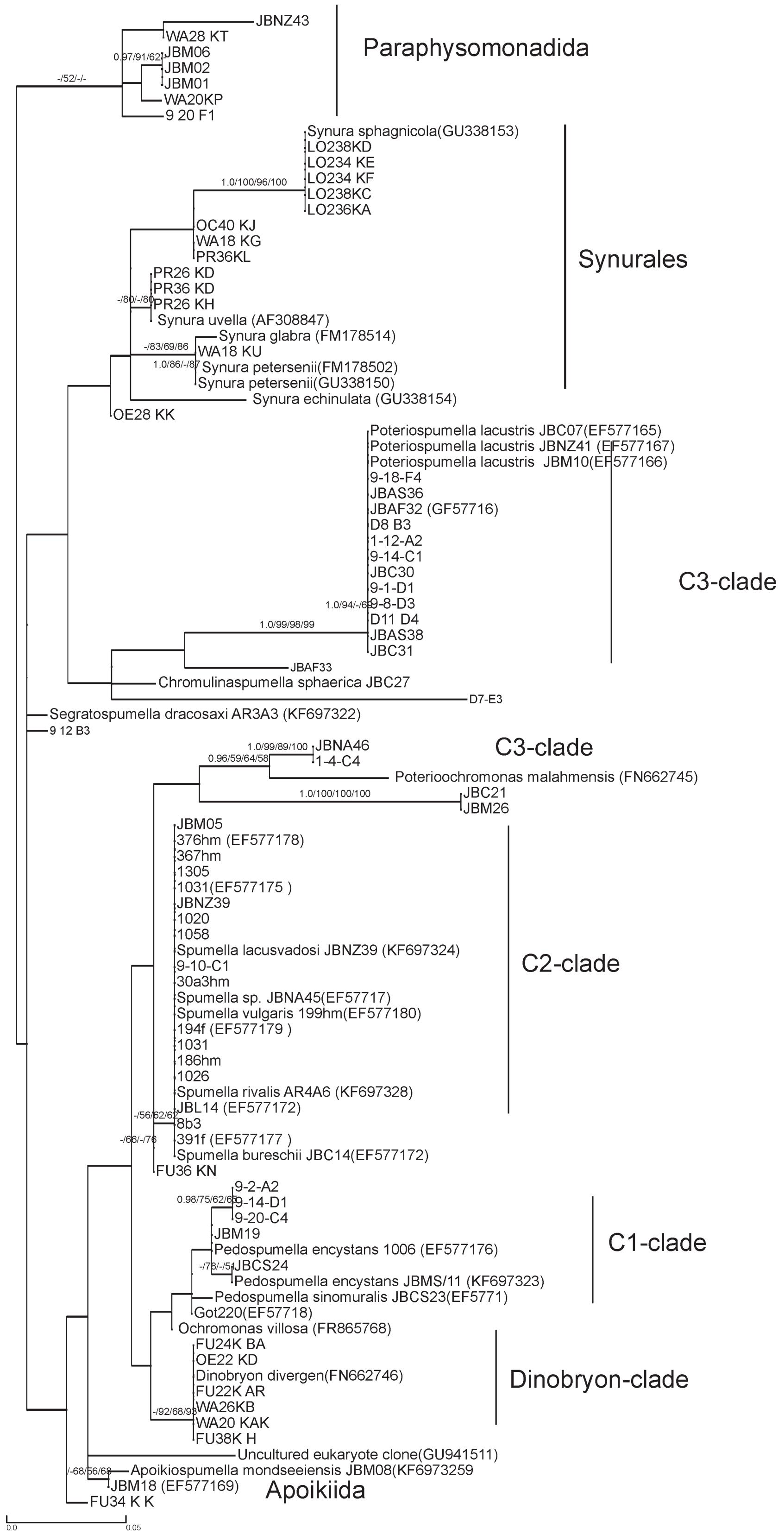

Figure S3. Phylogeny of the chrysophytes obtained by maximum likelihood inference of the 5.8S rDNA dataset. Values at the nodes indicate statistical support estimated by four methods—Bayesian inference (MB), maximum likelihood (ML), maximum parsimony (MP), distance (neighbor joining; NJ). Hyphens indicate support below 50% for ML,MP, NJ and below 0.95 for MB. Scale bar represents the expected number of substitutions per site.

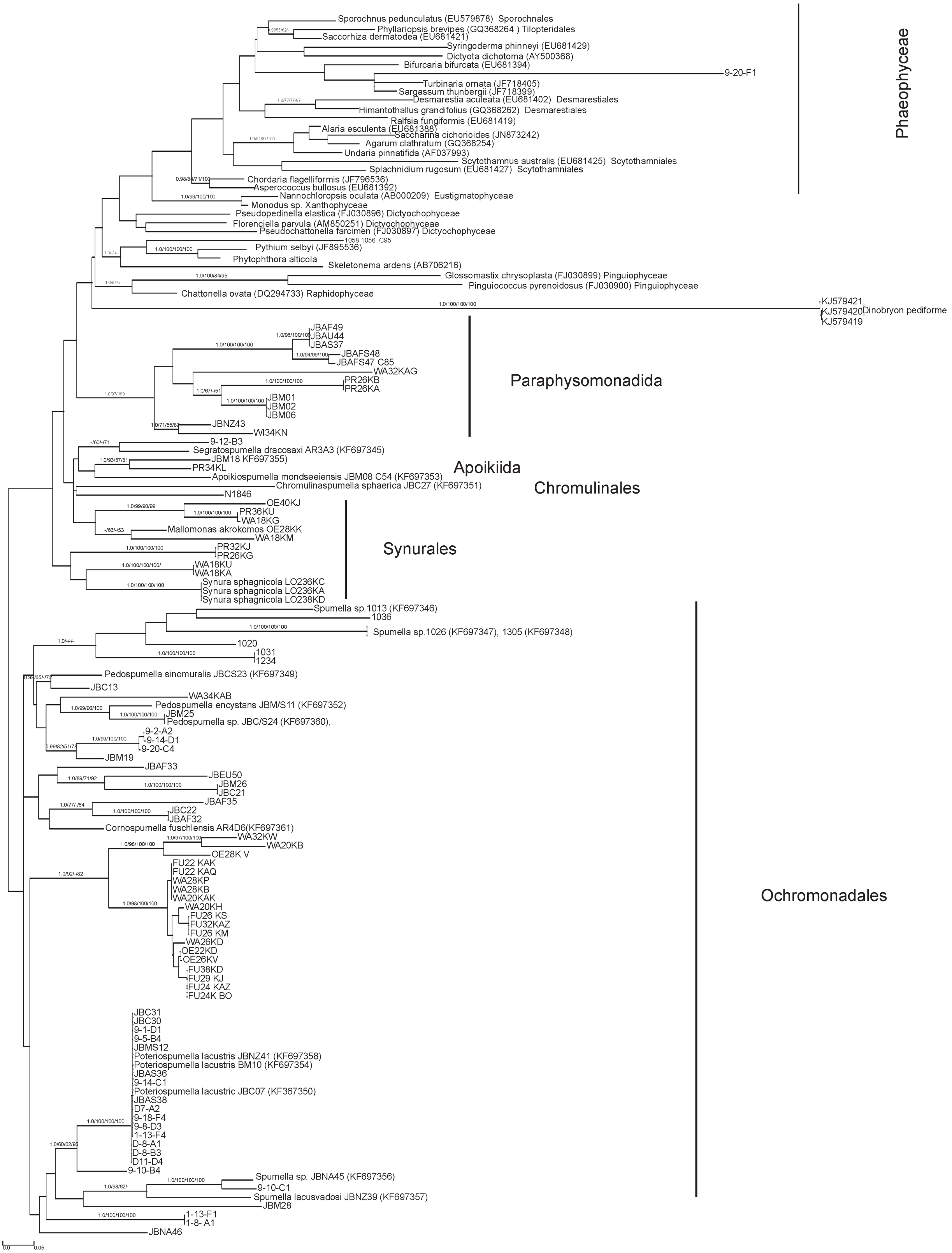

Figure S4. Complete phylogeny of the chrysophytes obtained by maximum likelihood inference of the COI dataset. Values at the nodes indicate statistical support estimated by four methods—Bayesian inference (MB), maximum likelihood (ML), maximum parsimony (MP), distance (neighbor joining; NJ). Hyphens indicate support below 50% for ML,MP, NJ and below 0.95 for MB. . Scale bar represents the expected number of substitutions per site.