File S1: Description of the construction of the Haptophyte 18S rRNA gene reference database.

The sequences were downloaded as a FASTA file from "The ribosomal protist database" (Guillou et al. 2013) (PR^2, http://ssu-rrna.org/pr2/Search/Search by Keywords/Haptophyta/All, originating from the GenBank v. 203, downloaded October 2014) including 968 haptophyte sequences. The file was opened in an Excel sheet to separate the taxonomy field into different columns. In addition, we included 26 sequences shorter than 800 bp, without cultured representatives, and 1 from a culture, which were phylogenetically placed and used as reference by Egge et al. (2015). Six additional sequences of newly released sequences (Sept 2015) of cultured species were added. Sequences were aligned by Mafft (v.7, automatic). Phylogenetic analyses were performed in Geneious (v. 8.1) by FastTree (v. 2.1.5, GTR, CAT) and RAxML (v. 7.2.8, GTR GAMMAI, Rapid bootstrapping and search for best ML tree), and by RAxML on the Abel computer cluster at UiO, as described below. The taxonomic placement of sequences from cultured strains was checked and environmental sequences were placed in well-supported clades based on phylogenetic trees in Fig. 2. All associated information related to the sequences was downloaded from NCBI as described on their database (see http://www.ncbi.nlm.nih.gov/). Information on sequence length, name and geographical origin of strain/clone and author and year of submission were extracted and transferred to an Excel-file using a script in python. The taxonomy was updated according to latest taxonomic revisions (Edvardsen et al. 2000, 2011, Jordan et al. 2004, Bendif et al. 2011, 2013, Andersen et al. 2014). The environmental sequences were checked for chimeras by uchime in usearch (v. 8.0, results for all sequences are shown in Table S1). Thirty-two chimeras were detected and removed, 26 were identified by uchime and additionally six were found by manual inspection of alignment and by BLAST of sequences with long branches. These are listed in Table S1, sheet 2. For the final tree the remaining 971 sequences and 5 outgroup sequences from Hacrobia (AF534709, AJ564771, JX988758, KJ762967, AF508268) were aligned in MAFFT online (v. 7, G-INS-I, default settings). The alignment was edited manually by eye in Geneious, and primer regions removed. Phylogenetic analyses based on the curated alignment (File S4) were performed with RAxML v. 8.026 (GTRCAT, 100 resamplings for bootstrap values) on the Abel computer cluster at UiO and kindly performed by Sandra Gran Stadniczeñko. Clades were collapsed into major clades (Fig. 2) or coloured according to taxonomic placement (Fig. S1).

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