

Figure S1: MIF copy number as a function of taxa, environment, and lifestyle. Box plot of the differences in MIF copy number according to the environment (**a**), the taxon (**b**) and the lifestyle (**c**) of species. Each box is delimited by the quartiles Q1 and Q3, whose variation Q3-Q1 corresponds to 50% of the species. The horizontal line in the centre of the box represents the median value. The two ends of the vertical bars correspond to the values of the first and last percentiles (C1 and C99) and delimit 98 % of the sample distribution. Extreme values (outliers) are indicated by a dot (below 2% of the sample distribution).

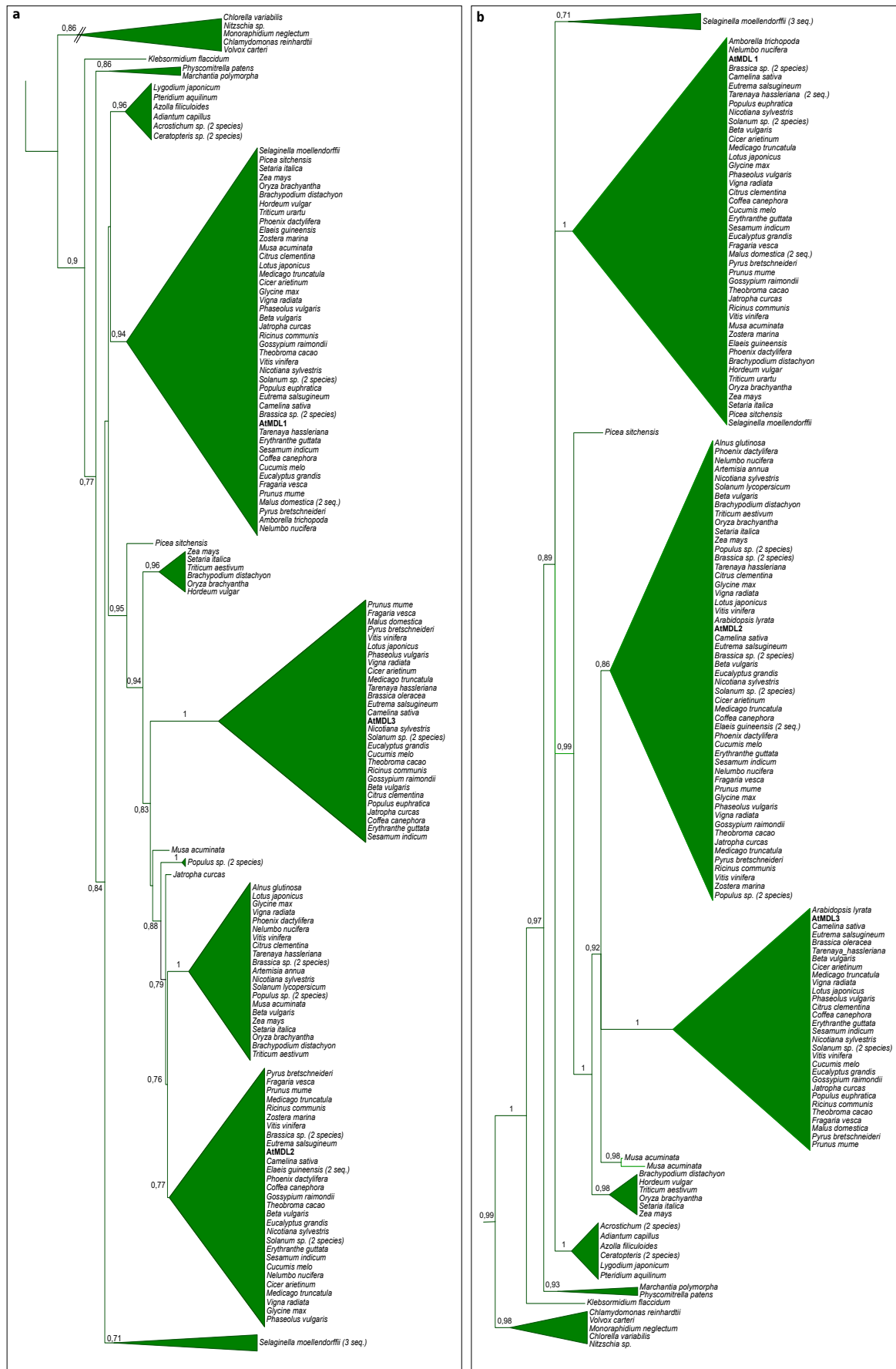


Figure S2: Plant MIF phylogeny. Phylogenetic analyses of plant MIF sequences using the Bayesian Inference (BI) method **(a)** and the maximum likelihood (ML) method **(b)**. The *Arabidopsis thaliana* MIF sequences (AtMDL) are shown in bold. Statistical confidence values are indicated next to each branch, when they were superior to 0.5 and 0.7, according to the BI method and the approximate likelihood-ratio test (aLRT) with maximum likelihood analyses, respectively.

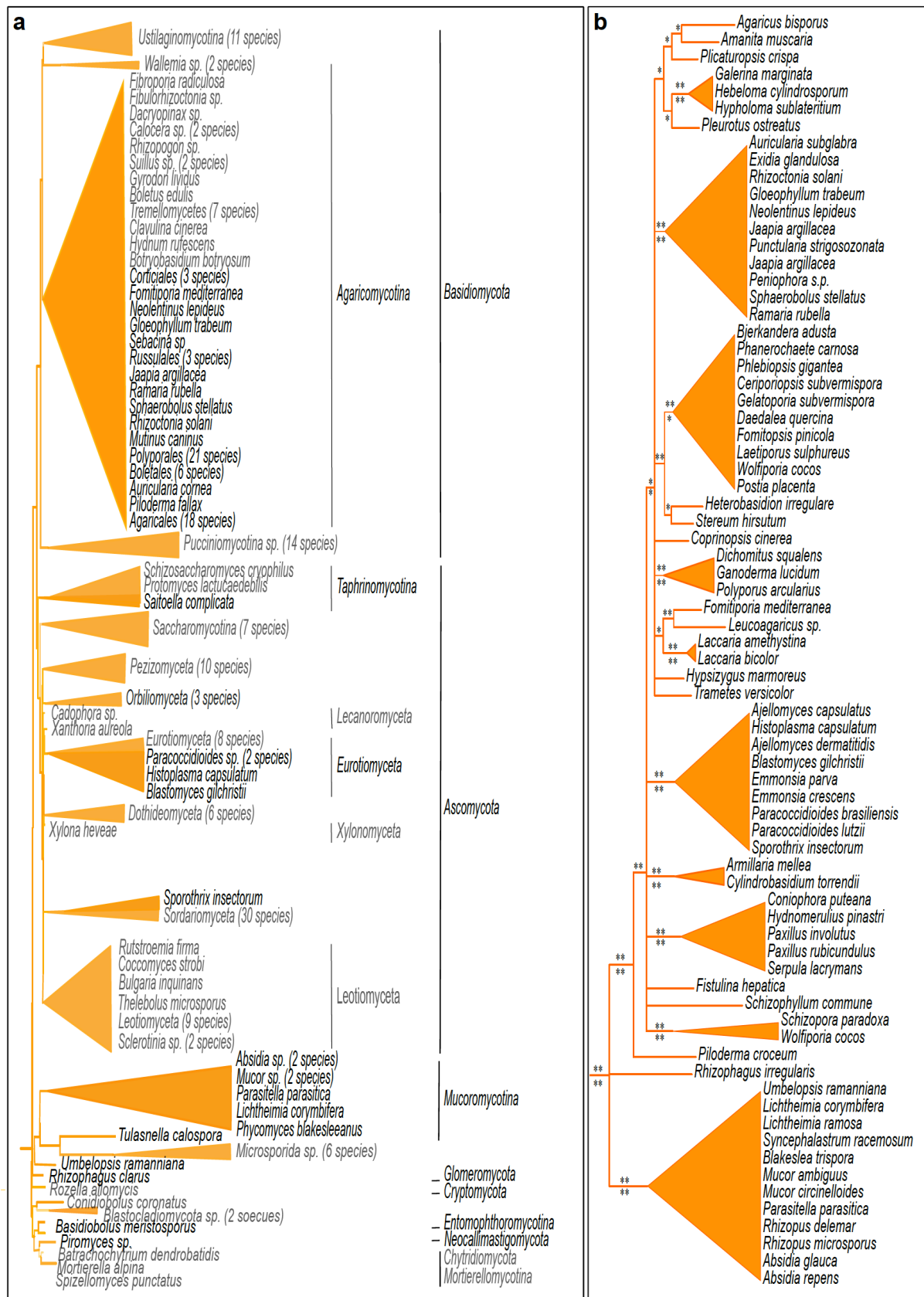


Figure S3: MIF phylogeny of fungal species. Results of Bayesian Inference (BI) analyses based on fungal 18S RNA sequences (**a**) and corresponding MIF sequences (**b**). Statistical confidence values are indicated next to each branch, when they were superior to 0.5 and 0.7, according to the BI method and the approximate likelihood-ratio test (aLRT) with maximum likelihood analyses, respectively. The species tree is consistent with the currently accepted phylogeny of fungi ⁷⁵. Species lacking MIF sequences are shown in grey.

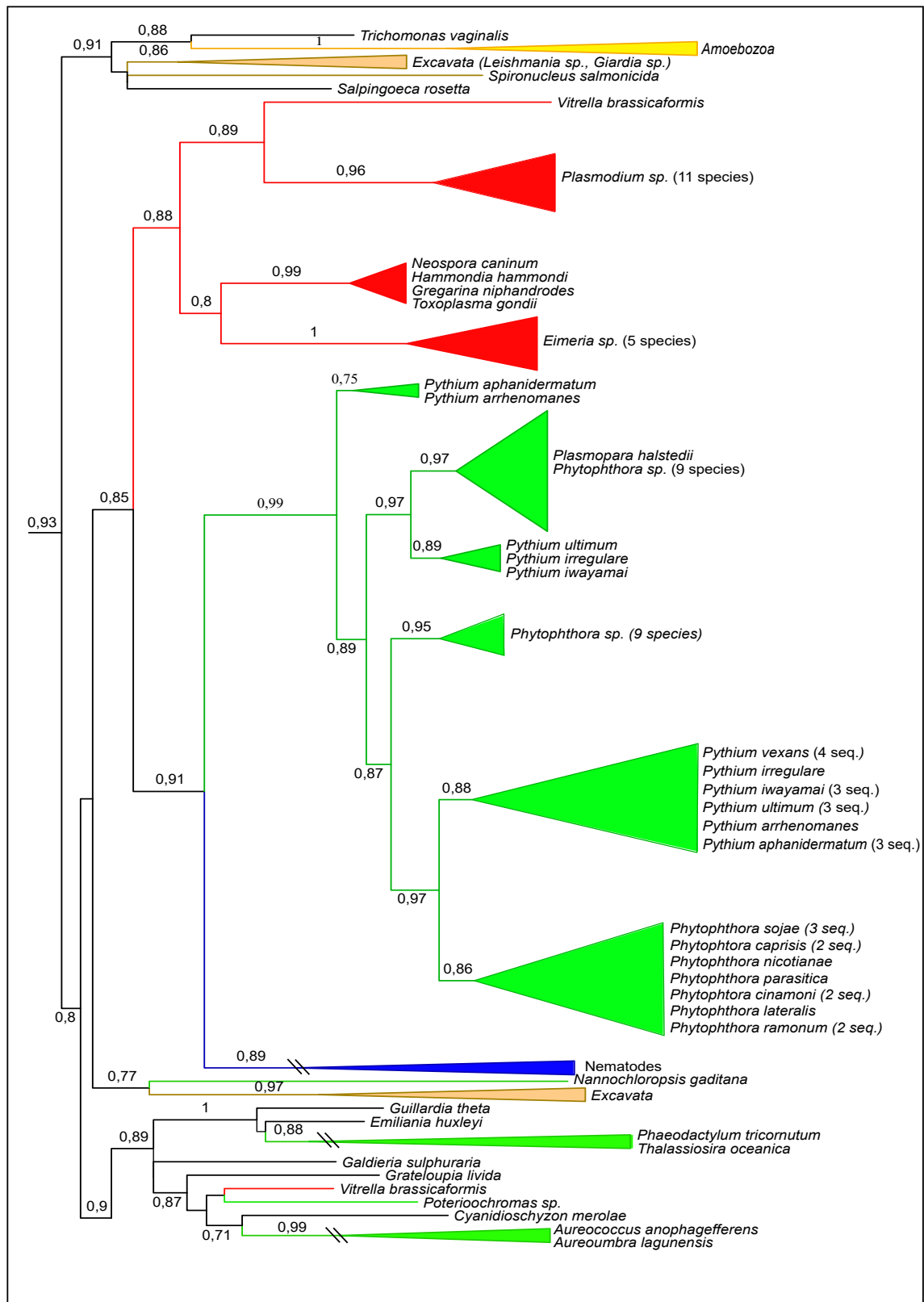


Figure S4: Maximum likelihood analyses of MIF sequences from *Stramenopila* and *Alveolata*. Results of maximum likelihood (ML) analysis of MIF sequences from *Stramenopila* and *Alveolata*. Statistical confidence values are indicated next to each branch when superior to 0.7 according to the approximate likelihood-ratio test (aLRT).

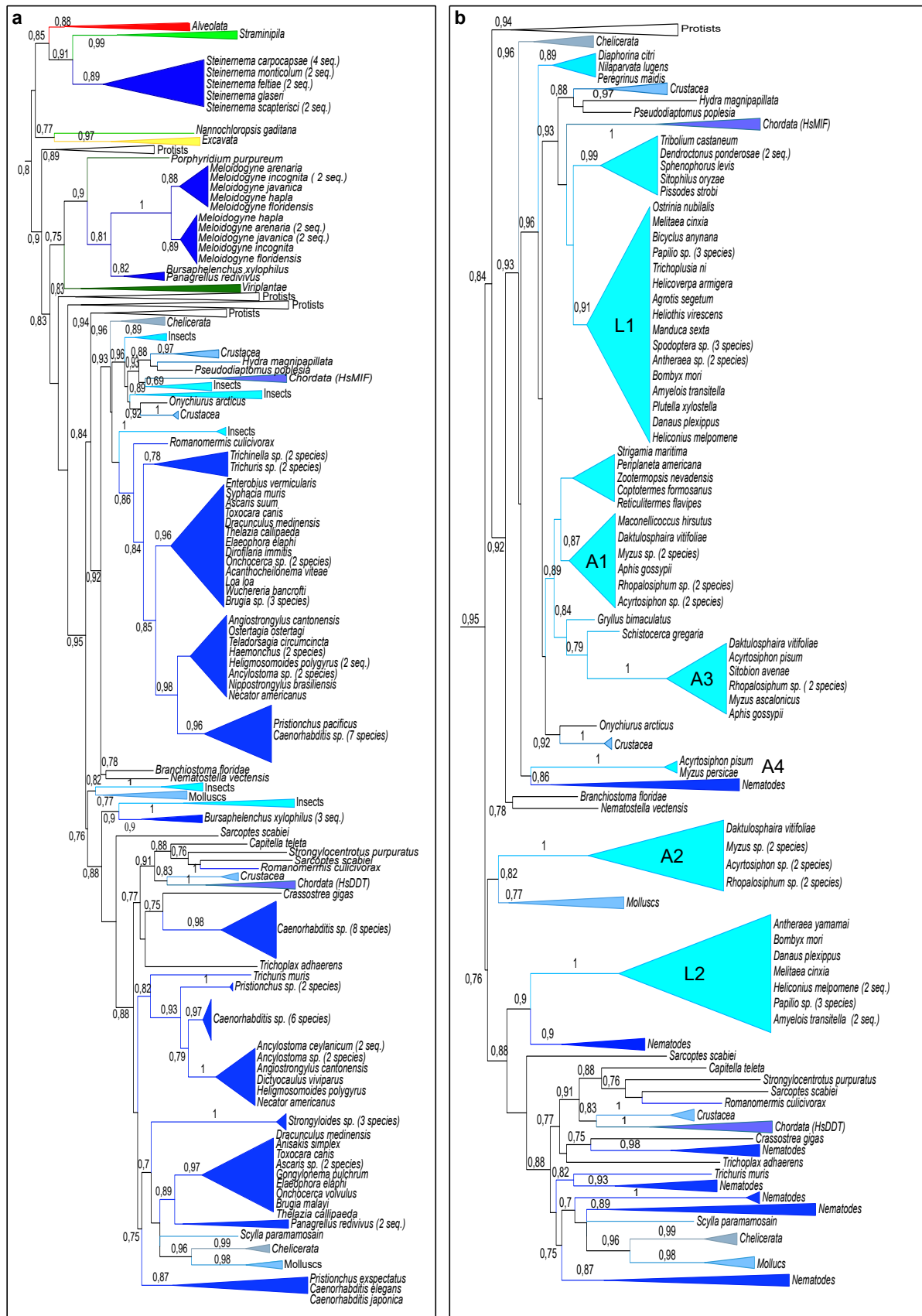


Figure S5: Maximum likelihood phylogeny of MIF sequences from nematodes and insects. Results of maximum likelihood (ML) analyses of MIF sequences from nematodes (a) and

insects (**b**). Statistical confidence values are indicated next to each branch when superior to 0.7 according to the approximate likelihood-ratio test (aLRT).