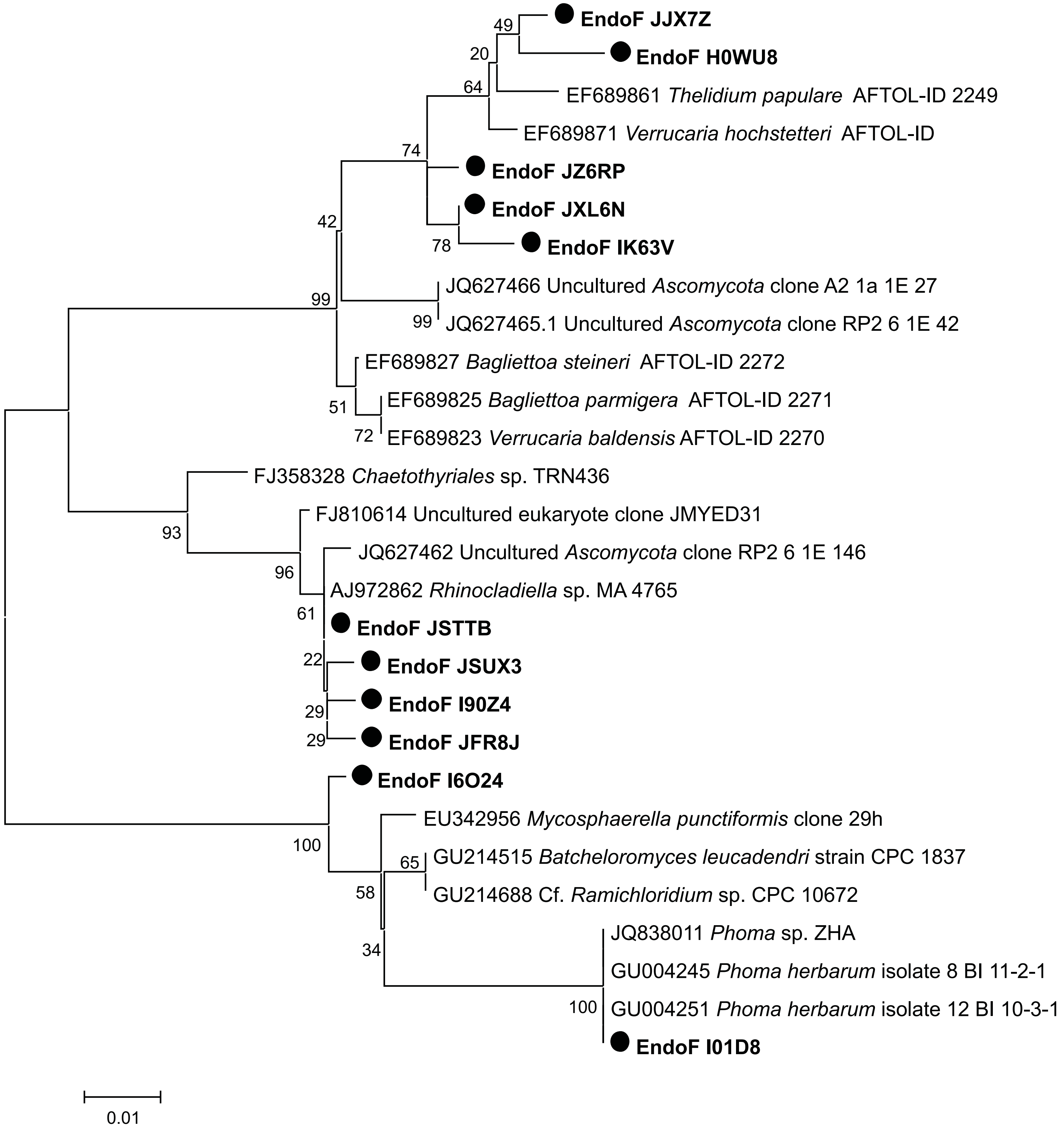
Supplemental Figure 1. Maximum likelihood (ML) phylogenetic tree illustrating the inferred relationship between 18S rRNA gene sequences (460bp) showing the position of fungal members of the GH endolithic community (● **bold)** related to the most similar GenBank sequences. Bootstrap values (expressed as percentages of 500 replications) are shown at branch nodes. Similar topologies were recovered in trees generated with the neighbor-joining algorithm. Bar, 0.1 substitutions per nucleotide position.

Supplemental Figure 2. Maximum likelihood (ML) phylogenetic tree illustrating the inferred relationship between 23S rRNA plastid targeting gene sequences (393bp) showing the position of pre-dominantly bacterial members and few algal members of the GH endolithic community (● **bold)** related to the most similar GenBank sequences. Bootstrap values (expressed as percentages of 500 replications) are shown at branch nodes. Similar topologies were recovered in trees generated with the neighbour-joining algorithm. Bar, 0.1 substitutions per nucleotide position.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● EndoF I6O24
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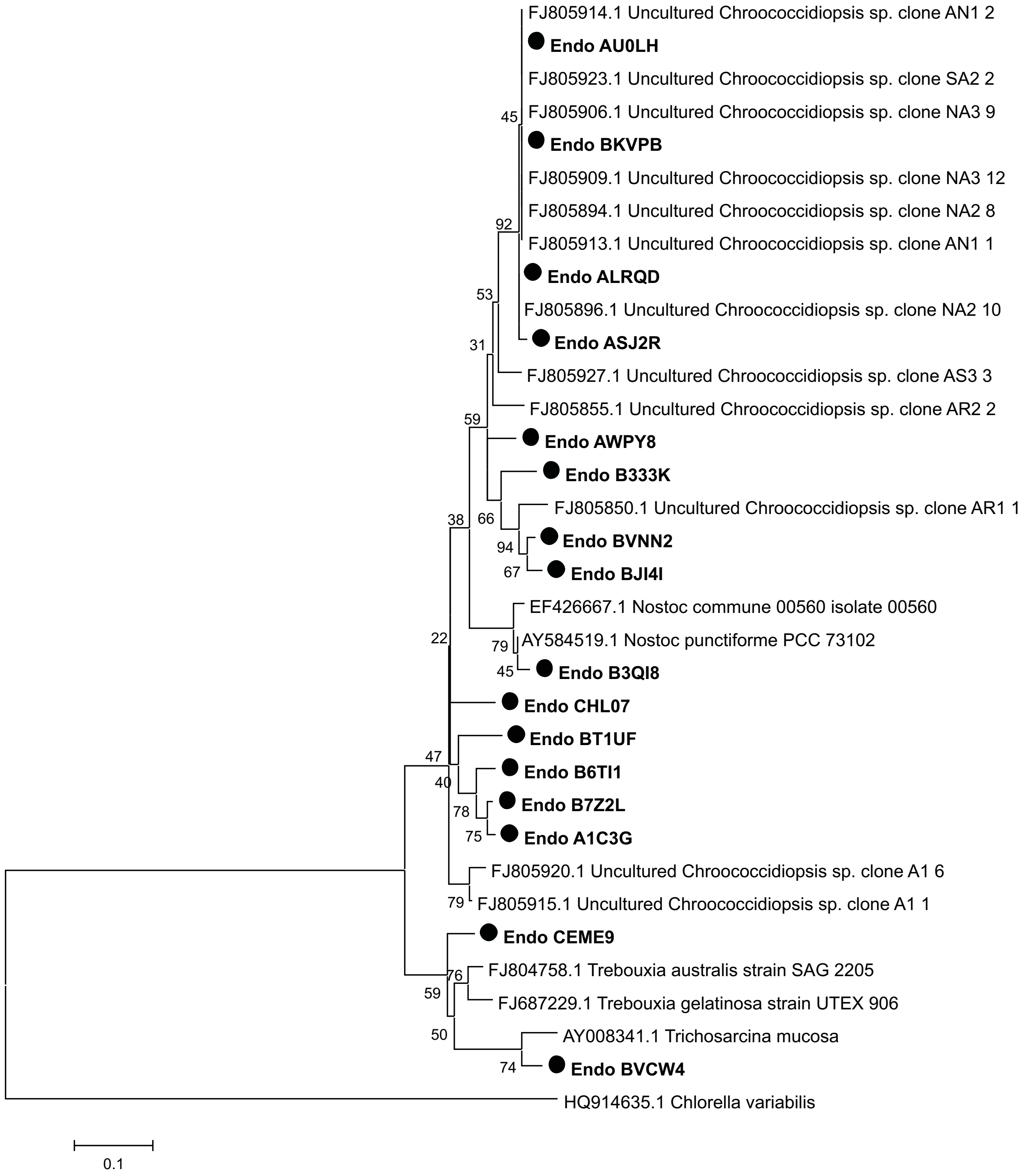
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