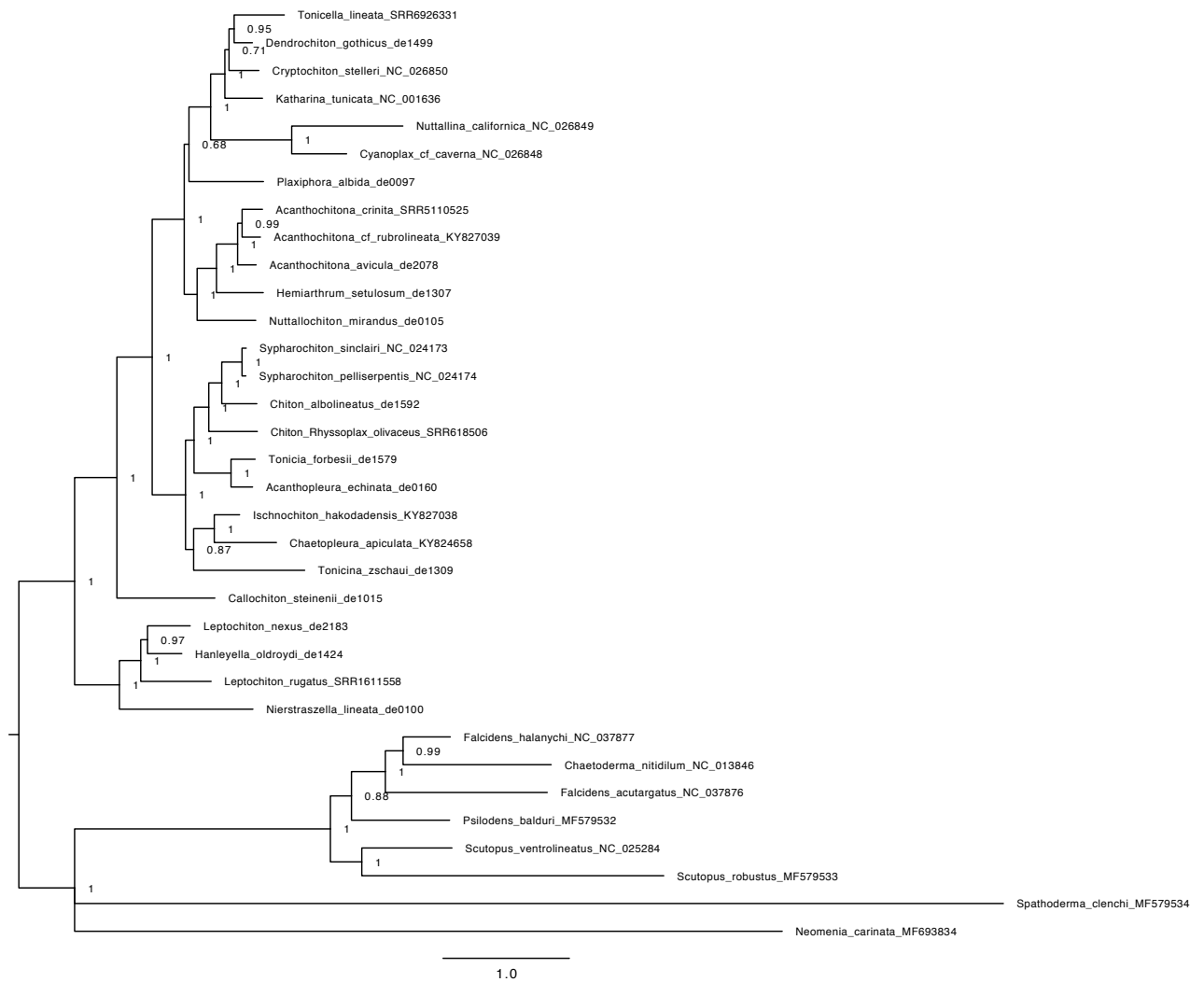
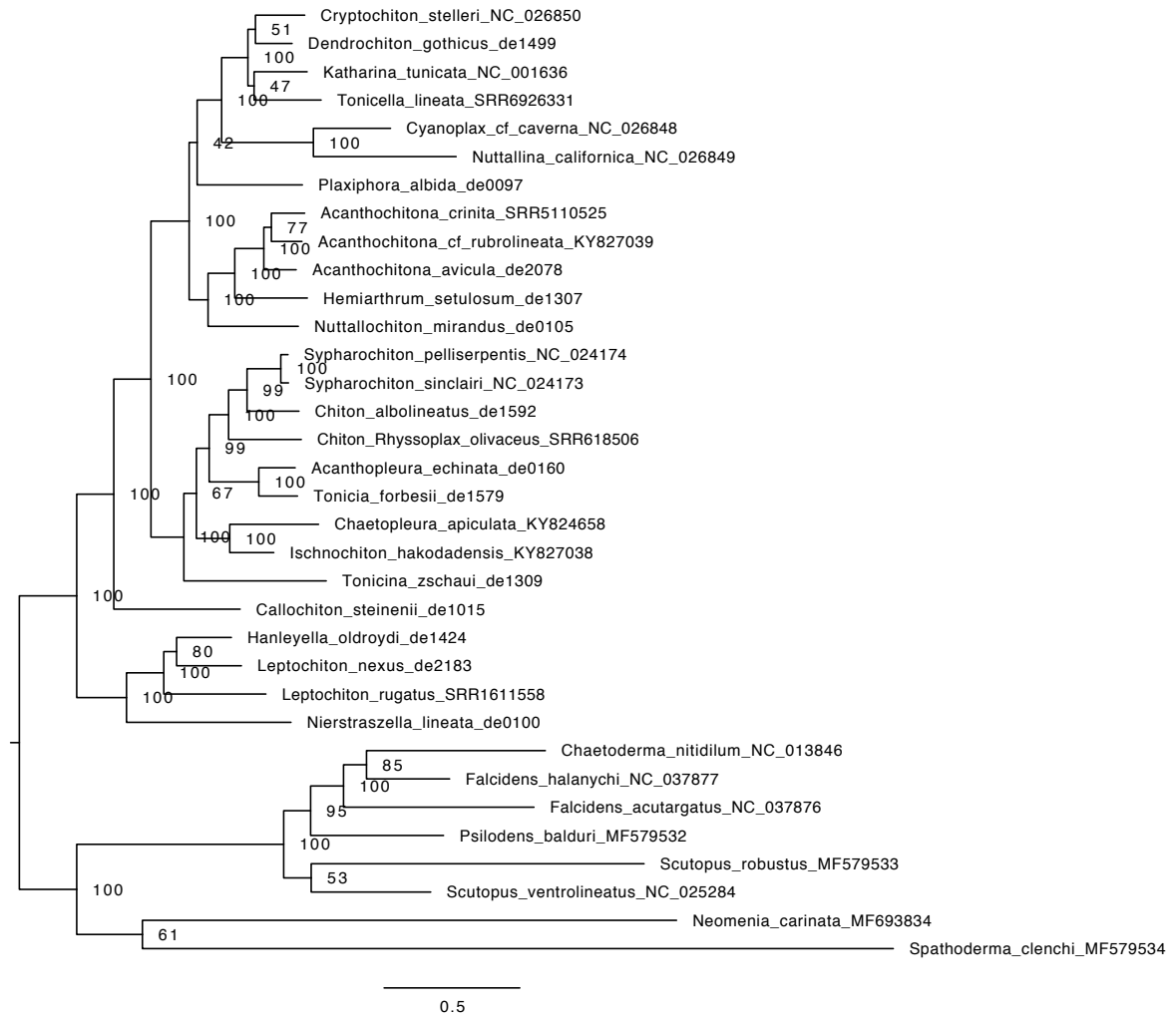


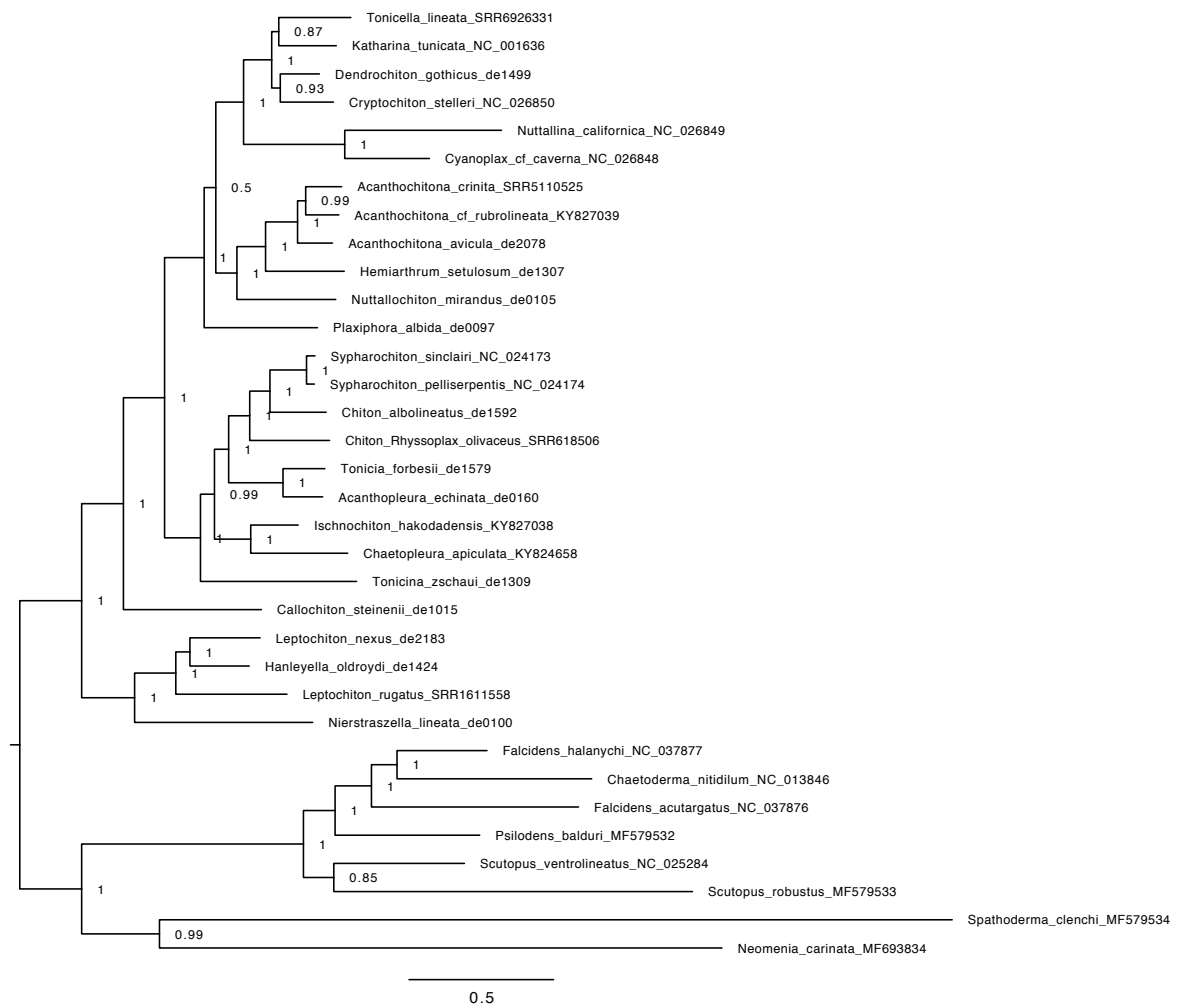
Partitioned Bayesian phylogram inferred from the combined (protein + rRNA) dataset in MrBayes. Numbers at nodes are posterior probabilities and scale bar is in expected substitutions site⁻¹.



Bayesian phylogram inferred from the protein dataset under the CAT-GTR+ Γ 4 model in PhyloBayes. Numbers at nodes are posterior probabilities and scale bar is in expected substitutions site⁻¹.



Maximum likelihood phylogram inferred from the protein dataset under the mtZOA+F+I+Γ4 model in IQTREE. Numbers at nodes are non-parametric bootstrap proportions (%) and scale bar is in expected substitutions site⁻¹.



Bayesian phylogram inferred from the protein dataset under the mtZOA+ Γ 4 model in PhyloBayes. Numbers at nodes are posterior probabilities and scale bar is in expected substitutions site⁻¹.