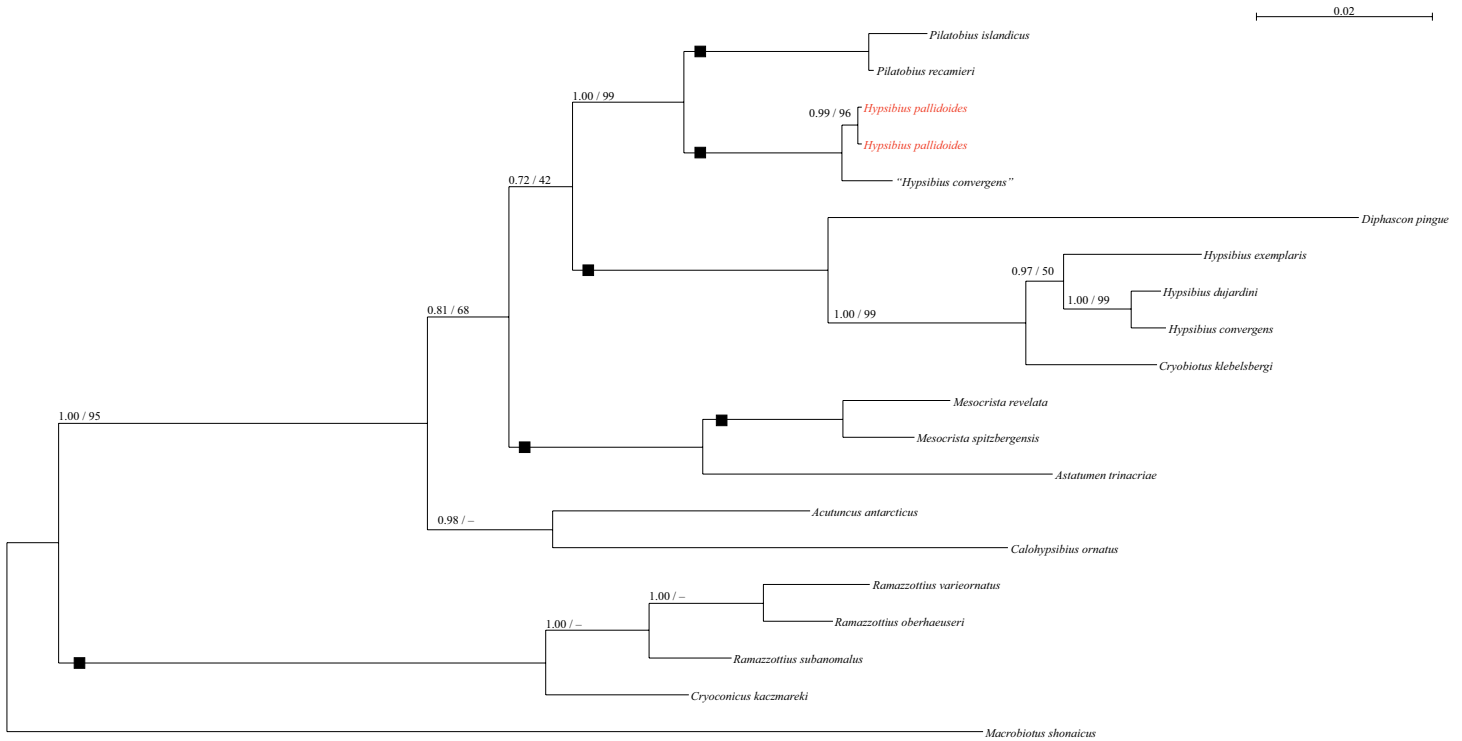


Supplementary Material 2



The phylogeny of Hysibioidae based on concatenated 18S + 28S sequences. Numbers at nodes indicate Bayesian posterior probability values (BI, first values) and bootstrap values (ML, second values). Black dots indicate the nodes supported by values of 1.0/100% with both methods. Scale bar and branch lengths refer to the Bayesian analysis.