



**Figure S2.** Phylogenetic relationships of *Coxobolellus* species based on maximum likelihood analysis (ML) and Bayesian inference (BI) of 458 bp of the 16S rRNA alignment. Numbers at nodes indicate branch support based on bootstrapping (ML) / posterior probabilities (BI). Scale bar = 0.06 substitutions/site. # indicates branches with <50% ML bootstrap support and <0.95 Bayesian posterior probability. - indicates non-supported branches.