**Legends to supplementary materials**

**Table S1.** Collection sites (coordinates and quadrats of central European zoological mapping grid) pertaining to Renicolidae specimens examined for the analysis of prevalence and intensity of infection, and identification numbers of the examined specimens deposited in the Commenius Museum, Přerov, Czech Republic.

**Table S2.** Alignment of trimmed ITS2 locus corresponding to nt. 1-582 (582 bp) of Prosthogonimus cuneatus KP192736, which consisted of partial 5.8S rDNA, full-length ITS2 and partial 28S rDNA sequence.

**Table S3.** Alignment of trimmed 28S rDNA locus corresponding to nt. 192-3495 (304 bp) of Lepidophyllum steenstrupi AY157175, which consisted of partial LSU rRNA coding sequence.

**Table S4.** Alignment of trimmed CO1 locus corresponding to nt. 119-683 (565 bp) of Renicola buchanani KF512572, which consisted of partial CO1 coding sequence, short non-coding region and partial tRNA-Thr coding sequence.

**Table S5.** Alignment of trimmed ITS2 locus corresponding to nt. 1-182 (182 bp) of Schistogonimus rarus KP192760, which consisted of partial ND1 coding sequence.

**Table S6.** Maximum likelihood fits of 24 nucleotide substitution models for the ITS2 locus (6 sequences with a total of 643 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information critetion, Akaike information criterion (corrected) and maximum likelihood values.

**Table S7**. Maximum likelihood fits of 24 nucleotide substitution models for the 28S rDNA locus (7 sequences with a total of 304 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information critetion, Akaike information criterion (corrected) and maximum likelihood values.

**Table S8.** Maximum likelihood fits of 24 nucleotide substitution models for the CO1 locus (17 sequences with a total of 565 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information critetion, Akaike information criterion (corrected) and maximum likelihood values.

**Table S9.** Maximum likelihood fits of 24 nucleotide substitution models for the ND1 locus (7 sequences with a total of 182 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information critetion, Akaike information criterion (corrected) and maximum likelihood values.

**Figure S1.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Brachylaimoidea ITS2 locus. Color of branches indicates Bayesian posterior probabilities.

**Figure S2.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Brachylaimoidea 28S rDNA locus. Color of branches indicates Bayesian posterior probabilities.

**Figure S3.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Brachylaimoidea CO1 locus. Color of branches indicates Bayesian posterior probabilities.

**Figure S4.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Brachylaimoidea ND1 locus. Color of branches indicates Bayesian posterior probabilities.