



**SUPPLEMENTARY FILE 1.** Bayesian analysis based on the 18S rDNA dataset. Values at the nodes indicate statistical support estimated by three methods—MrBayes posterior-node probability (left), maximum-likelihood bootstrap (middle), and maximum parsimony bootstrap (right). Asterisk represents full support. Scale bar shows the estimated number of substitutions per site. Newly sequenced strains are marked in bold. Those sequences containing the IB3 group I introns are marked by a triangle.