Figure S32. Trace plots of log likelihood (lnL) of phylogenetic trees of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.
Figure S33. Density plots of log likelihood (lnL) of phylogenetic trees of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset. Red values indicate values outside the 95% credibility intervals.
Figure S34. Trace plots of log prior parameters (lnPrior) of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.
Figure S35. Density plots of log prior parameters (lnPrior) of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset. Red values indicate values outside the 95% credibility intervals.
Figure S36. Tree topology trace plots of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.
Figure S37. Density plots of tree topology trace of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset. Red values indicate values outside the 95% credibility intervals.
Figure S38. Plots showing correlations between tree topology and continuous model parameters of the first run of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.
Figure S39. Plots showing correlations between tree topology and continuous model parameters of the second run of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.
Figure S40. Topological autocorrelation plots of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.
Figure S41. Plots showing cumulative split frequencies for 20 most variable clades of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset
Figure S42. Plots showing cumulative change in split frequencies of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset
Figure S43. Tree space heatmaps for 100 trees of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.
Figure S44. NMDS plots for 100 trees of two runs of the Phycas MCMC analyses of the unmasked 18S rRNA gene + ITS region dataset.