Figure S45. Trace plots of log likelihood (lnL) of phylogenetic trees of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93.
Figure S46. Density plots of log likelihood (lnL) of phylogenetic trees of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93. Red values indicate values outside the 95% credibility intervals.
Figure S47. Trace plots of log prior parameters (lnPrior) of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93.
Figure S48. Density plots of log prior parameters (lnPrior) of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93. Red values indicate values outside the 95% credibility intervals.
Figure S49. Tree topology trace plots of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93.
Figure S50. Density plots of tree topology trace of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93. Red values indicate values outside the 95% credibility intervals.
Figure S51. Plots showing correlations between tree topology and continuous model parameters of the first run of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93
Figure S52. Plots showing correlations between tree topology and continuous model parameters of the second run of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93
Figure S53. Topological autocorrelation plots of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93.
Figure S54. Plots showing cumulative split frequencies for 20 most variable clades of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93.
Figure S55. Plots showing cumulative change in split frequencies of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93.
Figure S56. Tree space heatmaps for 100 trees of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93
Figure S57. NMDS plots for 100 trees of two runs of the Phycas MCMC analyses of the 18S + 5.8S +28S rRNA gene dataset masked with a cut-off value of 0.93