

Supplementary figure legends

Figure S1. NJ tree of Rep amino acid sequences based on equal input model. Numbers on the branches represent the percentages of 1000 bootstrap samples supporting the branch; only values $\geq 80\%$ are shown.

Figure S2. 50% majority-rule consensus Bayesian tree based on JTT + Γ model. Only the topology, not the branch lengths are shown. Numbers on the branches represent Bayesian posterior probabilities.

