Supplementary Figure 1. Phylogenetic analysis of the relationships of Trypanosoma spp. based on the partial glycosomal glyceraldehyde phosphate dehydrogenase (gGAPDH).

The tree was inferred using the Minimum Evolution (ME, Kimura 2-parameter (K2P) distances) method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test using ME (1000 replicates) and Maximum Likelihood (ML, 100 replicates), and Bayesian Method (BM, posterior probability) are shown next to the branches. The ML model (K2P) included a discrete gamma distribution and allowed for invariable sites. The BM was based on K2P model with estimated discrete gamma distribution and proportion of invariable sites. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. There were a total of 826 positions in the final dataset.

