Additional File 4: Figure S2: Phylogenetic tree of NASP proteins from different eukaryotic lineages reconstructed using entire protein sequences. Tree topology corresponds to bootstrap consensus ML tree reconstructed under the rtREV+G+F model. Branch lengths do not reflect genetic distance. Posterior probability values are indicated as underlined whereas bootstrap values based on 1000 replicates for the ML tree are indicated in light-face and are only reported when at least ≥ 50%. For Bayesian analysis the average standard deviation of split frequencies from two runs was 0.0072. Different taxonomic groups are indicated in the right margin. *Trypanosoma cruzi* and *Trypanosoma brucei* were used as out groups to root the tree.