**Additional File 6: Figure S4. A:** Phylogenetic relationship among different *NASP* orthologs. Trees were reconstructed using nucleotide coding sequences with ML and MP methods. The tree topology corresponds to bootstrap consensus ML estimations under the GTR+G+I model. Branch lengths do not reflect genetic distance. Confidence values for ML and MP trees are based on 1000 bootstrap replicates and are indicated ($\geq$ 50%) in light-face and bold-face (underlined), respectively. *Trypanosoma cruzi* and *Trypanosoma brucei* were used as out groups to root the tree. **B:** Overall nucleotide diversity among four TPRs corresponding to the lineages represented in figure S4A. A sliding window approach was used to calculate the overall synonymous/ non-synonymous differences per site.
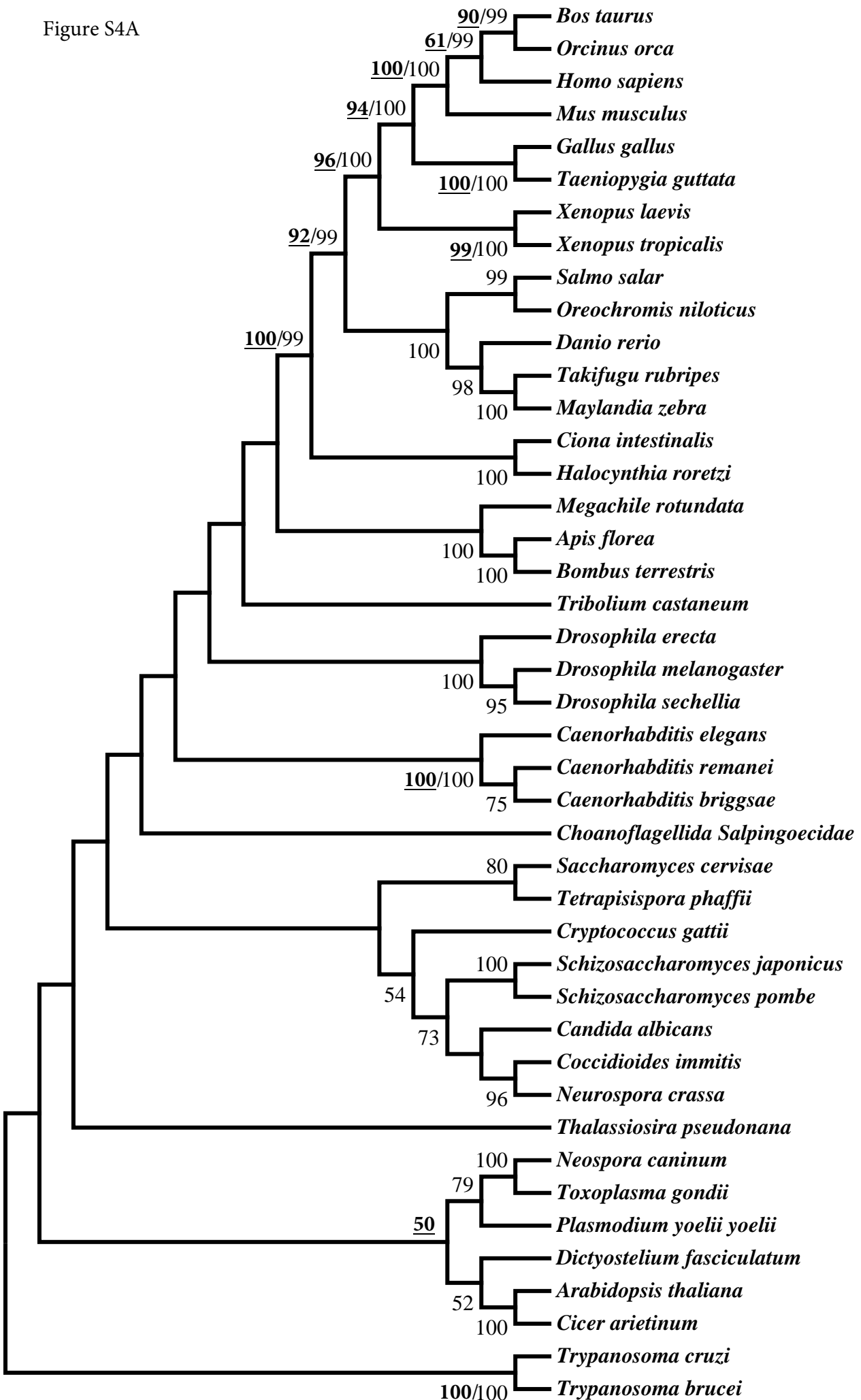
Figure S4A

Figure S4B