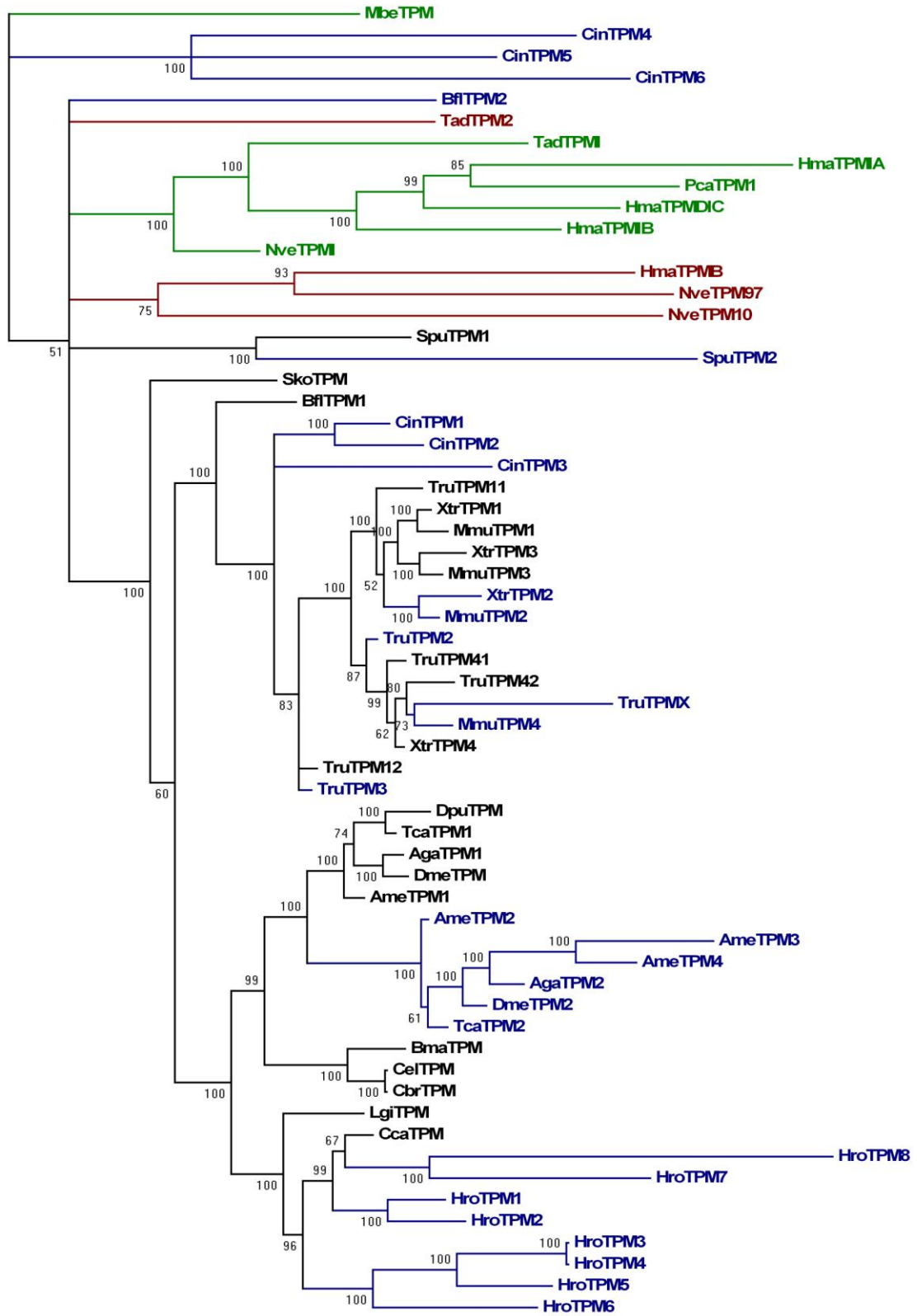


Figure S7

A)



B)

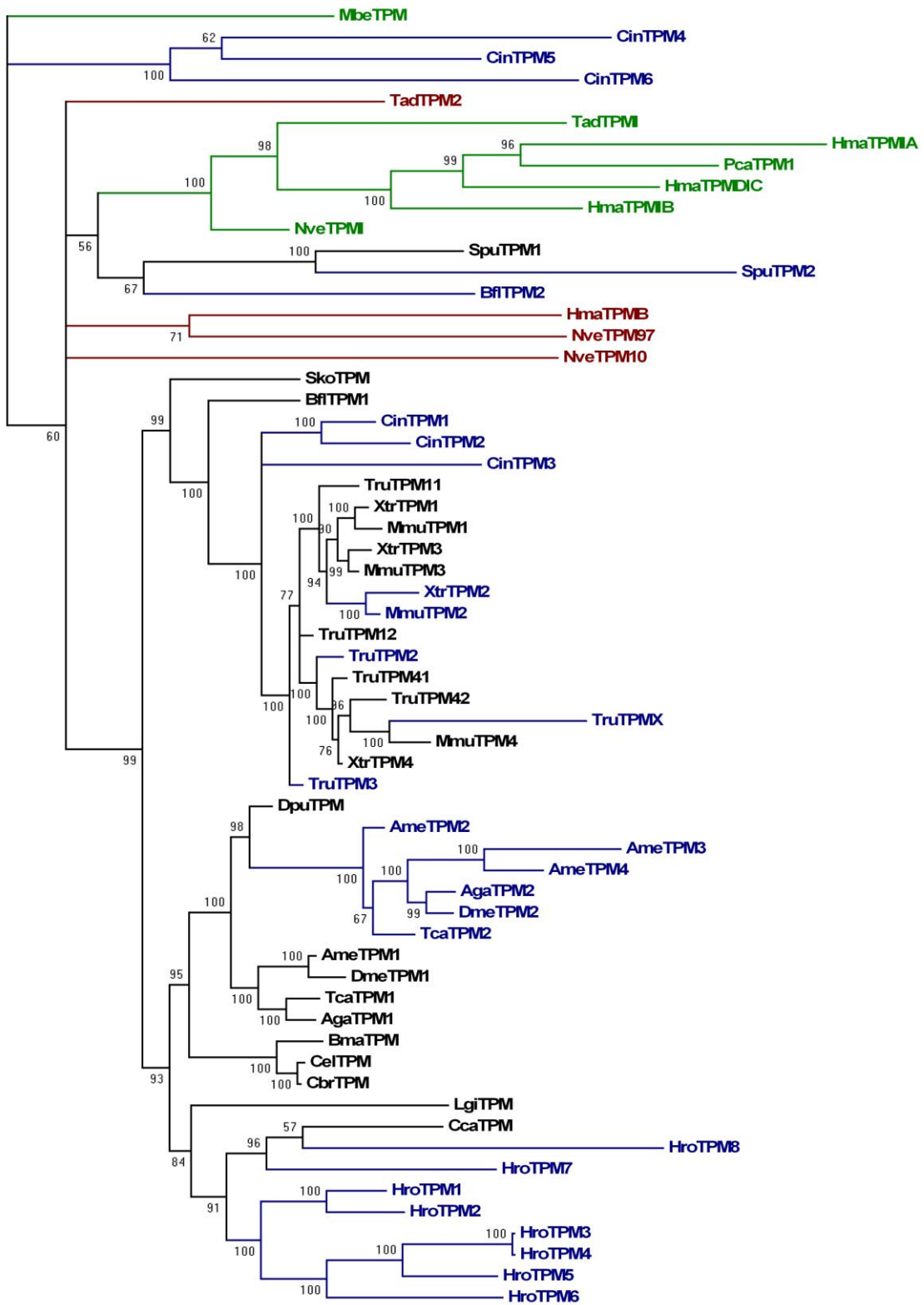


Figure S7 - Phylogenetic analysis of metazoan TPM genes.

Two independent randomly selected sets of exons 3 to 9 were generated to assess the global phylogenetic relationships among the TPM genes (see Methods). A) Bayesian inference tree using the first replicate estimated under the JTT + Γ model as recommended by Prottest. B) Bayesian inference tree using the second replicate estimated under the RtRev + Γ model as recommended by Prottest. In both cases, the choanoflagellate *Monosiga brevicollis* was used as outgroup. Species are abbreviated as follows: Aga, *Anopheles gambiae*; Ame, *Apis mellifera*; Bf, *Branchiostoma floridae*; Bma, *Brugia malayi*; Cbr, *Caenorhabditis briggsae*; Cca, *Capitella capitata*; Cel, *Caenorhabditis elegans*; Cin, *Ciona intestinalis*; Dme, *Drosophila melanogaster*; Dpu, *Daphnia pulex*; Hma, *Hydra magnipapillata*; Hro, *Helobdella robusta*; Lgi, *Lottia gigantea*; Mbr, *Monosiga brevicollis*; Mmu, *Mus musculus*; Nve, *Nematostella vectensis*; Pca, *Podocoryne carnea*; Sko, *Saccoglossus kowalevskii*; Spu, *Strongylocentrotus purpuratus*; Tad, *Trichoplax adhaerens*; Tca, *Tribolium castaneum*; Tru, *Takifugu rubripes*; and Xtr, *Xenopus tropicalis*. Numbers next to the nodes indicate posterior probabilities. Canonical non-bilaterian TPM genes are represented in green, whereas the more divergent ones are colored in red. All bilaterian genes with only one promoter are depicted in blue.