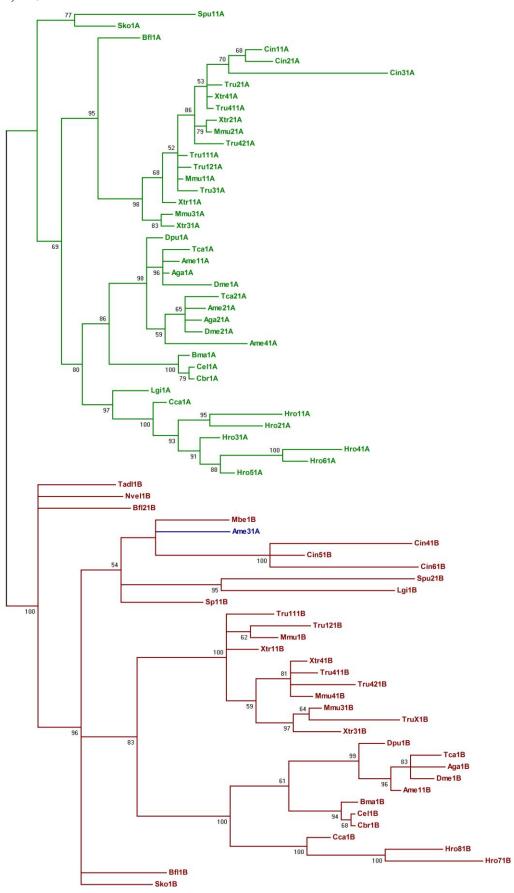
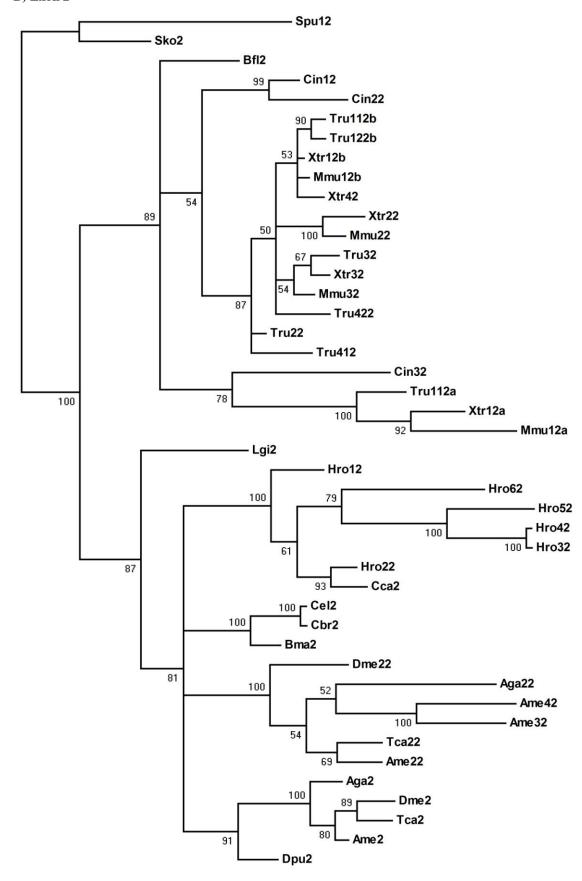
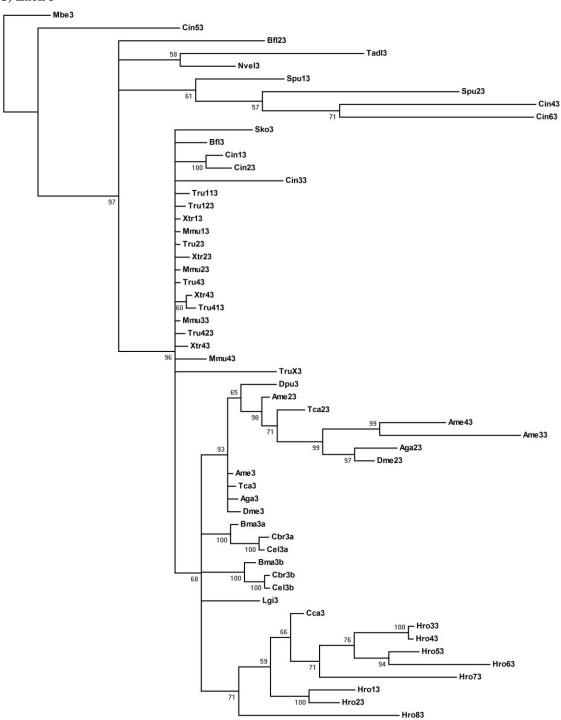
# Figure S3

## A) Exon 1

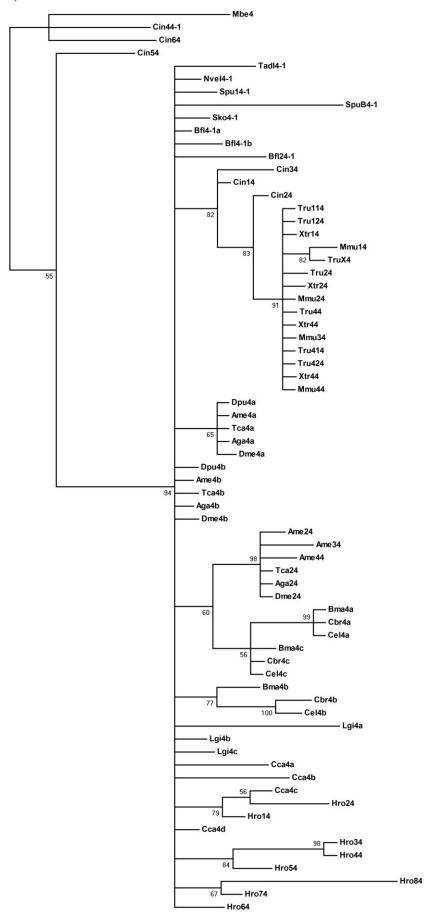




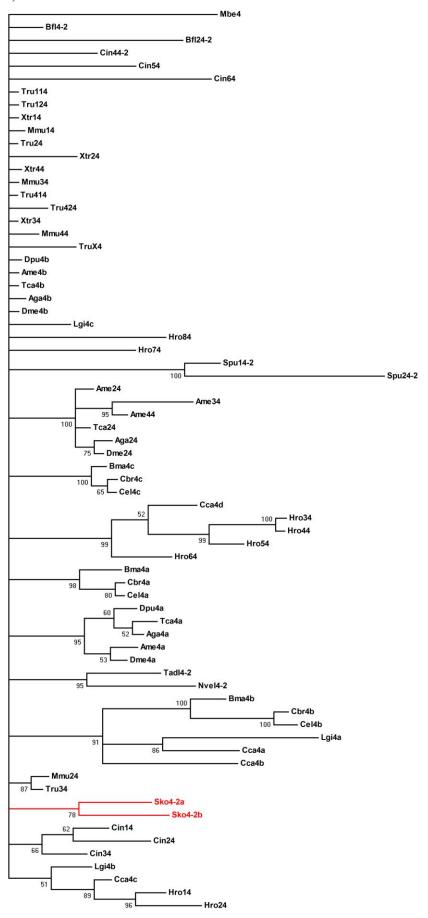
# C) Exon 3



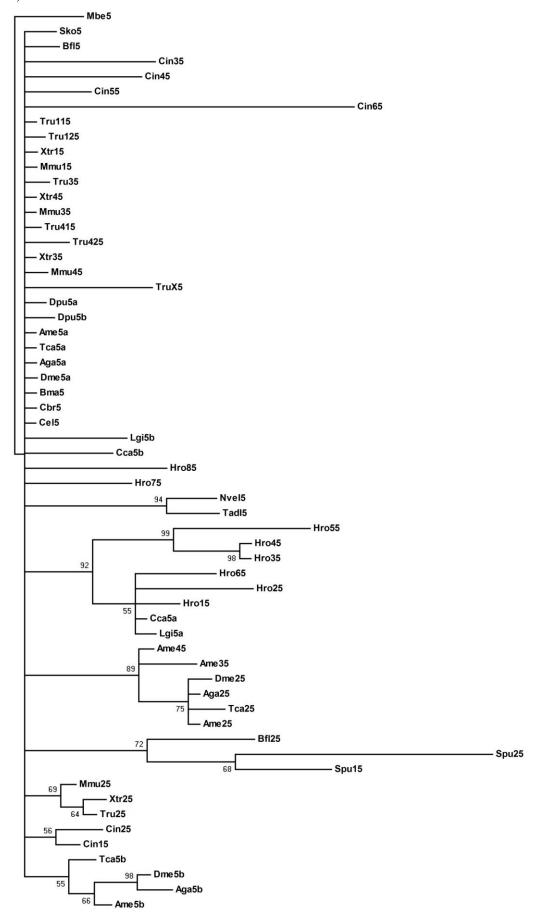
## **D) Exon 4.1**



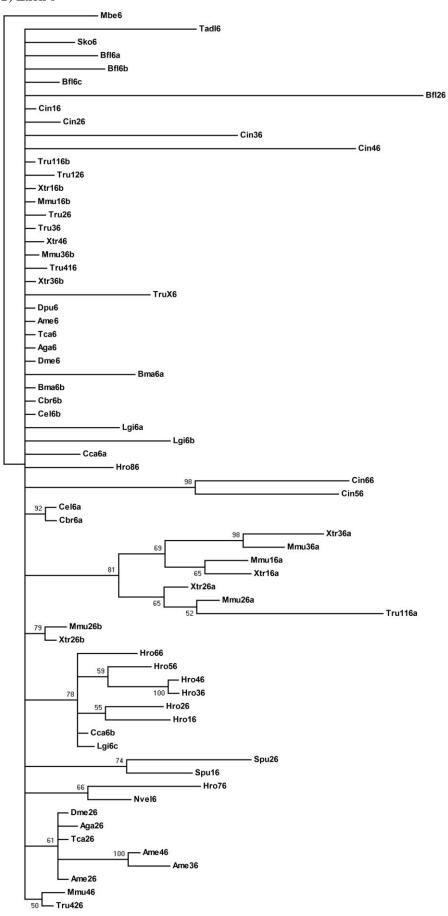
# E) Exon 4.2



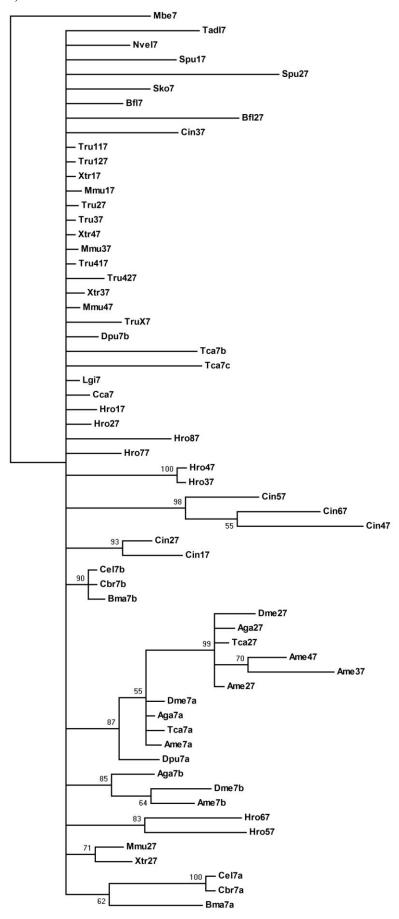
# F) Exon 5

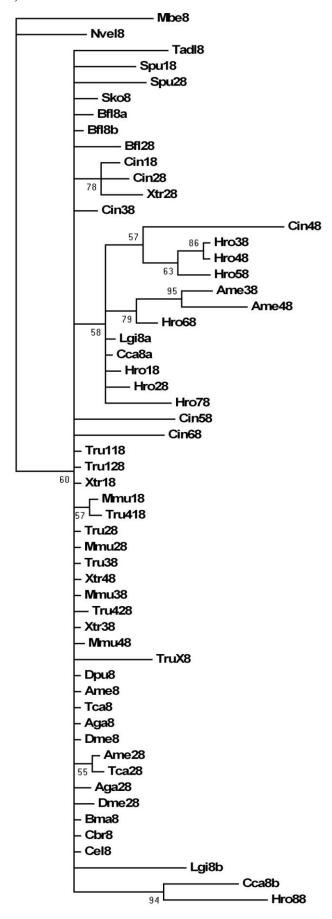


# G) Exon 6

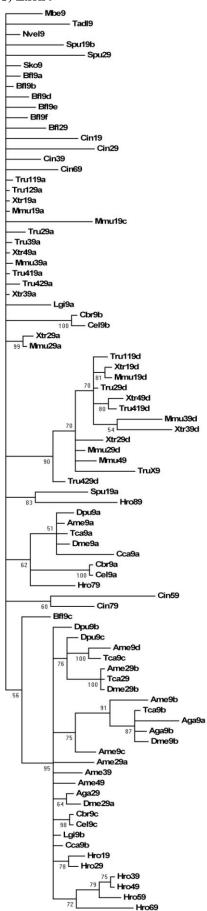


## H) Exon 7





#### J) Exon 9



#### Figure S3 - Phylogenetic analysis of the 10 ancestral TPM exons.

A) Bayesian inference tree of exons 1A and 1B estimated under the RtRev +  $\Gamma$  model as recommended by Prottest. B) Bayesian inference tree of exons 2 estimated under the RtRev +  $\Gamma$  model as recommended by Prottest. C) Bayesian inference tree of exons 3 estimated under the RtRev +  $\Gamma$  model as recommended by Prottest. D) Bayesian inference tree of exons 4.1 estimated under the JTT +  $\Gamma$  model as recommended by Prottest. E) Bayesian inference tree of exons 4.2 estimated under the JTT +  $\Gamma$  model as recommended by Prottest. F) Bayesian inference tree of exons 5 estimated under the JTT +  $\Gamma$  model as recommended by Prottest. G) Bayesian inference tree of exons 6 estimated under the JTT +  $\Gamma$  model as recommended by Prottest. H) Bayesian inference tree of exons 7 estimated under the RtRev +  $\Gamma$  model as recommended by Prottest. I) Bayesian inference tree of exons 8 estimated under the RtRev + I +  $\Gamma$  model as recommended by Prottest. J) Bayesian inference tree of exons 9 estimated under the JTT +  $\Gamma$  model as recommended by Prottest. Each taxon name includes the number of the TPM paralog within a given species (if any) followed by the number of the MATE exon, e. g. Tru119d corresponds to the MATE exon 9d of the TPM1.1 of Takifugu rubripes. 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; Hro, Helobdella robusta; Lgi, Lottia gigantea; Mbr, Monosiga brevicollis; Mmu, Mus musculus; Nve, Nematostella vectensis; 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.