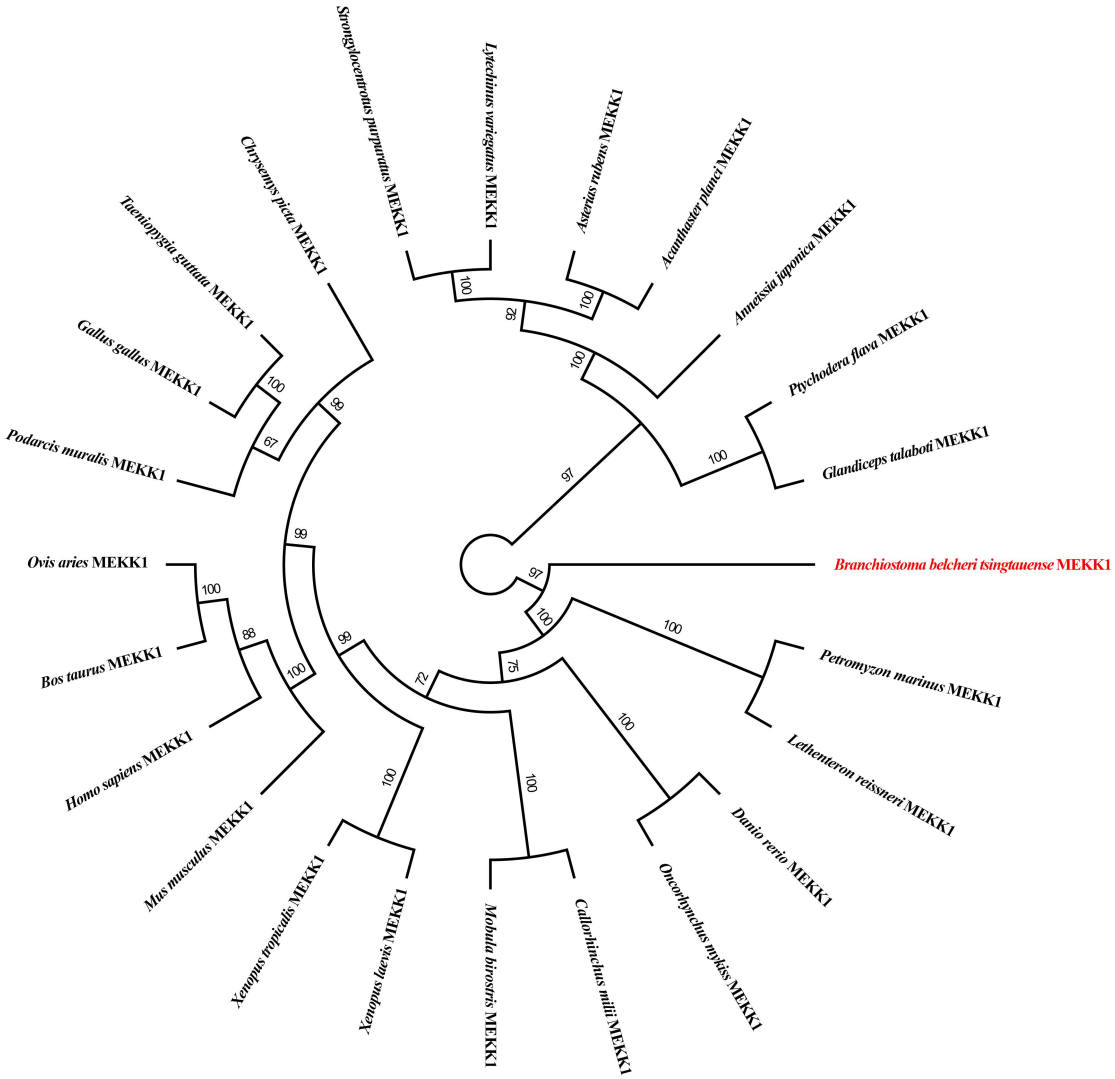

Figure S4 Phylogenetic analysis of AmphiMEKK1 and its homologs.

The maximum-likelihood method is used to construct the phylogenetic tree, with bootstrap values (1000 replicates) shown at the nodes. Echinoderms and hemichordates are used as the outgroup. The *Branchiostoma belcheri tsingtauense* sequence is highlighted in red. Model: JTT+F+R5**.**