

Figure S2

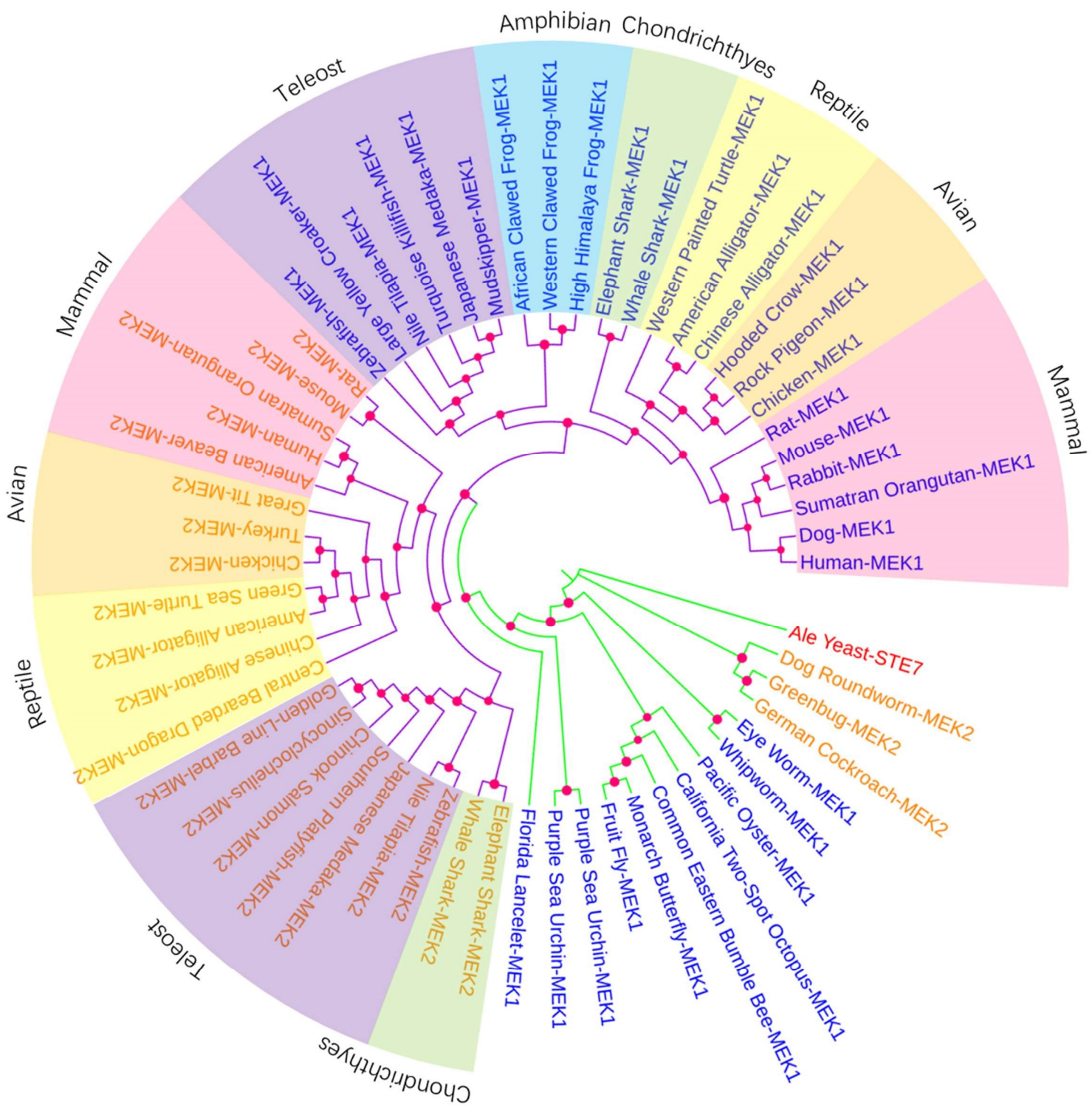


Figure S2. Phylogenetic trees of Mek1/2 from the indicated species. The tree was constructed using the neighbor-joining (NJ) algorithm with the Mega 4.1 program based on multiple sequence alignment by ClustalW. Blue font indicates Mek1s, and orange font indicates Mek2s, while the red font was STE7, a homologue of Meks from yeast. The purple branches show the Meks in vertebrates and green branches were Meks from invertebrates. Bootstrap values of 1000 replicates (%) are illustrated by pink dots. The accession numbers of selected sequences are listed in Table S1.