

Figure S15. Phylogenetic tree of 10 sequenced vertebrates. The tree was constructed with PhyML under GTR/JTT+gamma model based on CDS, protein, 1st, 2nd, 1st& 2nd, 3rd, 4d codon position of codon sequences in 3,181 genes. Each tree was run with 1,000 replications. All internal branches of the tree were 100% bootstrap supported. Note that all the tree

topologies are similar, supporting that S_g is closer to S_a .

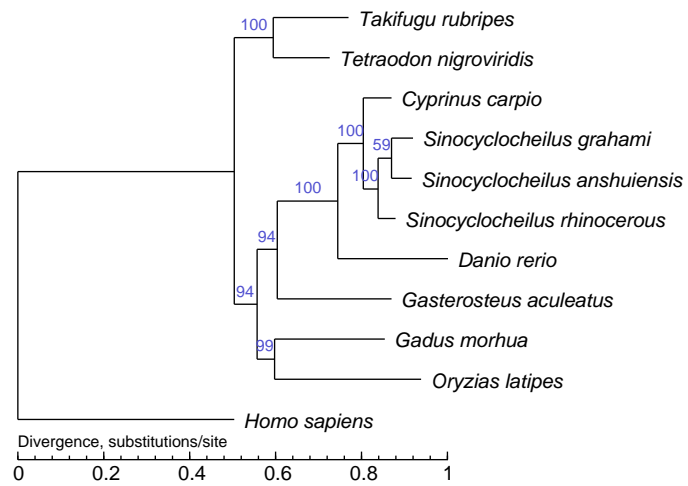


Figure S16. Phylogenetic tree based on mitochondrial CDS sequences of 10 vertebrate species with Bayes analysis.

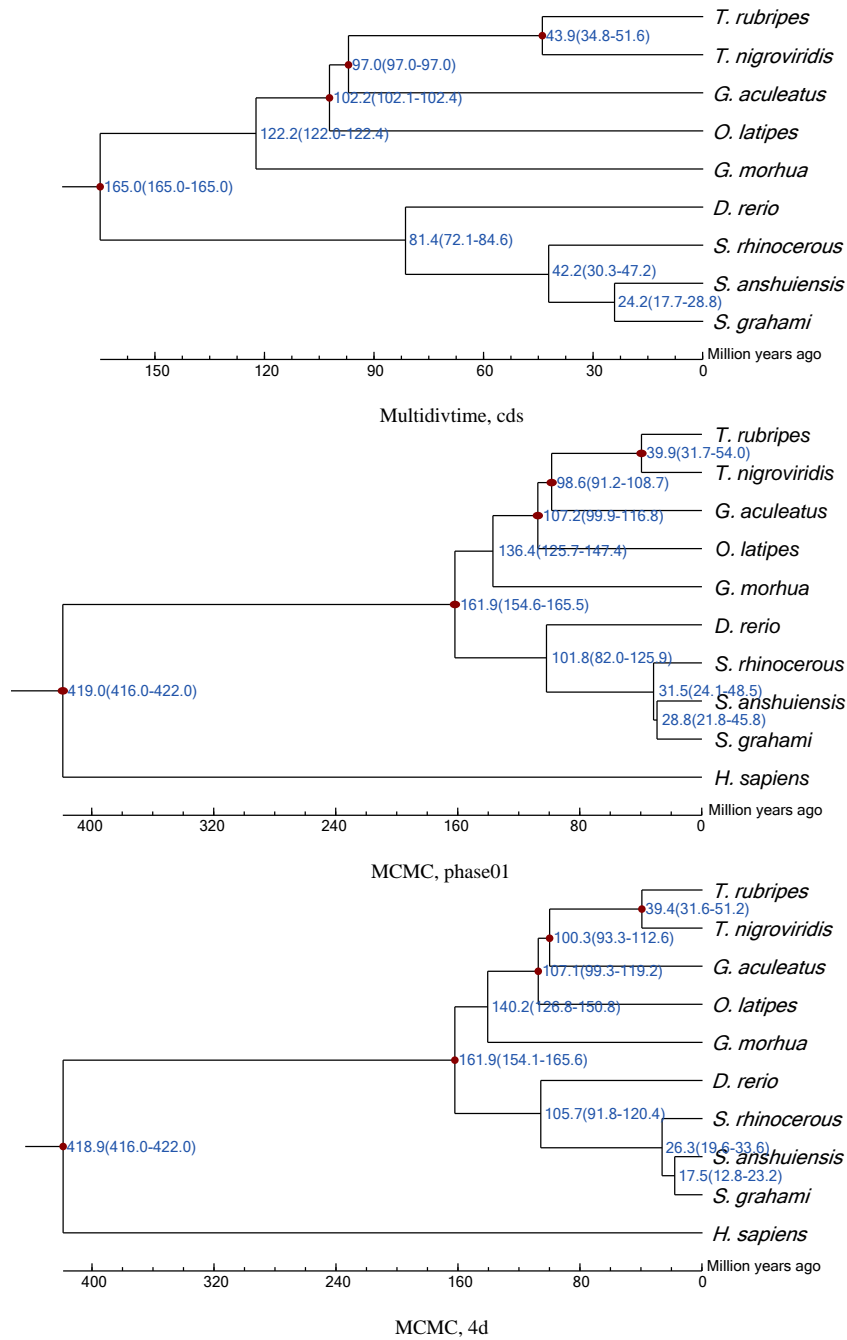


Figure S17. Divergence time of 10 sequenced vertebrates. The divergence time was estimated by PAML mcmctree or Multidivtime based on 1st & 2nd, CDS, and 4d codon position, respectively. The red dots indicated the reference divergence times from the TimeTree (<http://www.timetree.org/>).