



Figure S3 Phylogenetic tree of teleost *Ddx3a* genes used in PAML analysis. (A) Bayesian tree of teleost *Ddx3a* genes. Numbers at the nodes are Bayesian posterior probabilities. Scale bar = 0.05. (B) Maximum likelihood tree of teleost *Ddx3a* genes. Numbers at the nodes are bootstrap support values. Scale bar = 0.03. Phylogenetic reconstructions were based on the coding sequences of *Ddx3a* genes. The accession numbers of these genes at GenBank or Ensembl database are provided in Table S1.