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.