



Figure S1 (a) Maximum-likelihood nuclear phylogeny of *Nomorhamphus* and *Oryzias* reconstructed from the concatenating 272 and 148 transcripts, respectively. The numbers on branches show the maximum-likelihood bootstrap values. (b) Neighbor-joining population-averaged tree of *Nomorhamphus* and *Oryzias* based on the d_A values calculated from the 272 and 148 transcripts, respectively.