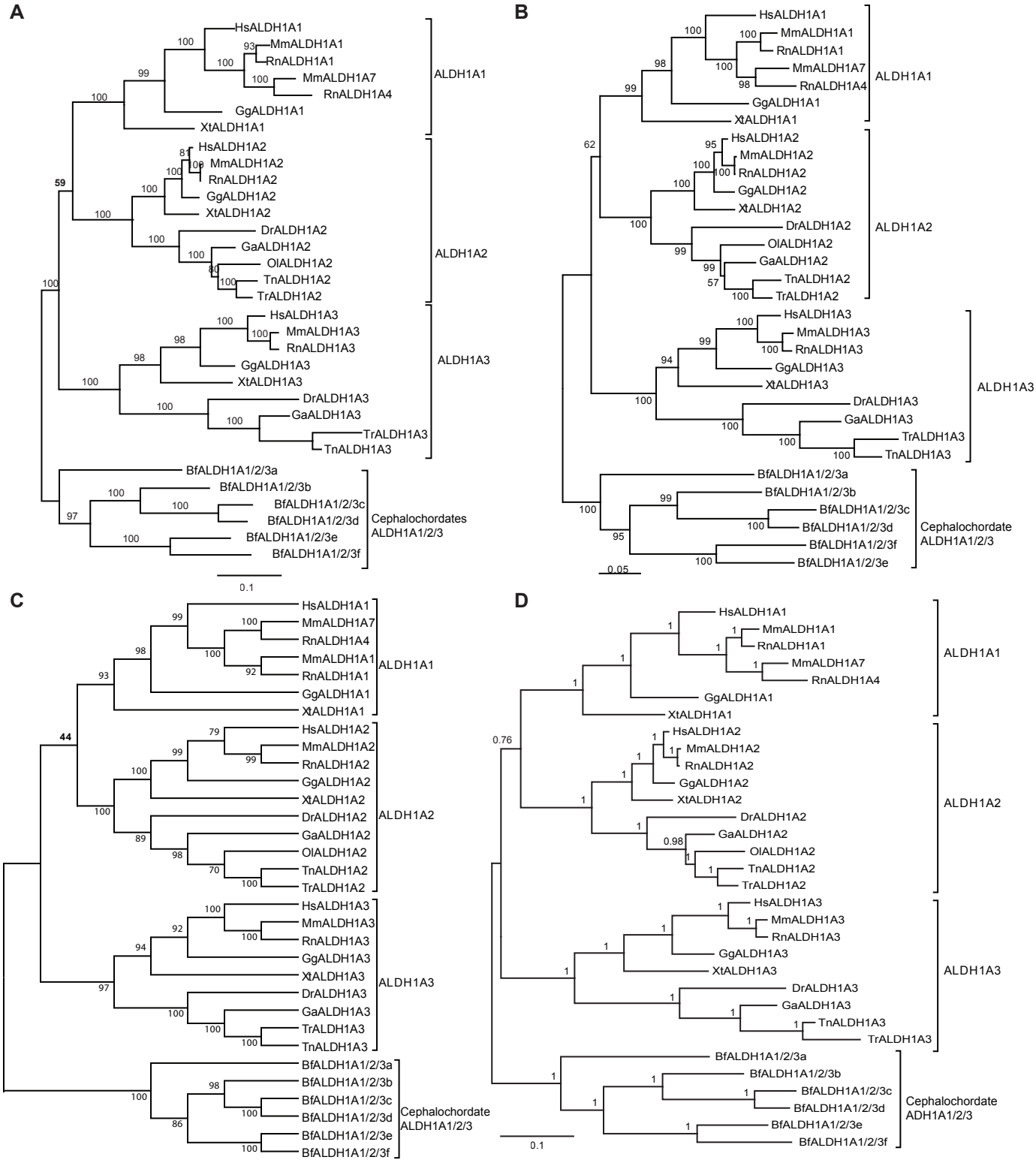

Figure S1. Phylogenetic trees of the vertebrate Aldh1A gene family, using the cephalochordate Aldh1A pro-orthologs to root the tree. The tree topology ((Aldh1a1, Aldh1a2), Aldh1a3) was obtained in all used phylogenetic methodologies: A: maximum-likelihood (ML); B: neighbor-joining (NJ); C: maximum-parsimony (MP); and D: bayesian method. Values in nodes indicate the boostrap values (A-C) and posterior probabilities (D) supporting each node of the trees. LG and JTT models rendered the same tree topology and minor differences in node support. Scale bar indicates amino-acid substitutions of branch lengths. Tetrapods: Hs, *Homo sapiens*; Mm, *Mus musculus*; Rn, *Rattus novergicus*; Gg, *Gallus gallus*; Xt, *Xenopus tropicalis*; Teleosts: Dr, *Danio rerio*; Ga, *Gasterosteus aculeatus*; Tn, *Tetraodon nigroviridis*; Tr, *Takifugu rubripes*; Cephalochordates: Bf, *Branchiostoma floridae*. Protein alingment is provided below. Accession numbers correspond to those in Cañestro et al., (2006) [59]

BfALDH1A1/2/3c
BfALDH1A1/2/3d
BfALDH1A1/2/3b
BfALDH1A1/2/3e
BfALDH1A1/2/3f
BfALDH1A1/2/3a
MmALDH1A1
RnALDH1A1
MmALDH1A7
RnALDH1A4
HsALDH1A1
GgALDH1A1
XtALDH1A1
TnALDH1A2
TrALDH1A2
OlALDH1A2
GaALDH1A2
DrALDH1A2
MmALDH1A2
RnALDH1A2
HsALDH1A2
GgALDH1A2
XtALDH1A2
MmALDH1A3
RnALDH1A3
HsALDH1A3
GgALDH1A3
XtALDH1A3
TnALDH1A3
TrALDH1A3
GaALDH1A3
DrALDH1A3