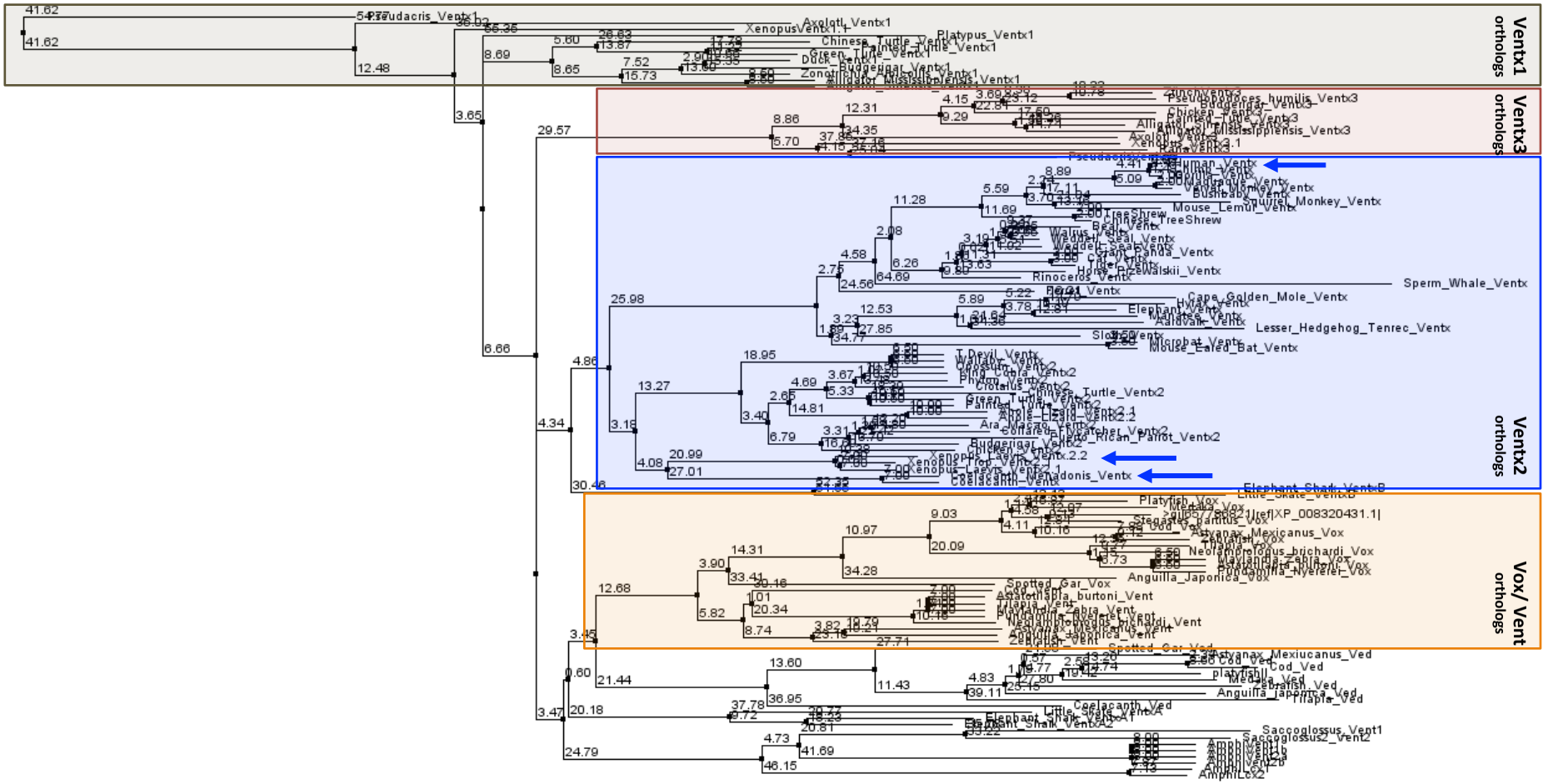

Supplementary file 2. Phylogenetic tree of *Ventx* deuterostome genes.

Boxes indicate members with orthology relationship, like coelacanth *Ventx*, *Xenopus Ventx2* and human *VENTX* (blue arrows). Sequences were collected from ENSEMBL, JGI, A-STAR and NCBI public databases (see Supplementary file 4). Ventx homeodomain sequences were aligned using Jalview software (RRID:SCR_006459) and the phylogenetic tree was obtained by Neighbor Joining analysis of percentage identity.