



**Figure S1** Vistaplots for four *Hivp* paralogs. Sequence similarity with a minimum of 50% identity between *A. burtoni* (top panel), *O. latipes* (second panel), *T. rubripes* (mid panel), *T. nigroviridis* (fourth panel), *D. rerio* (bottom panel) and *O. niloticus* (exon-intron structure on top of figure) are displayed in purple. Pink regions indicate conserved non-coding regions (CNEs). Arrows indicate the two identified CNEs in all four paralogs. Three CNEs were observed in *Hivp1* (A) and *Hivp2a* (B) in *A. burtoni*, of which two were commonly observed among teleosts. (C) Two cichlid-specific CNEs were observed in *Hivp2b*. (D) In *Hivp3b* four CNEs were observed.