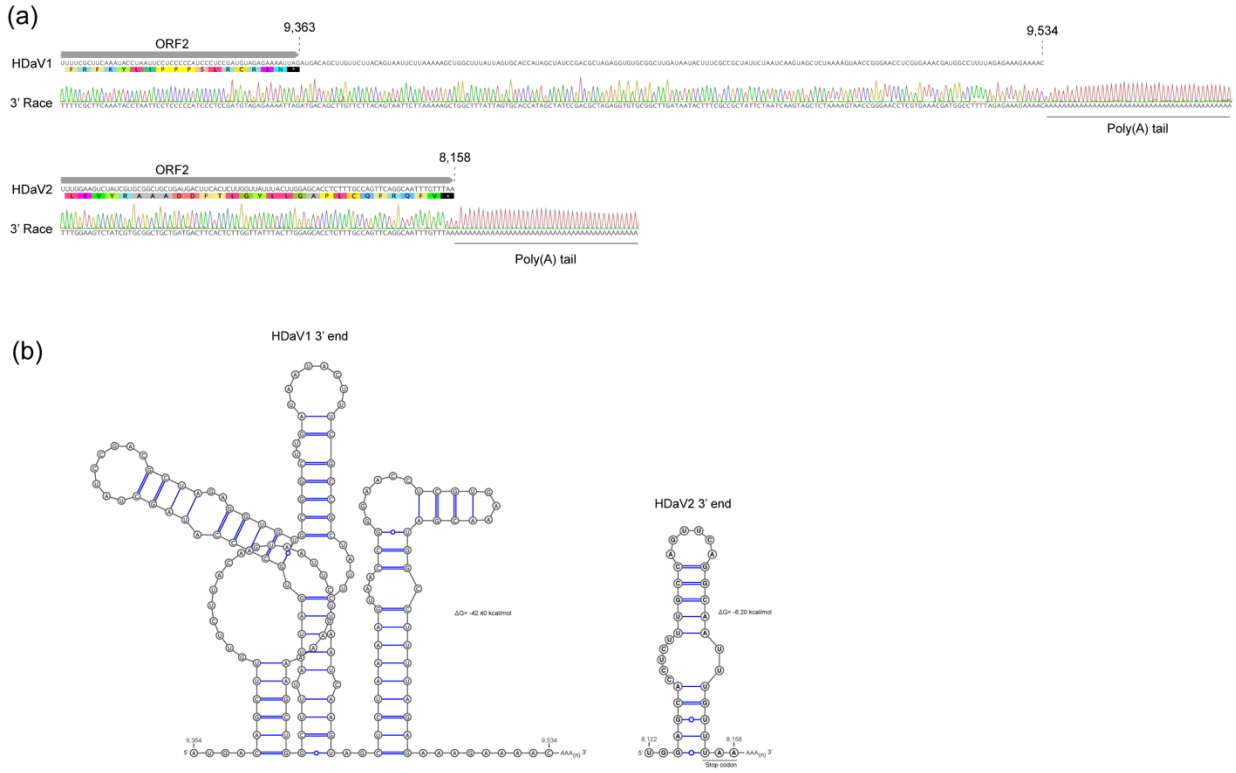
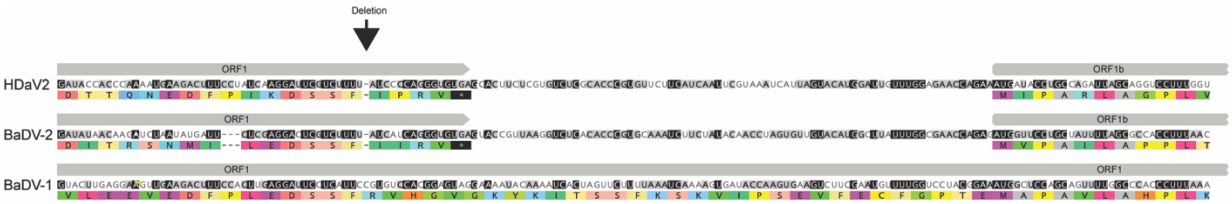



**Supplementary Figure 1.** The 3′ ends of HDaV1 and HDaV2 genomes. (a) Sanger sequencing of the 3′ RACE products. The ORF2 is presented as a grey arrow. (b) The optimal secondary structure predicted for the 3′ends of HDaV1 and HDaV2 using the RNAfold web server (http://rna.tbi.univie.ac.at//cgi-bin/RNAWebSuite/RNAfold.cgi).




**Supplementary Figure 2.** Alignment of a selected region of HDaV2 and two related viruses (BaDV-1 and BaDV-2). All ORFs are represented as arrows pointing from the 5′ to the 3′ end and are colored in grey. The protein translation is below the nucleotide sequence. The arrow shows a single nucleotide deletion that generates the two ORFs (ORF1 and ORF1b) in HDaV2 and BaDV-2.