



Fig 3. The topology of the molecular phylogenetic tree based on the full-length ORF1ab (A) and ORF2 (B) sequences of representative astrovirus species. The sequences from SMS-AstV-H1 are indicated as black triangle and SMS-AstV (GU985458). GenBank accession numbers and strain details are listed in Table S3. The scale bar indicates the estimated nucleotide sequence phylogenetic distance.