

Figure S1. Neighbor-joining tree based on alignments of the partial (319 nt) ORF1b sequences of avastroviruses. A single mamastrovirus (HAstV-3) was included as an outgroup. A distance matrix was constructed using the Kimura 2-parameter model of nucleotide substitutions (Kimura, 1980). The results of 1000 bootstrap pseudo-replicates are shown as percentage values on the branches (only values of 70% and above are shown). All analyses were performed with MEGA 4.0.

