

Fig. S4. Maximum likelihood phylogenetic tree of the capsid protein for representative members of the viral family *Astroviridae*. The scale bar represents units of substitutions per site. Genera are labeled with a black circle and recognized species are marked in grey boxes (MAstV, mammalian astrovirus; AAstV, avian astrovirus). Viruses identified in this study and the unclassified clades that they are assigned to are labeled in green. All bootstrap nodal support values are indicated if >70.

