

Fig. S5. Maximum likelihood phylogenetic tree of VP1 for members of the viral family *Caliciviridae*. The scale bar represents units of substitutions per site. Genera are labeled with a black circle. Representative viruses from currently recognized genogroups for the *Sapovirus* and *Norovirus* genera are shaded in grey boxes. Viruses identified in this study and the associated genogroups are labeled in green. All bootstrap nodal support values are indicated if >70.

