**Fig. S6**. Maximum likelihood phylogenetic tree of concatenated helicase/polymerase proteins for representative members of the *Hepe-Virga* clade. The scale bar represents units of substitutions per site. The hepe-like virus identified in this study and the clade that it is assigned to is labeled in green. All other recognized viral families are labeled in a grey box. All bootstrap nodal support values are indicated if >70.