



Figure S1: Maximum-likelihood phylogenetic tree based on syncytin-1-like sequences from bat host species obtained through NGS data. The host sequence identified in this study is highlighted in bold marked with a black circle. Branch support values are based on the Shimodaira-Hasegawa (SH-like) test. Only values equal to or greater than 95% are shown. Branch lengths are scaled to nucleotide substitutions per site.