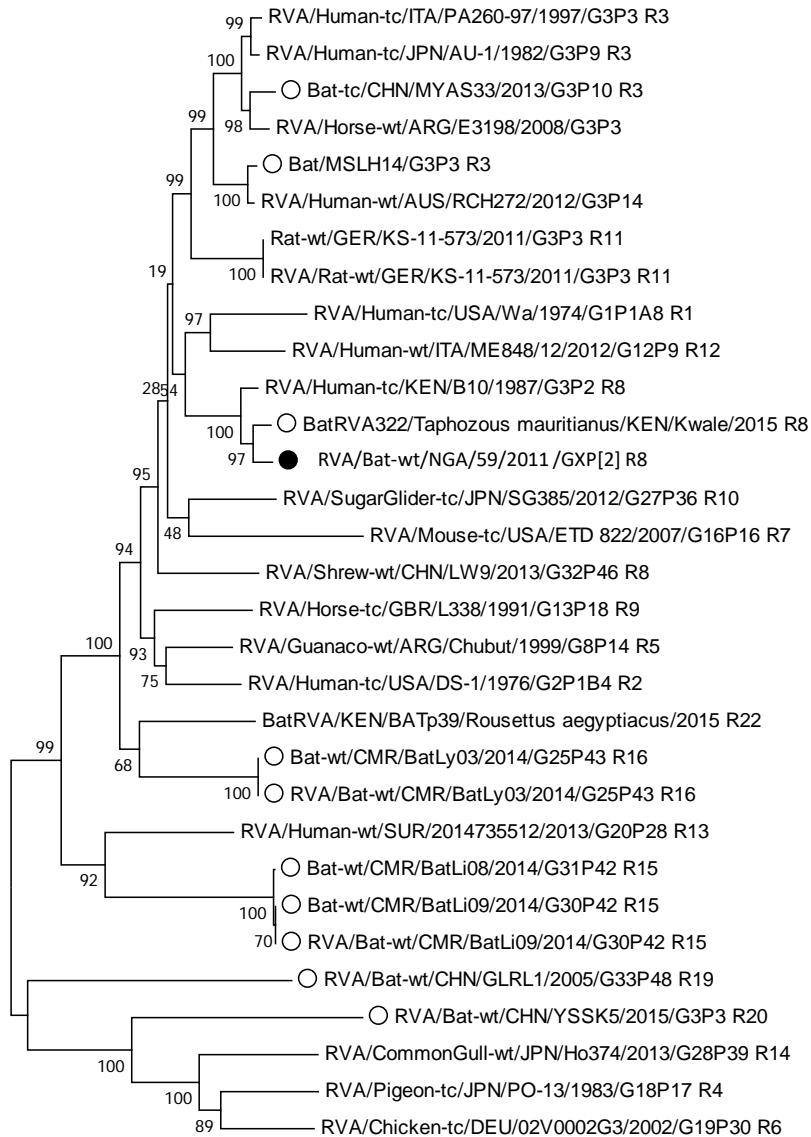


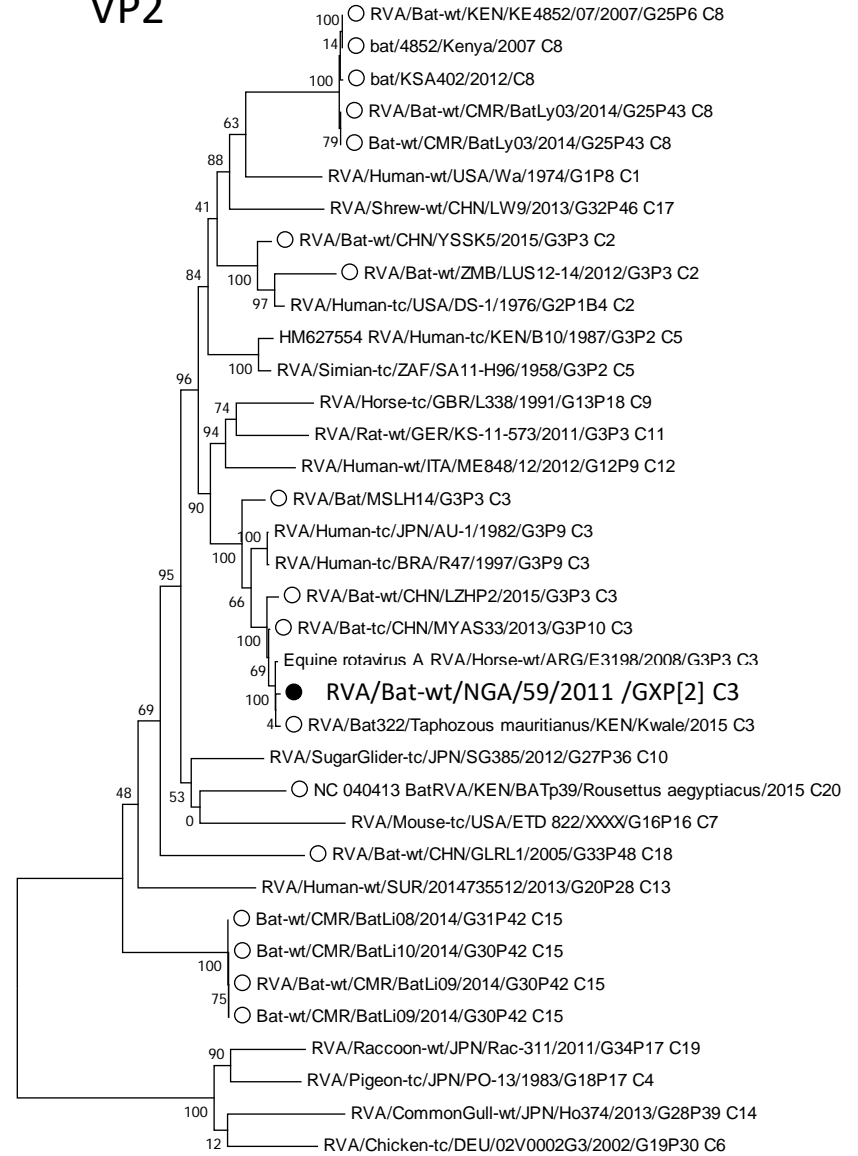
Supplementary Figure 2. Phylogenetic analysis of the available VP1, VP2, VP3, Vp4, VP6, NSP1, NSP2, and NSP3 bat rotavirus sequences. The bat rotavirus-related sequence from this study is indicated by solid circle while other known bat rotaviruses are indicated by empty circles. Phylogenetic trees were constructed using the maximum likelihood (ML) method available PhyML version 3.0 assuming a general time-reversible (GTR) model with a discrete gamma distributed rate variation among sites (G_4) and a SPR tree swapping algorithm.

VP1



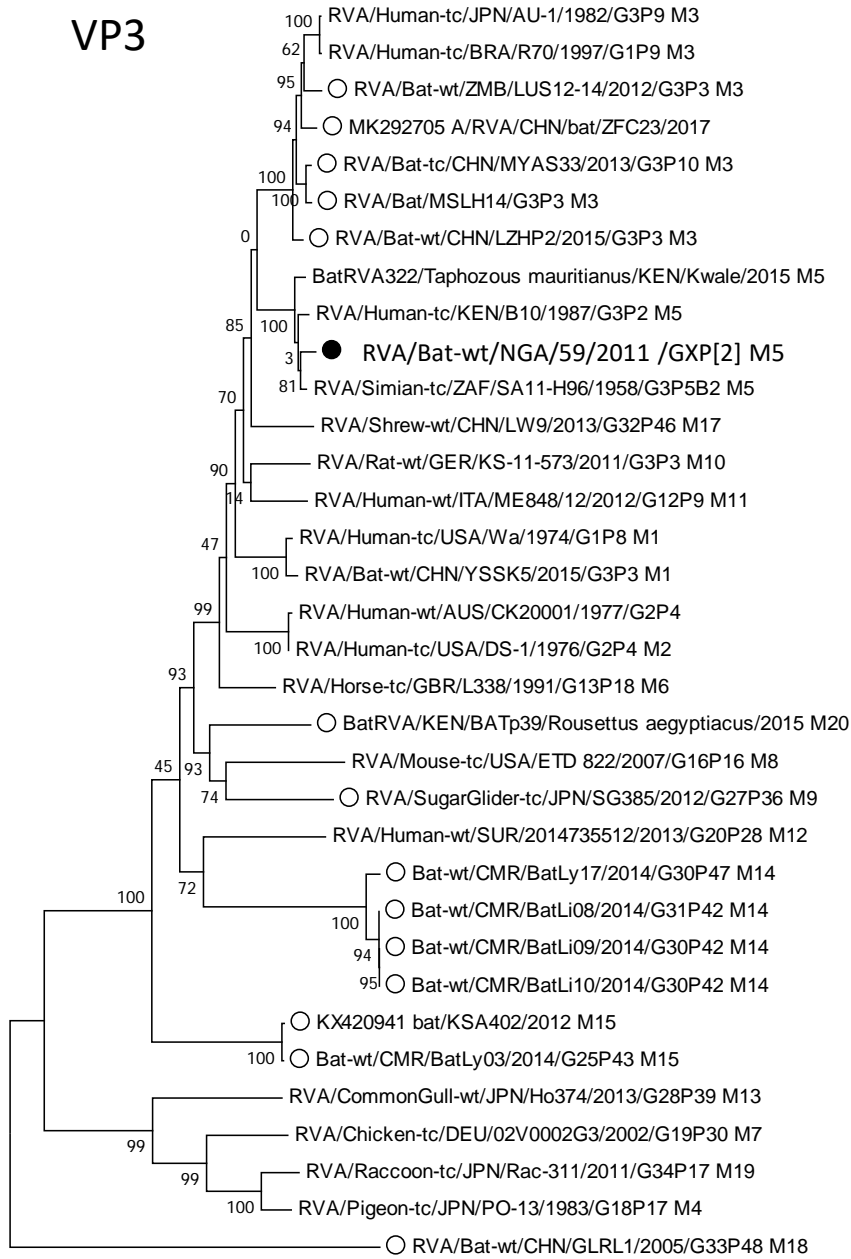
0.5

VP2

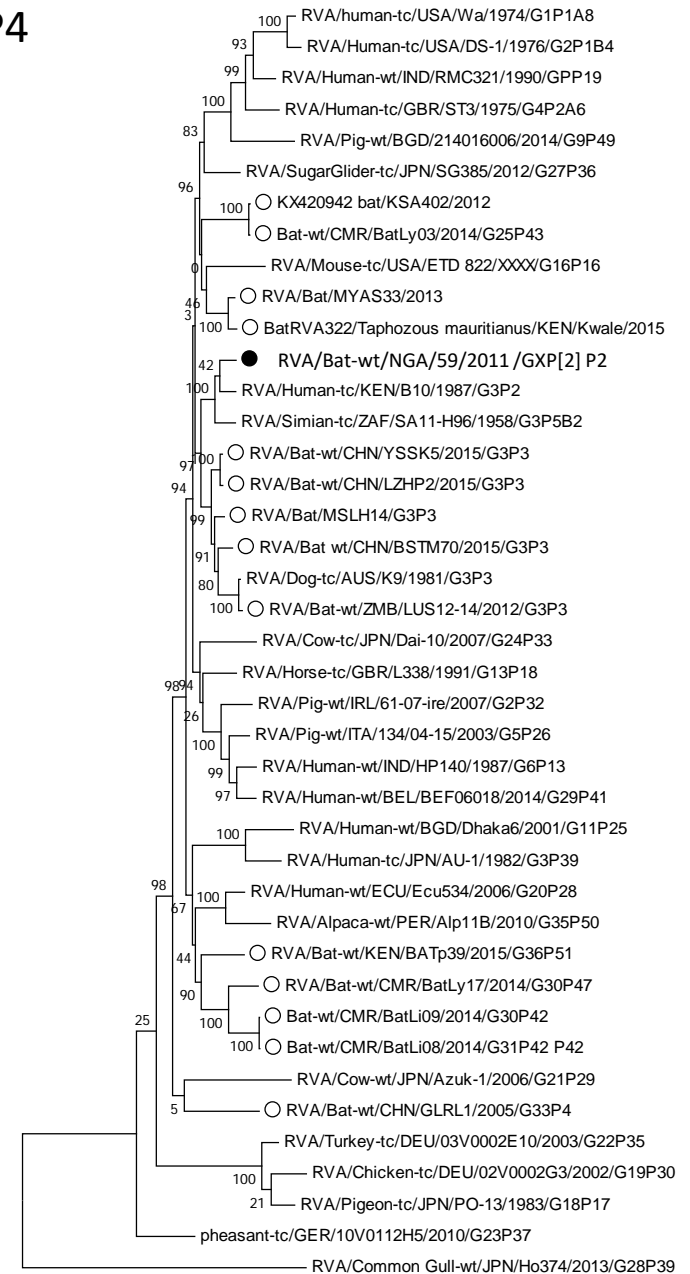


0.2

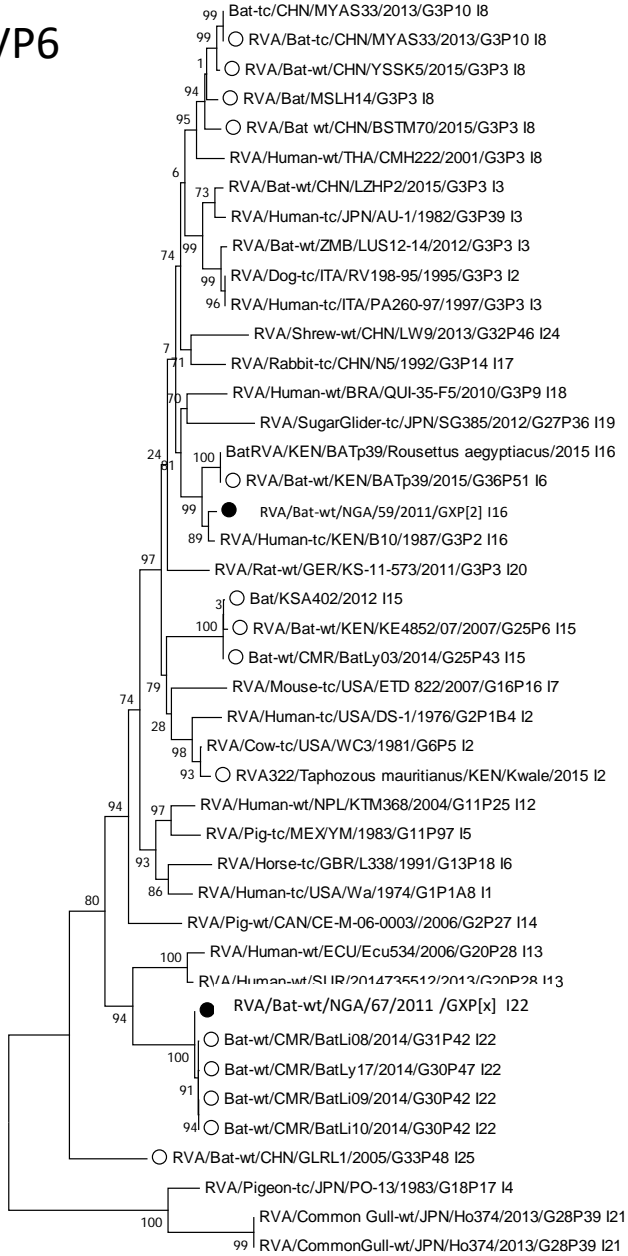
VP3



VP4

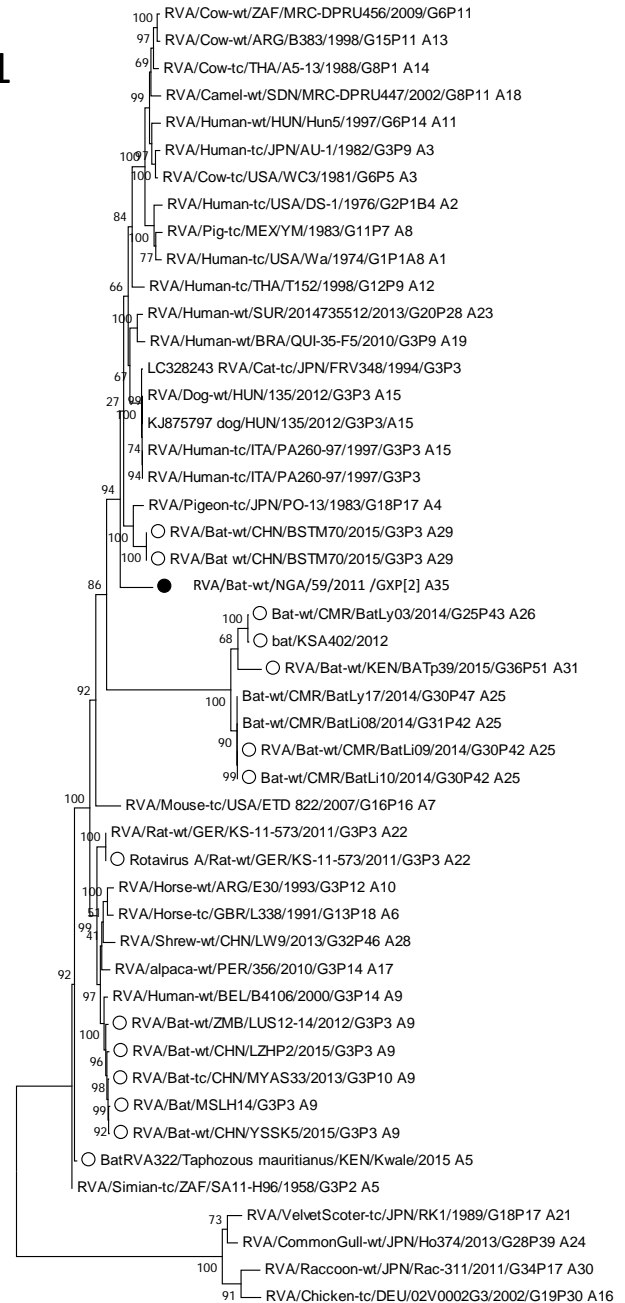


VP6



0.5

NSP1



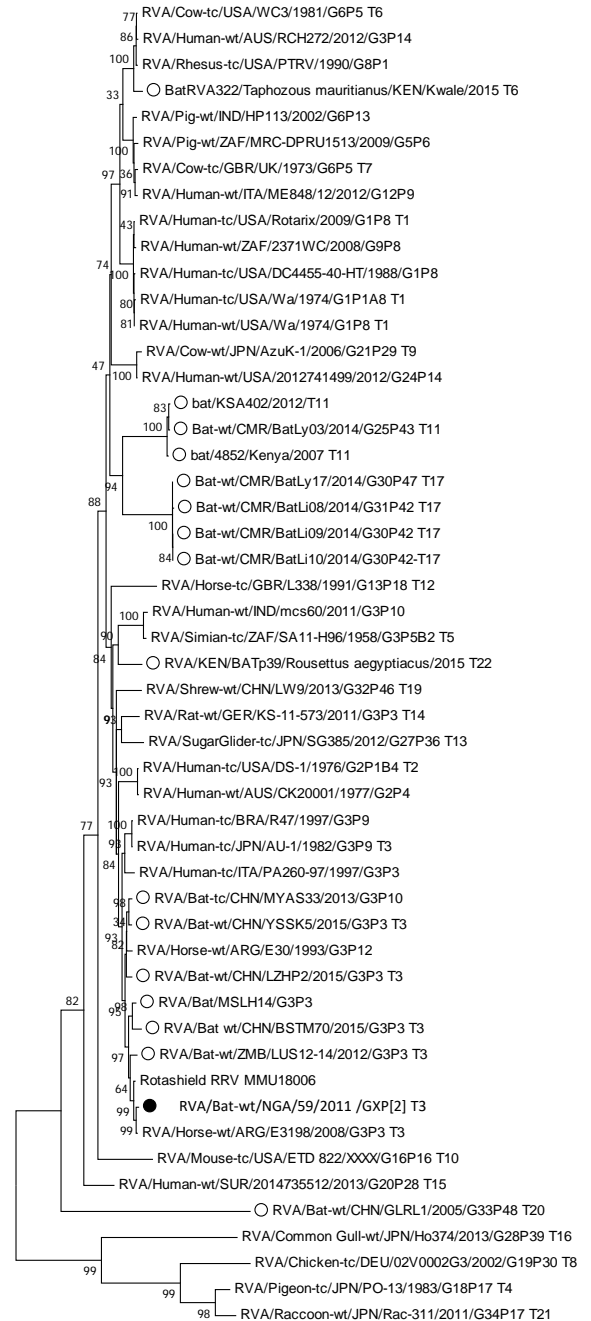
1

NSP2



0.5

NSP3



0.5