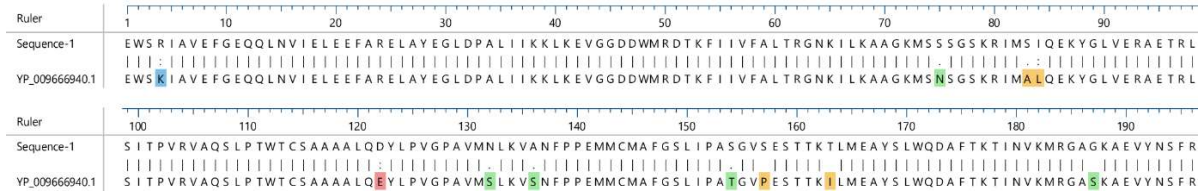
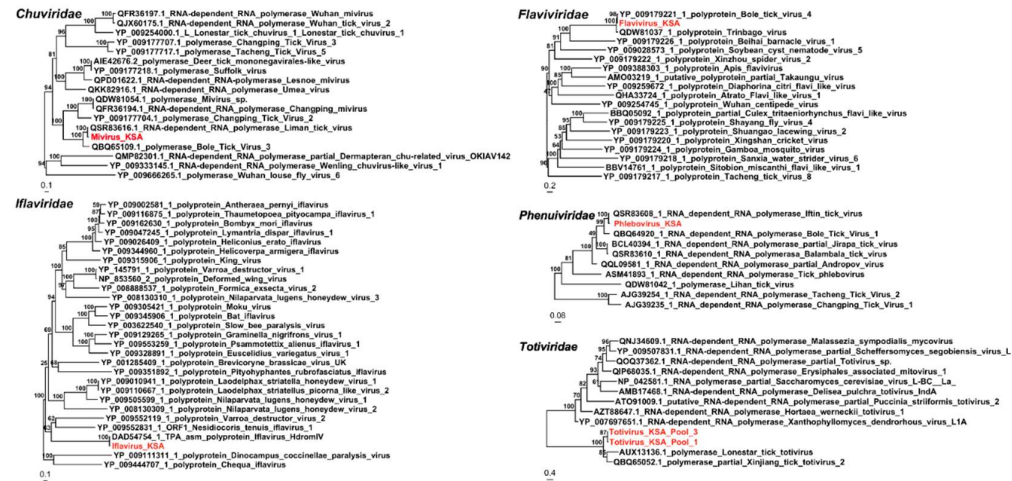


Protein alignment [Matrix: "BLOSUM62" Gap penalty: 10 Gap extension penalty: 1]

Sequence-1	YP_009666940.1	%Identity	%Similar	%Gaps	Identical	Similar	Count	Length	Score	Length
7>249	3>245	93.0%	97.9%	0.0%	226	238	0	0	1,173	243



**Figure S1.** BLOSUM62 score showing substitutions between the newly identified Guertu virus in Saudi Arabia and the strain (YP\_009666940.1) identified in China.



**Figure S2.** Phylogenetic trees of viruses that have not been associated with human diseases. The viruses detected in Saudi Arabia are marked with red colour.