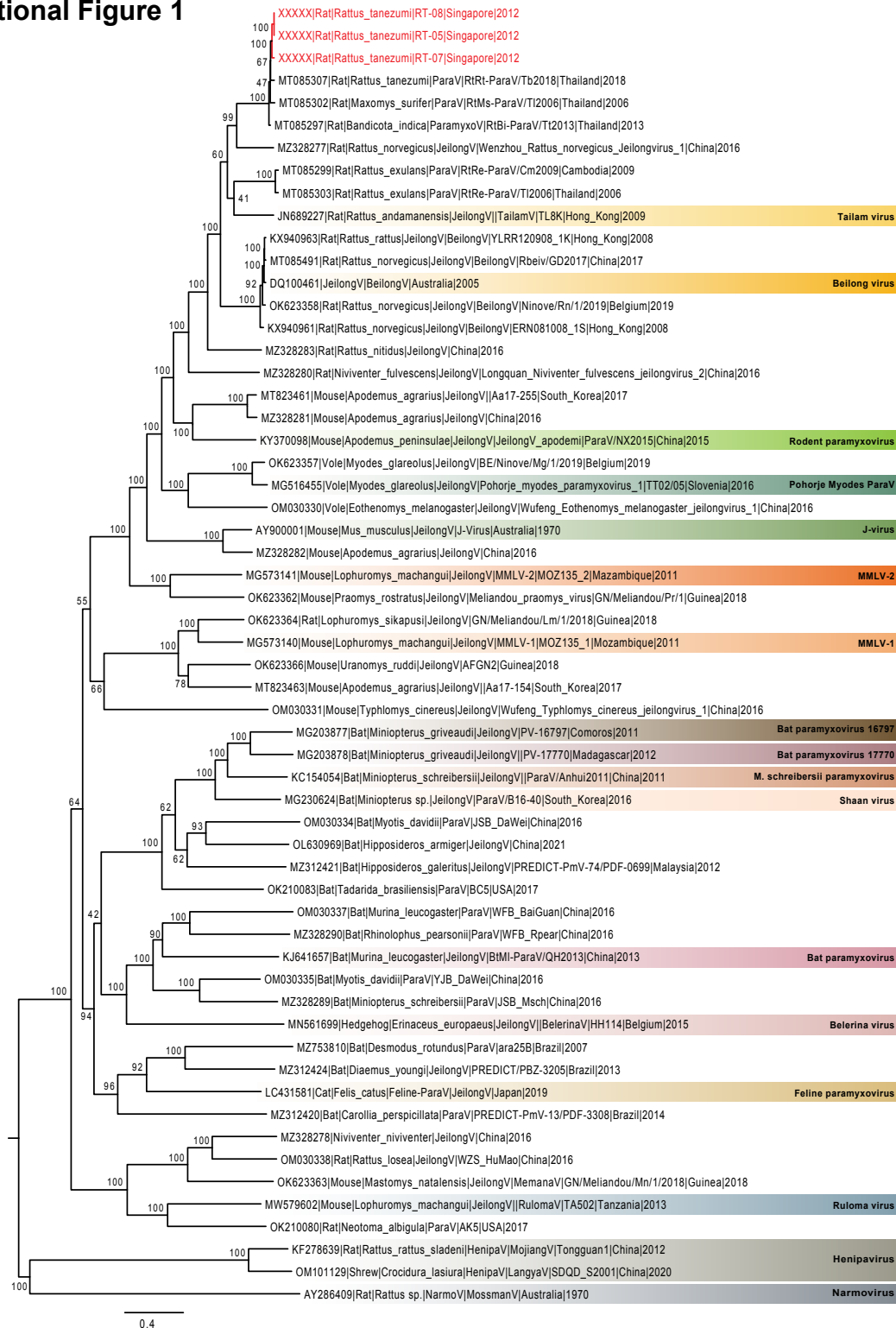


Additional Figure 1



Maximum likelihood phylogeny of full Jeilongvirus genomes generated using the GTR + GAMMA model in RaxML. Coloured taxa represent exemplar Jeilongvirus species. Red fonts indicate novel genomes generated from *Rattus tanezumi* in this study. Bootstrap values greater than 70% are indicated at branch nodes. The scale bar denotes nucleotide substitutions per site.