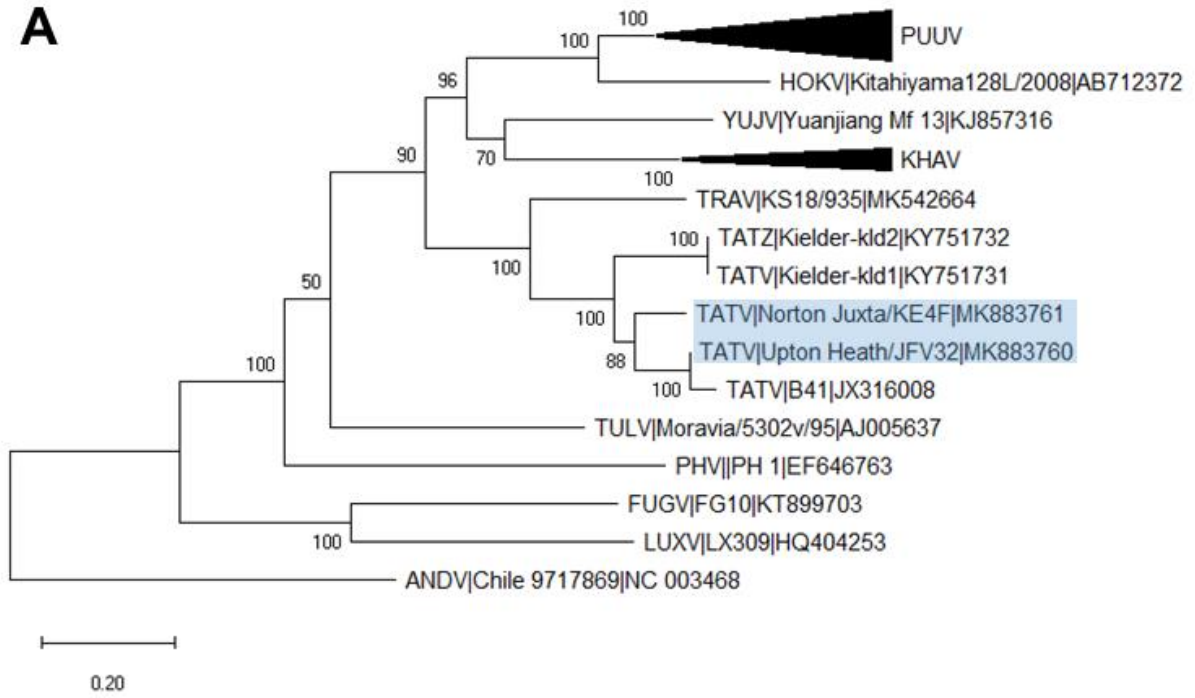
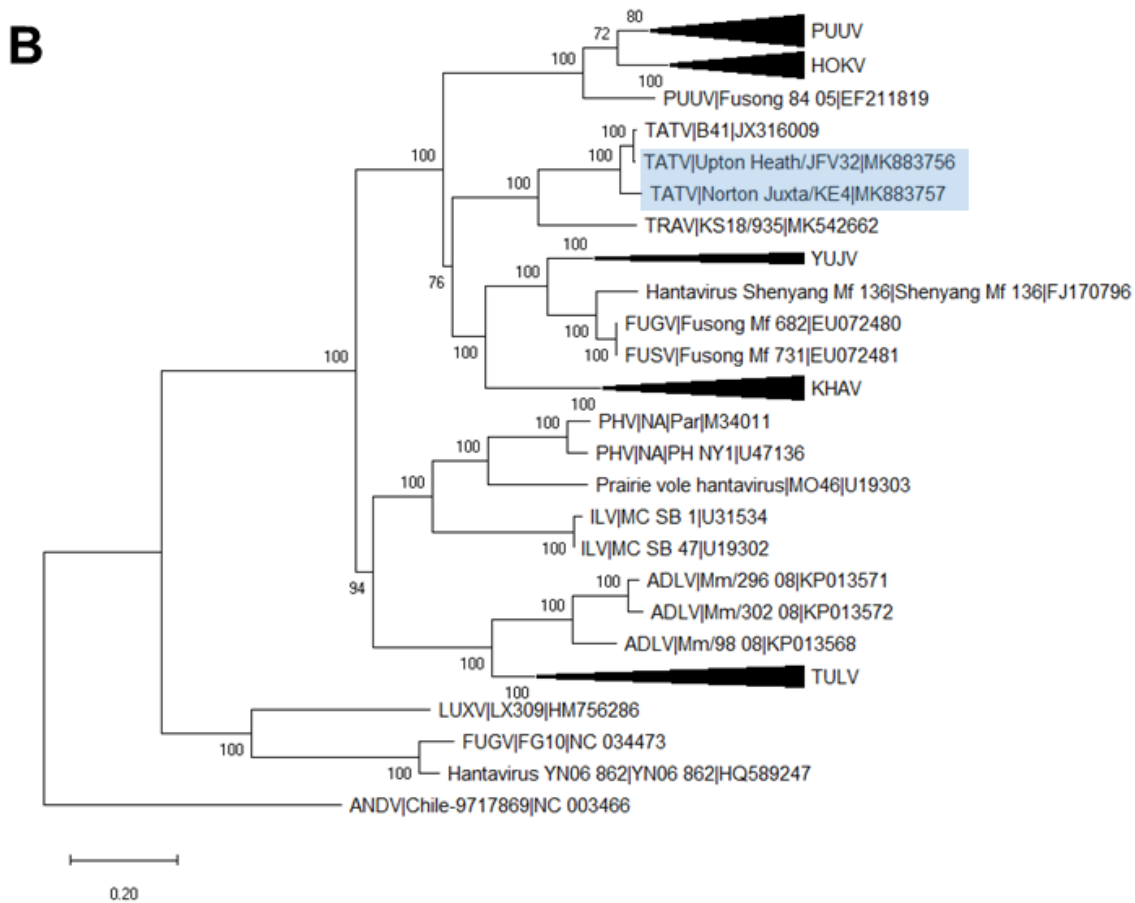


A





Supplementary Figure 1: Phylogenetic relationship of Tatenale virus Upton-Heath and Norton-Juxta, with available partial sequences of previous Tatenale virus sequences and other vole-associated orthohantavirus species. Representative partial sequences were obtained for L (A) and S (B) segments. Maximum Likelihood trees were created using the GTR+G+I model, branch lengths are drawn to a scale of nucleotide substitutions per site. Numbers above individual branches show bootstrap support after 50 replicates. Tatenale virus strains discovered in this study are highlighted with a blue box. Sequences are shown with the species name, strain name and the GenBank accession number. Black triangles represent a compressed species, specific subtree. PUUV, Puumala virus; HOKV, Hokkaido virus; FUSV, Fusong virus; YUJV, Yuanjiang virus; KHAV, Khabarovsk virus; TATV, Tatenale virus; PHV, Prospect Hill virus; ILV, Isla Vista virus; TULV, Tula virus; ADLV, Adler virus; LUXV, Luxi virus; FUGV, Fugong virus; TRAV, Traemmersee virus.