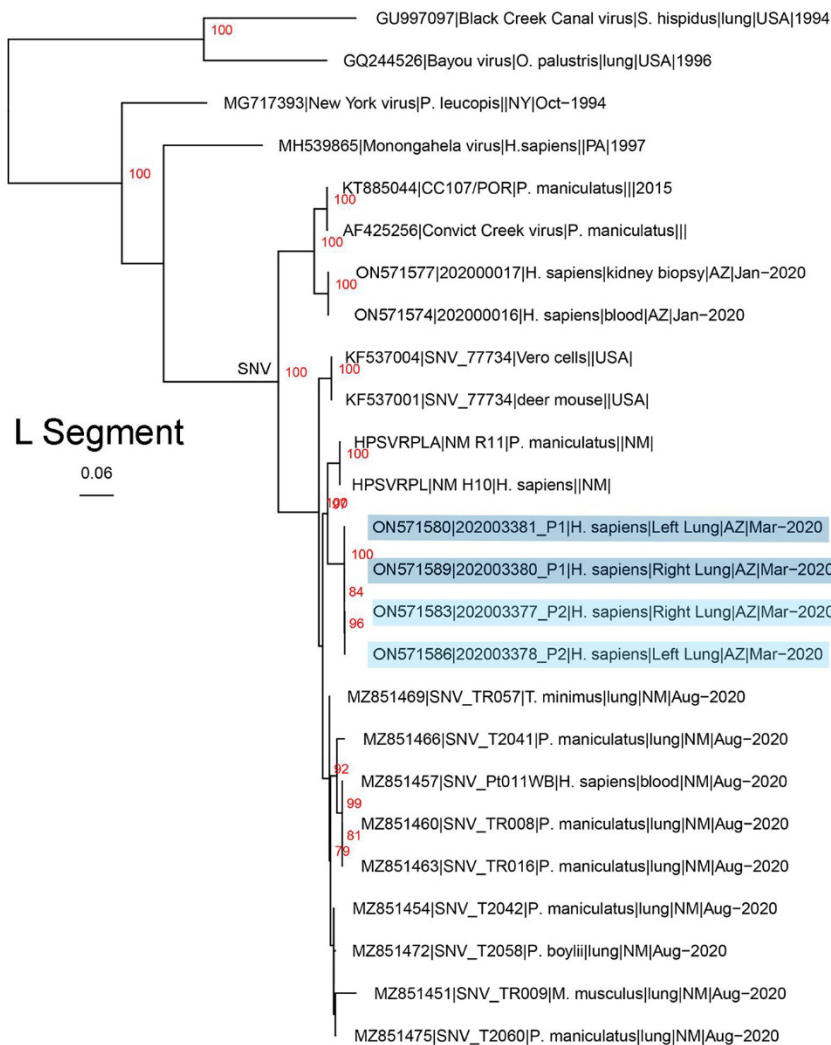


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Detection of Hantavirus During the COVID-19 Pandemic, Arizona, 2020

Appendix



Appendix Figure 1. Phylogenetic tree for *Orthohantavirus* long (L) segment. We inferred phylogenetic history of full-length SNV L segment using maximum-likelihood estimation. Phylogenetic trees were made using a nucleotide alignment of *Orthohantavirus* L segments.



Appendix Figure 2. Phylogenetic tree for *Orthohantavirus* medium (M) segment. We inferred phylogenetic history of full-length SNV M segment using maximum-likelihood estimation. Phylogenetic trees were made using a nucleotide alignment of *Orthohantavirus* M segments.