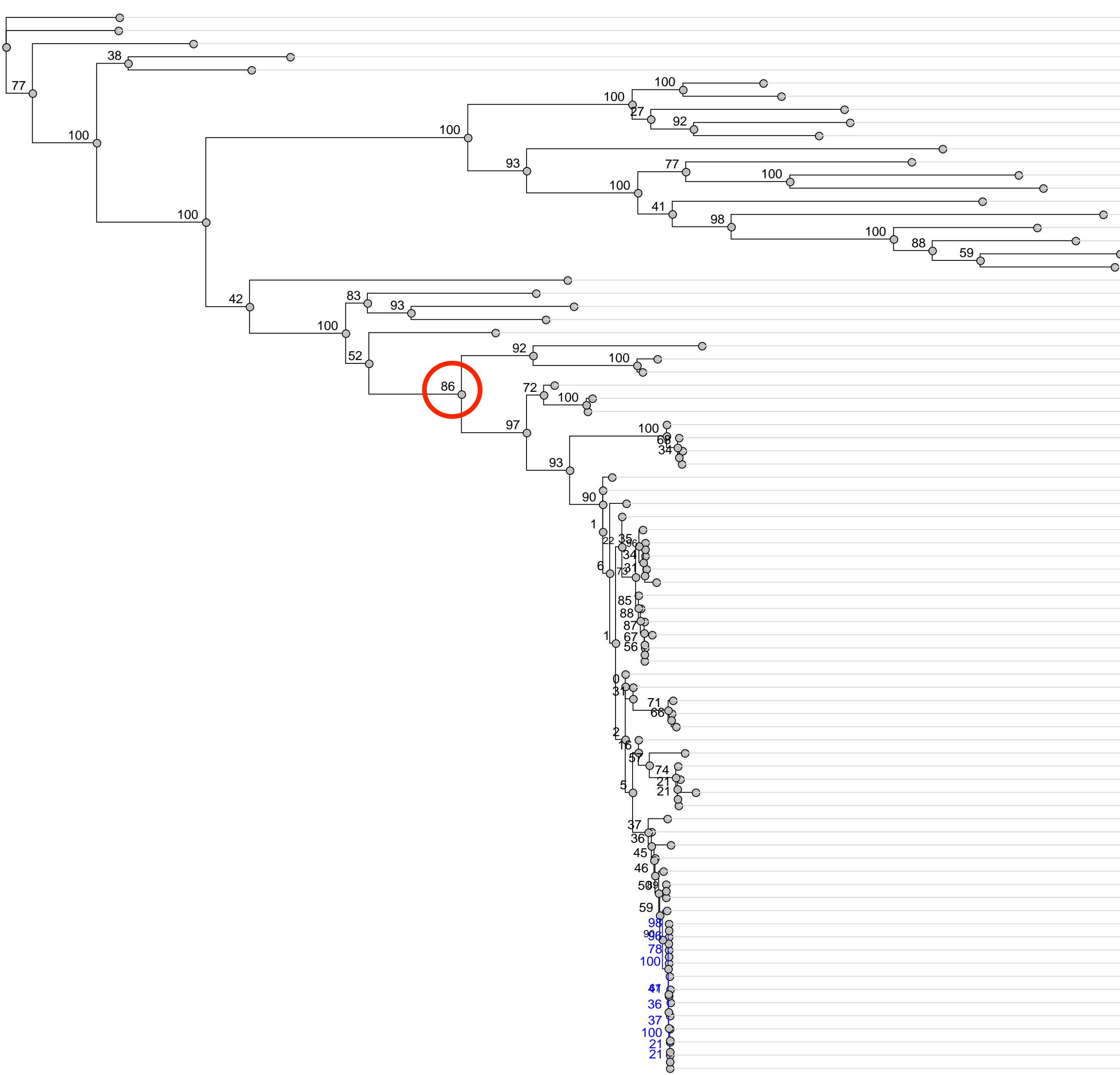


Supplementary Figures

Figure S1 (next page): Phylogeny of the hantavirus S genome segment based on a maximum-likelihood alignment of hantavirus nucleotide sequences collected from *Peromyscus maniculatus*. The sequence label in red is the Sin Nombre reference sequence from NCBI. *P. maniculatus* sequences highlighted in blue are used for orientation across the S, M, and L segments, since these sequences are all derived from a single study (1).



ref|NC_034527.1|_ [completeness=complete]_ [organism=Orthohantavirus_khabarovskense]_ [isolate=Fuyuan...
 ref|NC_055635.1|_ [completeness=complete]_ [organism=Orthohantavirus_tatenalense]_ [strain=Upton_Heat...
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 ref|NC_038384.1|_ [completeness=complete]_ [organism=Orthohantavirus_virus]_ [strain=Yongjia-Nc-58]_ [nat_ho...
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 gij|4097306|gb|U54580|_El_Moro_Canyon_hantavirus_strain_PM-Tx-169/PM-Tx-343_nucleocapsid_protein_(N)...
 gij|380857302|gb|JN097476|_Sin_Nombre_virus_strain_HV_H0460038_segment_S_nucleocapsid_protein_gene,...
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 gij|380857284|gb|JN097467|_Sin_Nombre_virus_strain_HV_H0020015_segment_S_nucleocapsid_protein_gene,...
 gij|1200319|gb|U32647|_Hantavirus_Monongahela-3_nucleocapsid_protein_gene,_partial_cds_[Monongahela...
 gij|1200315|gb|U32591|_Hantavirus_Monongahela-1_S_RNA_segment_nucleocapsid_protein_gene_complete_c...
 gij|1200321|gb|U32648|_Hantavirus_Monongahela-3_nucleocapsid_protein_gene,_partial_cds_[Monongahela...
 gij|1200317|gb|U32646|_Hantavirus_Monongahela-2_nucleocapsid_protein_gene,_partial_cds_[Monongahela...
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 gij|1171320|gb|U45018|_Hantavirus_sp._S_segment_nucleocapsid_protein_gene,_partial_cds_[NV_NY-R309...
 gij|549952|gb|U11436|_Four_Corners_hantavirus_isolate_PM-222_nucleocapsid_protein_gene,_partial_cds...
 gij|1171324|gb|U45020|_Hantavirus_sp._S_segment_nucleocapsid_protein_gene,_partial_cds_[NV_NY-R872...
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 gij|987548|gb|U33232|_Sin_Nombre_hantavirus_NV_CL-R341_nucleocapsid_protein_gene,_partial_cds_[NV_C...
 gij|987554|gb|U33235|_Sin_Nombre_hantavirus_NV_EU-R451_nucleocapsid_protein_gene,_partial_cds_[NV_E...
 gij|987610|gb|U33263|_Sin_Nombre_hantavirus_NV_WA-R211_nucleocapsid_protein_gene,_partial_cds_[NV_W...
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 gij|1171312|gb|U45014|_Hantavirus_sp._S_segment_nucleocapsid_protein_gene,_partial_cds_[NV_EU-R693...
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 gij|0|gb|MW177654|_Sin_Nombre_orthohantavirus_isolate_BV213_segment_S_nucleocapsid_protein_gene,_par...
 gij|987606|gb|U33259|_Sin_Nombre_hantavirus_NV_WA-R199_nucleocapsid_protein_gene,_partial_cds_[NV_W...
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 gij|0|gb|MW177648|_Sin_Nombre_orthohantavirus_isolate_BV86_segment_S_nucleocapsid_protein_gene,_part...
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Figure S2 (next page): Phylogeny of the hantavirus M genome segment based on a maximum-likelihood alignment of hantavirus nucleotide sequences collected from *Peromyscus maniculatus*. The sequence label in red is the Sin Nombre reference sequence from NCBI. *P. maniculatus* sequences highlighted in blue are used for orientation across the S, M, and L segments, since these sequences are all derived from a single study (1).

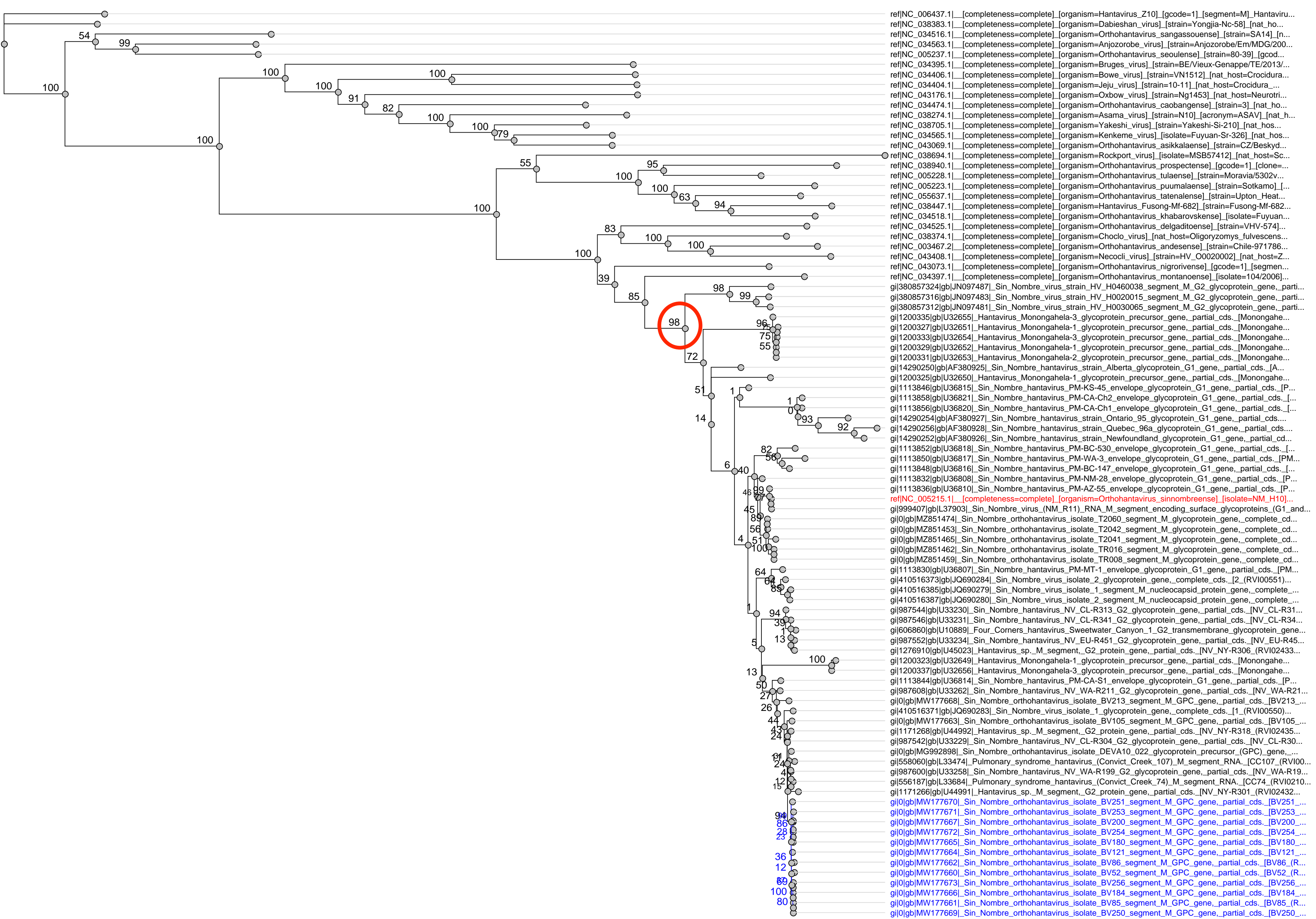


Figure S3 (next page): Phylogeny of the hantavirus L genome segment based on a maximum-likelihood alignment of hantavirus nucleotide sequences collected from *Peromyscus maniculatus*. The sequence label in red is the Sin Nombre reference sequence from NCBI. *P. maniculatus* sequences highlighted in blue are used for orientation across the S, M, and L segments, since these sequences are all derived from a single study (1).

