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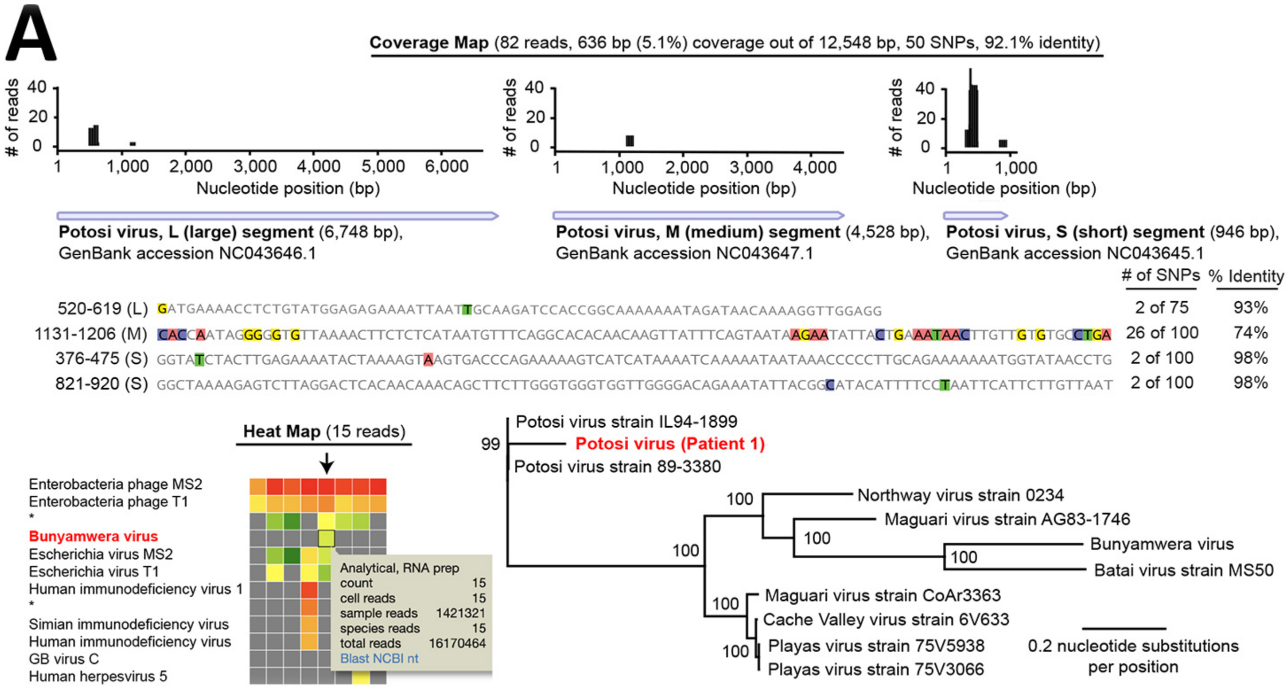
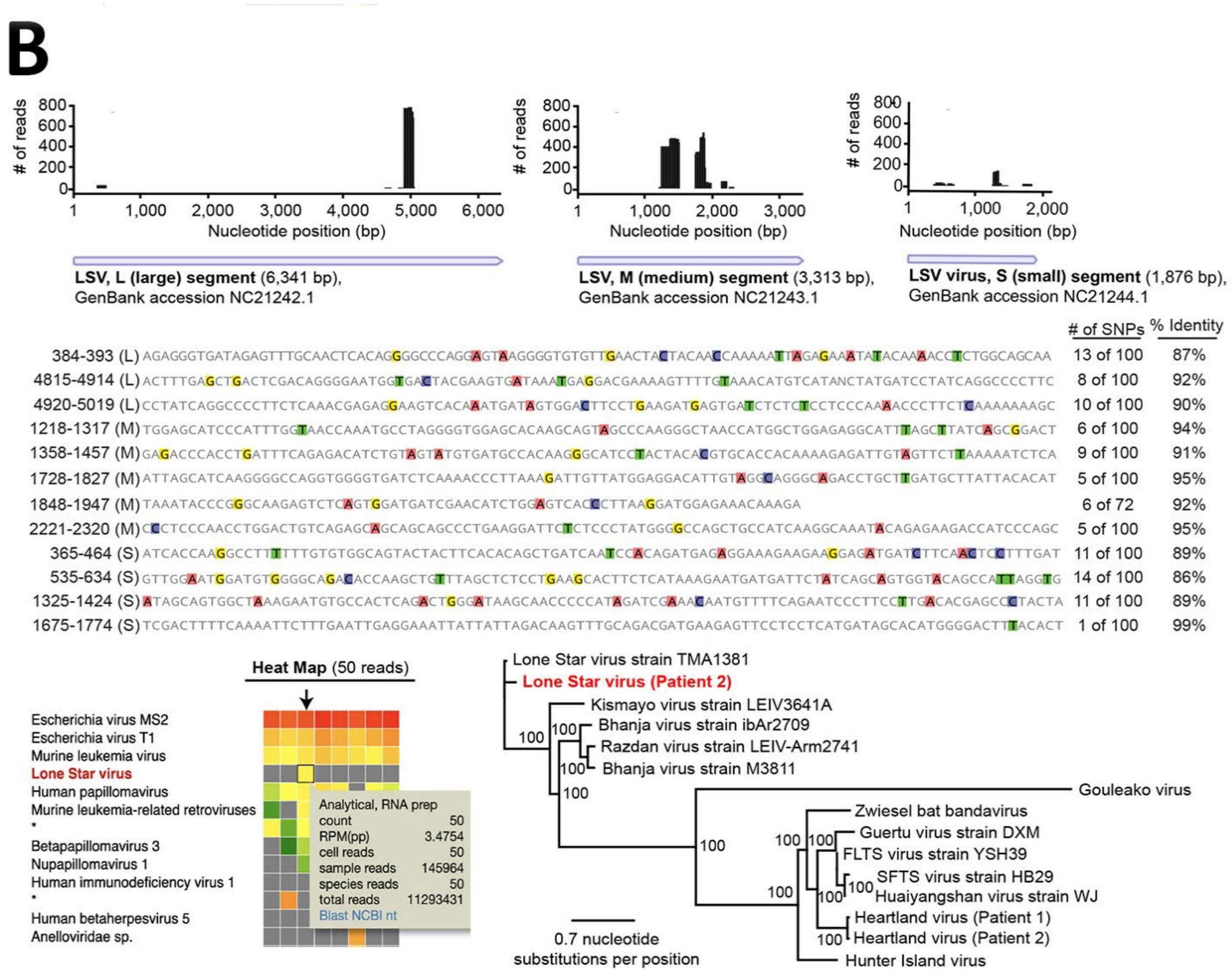
Two Human Cases of Fatal Meningoencephalitis Associated with Potosi and Lone Star Virus Infections, United States, 2020–2023

Appendix





A) Coverage map showing alignment of 72 reads to the 3 segments of the Potosi virus genome (top). Representative sequences of length <100 bp showing distribution of single-nucleotide polymorphisms and pairwise percentage identity compared to the reference Potosi virus genome (middle). Heat map showing detection of reads (n = 15) from an orthobunyavirus with homology to Bunyamwera virus in patient 1 cerebrospinal fluid (bottom left, arrow). Phylogenetic analysis identifies the patient 1 virus as Potosi virus (bottom right). B) Coverage map showing alignment of 2,460 reads to the 3 segments of the Lone Star virus genome (top). Representative sequences of length <100 bp showing distribution of single-nucleotide polymorphisms and pairwise percentage identity compared to the reference Lone Star virus genome (middle). Heat map showing detection of Lone Star virus reads (n = 50) in patient 2 cerebrospinal fluid (bottom left, arrow). Phylogenetic analysis confirms the patient 2 virus to be Lone Star virus (bottom right).