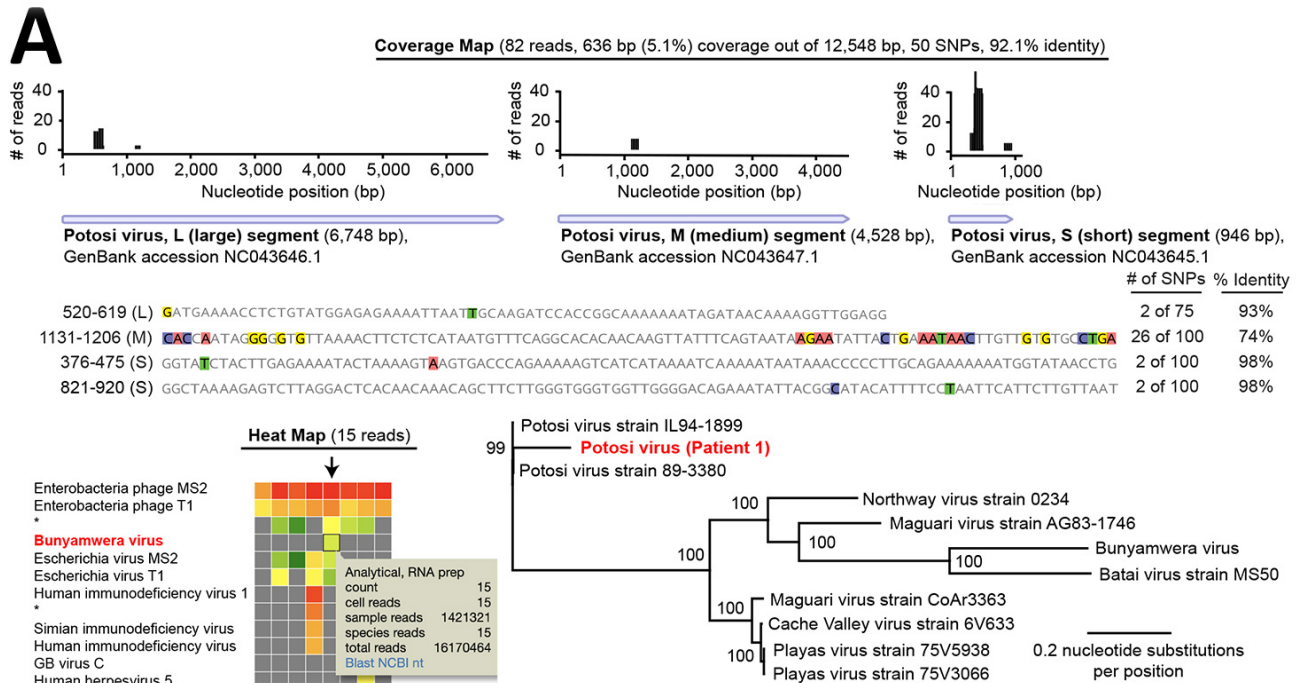


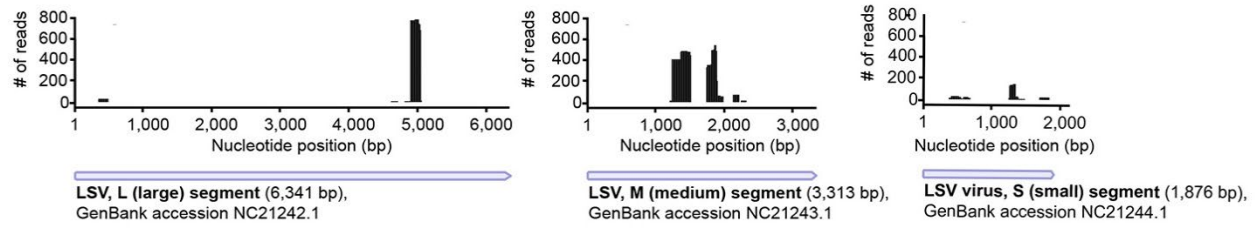
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Two Human Cases of Fatal Meningoencephalitis Associated with Potosi and Lone Star Virus Infections, United States, 2020–2023

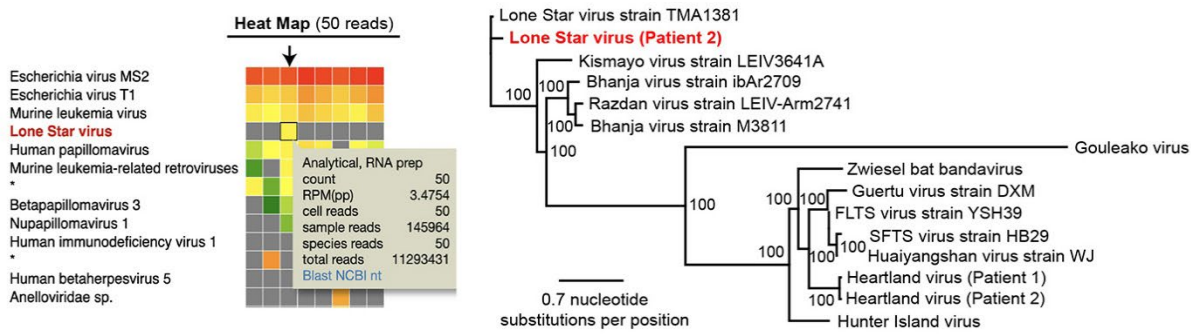
Appendix



B



	# of SNPs	% Identity
384-393 (L) AGAGGGTGATAGAGTTTGCAACTCACAGGGCCAGCAGTAAAGGGTGTGTGAACTACTACAACAAAAATTAGAGAAATACAAACCCTGGCAGCAA	13 of 100	87%
4815-4914 (L) ACTTTGAGCTGACTGCACAGGGGAATGCTGATACGAAGTCTAAAAGGACGAAAAAGTTTTGAAACATGTGCATANCTATGATCCTATCAGGCCCTTC	8 of 100	92%
4920-5019 (L) CCTATCAGGCCCTTCTCAAACGAGAGGAGTCAACAATGATAGTGGATTCCTGAAGATGAGTGAICTCTCCCTCCCAAACCCCTCTAAAAAAGC	10 of 100	90%
1218-1317 (M) TGGAGCATCCCATTTTGGTAACCAATGCCTAGGGTGGAGCACAAGCAGTACCCCAAGGGCTAACCATGGCTGGAGAGGCATTAGCTTATCAGCGACT	6 of 100	94%
1358-1457 (M) GAGCCACCTGATTTAGAGACATCTGTATGTGTATGCCACAAGGCCATCACTACAGTGCACCACAAAAGAGATTGTGTTCTAAAAATCTCA	9 of 100	91%
1728-1827 (M) ATTAGCATCAAGGGGCCAGGTGGGTGATCTCAAAACCCCTAAAGATTGTTATGGAGACATTGAGAGGGCAGACCTGCTGATGCTTATTACACAT	5 of 100	95%
1848-1947 (M) TAAATACCCGGCAAGAGTCTAGTGATGATCGAACATCTGCAGTCACTTAAAGGATGGAGAAAACAAAGA	6 of 72	92%
2221-2320 (M) CCCCCAACCTGGACTGTCAGAGCGCAGCAGCCCTGAAGGATTCCTCCCTATGGGCGCAGCTGCCATCAAGGCAAAACAGAGAAGACCATCCCAGC	5 of 100	95%
365-464 (S) ATCCACCAAGCCTTTTGTGTGGCAGTACTACTTACACAGCTGATCAACCCACAGATGAGGAAAGAAAGGACATGATTTCAATCTTTGAT	11 of 100	89%
535-634 (S) GTTGCATGATGTGGGCGACACCAAGCTGTTAGCTCTCCTGAAGCAGTCTCATAAAGAATGATGATTTATCAGCAGTGGTACAGCCATAGGCTG	14 of 100	86%
1325-1424 (S) ATAGCAGTGGCTAAGAATGTGCCACTCAGACTGGATAAGCAACCCCATAGATCCAAAATGTTTTGAGAATCCCTTCTGACAGAGCCCTACTA	11 of 100	89%
1675-1774 (S) TCGACTTTTCAAATTTGAAATTGAGGAAATTATTATTAGACAAGTTTGCAGACGATGAAGAGTTCTCTCTCATGATGACACATGGGGACTTACACT	1 of 100	99%



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).