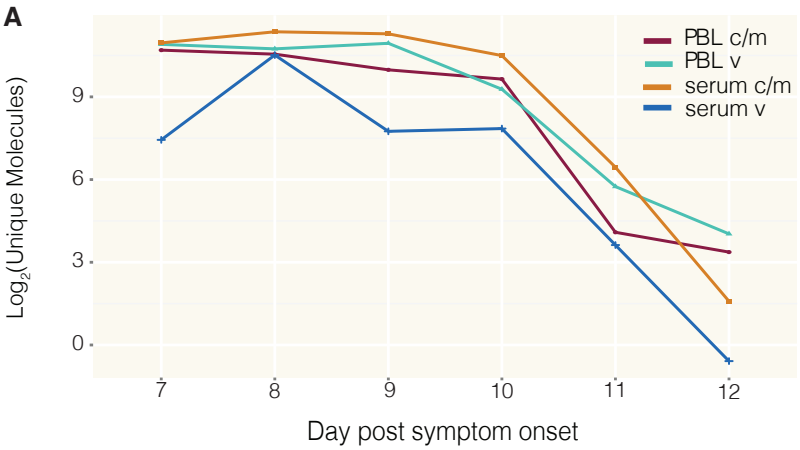
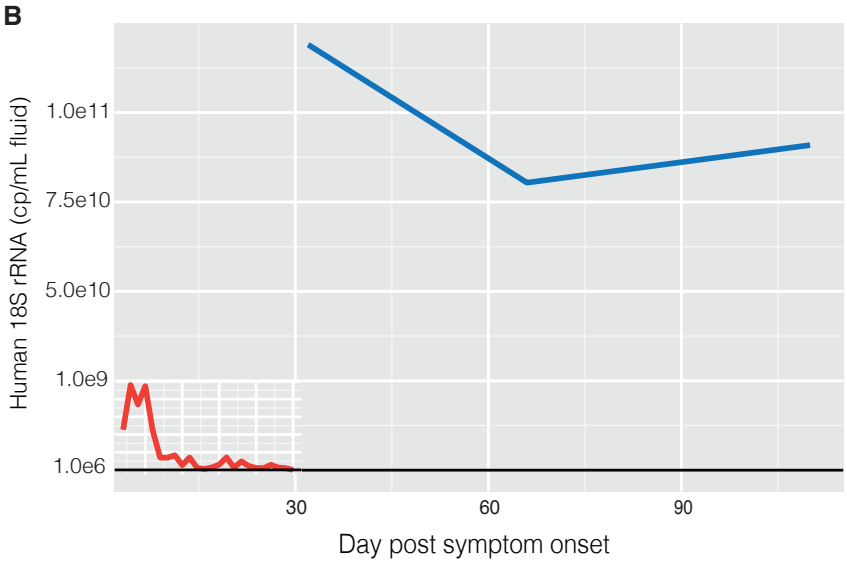
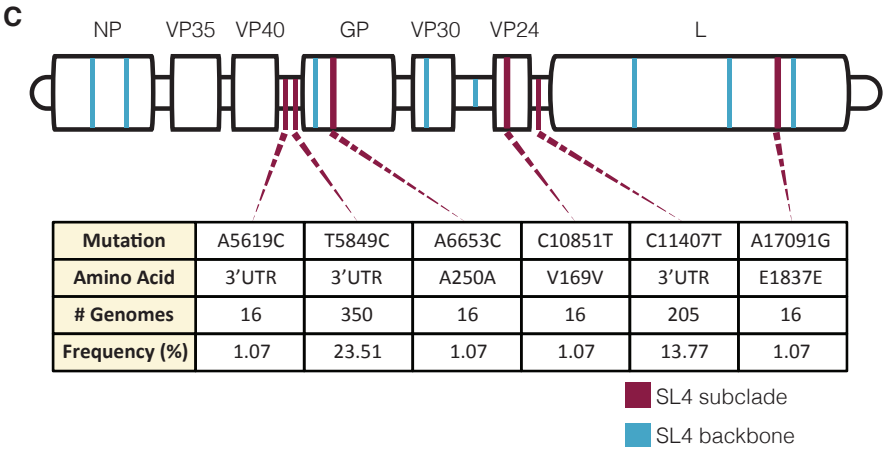
Figure S1







Mutation	A5619C	T5849C	A6653C	C10851T	C11407T	A17091G
Amino Acid	3'UTR	3'UTR	A250A	V169V	3'UTR	E1837E
# Genomes	16	350	16	16	205	16
Frequency (%)	1.07	23.51	1.07	1.07	13.77	1.07

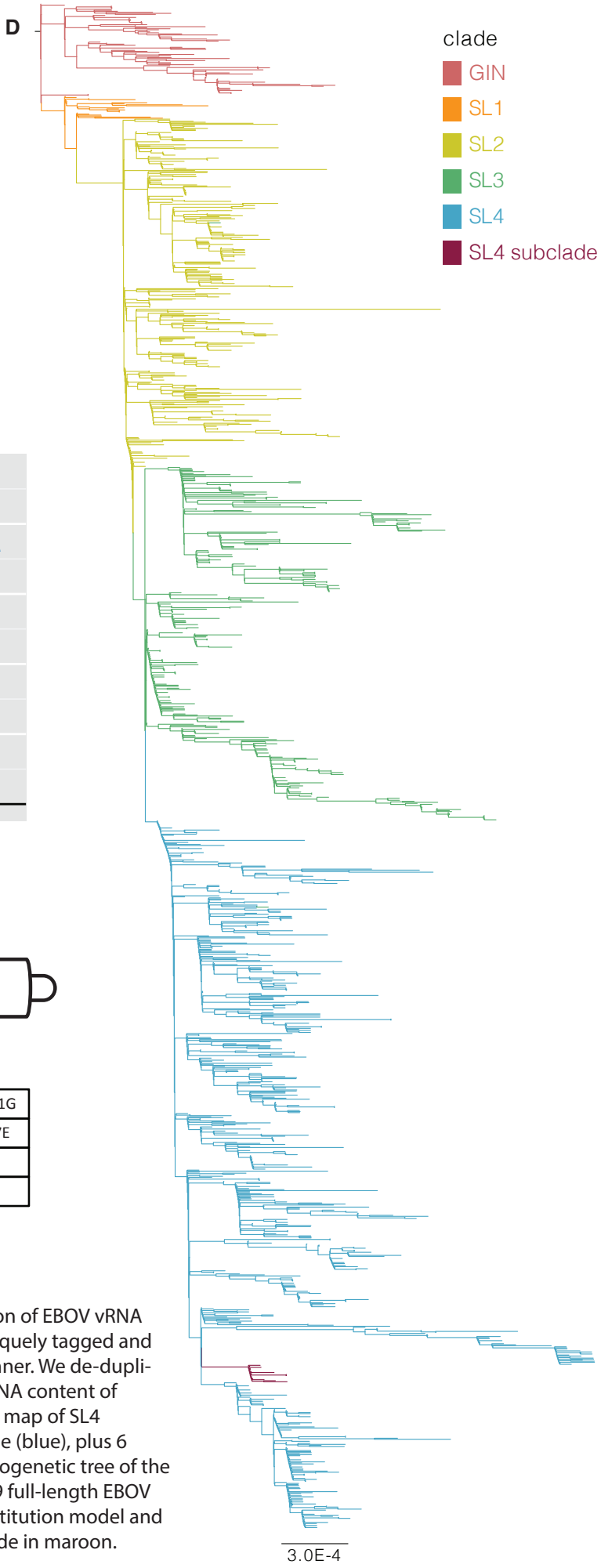


Figure S1. A) Single molecule tagged amplicon sequencing. Quantification of EBOV vRNA and c/mRNA in PBL samples collected during the acute infection. We uniquely tagged and amplified RNA molecules with random barcodes in a strand-specific manner. We de-duplicated reads and counted unique numbers of barcodes. B) Human 18S rRNA content of serum (red) versus semen (blue) samples based on RT-qPCR. C) Genomic map of SL4 subclade SNPs. All genomes in the SL4 subclade harbor the SL4 backbone (blue), plus 6 additional SNPs (maroon), 4 of which are unique to the subclade. D) Phylogenetic tree of the 2014-2016 EBOV outbreak. We generated a phylogenetic tree using 1489 full-length EBOV sequences collated by Diehl et al 2016. We used IQ-TREE with a GTR substitution model and 1000 bootstrap replicates. The patient sample falls within the SL4 subclade in maroon.