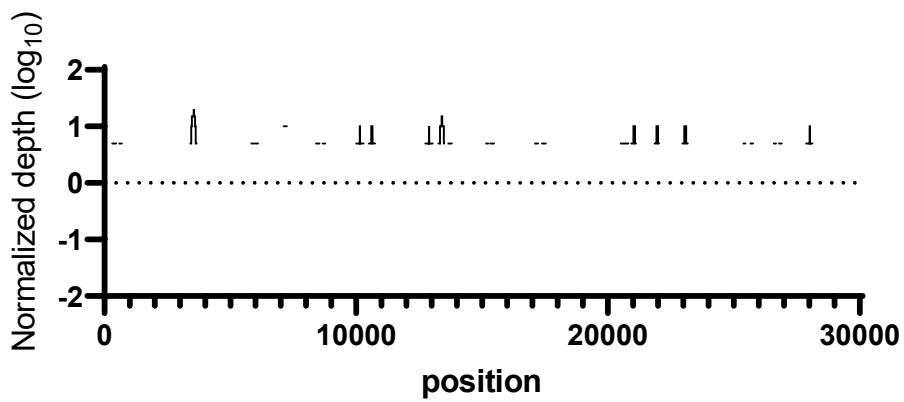


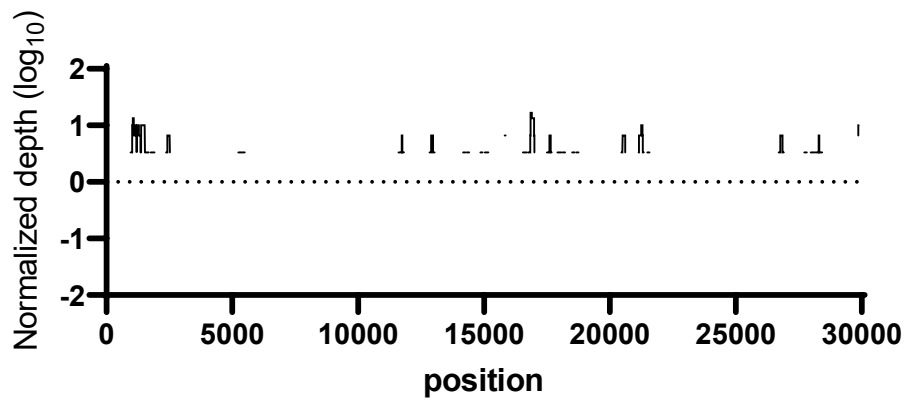
Figure S1. Depths of coverage at each position across the SARS-CoV-2 genome normalized to the average coverage obtained in the CS2022-0121 specimen by metagenomic sequencing (A), metagenomic sequencing after depletion of human rRNA (B), target capture sequencing (C), and target capture sequencing after depletion of human rRNA are shown (D). Average coverage is indicated by the dotted line. Areas where viral reads were not obtained are represented by gaps.

Figure S2. Depths of coverage at each position across the 8 segments (PB2, PB1, PA, HA, NP, NA, M, and NS) of the influenza A virus genome normalized to the average coverage obtained in the F16-31-UTM specimen by metagenomic sequencing (A), metagenomic sequencing after depletion of human rRNA (B), target capture sequencing (C), and target capture sequencing after depletion of human rRNA are shown (D). Average coverage is indicated by the dotted line. Areas where viral reads were not obtained are represented by gaps.

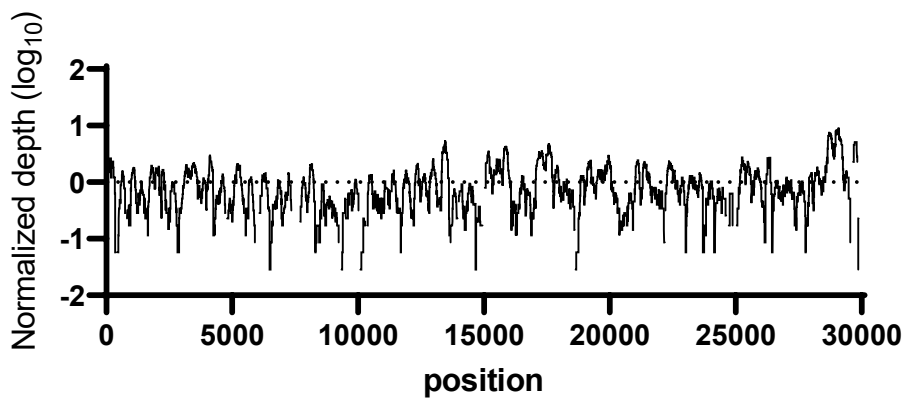
(A)



(B)



(C)



(D)

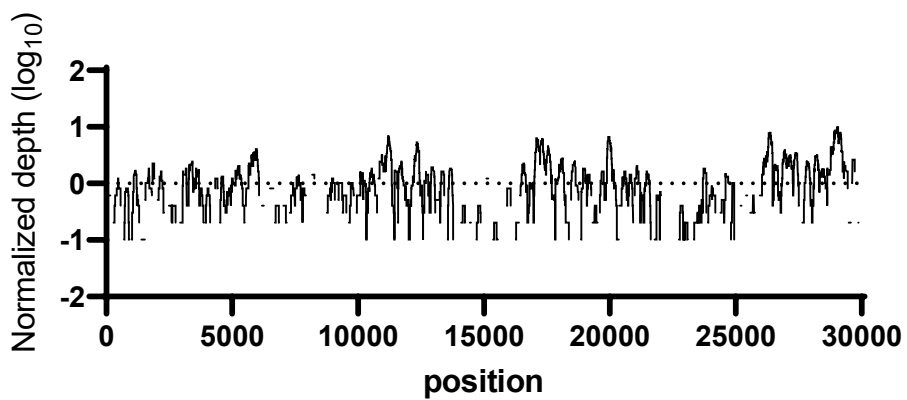


Figure S1

