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Author Correction: Mutations in viral nucleocapsid protein and endoRNase are discovered to associate with COVID19 hospitalization risk

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The original version of this Article contained an error in Figure 1, where an old version of the figure was mistakenly submitted for publication. The original Figure 1 and accompanying legend appear below.

The original Article has been corrected.

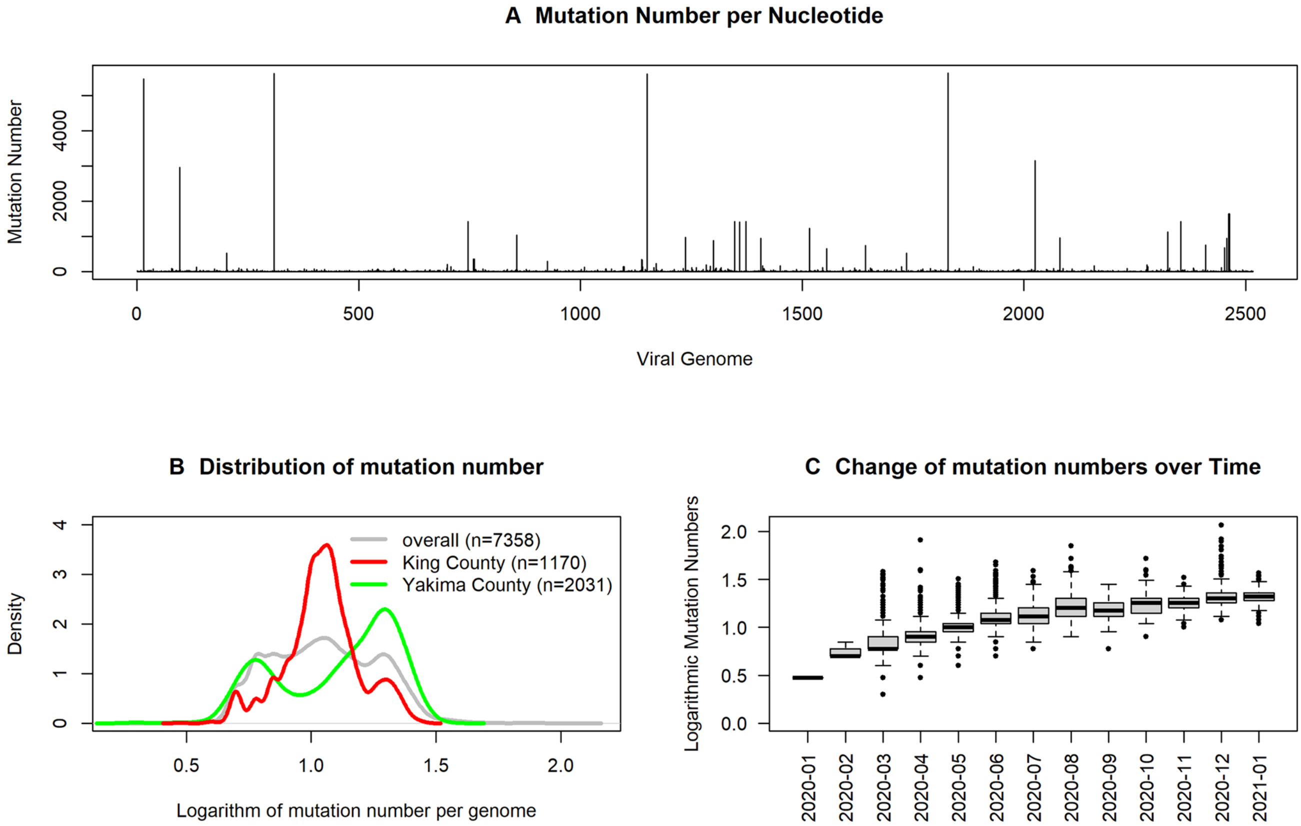

Figure 1. Results from analyzing 7137 viral genomes sequenced by laboratories in Washington state and deposited to GISAID. (**A**) Results from counting mutational numbers per nucleotide throughout the viral genome. Upper arrow indicates observed counts greater than 300. The viral genome is annotated with gene designations immediately below. (**B**) Computed q-values and maximum values of variant proportions in November 2020, December 2020, and January 2021, obtained from fitting generalized linear models to all individual SNVs. SNVs exceeding established threshold q-value and maximum proportions are highlighted in red (upper right corner). (**C**) Eight selected SNVs with significant and substantial temporalities are mapped using their locally averaged variant proportions over time from fitted generalized linear models (color key upper left).