Supplementary Material
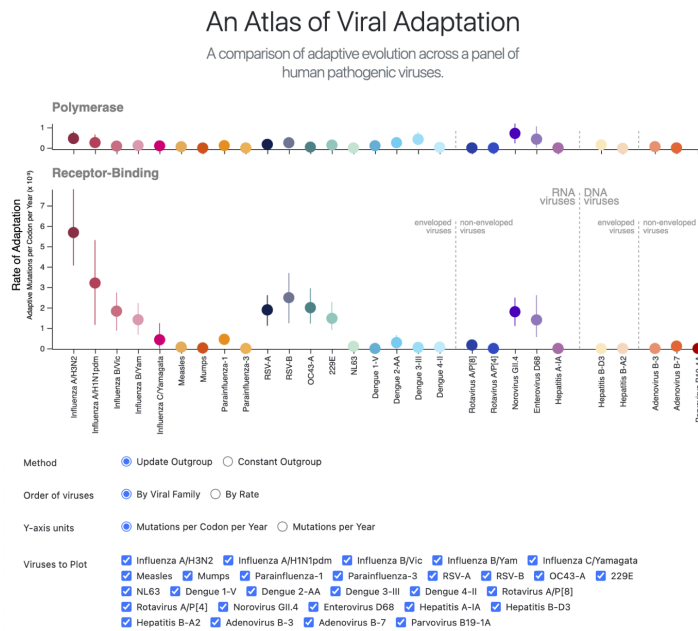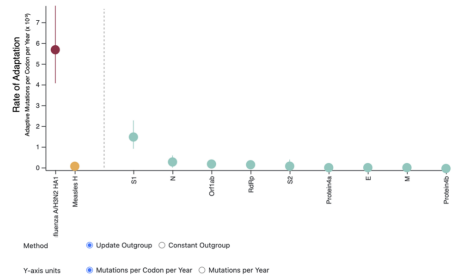
Figure S1: Screenshots of the interactive website presenting the results in this manuscript.
A) Screenshot of the main page, accessed at https://blab.github.io/atlas-of-viral-adaptation/.
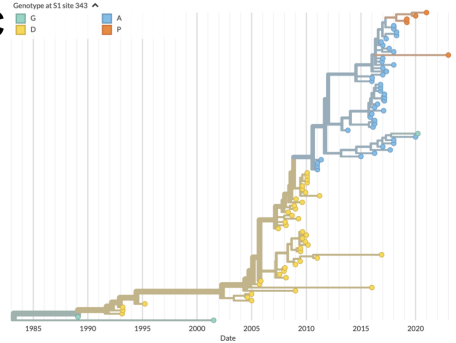Buttons allow the user to toggle the method used to calculate rate of adaptation (update outgroup or
constant outgroup), how the viruses are ordered in the plot (by rate or by viral family), the units the rate
is displayed in (per year or per codon per year), and which viruses shown on the plot. Hovering over any
of the points will display more information about that virus. Clicking on any point will redirect the user to
a virus-specific page that shows rates of adaptation across the genome of that virus. **B)** Screenshot of the
coronavirus 229E page. **C)** Screenshot of the 229E Nextstrain phylogeny that is paired with the analysis
and can accessed from the virus-specific page. In this example, the phylogeny is colored by the genotype at
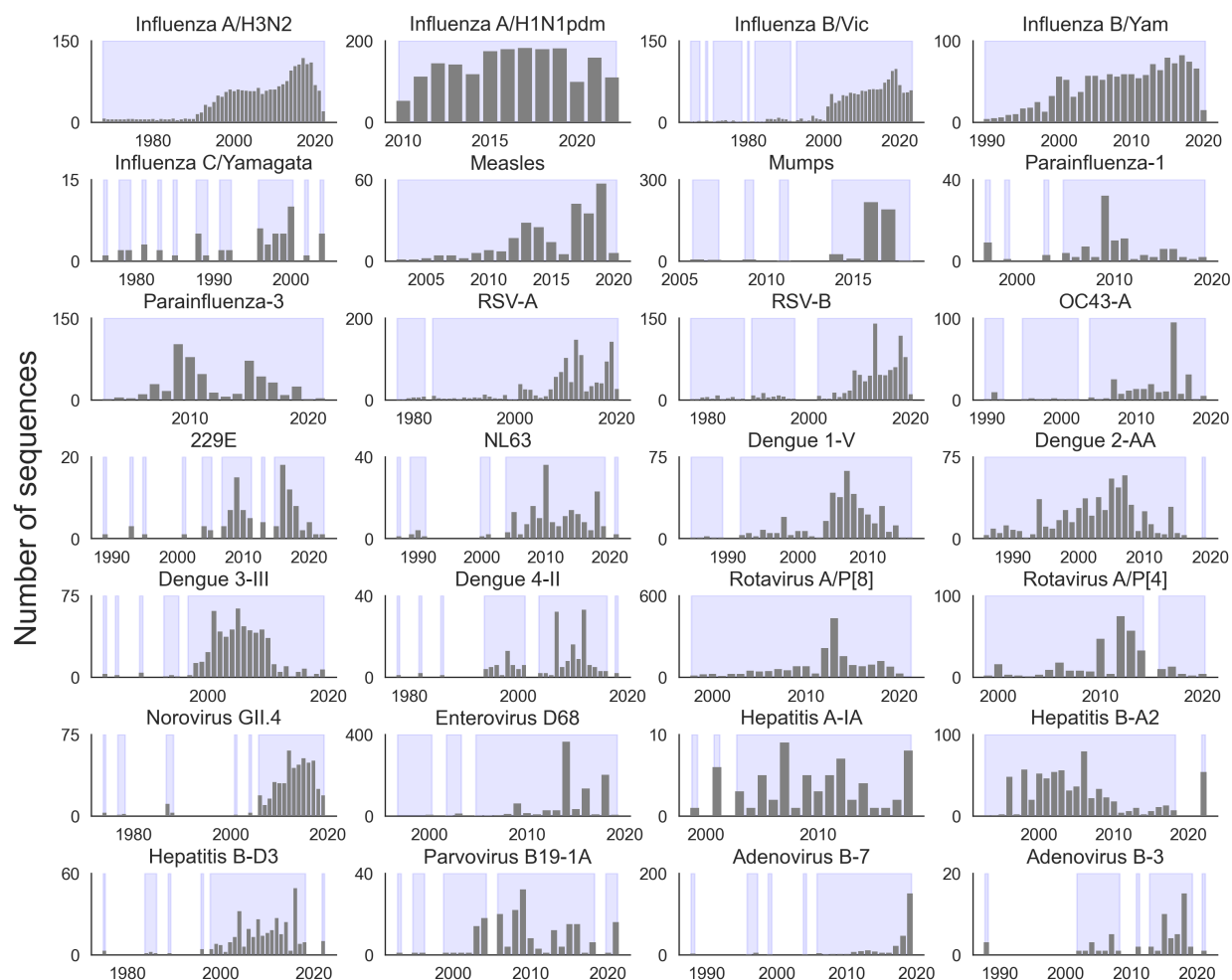amino acid 343, a residue which has experienced multiple fixation events.

Figure S2: Count of sequences per year for each virus in the panel. The number of receptor-binding gene sequences per year is shown for each virus. Because some years have one or a few sampled sequences and others have hundreds, we have highlighted each year with at least one sequence in blue to better show the distribution of samples over time.
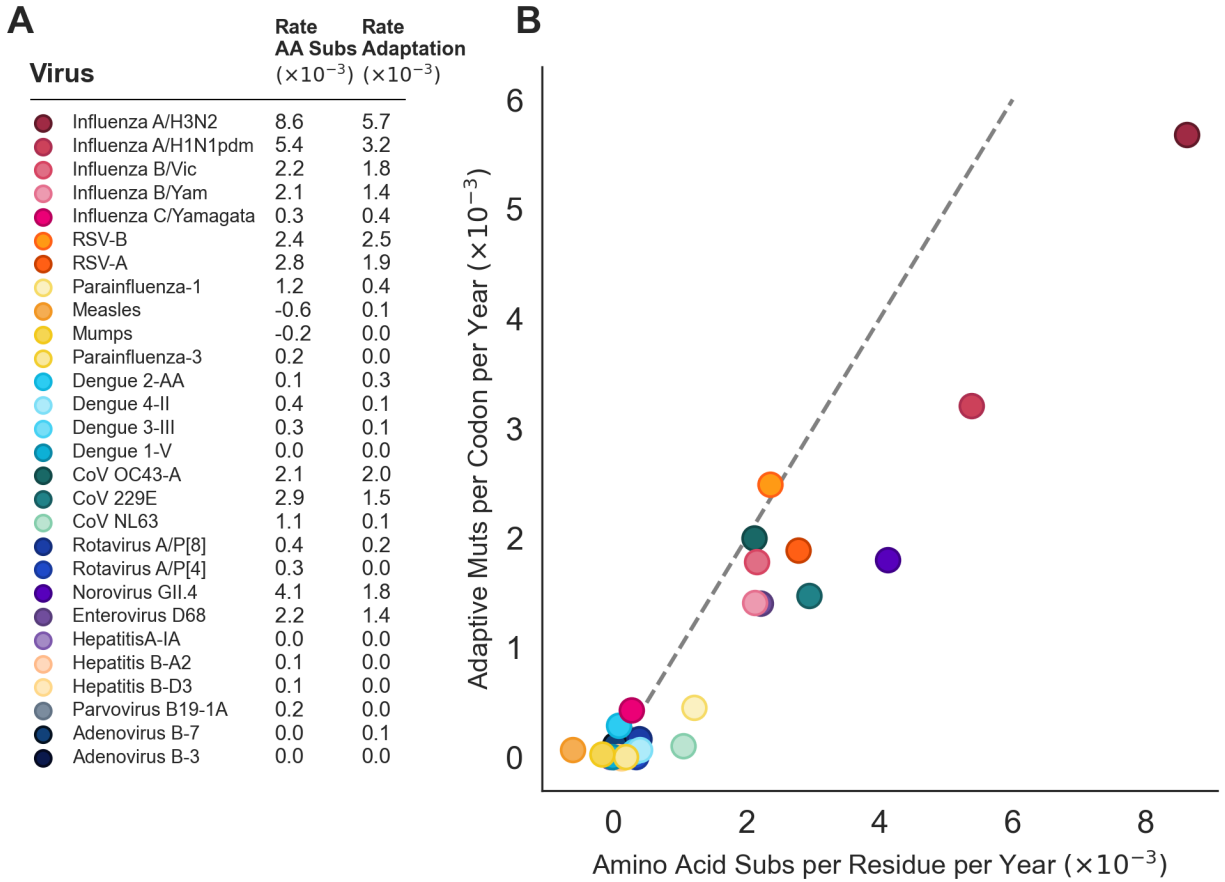
A

Virus	Rate AA Subs ($\times 10^{-3}$)	Rate Adaptation ($\times 10^{-3}$)
Influenza A/H3N2	8.6	5.7
Influenza A/H1N1pdm	5.4	3.2
Influenza B/Vic	2.2	1.8
Influenza B/Yam	2.1	1.4
Influenza C/Yamagata	0.3	0.4
RSV-B	2.4	2.5
RSV-A	2.8	1.9
Parainfluenza-1	1.2	0.4
Measles	-0.6	0.1
Mumps	-0.2	0.0
Parainfluenza-3	0.2	0.0
Dengue 2-AA	0.1	0.3
Dengue 4-II	0.4	0.1
Dengue 3-III	0.3	0.1
Dengue 1-V	0.0	0.0
CoV OC43-A	2.1	2.0
CoV 229E	2.9	1.5
CoV NL63	1.1	0.1
Rotavirus A/P[8]	0.4	0.2
Rotavirus A/P[4]	0.3	0.0
Norovirus GII.4	4.1	1.8
Enterovirus D68	2.2	1.4
HepatitisA-IA	0.0	0.0
Hepatitis B-A2	0.1	0.0
Hepatitis B-D3	0.1	0.0
Parvovirus B19-1A	0.2	0.0
Adenovirus B-7	0.0	0.1
Adenovirus B-3	0.0	0.0

Figure S3: Comparison of rates of amino acid substitution to rates of adaptation. A) Rate of amino acid substitution ($\times 10^{-3}$) and rate of adaptive evolution ($\times 10^{-3}$) is listed for each of the 28 viruses in the panel. **B)** Rate of amino acid substitution is plotted against rate of adaptive evolution for each virus, with color corresponding to the panel A. The dashed gray line is drawn at $X = Y$ to indicate the point where all amino acid substitutions are adaptive.