Supplementary Material

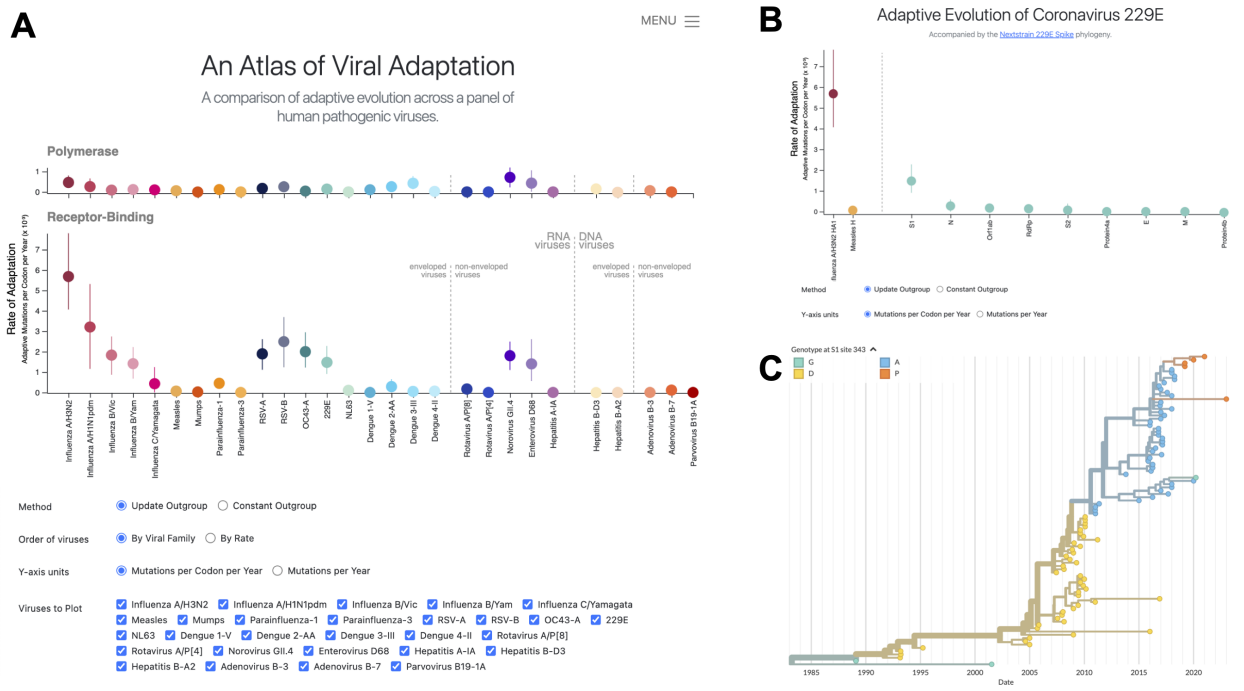

Figure S1: Screenshots of the interactive website presenting the results in this manuscript, related to Figure 3 and 4. A) Screenshot of the main page, accessed at https://blab.github.io/atlas-of-viral-adaptation/. Buttons allow the user to toggle the method used to calculate rate of adaptation (update 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.

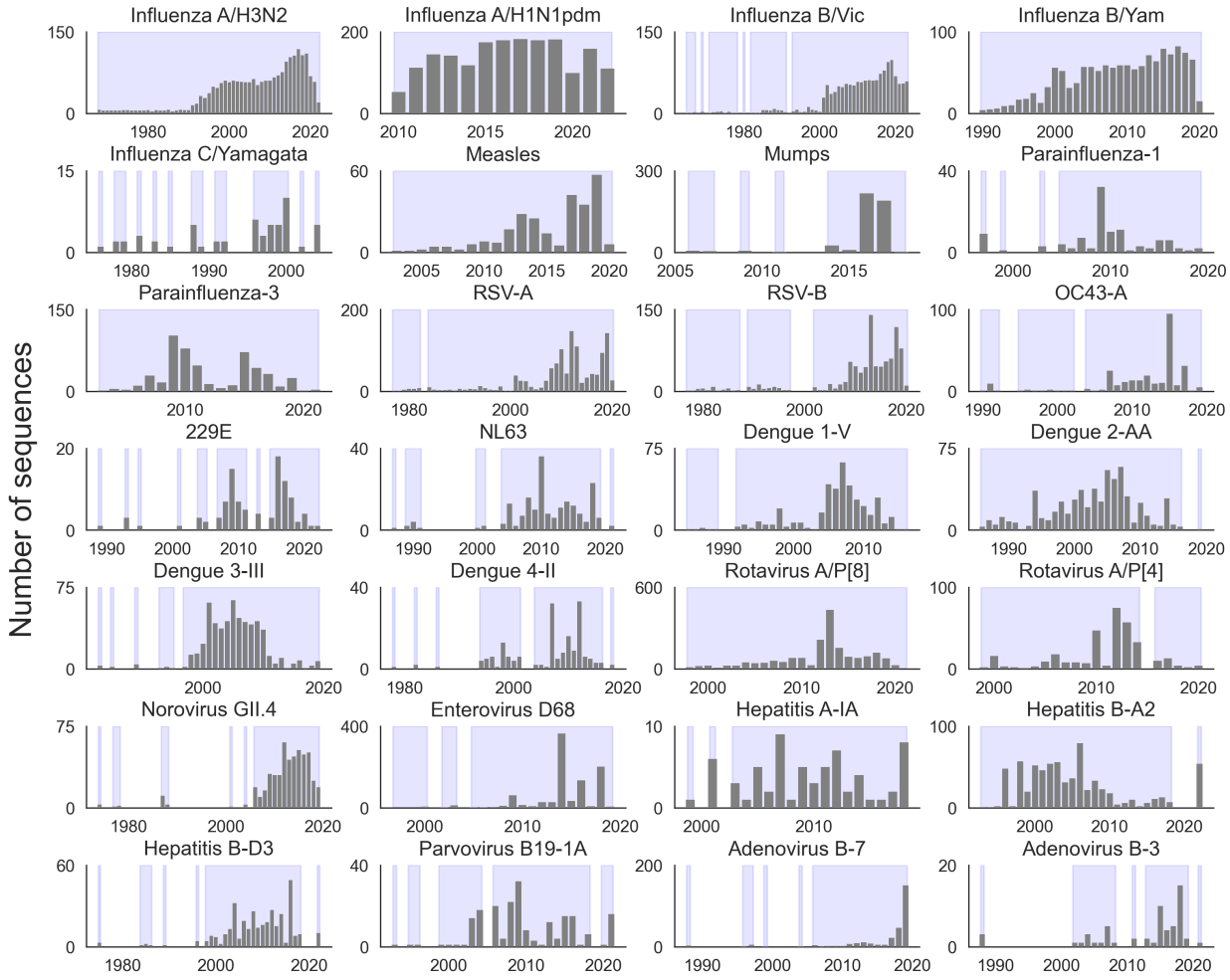

Figure S2: Count of sequences per year for each virus in the panel, related to STAR Methods. The number of receptor-binding gene sequences per year is shown for each virus. Because some years have one or a few sampled sequences and others have hundreds, we have highlighted each year with at least one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

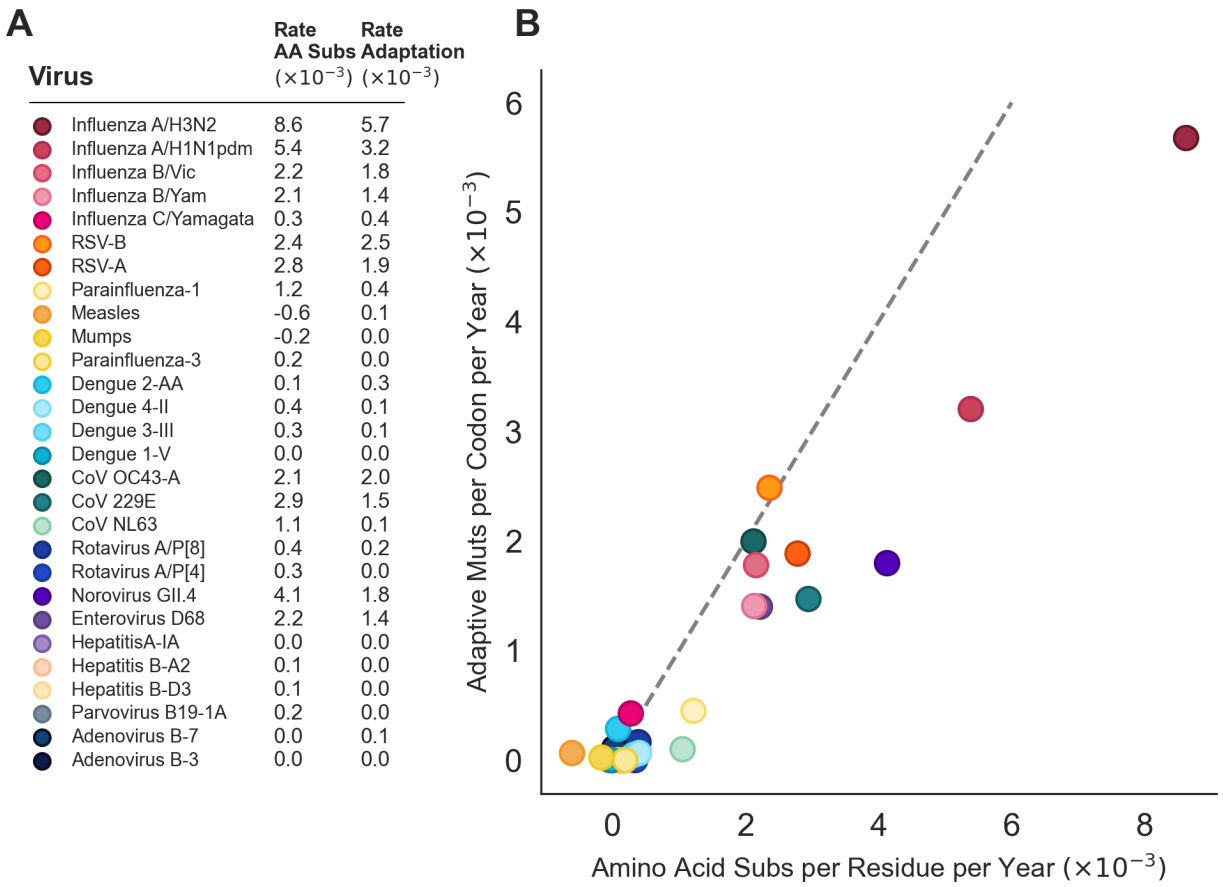

Figure S3: Comparison of rates of amino acid substitution to rates of adaptation, related to Figure 5. A) Rate of amino acid substitution ($\times 10^{-3}$) and rate of adaptive evolution ($\times 10^{-3}$) is listed for each of the 28 viruses in the panel. **B)** Rate of amino acid substitution is plotted 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.

Virus	RB	Polymerase	Surface	Non-Surface
Influenza A/H3N2	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza A/H1N1pdm	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza B/Vic	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza B/Yam	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza C/Yamagata	HEF1	PB1	HEF2	NP, PB2, P3, M, NS
RSV-B	G	L	F, SH	NS1, NS2, N, P, M
RSV-A	G	L	F, SH	NS1, NS2, N, P, M
Parainfluenza-1	HN	L	F	N, P, C, M
Measles	H	L	F	N, P, V, C, M
Mumps	HN	L	F, SH	NC, V, I, M
Parainfluenza-3	HN	L	F	N, P, C, M
Dengue 2-AA	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
Dengue 4-II	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
Dengue 3-III	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
Dengue 1-V	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
OC43-A	S1	RdRp	S2, HE	Orf1ab, E, M, N
229E	S1	RdRp	S2	Orf1ab, Protein 4A, Protein 4B, E, M, N
NL63	S1	RdRp	S2	Orf1ab, Protein 3, E, M, N
Rotavirus A/P[8]	VP4 (P)	R (VP1)	VP7 (G)	VP2, VP3, VP6, NSP1, NSP2, NSP3, NSP4
Rotavirus A/P[4]	VP4 (P)	R (VP1)	VP7 (G)	VP2, VP3, VP6, NSP1, NSP2, NSP3, NSP4
Norovirus GII.4	VP1	RdRp		p48, NTPase, p22, Vpg, 3CL-pro, VP2
Enterovirus D68	VP1	3D	VP2, VP3	VP4, 2A, 2B, 2C, 3A, 3B, 3C
Hepatitis A-IA	VP1	3D	VP2, VP3	VP4, 2A, 2B, 2C, 3A, 3B, 3C
Hepatitis B-A2	Large	Polymerase		Middle, Small, X, Core
Hepatitis B-D3	Large	Polymerase		Middle, Small, X, Core
Parvovirus B19-1A	VP1		VP2	NS, U7_5kDa, X, U11kDa
Adenovirus B-7	Fiber	Pol		E1A, E1B_55K, IVa2, pTp, pIIIA, Penton, Hexon, Protease, 100K
Adenovirus B-3	Fiber	Pol		E1A, E1B_55K, IVa2, pTp, pIIIA, Penton, Hexon, Protease, 100K

Table S1: Genes analyzed in this manuscript, for each virus, related to STAR Methods. For each virus, the receptor-binding (RB) and polymerase genes are listed, along with all other surface (but not receptor-binding) and non-surface (but not polymerase) genes that were analyzed in this study.