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Supplemental information

Comparative transmissibility of SARS-CoV-2 variants Delta and Alpha in New England, USA

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Supplementary Information

State	Alpha	Delta	Other	Total
Connecticut	3376	673	3110	**7159**
Maine	923	131	2267	**3321**
Massachusetts	7273	1872	7652	**16797**
New Hampshire	735	51	999	**1785**
Rhode Island	1347	147	1806	**3300**
Vermont	553	98	395	**1046**
All	**14207**	**2972**	**16229**	**33408**

Table S1. Number of genomes used in this study by state and variant category, related to Figure 1.

Pango Lineage	Number of Genomes	Pango Lineage	Number of Genomes	Pango Lineage	Number of Genomes
B.1.1.7	14207	B.1.617.1	18	B.1.160	2
B.1.2	3374	B.1.625	18	B.1.243.1	2
B.1.526	2989	B.1.177	14	B.1.284	2
B.1.617.2	2624	B.1.400	14	B.1.320	2
P.1	2535	B.1.1.207	13	B.1.333	2
B.1.517	986	B.1.1.28	13	B.1.351.3	2
B.1.429	654	B.1.582	13	B.1.36.8	2
B.1.596	487	B.1.609	13	B.1.395	2
B.1	439	C.36.3	13	B.1.404	2
B.1.575	397	B.1.466.1	11	B.1.428	2
R.1	342	B.1.1.231	10	B.1.574	2
AY.3	321	B.1.612	10	B.1.601	2
B.1.1.519	240	B.1.1.318	9	B.1.628	2
B.1.243	235	B.1.1.33	9	C.23	2
B.1.375	235	B.1.298	9	A.5	1
B.1.427	230	B.1.362	8	B.1.1.10	1
B.1.1.316	204	B.1.580	8	B.1.1.115	1
B.1.525	188	B.1.1.416	7	B.1.1.189	1
B.1.240	183	B.1.139	7	B.1.1.198	1
B.1.568	167	B.1.478	7	B.1.1.220	1
P.2	158	B.1.509	7	B.1.1.221	1
B.1.1	141	B.1.551	7	B.1.1.272	1
B.1.1.486	98	B.1.1.320	6	B.1.1.305	1
B.1.409	93	B.1.160.16	6	B.1.1.34	1
P.1.1	89	B.1.591	6	B.1.1.340	1
B.1.351	83	B.1.1.351	5	B.1.1.372	1
B.1.433	78	B.1.498	5	B.1.1.374	1
B.1.349	73	B.1.543	5	B.1.1.393	1
B.1.1.434	71	B.1.561	5	B.1.1.397	1
B.1.577	65	B.1.1.432	4	B.1.1.420	1
B.1.621.1	62	B.1.361	4	B.1.1.487	1
B.1.234	60	C.36.3.1	4	B.1.1.517	1
B.1.110.3	58	P.1.7	4	B.1.1.518	1
R.2	58	A	3	B.1.119	1
B.1.1.348	54	A.2.5.1	3	B.1.131	1
B.1.311	51	AY.2	3	B.1.153	1

C.37	50	B.1.1.135	3	B.1.258	1
B.1.626	46	B.1.1.274	3	B.1.280	1
B.1.621	44	B.1.1.485	3	B.1.302	1
B.1.1.222	43	B.1.1.523	3	B.1.336	1
B.1.111	43	B.1.241	3	B.1.346	1
B.1.1.192	38	B.1.265	3	B.1.36.1	1
B.1.1.524	36	B.1.36.10	3	B.1.36.29	1
A.2.5	34	B.1.396	3	B.1.378	1
B.1.1.265	31	B.1.473	3	B.1.420	1
B.1.603	30	B.1.517.1	3	B.1.446	1
B.1.588	27	B.1.623	3	B.1.510	1
B.1.595	24	B.1.630	3	B.1.556	1
B.1.1.304	23	P.1.2	3	B.1.563	1
B.1.369	23	AY.1	2	B.1.564	1
AY.3.1	22	B	2	B.1.575.1	1
A.2.5.2	21	B.1.1.1	2	B.1.594	1
B.1.448	21	B.1.1.312	2	B.1.602	1
A.23.1	19	B.1.1.317	2	B.1.617.3	1
B.1.565	19	B.1.1.329	2	B.1.631	1
B.1.604	19	B.1.1.368	2	C.31	1
B.1.1.25	18	B.1.1.411	2	C.36	1
B.1.324	18	B.1.1.464	2	P.1.3	1

Table S2. Number of genomes used in this study by pango lineage, related to Figure 1.

GISAID Submitting Lab	**CT**	**ME**	**MA**	**NH**	**RI**	**VT**	**Total**
Centers for Disease Control and Prevention	2560	738	7135	1469	1438	260	**13600**
Broad Institute	209	87	7826	279	1428	586	**10415**
Yale University	3194	13	117	14	6	0	**3344**
The Jackson Laboratory	928	2345	3	2	1	0	**3279**
Massachusetts State Public Health Laboratory	0	0	1480	0	2	194	**1676**
Rhode Island State Health Laboratory	0	0	0	0	346	0	**346**
Quest Diagnostics	64	12	196	21	10	3	**306**
Connecticut Department of Public Health	179	0	0	0	0	0	**179**
Health and Environmental Testing Laboratory	0	123	0	0	0	0	**123**
Brown University	0	0	0	0	55	0	**55**
University of Michigan	0	0	36	0	0	0	**36**
US Air Force School of Aerospace Medicine	1	2	0	0	7	0	**10**
UConn Health	9	0	0	0	0	0	**9**
New York University	4	1	0	0	0	0	**5**
University of Washington	0	0	0	0	0	3	**3**
Boston University	0	0	2	0	0	0	**2**
New England Biolabs	0	0	2	0	0	0	**2**
MSHS Pathogen Surveillance Program	1	0	0	0	0	0	**1**
All	**7149**	**3321**	**16797**	**1785**	**3293**	**1046**	**33391**

Note: 7 RI and 10 CT sequences were missing metadata on GISAID as of 10/4/2021

Table S3. Number of genomes used in this study by state and submitting lab, related to Figure 1.

	Emergence Period (Days)		
State	**60**	**90**	**120**
Connecticut	1.57	2.51	3.09
Maine	0.43	1.95	2.92
Massachusetts	1.30	1.37	2.98
New Hampshire	0.22	1.75	1.97
Rhode Island	1.30	1.98	3.30
Vermont	1.52	2.63	2.68

Table S4. Relative logistic growth rates by emergence period, related to Figure 2.

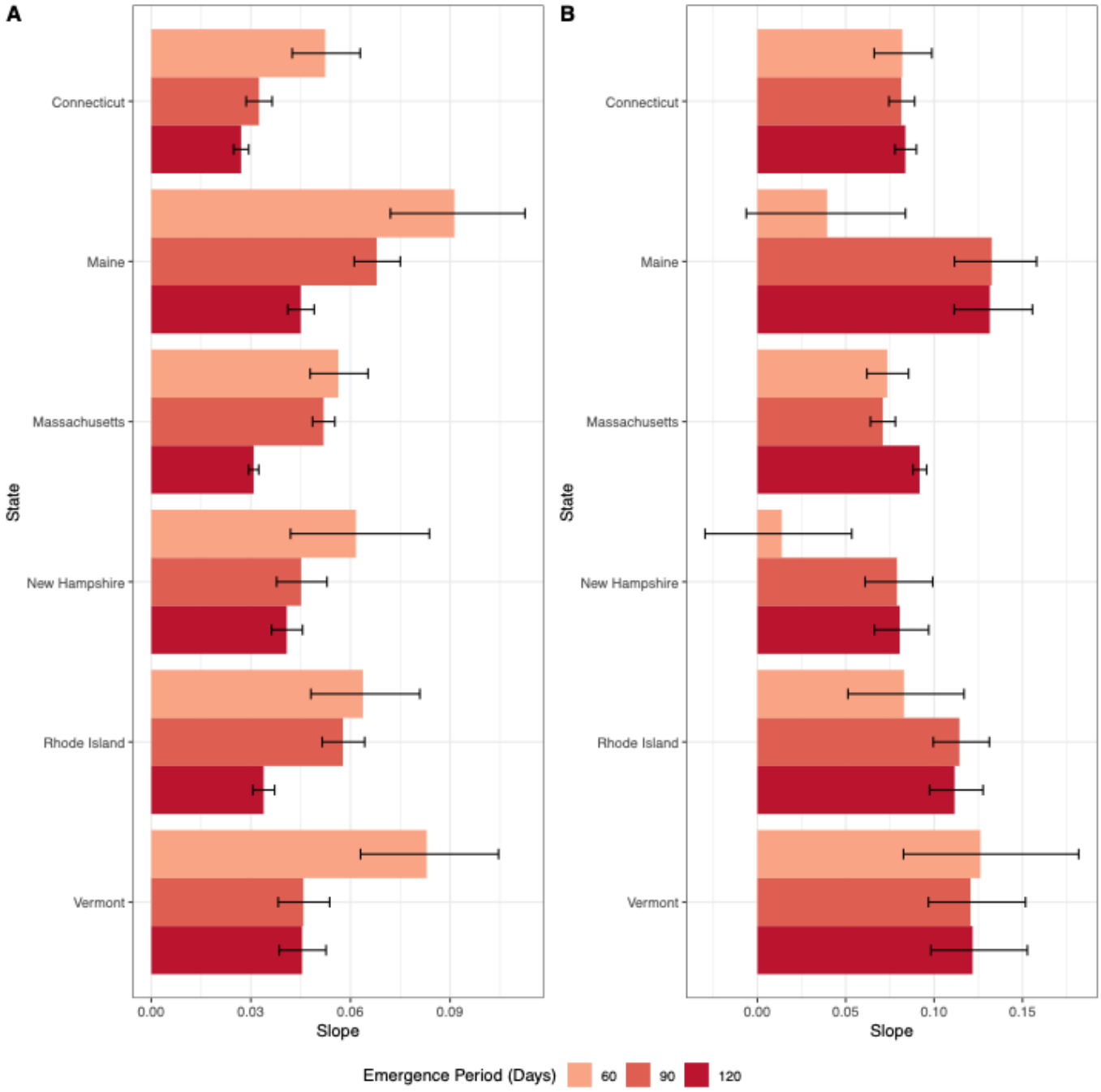

Figure S1. Logistic growth coefficients by length of emergence period, related to Figure 2C.
We conducted a sensitivity analysis varying our emergence period +/- 30 days from our selected 90-day emergence period to understand the effect on our logistic growth rate estimates for (A) Alpha and (B) Delta. Each bar represents the regression coefficients (slopes) of the logistic growth rate (the log odds of a given sequence belonging to each variant category) and its 95% confidence interval for each state and emergence period. We report the ratio of the regression coefficients (slopes) for Delta versus Alpha for each state and emergence period in **Table S4**. The number of state-specific Alpha and Delta genomes during their respective emergence for the 90-day period is reported in the legend for Figure 2. For the 60-day and 120-day Alpha emergence periods, we respectively had the following number of Alpha genomes for each state: Connecticut (N=290, N=2,780), Maine (N=99, N=856), Massachusetts (N=352, N=5,581), New Hampshire (N=70, N=635), Rhode Island (N=142, N=1,184), and Vermont (N=155, N=550). For the 60-day and 120-day Delta emergence periods, we respectively had the

following number of Delta genomes for each state: Connecticut (N=64, N=690), Maine (N=8, N=131), Massachusetts (N=181, N=1,689), New Hampshire (N=11, N=51), Rhode Island (N=17, N=147), and Vermont (N=9, N=98).

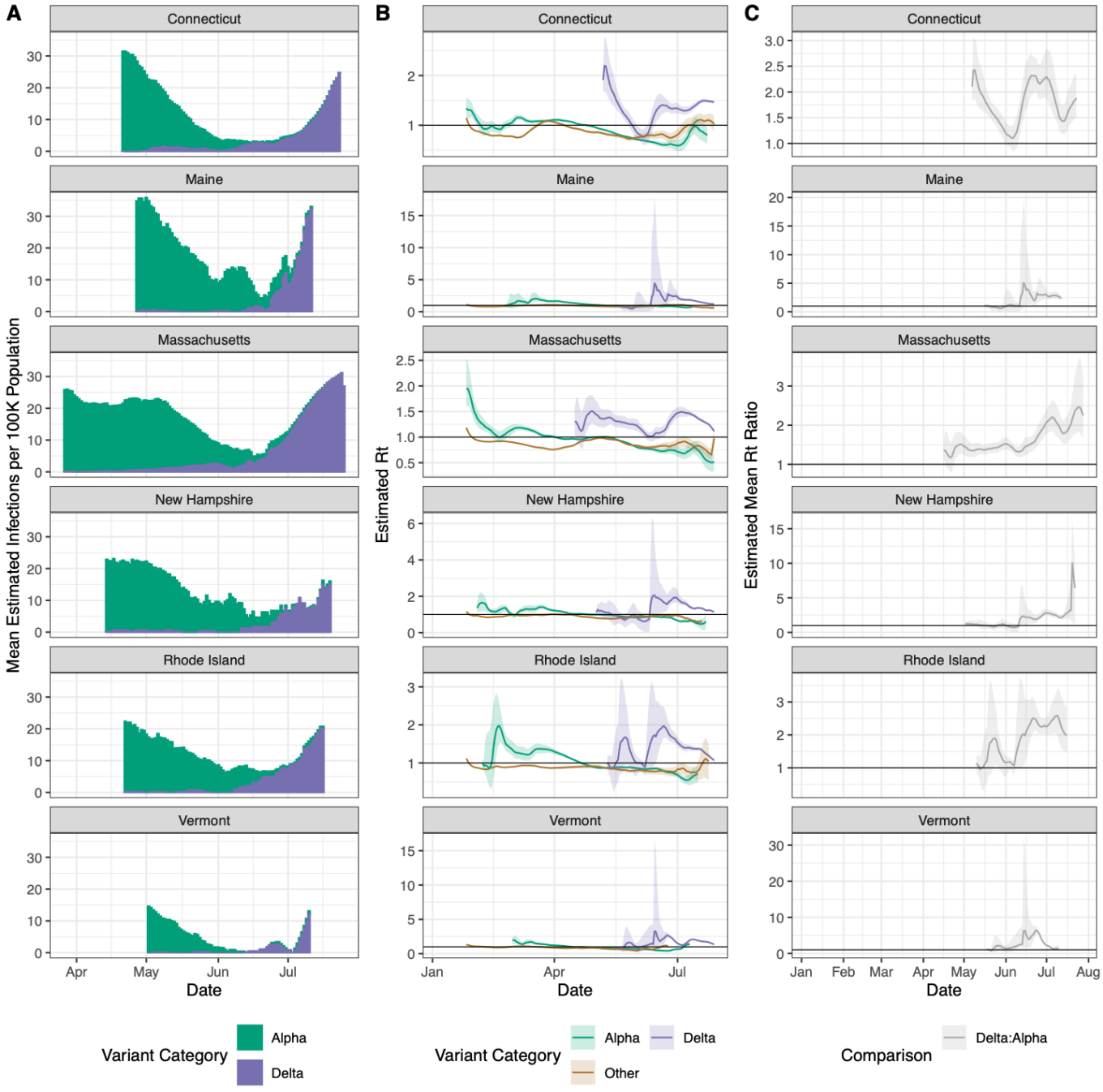

Figure S2. Estimated infections per 100K during co-circulation and comparison of variant effective reproductive numbers with full 95% confidence intervals, related to Figure 3.

(A) We used a multi-step bootstrap sampling approach to generate 1,000 samples containing the estimated number of variant-specific infections. We present the mean estimated Alpha and Delta infections per 100K population across the 1,000 bootstrapped samples during the mean co-circulation period described in the Methods section. Estimated variant-specific infections are used to calculate R_t.

(B) Estimated mean effective reproductive number R_t over time with 95% confidence intervals for each variant category calculated across the 1,000 bootstrapped samples described in (A).
(C) Daily mean ratios of R_t values for Delta compared to Alpha from (B) with 95% confidence intervals calculated across the 1,000 bootstrapped samples described in (A). Note the y-axes differ in both plots.

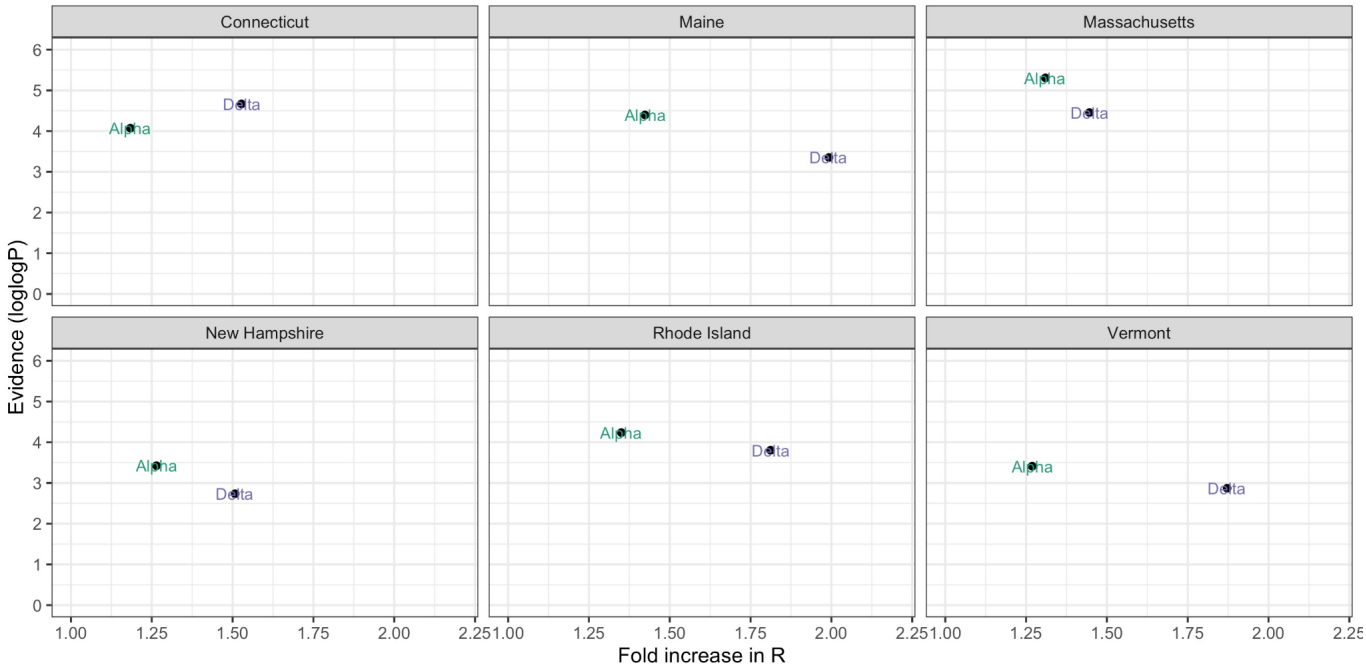

Figure S3. Multiplicative increase in R_t versus the strength of support by variant category and state during the initial 90-day emergence period following first detection, related to Figure 3.
We ran a binomial logistic regression with the variant category as the outcome and the number of days since the first detection as the predictor. The multiplicative increase is calculated by multiplying the regression coefficient by the mean generation interval of 5.2 days and exponentiating. The strength of support is the logged *p*-value for the coefficient. The number of state-specific Alpha and Delta genomes during their respective emergence for the 90-day period is reported in the legend for Figure 2.

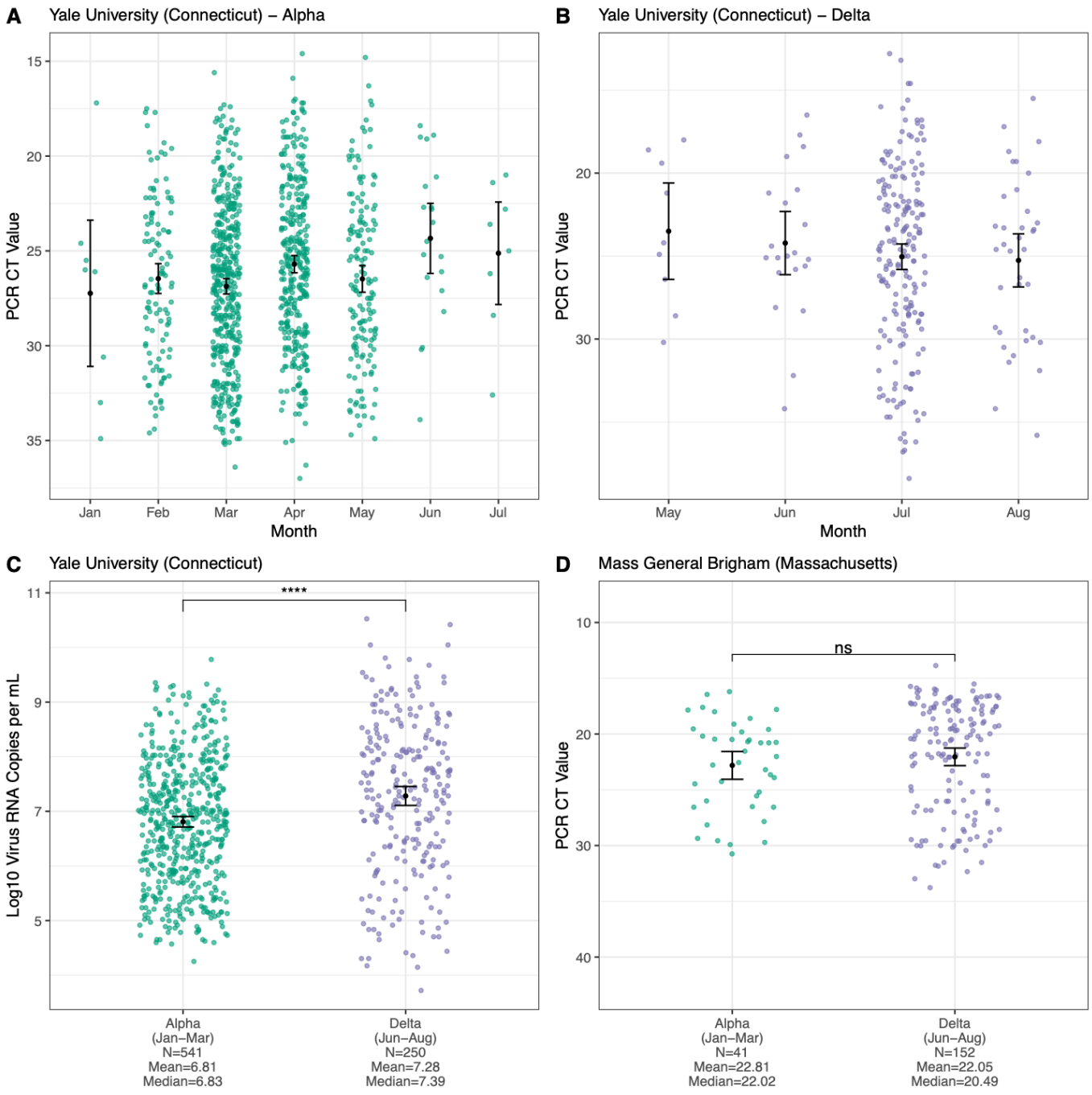
A
Yale University (Connecticut) – Alpha
PCR CT Value
15
20
25
30
35
Jan
Feb
Mar
Apr
May
Jun
Jul
Month
B
Yale University (Connecticut) – Delta
PCR CT Value
20
30
May
Jun
Jul
Aug
Month
C
Yale University (Connecticut)
Log10 Virus RNA Copies per mL
11
9
7
5
****
Alpha
(Jan–Mar)
N=541
Mean=6.81
Median=6.83
Delta
(Jun–Aug)
N=250
Mean=7.28
Median=7.39
D
Mass General Brigham (Massachusetts)
PCR CT Value
10
20
30
40
ns
Alpha
(Jan–Mar)
N=41
Mean=22.81
Median=22.02
Delta
(Jun–Aug)
N=152
Mean=22.05
Median=20.49

Figure S4. PCR CT monthly values, virus copy calculation, and additional ORF1a target, related to Figure 4.
(A) Monthly Alpha and **(B)** Delta PCR CT values. For Alpha, monthly sample sizes were as follows: Jan. N=8, Feb. N=112, Mar. N=425, Apr. N=332, May N=153, Jun. N=20, and Jul. N=8. There were no Alpha samples for August 2021. For Delta, monthly sample sizes were as follows: May N=9, Jun. N=21, Jul. N=192, and Aug. N=27.We plotted the CT values (inverted y-axis) of Yale University Alpha and Delta samples for months where data were available with the mean and 95% confidence intervals. We ran a one-way ANOVA for the Alpha and Delta samples, separately, to test for differences in mean CT values by month. We found a significant difference in monthly mean CT values for the Alpha samples, but not for the Delta samples. For the Alpha samples, we ran a post hoc Tukey's HSD test and found that only the March / April mean CT values were significantly different.
(C) Virus copy calculation from PCR CT values. We used a standardized curve to translate the Yale PCR CT values into log10 virus RNA copies per mL and added the mean and 95% confidence intervals. We removed 4 Alpha samples from early January 2021 that were tested using a different PCR assay. Alpha samples were again limited to January-March and Delta samples to June-August. The means of the Alpha (N=541) and Delta (N=250) samples were compared using a t-test.
(D) ORF1a target CT values. PCR CT values (inverted y-axis) plotted by variant category, limiting Alpha samples to January-March 2021 and Delta samples to June-August 2021 to account for their respective emergence periods. The means of the Alpha (N=41) and Delta (N=152) samples were compared using a t-test. The Mass General Brigham (Massachusetts) data are from the ORF1 gene of the Roche Cobas 6800 test (E gene data shown in **Figure 4**). One sample was dropped from the ORF1a analysis due to an NA value.