Table S1: Study cohort demographics information

N	60
age (median [range])	28.00 [19.00, 73.00]

race (%)	Asian	2 (3.3)
	Black	6 (10.0)
	Other	6 (10.0)
	White	46 (76.7)
gender (%)	Female	26 (43.3)
	Male	34 (56.7)
ethnicity (%)	Hispanic	10 (16.7)
	Non-Hispanic	50 (83.3)

Self-reported conditions:		
copd (%)	No	59 (98.3)
	Yes	1 (1.7)
asthma (%)	No	58 (96.7)
	Yes	2 (3.3)
cancer (%)	No	58 (96.7)
	Yes	2 (3.3)
immunodeficiency (%)	No	58 (96.7)
	Yes	1 (1.7)
	NA	1 (1.7)
anemia (%)	No	58 (96.7)
	Yes	1 (1.7)
	NA	1 (1.7)

Table S2. Comparing model fits to longitudinal viral load data from nasal swab samples using the corrected AIC (AICc) scores. The best overall model is the refractory cell model assuming that the parameter Φ covaries with the age of individuals and the parameters β, ρ covaries with viral type, i.e. non-B1.1.7 vs. B1.1.7 (its AICc score is bolded and underlined).

Model	Assumptions on β and π	Covariate		AICc
		Age	Viral type	
TCL model	Correlation	-	-	1924.9
	Fixed effect β	-	-	1944.4
	Fixed effect π	-	-	1932.9
	Correlation	t_0, β, δ, π	-	1926.4
	Correlation	t_0, β, π	-	1924.9
	Correlation	β, π	-	1926.8
	Correlation	β	-	1923.4
	Correlation	-	t_0, β, δ, π	1928.4
	Correlation	-	t_0, β	1926
	Correlation	-	β	1926.1
Refractory cell model	Correlation	-	-	1844.4
	Fixed effect β	-	-	1844
	Fixed effect π	-	-	1839.2
	Fixed effect β	$t_0, \beta, \delta, \pi, \Phi, \rho$	-	1846.4
	Fixed effect β	δ, Φ, ρ	-	1845.2
	Fixed effect β	Φ, ρ	-	1840.5
	Fixed effect β	Φ	-	1838
	Fixed effect β	ρ	-	1843.5
	Fixed effect β	Φ	$t_0, \beta, \delta, \pi, \Phi, \rho$	1850
	Fixed effect β	Φ	β, δ, ρ	1845.7
	Fixed effect β	Φ	β, ρ	**1836.1**
	Fixed effect β	Φ	β	1838.7
Viral production reduction model	Correlation	-	-	1932.3
	Fixed effect β	-	-	1938.6
	Fixed effect π	-	-	1939.9
	Correlation	$t_0, \beta, \delta, \pi, \gamma$	-	1936.5
	Correlation	β, π, γ	-	1933.9
	Correlation	β, π	-	1931.8
	Correlation	π	-	1937.6
	Correlation	β, π	$t_0, \beta, \delta, \pi, \gamma$	1933.4
	Correlation	β, π	β, π, γ	1940
Immune effector cell model	Correlation	-	-	1931
	Fixed effect β	-	-	1940.3
	Fixed effect π	-	-	1943.9
	Correlation	$t_0, \beta, \delta_1, \pi, t_1, \delta_2$	-	1940.9
	Correlation	β, π, δ_2	-	1937.8
	Correlation	π, δ_2	-	1935.4
	Correlation	δ_2	-	1932.4

	Correlation	-	$t_0, \beta, \delta_1, \pi, t_1, \delta_2$	1941.9
	Correlation	-	δ_1, t_1	1934.2
	Correlation	-	t_1	1927.5
Combined model	Correlation	-	-	1856.8
	Fixed effect β	-	-	1851.4
	Fixed effect π	-	-	1850
	Fixed effect π	$t_0, \beta, \delta_1, \Phi, \rho, t_1, \delta_2$	-	1860
	Fixed effect π	$\delta_1, \Phi, \rho, t_1, \delta_2$	-	1853.7
	Fixed effect π	$\Phi, \rho, t_1, \delta_2$	-	1850.6
	Fixed effect π	Φ, t_1, δ_2	-	1847.6
	Fixed effect π	t_1, δ_2	-	1845.8
	Fixed effect π	t_1	-	1842.4
	Fixed effect π	t_1	$t_0, \beta, \delta_1, \Phi, \rho, t_1, \delta_2$	1854.5
	Fixed effect π	t_1	$\beta, \delta_1, \rho, t_1, \delta_2$	1850.5
	Fixed effect π	t_1	$\beta, \delta_1, \rho, t_1$	1845.8
	Fixed effect π	t_1	β, ρ, t_1	1846.1
	Fixed effect π	t_1	ρ, t_1	1841.5
	Fixed effect π	t_1	ρ	1840.2

Table S3. Comparing model fits to longitudinal viral load data from saliva samples using the corrected AIC (AICc) scores. The best overall model is the immune effector cell model assuming that δ_1 and t_1 covary with viral type, i.e. non-B1.1.7 vs. B1.1.7 (its AICc score is bolded and underlined).

Model	Assumptions on $\boldsymbol{\beta}$ and $\boldsymbol{\pi}$	Covariate		AICc
		Age	Viral type	
TCL model	Correlation	-	-	2126.3
	Fixed effect - β	-	-	2179.1
	Fixed effect - π	-	-	2206.5
	Correlation	t_0, β, δ, π	-	2134.1
	Correlation	-	t_0, β, δ, π	2130.1
	Correlation	-	t_0, β, δ	2127.4
	Correlation	-	t_0, δ	2126.1
	Correlation	-	t_0	2128.7
	Correlation	-	δ	2125.6
Refractory cell model	Correlation	-	-	2110.9
	Fixed effect β	-	-	2139.6
	Fixed effect π	-	-	2132.5
	Correlation	$t_0, \beta, \delta, \pi, \Phi, \rho$	-	2122.6
	Correlation	β, π	-	2111.7
	Correlation	β	-	2111.9
	Correlation	π	-	2111.8
	Correlation	-	$t_0, \beta, \delta, \pi, \Phi, \rho$	2107.6
	Correlation	-	$t_0, \beta, \delta, \pi, \rho$	2107.8
	Correlation	-	t_0, β, π, ρ	2109.3
	Correlation	-	β, π, ρ	2113.2
	Correlation	-	β, ρ	2112
Viral production reduction model	Correlation	-	-	2099.7
	Fixed effect β	-	-	2139.9
	Fixed effect π	-	-	2179.3
	Correlation	$t_0, \beta, \delta, \pi, \gamma$	-	2104.2
	Correlation	δ, π, γ	-	2102.6
	Correlation	δ, γ	-	2103.1
	Correlation	δ	-	2101.2
	Correlation	-	$t_0, \beta, \delta, \pi, \gamma$	2096.5
	Correlation	-	$t_0, \beta, \delta, \gamma$	2100.8
	Correlation	-	t_0, δ, γ	2099.9
	Correlation	-	γ	2100.4
Immune effector cell model	Correlation	-	-	2078.4
	Fixed effect β	-	-	2118.2
	Fixed effect π	-	-	2155.4
	Correlation	$t_0, \beta, \delta_1, \pi, t_1, \delta_2$	-	2081.1
	Correlation	$t_0, \delta_1, t_1, \delta_2$	-	2078
	Correlation	t_0, δ_1, t_1	-	2079.1
	Correlation	t_0, δ_1	-	2076.9

	Correlation	t_0	-	2078.1
	Correlation	-	$t_0, \beta, \delta_1, \pi, t_1, \delta_2$	2079.3
	Correlation	-	$t_0, \beta, \delta_1, t_1, \delta_2$	2077.4
	Correlation	-	$t_0, \delta_1, t_1, \delta_2$	2078.7
	Correlation	-	t_0, δ_1, t_1	2076.6
	Correlation	-	δ_1, t_1	**2074.0**
	Correlation	-	δ_1	2078.2
	Correlation	-	t_1	2076.9
Combined model	Correlation	-	-	2095.7
	Fixed effect β	-	-	2080.9
	Fixed effect π	-	-	2081.8
	Fixed effect β	$t_0, \beta, \delta_1, \pi, \Phi, \rho, t_1, \delta_2$	-	2096.2
	Fixed effect β	π	-	2083.6
	Fixed effect β	-	$t_0, \beta, \delta_1, \pi, \Phi, \rho, t_1, \delta_2$	2084.8
	Fixed effect β	-	$t_0, \delta_1, \pi, \Phi, t_1$	2085
	Fixed effect β	-	t_0, δ_1, π, Φ	2081
	Fixed effect β	-	t_0, δ_1, Φ	2087.5
	Fixed effect β	-	t_0, δ_1	2087.4

Table S4. Estimated population parameter values from the best models, i.e., the refractory cell model for the nasal compartment and the effector cell model for the saliva compartment. The means and standard deviations are derived assuming that individual parameters follow log-normal distributions (except for t_0 and t_1).

Model	Parameter	Description	Mean (population estimate)	Standard deviation*
Refractory cell model (Nasal compartment)	t_0	Estimated time of infection in nasal relative to the day of diagnosis	-2.1 days	1.7 days
	β (non-B.1.1.7)	Infectivity parameter constant	4.92 x 10^{-9} mL/day	0.16
	β (B.1.1.7)		4.02 x 10^{-9} mL/day	
	δ	Death rate of infected cells	2.45 /day	0.24
	π	Composite parameter for virus production and sampling	376.3 /day	-
	Φ	Rate constant for the interferon-induced conversion of target cells to refractory cells	3.45 x 10^{-5} mL/day	1.1
	σ_{Φ}	Coefficient of the covariate, age, on Φ	-0.044	-
	ρ (non-B.1.1.7)	Rate at which refractory cells become target cells again	0.0119 /day	0.07
	ρ (B.1.1.7)		0.0123 /day	
Effector cell model (Saliva compartment)	t_0	Estimated time of infection in nasal relative to the day of diagnosis	-2.8 days	0.29 days
	β	Infectivity parameter constant	7.35 x 10^{-7} mL/day	1.9
	δ_1(non-B.1.1.7)	Death rate of infected cells in the absence of effector cell responses	0.58 /day	0.2
	δ_1(B.1.1.7)		0.05 /day	
	π	Composite parameter for virus production and sampling	4.16 /day	1.8
	t_1 (non-B.1.1.7)	Time when the effector cell response is developed relative to the day of diagnosis	11.1 days	3.5 days
	t_1 (B.1.1.7)		3.7 days	
	δ_2	The increase in infected cell killing due to the effector cell response	1.1 /day	0.35
	χ	Correlation between β and π	-0.955	-

* All the population parameters except for t_0 and t_1 are assumed to follow log-normal distributions in the population, and therefore, the report standard deviation is for a log-normal distribution. Parameters t_0 and t_1 and assumed to be normally distributed.

Table S5. Individual parameter values estimated from the best fit models, i.e. the refractory cell model and the effector cell model for viral dynamics in the nasal and saliva compartment respectively. 'NA' denotes individuals where data are not included in parameter estimation.

ID	Refectory cell model						Effector cell model					
	t_0 (day)	β (10^{-8} mL/day)	δ (/day)	π (/day)	Φ (10^{-6} /day)	ρ (/day)	t_0 (day)	β (10^{-8} mL/day)	δ_1 (/day)	π (/day)	t_1 (day)	δ_2 (/day)
432192	0.8	0.5	2.5	378.9	11.72	0.0120	-2.8	477.9	0.6	0.7	13.86	1.1
432568	4	0.5	2.5	378.9	17.18	0.0119	-2.8	49.3	0.6	5.5	11.05	1.1
432662	1.6	0.5	2.8	378.9	14.86	0.0119	-2.7	27.1	0.5	6.3	11.32	1.1
432686	2.3	0.5	2.4	378.9	12.65	0.0120	-2.8	28.8	0.5	7.4	14.7	1
432864	1.1	0.5	2.5	378.9	0.86	0.0120	-2.9	38.1	0.5	9.2	8.1	1.1
432870	0.6	0.5	2.8	378.9	23.63	0.0119	-2.7	28	0.6	7.1	9.74	1.1
433227	-0.6	0.5	2.4	378.9	5.73	0.0120	-2.8	31.7	0.5	7.4	11.03	1.1
433409	2.4	0.5	2.8	378.9	12.77	0.0118	-2.8	47.3	0.6	6.6	11.08	1.1
435729	3.6	0.5	2.3	378.9	8.79	0.0120	NA	NA	NA	NA	NA	NA
435772	-0.2	0.5	2.9	378.9	5.97	0.0118	-2.7	238.2	0.5	0.3	11.01	1.1
435786	3.2	0.5	2.1	378.9	6.69	0.0119	-2.9	31.8	0.6	9.7	11.82	1.2
435794	2.7	0.5	2.7	378.9	5.37	0.0119	-2.8	73.8	0.7	4.1	13.67	1
435805	2.6	0.5	2.2	378.9	7.22	0.0119	-2.8	23.6	0.5	10.9	13.25	1
435933	-2.4	0.5	3.1	378.9	15.52	0.0118	-2.9	199.9	0.5	1.7	9.66	1.1
435985	1.4	0.4	2.6	378.9	3.31	0.0120	-2.8	447.5	0.7	0.6	9.76	1.2
437388	3.1	0.5	2.3	378.9	15.46	0.0119	-2.8	30.3	0.6	6.6	11.04	1.1
438577	2.5	0.5	2.8	378.9	1.94	0.0118	-2.7	16.1	0.6	11.5	7.22	0.9
441582	1.1	0.5	2.1	378.9	17.92	0.0120	-2.8	317.2	0.6	1.1	5.85	1.4
441736	1.9	0.5	2.5	378.9	5.35	0.0119	-2.8	316.2	0.6	1	8	1.3
441925	2.3	0.5	2.5	378.9	8.11	0.0119	-2.9	76.8	0.6	4.7	10.79	0.9
442978	2.2	0.5	1.9	378.9	12.19	0.0119	-2.9	41.8	0.5	8.3	14.42	1
443108	1.4	0.5	2.7	378.9	2.32	0.0118	-2.8	24.2	0.6	8.6	11.51	1.1
443176	3.9	0.5	2.4	378.9	23.12	0.0119	-2.9	66.2	0.6	6	12.2	1.1
443240	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
444316	1.3	0.5	2.4	378.9	25.77	0.0121	-2.8	1619.5	0.6	0.2	5.68	1.3
444332	0.1	0.5	1.6	378.9	3.9	0.0121	-2.8	8.8	0.5	19.6	14.92	1
444349	2.2	0.5	3.2	378.9	14.01	0.0117	-2.8	189.8	0.7	1.5	12.75	1
444391	1.4	0.4	2.3	378.9	0.85	0.0119	-2.8	86.2	0.6	3.1	11.86	1
444446	2.7	0.5	2.6	378.9	5.75	0.0119	-2.8	10.8	0.5	24.8	14.47	1
444633	1.2	0.5	2.7	378.9	6.55	0.0120	-2.8	27.1	0.5	13.1	14.73	1
445534	3.2	0.5	2.7	378.9	21.37	0.0119	-2.9	275.5	0.6	1.5	6.87	1.5
445535	2.1	0.5	2.2	378.9	0.96	0.0119	-2.8	10.9	0.6	21.6	8.28	1.4

445602	0.3	0.5	2.4	378.9	12.4	0.0120	-2.8	0.2	0.5	712.9	10.21	0.9
446645	4.3	0.6	1.7	378.9	10.28	0.0122	-2.8	827.4	0.6	0.4	10.73	1.1
449474	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
449507	1.1	0.5	2.9	378.9	38.89	0.0119	-2.9	490.3	0.7	0.9	13.93	1.1
449527	4.7	0.6	2.1	378.9	24.93	0.0121	-2.8	250	0.6	1.3	6.42	1.1
449614	4.2	0.5	2.6	378.9	33.43	0.0120	-2.9	401	0.7	1.1	5.63	1.2
450241	2.2	0.4	1.9	378.9	1.54	0.0123	-2.7	159.4	0	1	10.87	1
450253	0.9	0.4	3.2	378.9	25.58	0.0122	-2.8	166.8	0	1.6	6.88	2.3
451146	NA	NA	NA	NA	NA	NA	-2.9	171.3	0	2	0.39	1.7
451152	1.1	0.5	2.4	378.9	12.88	0.0119	-2.8	3	0.6	60.6	10.97	1.1
451231	2.8	0.5	2.6	378.9	7.02	0.0119	-2.8	23.1	0.6	9.4	9.87	1.1
451346	2.4	0.5	2.6	378.9	6.9	0.0120	-2.8	259.7	0.6	1.1	8.49	1.2
451479	5.1	0.5	2.6	378.9	41.51	0.0119	-2.9	1812.4	0.7	0.3	10.01	1.2
451709	0.7	0.4	2	378.9	28.13	0.0125	-2.8	8.9	0	18.8	8.61	1.5
453058	2.7	0.5	1.4	378.9	1.83	0.0122	-2.9	10.9	0.6	35	11.04	1.1
453724	NA	NA	NA	NA	NA	NA	-2.7	337.2	0.6	0.2	7.73	1.6
459589	3.2	0.4	2.7	378.9	15.97	0.0122	-2.9	34.3	0	11	0.82	1.3
459597	-0.6	0.4	3.2	378.9	16.13	0.0122	-2.8	93.8	0	2.9	5.77	1.3
461379	2.9	0.4	2.5	378.9	5.72	0.0123	-2.8	182.6	0	1.6	0.54	0.9
461764	3	0.4	2.1	378.9	11	0.0125	-2.9	38.7	0	10.4	2.26	1.1
461771	2.4	0.4	2.4	378.9	5.33	0.0123	-2.7	137.5	0	1.5	2.23	0.8
469115	0.6	0.4	2.4	378.9	20.79	0.0124	-2.7	73.4	0	2.8	5.05	0.9
470855	0	0.5	2.7	378.9	33.4	0.0119	NA	NA	NA	NA	NA	NA
471467	-0.4	0.4	2.8	378.9	27.3	0.0122	-2.9	1	0	240	3.68	0.9
471588	2.6	0.4	1.9	378.9	6.53	0.0125	-2.8	20.5	0	13.4	3.82	0.8
471890	3	0.4	1.4	378.9	4.52	0.0126	-2.8	88.7	0	3.6	0.21	1.1
473097	5.3	0.4	2.8	378.9	9.24	0.0121	-2.9	88.2	0	4.2	1.68	1.1
473107	3.1	0.4	3	378.9	2.14	0.0122	-2.8	12.2	0	20.7	2.9	1.1

Table S6. The fixed parameters and their values in all viral dynamic models. The initial values of variables are set to 0 except for the two initial values listed below.

Parameter	Description	Values	Reference
T_0	Total number of (infection free) target cells	8×10^7 cells (nasal) and 1.08×10^8 cells (saliva)	See Supplementary Material
E_0	Initial number of infected cells	1 cell	See Supplementary Material
c	Virus clearance rate	10/day	(*2, 3*)
k	1/k is the eclipse period	4/day	(*2, 3*)

Table S7. Model comparison using AICc scores of three models describing the relationship between the viral genome load and cell culture positivity. In each model, we varied the assumption whether a parameter has random effects or only fixed effects. The lowest AICc score, indicating the best model, is bolded and underlined.

Model	Parameter assumptions		AICc
	Random effects	Fixed effect only	
Linear model	A	-	336.7
	-	A	481.6
Power-Law model	G, h	-	322
	h	G	319.6
	G	h	323.4
	-	h, G	349.2
Saturation model	J, h, K_m	-	319.2
	h, K_m	J	319.2
	J, K_m	h	325.4
	J, h	K_m	**<u>314.7</u>**
	J	h, K_m	322.1
	h	J, K_m	330.9
	K_m	J, h	323.7
	-	J, h, K_m	346

Table S8. The estimated parameters in the best-fit model to the paired RTqPCR and cell culture positivity data, i.e. the saturation model assuming K_m has fixed effect only. The population estimates of J, h and K_m are 10.5, 1.2 and 4.5x10^6 /mL, respectively.

ID	Parameter			ID	Parameter	
	J	h			J	h
432192	9.42	1.47		**444633**	12.02	1.54
432568	2.74	0.8		**445534**	18.28	1.18
432662	16.08	1.25		**445535**	18.87	1.08
432686	12.17	1.26		**445602**	14.75	1.09
432864	13.59	1.36		**446645**	13.53	1.71
432870	4.57	0.54		**449507**	9.05	0.7
433227	13.15	1.49		**449527**	11.51	1.28
433409	2.74	0.47		**449614**	11.34	1.58
435729	13.47	1.32		**450241**	17.96	1.74
435772	8.43	1.45		**450253**	2.49	0.87
435786	2.11	0.34		**451152**	12.22	1.38
435794	14.22	0.96		**451231**	11.89	1.25
435805	13.27	0.6		**451346**	15.87	1.22
435933	12.02	1.08		**451479**	10.97	1.21
435985	8.99	0.61		**451709**	15.6	1.76
437388	18.2	1.21		**453058**	4.08	1.1
438577	12.18	1.46		**459589**	9.69	1.55
441582	24.51	1.01		**459597**	1.4	0.72
441736	21.38	0.93		**461379**	8.92	1.49
441925	9.13	1.5		**461764**	3.18	1.2
442978	19.63	0.83		**461771**	14.5	1.97
443108	20.52	0.85		**469115**	8.65	1.38
443176	12.1	1.47		**470855**	9.43	1.61
444316	10.46	0.86		**471467**	12.29	1.58
444332	2.97	0.85		**471588**	0.63	0.54
444349	17.65	1		**471890**	2.29	0.96
444391	27.23	0.95		**473097**	16.3	1.56
444446	11.09	1.21		**473107**	19.37	1.38

Table S9: Viral genotype data

Participant ID number:	Date of enrollment:	Pangolin_lineage:
432192	12/2/20	B.1.576
432568	12/5/20	B.1.2
432662	12/6/20	B.1.2
432686	12/6/20	B.1.2
432864	12/8/20	B.1.1
432870	12/8/20	B.1.2
433227	12/11/20	B.1.2
433409	12/13/20	B.1.2
435729	1/4/21	B.1.582
435772	1/5/21	B.1.1.207
435786	1/5/21	B.1.2
435794	1/5/21	B.1.2
435805	1/5/21	B.1.2
435933	1/6/21	B.1.2
435985	1/6/21	B.1.2
437388	1/8/21	B.1.2
438577	1/9/21	B.1.311
441582	1/11/21	B.1.2
441736	1/11/21	B.1.2
441925	1/11/21	B.1.2
442978	1/12/21	B.1.2
443108	1/12/21	B.1.2
443176	1/12/21	B.1.2
443240	1/12/21	B.1.1.7
444316	1/13/21	B.1.577
444332	1/13/21	B.1.2
444349	1/13/21	B.1.596
444391	1/13/21	B.1.2
444446	1/13/21	B.1.568
444633	1/13/21	B.1.2
445534	1/14/21	B.1.2
445535	1/14/21	B.1.1.207
445602	1/14/21	B.1.2
446645	1/15/21	B.1.2
449474	1/18/21	B.1.2
449507	1/18/21	B.1.2
449527	1/18/21	B.1.2
449614	1/18/21	B.1.243
450241	1/20/21	B.1.1.7

450253	1/20/21	B.1.1.7
451146	1/27/21	B.1.1.7
451152	1/27/21	C.31
451231	1/28/21	B.1.2
451346	1/29/21	B.1.1.519
451479	1/30/21	B.1.2
451709	2/2/21	B.1.1.7
453058	2/5/21	B.1.2
453724	2/10/21	B.1.2
459589	2/20/21	B.1.1.7
459597	2/20/21	B.1.1.7
461379	3/3/21	B.1.1.7
461764	3/4/21	B.1.1.7
461771	3/4/21	B.1.1.7
469115	3/20/21	B.1.1.7
470855	3/23/21	P.1
471467	3/24/21	B.1.1.7
471588	3/24/21	B.1.1.7
471890	3/25/21	B.1.1.7
473097	3/28/21	B.1.1.7
473107	3/28/21	B.1.1.7

Table S10. CN values and the measured viral genome loads used for the viral genome load calibration curve for nasal samples.

CN value	N1 (/mL)	RP (/mL)	N2 (/mL)
17.39	386610.82	1453.94	451848.20
17.69	290396.11	193.97	264061.25
18.18	379840.39	66.18	347221.72
19.87	168508.79	1165.59	161205.60
20.05	75386.10	111.95	75100.57
21.97	66955.68	1390.31	65625.98
22.56	22409.81	601.38	21220.05
23.46	11620.21	2163.67	11656.56
24.45	6354.91	1063.48	6105.84
25.33	10905.32	19975.47	10490.55
26.32	3025.46	148.98	2958.09
27.31	374.47	347.19	356.28
28.54	172.40	94.92	158.30
29.56	103.01	53.38	103.01
29.76	117.64	180.78	100.81
32.17	593.24	7542.15	659.18
31.73	468.42	9176.54	292.74
36.71	122.78	28163.88	122.78
30.14	2001.28	8091.87	1879.87
34.64	987.01	16984.38	801.87
33.40	12465.10	7639.70	15569.42
30.20	1638.25	1501.62	1706.58
34.08	1451.78	2542.09	1270.18
31.53	2467.46	5310.41	2782.92
30.90	5200.57	41850.98	5511.03
33.52	1.00	13603.26	206.74
33.28	436.99	3689.54	312.11
31.71	2829.52	3410.98	2538.92
35.66	237.54	13214.54	772.21
34.62	393.83	151007.75	656.47
38.95	254.23	17640.56	572.12

Table S11. Ct values and the measured viral genome loads used for the viral genome load calibration curve for saliva samples.

Ct value	N gene load (/mL)		Ct value	N gene load (/mL)
1.80E+07	25.2		1.80E+04	35.5
1.80E+07	25.2		1.80E+04	36.2
1.80E+07	25.0		1.80E+04	37.7
1.80E+06	28.7		1.80E+03	38.4
1.80E+06	28.4		1.80E+03	37.8
1.80E+06	28.3		1.80E+03	37.8
1.80E+05	30.8		5.40E+04	33.6
1.80E+05	31.5		5.40E+04	33.4
1.80E+05	31.8		5.40E+04	34.5
1.80E+04	35.1		6.00E+03	38.9
1.80E+04	34.4		6.00E+03	35.2
1.80E+04	35.2		6.00E+03	36.2