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**Cross-sectional assessment of SARS-CoV-2 viral load by symptom status in  
Massachusetts congregate living facilities**

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**Brief summary:** In large-scale cross-sectional testing, nasopharyngeal SARS-CoV-2 viral loads from residents and staff of nursing homes were similar in those with or without symptoms at the time of testing early in the pandemic, though differences emerged as the local epidemic waned.

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## Abstract

Transmission of COVID-19 from people without symptoms confounds societal mitigation strategies. From April to June 2020, we tested nasopharyngeal swabs by RT-qPCR from 15,514 staff and 16,966 residents of nursing homes and assisted living facilities in Massachusetts. Cycle threshold (Ct) distributions were very similar between populations with (N = 739) and without (N = 2179) symptoms at the time of sampling (mean Ct 25.7 versus 26.4, ranges 12-38). However, as local cases waned, those without symptoms shifted towards higher Ct. With such similar viral load distributions, existing testing modalities should perform comparably regardless of symptoms, contingent upon time since infection.

**Keywords:** COVID-19; SARS-CoV-2; molecular diagnostics; viral load; symptoms

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## **Background**

A substantial fraction of severe acute respiratory syndrome coronavirus type 2 (SARS-CoV-2) spread occurs from infected individuals without symptoms of coronavirus disease 2019 (COVID-19) at the time of transmission [1]. We thus sought to understand the relative distributions of viral shedding in patients with and without symptoms. Several small studies found similar SARS-CoV-2 RNA shedding in infected individuals irrespective of symptoms [2–4], though the largest of these quantified viral load only after day 8 of infection, missing the period of maximal viral shedding [3]. Since nasopharyngeal viral load peaks near the time of symptom onset [1,5], routine symptom-driven testing often misses this peak, complicating the relationship between measured viral loads and transmissibility or severity.

As the local epidemic neared its peak in April 2020 (Supplementary Figure S1), in response to several outbreaks, the Commonwealth of Massachusetts initiated systematic viral testing of all staff and residents in all skilled nursing and assisted living facilities, along with a binary report of symptom status at the time of sampling. Here we compare estimated viral load distributions between individuals with and without symptoms at the time of testing.

## **Methods**

### *Study Population*

Between April 9 and June 9, 2020, nasopharyngeal (NP) swabs were collected from all residents and staff in all skilled nursing and assisted living facilities in Massachusetts, either by onsite staff or by the Massachusetts National Guard. The Broad Institute's CLIA-certified clinical laboratory received all specimens from 366 facilities; the remaining samples were tested at the Massachusetts Department

of Public Health State Public Health Laboratory (MASPHL) and are not included in this study. Testing was performed on 32,480 unique individuals at the Broad Institute. For the 6.7% of individuals tested more than once, only data from the first positive test are reported.

### *Symptom and Demographic Information*

Beginning in the second week of the testing program (April 17-23), a binary judgment of symptom status was reported by a clinician at each facility; if this adjudication was not possible, symptom status was coded as missing. Longitudinal information was not available about whether individuals without symptoms at the time of collection previously had or later developed symptoms, nor about duration or severity in those reporting symptoms. However, because most nursing facilities in Massachusetts during the study period required negative SARS-CoV-2 RT-PCR before accepting patients with known or suspected COVID-19, those testing positive would not include many post-symptomatic individuals convalescing from known COVID-19. Personal and demographic information were also collected (Supplementary Table S1).

### *Laboratory Testing*

NP swabs were placed in barcoded tubes with 3 mL of viral transport medium (VTM) and delivered on ice to the laboratory on the day of collection. RNA was extracted from 50 $\mu$ l of VTM using the MagMax-96 RNA extraction kit (Thermo Fisher) on a Bravo liquid handler platform (Agilent). One-step real-time reverse transcriptase–polymerase chain reaction (RT-qPCR) was performed on a QuantStudio 7 (Applied Biosystems), using a laboratory developed SARS-CoV-2 CDC assay protocol run under the FDA’s Emergency Use Authorization framework. Cycle threshold (Ct) values were reported for two viral probes, the N1 and N2 viral nucleocapsid protein gene regions, and a RNaseP human gene control (RP). The Ct value measures the number of amplification cycles required to

detect cDNA produced from viral RNA; a higher Ct value indicates less viral RNA in the sample. Ct values lower than 40 cycles for both N1 and N2 were designated positive (a single positive viral probe was reported as Inconclusive). Viral loads (copies/mL) were estimated by interpolation from a standard curve generated by serial dilutions of a synthetic RNA construct (Twist Biosciences, CA) containing the viral N2 target sequence (Supplementary Figure S2).

### *Analyses*

Ct values for the N1 and N2 probes in positive patients were averaged. One-way ANOVA and pooled t-tests were performed between subpopulations using SAS JMP software, version 13 (SAS Institute). This work was deemed exempt human subjects research by the Broad Institute Office of Research Subject Protection and approved with waiver of informed consent by the MA Department of Public Health's Institutional Review Board.

## **Results**

### *Positive rates by symptom status*

Across all facilities, 2654 of 16,966 residents (15.5%) and 624 of 15,514 staff (4.1%) tested positive for SARS-CoV-2. Tested residents were a mean of 82 years old (SD 13, range 17 – 114), 65% female, and 85% white, while tested staff were a mean of 45 years old (SD 15, range 16 – 101), 76% female, and 50% white. Supplementary Table S1 shows aggregate results by demographic group for the resident and staff cohorts. Among 13,341 residents who lacked symptoms at the time of swabbing, 1692 (12.7%) were positive, compared with 487 (3.7%) of 12,724 staff without symptoms. 699 (53.1%) of 1316 residents with symptoms tested positive, compared with 40 (18.2%) of 220 staff with symptoms (Supplementary Table S2).



### *Comparison of viral load between individuals with and without symptoms at the time of testing*

Among individuals testing positive, Ct values covered a broad range, from 11.6 to 37.7 cycles in individuals without symptoms and 11.9 to 37 cycles in individuals with symptoms (Figure 1), corresponding to viral loads ranging from 2 billion to 8 copies/mL, respectively. The Ct for the human host probe (RP) was more tightly distributed around a mean of 28.9 (SD 2.4) and 28.1 (SD 2.7) cycles for each population (Supplementary Figure S3), indicating reproducible sample collection and handling.

The distributions for the viral level were very similar between individuals with and without symptoms, with a statistically significant but clinically trivial difference in mean Ct of 0.71 cycles (25.7 vs 26.4,  $p=0.006$ ) and a slightly different proportion of individuals with  $Ct \geq 30$  cycles (29.2% for individuals with symptoms vs. 36% for those without) (Figure 1). Similarly, the mean Ct for the human host probe differed by 0.74 cycles ( $p=0.0001$ ) between these two populations (Supplementary Figure S3). For context, test developers and the FDA typically use a Ct difference of  $<3$  cycles as an indicator of substantial equivalence between viral testing methods. Furthermore, the observed differences in Ct are less than the typical variability in sampling efficiency, as reflected in the RP probe Ct distributions (SD 2.4 and 2.7 cycles).

### *Variation of viral loads over time*

During the study period, overall COVID-19 burden in the state peaked at  $>3000$  confirmed cases per day on April 17 (week 2 of the study) and declined thereafter, dropping over 7-fold by the end of the study period (Supplementary Figure S1). When the distribution of viral loads between individuals

with and without symptoms was compared over time, on a weekly basis, no difference was observed between the two populations, either in mean Ct value or range, during the time period that coincided with the peak outbreak of COVID-19 in Massachusetts (April 17-23) (Figure 2; Supplementary Figure S1). However, as cases waned over the course of the study, a gap emerged, with mean Ct value shifting higher in the population without symptoms while remaining essentially unchanged for symptomatic patients throughout the testing period. Specifically, individuals without symptoms tested during weeks 5 and 6 (May 7-20) had Ct values >3 cycles greater (less virus) than symptomatic individuals ( $p = 0.0013$  and  $0.0007$  for weeks 5 and 6, respectively).

#### *Effect of age and other demographic variables*

Although age dramatically affects COVID-19 severity, viral level did not vary significantly by symptom class in any age group over the entire study period, for either residents or staff (Supplementary Figures S4, S5). Across other demographic variables (sex, race, ethnicity, resident vs staff), statistically significant but numerically small differences were observed between those with and without symptoms in some categories ( $\Delta$ Ct range 0.8 - 1.2 cycles among demographic classes with  $p < 0.05$ ; Supplementary Figure S5).

#### **Discussion**

Because of frequent spread from individuals who do not show symptoms at the time of transmission [1], control measures that aim to substantially mitigate SARS-CoV-2 transmission require diagnosis of infected individuals who do not display symptoms at the time of testing [6]. By screening 16,966 residents and 15,514 staff of residential nursing facilities in Massachusetts, we generated quantitative RT-PCR data from 2179 subjects without and 739 with symptoms, the largest cohort of individuals without symptoms at the time of testing reported to date. The Ct distributions between

the two populations over the entire study period were remarkably similar, both overall and in each subgroup examined (age, sex, race, and ethnicity).

With or without symptoms, viral loads from NP swabs varied by 250 million-fold, consistent with prior studies [7] (Figure 1). As in other respiratory illnesses [8], it is plausible (but not proven) that infectivity of individuals with SARS-CoV-2 may relate to viral load [9]. Cross-sectional studies only report on viral load at the moment of sampling, whereas transmission may be better predicted by peak viral load; this peak is difficult to capture, particularly since it occurs very near the time of symptom onset [1,5]. Only careful prospective longitudinal studies have reliably captured this peak, but these have been small and in specialized populations [10]. Cross-sectional studies capture the distribution of viral loads at one moment in time that should include this peak in a subset of subjects, whereas convenience samples, such as those from symptomatic or hospitalized patients, often miss this peak entirely but have been the basis for most comparisons of viral load to date [11,12].

The mean and distribution of Ct values for individuals with and without symptoms were nearly identical at first, shortly after a surge in statewide cases (Supplementary Figure S1), before diverging in subsequent weeks as local prevalence subsided, when the mean viral load in individuals without symptoms declined (Figure 2). Since viral load peaks early during infection before waning slowly [1], viral loads at a given point in time depend on the distribution of time since infection for the population tested. Symptoms are typically displayed within a limited time period early in infection, close to the peak of viral shedding [1]. As a consequence, even if the distribution of viral levels over time is identical between individuals with and without symptoms, the set of individuals with symptoms at any given time is selected for more recent infections and thus higher viral levels

compared to individuals without symptoms. This dependence on epidemic dynamics of the relationship between symptom status and Ct may explain conflicting results seen in other cross-sectional studies [13]. During the rapid initial growth phase of a local epidemic, this skew in time-since-infection between those with and without symptoms is modest because the vast majority of infections are recent. Because the expected skew in time-since-infection is minimized in the rapid initial growth phase of a local epidemic, this period may provide a better representation of the prospective distribution of viral loads across individuals infected at roughly the same time, compared with a stable or declining local epidemic. As a local epidemic stabilizes or declines, this skew will increase, as symptomatic cases are still selected to reflect recent infection, while those without symptoms will on average be later since infection. This property of Ct distributions from a random cross-sectional sampling might even be used to estimate recent trends in disease incidence in a population [14].

This finding also has important implications for interpreting Ct distributions from cross-sectional or convenience samples of newly-discovered variants or of vaccinated individuals who become infected. A variant that is increasing in frequency in a population will have proportionally more recent cases than the wild-type strain it is displacing, which would tend to artifactually increase the average measured viral load, since variant cases would on average be newer. Conversely, soon after a vaccination rollout, cases in vaccinated individuals will decline rapidly over time, meaning cases found in vaccinated individuals will be more likely to have been acquired remotely than recently, whereas this constraint will not occur in unvaccinated individuals in the same population (until population immunity thresholds are approached). This discrepancy would tend to artifactually increase Ct (reduce observed viral load) simply due to a systematic difference in the time of sampling relative to peak shedding between the two populations. While altered peak viral load may be a plausible mechanism by which variants may increase [15] or vaccines may reduce transmissibility

[16], caution must be taken to disentangle these systematic sampling biases driven by epidemic dynamics [14], which are one important determinant among many that may affect observed Ct distributions.

The majority of positive tests from both residents (1692 of 2391, 70.8%) and staff (487 of 527, 92.4%) of all ages came from individuals without symptoms at the time of testing (Supplementary Figure S5). However, each group of individuals would have been depleted for symptomatic COVID-19 (residents with severe symptoms may have been transferred to hospitals, while most symptomatic staff would likely have stayed home), explaining the higher percentage compared with smaller-scale cross-sectional studies [17]. Modeling studies suggest that a substantial fraction of transmission occurs from people who are not symptomatic at the time, whether asymptomatic or presymptomatic [1], which is reinforced by contact-tracing studies [2,17]. Our finding that infected individuals without symptoms shed as much SARS-CoV-2 as those with symptoms underscores the need to expand beyond symptom-based screening as a sole tactic for detecting infected individuals and preventing transmission.

This study should be interpreted with certain caveats. First, without longitudinal follow-up, we cannot distinguish infected individuals who are permanently asymptomatic from those who are pre-symptomatic. However, both classes likely carry risk for transmitting the virus unwittingly [1,2,17] even while differing in their implications for contact tracing and COVID-19 pathogenesis. Second, with only a binary point-prevalence assessment of symptoms at the time of testing, we cannot resolve the relationship between viral load and concurrent or future symptom incidence or severity in this population. These are important avenues for future exploration in longitudinal studies. Third, nursing home residents and staff may differ with respect to stages or disease severity from other

populations, such as severely symptomatic individuals presenting to an acute setting for testing or requiring hospitalization [12], or asymptomatic individuals in different settings [2,3]. Nonetheless, these data represent Ct values for non-hospitalized individuals who did not seek acute testing, which represents the majority of COVID-19 cases and the vast majority of those at risk for ongoing transmission. Finally, RNA levels from NP swabs may not reflect viral loads in other body sites and cannot distinguish live virus from inactive or killed virus [9].

In summary, individuals with and without symptoms showed very similar distributions of SARS-CoV-2 viral loads, particularly early in the study during the peak of the local epidemic. Testing of asymptomatic individuals is under consideration in many settings, including contact tracing by public health departments and screening in workplaces or schools. While optimal implementation strategies and cost-effectiveness must be carefully considered, these findings build confidence in the technical feasibility of identifying asymptomatic individuals harboring SARS-CoV-2 by standard RT-PCR assays or other viral-directed diagnostics such as antigen testing, once timing of infection is considered, which may be less certain in those without symptoms.

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### **Conflict of interest**

None of the authors report a conflict of interest.

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### **Presentation at meetings**

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## References

1. He X, Lau EHY, Wu P, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nat Med*. **2020**; 26(5):672–675.
2. Chau NVV, Thanh Lam V, Thanh Dung N, et al. The natural history and transmission potential of asymptomatic SARS-CoV-2 infection. *Clin Infect Dis* [Internet]. **2020**; . Available from: <http://dx.doi.org/10.1093/cid/ciaa711>
3. Lee S, Kim T, Lee E, et al. Clinical course and molecular viral shedding among asymptomatic and symptomatic patients with SARS-CoV-2 infection in a community treatment center in the Republic of Korea. *JAMA Intern Med* [Internet]. **2020**; . Available from: <https://jamanetwork.com/journals/jamainternalmedicine/article-abstract/2769235>
4. Long Q-X, Tang X-J, Shi Q-L, et al. Clinical and immunological assessment of asymptomatic SARS-CoV-2 infections. *Nat Med*. **2020**; 26(8):1200–1204.
5. Cevik M, Tate M, Lloyd O, Maraolo AE, Schafers J, Ho A. SARS-CoV-2, SARS-CoV, and MERS-CoV viral load dynamics, duration of viral shedding, and infectiousness: a systematic review and meta-analysis. *Lancet Microbe*. **2021**; 2(1):e13–e22.
6. Gandhi M, Yokoe DS, Havlir DV. Asymptomatic Transmission, the Achilles' Heel of Current Strategies to Control Covid-19. *N. Engl. J. Med*. 2020. p. 2158–2160.
7. To KK-W, Tsang OT-Y, Leung W-S, et al. Temporal profiles of viral load in posterior oropharyngeal saliva samples and serum antibody responses during infection by SARS-CoV-2: an observational cohort study. *Lancet Infect Dis* [Internet]. Elsevier; **2020**; . Available from: <https://www.sciencedirect.com/science/article/pii/S1473309920301961>
8. Tsang TK, Cowling BJ, Fang VJ, et al. Influenza A Virus Shedding and Infectivity in Households. *J Infect Dis*. **2015**; 212(9):1420–1428.

9. Wölfel R, Corman VM, Guggemos W, et al. Virological assessment of hospitalized patients with COVID-2019. *Nature*. **2020**; 581(7809):465–469.
10. Kissler SM, Fauver JR, Mack C, et al. SARS-CoV-2 viral dynamics in acute infections [Internet]. *bioRxiv. medRxiv*; 2020. Available from: <http://medrxiv.org/lookup/doi/10.1101/2020.10.21.20217042>
11. Kanjilal S, Baker M, Woolley AE, et al. 427. Variation in SARS-CoV-2 molecular diagnostic test performance in symptomatic versus asymptomatic populations. *Open Forum Infectious Diseases*. Oxford University Press; **2020**; 7(Suppl 1):S280.
12. Magleby R, Westblade LF, Trzebucki A, et al. Impact of SARS-CoV-2 Viral Load on Risk of Intubation and Mortality Among Hospitalized Patients with Coronavirus Disease 2019. *Clin Infect Dis [Internet]*. **2020**; . Available from: <http://dx.doi.org/10.1093/cid/ciaa851>
13. Chung E, Chow EJ, Wilcox NC, et al. Comparison of Symptoms and RNA Levels in Children and Adults With SARS-CoV-2 Infection in the Community Setting. *JAMA Pediatr [Internet]*. **2021**; . Available from: <http://dx.doi.org/10.1001/jamapediatrics.2021.2025>
14. Hay JA, Kennedy-Shaffer L, Kanjilal S, et al. Estimating epidemiologic dynamics from cross-sectional viral load distributions [Internet]. *Science*. 2021. p. eabh0635. Available from: <http://dx.doi.org/10.1126/science.abh0635>
15. Kidd M, Richter A, Best A, et al. S-variant SARS-CoV-2 lineage B.1.1.7 is associated with significantly higher viral loads in samples tested by ThermoFisher TaqPath RT-qPCR. *J Infect Dis [Internet]*. **2021**; . Available from: <http://dx.doi.org/10.1093/infdis/jiab082>
16. Levine-Tiefenbrun M, Yelin I, Katz R, et al. Initial report of decreased SARS-CoV-2 viral load after inoculation with the BNT162b2 vaccine. *Nat Med [Internet]*. **2021**; . Available from: <http://dx.doi.org/10.1038/s41591-021-01316-7>

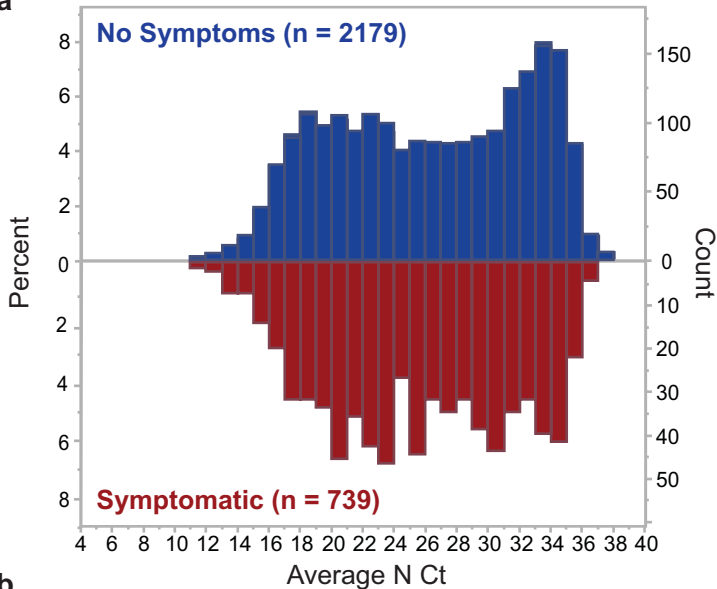
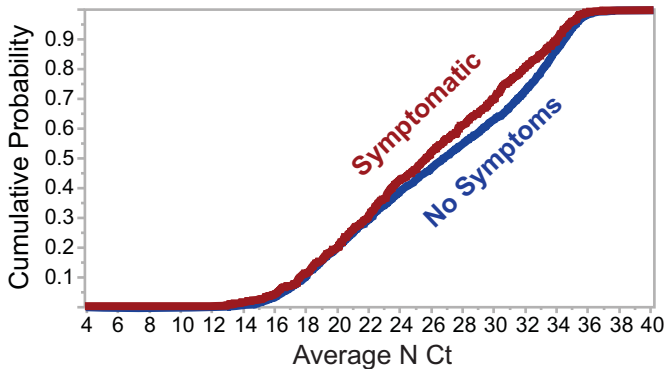
17. Buitrago-Garcia D, Egli-Gany D, Counotte MJ, et al. Occurrence and transmission potential of asymptomatic and presymptomatic SARS-CoV-2 infections: A living systematic review and meta-analysis. *PLoS Med.* **2020**; 17(9):e1003346.

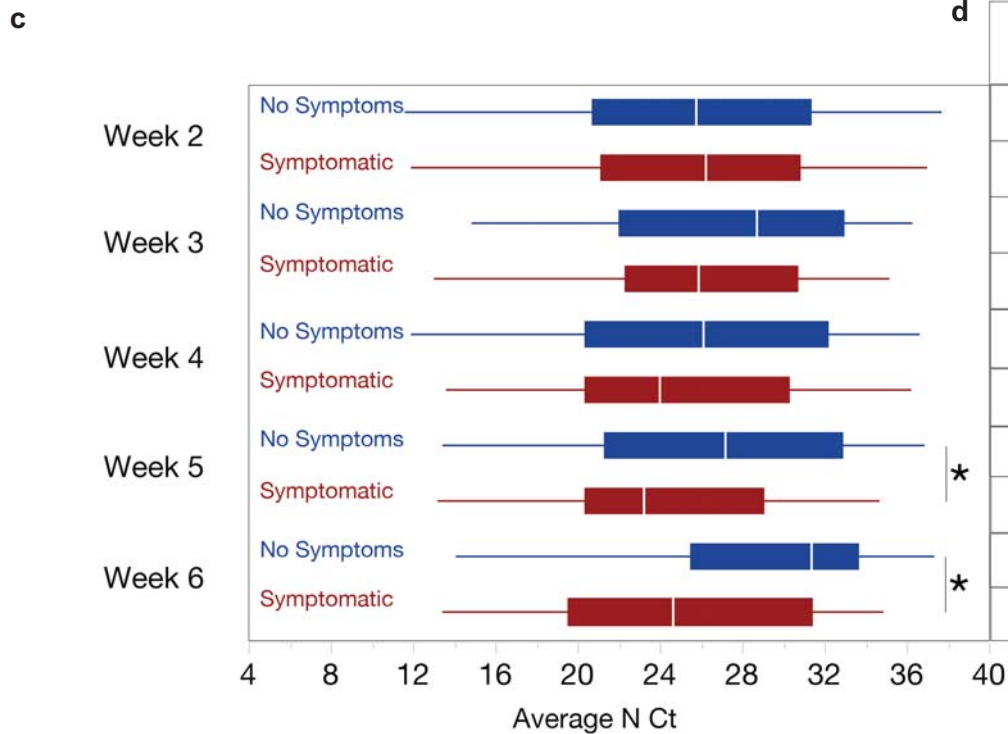
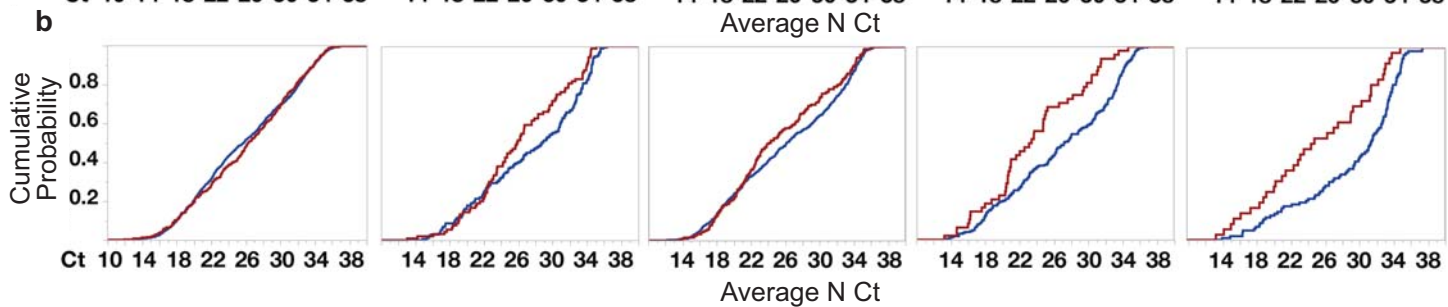
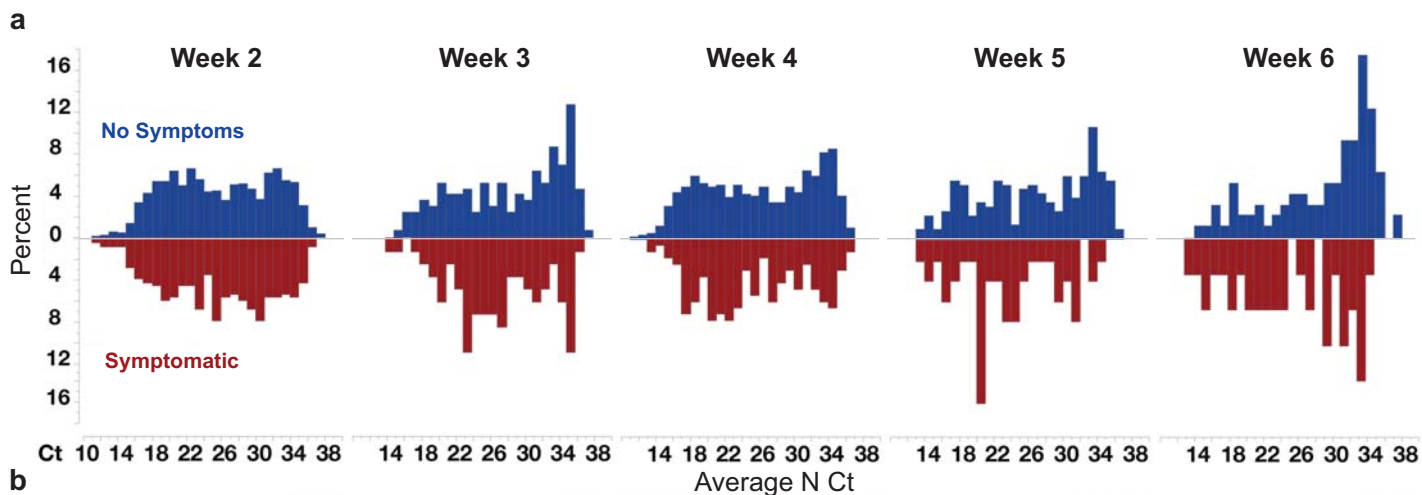
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## Figure Legends

**Figure 1. SARS-CoV-2 viral load distributions are very similar independent of symptom status at the time of testing.** Ct distributions using probes targeting the SARS-CoV-2 N gene (average of N1 and N2 probes) from patients without (blue) or with (red) symptoms at the time of testing are shown as binned histograms **(a)** and cumulative distributions **(b)**.

**Figure 2. Distributions of cycle thresholds diverged as the local epidemic waned, with individuals without symptoms shifting to lower viral loads (higher cycle thresholds).** **(a)** Ct distribution by symptom class by week of study (blue = no symptoms; red = with symptoms). Weeks with fewer than 20 data points in either category are not shown. Week 1 data are omitted, as symptom class was not captured. **(b)** Cumulative distribution plots of the data from (a). **(c)** Box-plots of the average viral N probe (N1 and N2) Ct by week and symptom class, with vertical line at median, colored boxes at IQR, and whiskers showing full range. Asterisk =  $p < 0.05$  within a sub-category. **(d)** Table of sample size, mean Ct, standard deviation (SD),  $\Delta$ Ct between symptom classes, and associated p-value.

**a****b**



**d**

N	Mean Ct (SD)	$\Delta$ Ct (Mean) (p-value)
1017	25.8 (6.0)	0.2 (0.57)
400	26.0 (5.9)	
173	27.5 (6.1)	1.3 (0.09)
89	26.2 (5.5)	
638	26.0 (6.4)	0.8 (0.12)
174	25.2 (6.1)	
227	26.8 (6.4)	3.2 (0.002)
48	23.6 (5.6)	
103	29.1 (5.9)	4.1 (0.0007)
36	25.0 (6.5)	