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SARS-CoV-2 Community Transmission disproportionately affects Latinx population during Shelter-in-Place in San Francisco

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Summary: By providing mass SARS-CoV-2 PCR/antibody testing, regardless of symptoms, in a San Francisco census tract, we determined that infections, most of which were asymptomatic, from diverse lineages continued circulating among low-income, Latinx persons 6-weeks into the city's shelter-in-place ordinance.

ABSTRACT

Background: There is urgent need to understand the dynamics and risk factors driving ongoing SARS-CoV-2 transmission during shelter-in-place mandates.

Methods: We offered SARS-CoV-2 reverse transcription-PCR and antibody (Abbott ARCHITECT IgG) testing, regardless of symptoms, to all residents (≥4 years) and workers in a San Francisco census tract (population: 5,174) at outdoor, community-mobilized events over four days. We estimated SARS-CoV-2 point prevalence (PCR-positive) and cumulative incidence (antibody or PCR-positive) in the census tract and evaluated risk factors for recent (PCR-positive/antibody-negative) versus prior infection (antibody-positive/PCR-negative). SARS-CoV-2 genome recovery and phylogenetics were used to measure viral strain diversity, establish viral lineages present, and estimate number of introductions.

Results: We tested 3,953 persons: 40% Latinx; 41% White; 9% Asian/Pacific Islander; and 2% Black. Overall, 2.1% (83/3,871) tested PCR-positive: 95% were Latinx and 52% asymptomatic when tested. 1.7% of census tract residents and 6.0% of workers (non-census tract residents) were PCR-positive. Among 2,598 tract residents, estimated point prevalence of PCR-positives was 2.3% (95%CI: 1.2-3.8%): 3.9% (95%CI: 2.0-6.4%) among Latinx vs. 0.2% (95%CI: 0.0-0.4%) among non-Latinx persons. Estimated cumulative incidence among residents was 6.1% (95%CI: 4.0-8.6%). Prior infections were 67% Latinx, 16% White, and 17% other ethnicities. Among recent infections, 96% were Latinx. Risk factors for recent infection were Latinx ethnicity, inability to shelter-in-place and maintain income, frontline service work, unemployment, and household income <$50,000/year. Five SARS-CoV-2 phylogenetic lineages were detected.

Conclusion: SARS-CoV-2 infections from diverse lineages continued circulating among low-income, Latinx persons unable to work from home and maintain income during San Francisco's shelter-in-place ordinance.

Key Words: community-based SARS-CoV-2 testing; asymptomatic SARS-CoV-2 infection; shelter-in-place; ethnic disparities; phylogenetic analysis

Introduction

In early 2020, multiple introductions of SARS-CoV-2 into the United States laid the foundation for the ongoing epidemic that has claimed over 100,000 U.S. lives in less than 6 months.[1] Some of the earliest clinical cases of COVID-19 were recognized in California,[2] and the state led the nation in issuing a state-wide shelter-in-place mandate on March 19.[3] San Francisco declared a local emergency on February 25 and issued a series of increasingly restrictive mandates on sizes of gatherings culminating in a shelter-in place order on March 16. Although peak hospitalization and death rates in San Francisco over the ensuing month were nearly 10-fold lower than hard-hit cities such as New York,[4] the pattern of disproportionately higher hospitalizations among Latinx communities was similar.[5] In San Francisco, 45% of reported COVID-19 cases are among Latinx people, who represent 15% of the city's population, and at San Francisco General Hospital, a large public hospital with a patient population that is 31% Latinx, 81% of COVID-19-related hospitalizations from March-May 2020 were among Latinx people.[6, 7]

Hospitalizations and deaths represent a small fraction of total SARS-CoV-2 infections.[8-10] Estimates of the burden of community SARS-CoV-2 infections from direct measurements have been difficult to obtain and compare because symptomatic testing programs capture only a proportion of cases,[11] the recognized symptoms associated with COVID-19 have expanded over time,[12] the assays used to identify infection have variable performance characteristics, and easily accessible testing programs are not in place for some of the most highly affected communities. Data on community transmission and ethnic disparities in SARS-CoV-2 infection, as opposed to COVID-19 disease[13], as well as systematic efforts to determine factors driving these disparities remain limited.[14]

To estimate the point prevalence and cumulative incidence of infection, determine risk factors for ongoing versus prior infection and characterize ongoing transmission and viral strain diversity with phylogenetic analyses, we offered population-based, universal PCR and antibody

testing for SARS-CoV-2 infection, regardless of symptoms, to all residents of a densely populated census tract within a majority Latinx community in San Francisco.

Methods

Unidos en Salud is a longitudinal study to characterize SARS-CoV-2 epidemiology and assess impact of public health measures within a US census tract in San Francisco. Six-weeks into the city's shelter-in-place ordinance, we provided cross-sectional, mass, low-barrier SARS-CoV-2 reverse transcription-PCR (RT-PCR) and antibody testing, regardless of symptoms, to residents (≥4 years) and people who work but may not reside in the census tract.

Study Setting and Community Mobilization

U.S. census tract 022901 is a population-dense, 16-square-block (0.1 square-mile) area in San Francisco's Mission District, with 5,174 residents of whom 58% are Latinx, 34% White/Caucasian, 5% Asian/Pacific Islander, and 1% Black/African American. Median per capita income was $40,420/year in 2018, with 34% of households earning <$50,000/year and 20% earning >$200,000/year.[15] In partnership with the Latino Task Force for COVID-19, an umbrella organization coordinating local Latinx community-based organizations, we distributed flyers, mobilized the community on local and social media, and offered online and door-to-door pre-registration within the census tract for testing appointments during the week prior to the testing campaign.

Testing Campaign

From April 25-28, 2020, we offered outdoor testing at public parks and schools to those who provided an address in the census tract or worked in the tract. On April 28, we expanded eligibility to residents of neighboring city blocks (two blocks north, three blocks east and one block south), responding to high community demand. During pre-registration, we conducted a brief survey. At the time of testing, we obtained verbal consent for participation and conducted COVID-19 symptom screening. Medical staff performed a fingerstick blood collection (500µL) for antibody testing and an oropharyngeal/mid-turbinate nasal swab for quantitative RT-PCR. Participants could opt out of either test. We contacted all PCR-positive persons to disclose results and perform a clinical assessment. We provided household support via a community-led team for PCR-positive participants and evaluated symptoms among all PCR-positive participants over 2 weeks following testing.

Laboratory assays

Swabs were collected in DNA/RNA Shield (Zymo Research) to inactivate virus and preserve RNA stability. RT-PCR of viral N and E genes and human RNAse P gene was performed on extracted RNA at a CLIA-certified laboratory operated by UCSF and the Chan Zuckerberg Biohub using a Laboratory Developed Test with a limit of detection of $\log_{10}$ 4.5 viral genome copies/mL. SARS-CoV-2-positive RNA samples were subjected to Primal-Seq Nextera XT version 2.0,[16] using the ARTIC Network V3 primers,[17] followed by paired-end 2 x 150bp sequencing on an Illumina NovaSeq platform. For antibody testing, the ARCHITECT SARS-CoV-2 IgG Emergency Use Authorization (EUA) assay (Abbott Laboratories, Abbott Park, IL, USA)[18] was performed on participants' plasma from the fingerstick collections, which is a research use of the test.

Study Outcomes

Outcomes included the estimated point prevalence of all PCR-positive infections, recent infections (PCR-positive and antibody-negative) and prior infections (antibody-positive and PCR-negative). Cumulative incidence of infection was defined as any PCR or antibody-positive result. Phylogenetics were used to measure strain diversity.

Statistical analyses

Proportions were compared using chi-squared tests and medians compared using Wilcoxon rank-sum tests. Cumulative incidence of infection was adjusted for RT-PCR and antibody test characteristics; 95% confidence intervals incorporating uncertainty in test characteristics were based on bootstrap. For census tract residents, we further adjusted for differences in age, sex, and race/ethnicity of participants compared to 2018 census estimates (**Supplementary Methods**). We used multivariate logistic regression for the dependent outcome of PCR-positivity among participants tested and included the independent variables sex, frontline worker status, household income and reporting a COVID-19 contact, based on *a priori* interest and univariate results. We did not adjust confidence intervals for multiple testing.

Bioinformatics and genomic analyses

A phylogenetic tree was constructed containing all 123 SARS-CoV-2 genomes from San Francisco County on GISAID[19] on May 22, 2020 together with the high-quality consensus genomes assembled from this study, using the nextstrain toolkit.[20] Global clade identification and naming follows the Nextstrain proposal,[21] and significance of population structure was computed by a permutation test was used for Hudson's FST (**Supplementary Methods**).[22]

Ethics Statement

The UCSF Committee on Human Research determined that the study met criteria for public health surveillance.

Role of the Funding Source

The study was supported by the Chan Zuckerberg Biohub, UCSF, and a Program for Breakthrough Biomedical Research award. ARCHITECT SARS-CoV-2 test kits were provided by Abbott Laboratories. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Results

Testing Uptake and Coverage

Overall, 3,953 persons were tested during the campaign. Of all persons tested, 53% were male, and 40% identified as Latinx, 41% White, 9% Asian/Pacific Islander, 2% Black, and 7% other/mixed ethnicity (**Table 1**). A significantly higher proportion of Latinx compared to non-Latinx participants reported annual household income <$50,000/year (62% vs. 19%), living with >5 persons/household (25% vs. 5%) and working frontline service jobs (43% vs. 17%, **Supplementary Table S1**). Estimated census tract testing coverage of adult residents (age ≥20 years) was 60%.

SARS-CoV-2 Infection by PCR testing

Among 3,871 tested by SARS-CoV-2 RT-PCR, 2.1% (83 people) tested PCR-positive: 1.7% (43/2,598; 95%CI: 1.2%-2.2%) of census tract residents, 6.0% (27/450; 95%CI: 4.0%-8.6%) of tract

workers and 1.6% (13/823; 95%CI: 0.8%-2.7%) of residents of neighboring city blocks. Among all persons tested, 237 (6.1%) reported symptoms compatible with COVID-19 of whom 31 (13.1%) tested PCR-positive. Twelve people (0.3% of all persons tested) reported having had a prior positive test for COVID-19, of whom five tested PCR-positive.

Among PCR-positive persons, 95% identified as Latinx, median age was 38 years (interquartile range [IQR]: 28-50 years), and 76% were male. Persons testing PCR-positive were significantly more likely than persons testing PCR-negative to identify as Latinx, report inability to shelter-in-place and maintain income, work frontline-service jobs or be unemployed, and live in households with income <$50,000/year and ≥3 persons/household (**Table 2**). Given that 95% of PCR-positive persons were Latinx, we limited our multivariate model to Latinx participants to evaluate risk factors for PCR-positivity within this group, and found significantly higher odds of PCR-positive infection if male (OR: 2.0, 95% CI: 1.1-3.6, p=0.02), working a frontline service job (OR: 2.6, 95% CI: 1.4-5.1, p=0.004, ref: non-frontline), household income <$50,000/year (OR: 8.9, 95% CI: 1.9-158, p=0.03, ref: >$100,000/year), or reporting a COVID-19 contact (OR: 3.6, 95%CI: 2.0-6.3, p<0.001).

Estimated point prevalence of PCR-positive infection in the census tract after adjusting for age and sex of participants in the testing campaign versus census demographics was 2.3% (95% CI: 1.2%-3.8%): 3.9% (95%CI: 2.0%-6.4%) among Latinx vs. 0.2% (95%CI: 0.0%-0.4%) among non-Latinx tract residents. Among Latinx people who worked in the census tract, unadjusted point prevalence of PCR-positive infection was 10.4% (95% CI: 7.0%-14.8%), compared to 0.0% (95% CI: 0.0%-2.0%) among non-Latinx workers.

Clinical characteristics of PCR-positive persons

Among 83 PCR-positive persons, 43 (52%) were asymptomatic at the time of testing. Two-week follow-up was obtained for 41 participants who were asymptomatic at the time of testing:

8/41 (20%) recalled mild symptoms that had resolved by the time of testing, 10 (24%) developed symptoms after testing (pre-symptomatic) and 23 (56%) remained asymptomatic. Based on reclassified symptom status among PCR-positive people, 39/80 (49%) were symptomatic at time of testing, 8 (10%) were previously symptomatic, 10 (12.5%) were pre-symptomatic, and 23 (29%) remained asymptomatic throughout infection. One PCR-positive person (1.3%) required hospitalization.

SARS-CoV-2 Cumulative Incidence and Recent vs. Prior Infections

Among 3,861 participants tested for SARS-CoV-2 antibodies, 3.4% (131) tested Ab-positive: 3.1% (80/2,545; 95%CI: 2.5%-3.9%) among census tract residents compared to 7.7% (34/442; 95%CI: 5.4%-10.6%) among tract workers and 2.1% (17/829; 95%CI: 1.2%-3.3%) among adjacent city block residents. Estimated cumulative incidence (Ab or PCR-positive) among tract residents was 4.4% (95% CI: 3.2%-5.6%) after adjusting for test characteristics and 6.1% (95%CI: 4.0%-8.6%) after further adjusting for participation (**Supplementary Table S2**).

Among all infections detected by PCR or Ab, 26% (48/182) were recent infection. 53% (96/182) were prior infection. Of the remaining infections, 18% (32/182) were PCR-positive/Ab-positive, and 3% (6/182) had PCR or antibody testing alone (**Supplementary Table S3**). Whereas prior infections occurred across a range of ethnic groups, employment types and household income levels, recent infections were predominantly among persons who identified as Latinx, worked frontline service jobs and lived in households with income <$50,000/year (**Figure 1**). Compared to individuals with prior infection, people with recent infection were significantly more likely to be of Latinx ethnicity (OR 10.1; 95% CI: 2.81-64.6, p=0.002, ref: non-Latinx ethnicity), report inability to shelter-in-place and maintain income (OR: 3.18; 95%CI: 1.10-11.6, p=0.048), work frontline service jobs (OR: 2.83; 95%CI: 1.21-6.93, p=0.019) or be unemployed (OR: 3.47; 95%CI: 1.08-11.3, p=0.035,

ref: non-frontline service jobs), and live in households with income <$50,000/year (OR: 19.3; 95%CI: 3.74-356, p=0.005; ref: household income >$100,000/year; **Supplementary Table S4**).

SARS-CoV-2 RNA levels and phylogenetic analysis

Median levels of virus as estimated by RT-PCR cycle thresholds were significantly higher among PCR-positive/Ab-negative persons compared to PCR-positive/antibody-positive persons, supporting our classification of recent infection (**Figure 2**). Among recently-infected individuals, median levels of virus by RT-PCR cycle threshold did not differ significantly between symptomatic (24, IQR: 19-25, range 11-35; N=27) and asymptomatic (24, IQR: 19-26, range 16-32; N=10; p=0.98) persons (**Figure 2**); additional comparisons by subgroup are in **Supplementary Figure S1**.

We recovered SARS-CoV-2 genomes from 59% (49/83) of the PCR-positive RNA samples. The recovered genomes were diverse and phylogenetically intermixed with samples from across San Francisco, including representatives from five globally circulating clades, showing multiple independent introductions (**Figure 3, Panel A**). Overall, 58% of PCR-positive participants shared a home with another PCR-positive participant identified in the testing campaign: sequences from such households were consistent with within-household transmission (**Figure 3, Panel B)**, with no variants detected in 65% of household links (N = 11/17, 95% CI 41%-83%). We found no significant population structure separating the Mission district samples from the rest of San Francisco (p=0.19).

Discussion

We found stark ethnic and economic disparities in who is at risk for ongoing infection six-weeks into San Francisco's shelter-in-place ordinance. The estimated point prevalence of PCR-positive infection among Latinx residents (3.9%) was twenty times that of non-Latinx residents (0.2%). Perhaps even more striking was that recent infections were concentrated almost exclusively among low-income, Latinx people working frontline jobs, whereas prior infections occurred among more ethnically and economically diverse individuals. In addition, the majority of PCR-positive infections were asymptomatic at the time of testing, and recently infected individuals had high levels of virus regardless of symptoms. These data show that San Francisco's COVID-19 epidemic has continuing transmission in subgroups of the city population that require urgent attention.

Heterogeneity among populations most affected by the COVID-19 epidemic exists across the U.S., within states and cities, and even within neighborhoods as shown here. Population-level epidemiologic data coupled with phylogenetic analyses can help identify, track and inform testing strategies, public health policies and measures to mitigate health and economic effects. Low-barrier, community-mobilized testing is foundational to these efforts. We sought to overcome some of the testing barriers in this census tract through our partnership with the community-led Latino Task Force in San Francisco, who provided explanations about COVID-19 and communicated the importance of testing to the community. Through this approach, we were able to test a large proportion of the population in a short period of time. To date, there are limited published data on population-level PCR testing in the US. Our estimated point prevalence of PCR-positive infection among residents (2.3%) was higher than an estimate (1.74%) from a statewide random population sample of persons aged $\geq$12 years in Indiana also obtained in late April 2020, [23] and notably higher than that of a community-wide testing study in the coastal town Bolinas, in the San Francisco Bay Area, in which no PCR-positive cases were identified.[24]

We determined that during shelter-in-place, COVID-19 transmission became increasingly concentrated in Latinx community members. The risk factors driving recent transmission among Latinx residents in our study were largely economic and highly correlated: low-income residents working frontline jobs who could not shelter-in-place and maintain their income. Unemployed residents may have experienced increased risk of PCR-positive infection as a consequence of seeking employment, particularly among day laborers. Given the evidence of within household transmission, confirmed by SARS-CoV-2 sequencing, we suspect that transmission was amplified in Latinx multi-generational and multi-family households – a byproduct of skyrocketing rental costs in the city.[25] These economic drivers and ethnic disparities observed at the community level here are reflected in COVID-19 hospitalizations and deaths widely reported in the US, in many settings disproportionately affecting Black/African American people.[13, 26, 27]

We observed high sequence diversity of SARS-CoV-2 infections in the census tract, similar to the diversity seen in San Francisco more broadly, suggestive of multiple independent introductions over time. Our data suggest that most recent infections during shelter-in-place are due to acquisition of virus when working in the census tract, with subsequent within-home transmission in high-density, low-income households. These findings should help dispel common, dangerous pitfalls in interpreting ethnic disparities in infection, such as biological explanations, supposed community behaviors or stigmatizing communities as transmission "hot spots" about which others have cautioned.[14]

Our results also highlight the importance of SARS-CoV-2 testing in both symptomatic and asymptomatic individuals. Symptom-based testing would have failed to detect over 40% of PCR-positive infections in this community, many of whom had high levels of virus. Overall, 29% of PCR-positive infections never developed symptoms, slightly lower than the proportion found (43%) in a population-based SARS-CoV-2 screening study from Iceland.[28] In our study, recently infected people had high levels of virus that did not differ significantly based on symptoms, a finding in line

with a recent cohort study from the Republic of Korea.[29] The clear implication of these findings is that testing strategies limited to symptomatic individuals and those seeking testing at health centers alone, will fail to limit transmission.

These results have several implications moving forward as shelter-in-place restrictions are lifted. First, more efforts are needed to address uncontrolled epidemics among sub-populations, especially vulnerable populations such as the Latinx community highlighted here. Expanded low-barrier testing, that is targeted, community-led and mobilized, and not limited to symptomatic persons, is needed. Testing needs to be coupled with social protection of job security and economic support for self-isolation and quarantine (i.e. "test and respond") and culturally responsive contact tracing. Our testing campaign contributed to policy change in San Francisco, with the mayor announcing on May 4, 2020 that essential workers would be eligible for free SARS-CoV-2 testing regardless of symptoms,[30] and then on May 28, 2020 that low-wage workers with COVID-19 would be provided funds to stay home and isolate ("Right to Recover").[31] In parallel, longitudinal, population-based cohorts that couple epidemiologic data with PCR and antibody testing and viral sequencing can provide evidence of effectiveness of public health measures and viral introductions over time, enabling evidence-based responses in a dynamic landscape.

Our study has several limitations. SARS-CoV-2 PCR tests do not detect all cases and antibody sensitivity may be lower in asymptomatic infection which could have resulted in underestimation of cumulative incidence. False positive antibody results could result in overestimation of cumulative incidence and misclassification of prior infections. Misclassification of prior infections could also result from infections that occurred, generated antibodies and resolved to PCR-negative over the six weeks following the shelter-in-place order. Fingerstick sampling could also impact antibody test performance. However, the EUA antibody test we used has been shown to have a high sensitivity (96.9-100%) at ≥17-22 days post symptom onset, and high specificity (≥99.6%) with venous drawn plasma,[32, 33] and our estimates of cumulative incidence accounted for sensitivity and specificity of

the PCR and antibody assays used. Second, selection bias in who chose to test may have affected our estimates. Although we adjusted for demographic differences between participants and community composition based on 2018 American Community Survey data, these data may not fully reflect tract demographics in 2020. However, population-based testing in a census tract allowed for greater clarity in understanding who did not participate. Lastly, we relied on self-reported symptoms and survey responses, which may have resulted in misclassification. With follow-up of PCR-positive participants over two weeks, we were able to further explore symptom status, allowing for monitoring and reclassification.

In conclusion, improving access to SARS-CoV-2 testing, regardless of symptoms, through community-led, low-barrier testing programs in vulnerable communities is feasible. Adding economic support and protections for low-income workers during isolation and quarantine could further increase testing and contribute to reducing community transmission and the massive disparities in SARS-CoV-2 infection observed in the U.S.

NOTES

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Potential Conflicts of Interest:

Mary Rodgers and John Hackett Jr. are employees and shareholders of Abbott Laboratories. Charles Y. Chiu is the director of the UCSF-Abbott Viral Diagnostics and Discovery Center (VDDC) and receives research support funding from Abbott Laboratories. M.G. reports grants from the NIH. V.J. reports grants from CDC/PEPFAR, outside the submitted work. D.H. reports grants from National Institutes of Health and The Gates Foundation, outside the submitted work. J.D. reports grants from Chan Zuckerberg Biohub, outside the submitted work. G.C. reports grants from National Institutes of Health and The Gates Foundation, outside the submitted work. All other authors have no potential conflicts.

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Tables

Table 1. Characteristics of persons participating in a population-based SARS-CoV-2 testing campaign in the study census tract (US Census tract 022901).

	Residents	**Workers**[1]	**Adjacent City Block Residents**	**Total**
N	2,653	460	840	3,953
Sex at birth, N (%)[2]				
Male	1236 (53%)	284 (62%)	418 (51%)	1938 (53%)
Female	1118 (47%)	173 (38%)	408 (49%)	1699 (47%)
Age category (years)				
4-10	78 (3%)	12 (3%)	28 (3%)	118 (3%)
11-17	100 (4%)	18 (4%)	23 (3%)	141 (4%)
18-50	1695 (64%)	278 (60%)	559 (67%)	2532 (64%)
51-70	633 (24%)	133 (29%)	185 (22%)	951 (24%)
>70	147 (6%)	19 (4%)	45 (5%)	211 (5%)
Race/Ethnicity[2]				
White/Caucasian	925 (40%)	112 (25%)	433 (53%)	1470 (41%)
Hispanic/Latinx	934 (40%)	265 (59%)	251 (31%)	1450 (40%)
Black/African American	59 (3%)	15 (3%)	11 (1%)	85 (2%)
Asian/Pacific Islander	239 (10%)	38 (8%)	55 (7%)	332 (9%)
Other	166 (7%)	22 (5%)	64 (8%)	252 (7%)

Occupation[2]				
Frontline Service Jobs				
Food/Beverage	176 (8%)	125 (28%)	70 (9%)	371 (11%)
Healthcare	128 (6%)	21 (5%)	43 (5%)	192 (5%)
Tradesperson (e.g. construction, plumbing) or Cleaning (e.g. janitor, housekeeper)/personal services (e.g. hairdresser)	244 (11%)	76 (17%)	75 (9%)	395 (11%)
Non-frontline Service Jobs				
Education	119 (5%)	13 (3%)	53 (6%)	185 (5%)
Finance, Sales & Technology	486 (21%)	31 (7%)	155 (19%)	672 (19%)
Student	191 (8%)	34 (8%)	71 (9%)	296 (8%)
Retired/homemaker	219 (10%)	23 (5%)	76 (9%)	318 (9%)
Unemployed	160 (7%)	27 (6%)	50 (6%)	237 (7%)
Other occupation	542 (24%)	91 (21%)	230 (28%)	863 (24%)
Household (HH) information[2]				
Number of people/HH				
1-2	807 (36%)	125 (31%)	338 (41%)	1270 (37%)
3-5	1092 (49%)	212 (53%)	417 (51%)	1721 (50%)

>5	313 (14%)	66 (16%)	68 (8%)	447 (13%)
Rooms/HH				
1-2	684 (32%)	154 (39%)	260 (32%)	1098 (33%)
3-4	898 (42%)	174 (44%)	338 (42%)	1410 (43%)
>4	535 (25%)	64 (16%)	208 (26%)	807 (24%)
Annual income/HH				
<$50,000/year	819 (36%)	253 (58%)	205 (25%)	1277 (36%)
$50,000-100,000/year	604 (27%)	105 (24%)	202 (25%)	911 (26%)
>$100,000/year	831 (37%)	78 (18%)	407 (50%)	1316 (38%)
Homeless	43 (2%)	12 (3%)	5 (1%)	60 (2%)
Past Medical History[2]				
Chronic lung disease	287 (12%)	54 (12%)	113 (14%)	454 (13%)
Chronic heart disease	120 (5%)	24 (5%)	35 (4%)	179 (5%)
Hypertension	325 (14%)	76 (17%)	81 (10%)	482 (13%)
Diabetes	148 (6%)	32 (7%)	33 (4%)	213 (6%)
Smoker[3]	540 (23%)	103 (23%)	174 (21%)	817 (23%)
COVID-19-related history				
Reported prior positive test for COVID-19	5 (0.2%)	1 (0.2%)	6 (0.7%)	12 (0.3%)
Reported having a personal contact diagnosed with COVID-19	175 (8%)	72 (16%)	69 (8%)	316 (9%)

Reported being able to shelter-in-place & maintain income	993 (47%)	79 (19%)	377 (49%)	1449 (44%)

[1]Includes workers and family members of people who reported working in the census tract.

[2]Excludes testing campaign participants with missing responses (i.e. not provided) during the testing survey.

[3]Tobacco or marijuana

Table 2. Characteristics of SARS-CoV-2 testing campaign participants who tested PCR-positive compared to PCR-negative, and factors associated with increased odds of PCR-positivity.

	PCR-positive (N=83)	PCR-negative (N=3,788)	Univariate risk of PCR-positivity (OR, 95% CI)	P value
Sex at birth (%)[1]				
Female	20 (24%)	1638 (47%)	*Ref*	
Male	63 (76%)	1845 (53%)	2.71 (1.64-4.69)	<0.001
Age category (years)				
4-10	4 (5%)	104 (3%)	*Ref*	
11-17	2 (2%)	127 (3%)	0.41 (0.06-2.14)	0.3
18-50	60 (72%)	2429 (64%)	0.64 (0.26-2.15)	0.4
51-70	14 (17%)	923 (24%)	0.39 (0.14-1.41)	0.11
>70	3 (4%)	205 (5%)	0.38 (0.07-1.76)	0.2
Race/Ethnicity[1]			*Ref: non-*	
White/Caucasian	1 (1%)	1441 (42%)	*Hispanic/Latinx*	
Hispanic/Latinx	79 (95%)	1348 (39%)		<0.001
Asian/Pacific Islander	2 (2%)	324 (9%)	28.3 (11.7-93.1)	
Other	1 (1%)	326 (9%)		
Occupation[1]				
Frontline Service Job	47 (64%)	902 (27%)	6.56 (3.86-11.6)	<0.001
Non-frontline Service Job	18 (24%)	2267 (67%)	*Ref*	
Unemployed	9 (12%)	220 (6%)	5.15 (2.18-11.3)	<0.001

Number of people/household[1]				
1-2	10 (14%)	1235 (37%)	*Ref*	
3-5	41 (58%)	1645 (50%)	3.08 (1.60-6.53)	0.002
>5	20 (28%)	420 (13%)	5.88 (2.79-13.2)	<0.001
Annual Household Income[1]				
>$100,000	2 (3%)	1287 (38%)	*Ref*	
$50-100,000	7 (9%)	889 (26%)	5.07 (1.22-34.1)	0.043
<$50,000	65 (88%)	1182 (35%)	35.4 (11.1-216)	<0.001
Past Medical History[1]				
Any underlying conditions	22 (29%)	971 (28%)	1.02 (0.61-1.66)	0.94
COVID-19-related history[1]				
Personal contact diagnosed with COVID-19	25 (32%)	286 (8%)	5.29 (3.19-8.57) *Ref*: no contacts	<0.001
Able to shelter-in-place and maintain income				
Yes	5 (7%)	1417 (45%)	*Ref*	<0.001
No	64 (93%)	1756 (55%)	10.3 (4.58-29.6)	

[1]Excludes testing campaign participants with missing responses (i.e. not provided) during the testing survey.

FIGURE LEGENDS

Figure 1: Characteristics of prior (PCR-negative and antibody-positive) versus recent (PCR-positive, antibody-negative) SARS-CoV-2 infections among persons participating in a population-based SARS-CoV-2 testing campaign in a densely populated census tract in San Francisco.

Figure 2: Quantitative levels of virus among participants with PCR-positive SARS-CoV-2 infections (N=80) by classification as asymptomatic, pre-symptomatic, and symptomatic for COVID-19 disease as determined over longitudinal follow-up (2 weeks post-testing), and stratified by antibody status with PCR+/Ab- persons considered consistent with recent infection.

Figure 3. Viral genomic diversity among PCR-positive participants. Panel A: phylogenetic tree containing Mission district samples (red) and other San Francisco samples (grey), x-axis marks the number of mutations with respect to the reference genome from Wuhan. Yellow arrows mark introductions of five major global clades (right brackets) to the study population. Panel B: tree subset to Mission district samples. Shape indicates district resident or worker and color indicates antibody status. Households with multiple PCR-positive persons are drawn in green and include markers for samples from which genomes could not be recovered. Asterisk marks a household outside of the district in which an unhoused person in the district spent time.

Figure 1

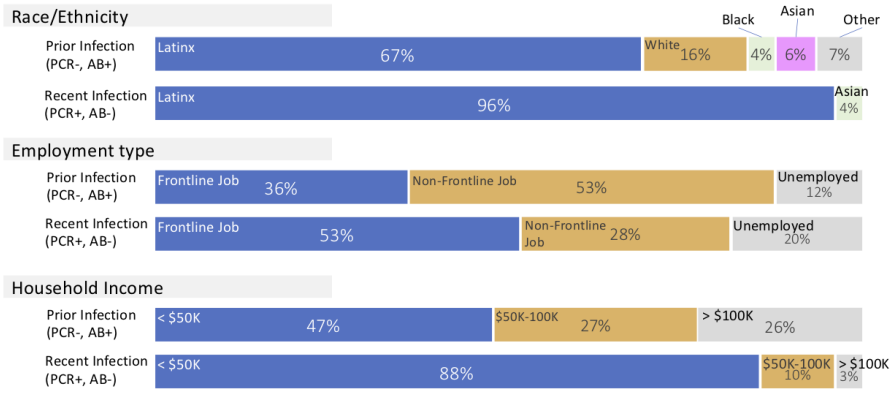

FIgure 2

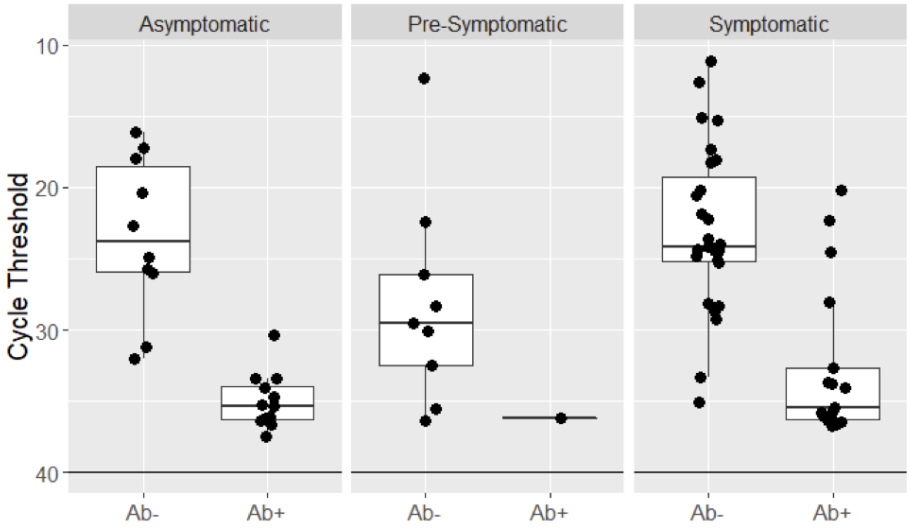
Asymptomatic
Pre-Symptomatic
Symptomatic
Cycle Threshold
10
20
30
40
Ab-
Ab+
Ab-
Ab+
Ab-
Ab+

Figure 3 high_res