Probability-Based Estimates of Severe Acute Respiratory Syndrome Coronavirus 2 Seroprevalence and Detection Fraction, Utah, USA

Matthew H. Samore, Adam Looney, Brian Orleans, Tom Greene, Nathan Seegert, Julio C. Delgado, Angela Presson, Chong Zhang, Jian Ying, Yue Zhang, Jincheng Shen, Patricia Slev, Maclean Gaulin, Mu-Jeung Yang, Andrew T. Pavia, Stephen C. Alder

We aimed to generate an unbiased estimate of the incidence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection in 4 urban counties in Utah, USA. We used a multistage sampling design to randomly select community-representative participants ≥12 years of age. During May 4–June 30, 2020, we collected serum samples and survey responses from 8,108 persons belonging to 5,125 households. We used a qualitative chemiluminescent microparticle immunoassay to detect SARS-CoV-2 IgG in serum samples. We estimated the overall seroprevalence to be 0.8%. The estimated seroprevalence-to-case count ratio was 2.5, corresponding to a detection fraction of 40%. Only 0.2% of participants from whom we collected nasopharyngeal swab samples had SARS-CoV-2–positive reverse transcription PCR results. SARS-CoV-2 antibody prevalence during the study was low, and prevalence of PCR-positive cases was even lower. The comparatively high SARS-CoV-2 detection rate (40%) demonstrates the effectiveness of Utah's testing strategy and public health response.

By May 2021, >150 million severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections and >3 million deaths from coronavirus disease (COVID-19) had been reported worldwide (*1*). The real infection count likely is much higher but continues to be a point of uncertainty. Case reporting underestimates the total number of SARS-CoV-2 infections because of underdetection of asymptomatic or mildly symptomatic cases and variation in the use and availability of diagnostic testing. Serologic testing provides an independent method to estimate the true cumulative incidence of SARS-CoV-2 infection because it relies on evidence of immune response as an indication of previous infection. Seroprevalence has been touted as a more standardized way to estimate the incidence of SARS-CoV-2 infection across different populations, but inconsistencies in test performance and sampling methods continue to cause challenges for use of seroprevalence.

In May 2020, the University of Utah (Salt Lake City, Utah, USA) launched the Utah Health and Economic Recovery Outreach project, in partnership with state government agencies, to collect community-based data on SARS-CoV-2 infection rates. Our goal was to estimate the cumulative incidence of SARS-CoV-2 infection to benchmark case detection in community populations based on public health surveillance. In addition to measuring SARS-CoV-2 seroprevalence, we collected nasopharyngeal swab samples to concurrently estimate the prevalence of reverse transcription PCR (RT-PCR) positivity. We applied methods of recruitment and analysis to minimize bias and maximize relevance for policymaking. We describe the results of the first phase of the project, which was conducted in the Wasatch Front, the major population center of Utah, comprising a chain of contiguous cities and towns stretched along the Wasatch Mountain Range.

Author affiliation: Veterans Affairs Salt Lake City Health Care System, Salt Lake City, Utah, USA (M.H. Samore); University of Utah, Salt Lake City (M.H. Samore, A. Looney, B. Orleans, T. Greene, N. Seegert, J.C. Delgago, A. Presson, C. Zhang, J. Ying, Y. Zhang, J. Shen, P. Slev, M. Gaulin, M.-J. Yang, A.T. Pavia, S.C. Alder)

DOI: https://doi.org/10.3201/eid2711.204435

Methods

Sampling Design and Participant Recruitment

We conducted serologic survey in 4 counties: Utah, Salt Lake, Davis, and Summit. The total estimated population of the study area is ≈2.2 million, which represents ≈68% of the population of Utah. Overall, 29% of the population is <18 years of age, compared with 22% of the US population (*2*). The fraction of residents of the 4 counties that are non-Hispanic White is 76%, which is higher than the US population of 60%. During March 14–June 30, 2020, the 4 counties reported 17,316 cases of SARS-CoV-2 infection (*3*).

We recruited and enrolled participants during May 4–June 30, 2020. The sampling frame consisted of a list of all residential addresses in the 4 counties curated by the state of Utah. The 657,870 total addresses were grouped hierarchically into 16,677 census blocks, 1,089 census block groups, 389 census tracts, and 229 groups of adjacent tracts, termed tract groups. We categorized tract groups into 15 strata based on combinations of county, ethnicity, median age, and reported positive case count from the Utah Department of Health.

We used 2 address-based probability sampling designs that differed in intensity of recruitment and geographic clustering. Both methods followed a random sampling design. Our primary sampling design included 11,563 addresses that were selected by randomly choosing 26 of the tract groups from the 15 strata, weighted by tract group population. We then selected ≈420 addresses from each tract group by first randomly choosing 30 census block groups per census tract group and then selecting 14 addresses per census block group. The geographic address clustering facilitated recruitment and data collection and followed methods recommended by the Centers for Disease Control and Prevention (https://www.cdc.gov/nceh/casper/sampling-methodology.htm).

Our secondary sampling frame comprised 14,012 addresses. We selected these addresses by proportionately oversampling the same strata as our primary sampling frame and excluding the tract groups selected in our primary sampling frame. The secondary sampling frame enabled us to expand the pool of participants and to broaden the geographic reach within the 4 counties.

To recruit our sample, we sent each address a postcard and a letter encouraging household members to participate. Participants were asked to complete a household survey, and household members ≥12 years of age were invited to take an individual participant survey and to undergo testing for IgG and viral RT-PCR at a specified mobile testing site. In our primary sampling frame, home addresses also were visited by a recruitment field team that attempted ≤3 in-person contacts. All household members who completed the survey and were tested received a $10 gift card as compensation for their time

Each mobile testing site location included 4 sequential drive-through stations. The first station collected basic information about the persons in the vehicle; the second conducted the viral RT-PCR sample via nasopharyngeal swab; the third conducted the IgG test via blood draw; and the last quality-checked participation, provided information about receiving test results, and responded to participant questions. The analyses described here are limited to persons who completed the participant survey and underwent serologic testing.

Laboratory Methods

We analyzed serum specimens by using the SARS-CoV-2 IgG assay (Abbott Laboratories, https://www.abbott.com) on an Architect i2000 instrument (Abbott Laboratories), according to the manufacturer's instructions. The SARS-CoV-2 IgG assay is a qualitative chemiluminescent microparticle immunoassay that detects IgG binding to an undisclosed epitope of the SARS-CoV-2 nucleocapsid protein. The assay relies on an assay-specific calibrator to report a ratio of specimen absorbance to calibrator absorbance. The assay can be interpreted as positive (ratio >1.4) or negative (ratio <1.4). The manufacturer reports a sensitivity of 86.4% (95% CI 65.1%–97.1%) 8–13 days after symptom onset and 100% (95% CI 95.9%–100%) ≥14 days after symptom onset, and a specificity of 99.6% (95% CI 99.1%–99.9%) (*4*,*5*). The manufacturer's estimate of sensitivity ≥14 days after symptom onset was derived from 88 symptomatic patients. However, other studies using this assay have reported lower sensitivities, ranging from 85% to 97%, when used in the general population (*6*–*8*). We observed that 20/24 (83.3%) participants who reported a prior positive SARS-COV-2 test >14 days before we collected serum samples were seropositive. By using a cutoff of 10 days after a prior positive SARS-COV-2, 25/30 (83.3%) participants who reported prior positive tests also were IgG positive. Therefore, we assumed a sensitivity of 83% in our primary analysis.

We used the cobas SARS-CoV-2 assay (Roche Diagnostics, https://www.roche.com) to detect viral RNA in nasopharyngeal swabs, according to the manufacturer's instructions. The cobas SARS-CoV-2 assay detects the nonstructural open reading frame (ORF) 1a/b region unique to SARS-CoV-2 at a limit

of detection of 1,800 copies/mL. All testing was performed at ARUP Laboratories (https://www.aruplab.com), a nonprofit national reference laboratory associated with the University of Utah.

For data analysis, we used a series of steps to account for the sampling design, nonresponse, demographic balance, and the sensitivity and specificity of the serology assay. The University of Utah Institutional Review Board designated this surveillance project nonresearch because it was launched to support public health and governmental response to the COVID-19 pandemic.

Statistical Methods

Sampling Design

We computed sampling design weights to account for varying probabilities of sampling of households (Appendix, https://wwwnc.cdc.gov/EID/article/27/11/20-4435-App1.pdf) (*9*). These weights depended primarily on the ratios of the numbers of sampled households to the total numbers of households within each stratum of the primary and secondary sampling designs (Appendix Tables 1–6). We computed 3 further sets of weights to account for nonresponse at the household, participant, and serology testing levels. We determined household response weights from estimated propensities of household response based on characteristics of the census block group where the household was located and participant response weights from estimated propensities of response by persons within households based on characteristics of the census block group and the primary household respondent. We determined serology response weights from estimated propensities for the provision of a serology sample based on participant survey responses.

We estimated propensities separately in the primary and secondary sampling designs by using nonparametric boosted regression for household and serology response and logistic regression for participant response (Appendix Table 1) (*10*). We used estimated propensities for membership in the primary versus the secondary design to align the secondary sampling design's characteristics to those of the primary sampling design. Multiplication of each of the described weights provided 2 sets of comprehensive weights that accounted for the design and nonresponse for the primary and secondary sampling designs. We then scaled the weights for 2 sampling designs based on the proportions of respondents in the 2 designs to provide a single final set of weights for estimating seroprevalence across the 4-county area. To prevent extreme variation in weights, we truncated weights that were either <10% or >10-fold greater than the median weight. Finally, we used iterative proportional fitting to optimize agreement of the marginal distributions of age, sex, Hispanic ethnicity, and education level between the weighted study sample and the US census data for the 4-county area (*11*).

Data Analysis

We defined the primary sampling units (PSUs) for data analysis by 54 census tracts included in the primary sampling design and mainly by block groups in the secondary sampling design. For Summit County, sampling was performed without clustering at the household level in the secondary sampling frame, so the household served as the PSU. We modeled the relationship of seroprevalence to predictor variables, such as county, demographic and clinical factors, behaviors, and attitudes, by using survey weighted generalized linear models for binary outcomes and assessed variability based on replicate jackknife weights (*12*,*13*). We tested for the presence of a detectable temporal trend in seroprevalence by including calendar time as a continuous variable in models relating seroprevalence to the Utah Department of Health case count. These analyses showed no trend for an effect of calendar time. Hence, we performed analyses for seroprevalence without adjustment for calendar time.

We corrected estimates of seroprevalence for assay error by applying the following formula:

$$\frac{\mathrm{P1} - (1 - \text{specificity})}{\text{sensitivity} + \text{specificity} - 1}$$

where P1 is the estimated prevalence within a given category of a predictor variable provided by the generalized linear models. We then used the parametric bootstrap to account for the sampling error and 95% CI of the manufacturer's estimate of specificity. We estimated the seroprevalence-to-case-count ratio by computing the ratio between the adjusted prevalence estimates we described in the previous section to the weighted average case count rates corresponding to the respondent's ZIP code 10–17 days before the respondent's serology test reported by the Utah Department of Health. The inverse of the ratio of adjusted prevalence and average case counts is the detection fraction, the estimated proportion of the total number of infections that were reported. We performed hypothesis tests comparing prevalence between categories directly on the estimates of seroprevalence without assay error adjustment because assay error adjustment does not affect equality of seroprevalences between subgroups when sensitivity plus specificity is >1.

Results

Participant Characteristics

During May 4–June 30, 2020, we randomly selected 11,563 households for a combined mailed recruitment and home visit and randomly selected another 14,012 households for mailed recruitment only. Altogether, 8,108 persons from 5,125 households completed surveys and testing for SARS-CoV-2 antibodies. Among participants, 5,791 were in the combined home visit and mailed recruitment frame and 2,317 were in the mailed recruitment only frame. The median age of participants was 44 (interquartile range [IQR] 30–62) years; only 9.3% of participants were 12–18 years of age (Tables 1, 2). Overall, 6.6% of participants self-reported ethnicity as Hispanic, compared with 15.3% of the 4-county population based on census data. The source population also differed from participants with respect to age distribution and education level. Accounting for response bias through iterative proportional fitting resolved these differences in county-level marginal distributions.

Estimated Seroprevalence

Among participants, 89 persons from 75 households were seropositive, corresponding to an unadjusted seroprevalence of 1.1% (Table 3). The 4-county seroprevalence adjusted for sampling fraction, nonresponse, and test performance was 0.8% (95% CI 0.1%–1.6%). We estimated adjusted SARS-CoV-2 seroprevalence to be 5.7% (95% CI 1.2%–19.4%) among persons residing in households where the primary language was Spanish and 2.7% (95% CI 0.6%–8.0%) among persons who self-reported as Hispanic; both estimates were significantly greater than the comparator groups (p = 0.01 for Spanish as primary language; p = 0.03 for self-report as Hispanic) (Table 3). Seroprevalence was 4.6% in Summit County, which includes the ski resort town, Park City, an early infection hot spot in Utah, and was significantly higher than the other counties (p = 0.03); the variation in seroprevalence across Utah, Salt Lake, and Davis counties was not statistically different.

Seroprevalence correlated with cumulative incidence estimated on the basis of reported case counts (Table 3). The adjusted seroprevalence was 2.2% in ZIP codes where cumulative incidence calculated from reported cases was >500/100,000 population compared with 0.2% in ZIP codes in where the reported cumulative incidence was ≤200/100,000 population. The overall seroprevalence-to-case count ratio was estimated to be 2.5 (95% CI 0.3–5.0), corresponding to a detected fraction of 0.40. This ratio was not statistically different across the 4 counties.

Other Descriptive Analyses

Among participants, 360 (4.4%) reported contact with a person with diagnosed COVID-19 and 26 (7.2%) of these participants were seropositive (Table 4). Among participants who reported contact with a family member with known SARS-CoV-2 infection, 14.4% were seropositive. In contrast, among 38 persons who reported exposure to SARS-CoV-2 infection in their role as healthcare workers, none were seropositive. Among 62 households with ≥2 members who tested positive, our analysis revealed 53 households with

Table 1. Characteristics of participants and households in a study of SARS-CoV-2 seroprevalence, Utah, United States

Household-level factors	No. (%) participating households	No. (%) participants, n = 8,108
County	n = 5,125	
Davis	1,023 (20)	1,703 (21.0)
Salt Lake	2,695 (52.6)	4,021 (49.6)
Summit, including Park City	283 (5.5)	345 (4.3)
Utah	1,124 (21.9)	2,039 (25.1)
No. participating household members	n = 5,088	
1	1,738 (34.2)	1,027 (12.7)
2	2,277 (44.8)	3,683 (45.4)
3	541 (10.6)	1,307 (16.1)
≥4	532 (10.5)	2,091 (25.8)
No. household members <12 years of age	n = 5,033	
0	3,537 (70.3)	5,407 (67.6)
1	589 (11.7)	1,053 (13.2)
2	499 (9.9)	850 (10.6)
3	239 (4.7)	424 (5.3)
≥4	169 (3.4)	269 (3.4)
Primary language spoken in household	n = 5,053	
English	4,866 (96.3)	7,785 (97.1)
Spanish	132 (2.6)	169 (2.1)
Other	55 (1.1)	61 (0.8)

*Participants completed a survey and had serum collected to test for SARS-CoV-2 IgG. n values indicate number of responses available in that category.
SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Table 2. Characteristics of participants in a study of SARS-CoV-2 seroprevalence, Utah, USA*

Characteristics	No. (%) participants, n = 8,108
Sex	
F	4,335 (53.5)
M	3,773 (46.5)
Age, y	
12–<18	755 (9.3)
18–<45	3,366 (41.5)
45–64	2,345 (28.9)
65–74	1,087 (13.4)
≥75	555 (6.8)
Ethnicity, n = 8044	
Hispanic	528 (6.6)
Non-Hispanic	7,516 (93.4)
Race, n = 7,839	
White	7,452 (95.1)
Black or African American	34 (0.4)
American Indian or Alaska Native	32 (0.4)
Asian	159 (2.0)
Native Hawaiian or other Pacific Islander	40 (0.5)
Multiracial	122 (1.6)
Underlying conditions	
Diabetes	508 (6.3)
Hypertension	1,078 (13.3)
Cardiovascular disease	354 (4.4)
Asthma	841 (10.4)
Emphysema	72 (0.9)
Cancer	130 (1.6)
Immunosuppressive therapy	79 (1.0)
Exposure, n = 8,084	
Contact with COVID-19 case	360 (4.5)
Prior testing	
Tested for COVID-19 at any time	716 (8.8)

*Participants completed survey and had serum collected to test for SARS-CoV-2 IgG. n values indicate number of responses available in that category COVID-19, coronavirus disease; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

exactly 1 seropositive member and 9 households with ≥1 seropositive member. Among the 123 members of 62 households with SARS-CoV-2–positive residents, 23 (18.7%) participants were seropositive. We assumed that infection for 1 of the infected members of each household was imported and that other household cases were transmissions from the index member of the household; thus, our crude estimate the secondary household attack rate was 12%.

Overall, 798 (9.9%) persons reported having a prior COVID-19 test. Among 30 participants who reported having a positive COVID-19 test ≥14 days before serum collection, 25 (83.3%) were SARS-CoV-2 seropositive; we used that figure to estimate the sensitivity of the serologic assay. Among seropositive participants, 7 (28.0%) reported a prior RT-PCR–positive SARS-CoV-2 test. If we assume a true seroprevalence of 0.8%, assay sensitivity of 83%, and specificity of 99.6%, the corrected point estimate for the detection fraction based on history of a prior positive RT-PCR test is 0.28/0.614 = 0.46, which is close to our estimated detection fraction based on the seroprevalence-to-case count ratio.

Among 6,251 participants from whom a nasopharyngeal swab specimen was collected, 14 (0.2%) had SARS-CoV-2 virus detected by RT-PCR; 9 (64.3%) of those persons were seropositive. The small number of positive RT-PCR tests precluded statistical analysis of factors associated with positivity or adjustment for response bias.

Discussion

By using a statistical sampling frame and adjusting for test performance and non-response, we estimated the prevalence of IgG to SARS-CoV-2 in 4 urban counties in Utah during May–June 2020 to be only 0.8%. Thus, consistent with other community surveys, most of the population lacked immunity to SARS-CoV-2. Comparing seroprevalence to the cumulative incidence of SARS-CoV-2 infection based on case reporting, we found that the estimated ratio of total-to-detected cases was 2.5, corresponding to a detection fraction of 40%. We found participants in Summit County had higher seroprevalence of 4.6%, which is compatible with the extensive outbreak in the resort community of Park City that began in March 2020. Seroprevalence was higher (2.7%) among persons who identified as Hispanic than among those who identified as non-Hispanic (0.5%); seroprevalence was 5.7% among persons who lived in a household where Spanish was the primary language, much higher than the 0.5% seroprevalence among persons who lived in households where English was the primary language. This finding adds to the substantial body of evidence regarding ethnic and racial disparities in the spread of SARS-CoV-2 across populations.

Our estimates of seroprevalence and of the seroprevalence-to-case count ratio are generally lower than has been reported in Utah and elsewhere in the United States during a similar time. Several seroprevalence studies conducted in the United States and other countries have been published (*14*–*24*) and use a variety of assays and sampling methods (*25*). Some studies have relied on convenience samples or did not adequately control for response bias. The specificity of serologic methods for SARS-CoV-2 testing varies widely, which can lead to substantial overestimation in a low-prevalence population (*26*). Not all studies have adjusted for test performance, and the differences in methods make comparisons between studies challenging.

Our project involved random sampling of >25,000 households and used intensive recruiting methods. Our analytical approach accounted for

multiple sources of error, including response bias and imperfect test performance. We also were able to generate an internal estimate of the detection fraction by using self-reported histories of prior RT-PCR test results. After accounting for test error, the estimate of the detection fraction based on participant histories was 0.46, a value that corroborates our population estimate of the detected fraction of 0.40.

We used a serologic test that is reported by the manufacturer to have a specificity at 99.6% (*4*,*5*); however, even at this level of accuracy, statistically accounting for false positive results is necessary given the low population prevalence of IgG to SARS-CoV-2. To better account for the possibility of reduced sensitivity when asymptomatic infections are included (*27*), we assumed a sensitivity of 83% because of an analysis of project participants who reported having had a positive RT-PCR test in the past. We note that our estimate of sensitivity is substantially lower than the manufacturer's estimate of sensitivity of 97.2% (*5*). Because antibody to nucleocapsid protein appears to decrease more rapidly than antibody to the spike protein, our analysis requires us to account for waning immunity (*27*,*28*). Our internal estimate of sensitivity is conditional on the distribution of time between infection and antibody testing for persons reported to be infected in our sample, which enhances its utility for adjusting the estimate of seroprevalence. Of note, among persons who reported having a prior test, 83% of serum samples were collected within 2 months following the previous RT-PCR SARS-CoV-2 test.

With these considerations in mind, our estimate of the detection fraction is substantially higher than what has been reported in other serologic surveys. A study that used residual clinical samples collected during March–May 2020 to measure SARS-CoV-2 antibody at 10 US sites estimated a detection fraction of 0.10 for residents of the country (*17*). That study estimated the seroprevalence in Utah at 2.2% (95% CI 1.2%–3.4%), and those CIs overlap with our estimate. Similarly, our estimate of seroprevalence is lower than what has been reported in most other geographic regions during a comparable period of the pandemic. In a meta-analysis that included 17 studies, the seroprevalence was estimated to be <1% in 5 of the studies examined (*29*). In another study, the projected prevalence of SARS-CoV-2 antibodies was 9.2% in the US adult population, based on an analysis of 28,000

Table 3. Overall and subgroup-specific seroprevalence of participants in a study of SARS-CoV-2 seroprevalence, Utah, USA*

Characteristics	Total	No. (%) seropositive	Adjusted seroprevalence, % (95% CI)†	p value
Overall	8,108	89 (1.1)	0.8 (0.1–1.6)	
County				
Davis	1,703	16 (0.9)	0.1 (0–1.3)	0.06
Salt Lake	4,021	38 (0.9)	0.7 (0–1.8)	
Summit, including Park City	345	10 (2.9)	4.6 (1.0–15.1)	
Utah	2,039	25 (1.2)	1.2 (0.1–3.4)	
Sex				
M	3,773	41 (1.1)	0.7 (0–1.6)	0.65
F	4,293	48 (1.1)	0.9 (0.2–1.9)	
Age, y				
<45	4,119	39 (0.9)	0.9 (0.1–2.1)	0.62
45–64	2,345	31 (1.3)	0.8 (0.1–1.7)	
≥65	1,642	19 (1.2)	0.4 (0–1.4)	
Ethnicity				
Non-Hispanic	7,516	75 (1)	0.5 (0–1.1)	0.03
Hispanic	528	14 (2.7)	2.7 (0.6–8.0)	
Primary language spoken in household				
English	7,785	78 (1)	0.5 (0–1.2)	0.01
Spanish	169	11 (6.5)	5.7 (1.2–19.4)	
No. participants in household				
1	1,027	15 (1.5)	0.7 (0–1.8)	0.60
2	3,683	35 (1)	0.5 (0–1.7)	
≥3	3,398	39 (1.1)	1.0 (0.2–2.3)	
No. participants <12 years of age				
0	5,407	64 (1.2)	0.6 (0–1.3)	0.33
≥1	2,596	20 (0.8)	1.1 (0.1–3)	
Cumulative incidence per 100,000 residents in participant's ZIP code				
<200	3,718	26 (0.7)	0.2 (0–0.9)	0.02
200–500	3,012	34 (1.1)	0.8 (0.1–2.0)	
>500	1,378	29 (2.1)	2.2 (0.6–5.5)	

*Participants completed survey and had serum collected to test for SARS-CoV-2 IgG. COVID-19, coronavirus disease; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.
†Adjusted for sampling design and test sensitivity (0.83) and specificity (0.996)

Table 4. Relationship between COVID-19 exposures and serologic results of participants in a study of SARS-CoV-2 seroprevalence, Utah, USA*

Exposures	Total	No. (%) seronegative, n = 8,019	No. (%) seropositive, n = 89	% Adjusted seroprevalence (95% CI)†
Contact with diagnosed COVID-19 case	360	334 (92.8)	26 (7.2)	8.5 (3.3–19.5)
Participant's relationship with contact				
Family member	97	83 (85.6)	14 (14.4)	14.8 (4.0–40.8)
Friend	42	38 (90.5)	4 (9.5)	14.0
Healthcare worker‡	38	38 (100)	0 (0)	0.0
Coworker	105	102 (97.1)	3 (2.9)	3.4
Other	78	73 (93.6)	5 (6.4)	3.1 (0.3–12.9)
Reside in household with ≥1 seropositive person	123	100 (81.3)	23 (18.7)	24.9 (10.5–48.7)

*COVID-19, coronavirus disease; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.
†Adjusted for sampling design and test sensitivity (0.83) and specificity (0.996). Confidence intervals are omitted for subgroups with fewer than 5 seropositive persons.
‡Participant reported that their exposure was related to their work as a healthcare worker.

dialysis patients; in Utah it was 3.1%. Discrepancies between results of other studies and our findings are likely due to our use of probabilistic sampling to reduce bias (*30*).

Our results suggest that Utah's public health response to SARS-COV-2 was effective in case detection. Factors that likely contributed to the success of Utah's approach to case detection include early expansion of access to testing, mobile testing that targeted heavily impacted communities, and a strong commitment to contact tracing and contact testing by the state and local health departments. This conclusion also is supported by our finding that 29% of seropositive persons reported exposure to a known case.

We observed that seropositivity was much more frequent than RT-PCR positivity, a finding that contrasts with selected other studies that combined viral detection and measurement of seroprevalence. For example, among randomly sampled residents of the US state of Indiana, the unadjusted prevalence of a positive RT-PCR was 1.74%, compared with an unadjusted SARS-CoV-2 seroprevalence of 1.01% (*31*). The ratio of prevalence of antibody detection to prevalence of viral detection, as observed in our community survey, suggests that infections were accumulating linearly rather than exponentially during the study period.

One limitation of our study is that it covers the early period of the COVID-19 pandemic, which reflects the cumulative incidence of SARS-CoV-2 infection through mid-June 2020. An updated analysis is needed to examine the secular trend in seroprevalence and determine whether the detection fraction continues to be high. Additional data also will enhance the feasibility of examining possible geographically localized hot spots. Our application of weighting and iterative proportional fitting should minimize nonresponse bias because of ethnicity and other measured factors at each stage of the sampling. However, our analytic approach cannot fully account for all sources of bias, particularly due to unmeasured factors that influenced the decision to participate at the household level. Thus, despite weighting techniques, the generalizability of our results might be limited by residual bias due to nonresponse. Nonetheless, our sampling frame likely reflects population seroprevalence more accurately than convenience-based samples. Recruitment efforts should focus on increasing the ease and appeal of participation of a wide range of demographic and geographic groups, especially for populations that traditionally have lower response rates and have been disproportionately affected by the COVID-19 pandemic.

In conclusion, we used a project design in which we randomly selected all participants, detected SARS-CoV-2 antibodies with a highly specific assay, applied rigorous analytical methods to account for bias and test error, and analyzed survey responses to support population-level inferences. The most distinctive finding in our analysis was that the detection fraction was estimated to be 40%. Further analysis is needed to determine whether this pattern has continued in subsequent months of the COVID-19 pandemic and to assess the factors that influence SARS-CoV-2 transmission and detection. High rates of testing and enhanced case detection are key initial steps for effective public health response.

This article was preprinted at https://www.medrxiv.org/content/10.1101/2020.10.26.20219907v1.

Acknowledgments

We thank Kristina Stratford for project management and for supporting data collection. We thank Elizabeth Rabon, Alicen Bringard, Jeanette Nelson, and Jill Stephenson for managing field operations and for administering the different parts of this project. We thank Carrie Milligan for review and editing of this manuscript.

This project was funded by a State of Utah Cooperative Contract (contract no. AR3473), with support in part from the University of Utah Study Design and Biostatistics Center, which receives funding from the National Center for Research Resources and the National Center for Advancing Translational Sciences, NIH (grant no. UL1TR002538).

About the Author

Dr. Samore chairs the Division of Epidemiology in the Department of Internal Medicine, University of Utah School of Medicine. He also directs the Department of Veterans Affairs IDEAS Center of Innovation in Salt Lake City, Utah. His research interests focus on infectious diseases and biomedical informatics.

References

1. Center for Systems Science and Engineering at Johns Hopkins University. COVID-19 dashboard. 2020 [cited 2021 May 3]. https://coronavirus.jhu.edu/map.html
2. United States Census Bureau. Quick facts 2020 [cited 2020 October 23]. https://www.census.gov/quickfacts/fact/table/US,daviscountyutah,summitcountyutah,utahcountyutah,UT/PST045219
3. Kem C. Gardner Policy Institute of the University of Utah. US Census Bureau estimates for race and Hispanic origin, vintage 2019 [cited 2020 Oct 5]. https://gardner.utah.edu/demographics/current-census-bureau-estimates
4. Abbott Laboratories Diagnostics Division. SARS-CoV-2 IgG reagent kit for use with Architect, June 2020 [package insert] [cited 2021 May 3]. https://www.fda.gov/media/137383/download
5. Abbott Laboratories Diagnostics Division. SARS-CoV-2 IgG calibrator kit for use with Architect, April 2020 [package insert] [cited 2021 May 3]. https://www.henryschein.com/assets/Medical/Abbott%20IFU%20-%20Calibration.pdf
6. Perkmann T, Perkmann-Nagele N, Breyer MK, Breyer-Kohansal R, Burghuber OC, Hartl S, et al. Side by side comparison of three fully automated SARS-CoV-2 antibody assays with a focus on specificity. Clin Chem. 2020;66:1405–13. https://doi.org/10.1093/clinchem/hvaa198
7. Theel ES, Harring J, Hilgart H, Granger D. Performance characteristics of four high-throughput immunoassays for detection of IgG antibodies against SARS-CoV-2. J Clin Microbiol. 2020;58:e01243-20. https://doi.org/10.1128/JCM.01243-20
8. Bryan A, Pepper G, Wener MH, Fink SL, Morishima C, Chaudhary A, et al. Performance characteristics of the Abbott Architect SARS-CoV-2 IgG assay and seroprevalence in Boise, Idaho. J Clin Microbiol. 2020;58:e00941-20. https://doi.org/10.1128/JCM.00941-20
9. Valliant R, Dever JA, Kreuter F. Practical tools for designing and weighting survey samples. New York: Springer; 2013.
10. Ridgeway G, McCaffrey D, Morral A, Burgette L, Griffin BA. Toolkit for weighting and analysis of nonequivalent groups: a tutorial for the twang package. Santa Monica (CA, USA): RAND Corporation; 2017 [cited 2021 May 3]. https://www.rand.org/pubs/tools/TL136z1.html
11. Lumley T. Post-stratification, raking and calibration. In: Complex surveys: a guide to analysis using R, volume 565. Hoboken (NJ, USA): John Wiley & Sons; 2011. p. 135–56.
12. Shao J, Tu D. The jackknife and bootstrap. New York: Springer-Verlag Inc; 1995.
13. Lumley T. Complex surveys: a guide to analysis using R, vol. 565. Hoboken (NJ, USA): John Wiley & Sons; 2011.
14. Bendavid E, Mulaney B, Sood N, Shah S, Ling E, Bromley-Dulfano R, et al. COVID-19 antibody seroprevalence in Santa Clara County, California. Int J Epidemiol. 2021;50:410–9. https://doi.org/10.1093/ije/dyab010
15. Biggs HM, Harris JB, Breakwell L, Dahlgren FS, Abedi GR, Szablewski CM, et al.; CDC Field Surveyor Team. Estimated community seroprevalence of SARS-CoV-2 antibodies—two Georgia Counties, April 28–May 3, 2020. MMWR Morb Mortal Wkly Rep. 2020;69:965–70. https://doi.org/10.15585/mmwr.mm6929e2
16. Flannery DD, Gouma S, Dhudasia MB, Mukhopadhyay S, Pfeifer MR, Woodford EC, et al. SARS-CoV-2 seroprevalence among parturient women in Philadelphia. Sci Immunol. 2020;5:eabd5709. https://doi.org/10.1126/sciimmunol.abd5709
17. Havers FP, Reed C, Lim T, Montgomery JM, Klena JD, Hall AJ, et al. Seroprevalence of Antibodies to SARS-CoV-2 in 10 Sites in the United States, March 23–May 12, 2020. JAMA Intern Med. 2020 Jul 21 [Epub ahead of print]. https://doi.org/10.1001/jamainternmed.2020.4130
18. Self WH, Tenforde MW, Stubblefield WB, Feldstein LR, Steingrub JS, Shapiro NI, et al.; CDC COVID-19 Response Team; IVY Network. Seroprevalence of SARS-CoV-2 among frontline health care personnel in a multistate hospital network—13 academic medical centers, April–June 2020. MMWR Morb Mortal Wkly Rep. 2020;69:1221–6. https://doi.org/10.15585/mmwr.mm6935e2
19. Sood N, Simon P, Ebner P, Eichner D, Reynolds J, Bendavid E, et al. Seroprevalence of SARS-CoV-2–specific antibodies among adults in Los Angeles County, California, on April 10–11, 2020. JAMA. 2020;323:2425–7. https://doi.org/10.1001/jama.2020.8279
20. Sutton M, Cieslak P, Linder M. Notes from the field: seroprevalence estimates of SARS-CoV-2 infection in convenience sample—Oregon, May 11–June 15, 2020. MMWR Morb Mortal Wkly Rep. 2020;69:1100–1. https://doi.org/10.15585/mmwr.mm6932a4
21. Percivalle E, Cambiè G, Cassaniti I, Nepita EV, Maserati R, Ferrari A, et al. Prevalence of SARS-CoV-2 specific neutralising antibodies in blood donors from the Lodi Red Zone in Lombardy, Italy, as at 06 April 2020. Euro Surveill. 2020;25:2001031. https://doi.org/10.2807/1560-7917.ES.2020.25.24.2001031
22. Pollán M, Pérez-Gómez B, Pastor-Barriuso R, Oteo J, Hernán MA, Pérez-Olmeda M, et al.; ENE-COVID Study Group. Prevalence of SARS-CoV-2 in Spain (ENE-COVID): a nationwide, population-based seroepidemiological study. Lancet. 2020;396:535–44. https://doi.org/10.1016/S0140-6736(20)31483-5
23. Stringhini S, Wisniak A, Piumatti G, Azman AS, Lauer SA, Baysson H, et al. Seroprevalence of anti-SARS-CoV-2 IgG antibodies in Geneva, Switzerland (SEROCoV-POP): a population-based study. Lancet. 2020;396:313–9. https://doi.org/10.1016/S0140-6736(20)31304-0
24. Xu X, Sun J, Nie S, Li H, Kong Y, Liang M, et al. Seroprevalence of immunoglobulin M and G antibodies against SARS-CoV-2 in China. Nat Med. 2020;26:1193–5. https://doi.org/10.1038/s41591-020-0949-6
25. Shook-Sa BE, Boyce RM, Aiello AE. Estimation without representation: early severe acute respiratory syndrome coronavirus 2 seroprevalence studies and the path forward. J Infect Dis. 2020;222:1086–9. https://doi.org/10.1093/infdis/jiaa429

26. Sempos CT, Tian L. Adjusting coronavirus prevalence estimates for laboratory test kit error. Am J Epidemiol. 2020;190:109–15. https://doi.org/10.1093/aje/kwaa174
27. Long QX, Tang XJ, Shi QL, Li Q, Deng HJ, Yuan J, et al. Clinical and immunological assessment of asymptomatic SARS-CoV-2 infections. Nat Med. 2020;26:1200–4. https://doi.org/10.1038/s41591-020-0965-6
28. Peluso MJ, Takahashi S, Hakim J, Kelly JD, Torres L, Iyer NS, et al. SARS-CoV-2 antibody magnitude and detectability are driven by disease severity, timing, and assay. Sci Adv. 2021;7:eabh3409. https://doi.org/10.1126/sciadv.abh3409
29. Byambasuren O, Dobler CC, Bell K, Rojas DP, Clark J, McLaws ML, et al. Comparison of seroprevalence of SARS-CoV-2 infections with cumulative and imputed COVID-19 cases: systematic review. PLoS One. 2021;16:e0248946. https://doi.org/10.1371/journal.pone.0248946
30. Anand S, Montez-Rath M, Han J, Bozeman J, Kerschmann R, Beyer P, et al. Prevalence of SARS-CoV-2 antibodies in a large nationwide sample of patients on dialysis in the USA: a cross-sectional study. Lancet. 2020;396:1335–44. https://doi.org/10.1016/S0140-6736(20)32009-2
31. Menachemi N, Yiannoutsos CT, Dixon BE, Duszynski TJ, Fadel WF, Wools-Kaloustian KK, et al. Population point prevalence of SARS-CoV-2 infection based on a statewide random sample—Indiana, April 25–29, 2020. MMWR Morb Mortal Wkly Rep. 2020;69:960–4. https://doi.org/10.15585/mmwr.mm6929e1

Address for correspondence: Matthew H. Samore, University of Utah 50 N Medical Dr, Salt Lake City, UT 84132, USA; email: matthew.samore@hsc.utah.edu

Article DOI: https://doi.org/10.3201/eid2711.204435

Probability-Based Estimates of Severe Acute Respiratory Syndrome Coronavirus 2 Seroprevalence and Detection Fraction, Utah, United States

Appendix

Statistical Methods

Complex Survey Design and Assay Error

Our statistical analyses incorporated several steps to account for nonresponse, demographic balance, and the sensitivity and specificity of the serology assay. We describe these steps below.

Step 1: Accounting for the sampling design. We estimated the probability (Pr) that a household was sampled in the primary sampling design as

Pr[household sampled] = Pr[tractgroup sampled] × ([no. of households sampled in tractgroup]/[no. viable addresses in tractgroup])

In strata for which ≥1 tractgroup was sampled, we approximated the probability that a given tractgroup was sampled as the product of the number of tractgroups sampled in that stratum and the probability of selection on a single draw. In the secondary sampling design, we approximated the probability that a household was targeted for sampling as the proportion of viable households within each stratum that were designated for sampling.

Step 2: Accounting for nonresponse. We estimated probabilities of response based on propensity models that used available information at the household, participant, and serology testing levels. We fit the propensity models separately for the primary and secondary sampling designs by using predictor variables (Appendix Table 1). We used boosted regression as implemented in the R TWANG statistical package (*1*) to estimate the propensities for a sampled household to respond to the household survey and for a survey respondent to provide serology

samples. We used logistic regression to estimate the propensities for participants to provide survey results among responding households. We computed weights to adjusted for overall nonresponse to serology testing as follows:

$$SW_{CIA1}(i) = \left\{ \frac{1}{(\Pr(HH\ sampled) \times (\Pr(HH\ responds|HH\ sampled)) \times (\Pr(Ind\ Responds|HH\ responds) \times (\Pr(Ind\ Serology\ test|Ind\ Responds))} \right\}$$

where Pr(*HH sampled*) represents the sampling design probabilities for each household, Pr(*HH responds|HH sampled*) represents propensity score for household response, and Pr(*Ind Responds|HH responds*) represents propensity score for participant response, and Pr(*Ind serology test|Ind responds*) represents propensity score for serology test response (*2*).

Step 3: Aligning secondary sampling design to the primary sampling design. The primary sampling design included both mail-push-to-web survey and in-person interviews, providing a duplicative contact strategy with 2 modes of contact, whereas the secondary sampling design includes only the mail-push-to-web survey. Thus, we considered the primary sampling design to be less susceptible to nonresponse bias than the secondary sampling design. Therefore, we estimated a further set of propensity scores to reweight the participants providing serology samples in the secondary sampling frame to align the characteristics of the of the secondary sampling design to the primary sampling design. The propensity scores defining these weights also were estimated by using boosted regression and the following predictor variables obtained from participant responses to the survey: sex age; Hispanic ethnicity; education; believes social distancing is important; works outside the home at least a few times per week; level of COVID-19 concern; self-reported general health; self-report of being sick since March 1, 2020; and known contact with someone who with diagnosed COVID-19.

After obtaining propensity scores, we computed inverse probability of treatment weights to estimate average treatment affect in the treated (ATT) by using the following formula for each participant who provided a serum sample:

$$W_{CIAi}^{P} = \frac{Z_i}{1} + e_{CIAi}\frac{1-Z_i}{1-e_{CIAi}}$$

where Z_i, the "treatment", indicates membership in the primary sampling design. We then updated the sampling weights by using the following formula:

$$SW_{CIA2}(i) = SW_{CIA1}(i) \times W_{CIAi}^{P}$$

Step 4: Averaging weights across sampling designs. We treated the weighted samples from the primary and secondary sampling designs as both representing the same population. Then we computed the weighted average of the weights across the primary and secondary designs based on the proportion of respondents from each individual sampling design relative to the total number of respondents.

Step 5: Weight trimming. We implemented weight trimming to reduce the variability in the sampling weights separately in each county (*3*). Weights that were <10% of the median weight were increased to 10% of the median, and weights that exceeded the median weight by a factor >10 were reduced to 10× the median.

Step 6: Iterative proportional fitting. Because nonresponse adjustments are limited to variables known at each step, imbalances in known characteristics might still differ between the sample and target population, even after applying the nonresponse weighs. Hence, we applied an additional calibration step by implementing iterative proportional fitting, often referred to as raking, to align the marginal distributions of age, sex, Hispanic ethnicity, and education between the weighted study sample and the population of the 4-county target population (*4*). We derived the population marginal distributions by using the 2018 Census American Community Survey 5-year estimates (*5*). The raking step was implemented using the following categorizations: age, categorized as 12–29, 30–59, or ≥60 years, by county; sex, categorized as male or female, by county; ethnicity, categorized as Hispanic versus non-Hispanic, by county but Davis County, due to insufficient sample size, was collapsed with Salt Lake County; education, categorized as completing 4-year college versus all others (including those <25 years of age), by county.

Strata and Primary Sampling Units

In addition to incorporating the appropriate weights, statistical analyses must also account for the strata within each sampling design and clustering of outcomes between different participants in the same primary sampling units (PSUs) within the same stratum. The information on the amount of variation in seroprevalence between the census tract groups, the true PSUs of the primary sampling design, was limited, because the primary sampling design had only 26 census tract groups across 15 strata, and 6/15 strata included only a single tract group. Possibly as a consequence of this limitation, variation in the estimated prevalence across the 26 tract groups within strata was less than expected by chance, preventing estimation of a clustering

effect. Therefore, we used the 54 census tracts rather than the census tract groups as the PSUs for the primary sampling design. For data analysis we also combined age strata among Salt Lake County low-prevalence Hispanic population; we also combined age strata among Salt Lake County low-prevalence non-Hispanic population due to insufficient census tracts within the individual strata. For the secondary sampling design, we used the more numerous block groups as the PSU in statistical analyses for all strata in which block groups were the true PSUs. For Park City, the used the household as the PSU in the secondary sampling design, and thus the household itself served as the PSU in data analysis.

Data Analysis

We constructed jackknife replicate weights (*6*), which we then applied in statistical analyses to estimate standard errors and perform statistical inference. Jackknife provides a largely model-free approach for estimating variability while accounting for correlations in outcomes between respondents in the same PSU, and naturally accounts for the use of different PSUs in the primary and secondary sampling designs. We modeled the relationship of seroprevalence and other outcomes, such as self-reported COVID-19 concern and self-reported social distancing, to predictor variables, such as county, demographic, and clinical factors, and behaviors and attitudes, by using survey-weighted generalized linear models for a binary outcome and assessed variability based on the replicate jackknife weights. We implemented these analyses by using the Survey package of R (R Foundation for Statistical Computing, https://www.r-project.org). We tested for the presence of a detectable temporal trend in seroprevalence by including calendar time as a continuous variable in models relating seroprevalence to the Utah Department of Health May 20, 2020 case count and calendar time. These analyses showed no trend for an effect of calendar time. Hence, analyses for seroprevalence are presented without adjustment for a secular trend in calendar time.

Adjusting Estimates of Seropositivity for Assay Error

Direct estimates of seroprevalence based on the proportion of tested respondents with positive serology assays are biased because the sensitivity and specificity of the test is expected to be <100%. Given relatively low seroprevalence, estimates of seroprevalence are especially strongly affected by the specificity of the test. As recommended by the Abbott Architect SARS-CoV-2 IgG package insert (*7*,*8*), we estimated specificity as 0.996, based on an evaluation of

1,070 samples obtained before the COVID-19 outbreak, including 73 samples from persons with other respiratory illnesses. This evaluation found that the assay incorrectly classified 4 of these 1,070 "true negative" samples as positive for COVID-19. We estimated a sensitivity of 0.83 which corresponded to the 25/30 respondents who reported having had a positive COVID-19 diagnosis and whose serology results were obtained $\geq$1 week later and were also positive. In sensitivity analyses we also considered a sensitivity estimate of 0.972, which is the proportion of 107 samples from subjects known to have COVID-19 that led to positive test results (104/107). These 107 samples included 73 from subjects with onset of COVID-19 symptoms at least 14 days before the test, and 34 subjects whose onset of COVID-19 symptoms was between 8 and 13 days before the test. Given these estimates of sensitivity and specificity, we then provided corrected estimates of seroprevalence by applying the formula (P1 – (1 – specificity))/(sensitivity + specificity – 1), where P1 is the estimated prevalence provided as described above. Finally, we used a parametric bootstrap resampling approach to account for the sampling error in the Abbott estimate of specificity when presenting lower and upper 95% confidence limits.

We did not further expand confidence limits to account for uncertainty in sensitivity. Instead, we conducted sensitivity analyses that evaluated how our estimates of seroprevalences are modified under different assumed values for the true sensitivity, which are compatible with the previous studies described in the prior paragraph.

References

1. Ridgeway G, McCaffrey D, Morral A, Burgette L, Griffin BA. Toolkit for weighting and analysis of nonequivalent groups: a tutorial for the twang package. Santa Monica, CA: RAND Corporation; 2017.

2. Valliant R, Dever JA, Kreuter F. Practical tools for designing and weighting survey samples. New York: Springer; 2013.

3. Lumley T. Complex surveys: a guide to analysis using R, volume 565. Hoboken (New Jersey, USA): John Wiley & Sons; 2011.

4. Lumley T. Post-stratification, raking and calibration. In: Complex surveys: a guide to analysis using R, volume 565. Hoboken (New Jersey, USA): John Wiley & Sons; 2011. p. 135–56.

5. US Census Bureau. American community survey, 2018: American community survey 5-year estimates [cited 2020 Aug 22]. https://data.census.gov/cedsci

6. Shao J, Tu D. The jackknife and bootstrap. New York: Springer-Verlag Inc; 1995.

7. Abbott Laboratories Diagnostics Division. SARS-CoV-2 IgG reagent kit for use with Architect, June 2020 [package insert]. [cited 2021 May 3]. https://www.fda.gov/media/137383/download

8. Abbott Laboratories Diagnostics Division. SARS-CoV-2 IgG calibrator kit for use with Architect, April 2020 [package insert] [cited 2021 May 3]. https://www.henryschein.com/assets/Medical/Abbott%20IFU%20-%20Calibration.pdf

Appendix Table 1. Predictor variables in propensity score nonresponse models used in a study of SARS-CoV-2 seroprevalence, Utah, United States*

Models and predictors
Household response propensity model
Location Predictors
1A) Tract group (primary sampling design only)
1B) Serology testing location (secondary sampling design only)
Predictors from U.S. Census
1) % of the population ≥14 y of age
2) Median age
3) % Hispanic
4) % not entering college
5) % of families with annual income <$60,000
6) % of families with annual income <$40,000
Individual response propensity model
Location Predictors
1A) Tract group (primary sampling design only)
1B) Serology testing location (secondary sampling design only)
Predictors from U.S. Census
1) % of families with annual income <$40,000
Predictors from household survey
1) Implements social distancing
2) Degree of concern over COVID-19
3) Regularly leaves the home for work, medical treatment, groceries, or to go to restaurants
4) General health
5) Hispanic ethnicity
6) Education level
7) Has been tested previously for COVID-19
8) Degree of concern that others should social distance
Serology response propensity model
Location Predictors
1A) Tract group (primary sampling design only)
1B) Serology testing location (secondary sampling design only)
Predictors from individual survey
1) Implements social distancing
2) Degree of concern over COVID-19
3) Regularly leaves the home for work, medical treatment, groceries, or to go to restaurants
4) General health
5) Respondent's age
6) Respondent's sex
7) Hispanic ethnicity
8) Education level
9) Has been tested previously for COVID-19
10) Degree of concern that others should social distance

*COVID-19, coronavirus disease; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Appendix Table 2. Household response rates in a study of SARS-CoV-2 seroprevalence, Utah, United States*

	Primary sampling design‡			Secondary sampling design§		
Stratum†	No. responded	No. approached	Response rate, %	No. responded	No. approached	Response rate, %
Davis County						
High prevalence	375	833	45	–	–	–
Low prevalence	374	1,036	36.1	–	–	–
High-low	–	–	–	274	2,125	12.9
Salt Lake County						
High prevalence						
Hispanic old	364	1,316	27.7	–	–	–
Hispanic young	210	834	25.2	–	–	–
Hispanic young and old	–	–	–	186	2,280	8.2
Non-Hispanic old	283	868	32.6	135	912	14.8
Non-Hispanic young	289	876	33	49	462	10.6
Low prevalence						
Hispanic old	131	415	31.6	36	456	7.9
Hispanic young	160	412	38.8	33	462	7.1
Non-Hispanic old	471	1,225	38.4	146	912	16
Non-Hispanic young	157	406	38.7	45	462	9.7
Summit County	165	876	18.8	118	3,205	3.7
Utah County						
High prevalence						
Hispanic	258	818	31.5	88	912	9.6
Non-Hispanic	146	416	35.1	47	456	10.3
Low prevalence						
Hispanic	161	411	39.2	–	–	–
Non-Hispanic	294	821	35.8	–	–	–
Hispanic and non-Hispanic	–	–	–	130	1,368	9.5

*SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

†Prevalence refers to the incidence proportion of SARS-COV-2 infection based on reported SARS-CoV-2 case counts at the time that data collection began.

‡In the primary sampling design, we operationally defined household approaches as a visit by the field team or the initiation of the online survey in response to the mailer sent to the household. Respondents were households that completed key portions of the household survey or ≥1 individual survey. We estimated the response rates as the ratio of these 2 quantities.

§In the secondary sampling design, we defined household approaches as households being sent the mailer. We used different definitions between the 2 sampling designs because the principal sampling method in the primary sampling design was door-to-door contact by the field team, with mailings playing a secondary role, while in the secondary sampling design the only sampling method was the mailer.

Appendix Table 3. Participant response rates for surveys in 4 counties in a study of SARS-CoV-2 seroprevalence, Utah, United States*

	Primary sampling design‡			Secondary sampling design§		
Stratum†	No. responded	No. approached	Response rate, %	No. responded	No. approached	Response rate, %
Davis County						
High prevalence	741	950	78	–	–	–
Low prevalence	764	1,100	69.5	–	–	–
High-low prevalence	–	–	–	576	697	82.6
Salt Lake County						
High prevalence						
Hispanic old	614	774	79.3	–	–	–
Hispanic young	325	505	64.4	–	–	–
Hispanic young and old	–	–	–	348	404	86.1
Non-Hispanic old	518	639	81.1	275	315	87.3
Non-Hispanic young	471	590	79.8	96	107	89.7
Low prevalence						
Hispanic old	258	340	75.9	69	82	84.1
Hispanic young	314	457	68.7	69	83	83.1
Non-Hispanic old	908	1233	73.6	314	354	88.7
Non-Hispanic young	340	514	66.1	92	99	92.9
Summit County	160	177	90.4	171	202	84.7
Utah County						
High prevalence						
Hispanic	524	706	74.2	195	234	83.3
Non-Hispanic	305	413	73.8	124	147	84.4
Low prevalence						
Hispanic	352	532	66.2	–	–	–
Non-Hispanic	598	843	70.9	–	–	–
Hispanic and non-Hispanic	–	–	–	312	378	82.5

*We defined individual response rates in both sampling designs as the proportion of persons ≥12 years of age in responding households that completed the survey. SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

†Prevalence refers to the incidence proportion of SARS-COV-2 infection based on reported SARS-CoV-2 case counts at the time that data collection began.

‡In the primary sampling design, we operationally defined household approaches as a visit by the field team or the initiation of the online survey in response to the mailer sent to the household. Respondents were households that completed key portions of the household survey or ≥1 individual survey. We estimated the response rates as the ratio of these 2 quantities.

§In the secondary sampling design, we defined household approaches as households being sent the mailer. We used different definitions between the 2 sampling designs because the principal sampling method in the primary sampling design was door-to-door contact by the field team, with mailings playing a secondary role, while in the secondary sampling design the only sampling method was the mailer.

Appendix Table 4. Serology response rates in 4 counties in a study of SARS-CoV-2 seroprevalence, Utah, United States*

	Primary sampling design‡			Secondary sampling design§		
Stratum†	No. responded	No. approached	Response rate, %	No. responded	No. approached	Response rate, %
Davis County						
High prevalence	593	746	79.5	–	–	–
Low prevalence	594	791	75.1	–	–	–
High-low prevalence	–	–	–	516	598	86.3
Salt Lake County						
High prevalence						
Hispanic old	512	651	78.6	–	–	–
Hispanic young	201	348	57.8	–	–	–
Hispanic young and old	–	–	–	287	361	79.5
Non-Hispanic old	429	534	80.3	245	289	84.8
Non-Hispanic young	352	489	72	87	100	87
Low prevalence						
Hispanic old	217	272	79.8	63	69	91.3
Hispanic young	227	332	68.4	60	73	82.2
Non-Hispanic old	732	958	76.4	274	320	85.6
Non-Hispanic young	252	356	70.8	83	93	89.2
Summit County	218	277	78.7	127	179	70.9
Utah County						
High prevalence						
Hispanic	441	554	79.6	171	195	87.7
Non-Hispanic	261	329	79.3	124	141	87.9
Low prevalence						
Hispanic	288	363	79.3	–	–	–
Non-Hispanic	474	619	76.6	–	–	–
Hispanic and non-Hispanic	–	–	–	280	331	84.6

*We defined serology response rates in both sampling designs as the proportion of survey respondents who also provided a serology sample. SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

†Prevalence refers to the incidence proportion of SARS-COV-2 infection based on reported SARS-CoV-2 case counts at the time that data collection began.

‡In the primary sampling design, we operationally defined household approaches as a visit by the field team or the initiation of the online survey in response to the mailer sent to the household. Respondents were households that completed key portions of the household survey or ≥1 individual survey. We estimated the response rates as the ratio of these 2 quantities.

§In the secondary sampling design, we defined household approaches as households being sent the mailer. We used different definitions between the 2 sampling designs because the principal sampling method in the primary sampling design was door-to-door contact by the field team, with mailings playing a secondary role, while in the secondary sampling design the only sampling method was the mailer.

Appendix Table 5. Overall response rates in 4 counties in a study of SARS-CoV-2 seroprevalence, Utah, United States*

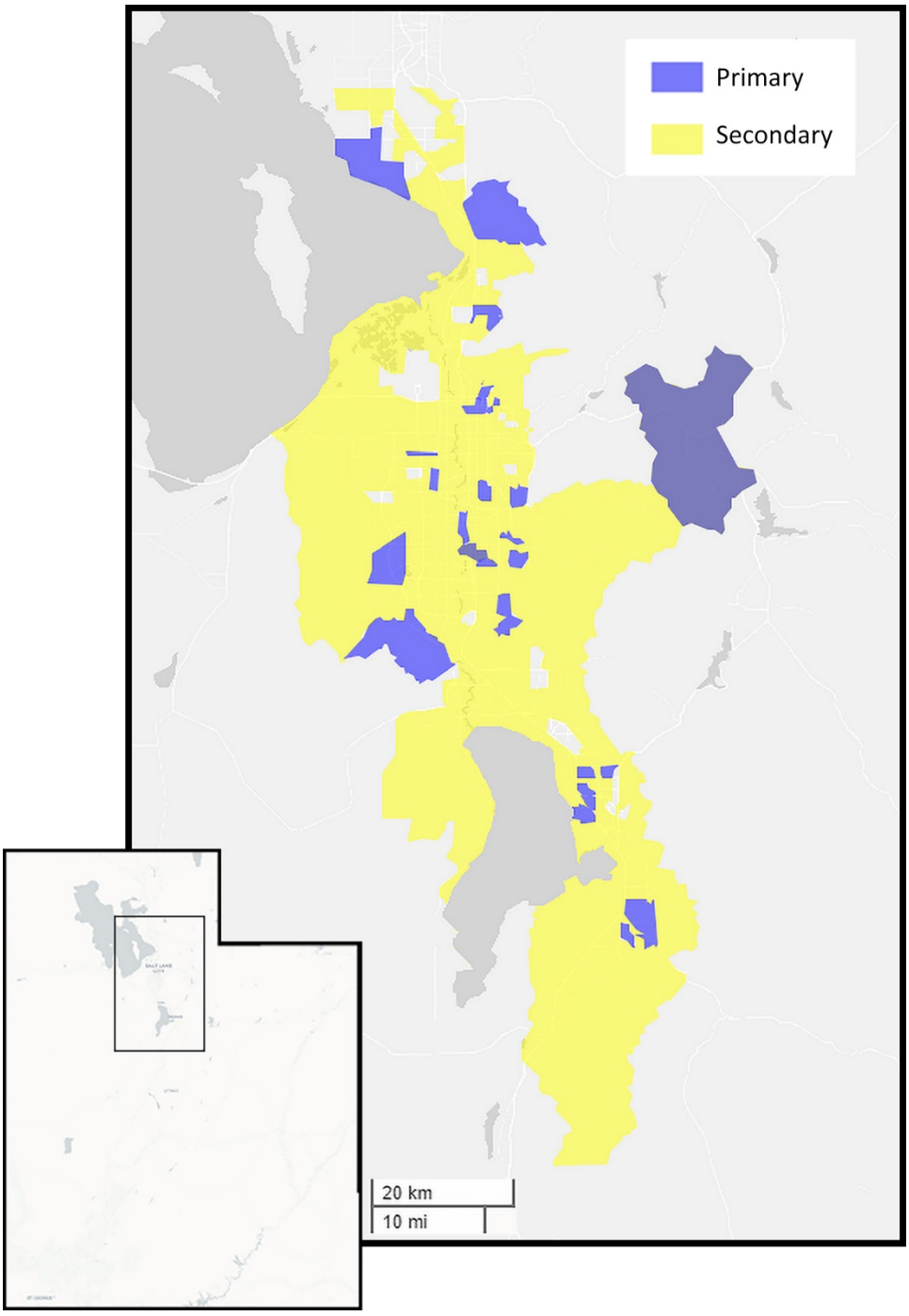
Stratum†	Sampling design, % response	
	Primary‡	Secondary§
Davis County		
High prevalence	27.9	–
Low prevalence	18.8	–
High-low prevalence	–	9.2
Salt Lake County		
High prevalence		
Hispanic old	17.3	–
Hispanic young	9.4	–
Hispanic young and old	–	5.6
Non-Hispanic old	21.2	11
Non-Hispanic young	19	8.3
Low prevalence		
Hispanic old	19.1	6.1
Hispanic young	18.2	4.8
Non-Hispanic old	21.6	12.1
Non-Hispanic young	18.1	8
Summit County	13.4	2.2
Utah County		
High prevalence		
Hispanic	18.6	7
Non-Hispanic	20.5	7.6
Low prevalence		
Hispanic	20.6	–
Non-Hispanic	19.4	–
Hispanic and non-Hispanic	–	6.6

*We estimated overall response as the products of the household, individual, and serology level response rates from Appendix Tables 3, 4, and 5. SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.
†Prevalence refers to the incidence proportion of SARS-COV-2 infection based on reported SARS-CoV-2 case counts at the time that data collection began.
‡In the primary sampling design, we operationally defined household approaches as a visit by the field team or the initiation of the online survey in response to the mailer sent to the household. Respondents were households that completed key portions of the household survey or ≥1 individual survey. We estimated the response rates as the ratio of these 2 quantities.
§In the secondary sampling design, we defined household approaches as households being sent the mailer. We used different definitions between the 2 sampling designs because the principal sampling method in the primary sampling design was door-to-door contact by the field team, with mailings playing a secondary role, while in the secondary sampling design the only sampling method was the mailer.

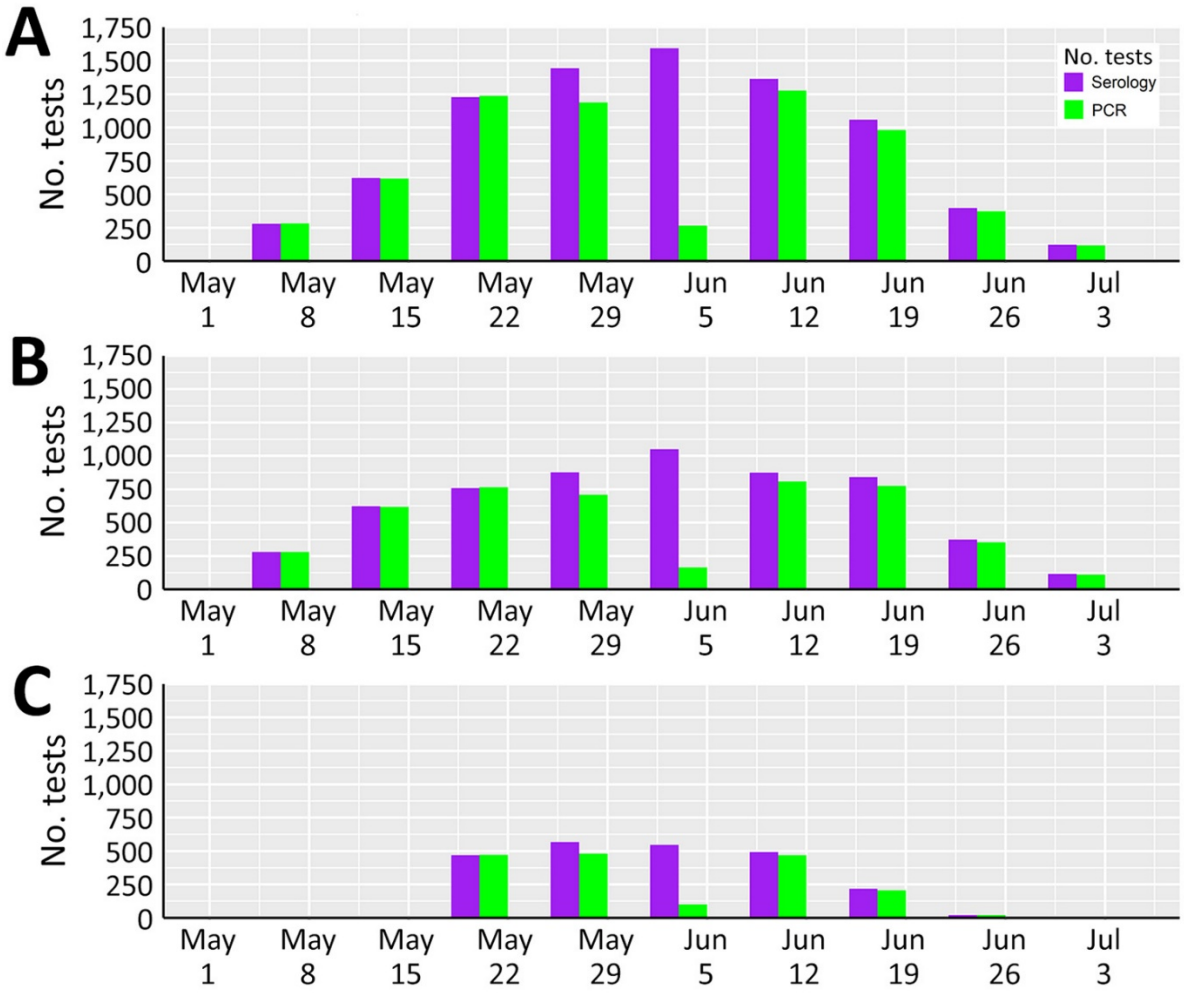
Appendix Table 6. Summaries of the mean relative weights applied to various subgroups of respondents in a study of SARS-CoV-2 seroprevalence, Utah, United States*

Variable	Sample size	Relative mean analysis weight†
Age group, y		
12–17	755	1.6
18–44	3,366	1.2
45–64	2,345	0.9
65–74	1,087	0.6
75–84	477	0.6
≥85	78	0.6
Sex		
M	3,773	1.1
F	4,293	0.9
Ethnicity		
Hispanic	528	2.3
Non-Hispanic	7,516	0.9
Education Level		
High school or less	1,681	1.7
Some college or technical school	2,022	1.4
College graduate	4,281	0.5
General Health		
Excellent	2,404	1
Very Good	3,443	1
Good	1,792	1
Fair/Poor	444	1
Chronic Medical Conditions		
None	5,567	1.1
Asthma only	841	1
≥1 chronic condition other than asthma	1,700	0.8

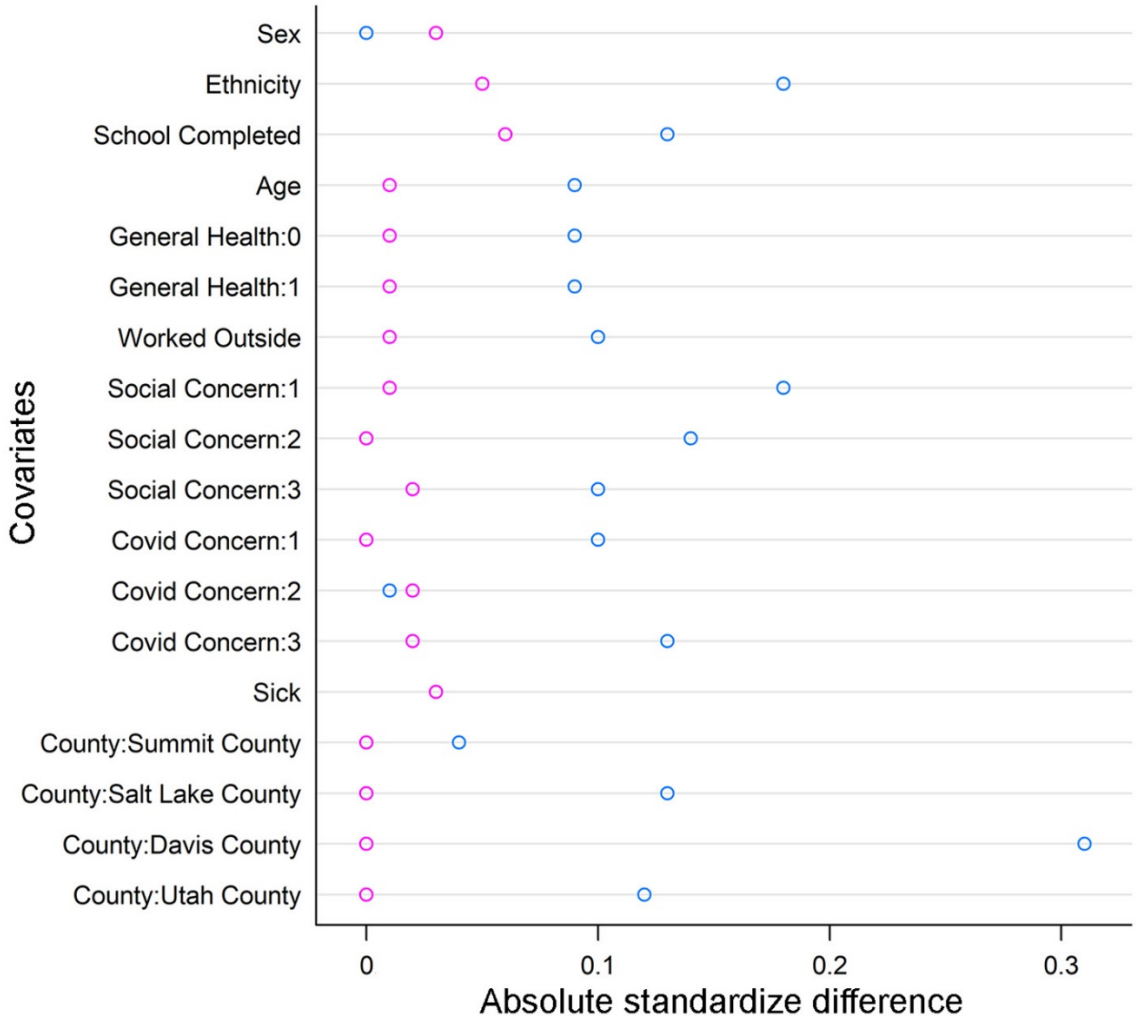
*The ratios of the mean analysis sampling weights within the designated subgroup compared with the overall mean sampling rate for analyses of the serology results are shown. These ratios indicate the relative amount of influence of individual respondents with different characteristics. The weights incorporate adjustments for nonresponses at the household, individual, and serology levels and the propensity score adjustment used to align the characteristics of respondents in the secondary sampling design to respondents in the primary sampling design and to the final iterative proportional fitting step to align the weighted characteristics of the study population to the U.S. census.
†Relative mean analysis weight = mean × (weights for subgroup)/mean × (weight for everyone), where weights are the final analysis weights that account for sampling design and all postsurvey adjustments.



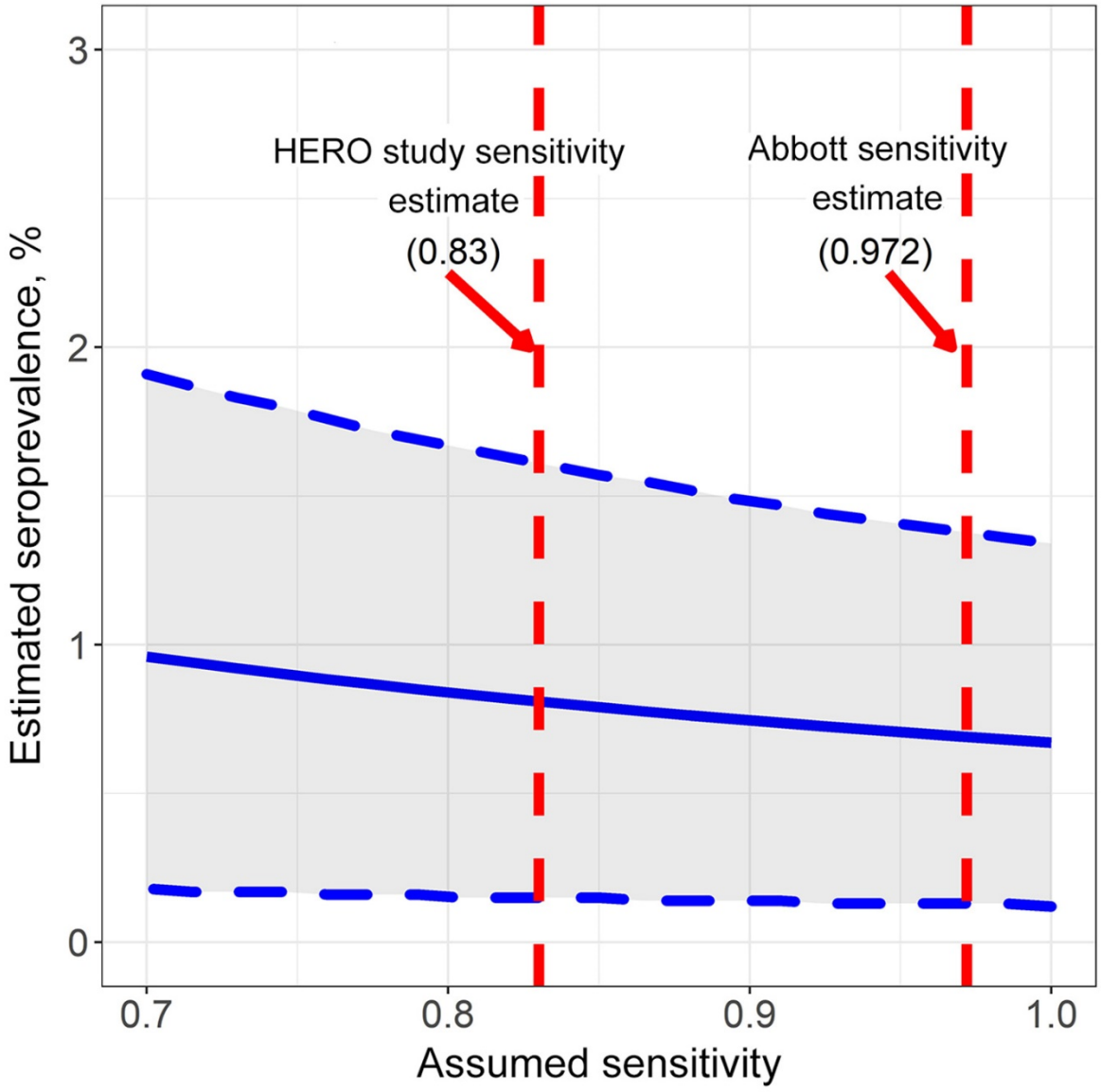
Appendix Figure 1. Geographic locations of the primary or secondary sampling designs in a study of SARS-CoV-2 seroprevalence, Utah, United States. The figure illustrates that the primary sampling locations are spread across 4 counties and that a large fraction of the counties were sampled either in the primary or secondary sampling design. Inset shows Utah with the 4-country area shown by box. SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.



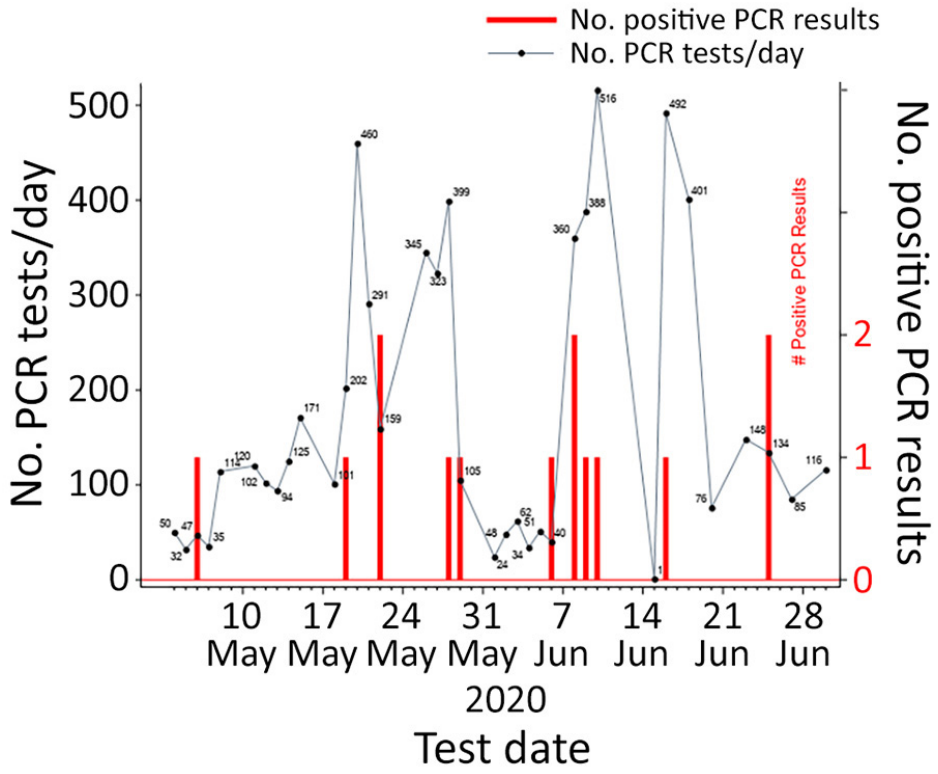
Appendix Figure 2. Timing of serology and PCR samples in a study of SARS-CoV-2 seroprevalence, Utah, United States. Top, extended sampling design; middle, primary sampling design; bottom, secondary sampling design. Extended sampling design refers to collection of all 5,125 responding households, including households in both the primary and secondary sampling designs. SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.



Appendix Figure 3. Propensity matching of secondary to primary sampling design respondents in a study of SARS-CoV-2 seroprevalence, Utah, United States. Blue circles represent the standardized mean differences in each factor between the primary and secondary sampling designs after application of sampling weights that account for nonresponse at the household, individual, and serology testing levels. Pink circles represent the standardized mean differences after the additional propensity score weighting to bring the characteristics of the respondents in the secondary sampling design into alignment with the characteristics of the respondents in the primary sampling design. The shift in the pink circles relative to the blue circles indicates the effect of the propensity adjustment to align the secondary design sample to match the primary design sample.



Appendix Figure 4. Dependence of percent seropositivity on assumed sensitivity of the serology assay used for analyses in a study of SARS-CoV-2 seroprevalence, Utah, United States. Our primary estimates of seroprevalence are based on estimates of 0.83 sensitivity, selected on the basis of the fraction of respondents (25/30) who self-reported having a prior positive COVID-19 test and subsequently had a positive serology test ≥1 week after their reported positive COVID-19 test. We considered a relatively wide range for sensitivity to address speculation that IgG concentrations might wane over time and become undetectable by the assay at some point. The graph shows the relationship between the estimated seroprevalence across the 4-county area with the assumed sensitivity if specificity is assumed to be 0.996. COVID-19, coronavirus 19; HERO, Health and Economic Recovery Outreach program in Utah; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.



Appendix Figure 5. Positive PCR tests and total number of PCR tests performed on participants in a study of SARS-CoV-2 seroprevalence, Utah, United States. Gray curve indicates the number of PCR tests performed each day; red bars indicate number of PCR-positive results per week. The drop-off in the gray curve in late May and early June reflects a temporary period during which PCR tests were administered only when specifically requested by the respondent. The study subsequently reinitiated broad PCR testing in response to the increased COVID-19 case counts reported in the 4-county area. COVID-19, coronavirus 19; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.