

# Severe Acute Respiratory Syndrome Coronavirus 2 Transmission in Georgia, USA, February 1–July 13, 2020

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The serial interval and effective reproduction number for coronavirus disease (COVID-19) are heterogeneous, varying by demographic characteristics, region, and period. During February 1–July 13, 2020, we identified 4,080 transmission pairs in Georgia, USA, by using contact tracing information from COVID-19 cases reported to the Georgia Department of Public Health. We examined how various transmission characteristics were affected by symptoms, demographics, and period (during shelter-in-place and after subsequent reopening) and estimated the time course of reproduction numbers for all 159 Georgia counties. Transmission varied by time and place but also by persons' sex and race. The mean serial interval decreased from 5.97 days in February–April to 4.40 days in June–July. Younger adults (20–50 years of age) were involved in most transmission events occurring during or after reopening. The shelter-in-place period was not long enough to prevent sustained virus transmission in densely populated urban areas connected by major transportation links.

Coronavirus disease (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). After it was first reported in Wuhan, China, in December 2019, COVID-19 spread rapidly across the world as an ongoing global pandemic. As of July 9, 2021, most confirmed COVID-19 cases (33,792,898 cases) and deaths (606,487) in the world were in the United States (1), and 906,136 confirmed cases and 18,544 deaths were in the state of Georgia (2).

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Transmission of COVID-19 varies by region (3,4), setting (long-term care facilities, prisons, and factories) (5), population demographics (age, sex, and race), and even among individual persons (physiologic and behavioral differences) (6). During the early phases of transmission in the United States, new cases were mainly imported by travelers and transmission was associated with human mobility (7). Local transmission was more intense in regions with high population density and in populations with frequent social contacts (3,8,9). When SARS-CoV-2 was introduced into high-risk settings (e.g., long-term care facilities), transmission rates were intense, and the outcomes were often fatal (10).

To study transmission of SARS-CoV-2, we examined the serial interval for symptom onset (defined as the time interval between symptom onset in a primary case-patient and symptom onset in a secondary case-patient infected by the primary case-patient) and the effective reproduction number  $R_t$  (the expected number of cases directly caused by any single infectious person).  $R_t$  has been shown to vary strongly; some case-patients have caused superspreading events (11,12). Such heterogeneity influences the spread as well as the control of COVID-19, as documented by studies of nonpharmaceutical interventions in China (13,14) and Europe (15) at the province and country levels.

After the first case of COVID-19 was reported in the state of Georgia on March 2, 2020, a series of events and interventions followed (Appendix Table 1, <https://wwwnc.cdc.gov/EID/article/27/10/21-0061-App1.pdf>). On April 3, state officials announced a shelter-in-place order, requiring all residents and visitors to remain in their residence and take every possible precaution to limit social interactions. On

April 24, officials allowed some businesses to reopen, and on April 30 the shelter-in-place order was lifted. On June 1, state officials further relaxed restrictions. During June–July 2020, as new COVID-19 cases continued to surge in Georgia and other states, knowing how shelter-in-place and the subsequent reopening events affected the transmission of SARS-CoV-2 in different regions became crucial.

Identifying a large number of the primary and secondary case-patient pairs enabled us to estimate the distribution of the serial interval for symptom onset. Using the serial interval distribution, we can estimate the time-varying  $R_t$  (16). With  $R_t$ s over time, we can study the spatial distribution of transmission across all 159 Georgia counties as well as the effects of shelter-in-place and subsequent gradual reopening.

The Georgia Department of Public Health (GDPH) Institutional Review Board determined that this analysis was exempt from the requirement for review and approval, and informed consent was not required. This activity was reviewed by the Centers for Disease Control and Prevention and was consistent with their applicable policy and with federal law.

## Methods

### Data Source

GDPH provided data for all 118,491 confirmed COVID-19 cases in all 159 counties of Georgia during February 1–July 13, 2020. Available data included demographic characteristics (age, sex, and race), clinical characteristics (dates of symptom onset, recorded symptoms, hospitalization, and ventilator use), and social contacts (contacts between confirmed case-patients and if cases were part of a confirmed outbreak) (Table; Appendix Table 2). Missing values in the data were common; large percentages of values for clinical characteristics were missing. With regard to events possibly driving transmission, periods were categorized as early transmission and shelter-in-place during February–April, after reopening (shelter-in-place order was lifted) in May, and further reopening (more restrictions were relaxed) during June–July (Appendix Table 1). For this study, we defined a COVID-19 case as SARS-CoV-2 infection confirmed by reverse transcription PCR irrespective of clinical signs and symptoms.

### Tracked Pairs: Serial Intervals and Characteristics of Transmission

On the basis of reported contacts with confirmed case-patients, we identified pairs of primary and secondary case-patients by using the following procedure.

First, most transmission pairs could be established as a unique close contact with a confirmed case-patient. We assumed that symptom onset for any primary case-patient in a confirmed pair occurred before symptom onset of the secondary case-patient. Second, when an outbreak involved multiple cases, we assigned primary case-patients according to review of the epidemiologic time lines. Usually, there was 1 case-patient whose symptom onset was several days earlier than that of the rest of the case-patients in the cluster, and this case-patient was designated as the primary case-patient. Thus, serial intervals were assumed to be always positive. To examine the influence of ignoring negative serial intervals on  $R_t$  estimation, we conducted a sensitivity analysis (Appendix Supplemental Material C). Transmission pairs with serial intervals >15 days were dropped because such long intervals are unlikely, as shown in previous studies (17,18). We modeled the serial interval as a gamma distribution and obtained maximum-likelihood estimators of shape and scale parameters. Furthermore, we explored whether the duration of the serial interval varied by demographic characteristics, various disease symptoms, and periods of symptom onset for primary case-patients. The large numbers of tracked case-patient pairs also enabled us to examine variation in transmission within and between different groups by age, sex, and race.

### Confirmed Cases: Reproduction Numbers

We estimated probabilities of transmission between any pairs of case-patients in an outbreak by using a transmission probability matrix method (Appendix Supplemental Material B) (16). Using GDPH data for confirmed COVID-19 cases during February 1–July 13, 2020, we estimated  $R_t$ s by date, and we used dates of symptom onset and social contact information (wherever available) in each county independently by estimating the transmission probability matrix.

Among 118,491 confirmed cases, the date of symptom onset was missing for 48,893 (41.3%). These missing symptom-onset dates were imputed according to dates of first specimen collection if available or dates of laboratory report if not (Appendix Supplemental Material A).

The most recent data are incomplete because not all incident cases have been reported and not all persons have become symptomatic. Therefore, estimates of  $R_t$  approaching the present date are biased. Because one of our study goals was to examine the timing and magnitude of the first 2 waves of SARS-CoV-2 transmission in Georgia (and not to nowcast transmission), we removed  $R_t$  estimates of the most

## RESEARCH

recent 4 weeks (June 16–July 13) from the analysis. SARS-CoV-2 transmission in Georgia seemed to include multiple waves and varied considerably among counties. The time-varying average  $R_t$  estimates were smoothed by using LOESS regression, and local maximums/minimum were identified for each individual county. On the basis of our review of the epidemic curves and curves, we defined the following 5 transmission patterns:

- Consistent spreading: there was sustained transmission of SARS-CoV-2 ( $R_t > 1$ ) during the shelter-in-place period. Consequently, numbers of cases remained high and increased rapidly at reopening.

- Two strong waves: a first wave of early transmission was followed by a slowdown ( $R_t < 1$ ) during the shelter-in-place period and a new surge in cases ( $1 \leq R_t < 2$ ) after reopening.
- Strong first wave: there was a considerable number of cases during the initial period of the outbreak. During the shelter-in-place period, spreading was controlled; after reopening no new surge in cases occurred ( $R_t < 1$ ).
- Strong second wave: there were few cases during the early transmission period, but new cases surged ( $R_t \geq 2$ ) after reopening.
- Small case number (<200): SARS-CoV-2 transmission was rare.

**Table.** Demographic and clinical information for persons with confirmed coronavirus disease, Georgia, USA, during 3 periods, February 1–July 15, 2020

Variable	February–April, no. (%), n = 31,575*	May, no. (%), n = 19,270†	June–July, no. (%), n = 67,646‡	Total, no. (%), n = 118,491§
<b>Sex</b>				
M	13,770 (43.6)	9,142 (47.4)	30,247 (44.7)	53,159 (44.9)
F	17,308 (54.8)	9,747 (50.6)	33,828 (50)	60,883 (51.4)
Missing	497 (1.6)	381 (2.0)	3,571 (5.3)	4,449 (3.7)
<b>Race</b>				
Black	13,010 (41.2)	4,639 (24.1)	13,878 (20.5)	31,527 (26.6)
White	11,418 (36.2)	7,168 (37.2)	17,500 (25.9)	36,086 (30.5)
Other	2,818 (8.9)	2,029 (10.5)	6,158 (9.1)	11,005 (9.3)
Missing	4,329 (13.7)	5,434 (28.2)	30,110 (44.5)	39,873 (33.6)
<b>Hospitalized</b>				
Yes	6,714 (21.3)	2,099 (10.9)	4,523 (6.7)	13,336 (11.3)
No	15,627 (49.5)	10,729 (55.7)	27,926 (41.3)	54,282 (45.8)
Missing	9,234 (29.2)	6,442 (33.4)	35,197 (52)	50,873 (42.9)
<b>Ventilator use</b>				
Yes	1,046 (3.3)	184 (1.0)	258 (0.4)	1,488 (1.3)
No	12,188 (38.6)	8,404 (43.6)	19,313 (28.6)	39,905 (33.7)
Missing	18,341 (58.1)	10,682 (55.4)	48,075 (71.1)	77,098 (65.0)
<b>Abnormal chest radiograph finding</b>				
Yes	2,602 (8.2)	494 (2.6)	742 (1.1)	3,838 (3.2)
No	10,151 (32.1)	8,081 (41.9)	18,246 (27.0)	36,478 (30.8)
Missing	18,822 (59.6)	10,695 (55.5)	48,658 (71.9)	78,175 (66.0)
<b>Death</b>				
Yes	2,127 (6.7)	558 (2.9)	320 (0.5)	3,005 (2.5)
No	15,766 (49.9)	10,183 (52.8)	26,304 (38.9)	52,253 (44.1)
Missing	13,682 (43.3)	8,529 (44.3)	41,022 (60.6)	63,233 (53.4)
<b>Fever</b>				
Yes	10,094 (32.0)	4,005 (20.8)	11,787 (17.4)	25,886 (21.8)
No	8,489 (26.9)	7,951 (41.3)	19,655 (29.1)	36,095 (30.5)
Missing	12,992 (41.1)	7,314 (38)	36,204 (53.5)	56,510 (47.7)
<b>Cough</b>				
Yes	12,417 (39.3)	4,992 (25.9)	15,319 (22.6)	32,728 (27.6)
No	6,462 (20.5)	7,059 (36.6)	16,434 (24.3)	29,955 (25.3)
Missing	12,696 (40.2)	7,219 (37.5)	35,893 (53.1)	55,808 (47.1)
<b>Shortness of breath</b>				
Yes	8,504 (26.9)	2,952 (15.3)	7,325 (10.8)	18,781 (15.9)
No	9,807 (31.1)	8,960 (46.5)	23,542 (34.8)	42,309 (35.7)
Missing	13,264 (42)	7,358 (38.2)	36,779 (54.4)	57,401 (48.4)
<b>Diarrhea</b>				
Yes	4,410 (14)	1,971 (10.2)	6,072 (9.0)	12,453 (10.5)
No	12,718 (40.3)	9,589 (49.8)	23,936 (35.4)	46,243 (39.0)
Missing	14,447 (45.8)	7,710 (40.0)	37,638 (55.6)	59,795 (50.5)

\*Median age (Q1–Q3) 51 (37–65) y.

†Median age (Q1–Q3) 43 (28–59) y.

‡Median age (Q1–Q3) 34 (23–50) y.

§Median age (Q1–Q3) 40 (26–56) y.

We generated maps to spatially examine the spreading of the COVID-19 first wave. We evaluated the effect of shelter-in-place, reopening, and further reopening by the trend of reproduction numbers before and after those events in different regions of Georgia.

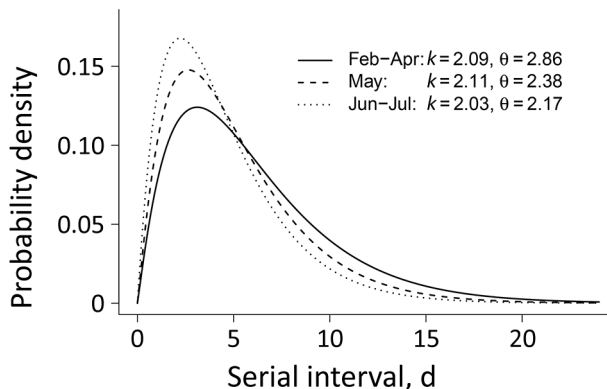
## Results

### Tracked Pairs: Serial Intervals

On the basis of 4,080 tracked pairs of primary and linked secondary case-patients in Georgia (Appendix Table 3), we estimated the serial interval distribution as a gamma distribution with a mean (10th–90th percentile) of 4.99 (1.32–9.71) days. Generally, the serial interval was longer when outcomes for primary case-patients were severe, such as hospitalization, undergoing ventilation, having an abnormal chest radiograph result, or death as final outcome (Appendix Table 4). Specific signs/symptoms in primary case-patients (i.e., fever, cough, shortness of breath, or diarrhea) did not shorten serial intervals. Serial intervals did not differ across demographic categories (i.e., age, sex, race, or location). The mean (10th–90th percentile) serial interval was 5.97 (1.65–11.50) days in February–April, 5.03 (1.41–9.65) days in May, and 4.40 (1.18–8.52) days in June–July (Figure 1). The average serial interval became shorter over time: from 5.97 (1.65–11.50) days in February–April, to 5.03 (1.41–9.65) days in May, and then to 4.40 (1.18–8.52) days in June–July (Appendix Figure 1).

### Tracked Pairs: Characteristics of Transmission

To study the variation in transmission by demographic characteristic (i.e., age, sex, and race), the observed frequencies in transmission pairs can be



**Figure 1.** Estimated serial interval distribution for 3 periods in study of severe acute respiratory syndrome coronavirus 2 transmission in Georgia, USA: early transmission and shelter-in-place (February–April 2020); after reopening (May); and further reopening (June–July).  $k$  and  $\theta$  indicate the scale and shape parameters for the gamma distribution. The y-axis represents the estimated probability density of having a certain serial interval.

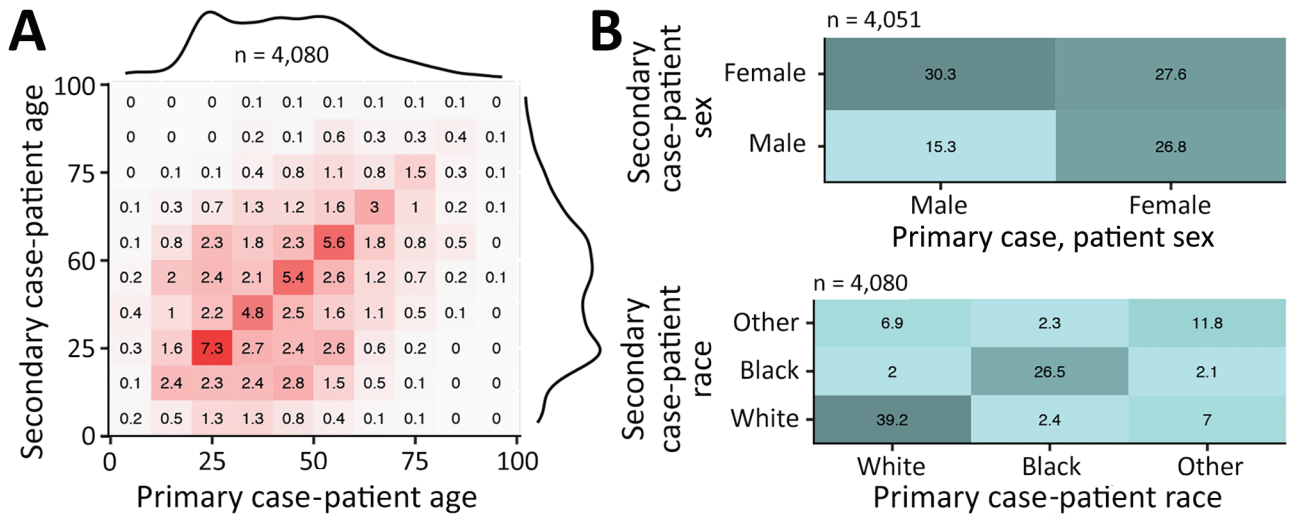
shown in a matrix (Figure 2, panels A, B). Male case-patients were twice as likely to transmit infection to a female than a male contact, whereas female case-patients were equally likely to transmit infection to a male or a female contact. Transmission between races was strongly assortative. White and Black persons were more likely to transmit infection to persons of their own races than to persons of other races; White persons were 4.4 times as likely to transmit infection to White persons, and Black persons were 5.6 times as likely to transmit infection to Black persons.

SARS-CoV-2 seemed to mainly spread from adults 20–60 years of age during February–July 2020; transmission between children (<20 years) and elderly persons (>60 years) was observed less often, suggesting that transmission occurred more frequently between persons of similar ages (Figure 3, panels A–D). Transmission between persons of different sexes was mainly among those in the same age group. Cases in persons 10–30 years of age were associated with most transmission pairs of the same sex. Over the study period, most transmission pairs shifted from 40–70 years of age (median age for primary case-patients was 52 years and for secondary case-patients was 50 years) in February–April to 20–50 years of age (primary case-patient median age 36 years and secondary case-patient median age 34 years) in June–July (Figure 4).

### Temporal and Spatial Patterns of Transmission

During February and March,  $R_t$  were >1 and then decreased until late April and early May, considered the first wave in Georgia.  $R_t$  usually decreased to a (mathematical) local minimum during the shelter-in-place period and started to increase again as the second wave began. As during the first wave,  $R_t$ s peaked and then started to decrease again during the second wave (Figure 5). Although the number of reported cases was lower in first wave,  $R_t$  was much higher in the first wave ( $\approx 3.5$ ) than in the second wave ( $\approx 1.7$ ).

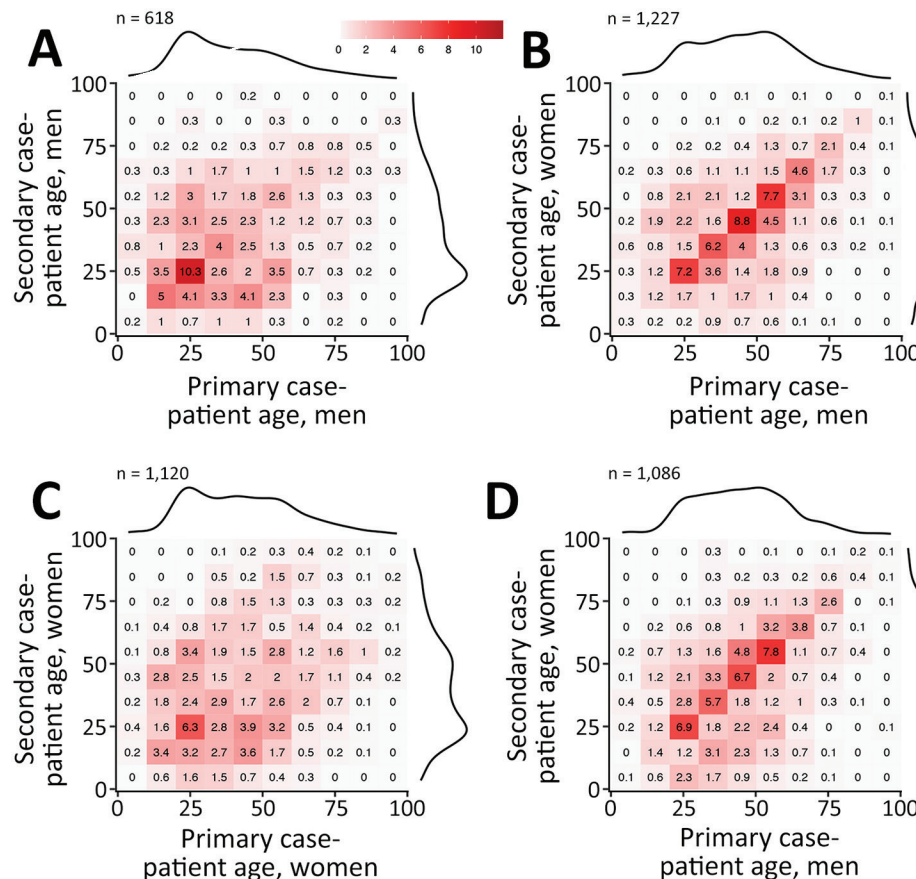
Although the general pattern of SARS-CoV-2 transmission was similar across all counties, the dates of local maximums/minimum (i.e., first peak, local minimum, and second peak) and the magnitude of  $R_t$  at these extremes varied among counties. The peak dates for the first wave in counties with cumulative case numbers was >200 cases by July 13, 2020 (Figure 6, panel A). At that time, counties with high numbers of COVID-19 cases were located around cities and along highways. Starting in early February, COVID-19 spread radially and along the interstate highway from Atlanta and Albany, the 2 initial outbreak sources. Outbreaks occurred later in other



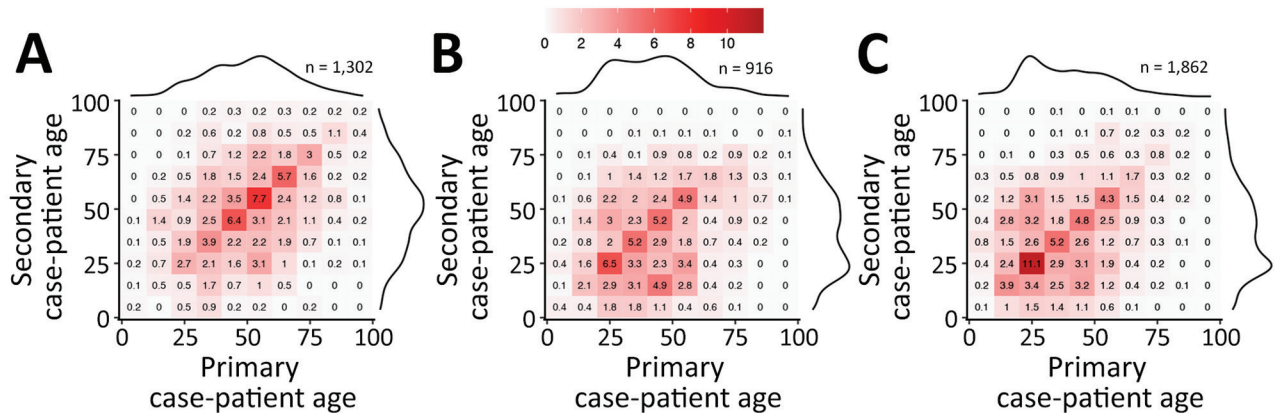
**Figure 2.** Patterns of severe acute respiratory syndrome coronavirus 2 transmission by patient age (A), sex (B), and race (B), based on 4,080 tracked pairs of coronavirus disease cases from Georgia, USA, during February–July 2020. The matrix graphs show numbers of transmission pairs as a percentage of the total, with primary case-patients as columns and their secondary case-patients as rows. Darker colors indicate a higher percentage of fraction of tracked pairs observed. In panel A, marginal totals are shown as density curves to illustrate the age distribution of case-patients.

cities, including Augusta and Savannah. A total of 65 (74.7%) of 87 counties with >200 cumulative cases by July 13th reached a local minimum in  $R_t$  during the

shelter-in-place period (April 3–April 30) (Figure 7). After reopening, many counties experienced a second wave of COVID-19 and increased numbers of cases



**Figure 3.** Patterns of severe acute respiratory syndrome coronavirus 2 transmission according to patient sex and age, based on 4,080 tracked pairs of coronavirus disease cases in Georgia, USA, February–July 2020. A) Male-to-male transmission; B) male-to-female transmission; C) female-to-female transmission; D) female-to-male transmission. The matrix graphs show numbers of transmission pairs as a percentage of the total, with primary case-patients as columns and their secondary case-patients as rows. Darker colors indicate a higher percentage of fraction of tracked pairs observed. Marginal totals are shown as density curves to illustrate the age distribution of case-patients.



**Figure 4.** Patterns of severe acute respiratory syndrome coronavirus 2 transmission in Georgia, USA, February–July 2020, by age group, in 3 successive periods. A) Early transmission and shelter-in-place (February–April); B) after reopening (May); C) further reopening (June–July). The matrix graphs show numbers of transmission pairs as a percentage of the total, with primary case-patients as columns and their secondary case-patients as rows. Darker colors indicate a higher percentage of fraction of tracked pairs observed. Marginal totals are shown as density curves to illustrate the age distribution of case-patients.

were reported. On the basis of the magnitude of  $R_t$  at the first peak, local minimum, and second peak, we categorized case data into the 5 transmission patterns (Figure 5; Appendix Figures 11–169).

Consistent spreading occurred in Georgia counties around some major cities (e.g., Atlanta, Athens, Columbus, Savannah) and counties along interstate highways (Figure 6, panel B). In counties bordering other counties with consistent spreading, there were 2 strong waves or only a strong second wave. An early intense first wave but not a strong second wave occurred in counties around the city of Albany (Lee, Sumter, Terrell, Mitchell, Crisp, and Dooly Counties). Fewer cases occurred in counties not connected by interstate highways.

## Discussion

During February–July, the estimated serial intervals for onset of COVID-19 symptoms in the state of Georgia seemed to become shorter (Figure 1). Such a phenomenon was also observed in mainland China during January–February 2020 (19). Shorter serial intervals imply more rapid transmission. During February–July, disease prevalence increased in Georgia; by August 25, Georgia had the fifth highest number of confirmed COVID-19 cases in the United States. One cause of contracting serial intervals could be that persons had more contacts after reopening; in particular, younger persons (20–50 years) might play a larger role in SARS-CoV-2 transmission. Also, Kenah et al. showed that increasingly more infectious case-patients are present in the local population, competing to infect susceptible persons, and the expected time until a new infection is shortened (20).

The serial interval estimation could also be affected by changing testing practices and contact tracing over the duration of the pandemic. COVID-19 testing capacity and contact tracing ability in Georgia were limited during earlier stages of the pandemic; thus, identification and isolation of COVID-19 case-patients and their close contacts were often delayed. With improved testing capacity, symptomatic case-patients were tested more promptly and isolated more quickly, which led to fewer exposures during their infectious periods. Rapid isolation and contact tracing could truncate transmission and lead to shorten serial intervals. More recent data collected when testing and contact tracing have improved are less likely to be affected by delayed testing and isolation. Contraction of serial intervals continued into May through early July, so the changes may still be explained at least partly by increased prevalence and increased contact rates (Figure 1).

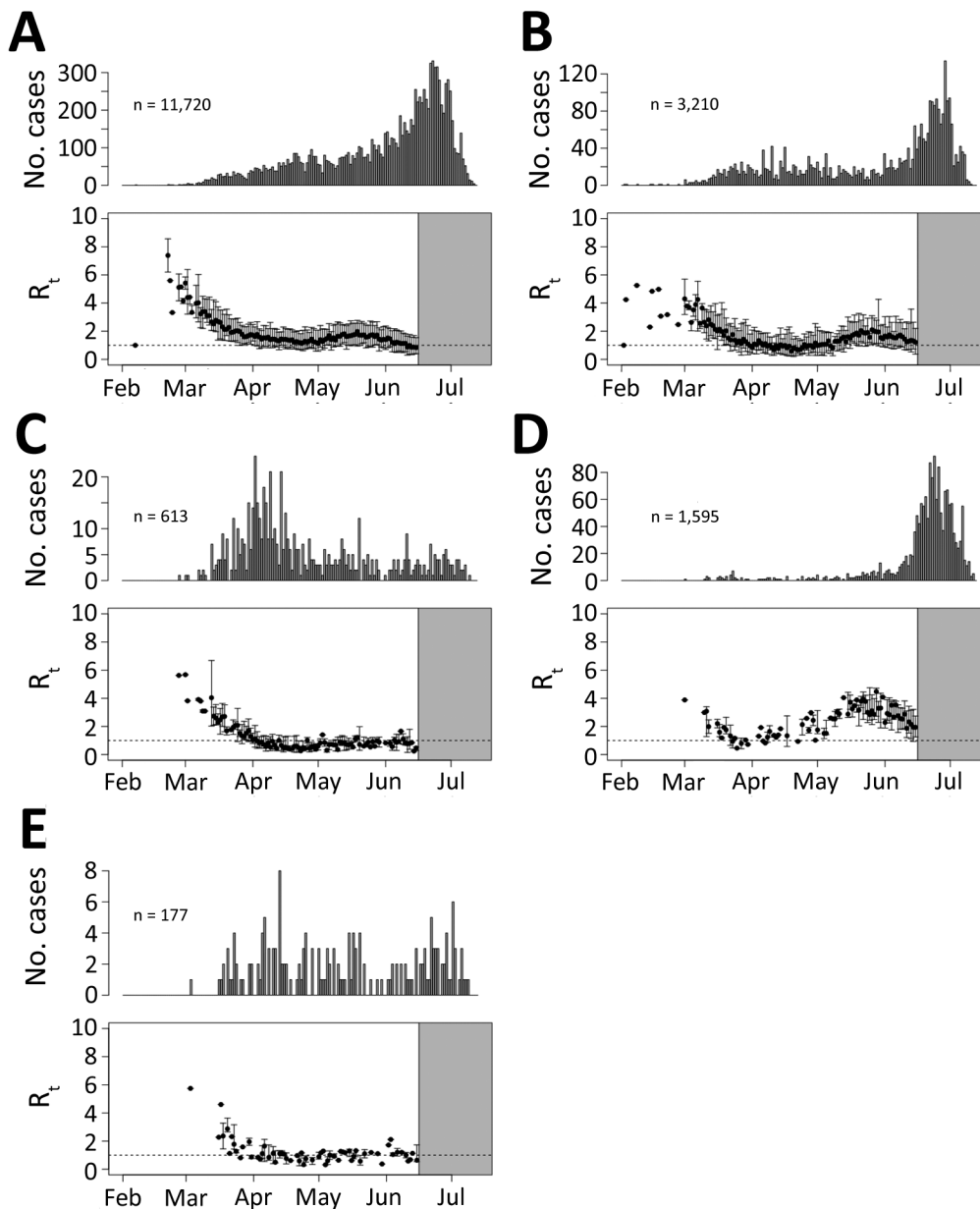
Transmission of a respiratory infection such as COVID-19 depends on behavioral factors and in particular on social contacts. Studies of contact behavior have shown that persons tend to have social contact with peers of similar age and demographic backgrounds (21). The tracked transmission pairs in this study show that such assortative mixing also applies to SARS-CoV-2 transmission (Figure 2). The transmission pairs in this study were more likely to be tracked when case-patients knew each other (e.g., family members, friends, or colleagues), whereas transmission in public spaces (e.g., stores or restaurants) usually could not be tracked. Transmission occurs frequently among persons in the same age group and less frequently among those in different age

groups (Figure 3), although transmission may have been across generations (e.g., between parents and children, or grandparents and grandchildren) (22).

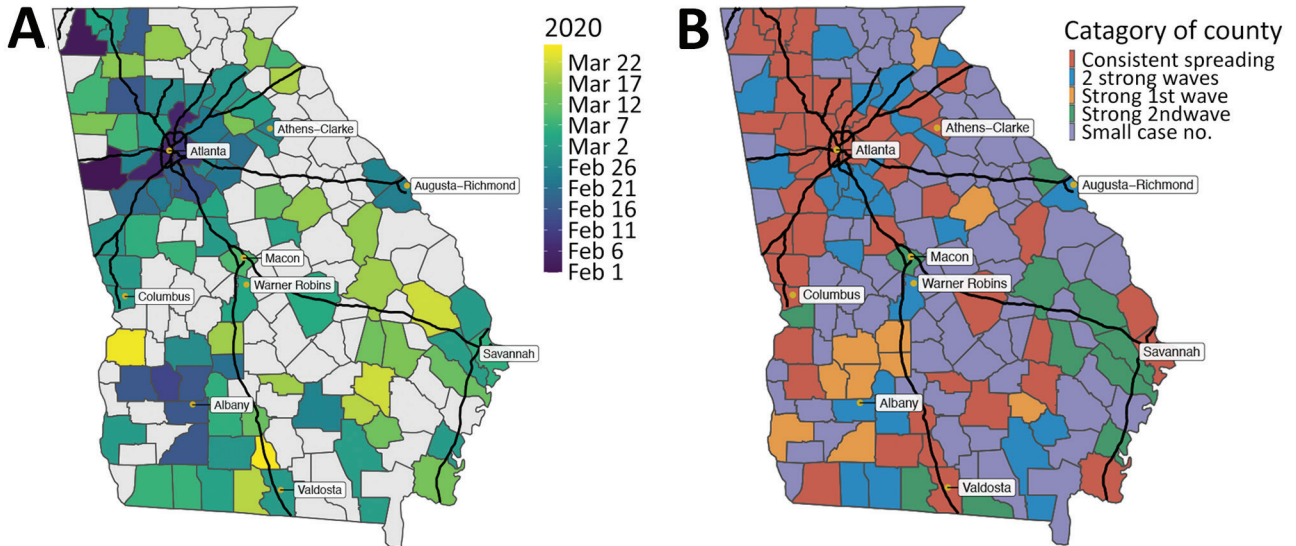
A primary case-patient who was male was more likely to transmit infection to a female contact than to a male contact. Female case-patients were infected by male case-patients across a wide range of ages (Figure 3, panel B), and male case-patients were mainly infected by young male case-patients (Figure 3, panel A). A possible explanation may be that female persons tend to be caregivers, taking care of sick persons in the household, and young male persons may be more likely to acquire infection outside the household.

Similar to the serial interval, transmission patterns also changed as the pandemic continued. The major contribution to spreading SARS-CoV-2 shifted over time to the younger generation. This shift could be caused by elderly persons becoming more careful to protect themselves from infection by taking measures such as staying at home, wearing face masks in public spaces, and observing good hand hygiene. At the same time, younger persons might have been less compliant with quarantine measures and more likely to attend indoor gatherings such as parties or to have visited bars, gyms, and clubs while not wearing face masks.

Previous pandemics, such as the 1918 influenza and the 2009 swine influenza (H1N1) pandemics,



**Figure 5.** Examples of the 5 categories of severe acute respiratory syndrome coronavirus 2 spreading patterns in counties in Georgia, USA, February–July 2020. Shown are epidemic curves from the start of the outbreak until July 13, 2020, and effective reproduction number ( $R_t$ ) estimates until June 15, in Gwinnett (A), Clayton (B), Sumter (C), Glynn (D), and Dawson (E) Counties. Tick marks indicate the first day of the month. The x-axis represents the date of symptom onset for patients with confirmed cases. The y-axis in the top plot shows the number of cases; the y-axis in the bottom plot shows the estimated median reproduction numbers. Error bars represent 2.5th–97.5th percentile ranges of  $R_t$ s. The gray area shows where  $R_t$  estimates were truncated on June 15.

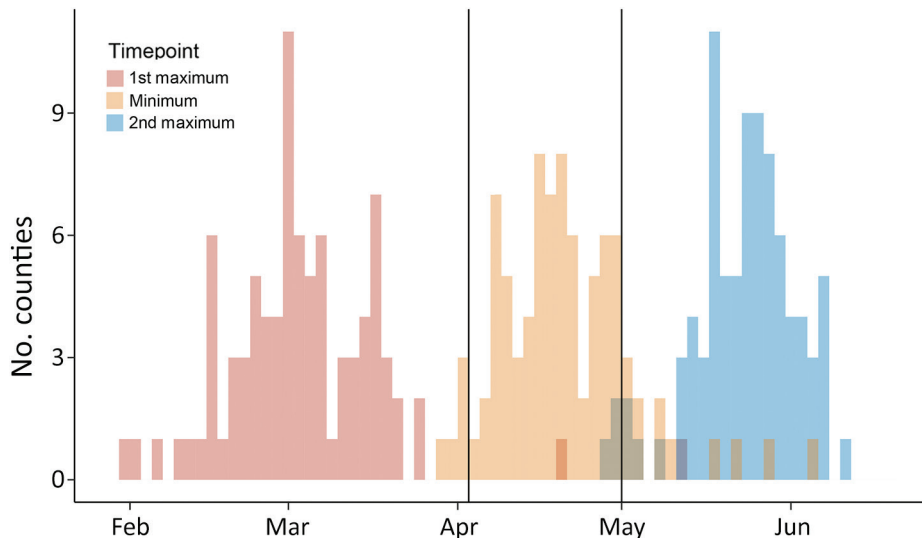


**Figure 6.** Spatial patterns of transmission of severe acute respiratory syndrome coronavirus 2 in Georgia, USA, February–July 2020. A) Date of reaching the peak (local maximum of effective reproduction number) for the first wave; B) spatial distribution of the 5 categories of virus transmission patterns by June 15, 2020. The black lines represent interstate highways.

caused multiple waves of infections (23). In Georgia, we have so far observed 2 waves of SARS-CoV-2 transmission separated by the shelter-in-place period. The COVID-19 cases of the first wave were first observed in Atlanta, the state capital with one of the busiest US airports, and Albany, the eighth largest city in Georgia. The outbreak in Albany resulted from 2 superspreading funeral events. However, the connectivity of these 2 cities differs: Atlanta is a transportation hub that connects multiple interstate highways, whereas Albany has no interstate highways. During the first wave, SARS-CoV-2 spread radially from both cities to the surrounding areas. For Atlanta, cases also started to appear along the interstate highways

(Figure 6, panel A). Concentrations of increased transmission along highways, as links connecting population centers, suggest that commuter links might have been effective transmission links.

During the shelter-in-place period (April 3–April 30), SARS-CoV-2 transmission slowed and  $R_s$  reached a local minimum in most counties. However, before reopening,  $R_s$  were still  $>1$  in many counties even at the local minimum, indicating continued disease spread (Figure 6, panel B). After reopening, transmission again increased across Georgia. These data suggest that the 3 or 4 weeks of shelter-in-place orders were not long enough to sufficiently suppress SARS-CoV-2 transmission (local and imported) in



**Figure 7.** Distributions of estimated dates of first maximum, minimum, and second maximum in effective reproduction numbers for severe acute respiratory syndrome coronavirus 2 transmission in 87 counties in Georgia, USA, with 200 cumulative cases by July 13, 2020, and dates of key events possibly driving virus transmission.



densely populated urban areas connected by major transportation links.

Thus far, the second wave has been heterogeneous in time and magnitude in different counties. Local prevalence was different at the time of reopening, and counties where prevalence was high (i.e., counties bordering cities and along interstate highways) experienced a stronger second wave. Counties not connected by major transportation links (e.g., around Albany) often also saw a second wave of COVID-19 but on a relatively small scale. Some counties that experienced an early and intense first wave (e.g., Lee, Sumter, Terrell, and Mitchell) did not experience a second wave. Possibly, inhabitants of those counties were more compliant with the prevention and control measures.

A limitation of our study is that although data were available for >100,000 cases, clinical information and contacts with a confirmed case-patient were missing on some records. Absence of clinical information may depend on several factors. For example, reporting rates tend to be lower and clinical information more frequently missing for case-patients with mild or no symptoms than for case-patients with severe symptoms. A subgroup analysis showed similar distributions of serial intervals for transmission pairs with complete clinical information and transmission pairs with missing clinical information. This finding lends credibility to the assumption that the absence of clinical information does not affect the overall serial interval.

Data on tracked pairs were not missing at random because contact tracing is voluntary and its capacity was limited during the early stages of the pandemic. Tracked pairs were more likely to be recorded when they involved known contacts. Identifying transmission links in public spaces or within clusters of cases remains challenging.

In this study, presymptomatic transmission leading to negative serial intervals was ignored because infectors could rarely be determined by exposure information or travel history. On the basis of the sensitivity analysis (Appendix Supplemental Material C), the influence of a small proportion of negative serial intervals on  $R_t$  estimates could safely be ignored.

When examining the time course of transmission of SARS-CoV-2 in Georgia, asymptomatic transmission was ignored. The observed numbers of case-patients thus underestimate the numbers of infected (infectious) persons, but this underestimation does not imply that  $R_t$  is underestimated by the same amount. Both the numbers of primary case-patients (transmitting infection) and the numbers of secondary

case-patients (acquiring infection) are underestimated, so the estimated rate of increase is likely to be less affected (24).

In conclusion, transmission of SARS-CoV-2 in Georgia changed over time during February–July 2020. The mean serial interval decreased from 5.97 days in February–April to 4.40 days in June–July. The younger population (20–50 years of age) was involved in most transmission events during or after reopening subsequent to the shelter-in-place period. By mid-July, 2 waves of SARS-CoV-2 transmission were apparent, separated by the shelter-in-place period in Georgia. Transmission was more intense in counties around major cities and along interstate highways. These transmission patterns can be used to help predict and guide states in COVID-19 prevention and control according to population and region.

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Y.W. and P.T. conceived the study and developed the methods. Y.W., C.S., Y.C., and C.A. conducted literature reviews. Y.W., C.S., and Y.C. produced the estimates and created figures and tables. Y.W. and P.T. wrote the first draft of the manuscript and led the writing of subsequent drafts. B.L., L.E., M.T., C.S., C.A., and M.L. provided critical feedback on the first draft and contributed to the writing of subsequent drafts of the manuscript. M.L. and B.L. acquired the funding for the research.

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# Severe Acute Respiratory Syndrome Coronavirus 2 Transmission in Georgia, USA, February 1–July 13, 2020

## Appendix

### Supplemental Material A. Imputation for Symptom Onset Dates

Among 118,497 confirmed cases between February 1–July 13, 2020, 48,893 (41.3%) cases had missing symptom onset dates. For each case, dates were also recorded when the first specimen was collected for testing and when the case was confirmed and reported. The delay of testing can be calculated as the difference between the date of first specimen collected and the date of symptom onset. And the delay of reporting can be calculated as the difference between the date of laboratory report and the date of symptom onset. Appendix Figure 2 (a) and (b) shows that the average delay of testing decreased gradually over time while the average delay of reporting was only stabilized after June 2020. We imputed the delay of testing (or the delay of reporting) using two negative binomial regression models with the date of first specimen collected or date of laboratory report as the predictor to account for decreasing trend of the delays. Missing symptom onset dates can be imputed based on the models and the date of first specimen collected (or date of laboratory report). Since the delay of testing was more stable compared to delay of reporting, the model with the date of first specimen collected as predictor was prioritized over the model with the date of laboratory report as predictor during the imputation. The procedure of imputation can be summarized as a flow chart (Appendix Figure 3). Appendix Figure 2 compares observed and imputed delays of testing and reporting.

To assess the impact of imputing large proportion of missing symptom onset on the  $R_t$  estimation results, we repeated the analysis omitting cases with missing symptom onset in Clayton, Glynn, and Sumter counties. Appendix Figures 4–6 show the comparison of  $R_t$  estimation with and without imputed symptom onsets.

## Supplemental Material B. Transmission Probability Matrix Method

Based on the transmission probability matrix method proposed by Teunis et al (*1*), we estimated probabilities of transmission between any pairs of case-patients in an outbreak. For an outbreak with  $n$  observed case-patients, a transmission probability matrix  $V_{n \times n}$  can be defined with any element  $v_{i,j}$  representing the probability that case-patient  $i$  was infected by case-patient  $j$ . When two cases are linked by their serial interval, the likelihood of transmission between these two case-patients can be calculated using the serial interval distribution as a kernel density (*1*). Additional information at an individual level (e.g., evidence of social contact between case-patients  $i$  and  $j$ ) is accounted for by a  $n \times n$  weighting matrix (*1*). The transmission probability matrix  $V$  can be estimated in a Markov chain Monte Carlo procedure (*1,2*).

When the transmission probability matrix is known, it can be used to calculate reproduction numbers. Elements of row  $i$  show the probabilities of case-patient  $i$  having received their infection from any other case-patient in the observed population. Rows of  $V$  must therefore add to 1. Likewise, elements of column  $j$  show the probabilities that case-patient  $j$  has transmitted their infection to any other case-patient in the observed population. Columns of  $V$  therefore add to an estimate of the number of cases infected by case-patient  $j$ : its reproduction number.

## Supplemental Material C. Sensitivity Analysis of Ignoring Negative Serial Intervals

Pre-symptomatic transmission resulting in negative serial intervals, is possible for COVID-19. Unlike the early outbreak studies in China (*3,4*), we could not use the travel history to identify potential exposure and infer the direction of transmission in our study at the state of Georgia. When the onset dates of the two cases in a pair were close, their order (who was infector, who was infectee) could not always be verified. Since the proportion of transmission pairs with negative serial interval was found to be small (*3,4*), we ignored negative serial intervals and assumed the person with earlier symptom onset was the infector. We conducted a sensitivity analysis to examine the impact of this assumption on the  $R_t$  estimates. Instead of arbitrarily assigning the subject with earlier symptom onset to be the infector, we can swap the infector and infectee for such pairs. As it seems implausible that such reversed order should

occur when the onset dates are several days apart, we only deal with small negative serial intervals: -3 – -1 days and a minor fraction (10%). Appendix Figure 7 shows the empirical and estimated cumulative density function (CDF) of serial interval distribution with and without negative interval. Although negative serial intervals would drastically change the transmission network (who infected whom), this would not necessarily influence the average reproduction number of infectious subjects. In an earlier publication by Wang and Teunis (2), we have established that negative serial intervals have only minor influence on reproduction number estimates. Appendix Figures 8–10 show comparisons of  $R_t$  for three counties (Clayton, Glynn, Sumter): ignoring negative serial intervals did not impact the estimation of  $R_t$ .

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**Appendix Table 1.** COVID-19 pandemic situation and state government responses\*

Date	Situation and Response
January 20, 2020	First COVID-19 case reported in the United States.
March 2, 2020	First COVID-19 case reported in the state of Georgia.
March 14, 2020	Georgia governor declared a public health emergency.
March 23, 2020	Large gatherings were banned and shelter-in-place order was issued for “medically fragile” population.
March 24, 2020	Bars and clubs were ordered to close.
April 1, 2020	All K–12 schools were closed.
April 3, 2020	Statewide shelter-in-place order was issued.
April 24, 2020	Some businesses (gyms, fitness centers, bowling alleys, body art studios, barbers, cosmetologists, hair designers, nail care artists, estheticians, their respective schools, and massage therapists) were allowed to reopen with minimum basic operations.
April 27, 2020	More businesses (theaters, private social clubs, and restaurant dine-in services) were allowed to reopen with social distancing and sanitation mandates.
April 30, 2020	Reopening: Statewide shelter-in-place order was lifted.
June 1, 2020	Further Reopening: Limits on the size of public gathering were relaxed: bars and nightclubs were allowed to reopen, sports events could resume, and summer schools and camps were allowed to begin sessions.

\*Executive orders from Georgia governor available at <https://gov.georgia.gov/executive-action/executive-orders/2020-executive-orders>.

**Appendix Table 2.** Data of available information about demographics, epidemiological timelines, clinical outcomes, and contact tracing

Variable	Description	Value
<b>Demographics</b>		
UID	Unique identifier (UID) associated with patient	patient UID
Age	Patient’s age	Positive Integer
Sex	Patient’s sex	Male; Female
Race	Patient’s race	Black; White; Other
County	County of residence	159 counties in Georgia
<b>Epidemiological Time lines</b>		
Reported date	Date of first report to public health	Date
Symptom onset	Date of symptom onset	Date
Date of sample collection	Date of first specimen collection	Date
<b>Clinical Outcomes</b>		
Hospitalized	Hospitalization of patient during illness	Yes; No
Ventilator	Patient received intubation or mechanical ventilation during hospitalization	Yes; No
Abnormal Chest X-ray	Patient had an abnormal chest X-ray	Yes; No
Death	Death occurred as a result of COVID-19 infection and was reported to public health	Yes; No
Fever	Fever of a >100.4 recorded by patient or medical provider	Yes; No
Cough	Cough (new onset or worsening of chronic cough)	Yes; No
Short of Breath	Shortness of breath (dyspnea)	Yes; No
Diarrhea	Diarrhea ( $\geq 3$ loose/looser stools in 24 hours period)	Yes; No
<b>Contact Tracing</b>		
Close Contact	Unique identifier of confirmed COVID-19 case to which patient was exposed	Patient UID
Outbreak	Is this case part of an outbreak?	Yes; No
Outbreak ID	If this is part of an outbreak, outbreak ID?	Outbreak ID

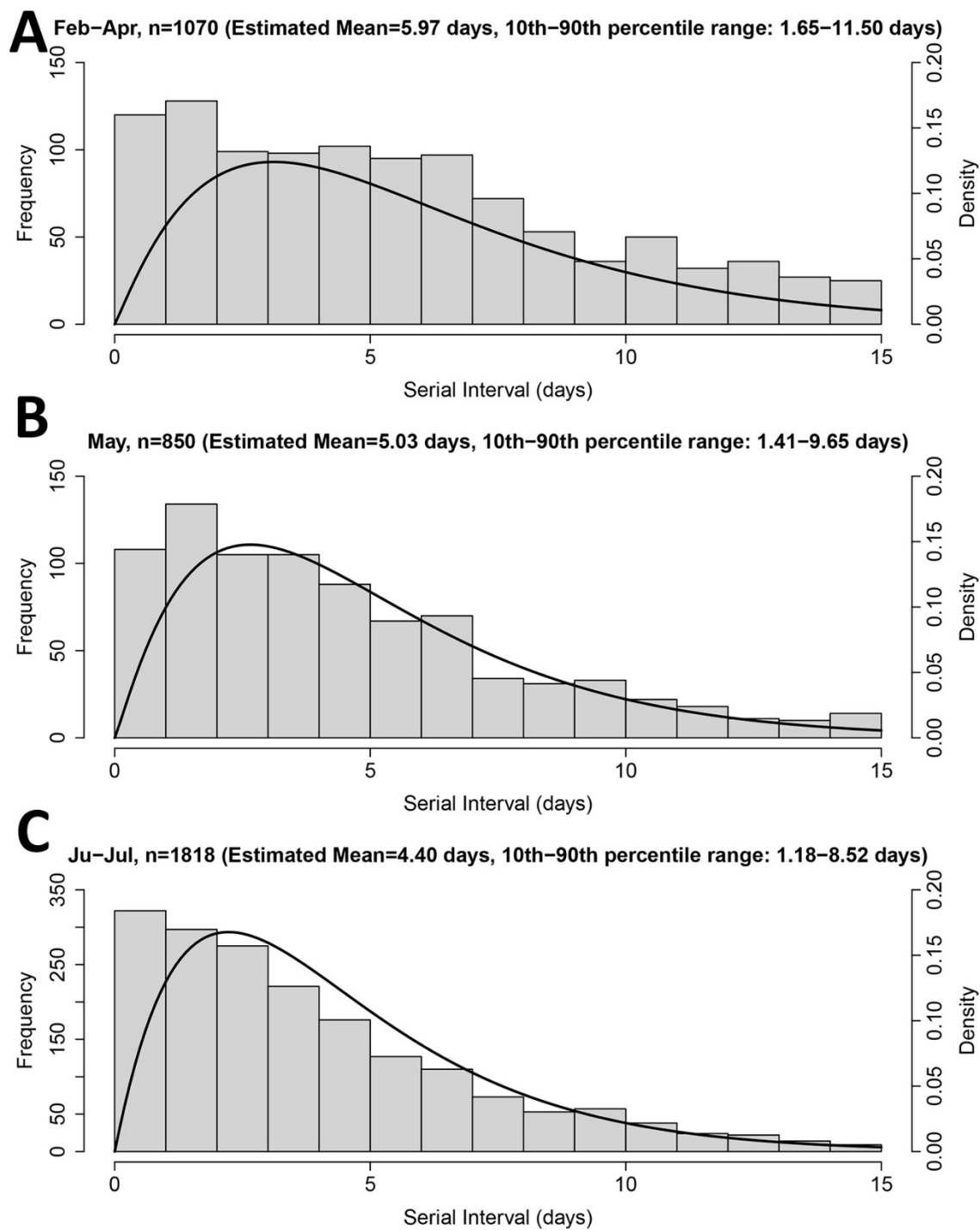
**Appendix Table 3.** Clinical outcomes and demographic information for 4080 tracked pairs of primary case-patients and secondary case-patients.

Variable	Primary Case-patient		Secondary Case-patient	
	Yes (%)	No (%)	Yes (%)	No (%)
Clinical Outcomes				
Hospitalized	737 (18.1)	3,232 (79.2)	504 (12.4)	3,486 (85.4)
Ventilator Use	121 (3.0)	3,139 (76.9)	92 (2.3)	3,246 (79.6)
Abnormal Chest X-ray	370 (9.1)	2,697 (66.1)	216 (5.3)	2,909 (71.3)
Death	154 (3.8)	3,436 (84.2)	99 (2.4)	3,552 (87.1)
Fever	2,056 (50.4)	1,723 (42.2)	1,654 (40.5)	2,141 (52.5)
Cough	2,662 (65.2)	1,197 (29.3)	2,283 (56)	1,569 (38.5)
Short of Breath	1,438 (35.2)	2,323 (56.9)	1,129 (27.7)	2,640 (64.7)
Diarrhea	1,093 (26.8)	2,565 (62.9)	916 (22.5)	2,792 (68.4)
Demographics				
Sex	Male (%)	Female (%)	Male (%)	Female (%)
	1,851 (45.4)	2,220 (54.4)	1,707 (41.8)	2,352 (57.6)
Race	White (%)	Black (%)	White (%)	Black (%)
	1,959 (48.0)	1,273 (31.2)	1,978 (48.5)	1,247 (30.6)
Age	Mean	SD	Mean	SD
	42.7	18.3	40.8	20.4

**Appendix Table 4.** Serial interval by subgroup with different clinical characteristics and demographic characteristics.

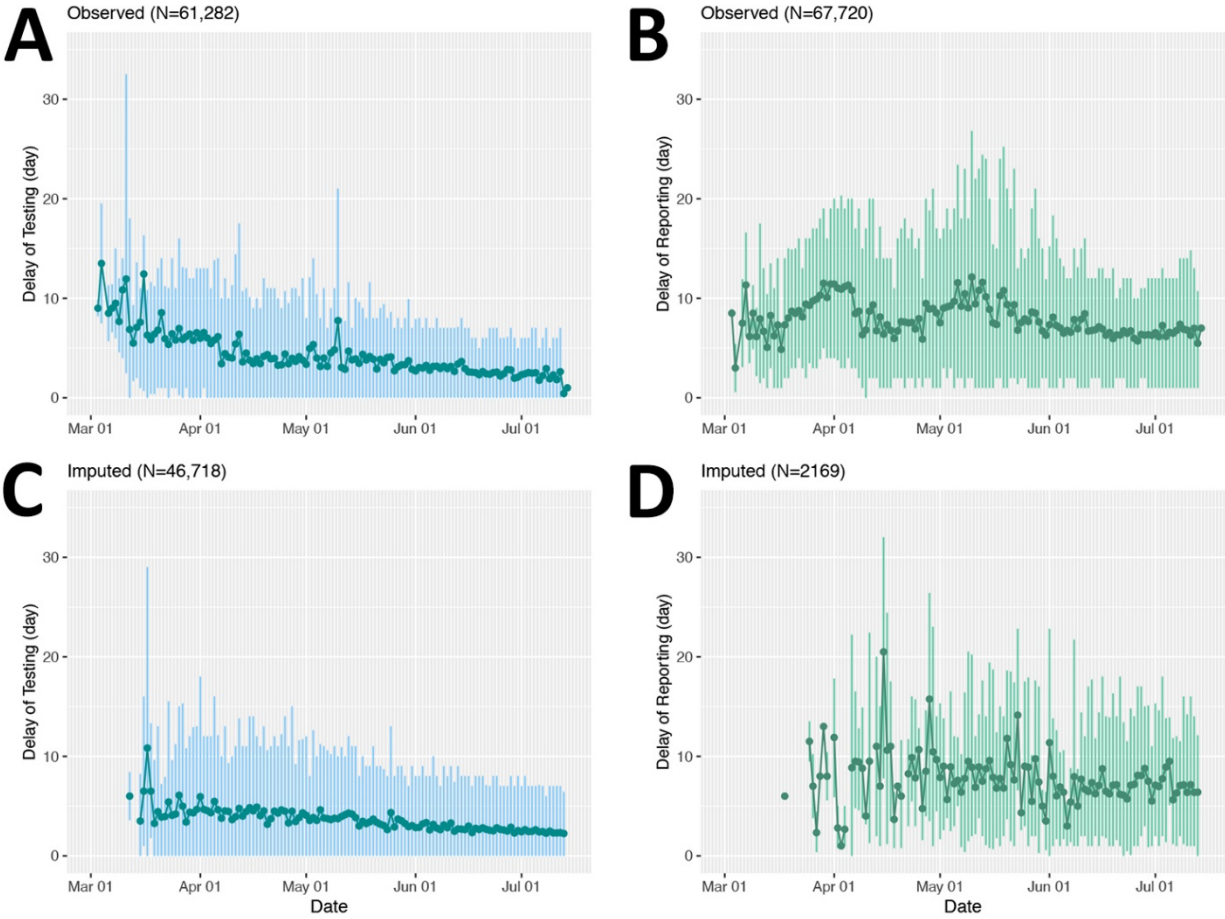
Subgroup	n	Mean (day)	10th–90th Percentile Range (day)	Shape	Scale
Clinical Outcome					
Hospitalized+	650	5.69	1.55–11.00	2.05	2.77
Hospitalized-	2,986	4.84	1.29–9.41	2.00	2.42
Ventilator+	106	6.28	1.83–11.93	2.21	2.84
Ventilator-	2,877	4.93	1.32–9.57	2.02	2.44
Abnormal Chest X-ray+	307	6.13	1.80–11.64	2.22	2.76
Abnormal Chest X-ray-	2,492	4.84	1.31–9.36	2.04	2.37
Death+	133	5.91	1.61–11.42	2.06	2.87
Death-	3,153	4.95	1.34–9.60	2.03	2.44
Fever+	1,889	5.12	1.40–9.88	2.06	2.48
Fever-	1,575	4.87	1.26–9.55	1.94	2.51
Cough+	2,435	5.09	1.38–9.85	2.05	2.49
Cough-	1,096	4.79	1.22–9.42	1.92	2.50
Short of Breath+	1,302	5.25	1.44–10.12	2.07	2.54
Short of Breath-	2,140	4.81	1.26–9.38	1.98	2.43
Diarrhea+	993	5.22	1.31–10.30	1.88	2.77
Diarrhea-	2,349	4.87	1.32–9.41	2.05	2.37
Age					
20-	412	4.10	1.07–8.00	1.96	2.09
20–40	1,369	4.78	1.30–9.24	2.05	2.33
40–60	1,330	5.29	1.44–10.23	2.05	2.58
60+	618	5.47	1.45–10.66	1.99	2.75
Sex					
Male	1,720	4.85	1.26–9.47	1.96	2.47
Female	2,009	5.11	1.39–9.89	2.05	2.50
Race					
Black	1,147	5.39	1.46–10.43	2.04	2.64
White	1,790	4.73	1.22–9.25	1.95	2.43
Other	801	4.99	1.32–9.69	2.00	2.49
Resident Area					
Metro Atlanta	839	4.88	1.33–9.43	2.06	2.37
Out of Metro Atlanta	2,899	5.02	1.33–9.78	1.99	2.53
Time Period					
Feb–Apr	1,070	5.97	1.65–11.50	2.09	2.86
May	850	5.03	1.41–9.65	2.11	2.38
Jun–Jul	1,818	4.40	1.18–8.52	2.03	2.17
Total	3,738	4.99	1.33–9.71	2.00	2.49

Subgroups were defined based on the primary case-patient characteristics. Characteristics variables were defined in Appendix Table 2. For clinical characteristics, “+” represents yes and “-” represents. The shape and scale parameters of gamma distributions were estimated using maximum likelihood estimator.

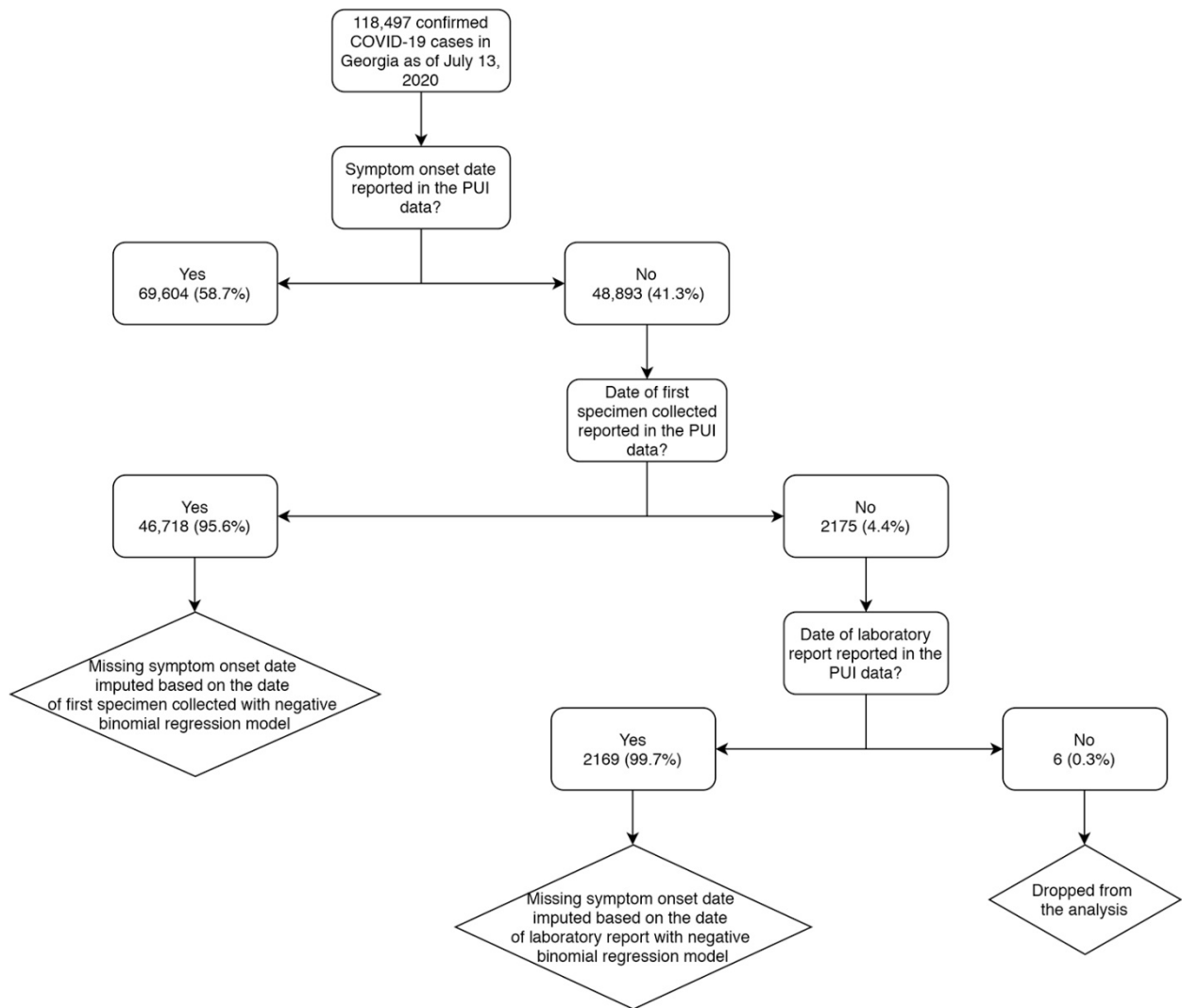


**Appendix Figure 1.** The observed (histograms) and estimated (density plot) distribution of the serial interval during three time periods: Early transmission and shelter-in-place (Feb–Apr); after reopening (May); further reopening (Jun–Jul).

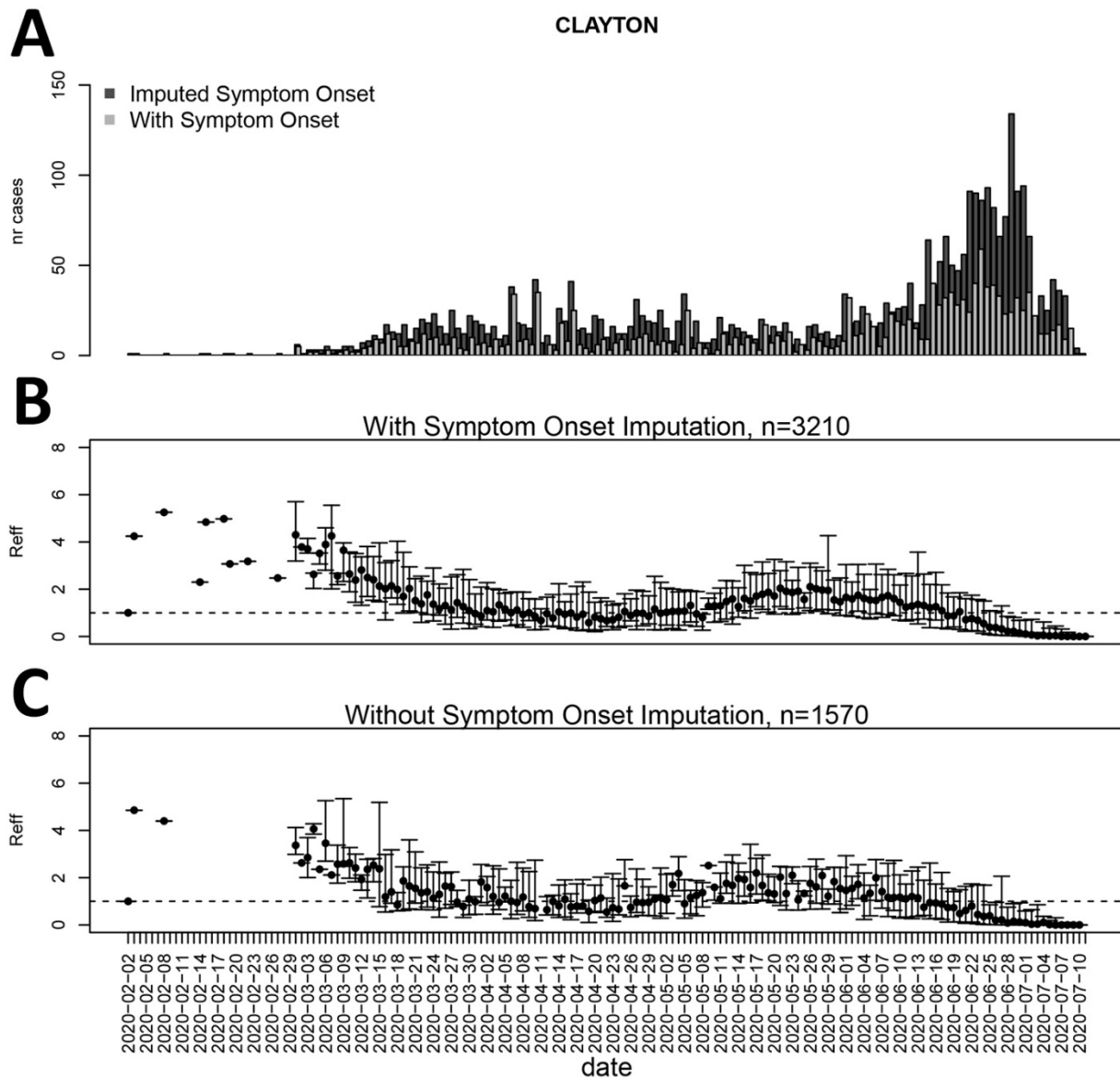




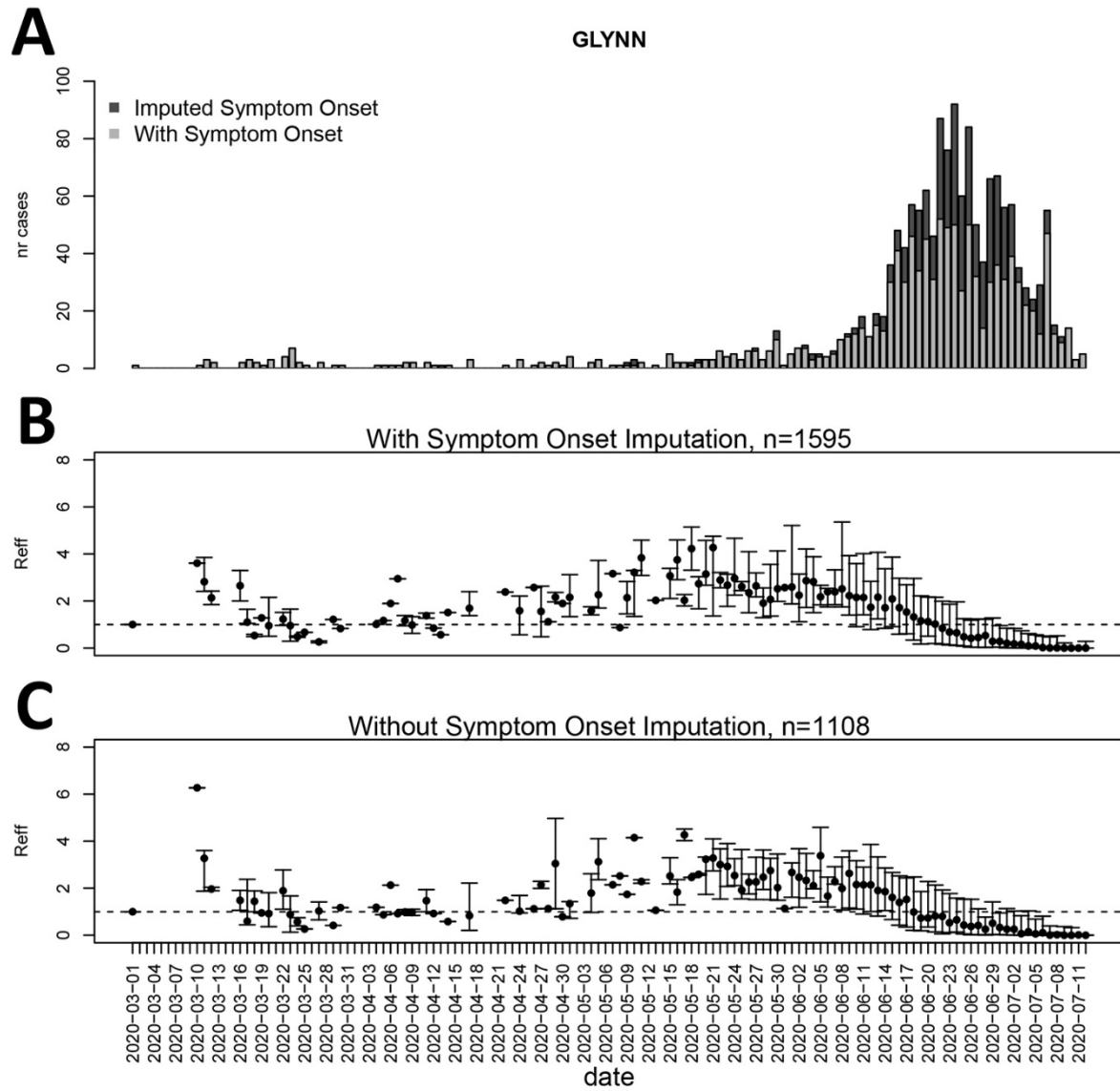
**Appendix Figure 2.** The observed (a) and imputed (c) delay between the date of first specimen collection and the date of symptom onset, and the observed (b) and imputed (d) delay between the date of laboratory report and the date of symptom onset between March 1–July 13, 2020. The solid lines represent the mean delay and the error bars represent the 10th and 90th percentile range.



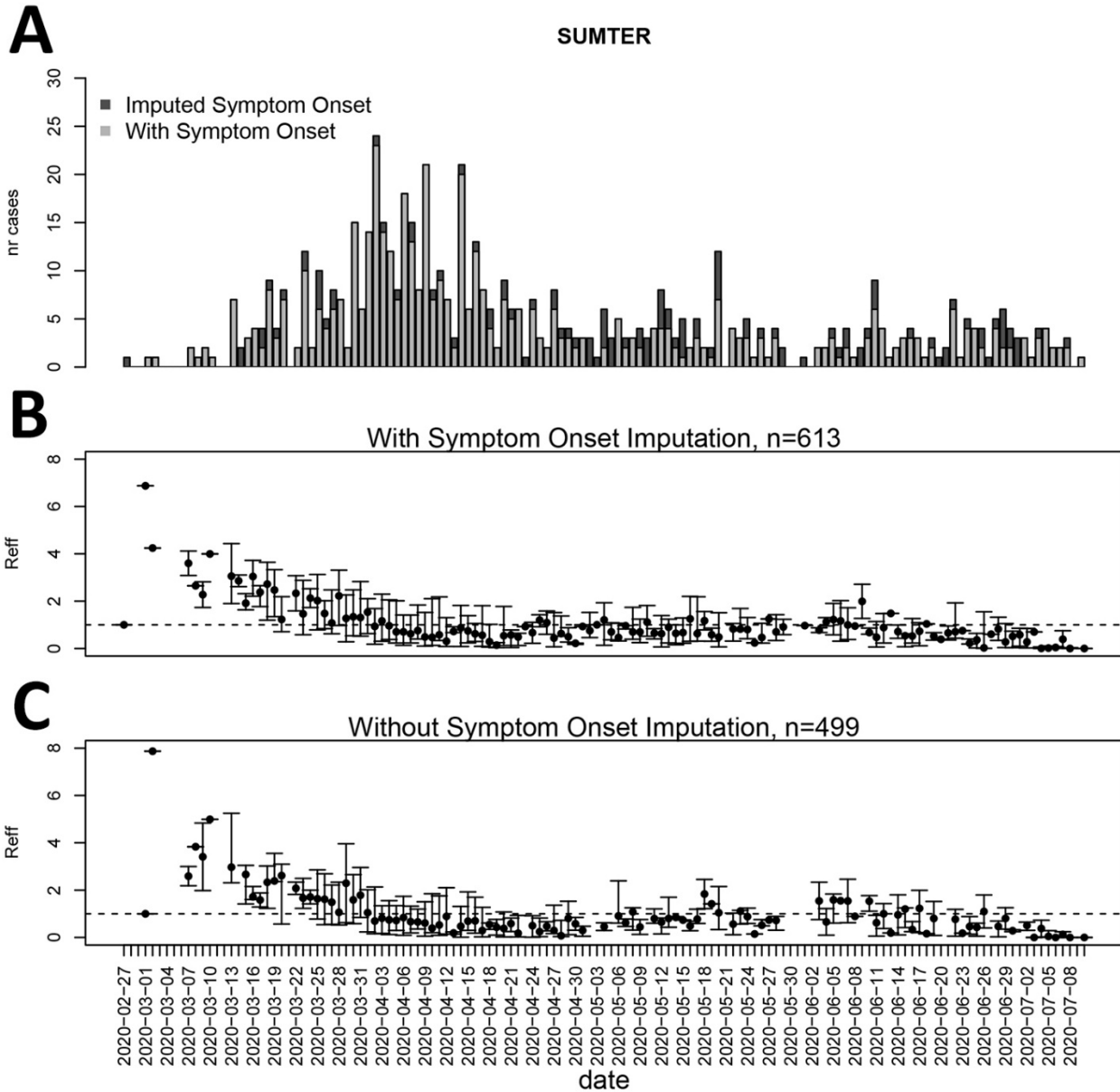
**Appendix Figure 3.** The flow chart of the imputation procedure for missing symptom onset dates.



**Appendix Figure 4.** Epidemic curves and corresponding reproduction number estimates with and without imputed missing symptom onset until July 13th in Clayton county.

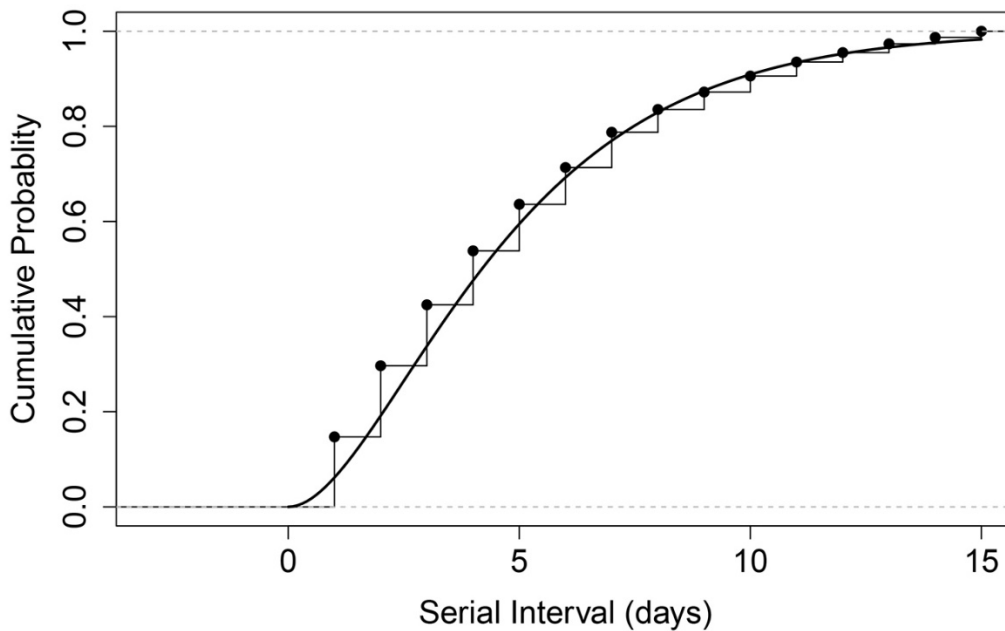


**Appendix Figure 5.** Epidemic curves and corresponding reproduction number estimates with and without imputed missing symptom onset until July 13th in Glynn county.

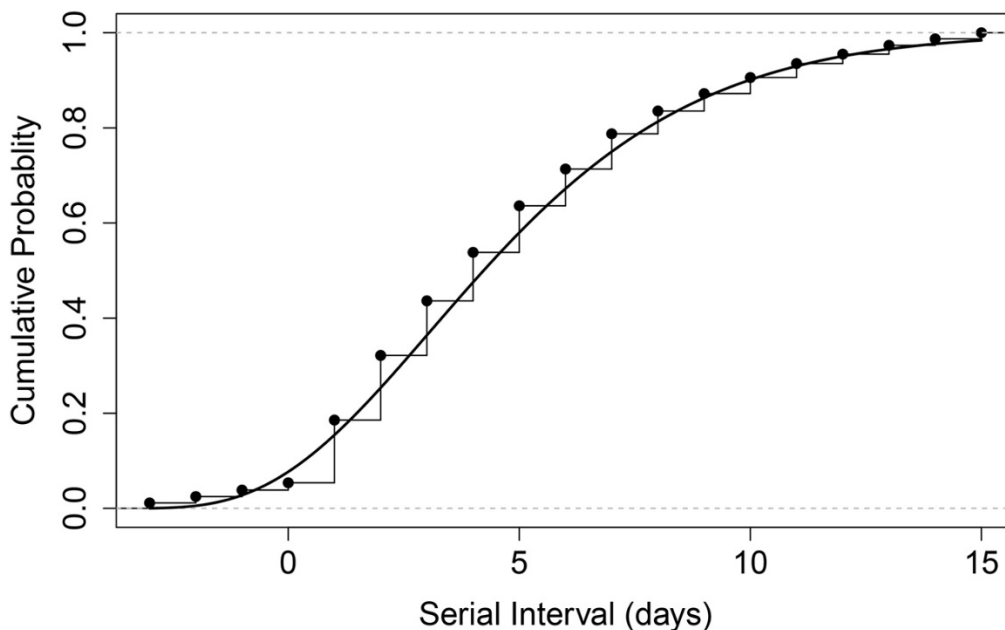


**Appendix Figure 6.** Epidemic curves and corresponding reproduction number estimates with and without imputed missing symptom onset until July 13th in Sumter county.

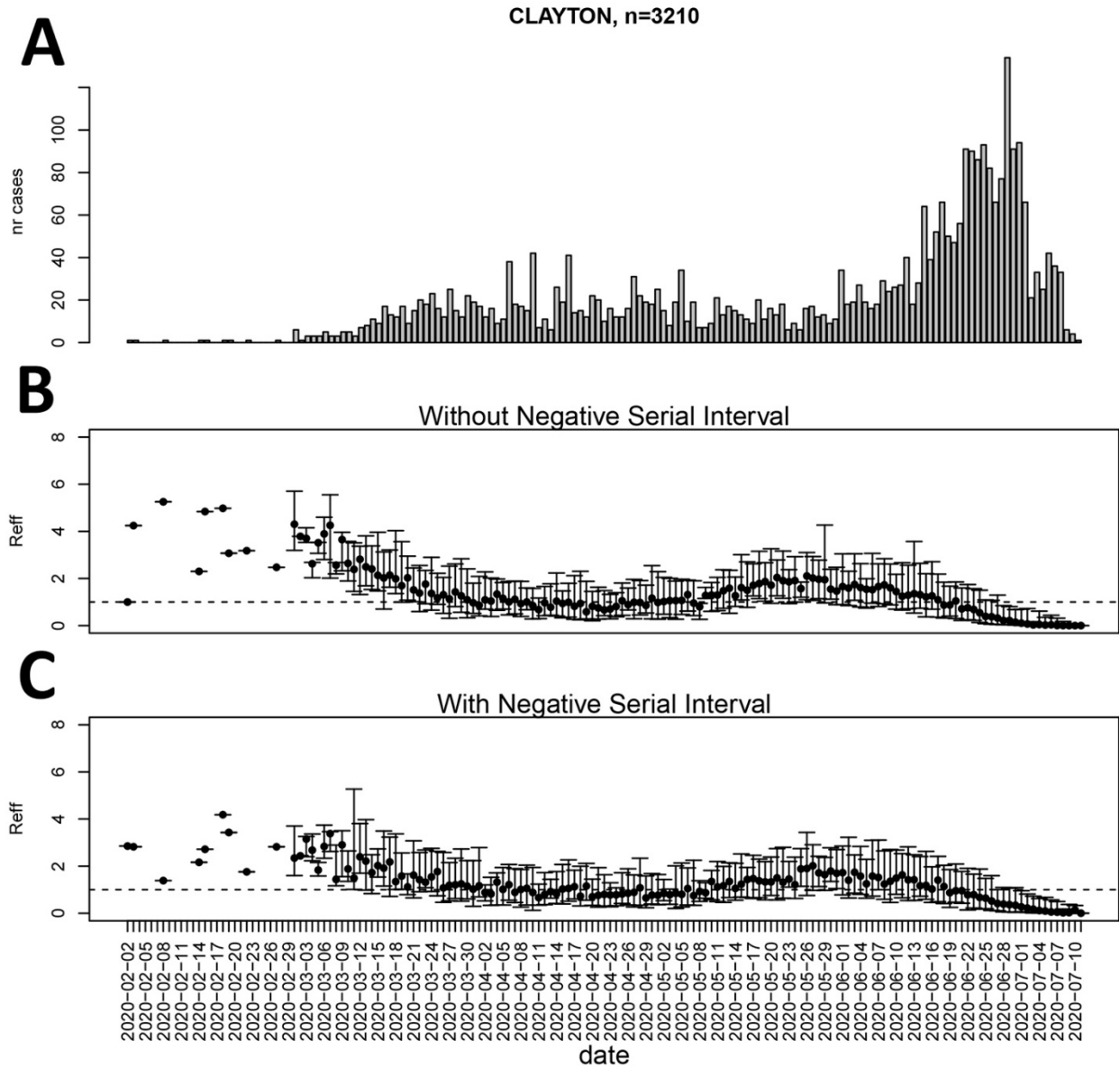
**A** Without Negative Serial Intervals  
(Estimated Mean: 4.99 days, 10th–90th percentile range: 1.32–9.71 days)



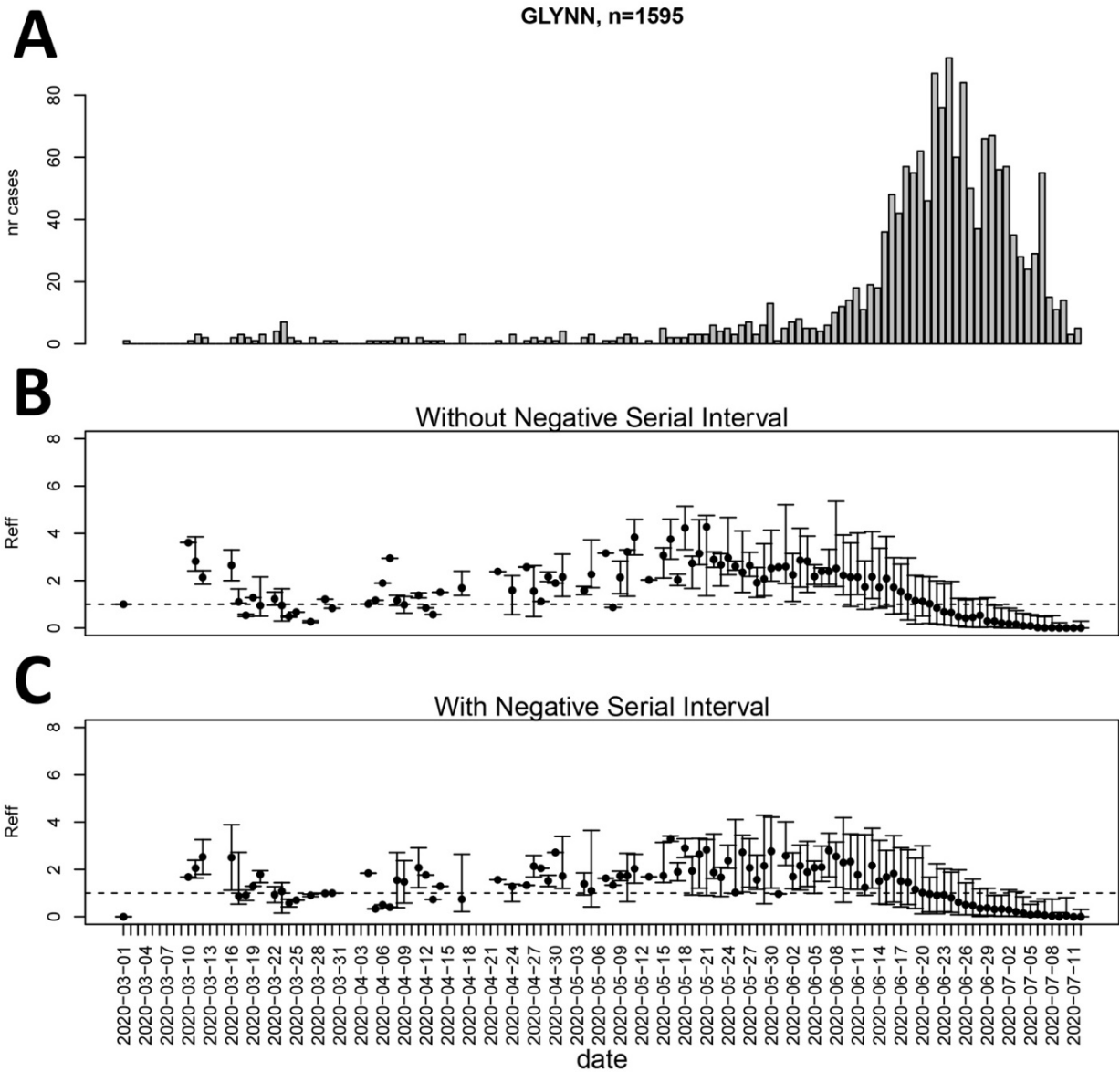
**B** With Negative Serial Intervals  
(Estimated Mean: 4.79 days, 10th–90th percentile range: 0.34–9.97 days)



**Appendix Figure 7.** The empirical cumulative distribution and estimated cumulative distribution of the serial interval ignoring negative serial intervals (top) and considering a proportion (10%) of negative serial intervals.

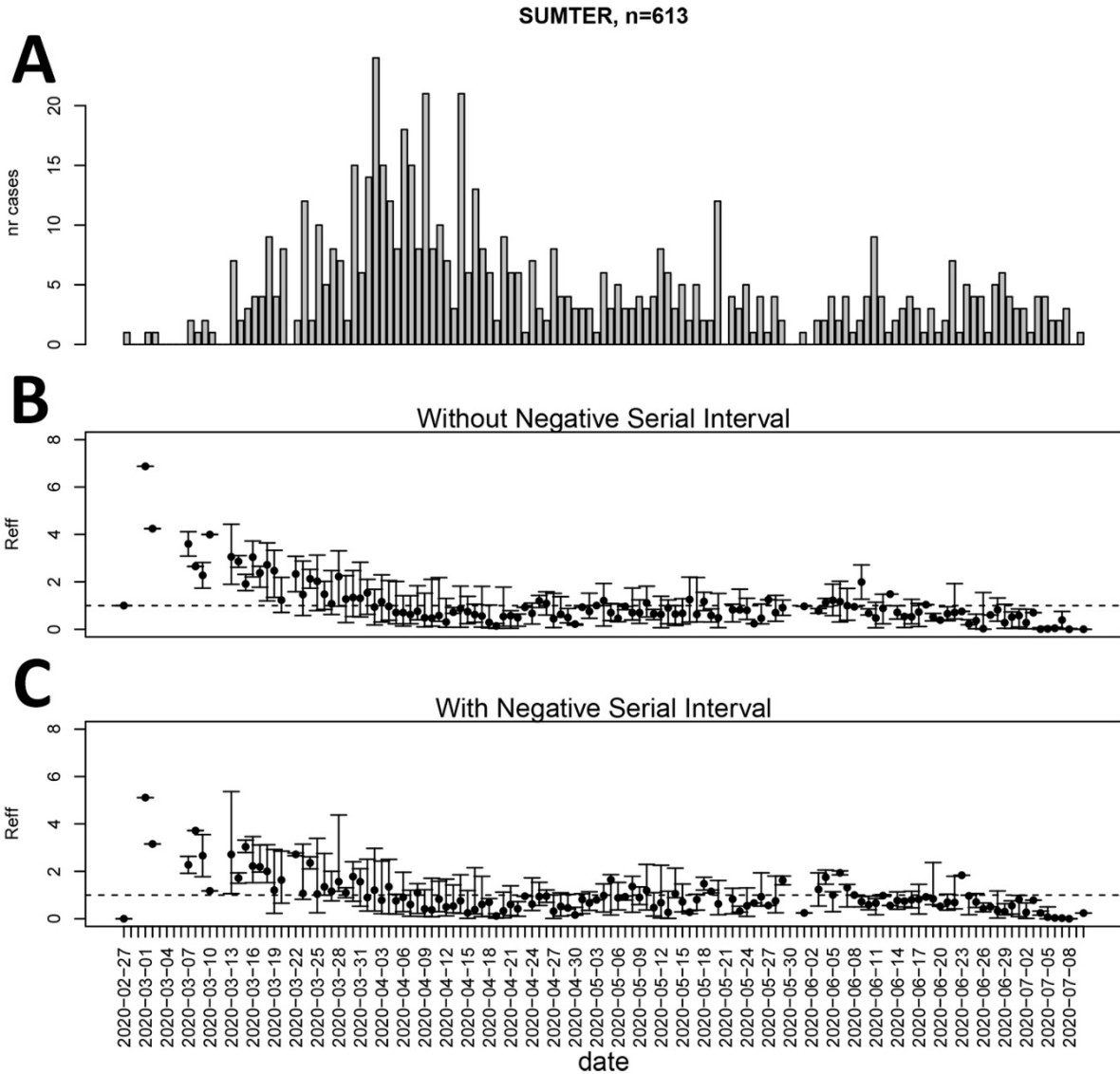


**Appendix Figure 8.** Epidemic curves and corresponding reproduction number estimates with and without considering negative serial intervals until July 13th in Clayton county.



**Appendix Figure 9.** Epidemic curves and corresponding reproduction number estimates with and without considering negative serial intervals until July 13th in Glynn county.

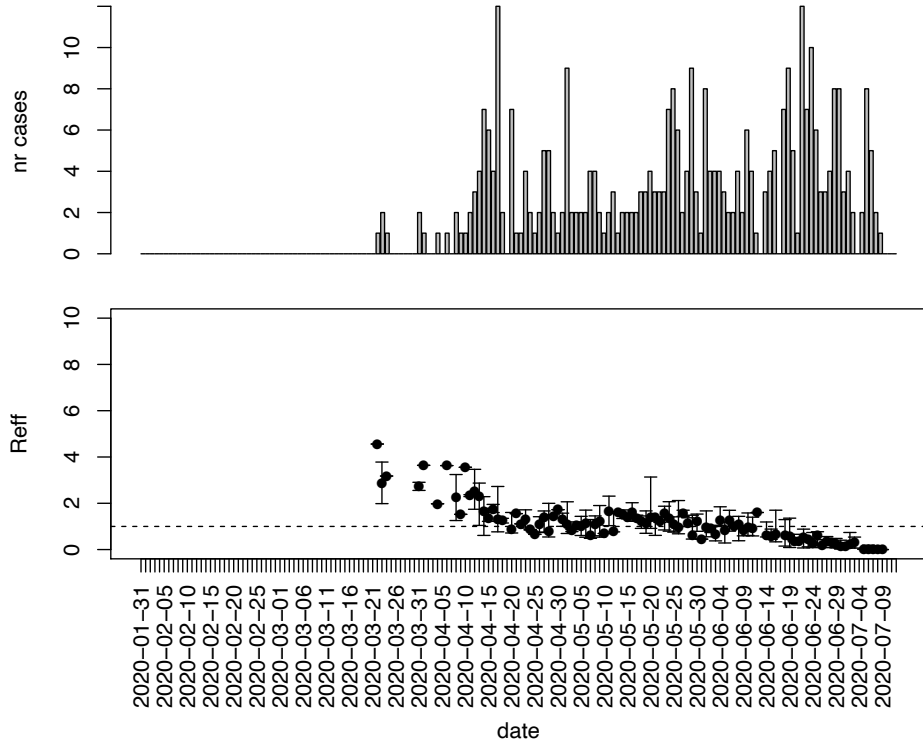




**Appendix Figure 10.** Epidemic curves and corresponding reproduction number estimates with and without considering negative serial intervals until July 13th in Sumter county.

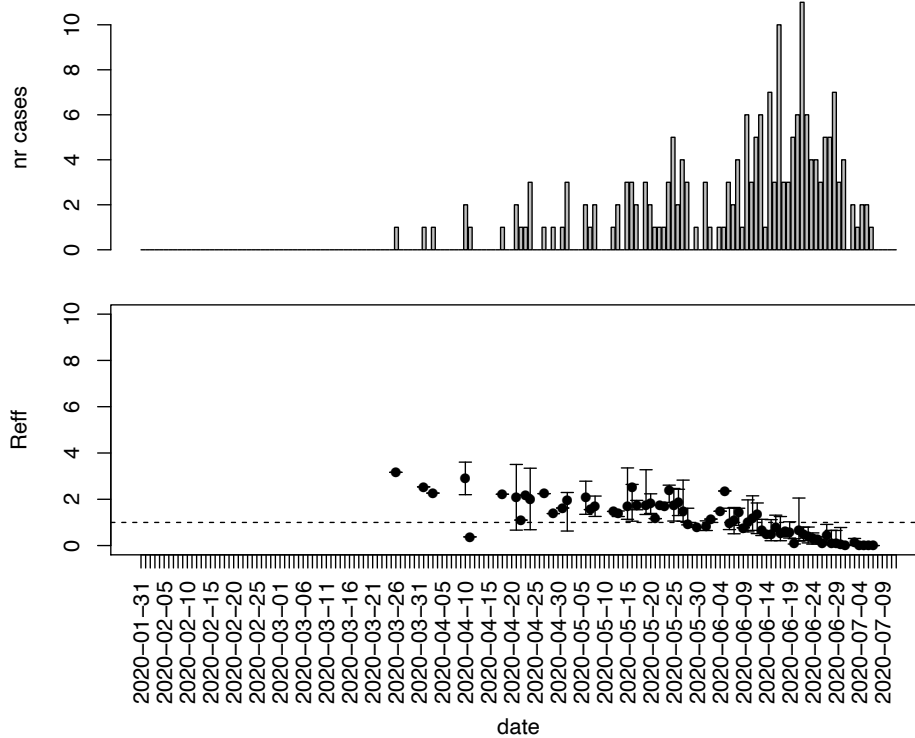
**Appendix Figures 11–169** (following pages). Epidemic curves and reproduction number estimates until July 13th for all counties in Georgia.

APPLING, n=353

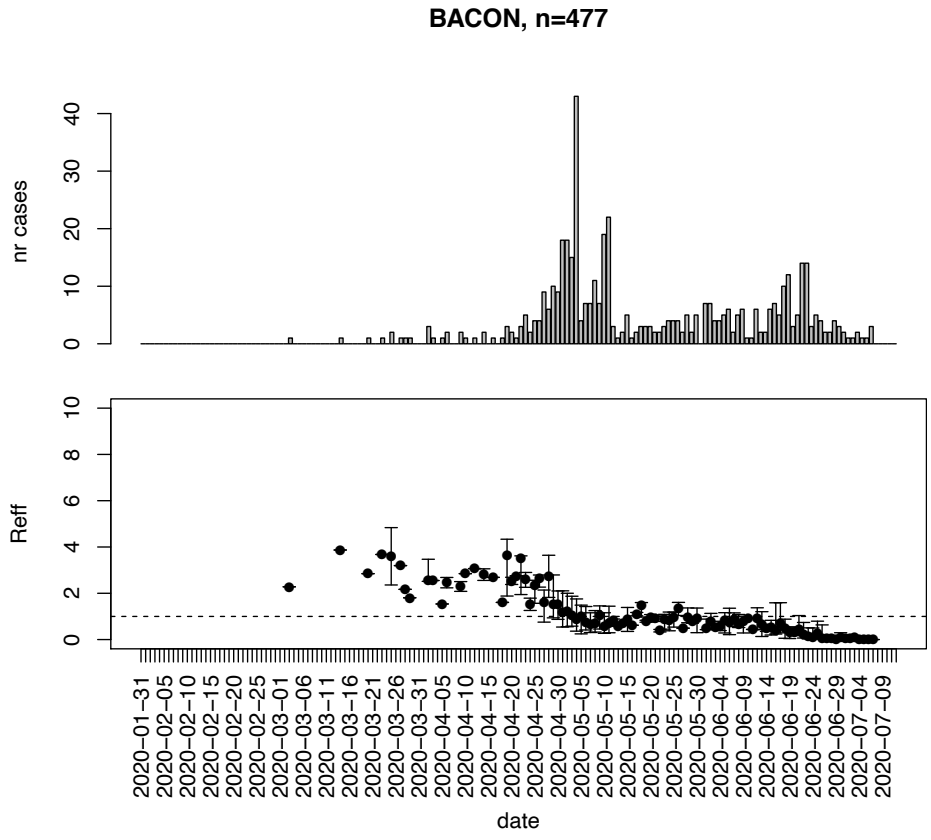


Appendix Figure 11. Epidemic curves and reproduction number estimates until July 13th in Appling county.

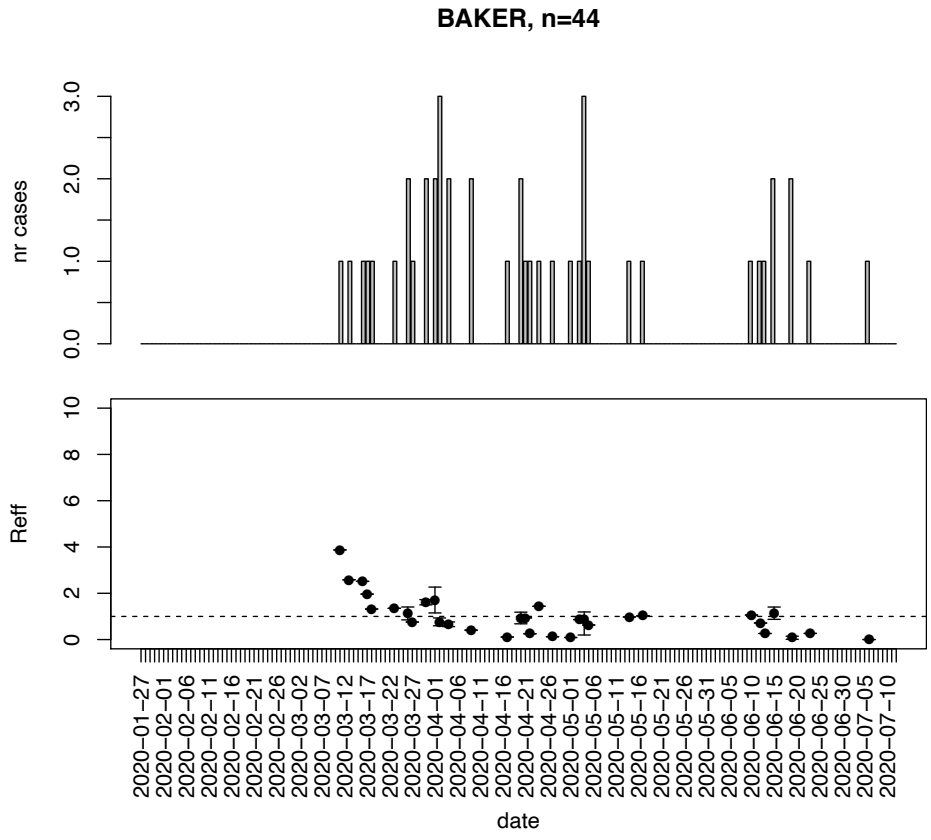
ATKINSON, n=196



Appendix Figure 12. Epidemic curves and reproduction number estimates until July 13th in Atkinson county.

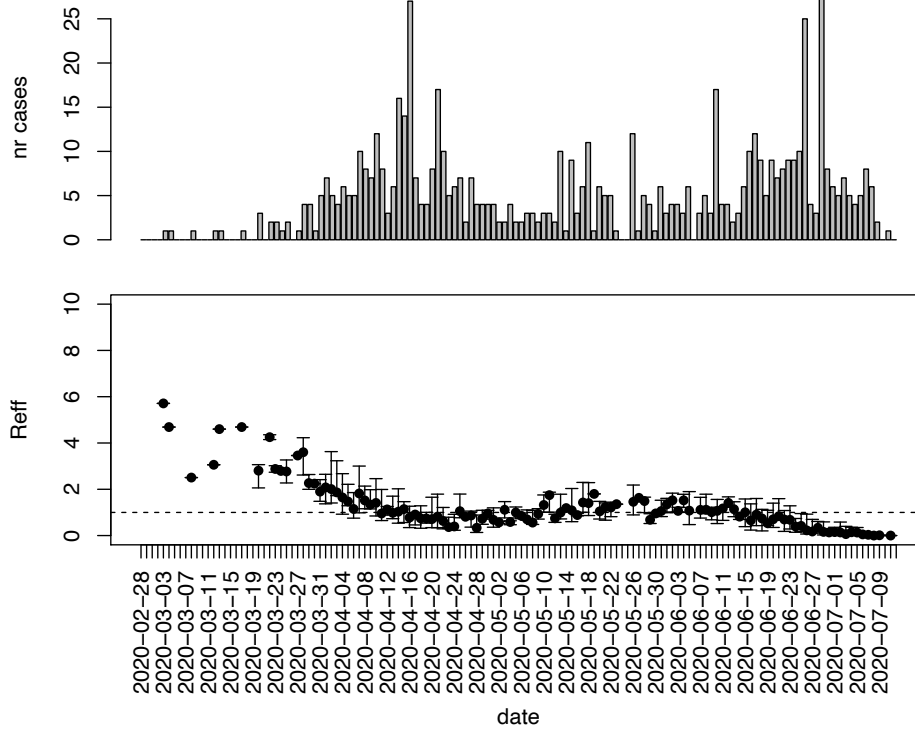


Appendix Figure 13. Epidemic curves and reproduction number estimates until July 13th in Bacon county.

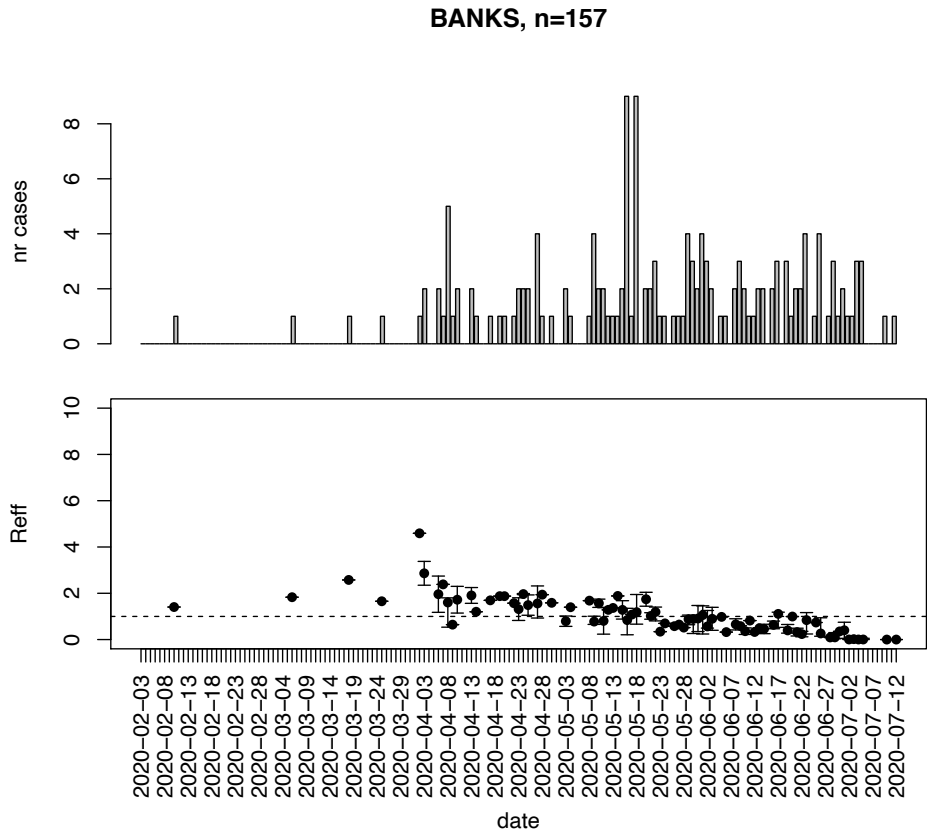


Appendix Figure 14. Epidemic curves and reproduction number estimates until July 13th in Baker county.

**BALDWIN, n=654**

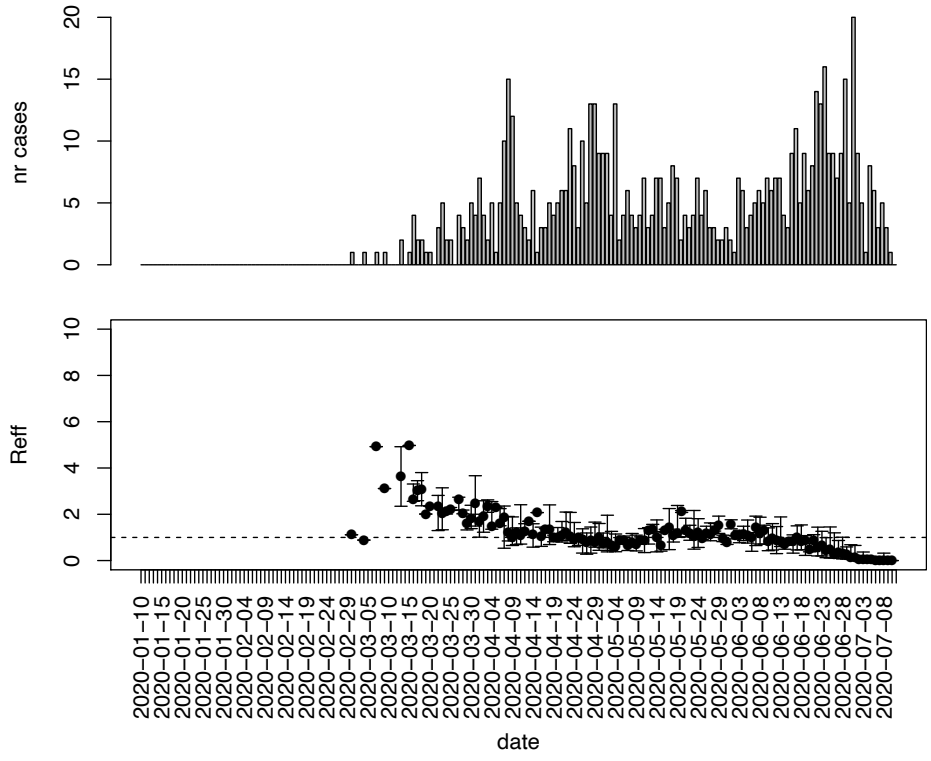


Appendix Figure 15. Epidemic curves and reproduction number estimates until July 13th in Baldwin county.



Appendix Figure 16. Epidemic curves and reproduction number estimates until July 13th in Banks county.

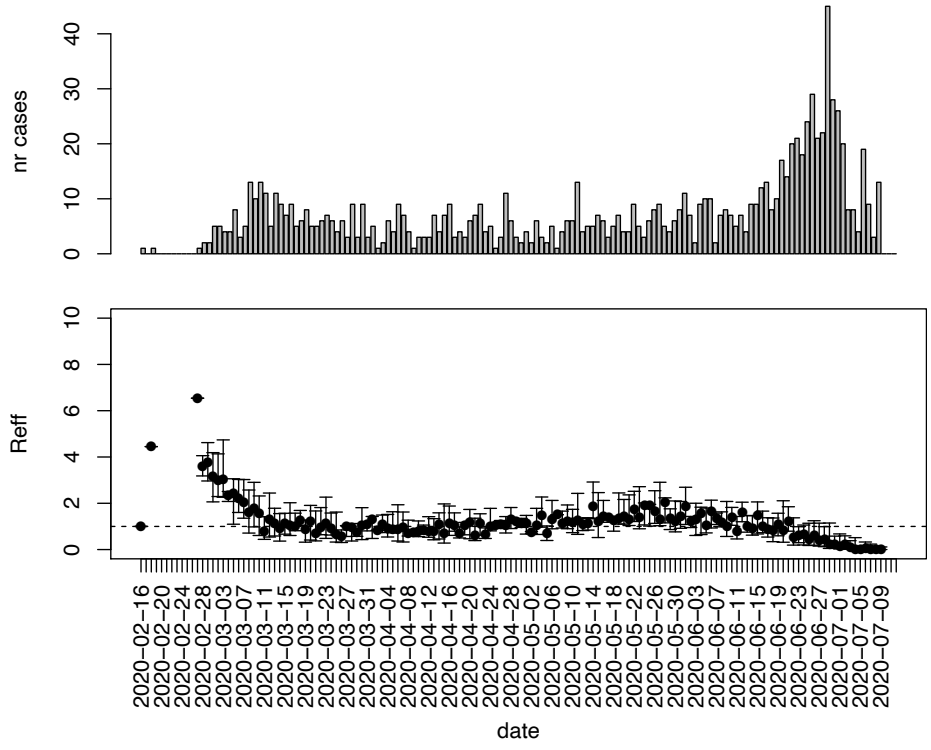
**BARROW, n=664**



Appendix Figure 17. Epidemic curves and reproduction number estimates until July 13th in Barrow county.

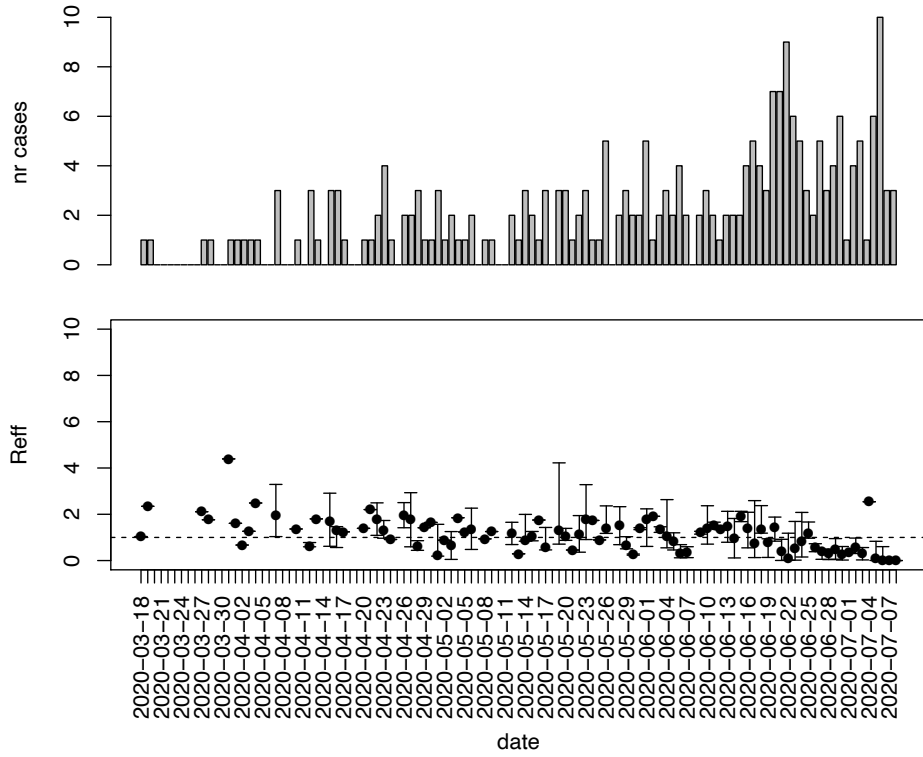


**BARTOW, n=1040**



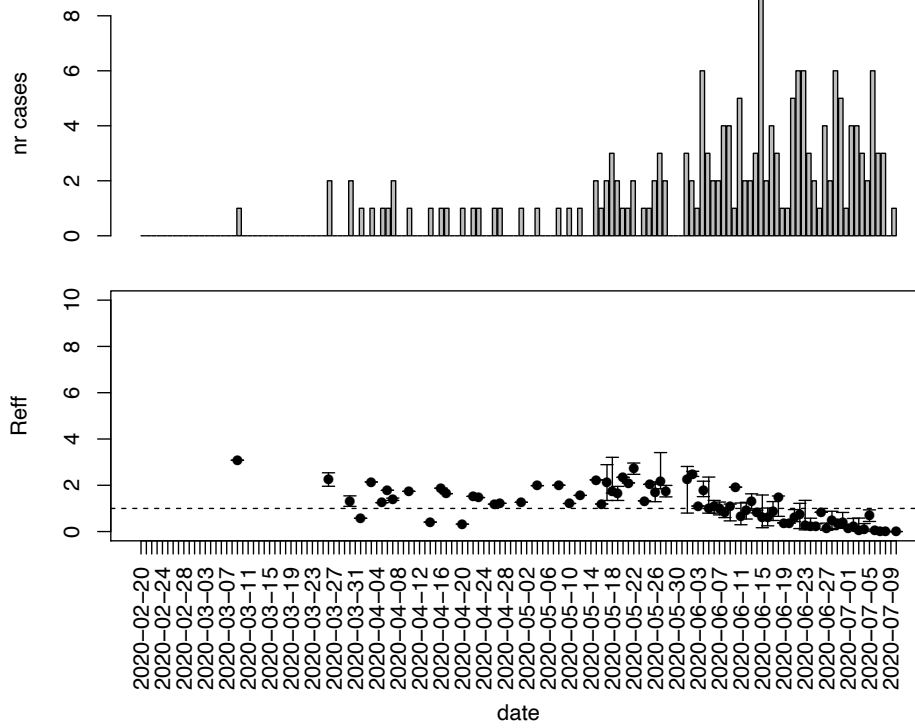
Appendix Figure 18. Epidemic curves and reproduction number estimates until July 13th in Bartow county.

**BEN HILL, n=233**



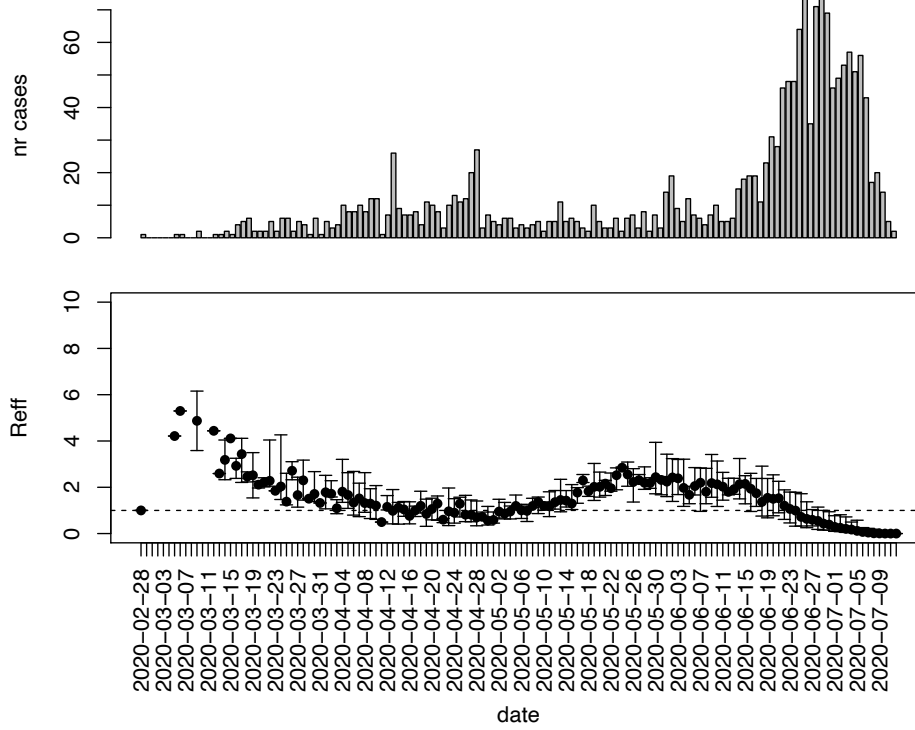
Appendix Figure 19. Epidemic curves and reproduction number estimates until July 13th in Ben Hill county.

**BERRIEN, n=175**



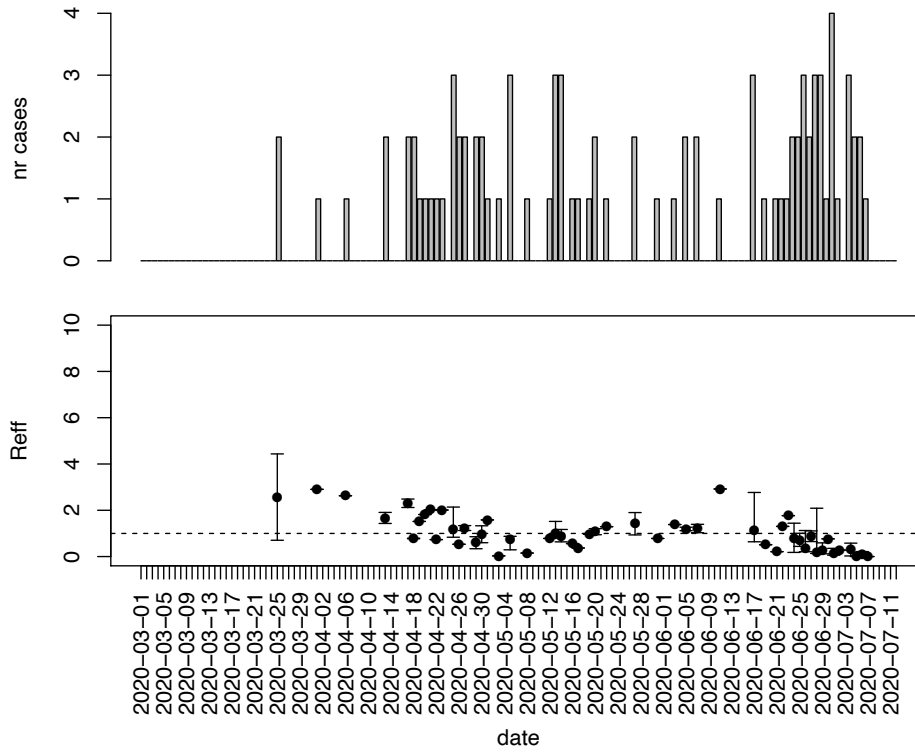
Appendix Figure 20. Epidemic curves and reproduction number estimates until July 13th in Berrien county.

**BIBB, n=1719**



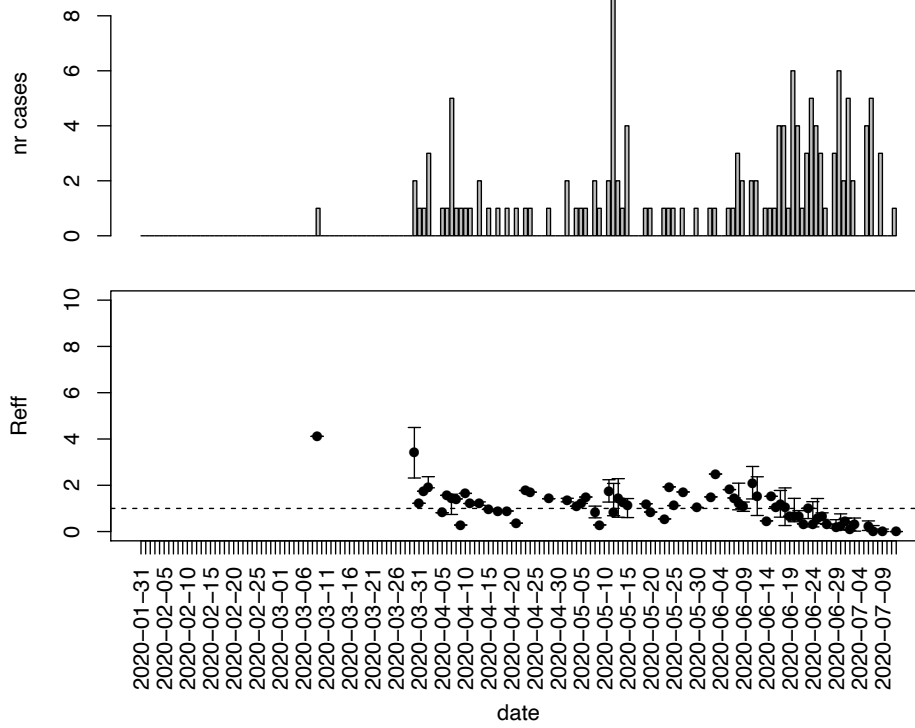
Appendix Figure 21. Epidemic curves and reproduction number estimates until July 13th in Bibb county.

**BLECKLEY, n=90**



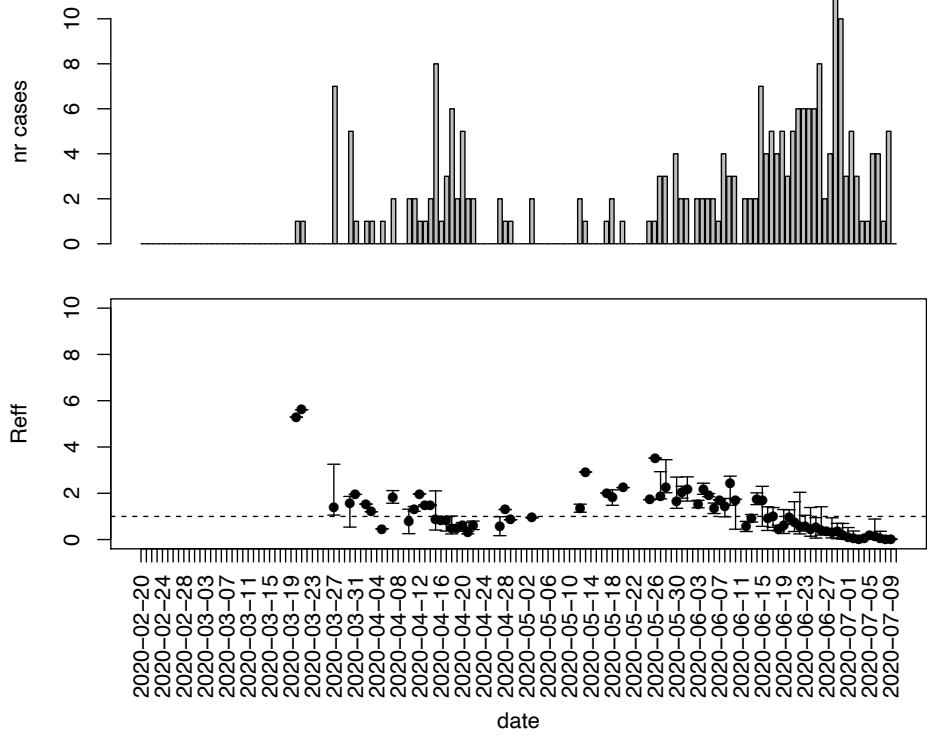
Appendix Figure 22. Epidemic curves and reproduction number estimates until July 13th in Bleckley county.

**BRANTLEY, n=144**



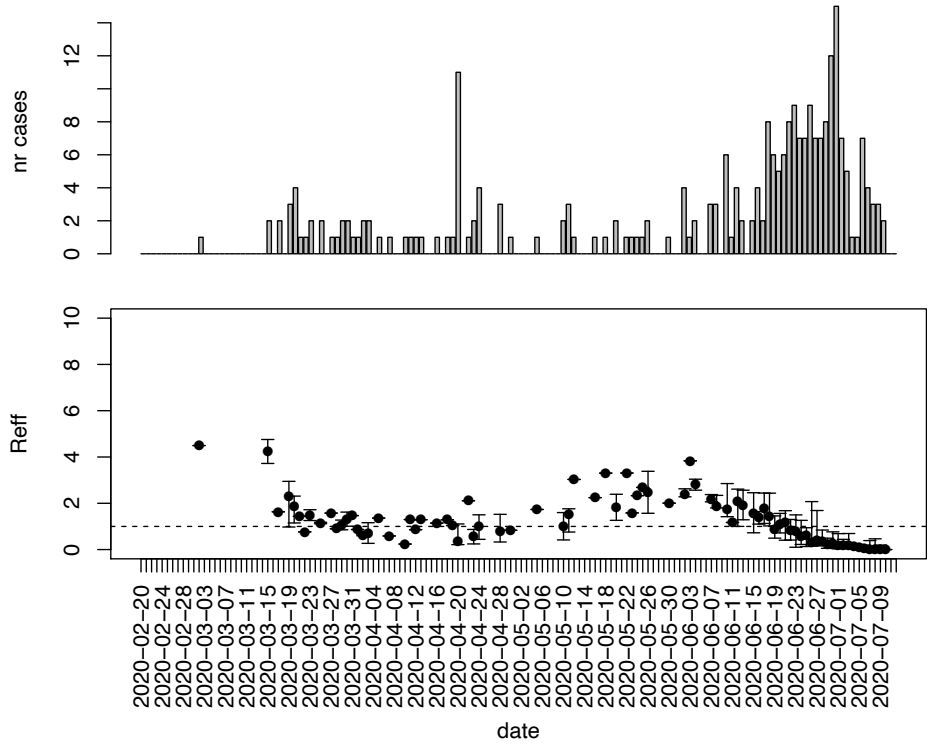
Appendix Figure 23. Epidemic curves and reproduction number estimates until July 13th in Brantley county.

**BROOKS, n=230**



Appendix Figure 24. Epidemic curves and reproduction number estimates until July 13th in Brooks county.

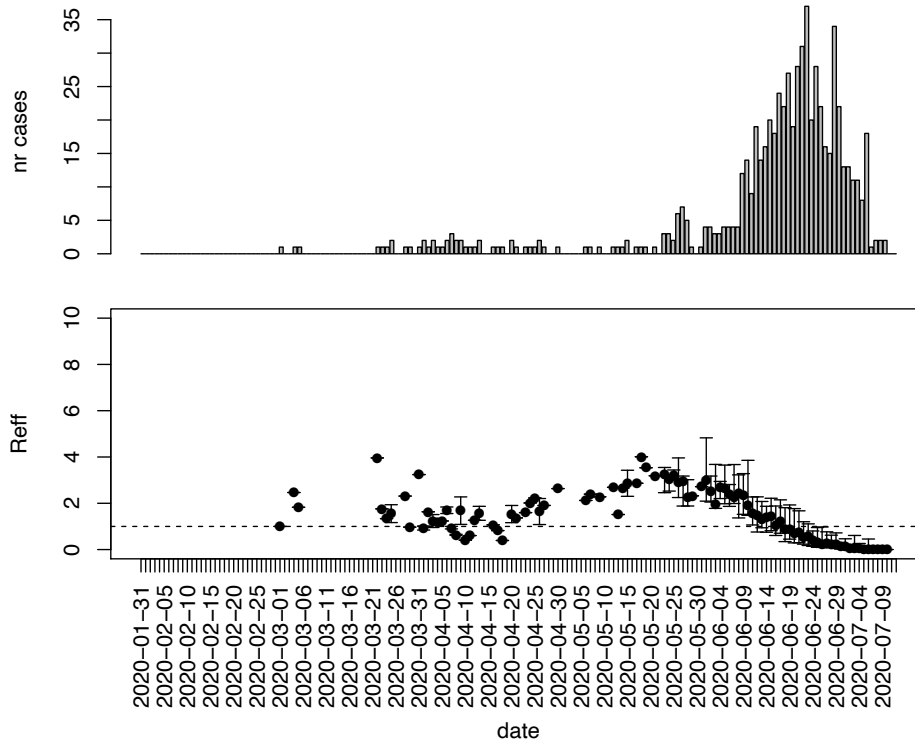
**BRYAN, n=260**



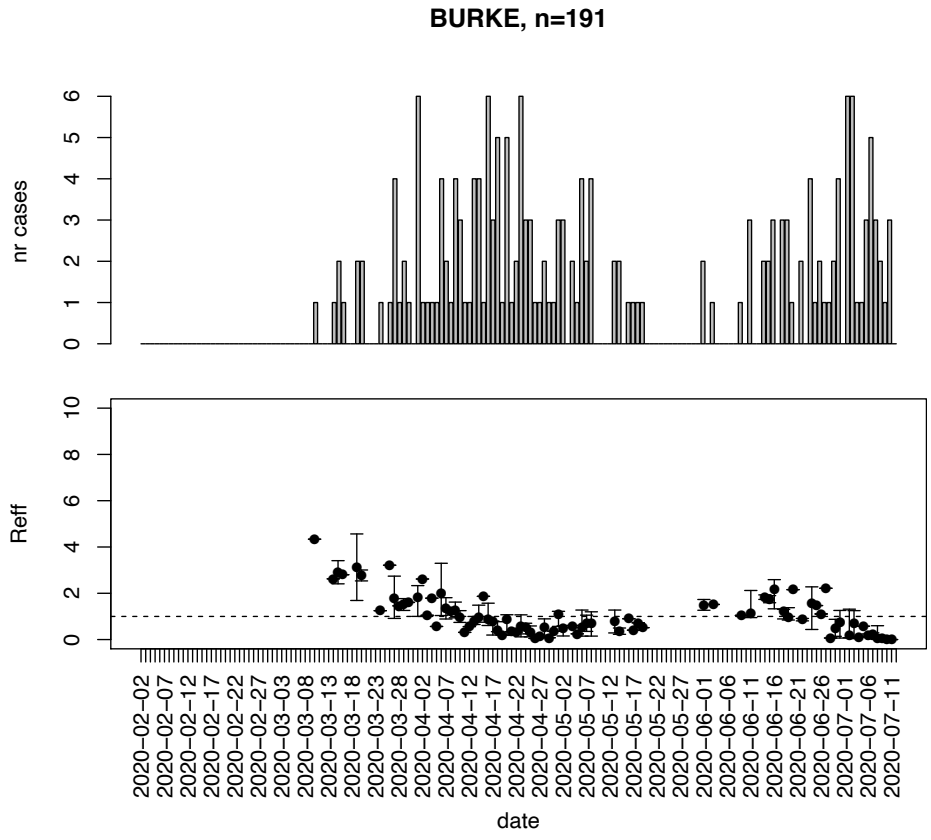
Appendix Figure 25. Epidemic curves and reproduction number estimates until July 13th in Bryan county.



**BULLOCH, n=663**

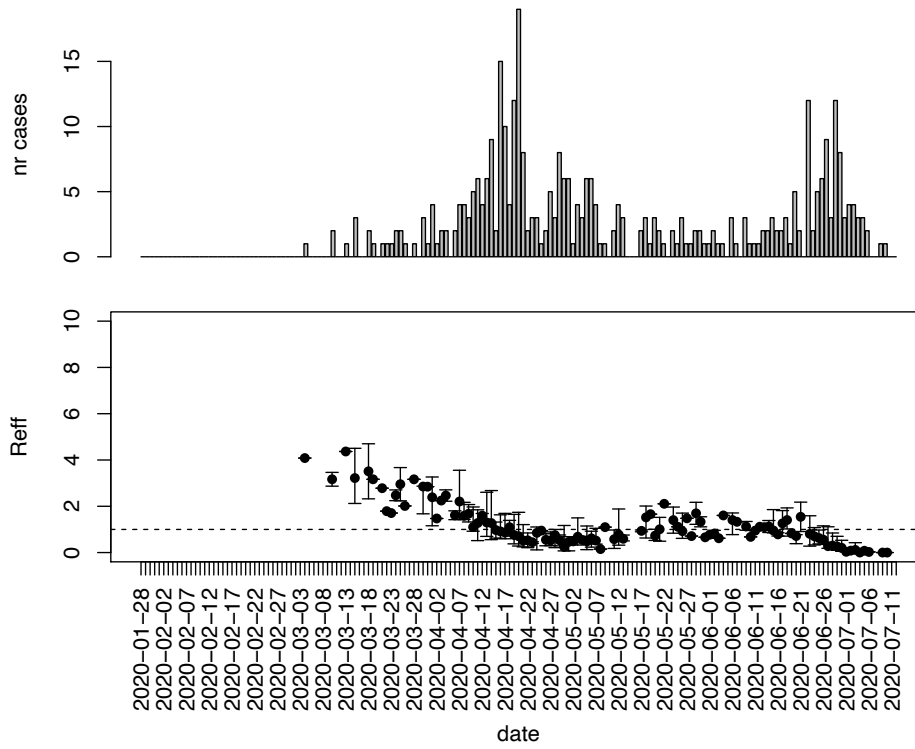


Appendix Figure 26. Epidemic curves and reproduction number estimates until July 13th in Bulloch county.



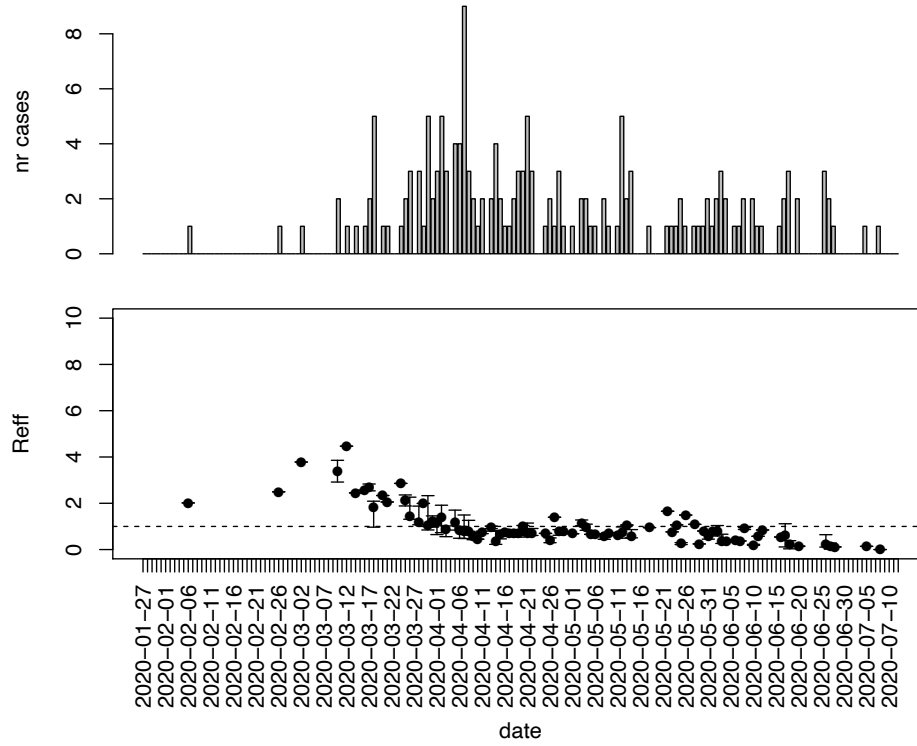
Appendix Figure 27. Epidemic curves and reproduction number estimates until July 13th in Burke county.

BUTTS, n=359



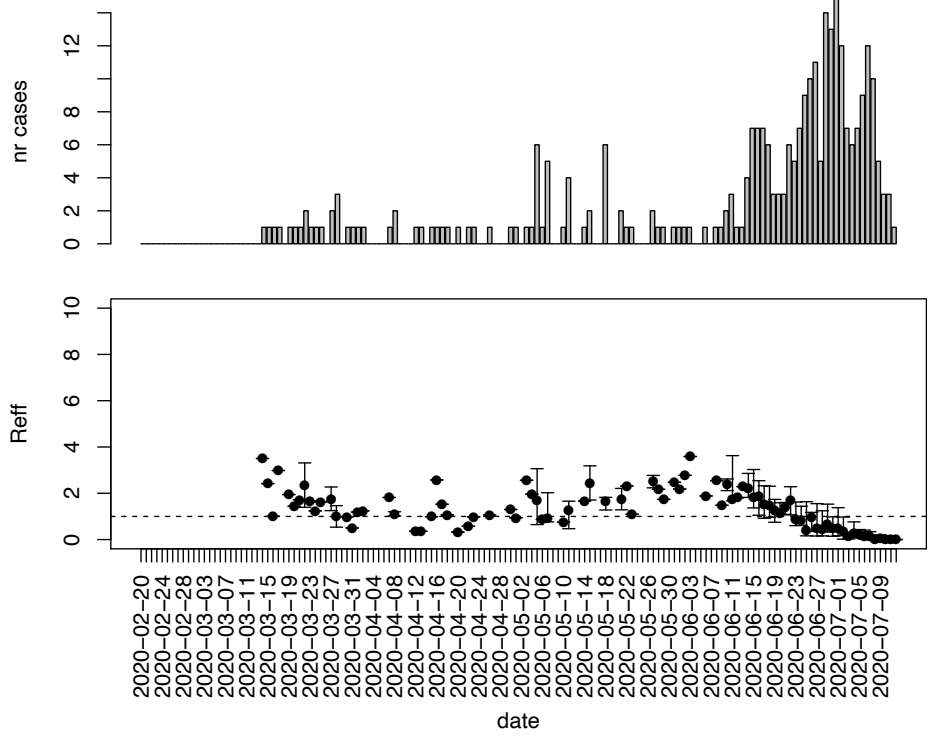
Appendix Figure 28. Epidemic curves and reproduction number estimates until July 13th in Butts county.

CALHOUN, n=169



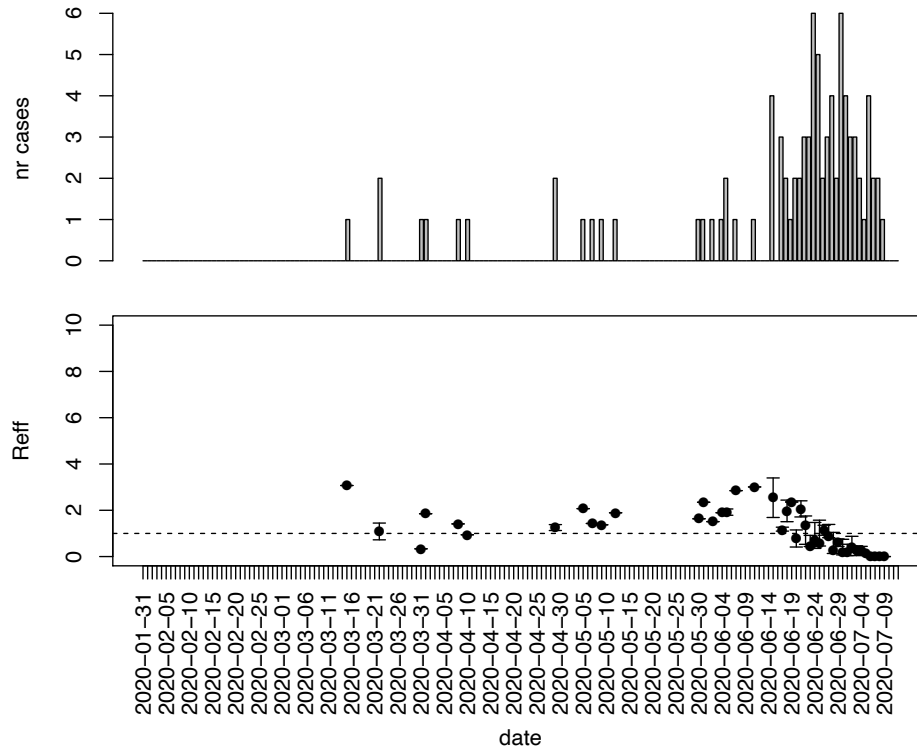
Appendix Figure 29. Epidemic curves and reproduction number estimates until July 13th in Calhoun county.

CAMDEN, n=296



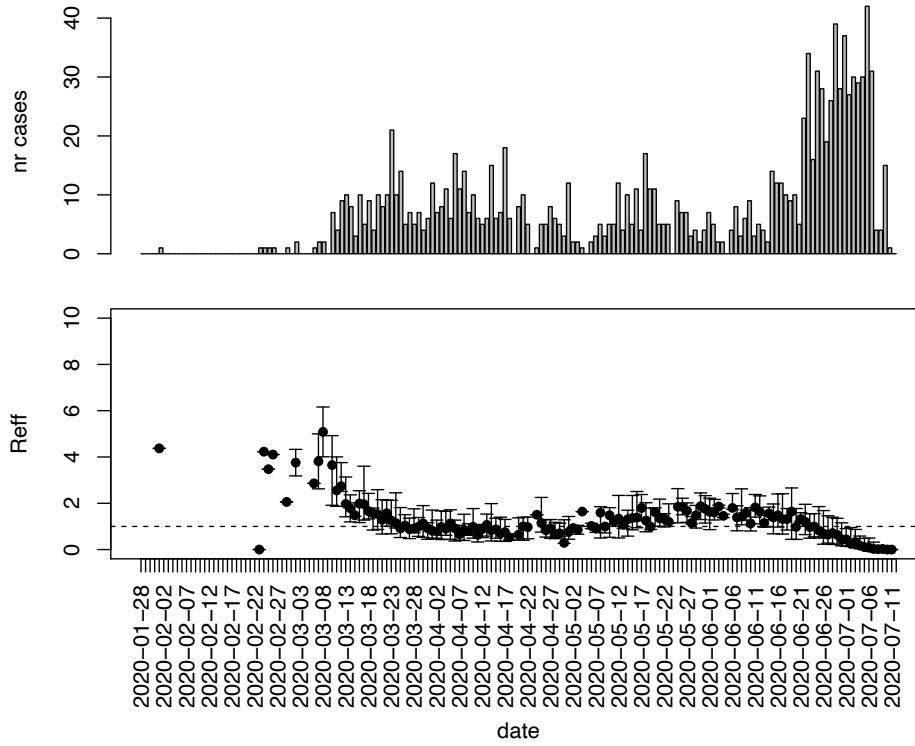
Appendix Figure 30. Epidemic curves and reproduction number estimates until July 13th in Camden county.

CANDLER, n=91



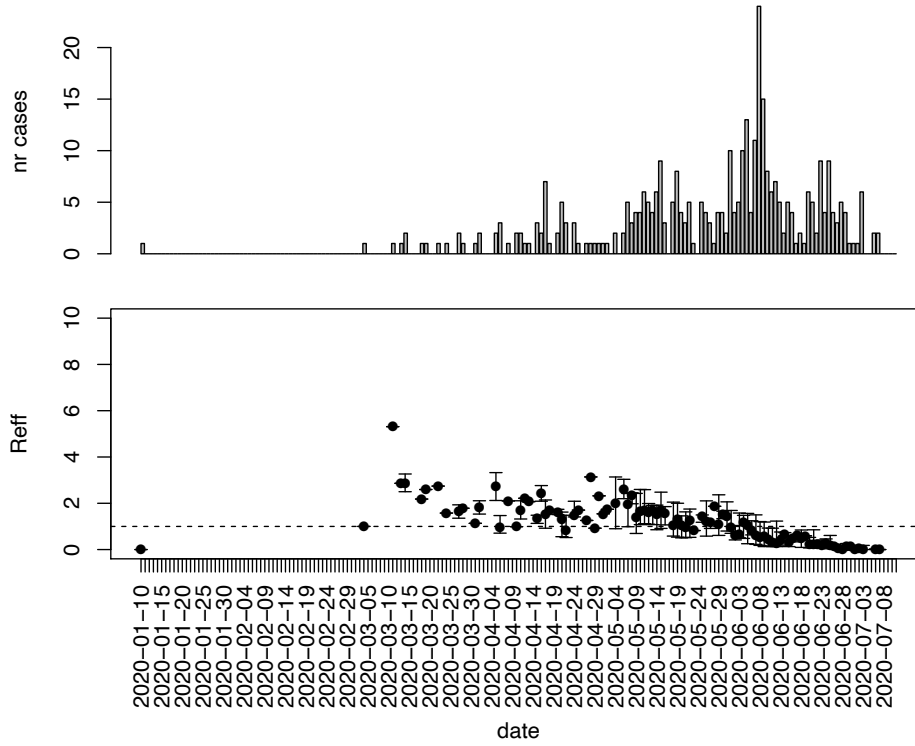
Appendix Figure 31. Epidemic curves and reproduction number estimates until July 13th in Candler county.

**CARROLL, n=1219**



Appendix Figure 32. Epidemic curves and reproduction number estimates until July 13th in Carroll county.

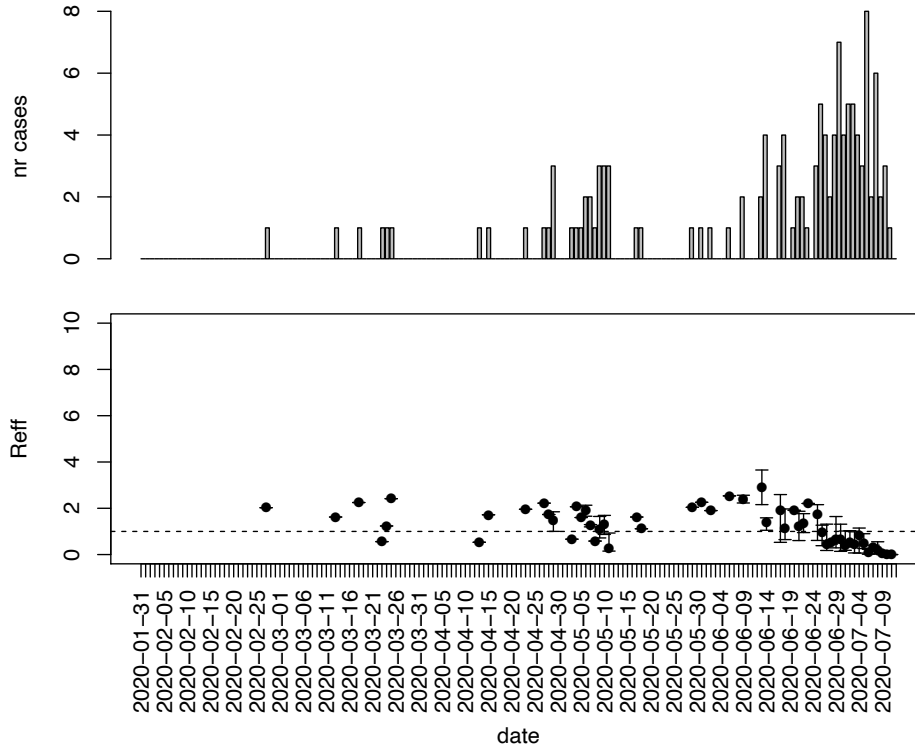
CATOOSA, n=364



Appendix Figure 33. Epidemic curves and reproduction number estimates until July 13th in Catoosa county.

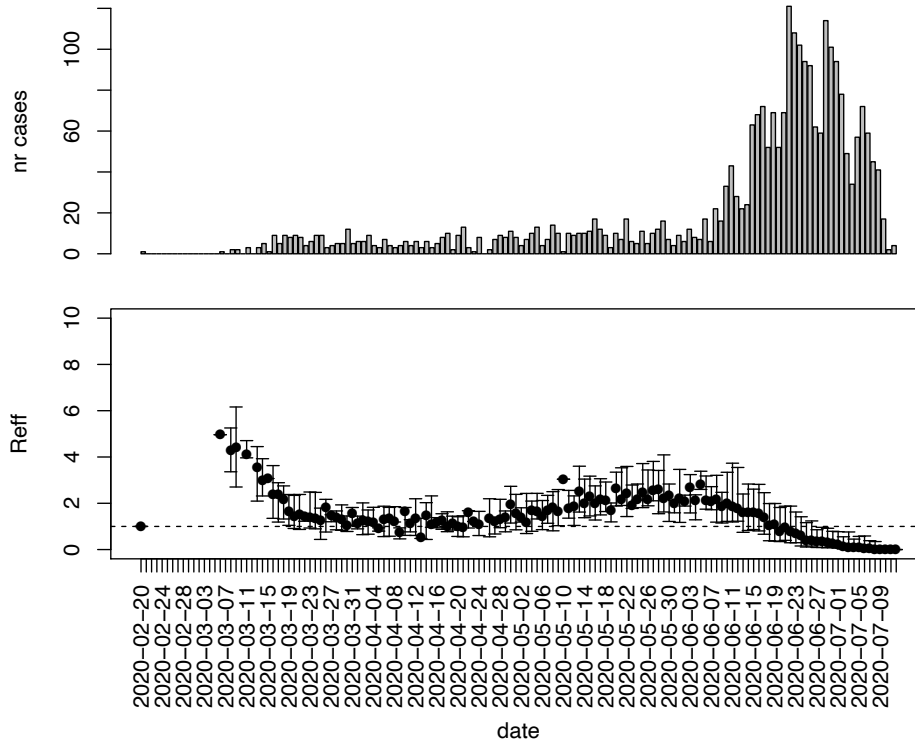


**CHARLTON, n=126**



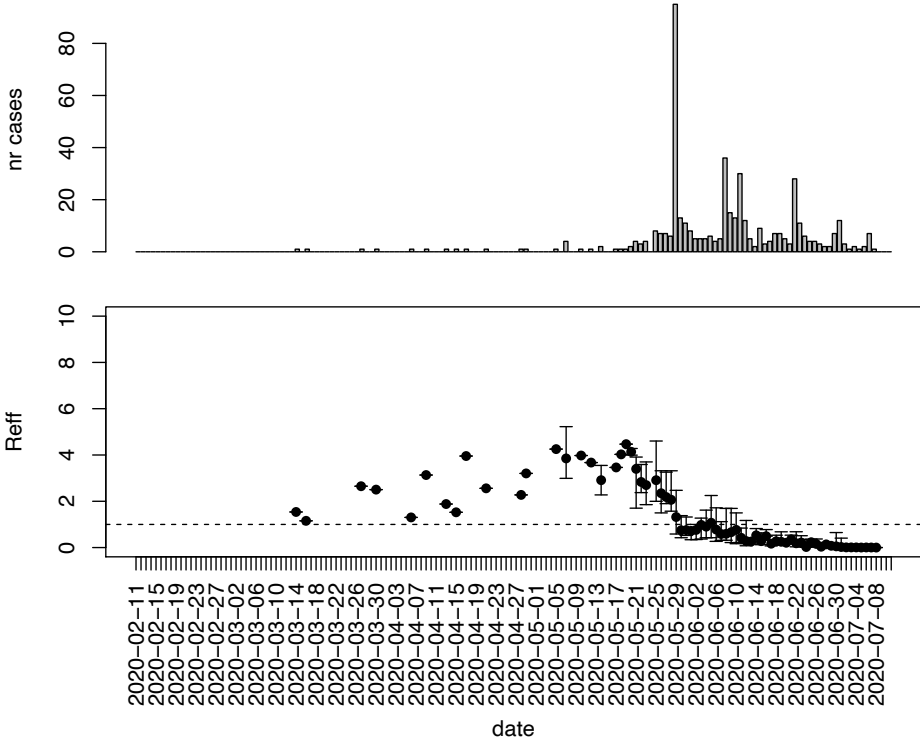
Appendix Figure 34. Epidemic curves and reproduction number estimates until July 13th in Charlton county.

CHATHAM, n=2680



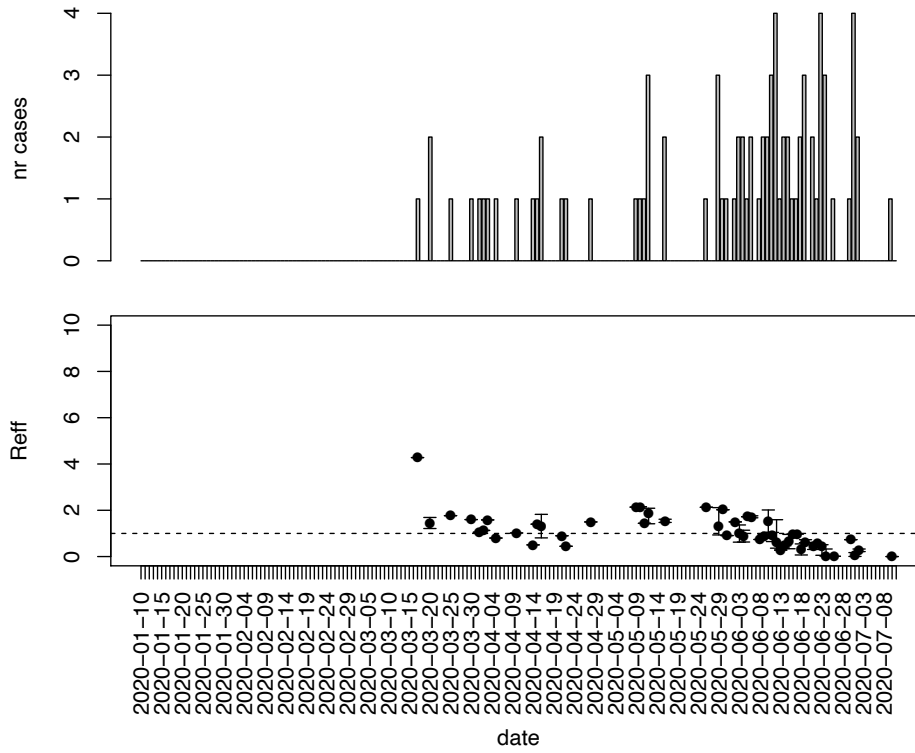
Appendix Figure 35. Epidemic curves and reproduction number estimates until July 13th in Chatham county.

CHATTAHOOCHEE, n=469



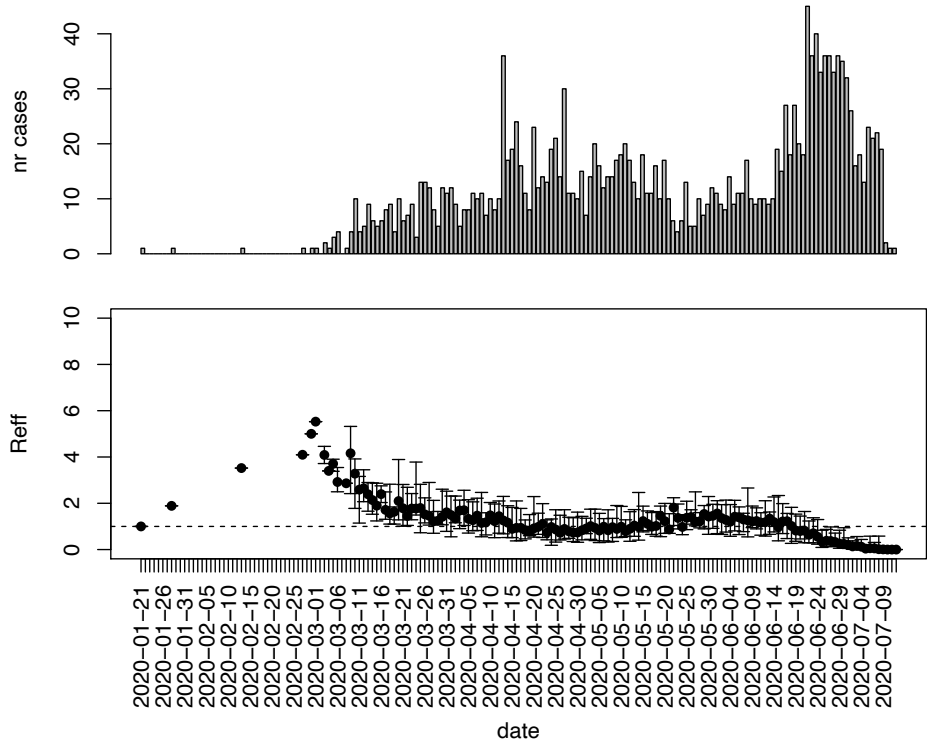
Appendix Figure 36. Epidemic curves and reproduction number estimates until July 13th in Chattahoochee county.

CHATTOOGA, n=82



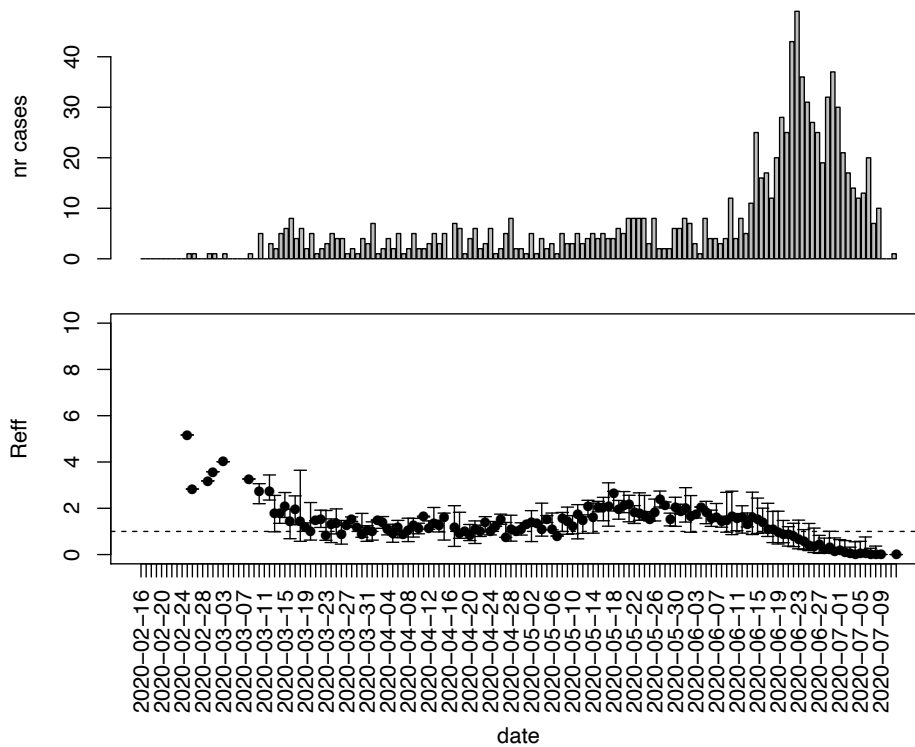
Appendix Figure 37. Epidemic curves and reproduction number estimates until July 13th in Chattooga county.

CHEROKEE, n=1807



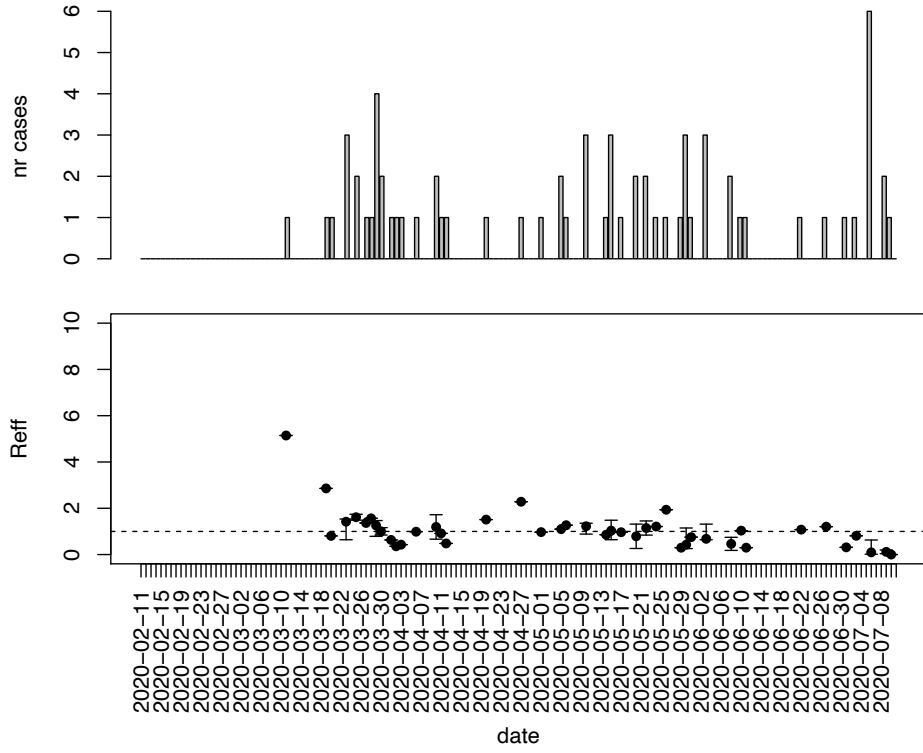
Appendix Figure 38. Epidemic curves and reproduction number estimates until July 13th in Cherokee county.

CLARKE, n=989



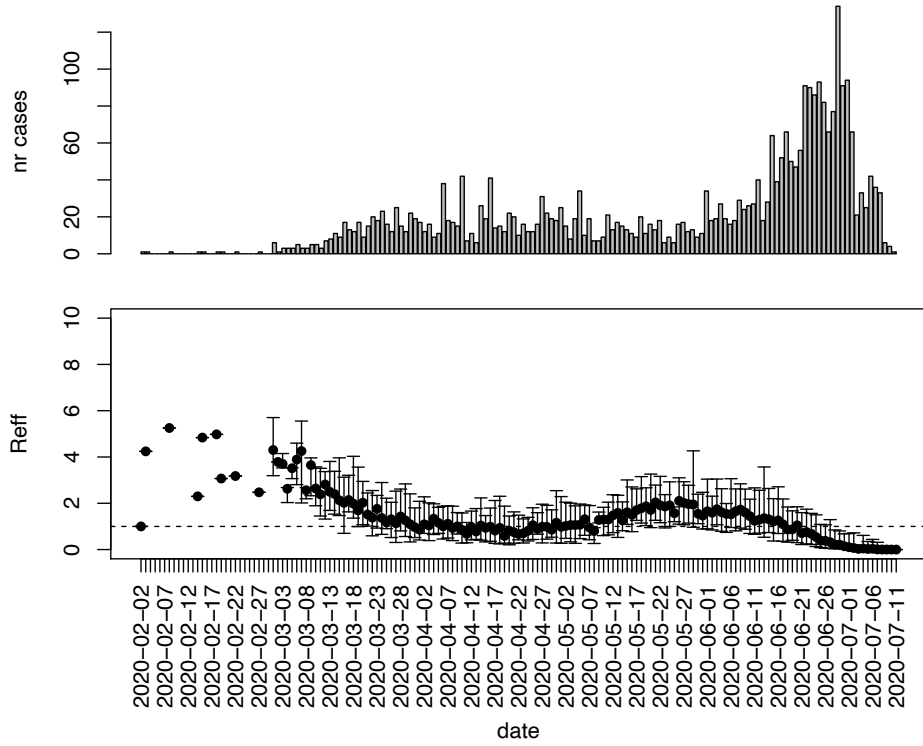
Appendix Figure 39. Epidemic curves and reproduction number estimates until July 13th in Clarke county.

CLAY, n=69



Appendix Figure 40. Epidemic curves and reproduction number estimates until July 13th in Clay county.

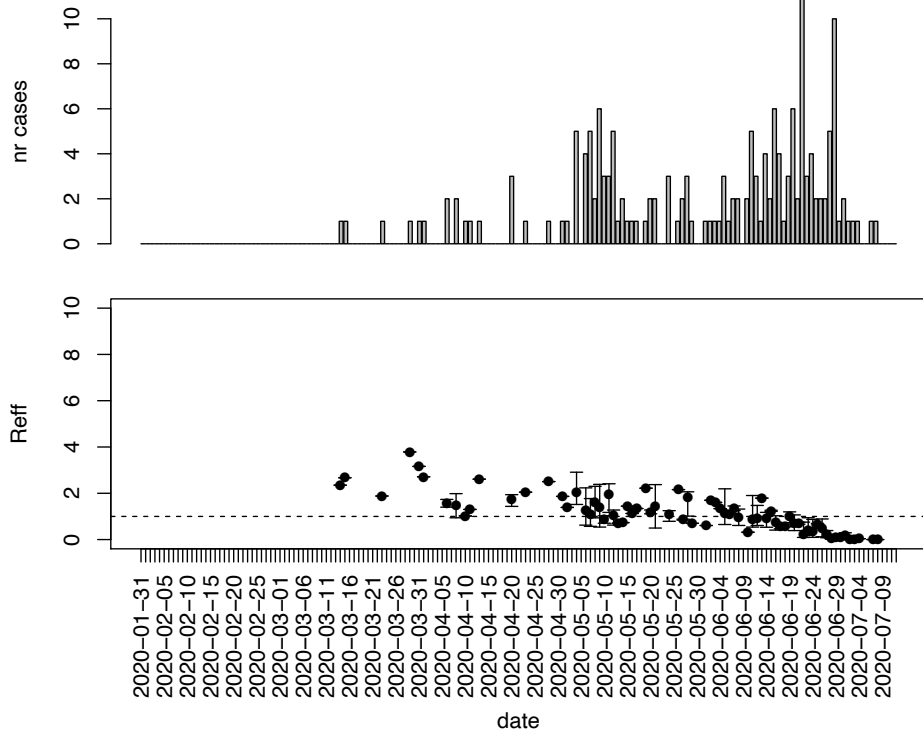
CLAYTON, n=3210



Appendix Figure 41. Epidemic curves and reproduction number estimates until July 13th in Clayton county.

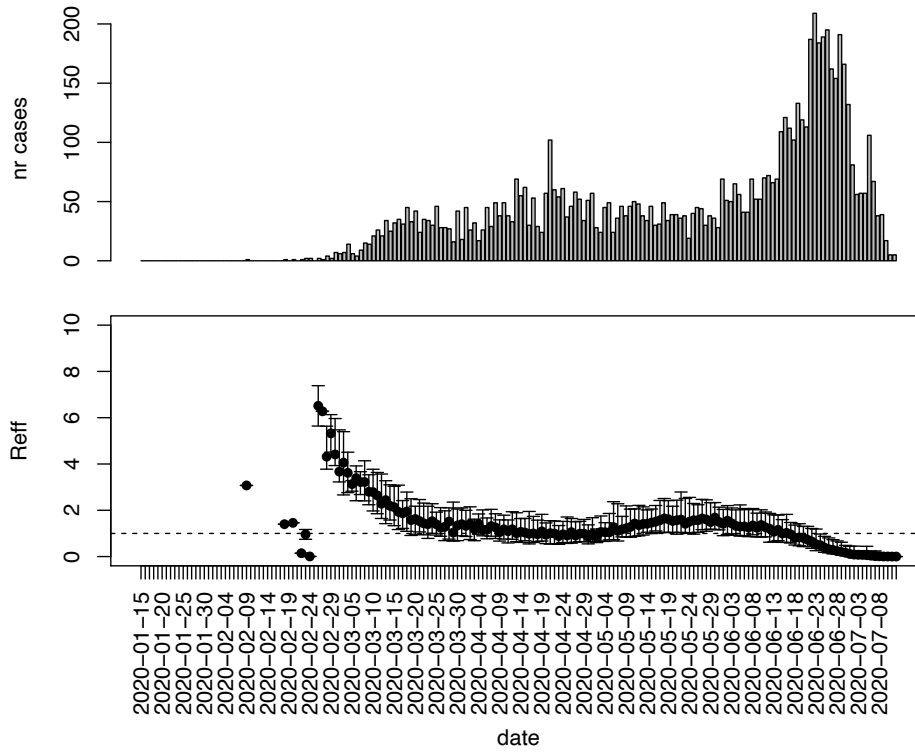


CLINCH, n=172



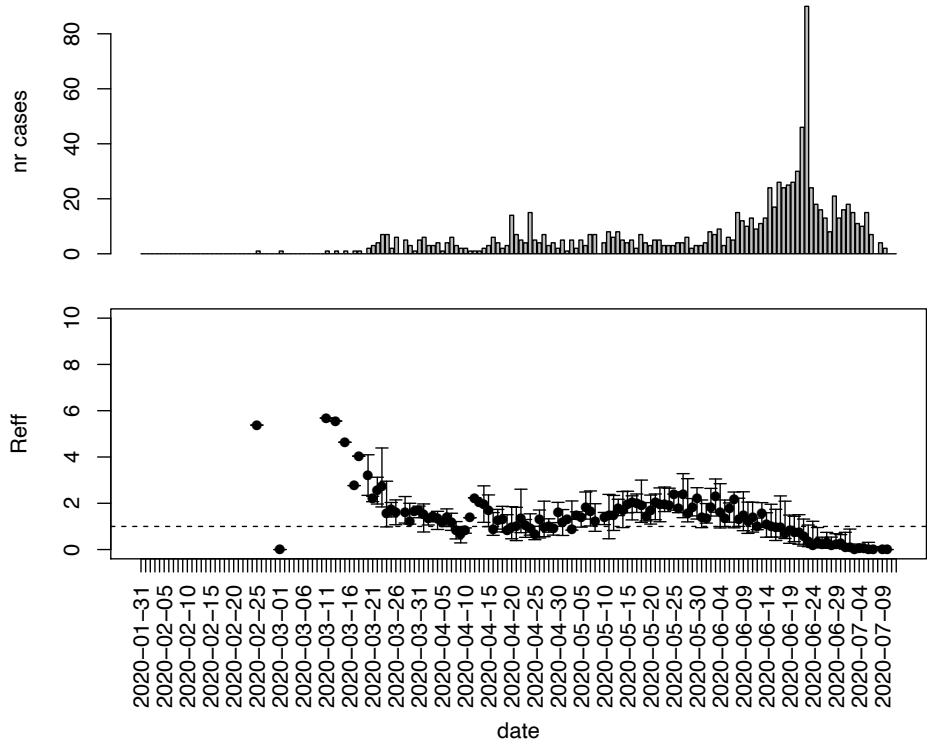
Appendix Figure 42. Epidemic curves and reproduction number estimates until July 13th in Clinch county.

COBB, n=7247



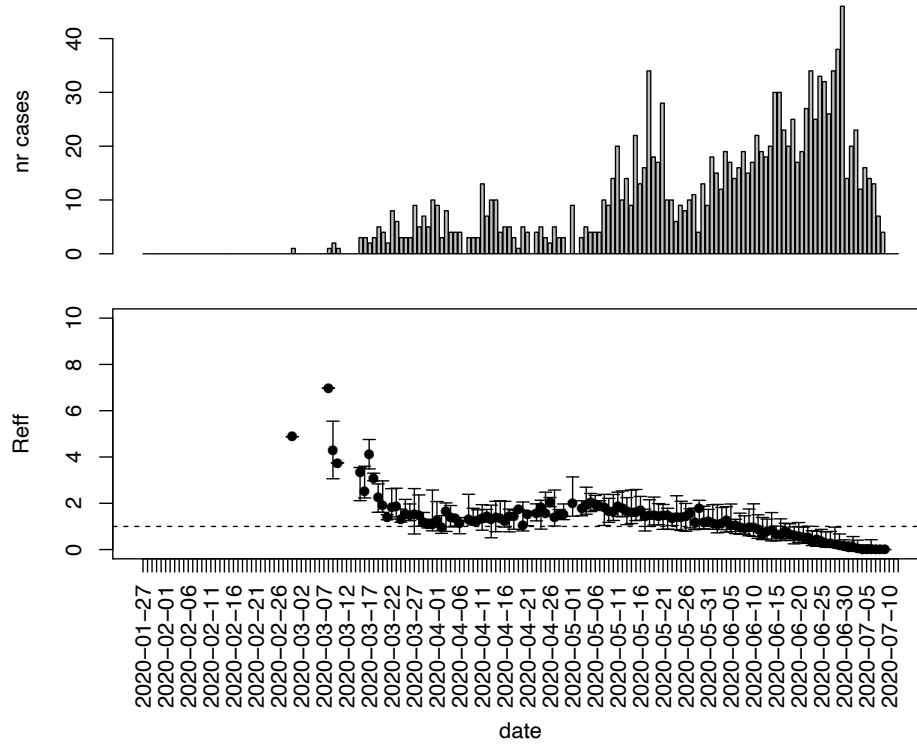
Appendix Figure 43. Epidemic curves and reproduction number estimates until July 13th in Cobb county.

COFFEE, n=955



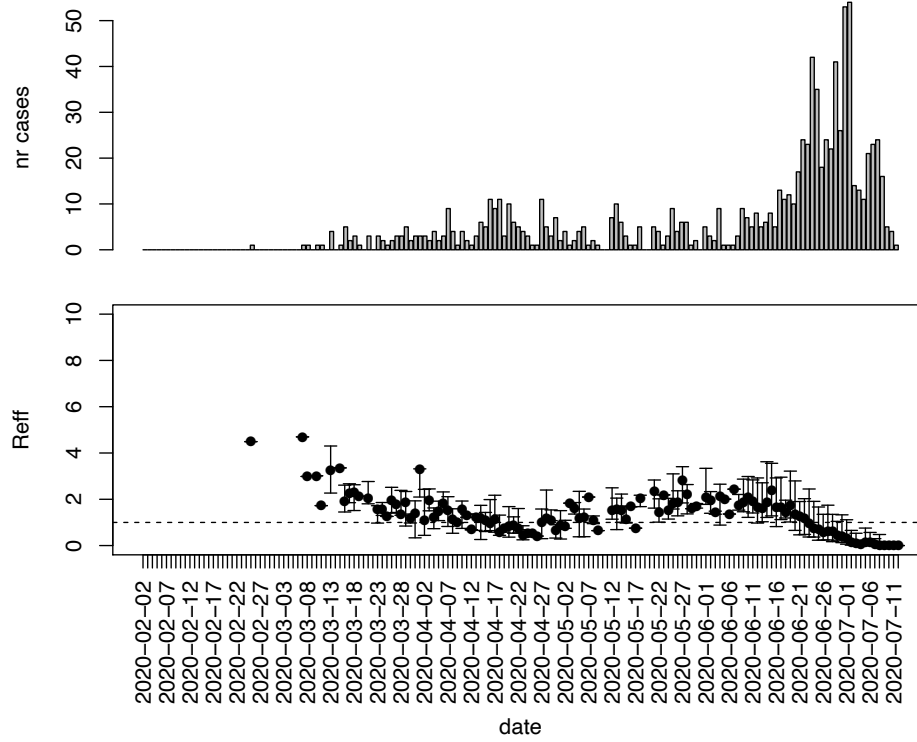
Appendix Figure 44. Epidemic curves and reproduction number estimates until July 13th in Coffee county.

COLQUITT, n=1395



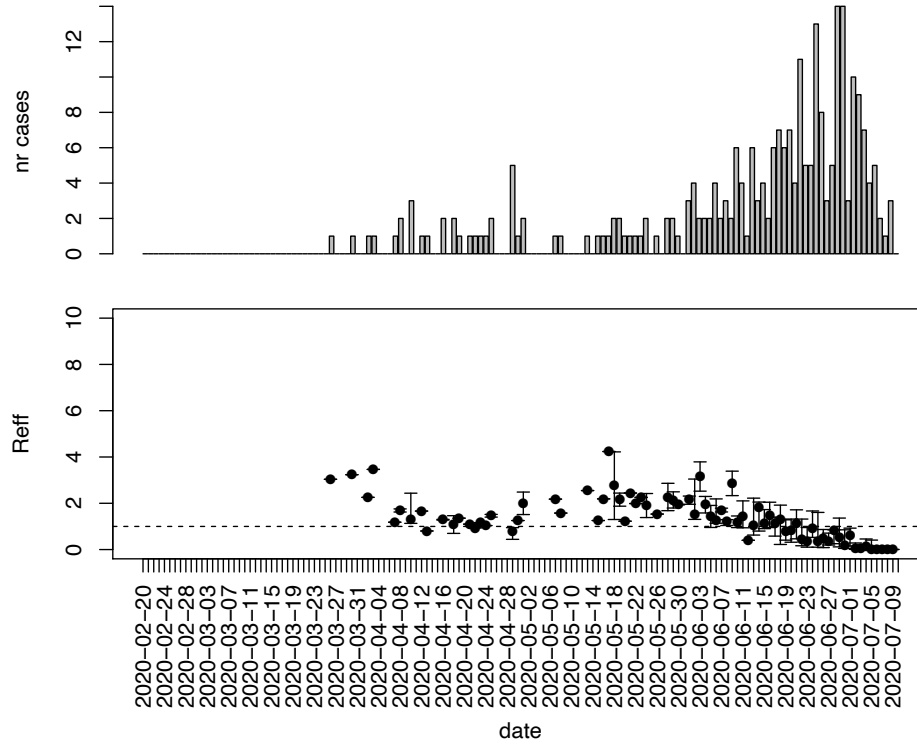
Appendix Figure 45. Epidemic curves and reproduction number estimates until July 13th in Colquitt county.

COLUMBIA, n=921



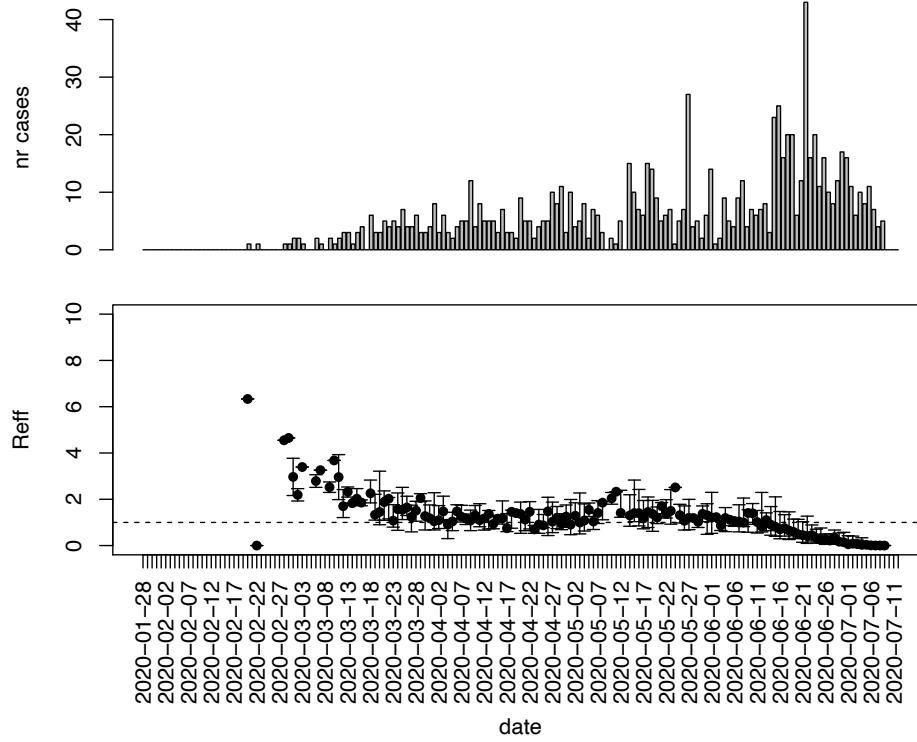
Appendix Figure 46. Epidemic curves and reproduction number estimates until July 13th in Columbia county.

COOK, n=255

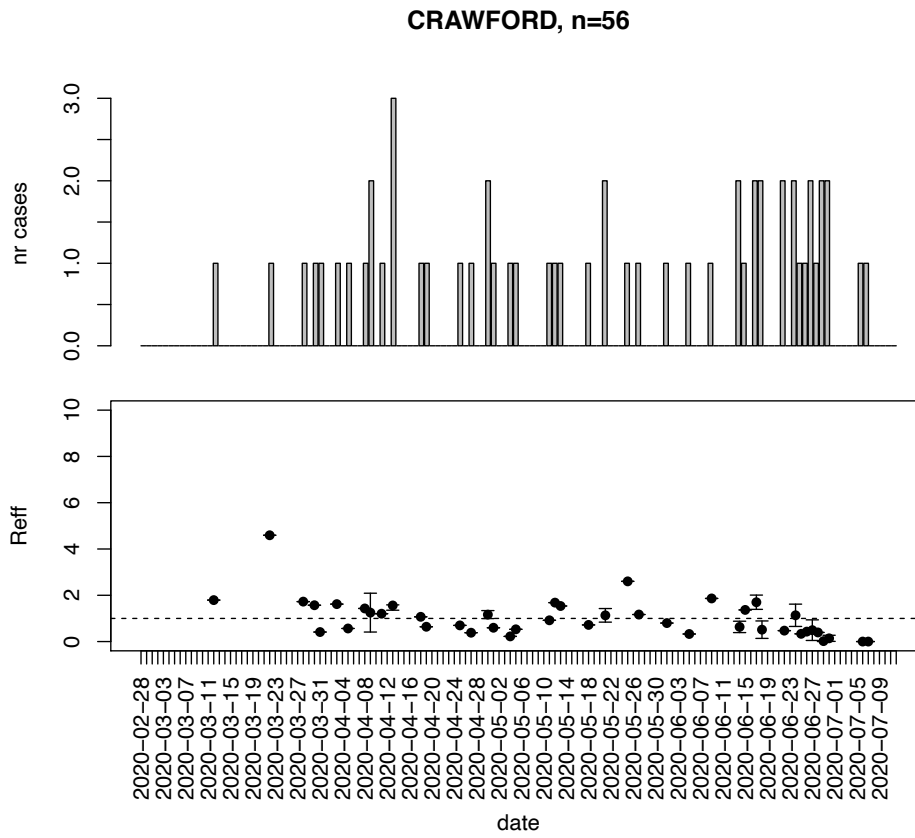


Appendix Figure 47. Epidemic curves and reproduction number estimates until July 13th in Cook county.

COWETA, n=900



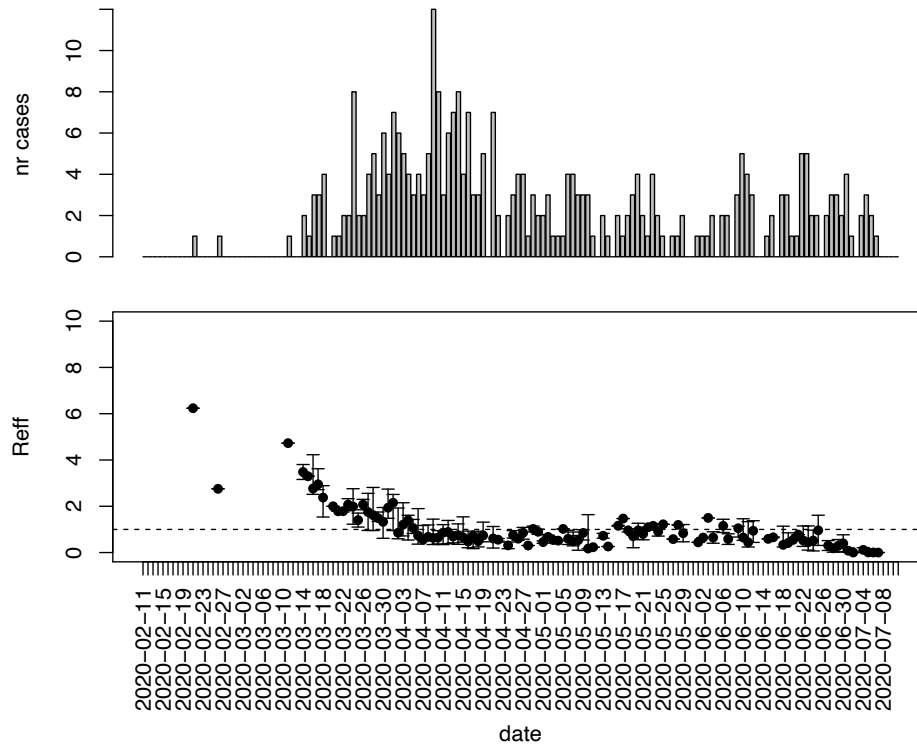
Appendix Figure 48. Epidemic curves and reproduction number estimates until July 13th in Coweta county.



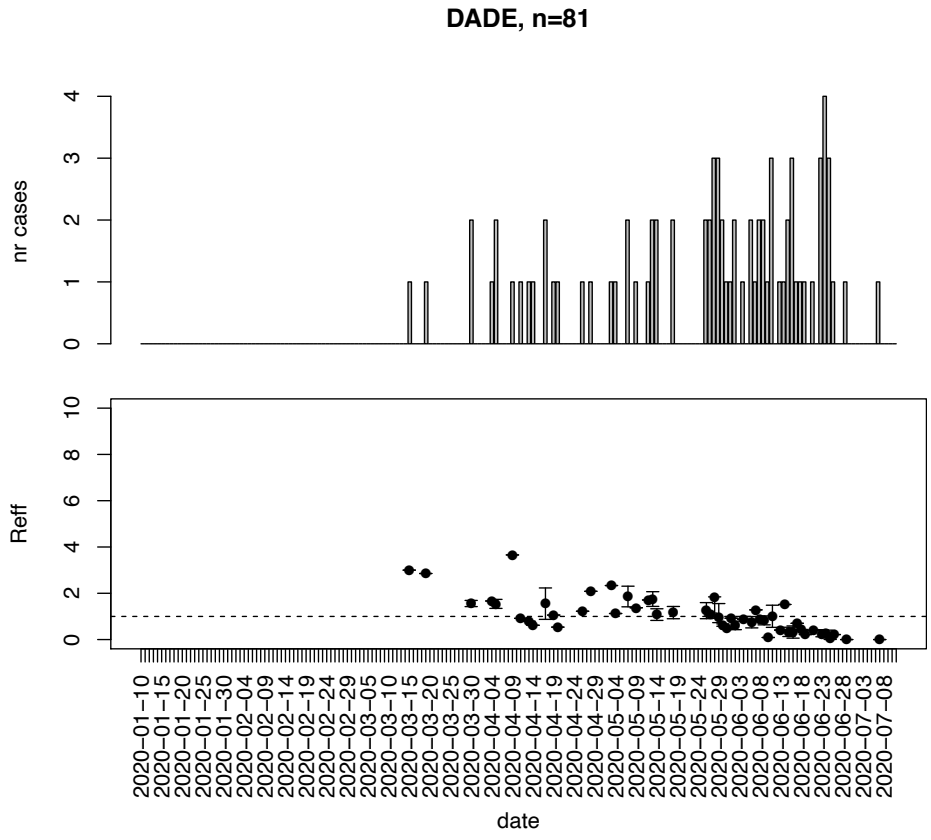
Appendix Figure 49. Epidemic curves and reproduction number estimates until July 13th in Crawford county.



CRISP, n=314

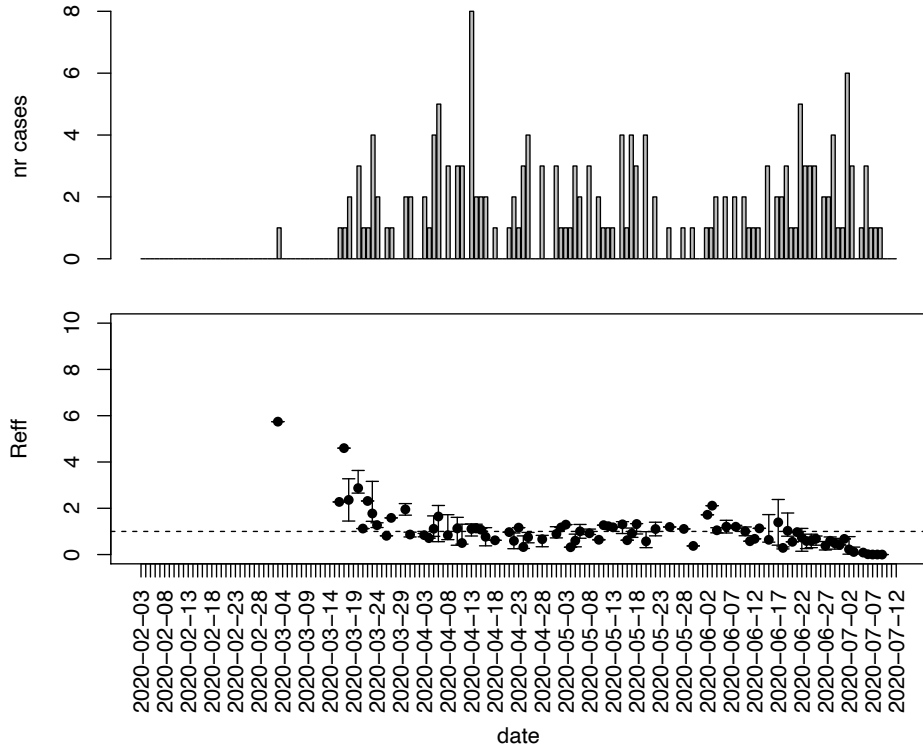


Appendix Figure 50. Epidemic curves and reproduction number estimates until July 13th in Crisp county.



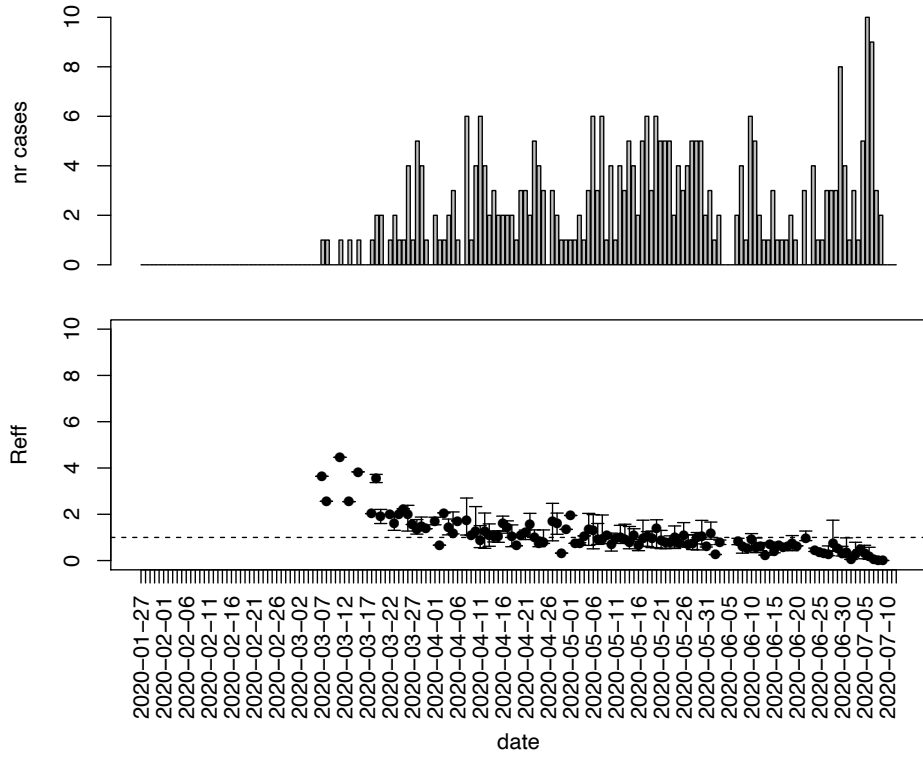
Appendix Figure 51. Epidemic curves and reproduction number estimates until July 13th in Dade county.

DAWSON, n=177



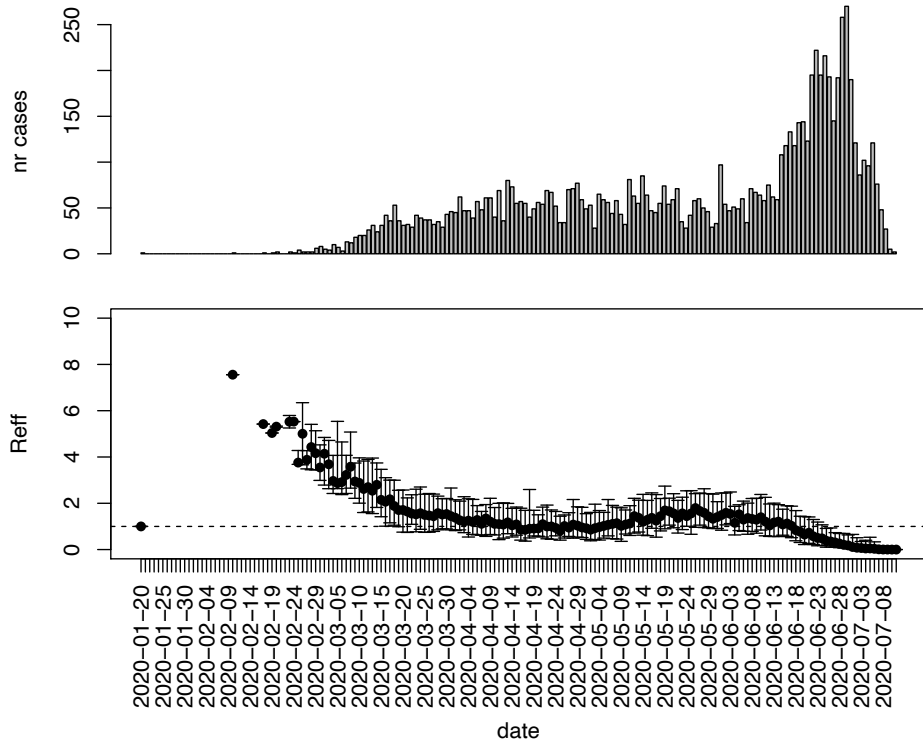
Appendix Figure 52. Epidemic curves and reproduction number estimates until July 13th in Dawson county.

DECATUR, n=315



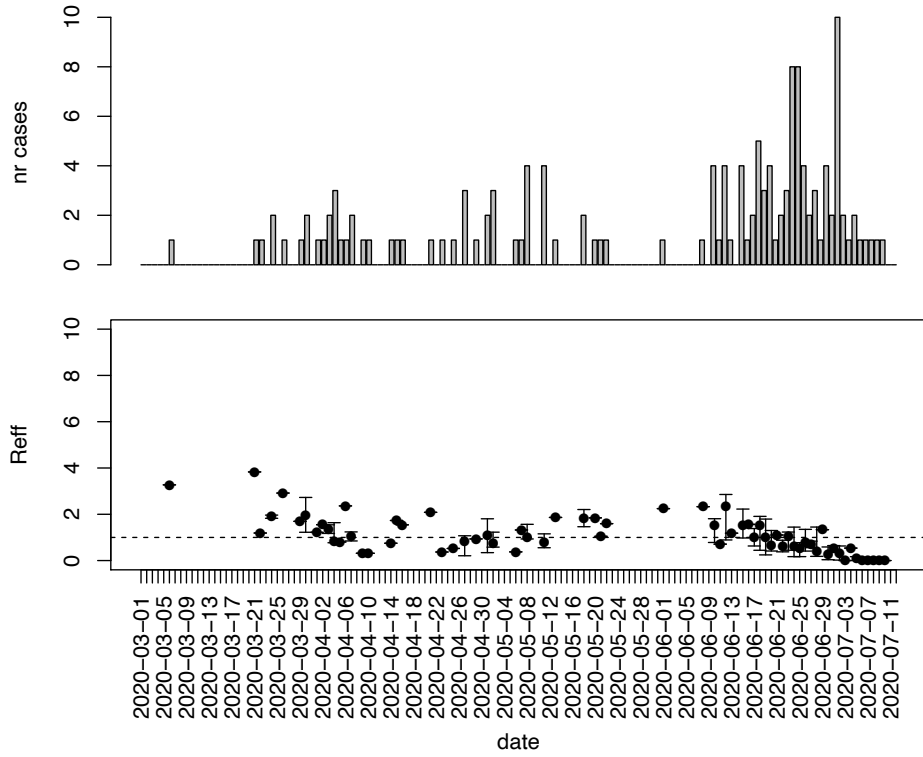
Appendix Figure 53. Epidemic curves and reproduction number estimates until July 13th in Decatur county.

DEKALB, n=8636



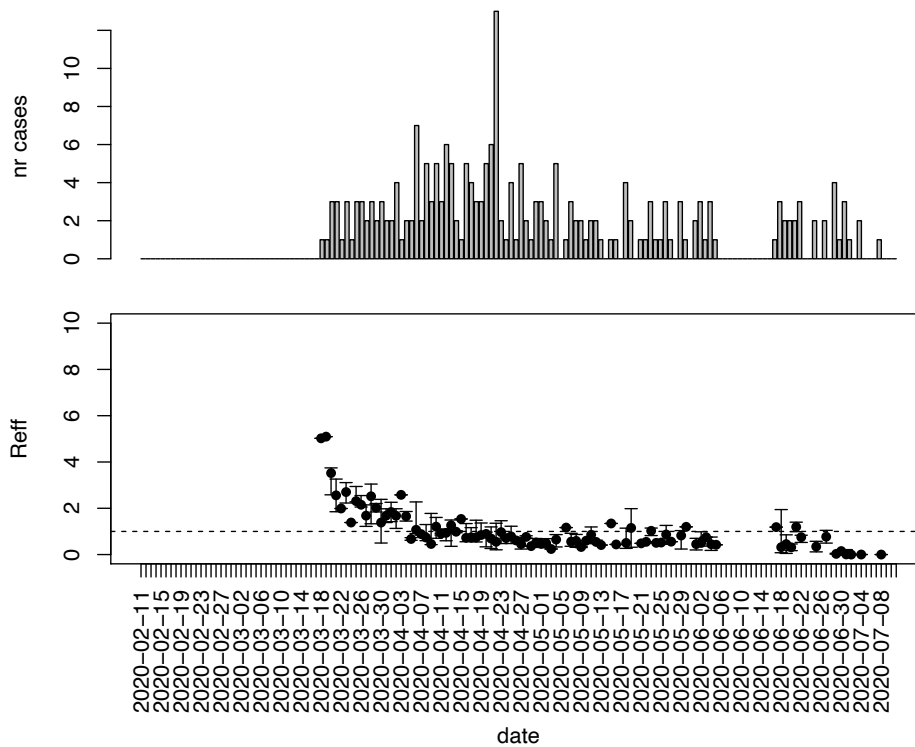
Appendix Figure 54. Epidemic curves and reproduction number estimates until July 13th in Dekalb county.

DODGE, n=142



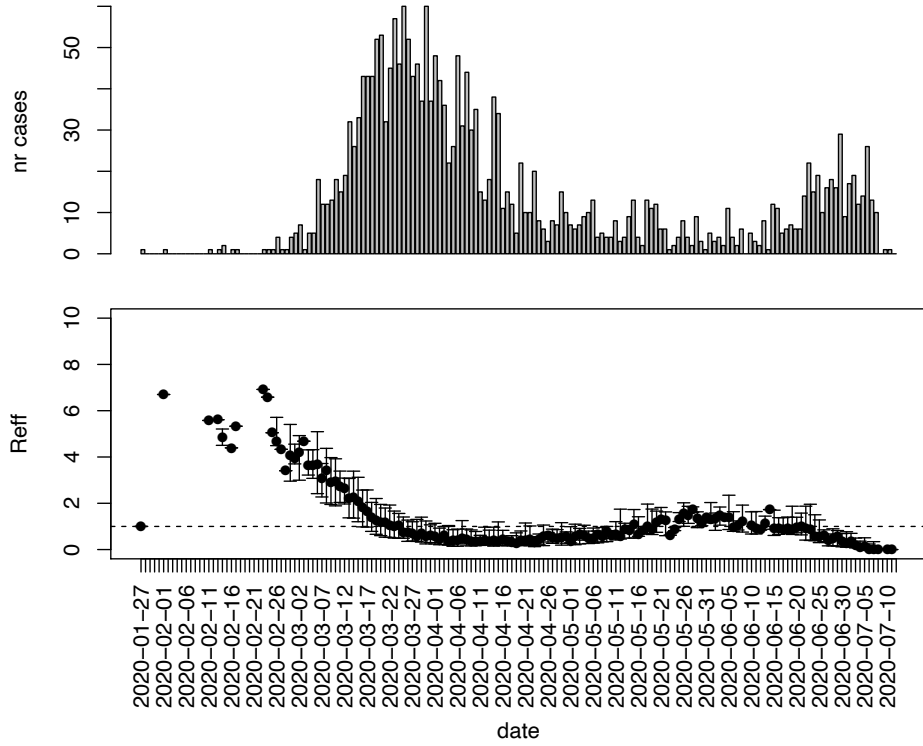
Appendix Figure 55. Epidemic curves and reproduction number estimates until July 13th in Dodge county.

DOOLY, n=226



Appendix Figure 56. Epidemic curves and reproduction number estimates until July 13th in Dooly county.

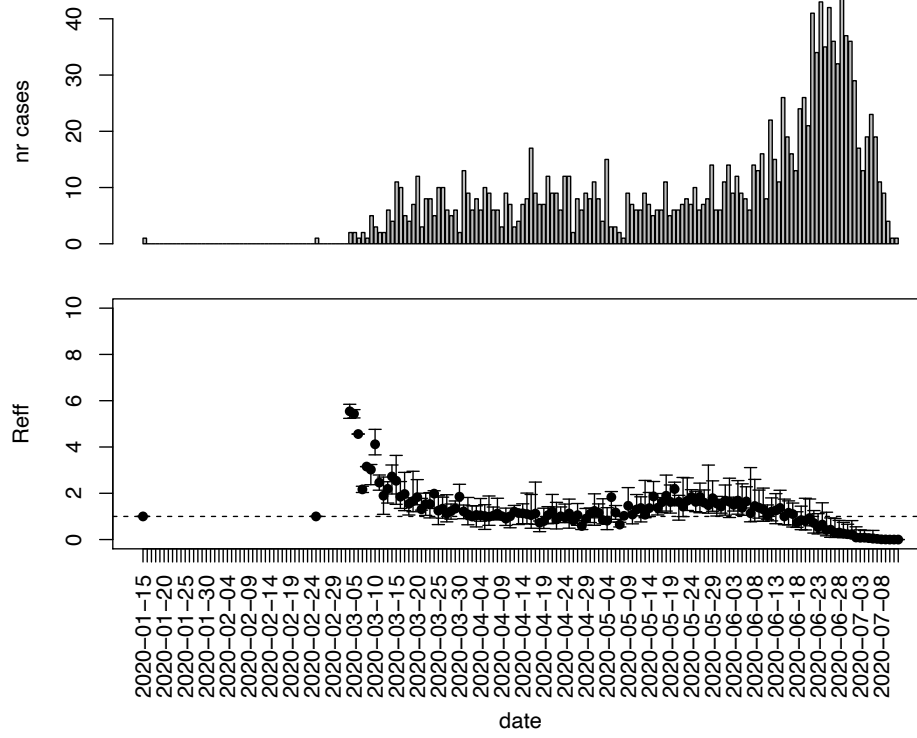
DOUGHERTY, n=2217



Appendix Figure 57. Epidemic curves and reproduction number estimates until July 13th in Dougherty county.

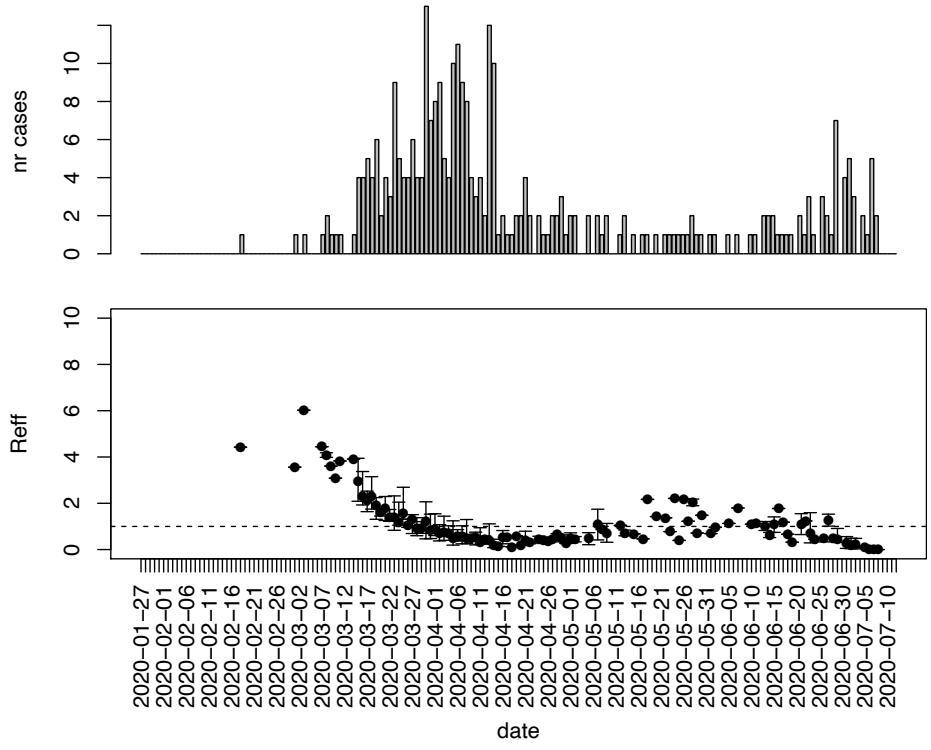


DOUGLAS, n=1445



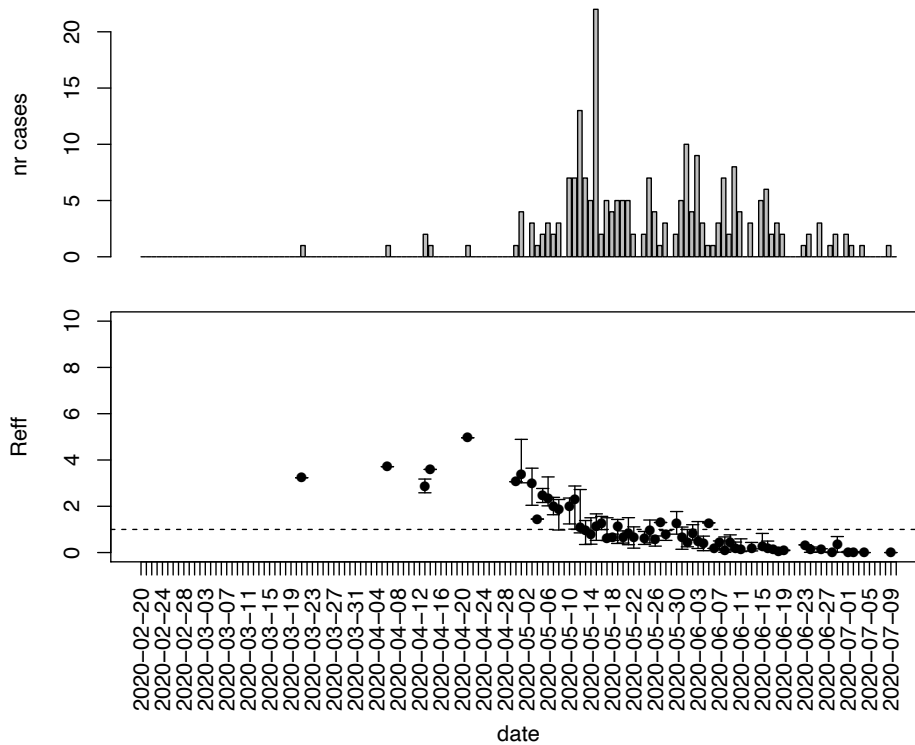
Appendix Figure 58. Epidemic curves and reproduction number estimates until July 13th in Douglas county.

**EARLY, n=310**



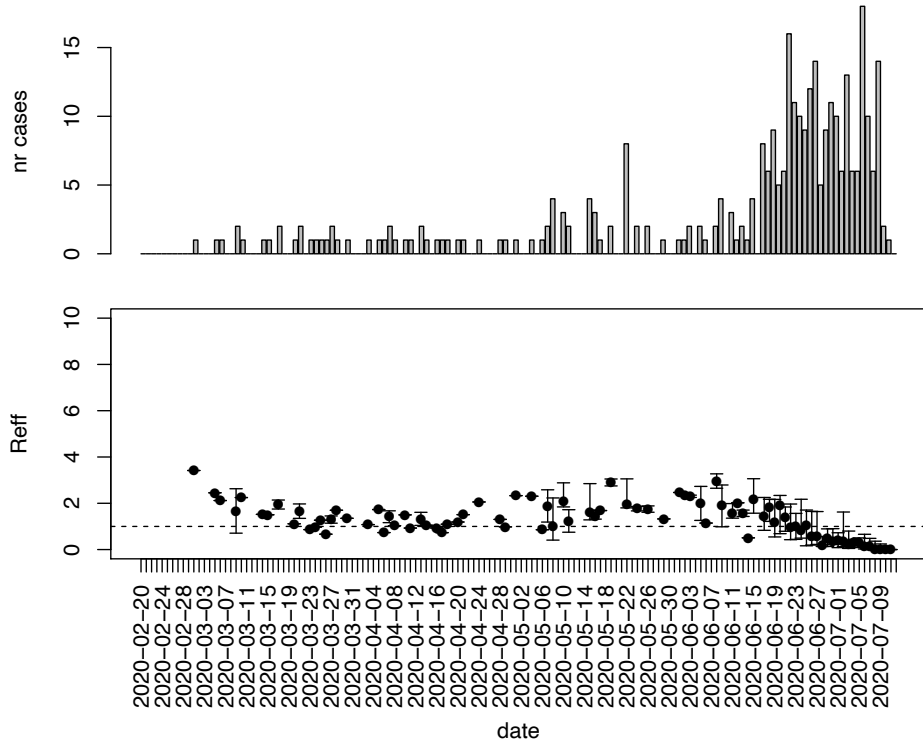
Appendix Figure 59. Epidemic curves and reproduction number estimates until July 13th in Early county.

### ECHOLS, n=225



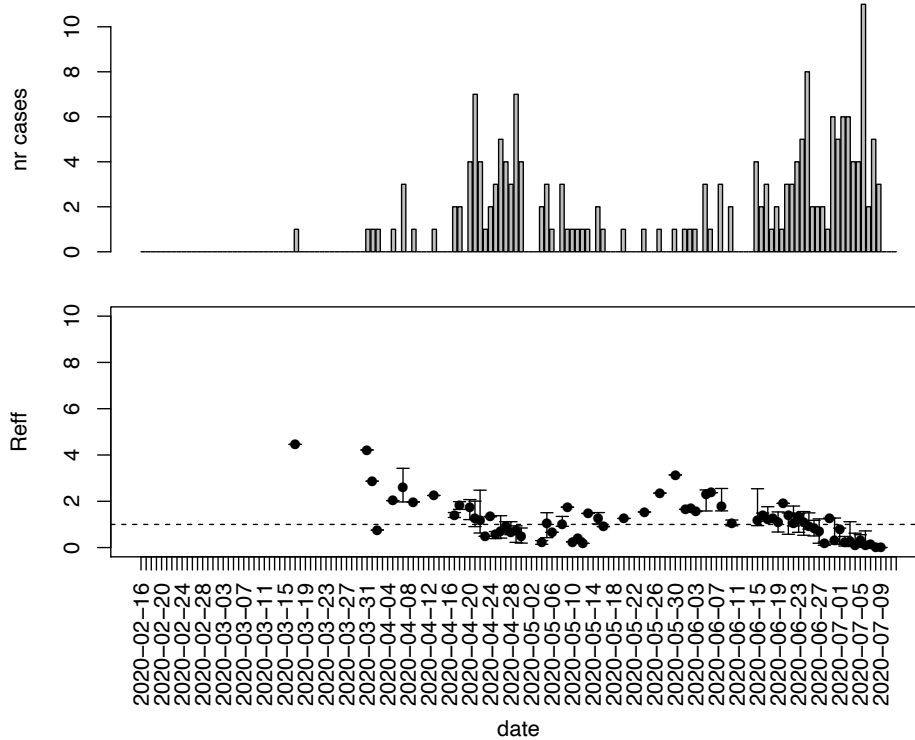
Appendix Figure 60. Epidemic curves and reproduction number estimates until July 13th in Echols county.

EFFINGHAM, n=324



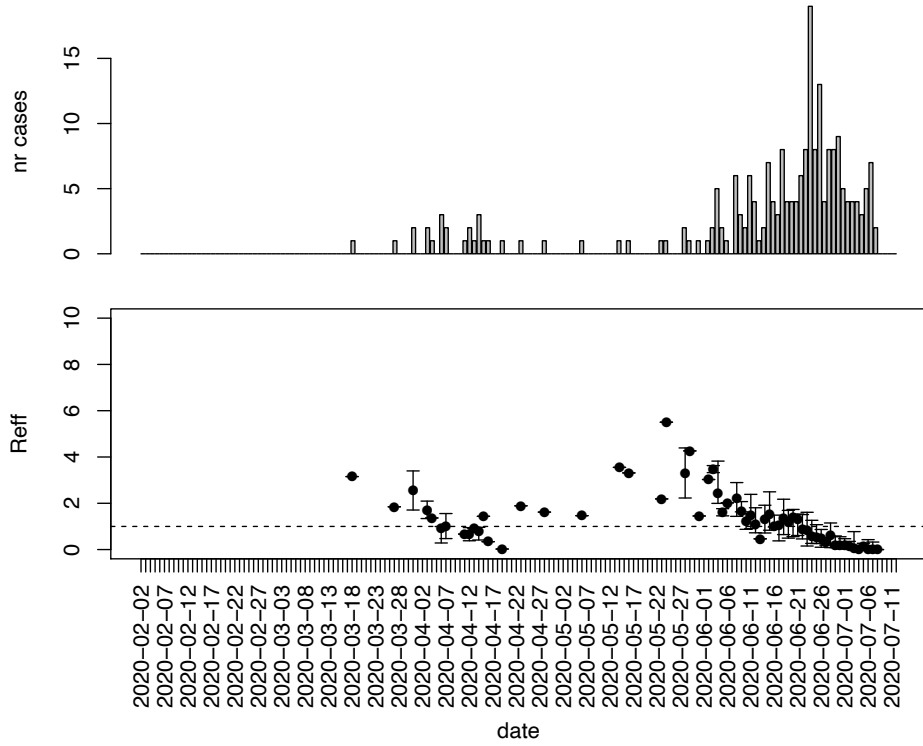
Appendix Figure 61. Epidemic curves and reproduction number estimates until July 13th in Effingham county.

ELBERT, n=186



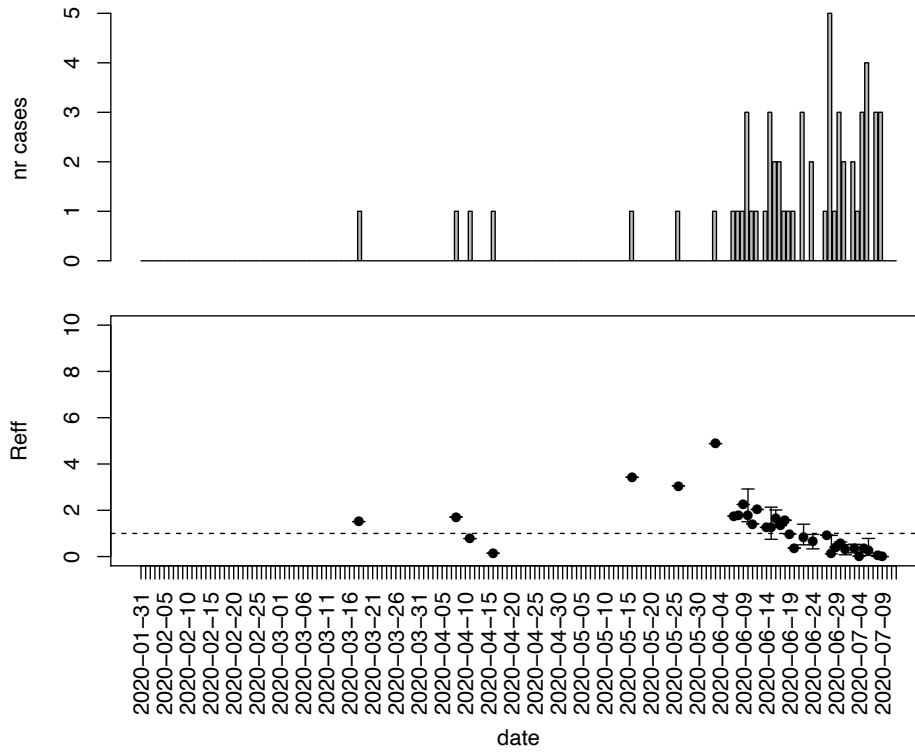
Appendix Figure 62. Epidemic curves and reproduction number estimates until July 13th in Elbert county.

EMANUEL, n=219

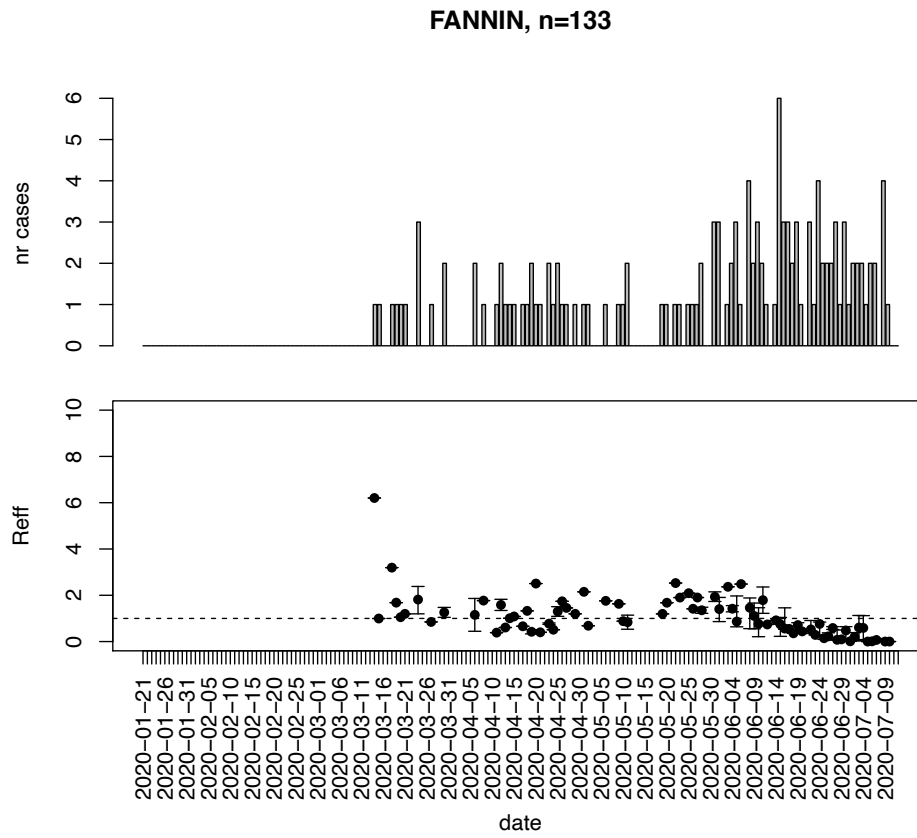


Appendix Figure 63. Epidemic curves and reproduction number estimates until July 13th in Emanuel county.

EVANS, n=59



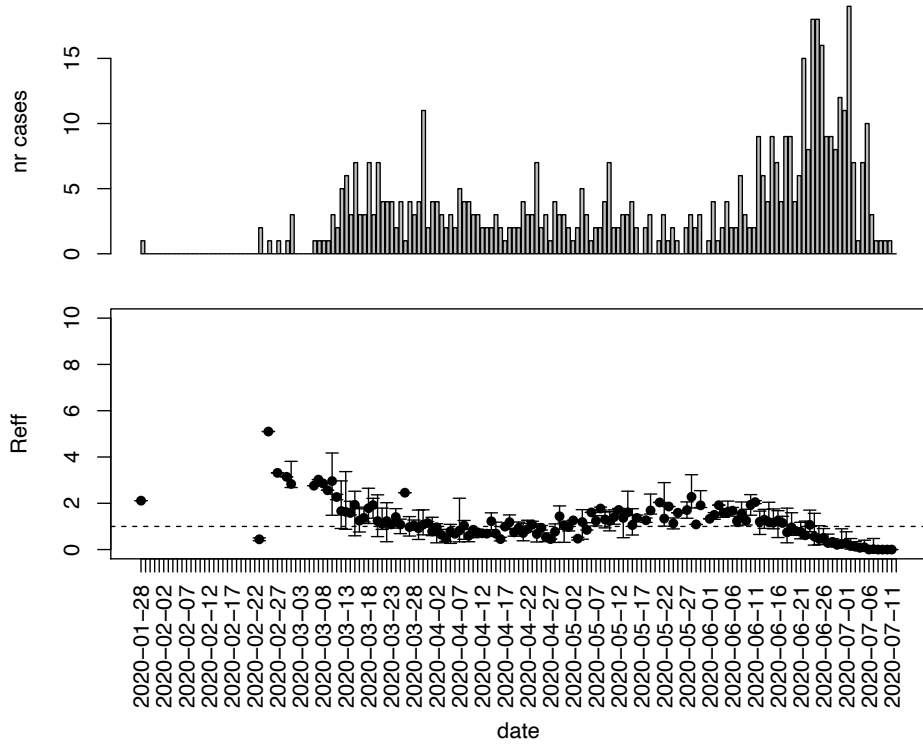
Appendix Figure 64. Epidemic curves and reproduction number estimates until July 13th in Evans county.



Appendix Figure 65. Epidemic curves and reproduction number estimates until July 13th in Fannin county.

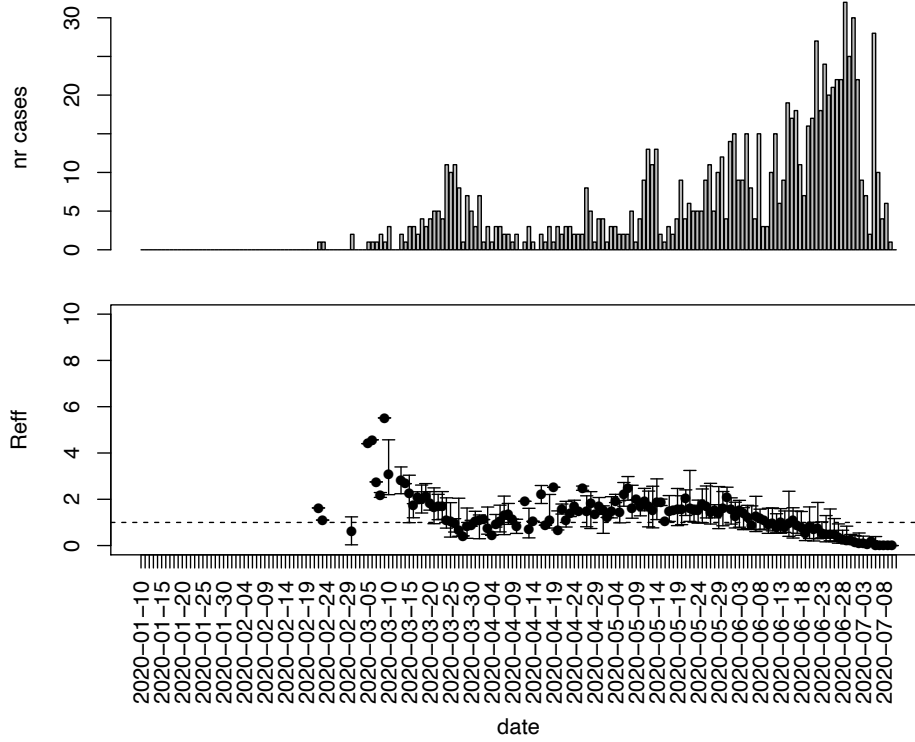


FAYETTE, n=532



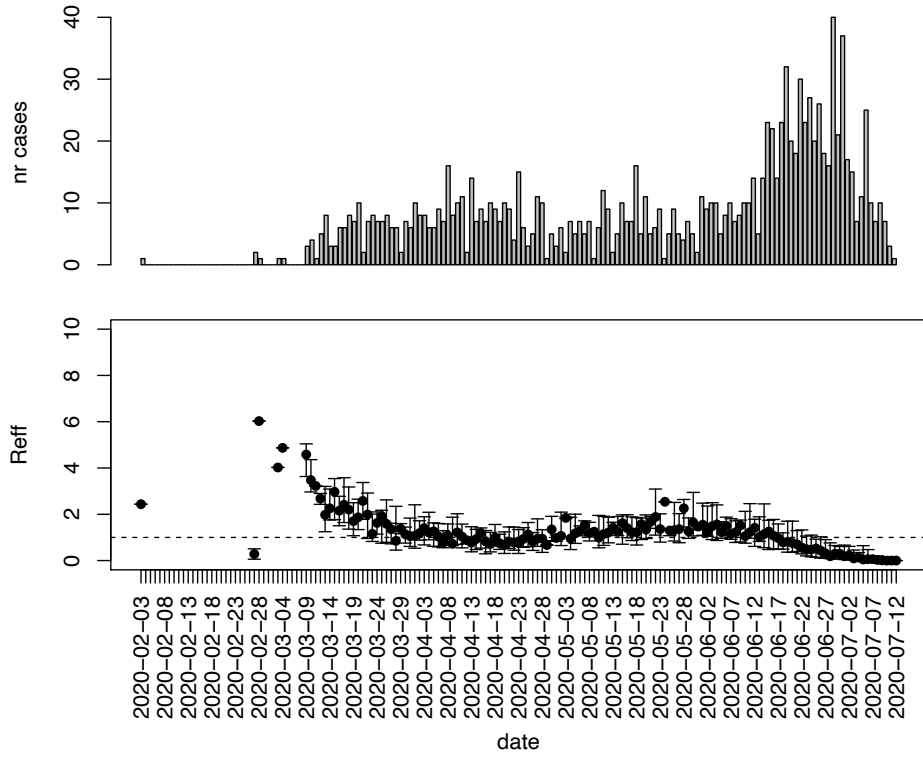
Appendix Figure 66. Epidemic curves and reproduction number estimates until July 13th in Fayette county.

FLOYD, n=917



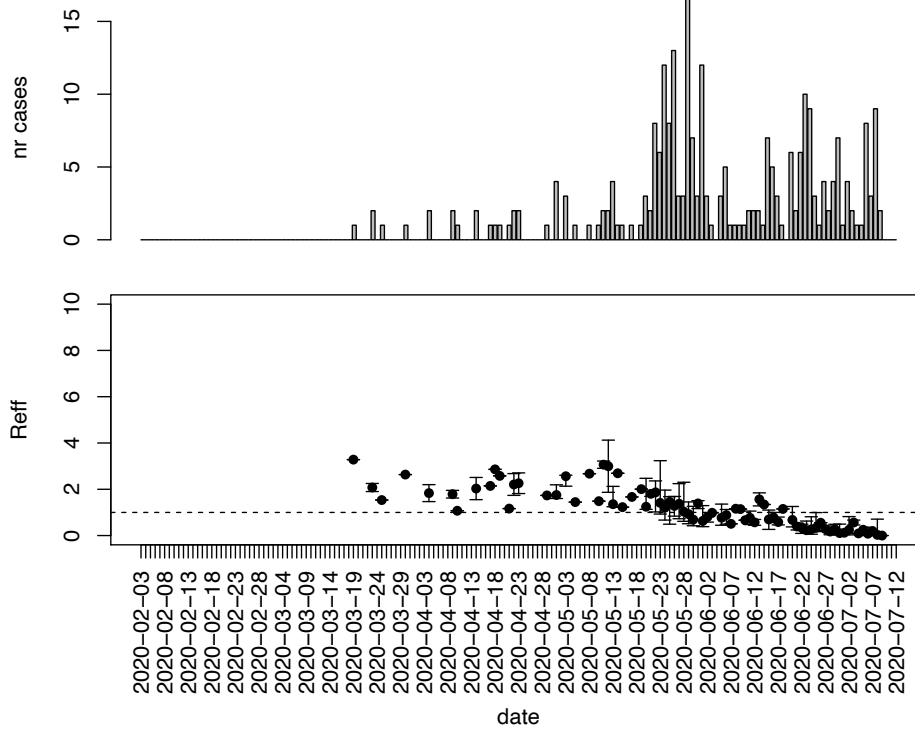
Appendix Figure 67. Epidemic curves and reproduction number estimates until July 13th in Floyd county.

FORSYTH, n=1224



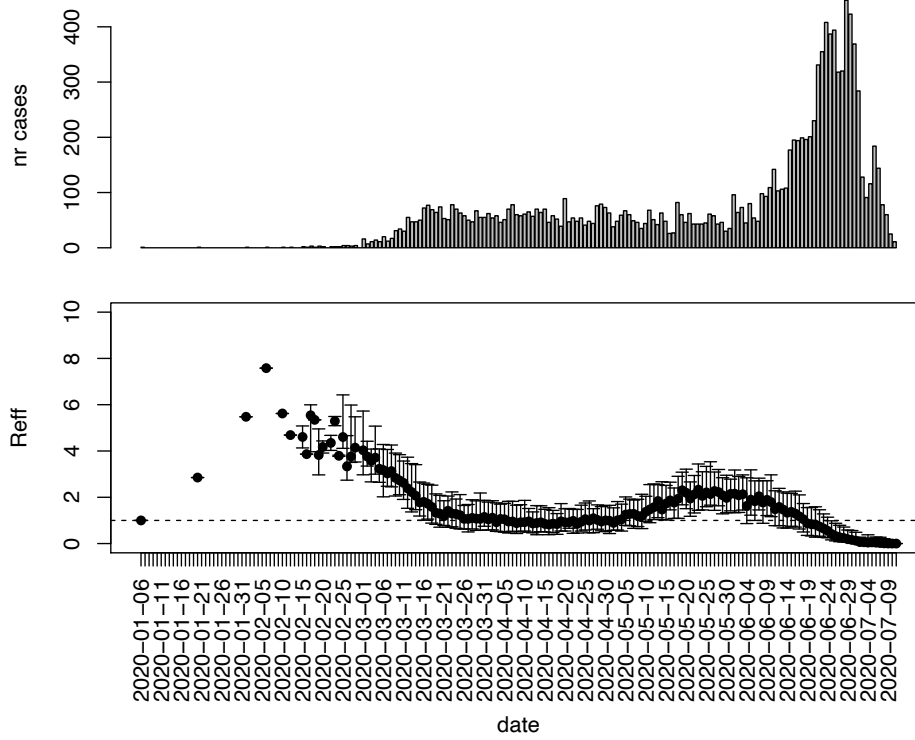
Appendix Figure 68. Epidemic curves and reproduction number estimates until July 13th in Forsyth county.

FRANKLIN, n=264



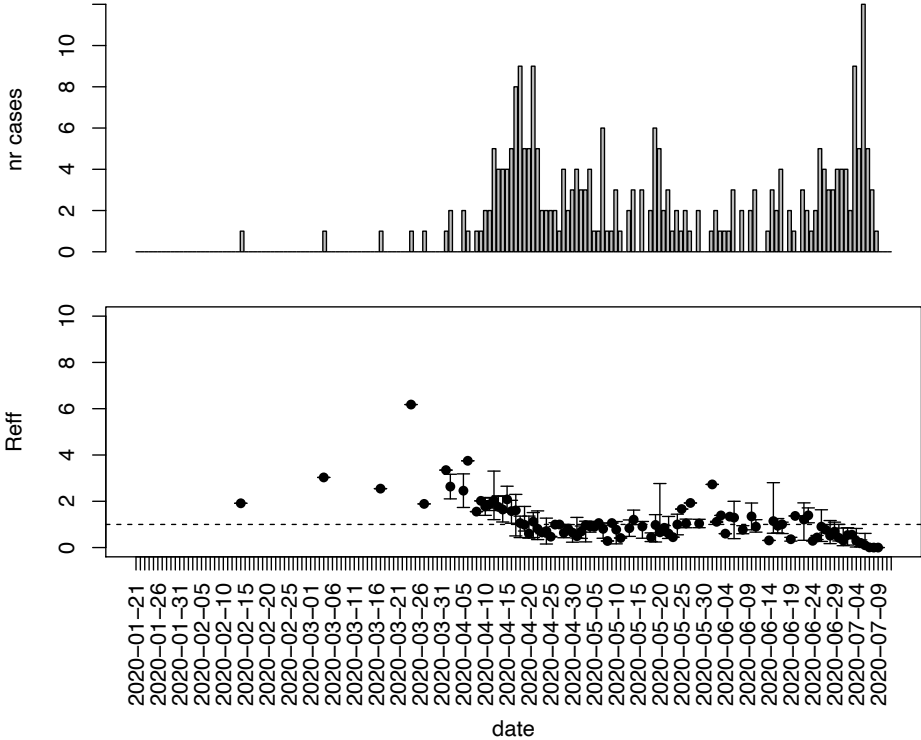
Appendix Figure 69. Epidemic curves and reproduction number estimates until July 13th in Franklin county.

FULTON, n=12232

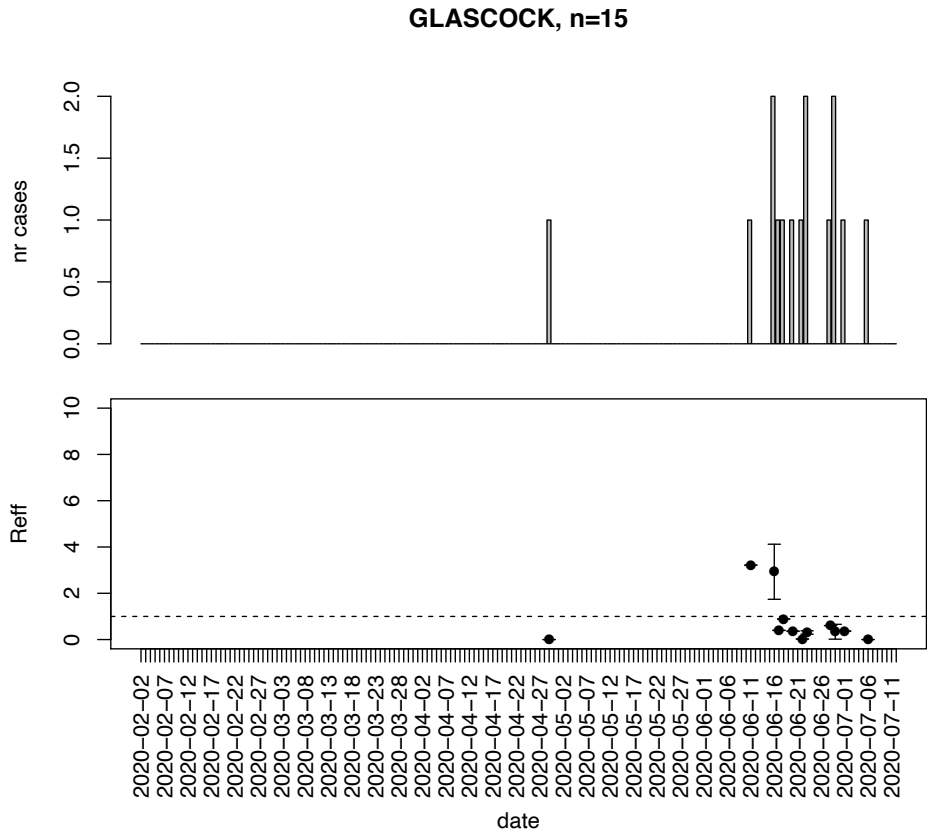


Appendix Figure 70. Epidemic curves and reproduction number estimates until July 13th in Fulton county.

GILMER, n=262

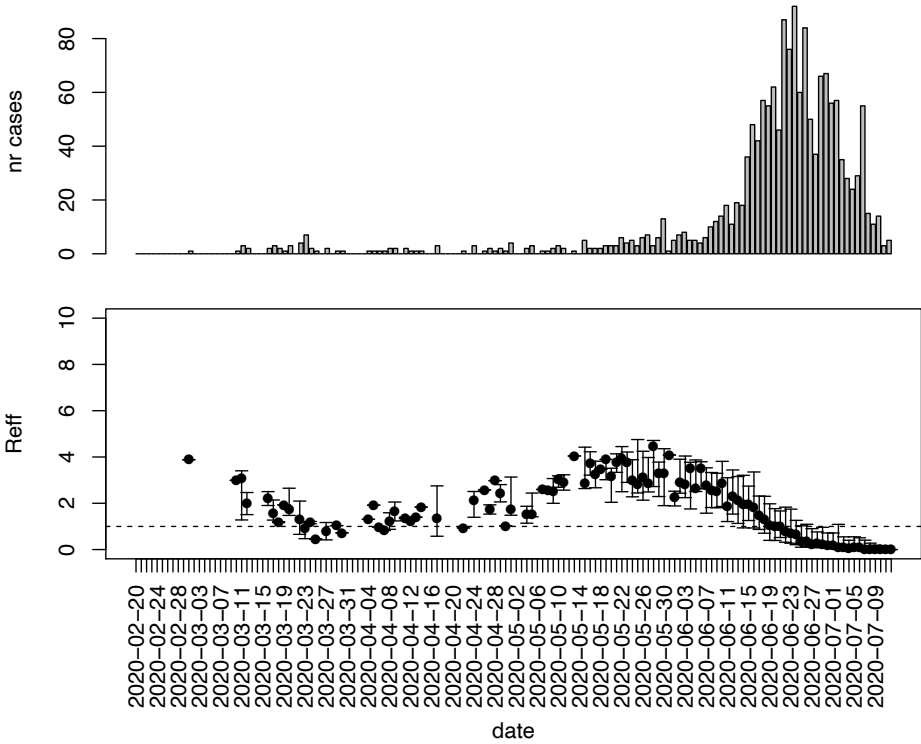


Appendix Figure 71. Epidemic curves and reproduction number estimates until July 13th in Gilmer county.



Appendix Figure 72. Epidemic curves and reproduction number estimates until July 13th in Glascock county.

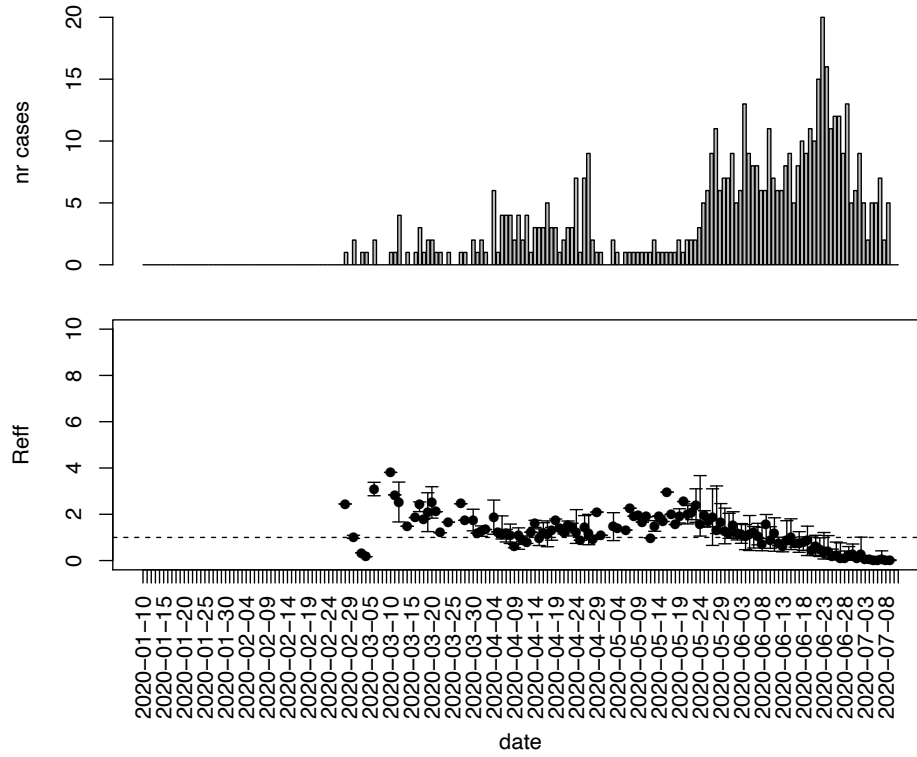
GLYNN, n=1595



Appendix Figure 73. Epidemic curves and reproduction number estimates until July 13th in Glynn county.

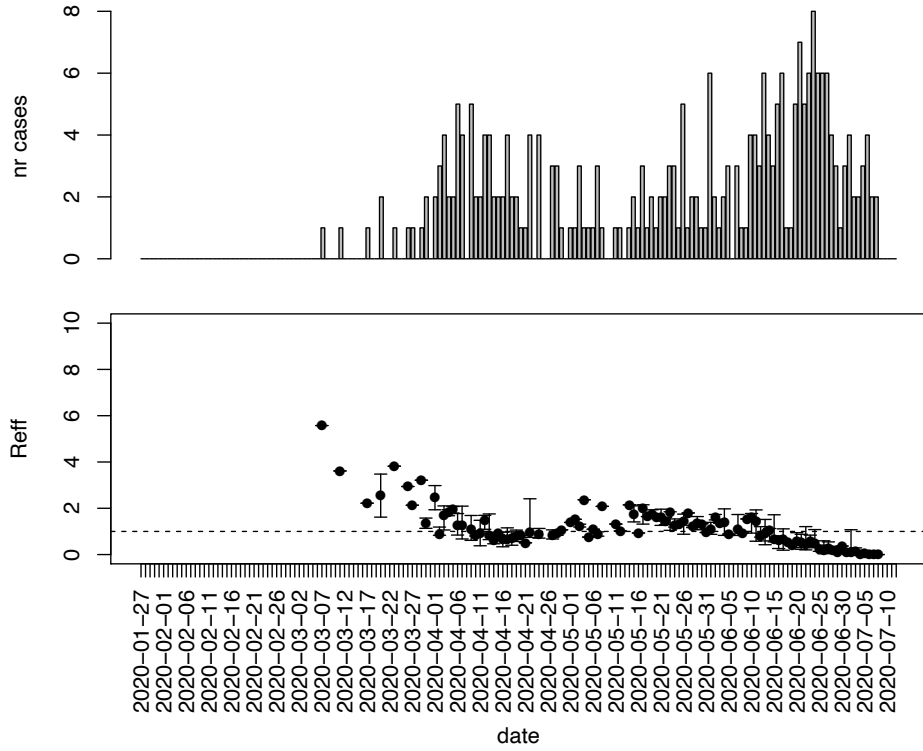


GORDON, n=532



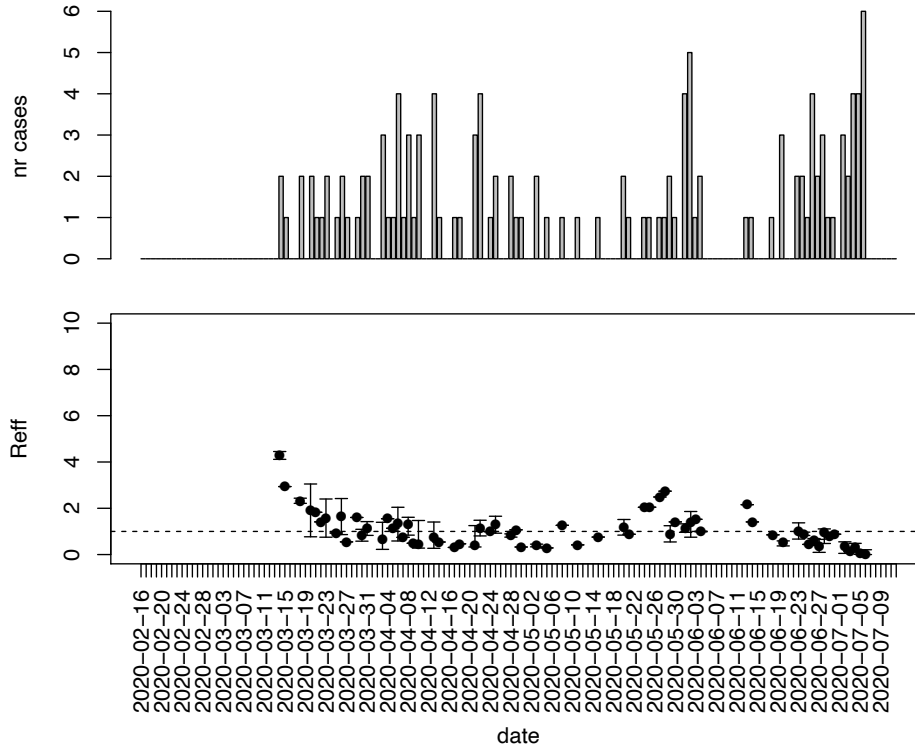
Appendix Figure 74. Epidemic curves and reproduction number estimates until July 13th in Gordon county.

GRADY, n=264



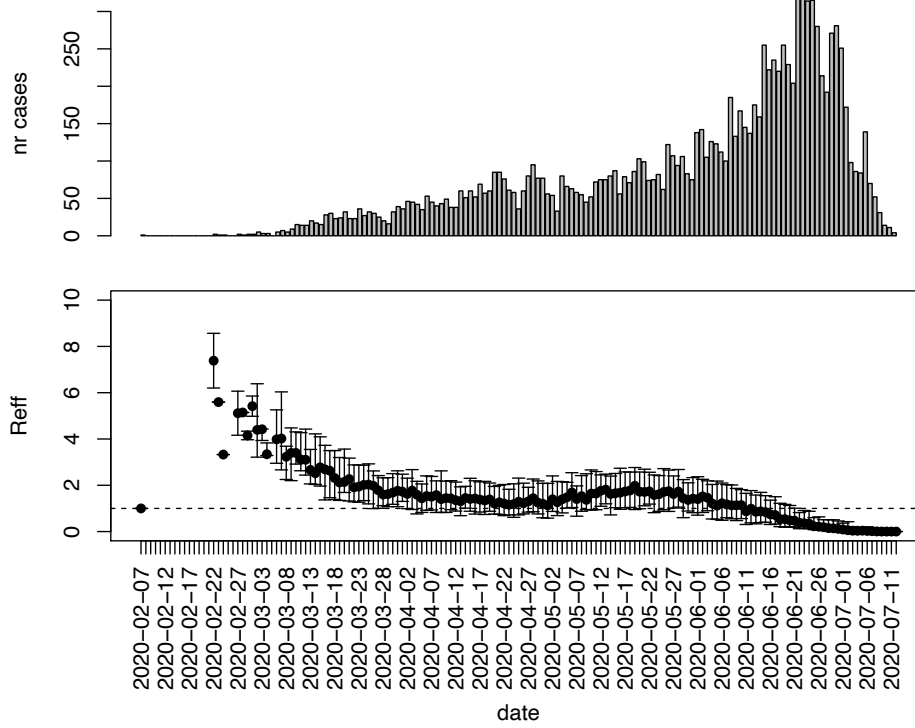
Appendix Figure 75. Epidemic curves and reproduction number estimates until July 13th in Grady county.

GREENE, n=127



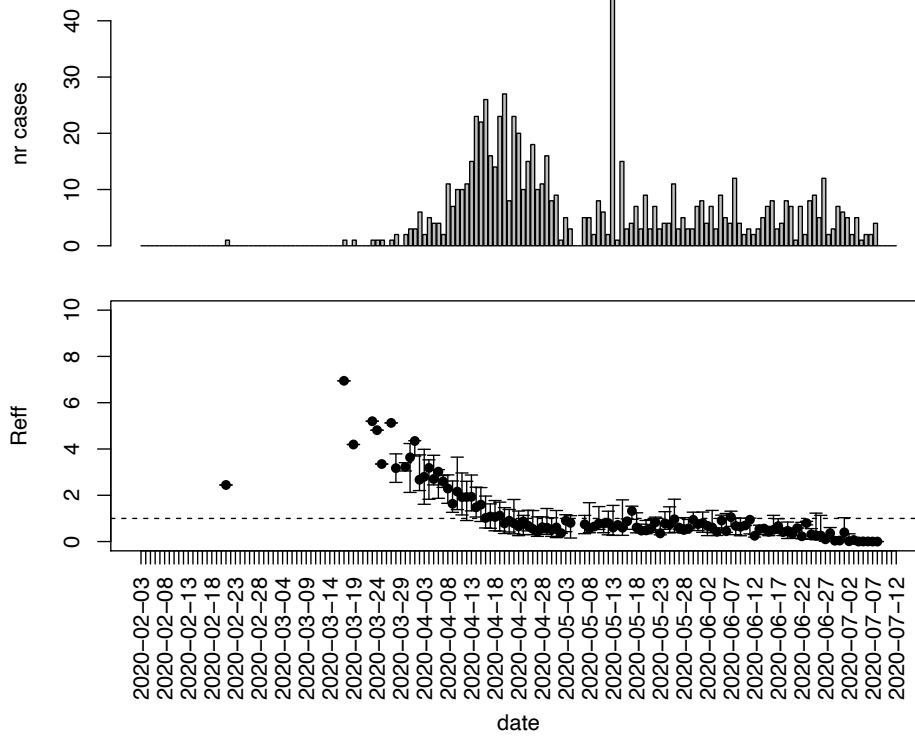
Appendix Figure 76. Epidemic curves and reproduction number estimates until July 13th in Greene county.

**GWINNETT, n=11720**

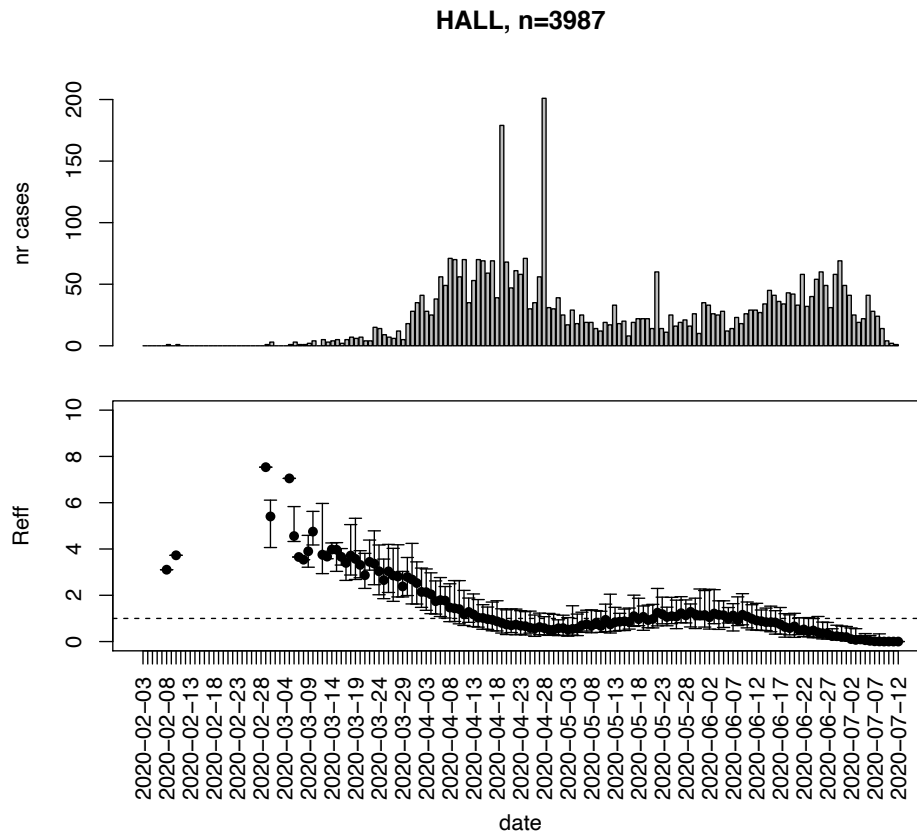


Appendix Figure 77. Epidemic curves and reproduction number estimates until July 13th in Gwinnett county.

HABERSHAM, n=770

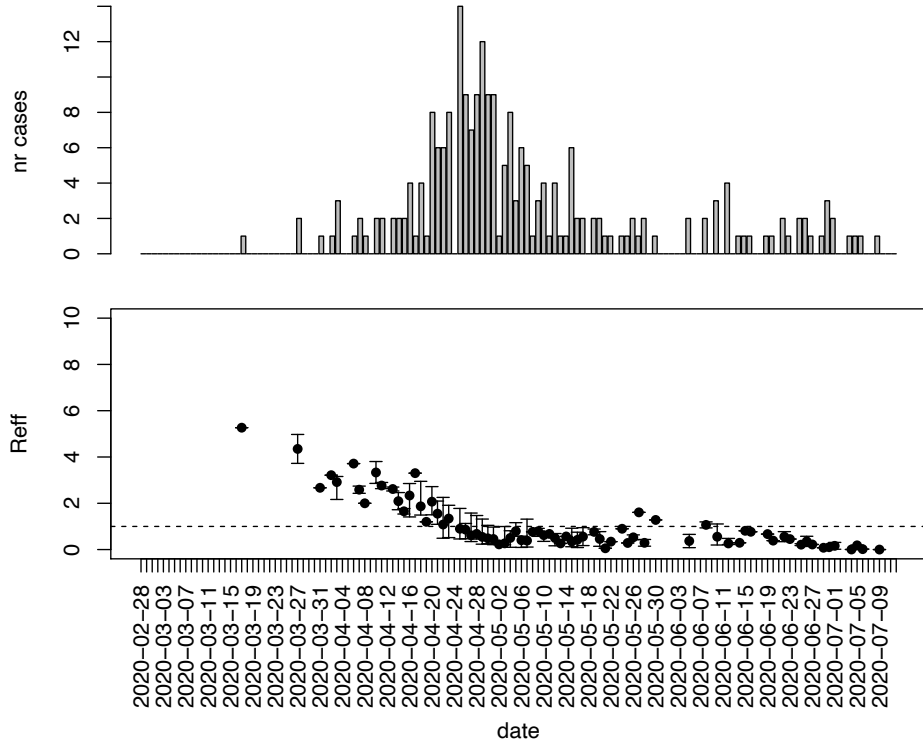


Appendix Figure 78. Epidemic curves and reproduction number estimates until July 13th in Habersham county.



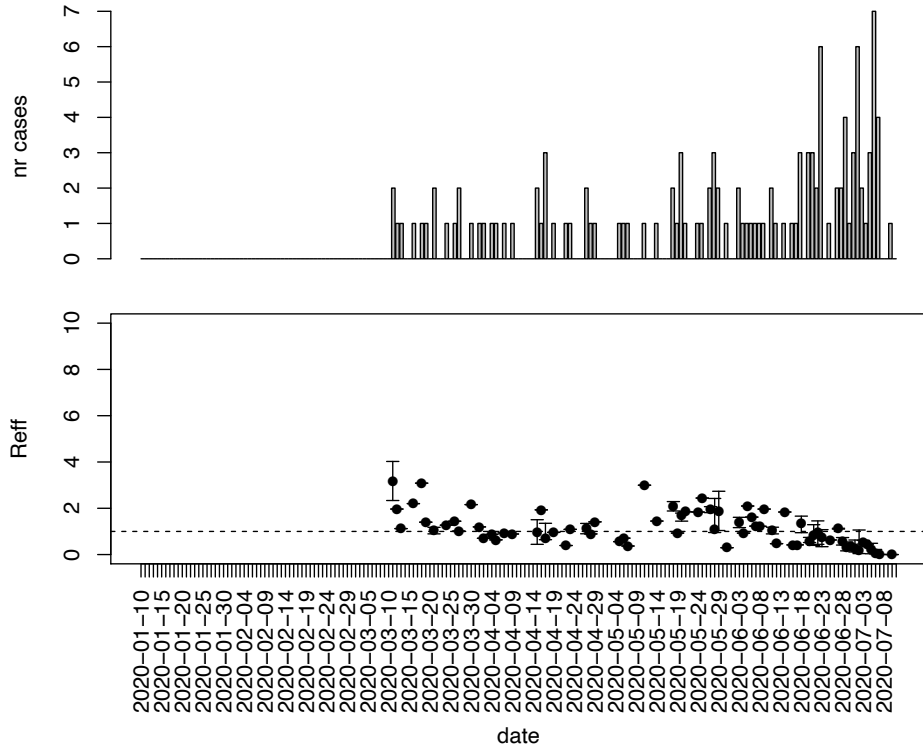
Appendix Figure 79. Epidemic curves and reproduction number estimates until July 13th in Hall county.

HANCOCK, n=230



Appendix Figure 80. Epidemic curves and reproduction number estimates until July 13th in Hancock county.

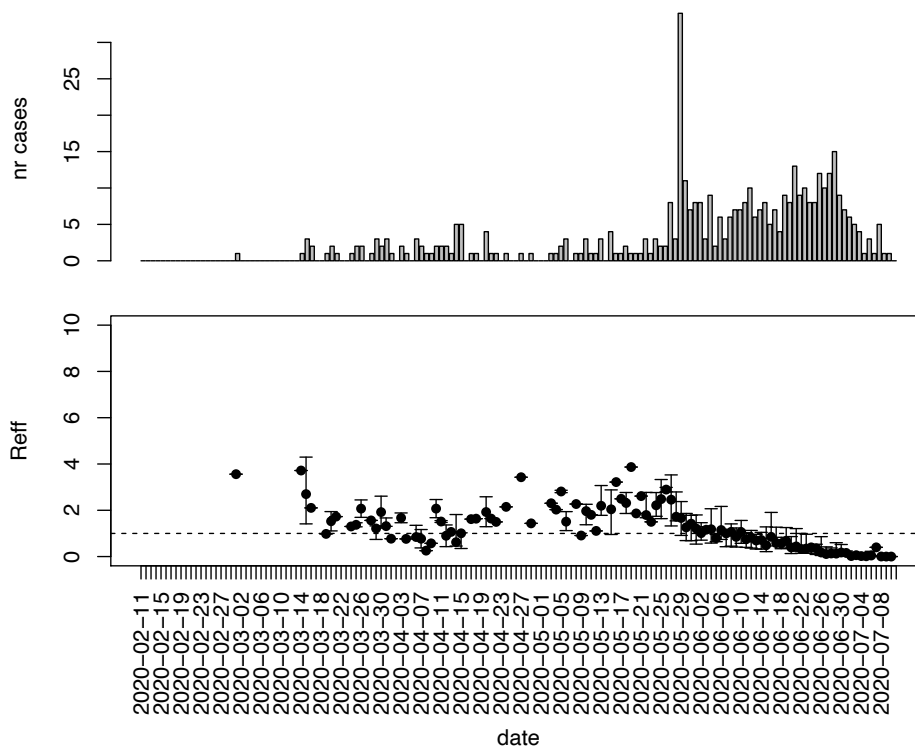
HARALSON, n=123



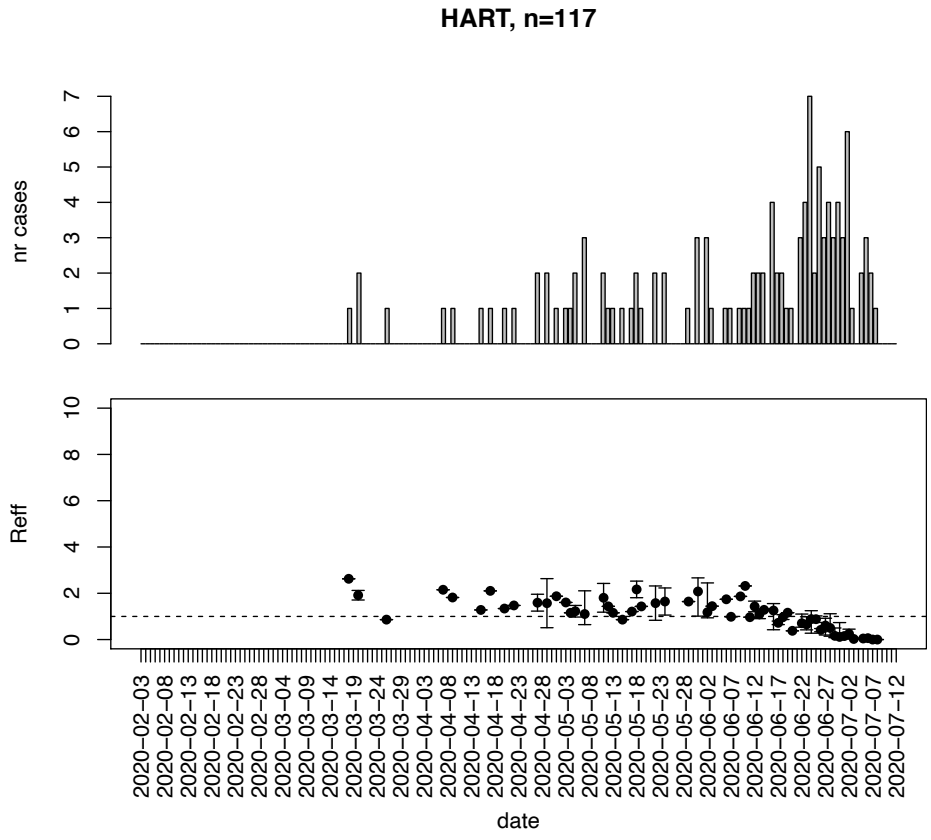
Appendix Figure 81. Epidemic curves and reproduction number estimates until July 13th in Haralson county.



HARRIS, n=437

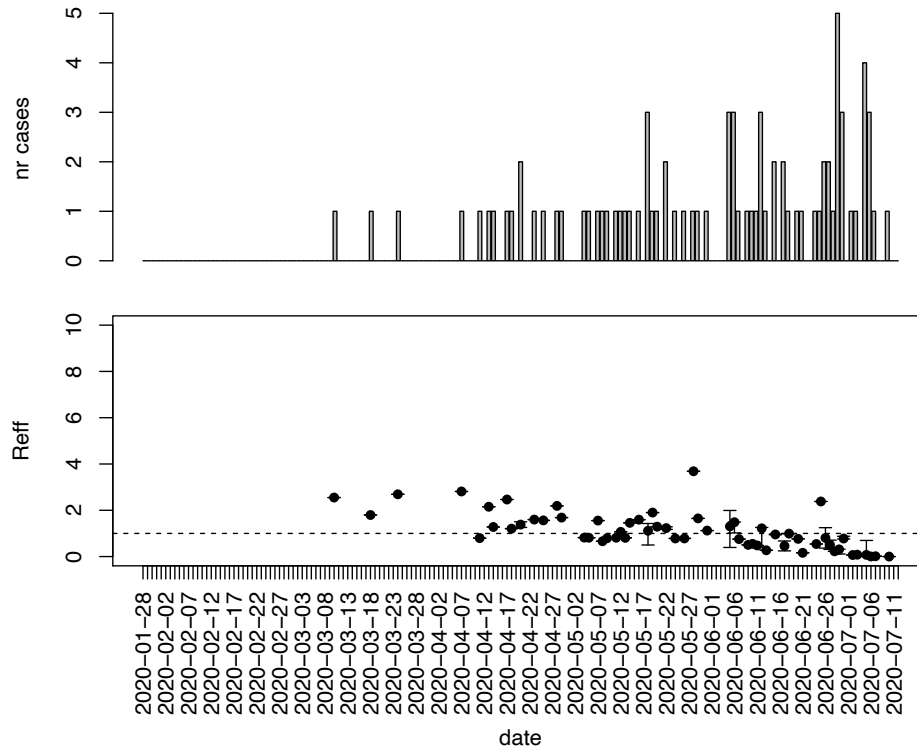


Appendix Figure 82. Epidemic curves and reproduction number estimates until July 13th in Harris county.



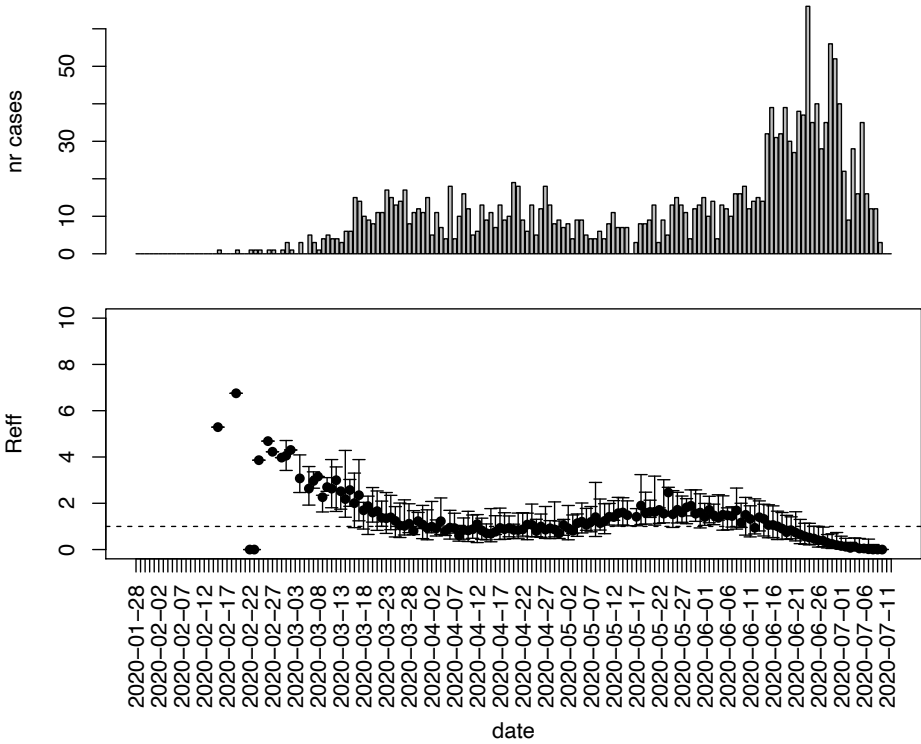
Appendix Figure 83. Epidemic curves and reproduction number estimates until July 13th in Hart county.

HEARD, n=84



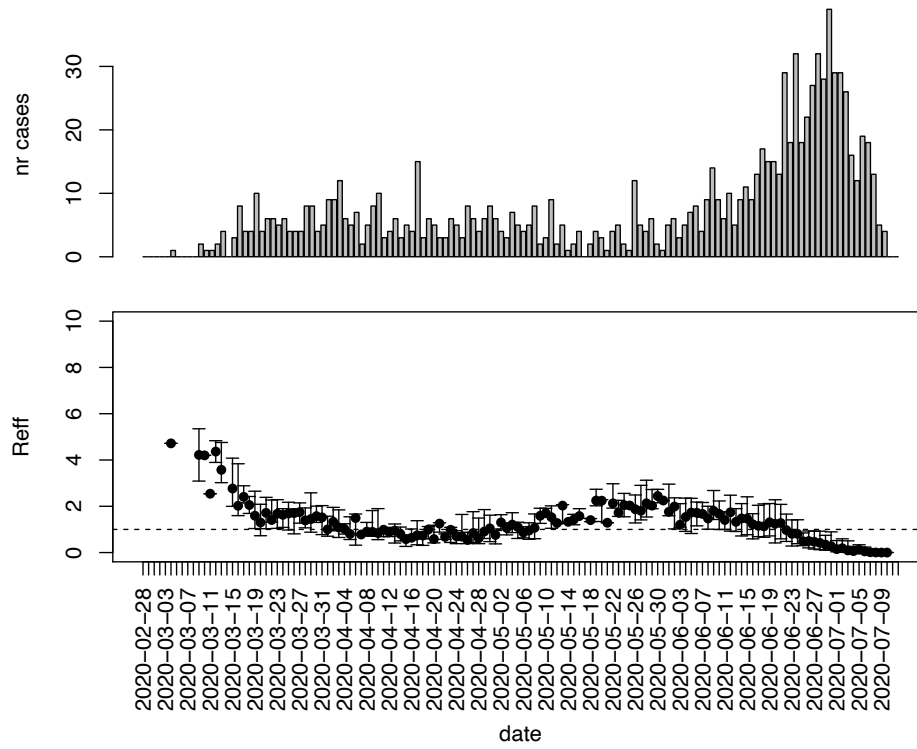
Appendix Figure 84. Epidemic curves and reproduction number estimates until July 13th in Heard county.

HENRY, n=1799



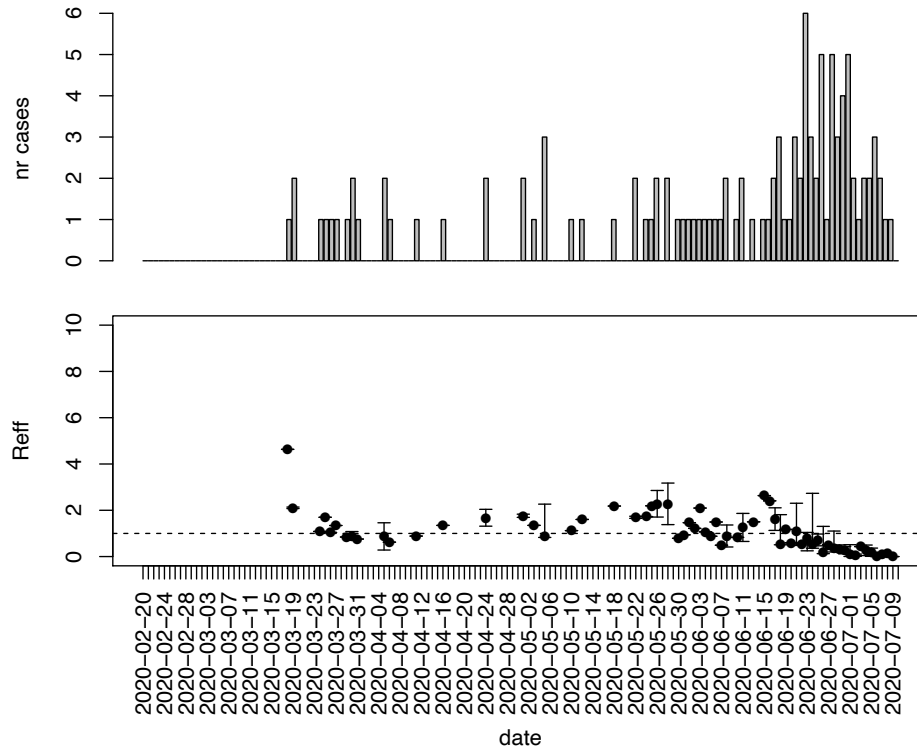
Appendix Figure 85. Epidemic curves and reproduction number estimates until July 13th in Henry county.

HOUSTON, n=1014



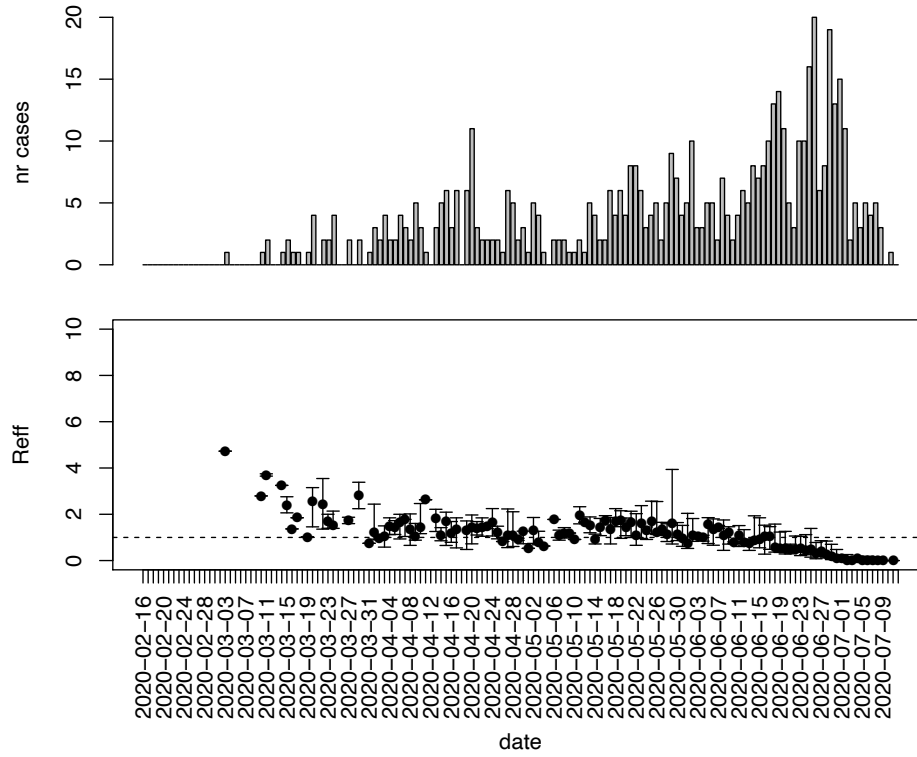
Appendix Figure 86. Epidemic curves and reproduction number estimates until July 13th in Houston county.

IRWIN, n=112



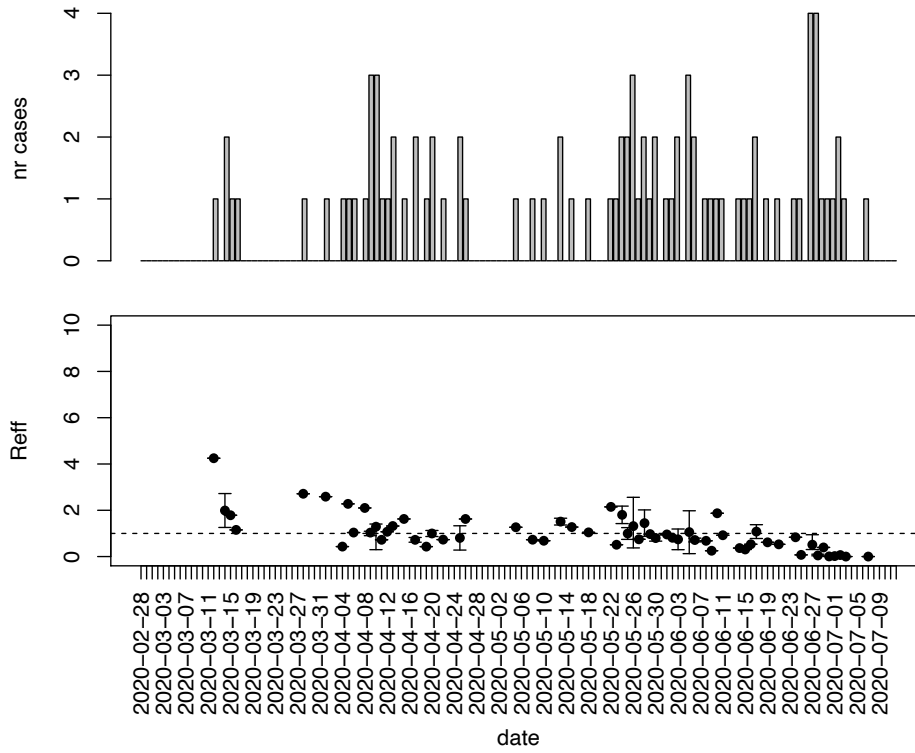
Appendix Figure 87. Epidemic curves and reproduction number estimates until July 13th in Irwin county.

JACKSON, n=538



Appendix Figure 88. Epidemic curves and reproduction number estimates until July 13th in Jackson county.

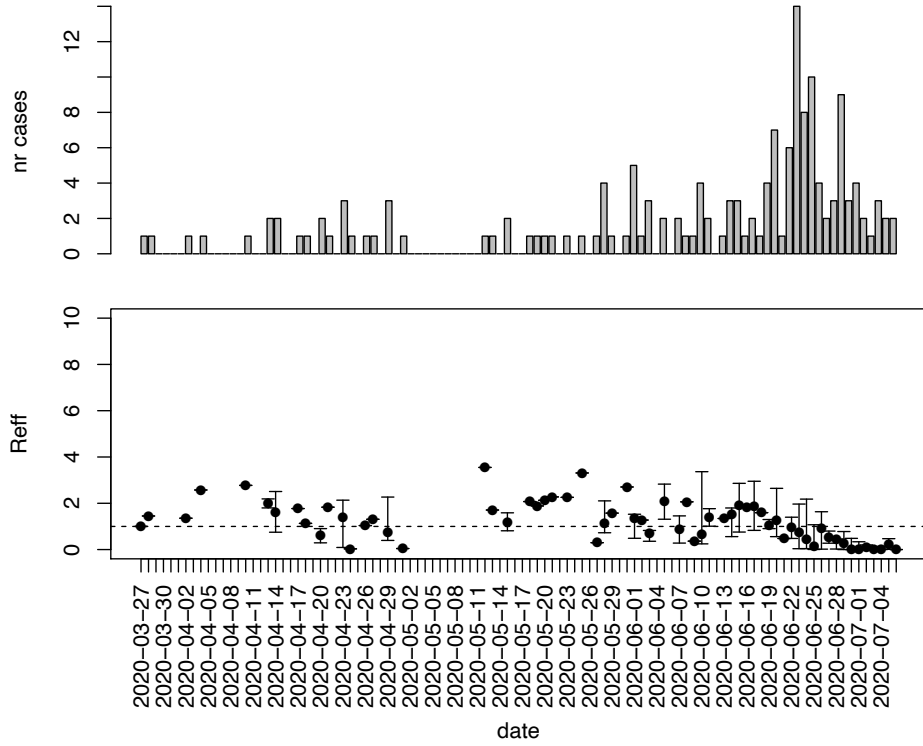
JASPER, n=90



Appendix Figure 89. Epidemic curves and reproduction number estimates until July 13th in Jasper county.

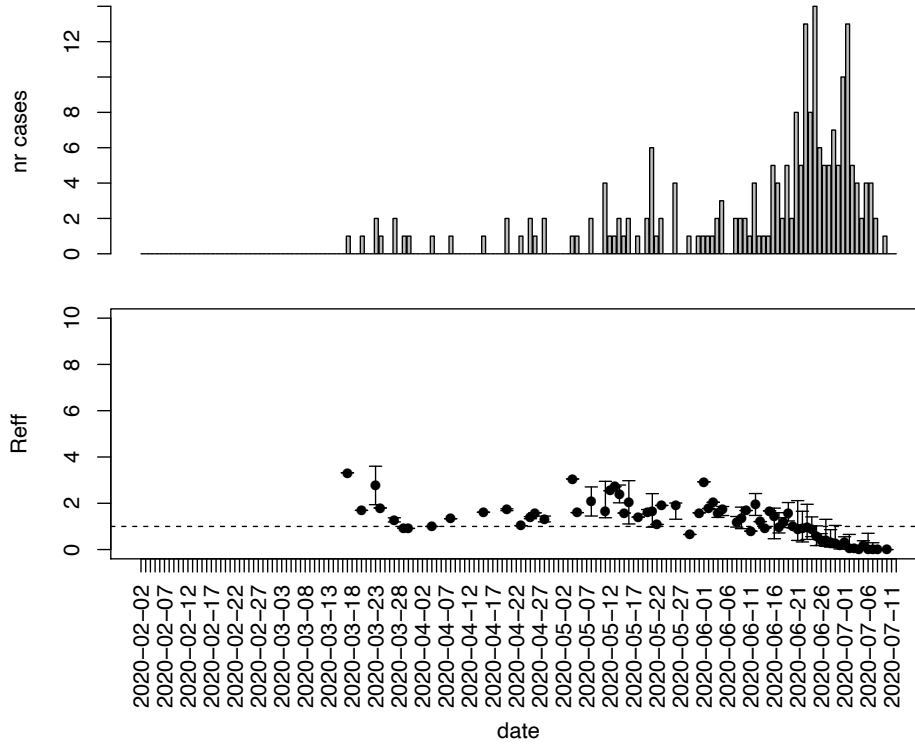


JEFF DAVIS, n=158



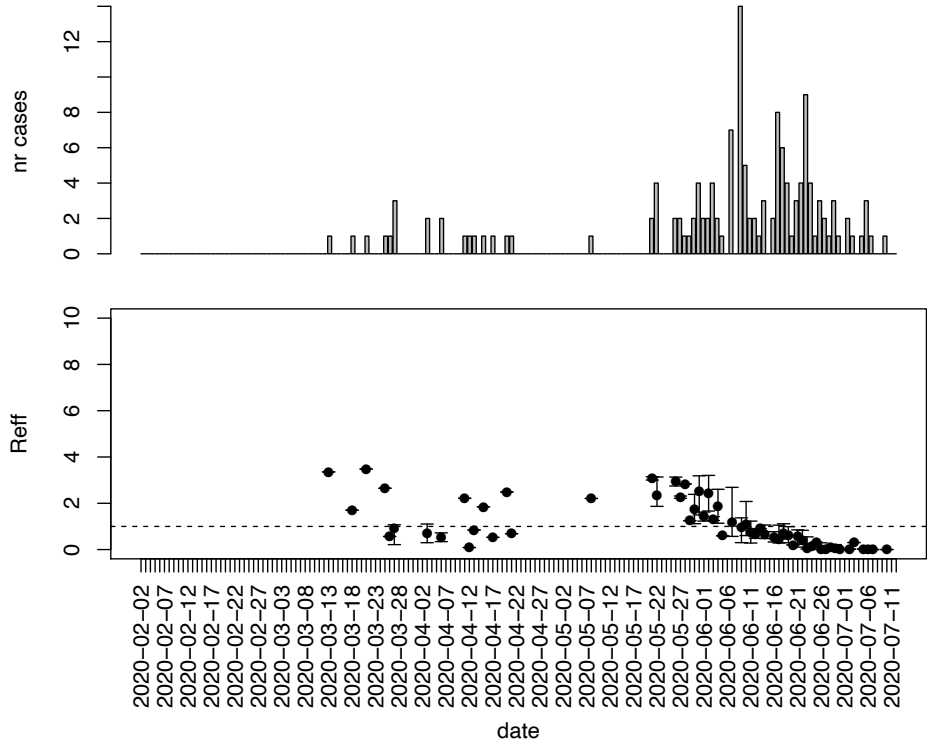
Appendix Figure 90. Epidemic curves and reproduction number estimates until July 13th in Jeff Davis county.

JEFFERSON, n=214



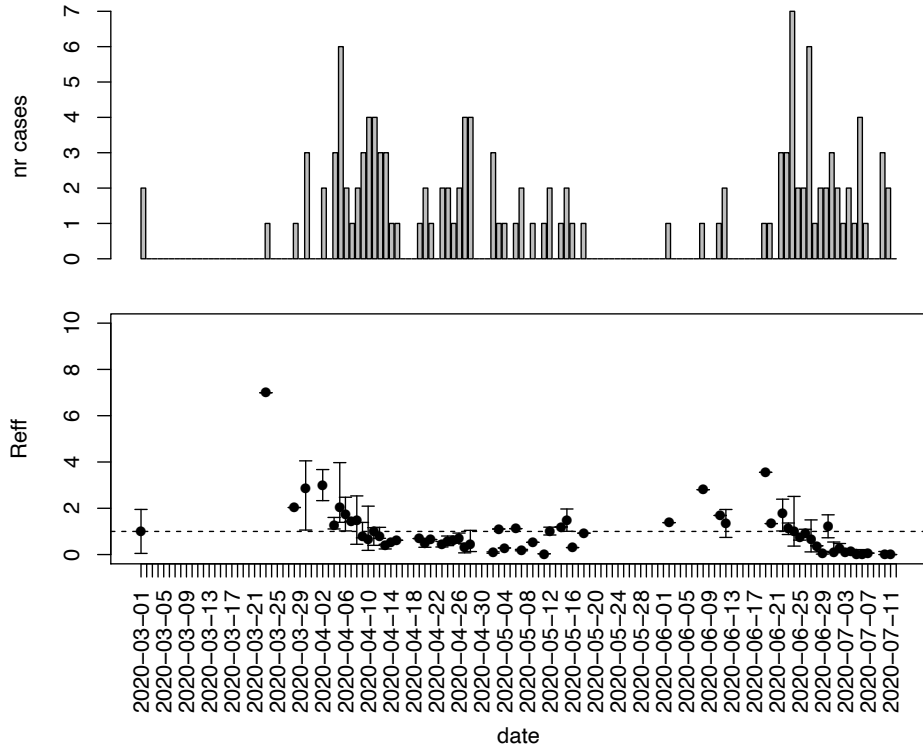
Appendix Figure 91. Epidemic curves and reproduction number estimates until July 13th in Jefferson county.

JENKINS, n=144



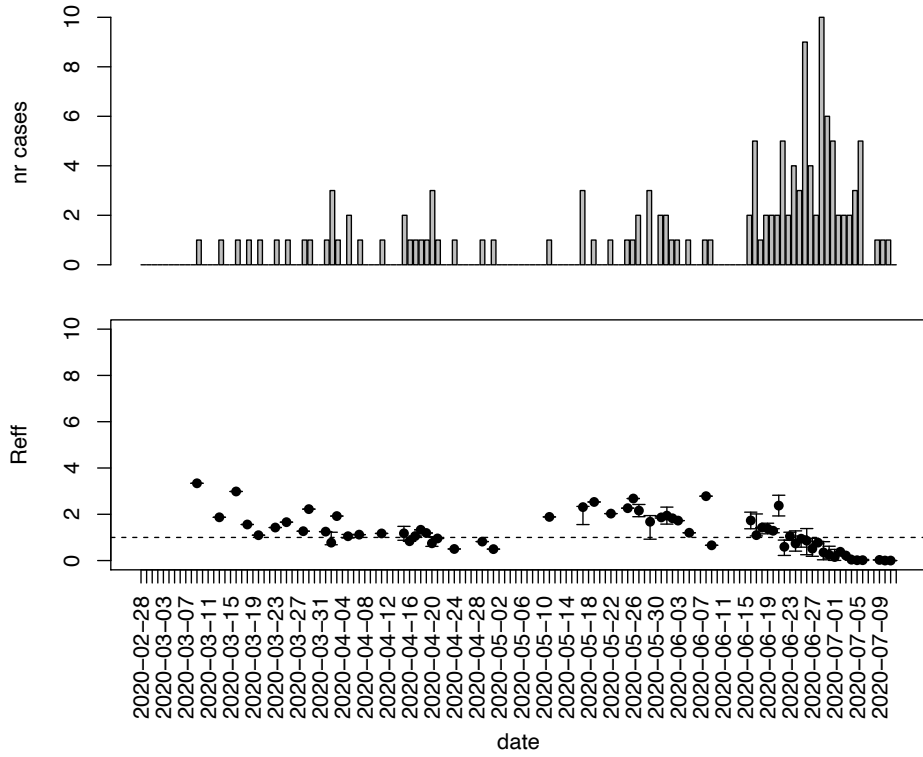
Appendix Figure 92. Epidemic curves and reproduction number estimates until July 13th in Jenkins county.

JOHNSON, n=132



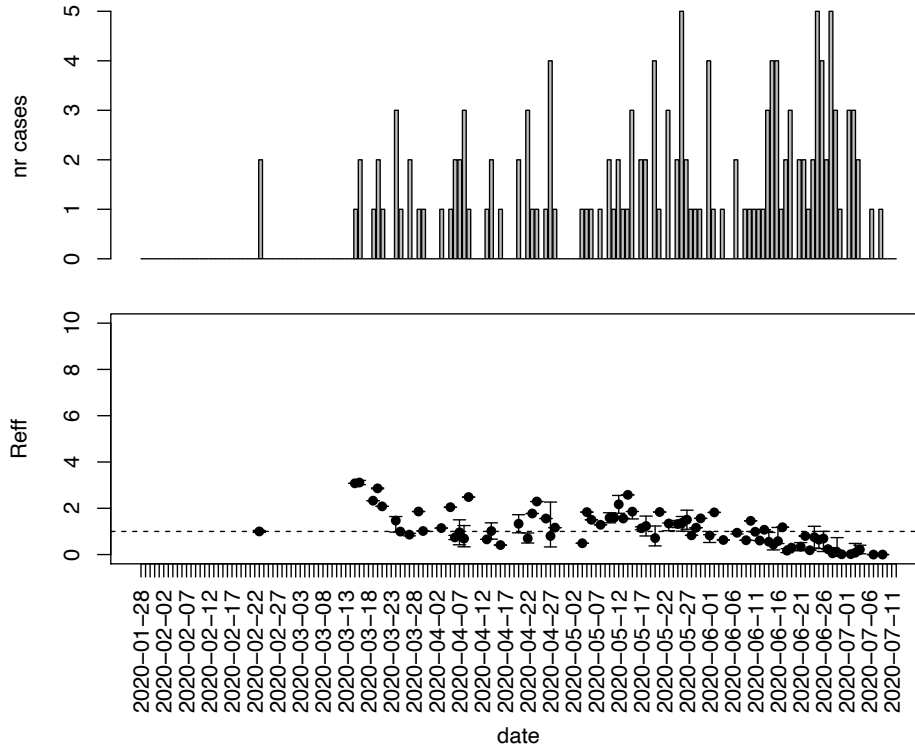
Appendix Figure 93. Epidemic curves and reproduction number estimates until July 13th in Johnson county.

JONES, n=134



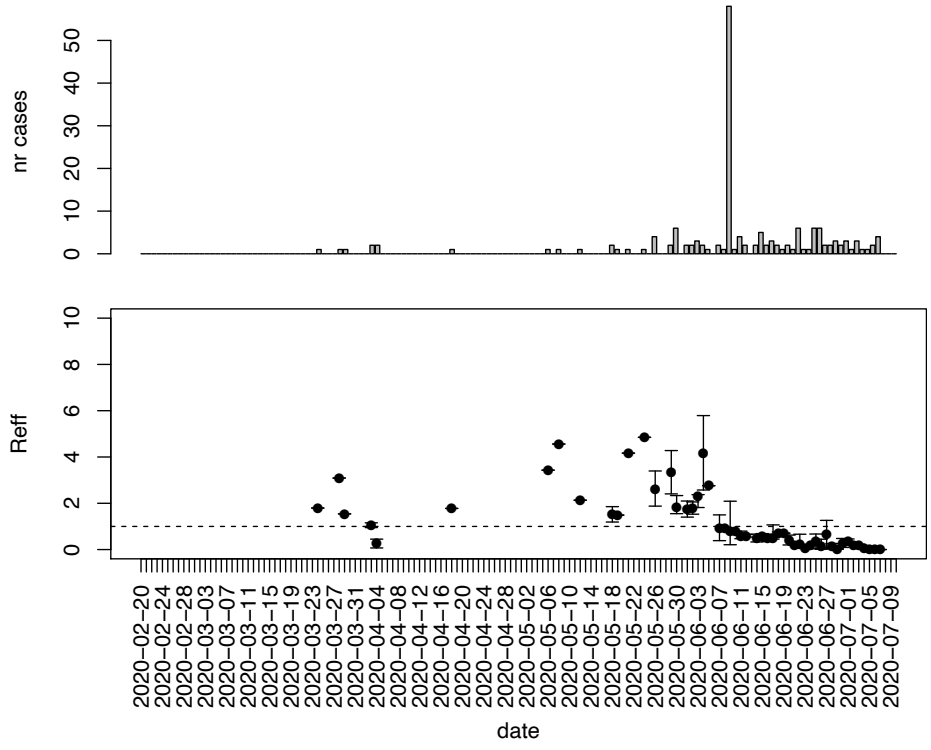
Appendix Figure 94. Epidemic curves and reproduction number estimates until July 13th in Jones county.

LAMAR, n=149



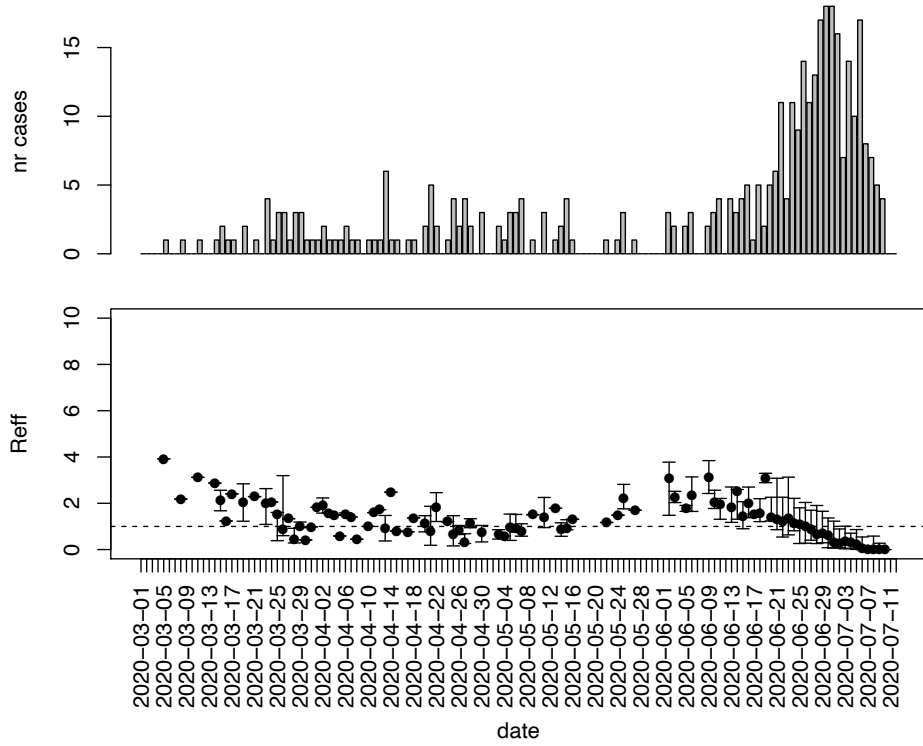
Appendix Figure 95. Epidemic curves and reproduction number estimates until July 13th in Lamar county.

LANIER, n=168



Appendix Figure 96. Epidemic curves and reproduction number estimates until July 13th in Lanier county.

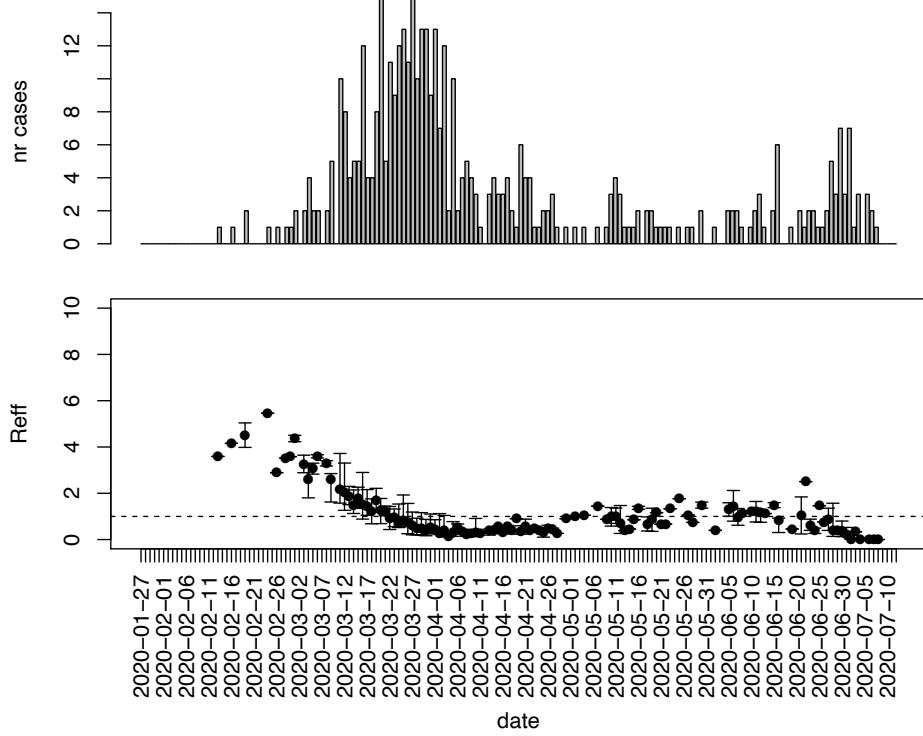
LAURENS, n=378



Appendix Figure 97. Epidemic curves and reproduction number estimates until July 13th in Laurens county.

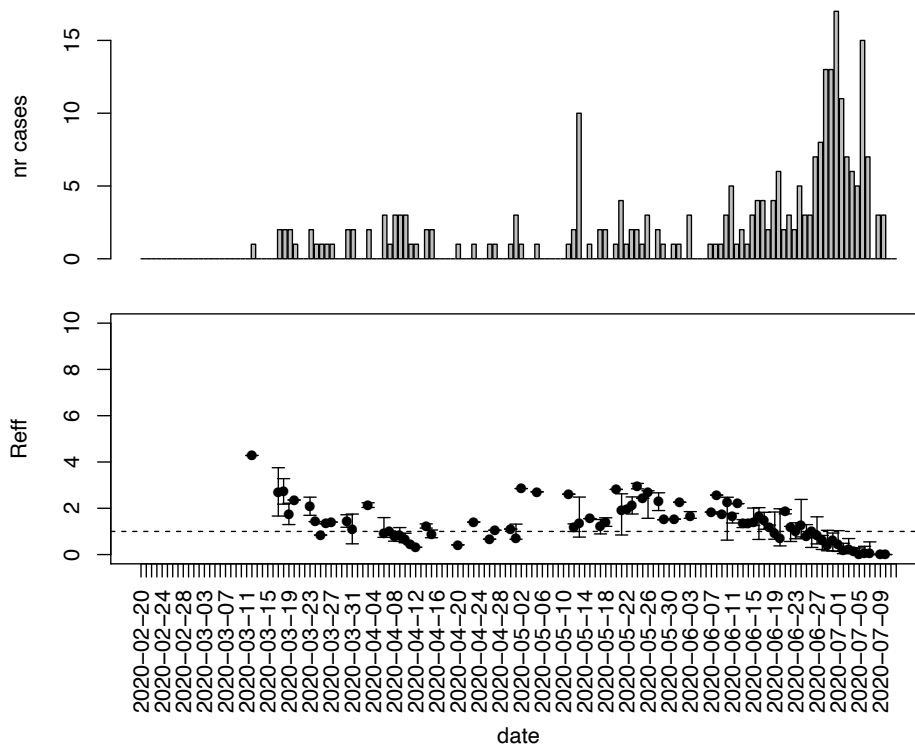


LEE, n=433



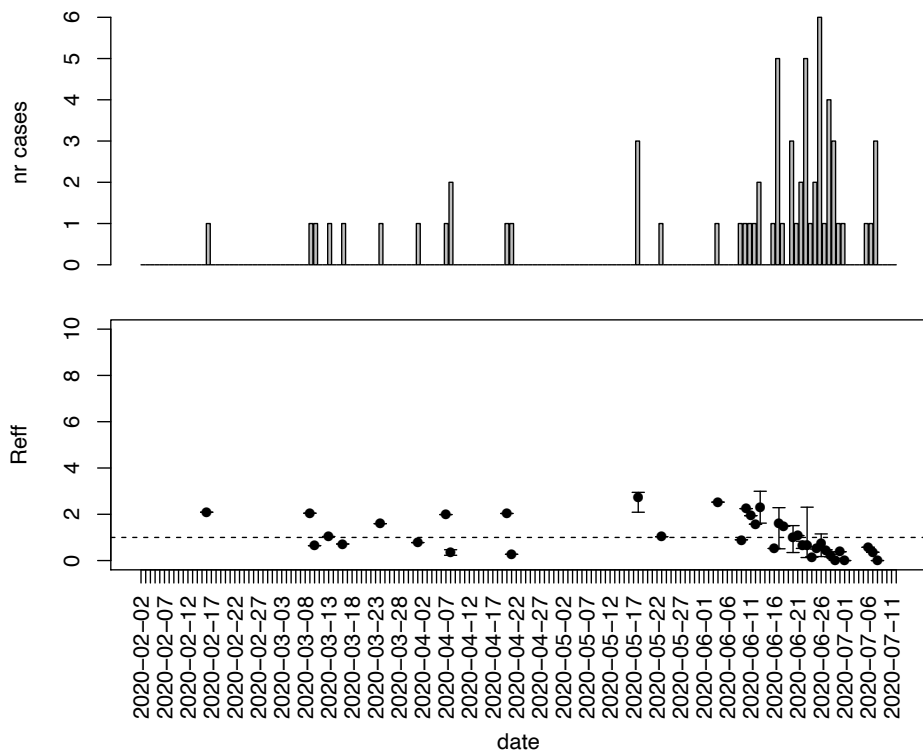
Appendix Figure 98. Epidemic curves and reproduction number estimates until July 13th in Lee county.

LIBERTY, n=260

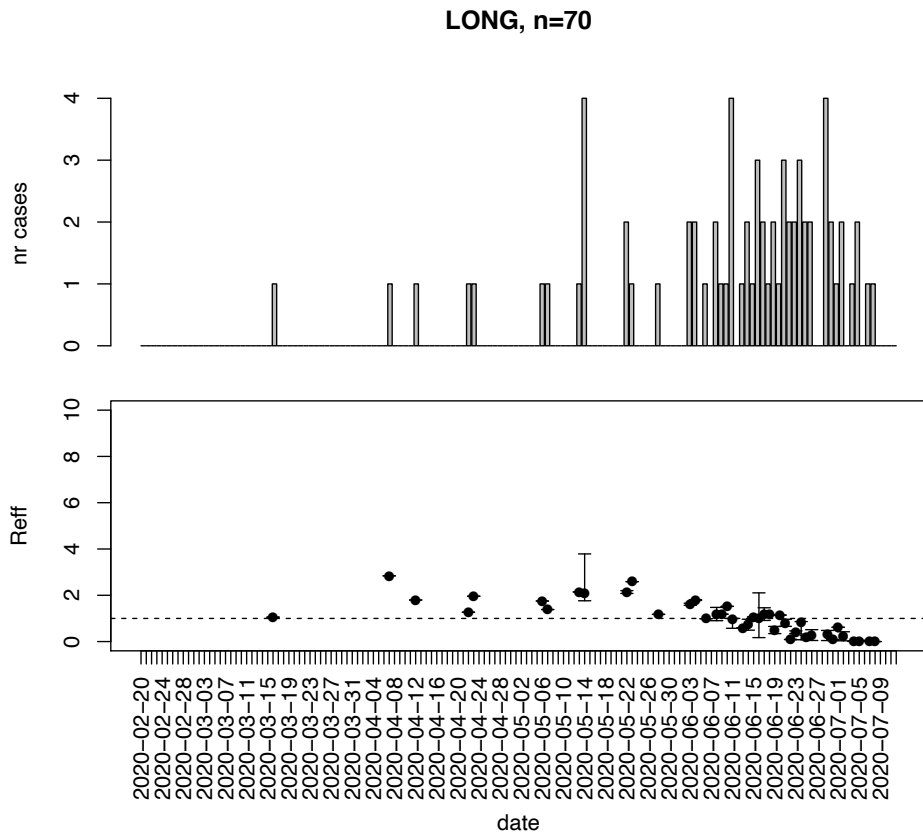


Appendix Figure 99. Epidemic curves and reproduction number estimates until July 13th in Liberty county.

LINCOLN, n=65

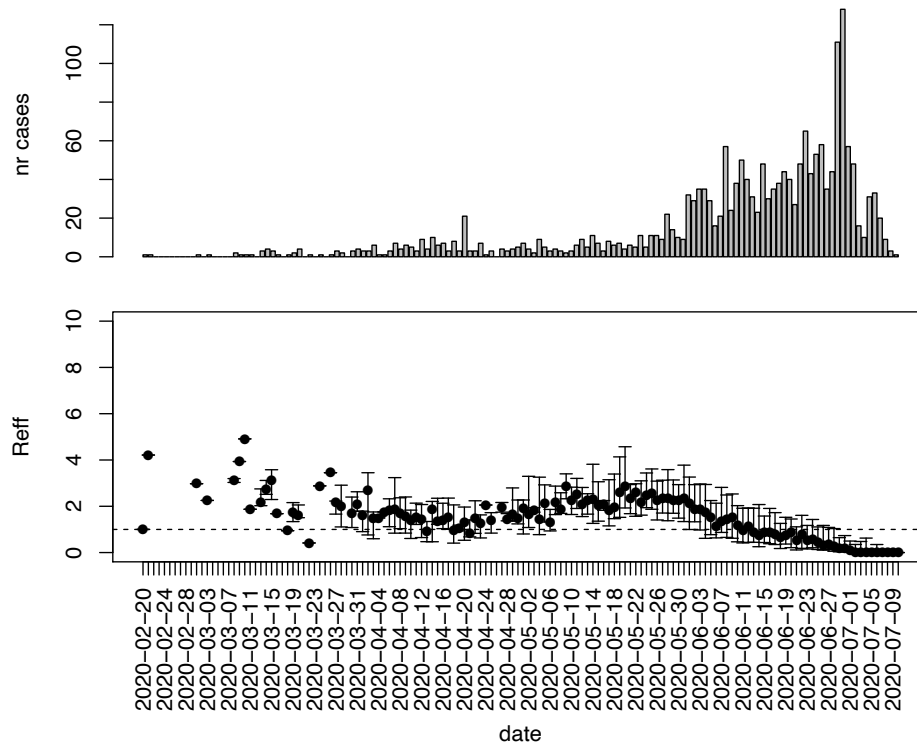


Appendix Figure 100. Epidemic curves and reproduction number estimates until July 13th in Lincoln county.



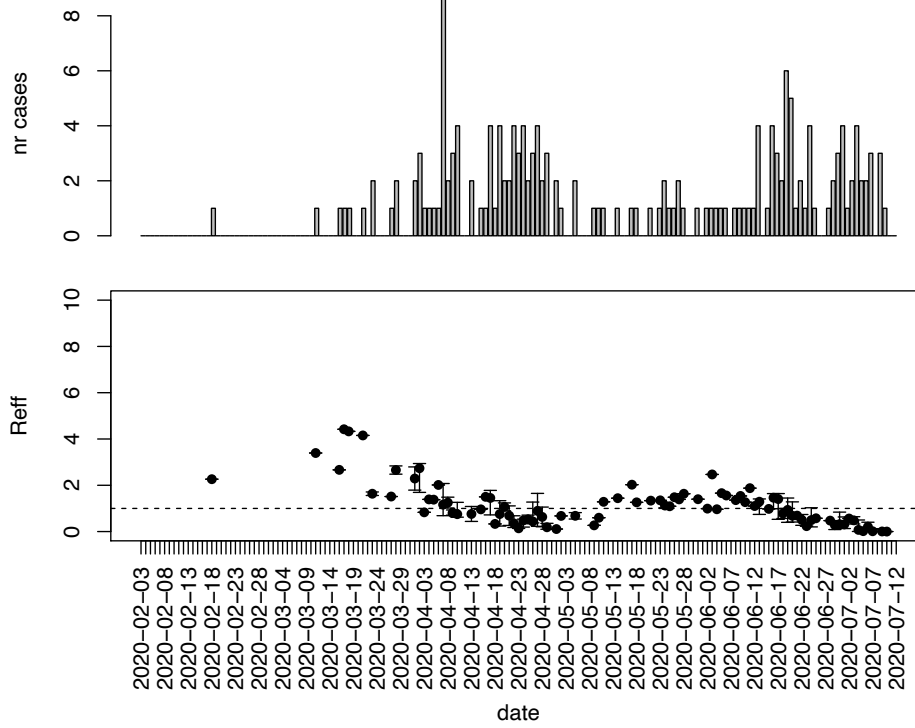
Appendix Figure 101. Epidemic curves and reproduction number estimates until July 13th in Long county.

LOWNDES, n=1944

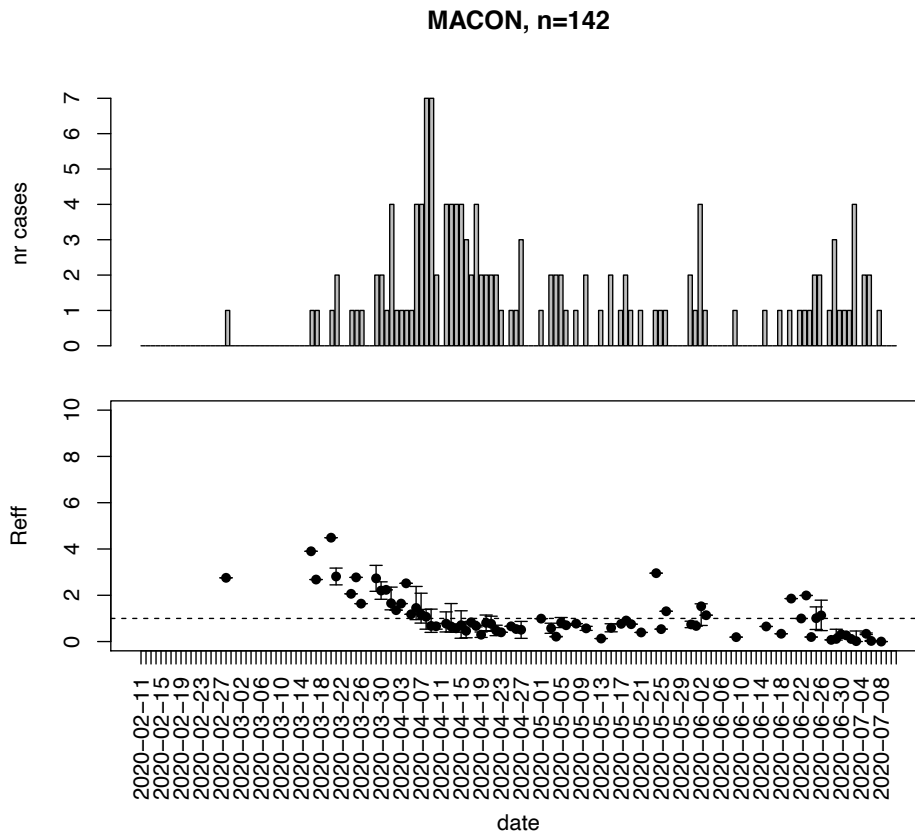


Appendix Figure 102. Epidemic curves and reproduction number estimates until July 13th in Lowndes county.

LUMPKIN, n=173

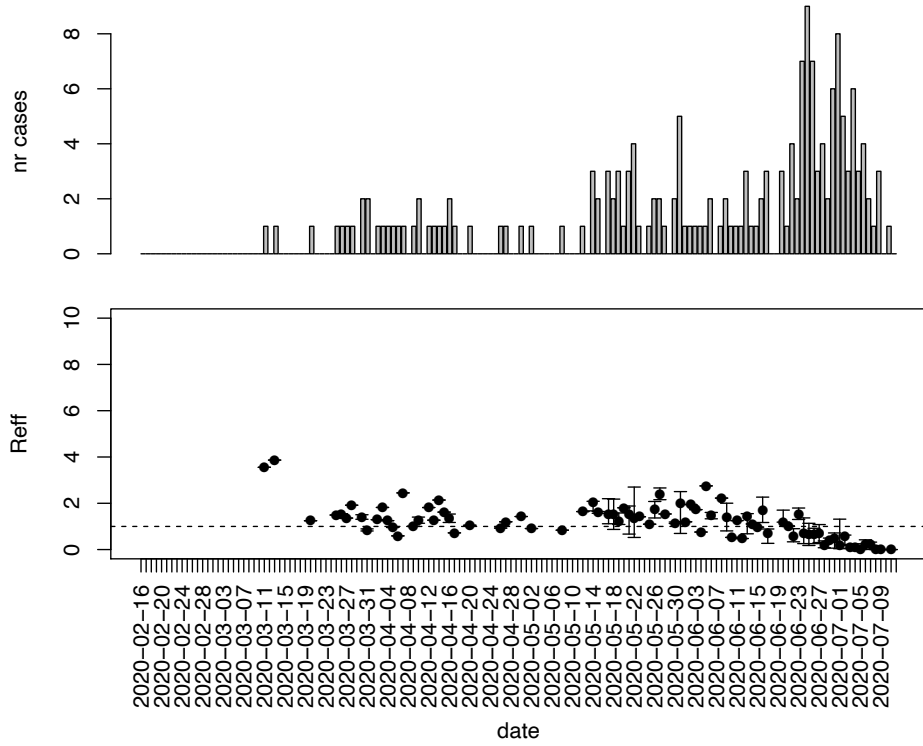


Appendix Figure 103. Epidemic curves and reproduction number estimates until July 13th in Lumpkin county.



Appendix Figure 104. Epidemic curves and reproduction number estimates until July 13th in Macon county.

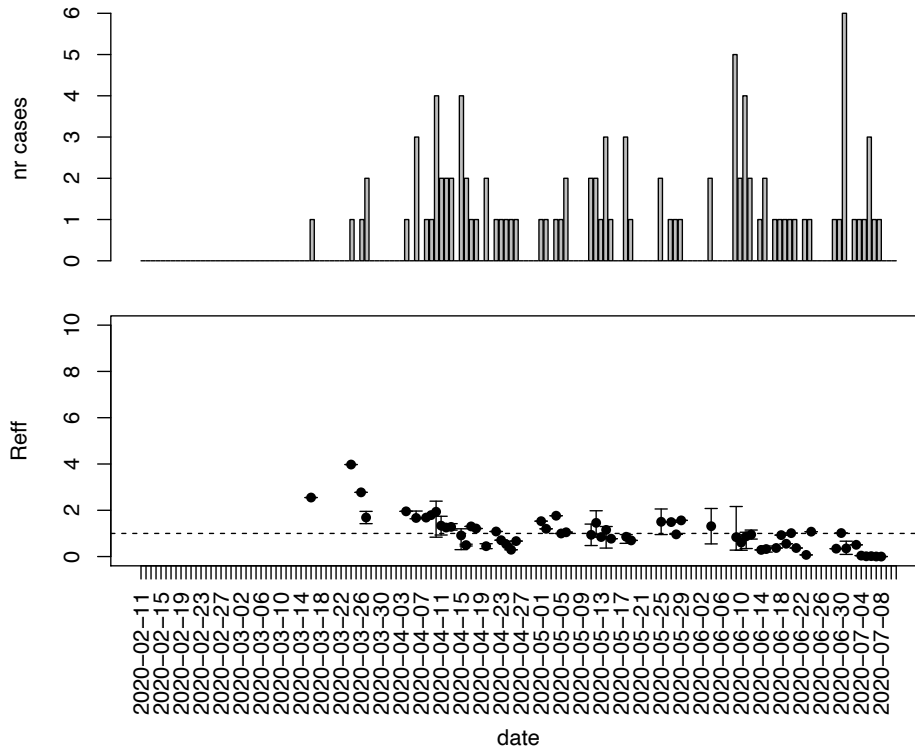
MADISON, n=176



Appendix Figure 105. Epidemic curves and reproduction number estimates until July 13th in Madison county.

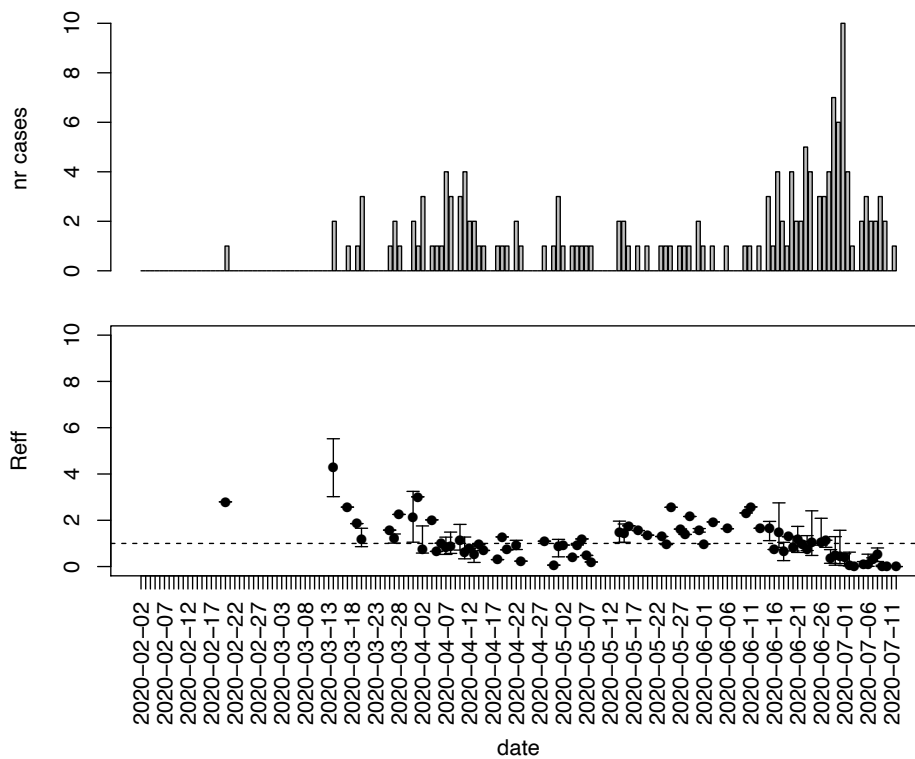


MARION, n=101



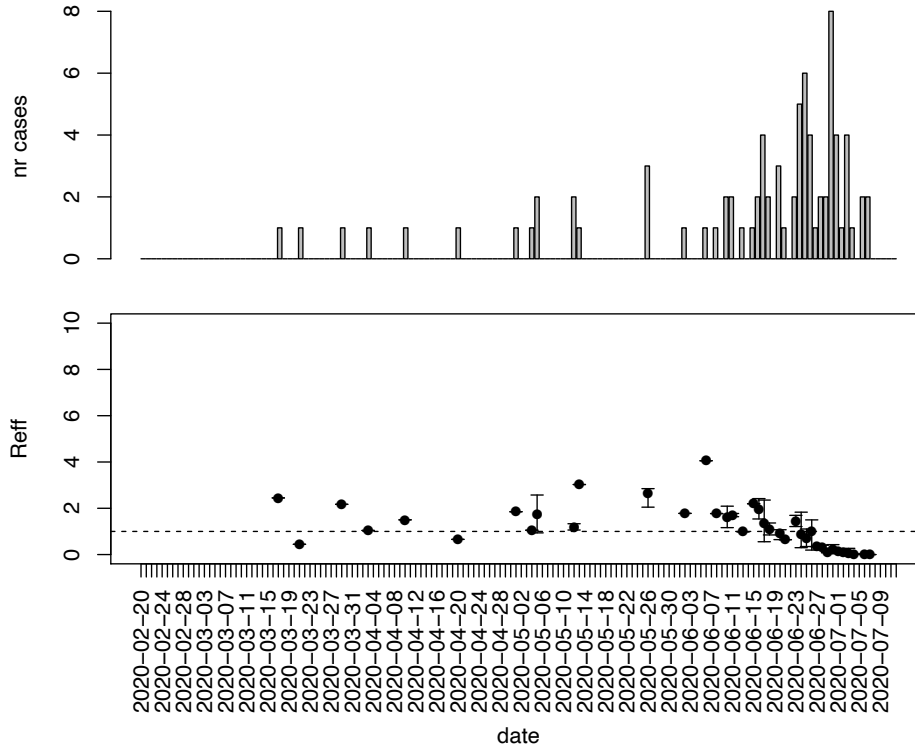
Appendix Figure 106. Epidemic curves and reproduction number estimates until July 13th in Marion county.

MCDUFFIE, n=160



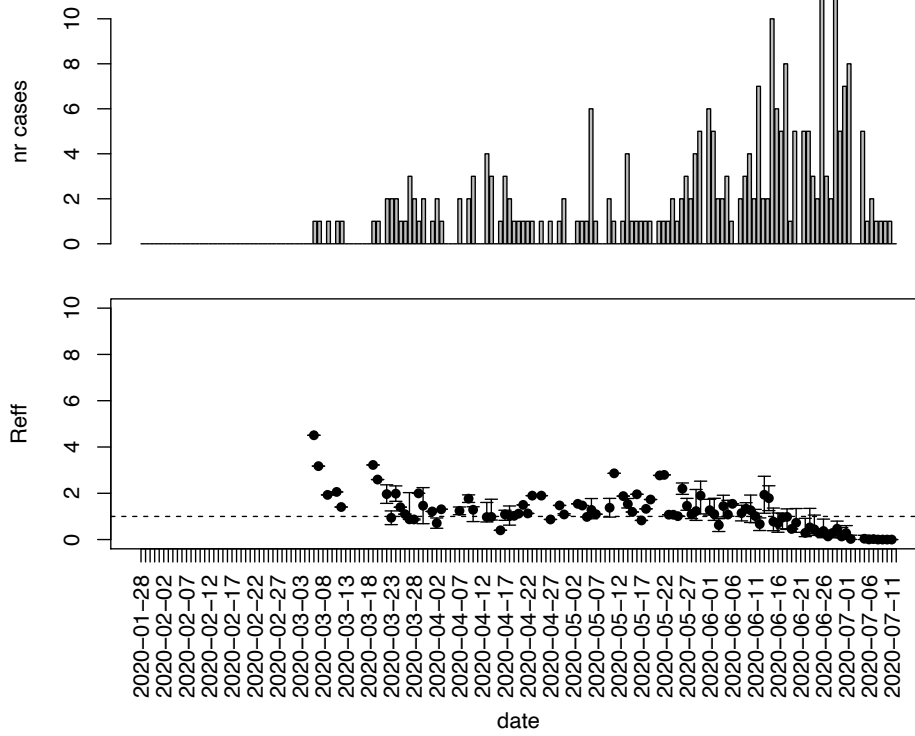
Appendix Figure 107. Epidemic curves and reproduction number estimates until July 13th in Mcduffie county.

MCINTOSH, n=81

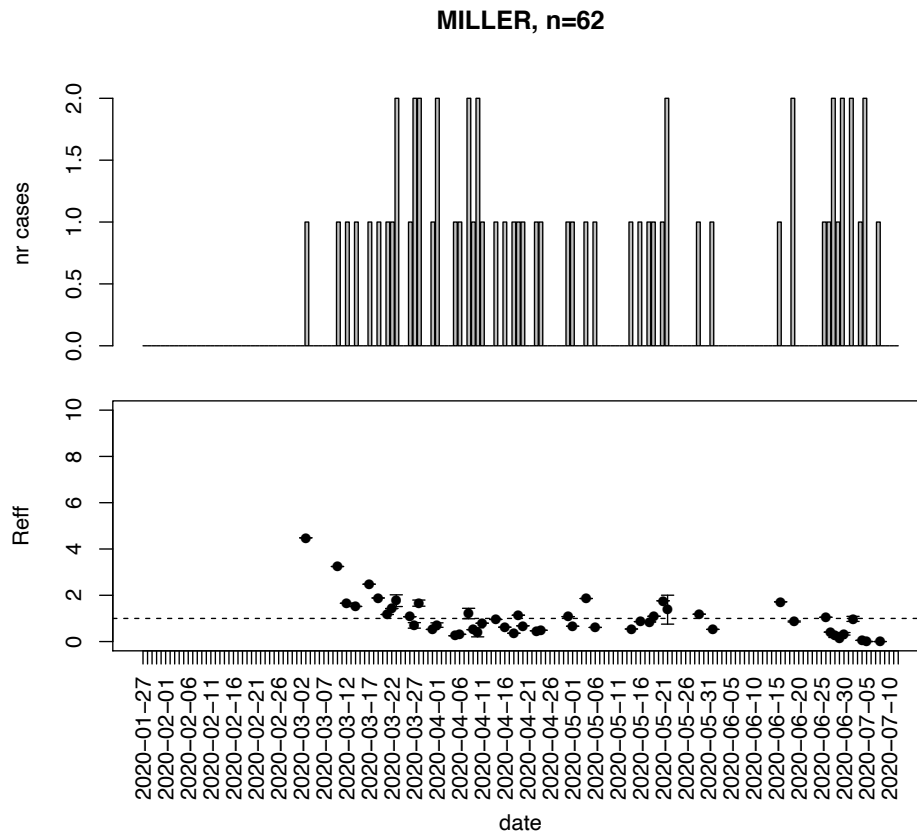


Appendix Figure 108. Epidemic curves and reproduction number estimates until July 13th in McIntosh county.

MERIWETHER, n=252

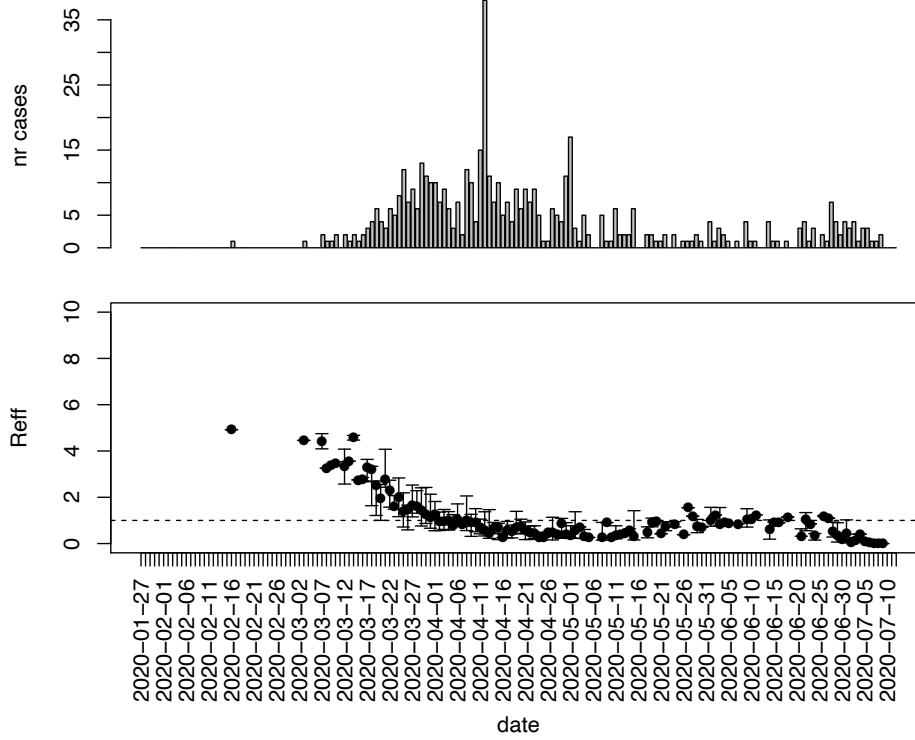


Appendix Figure 109. Epidemic curves and reproduction number estimates until July 13th in Meriwether county.



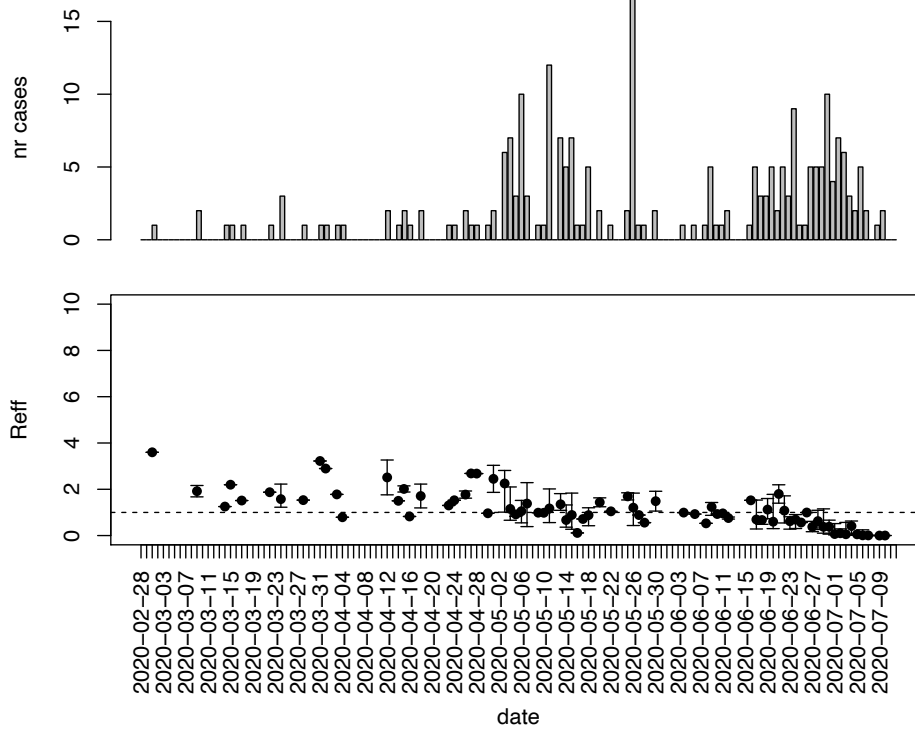
Appendix Figure 110. Epidemic curves and reproduction number estimates until July 13th in Miller county.

MITCHELL, n=506



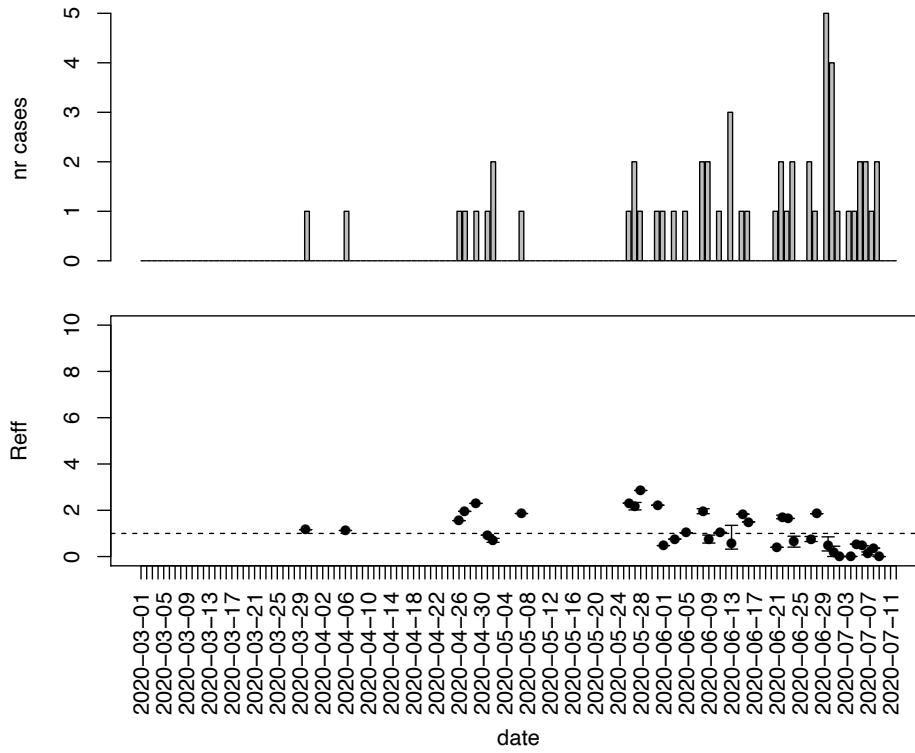
Appendix Figure 111. Epidemic curves and reproduction number estimates until July 13th in Mitchell county.

MONROE, n=234



Appendix Figure 112. Epidemic curves and reproduction number estimates until July 13th in Monroe county.

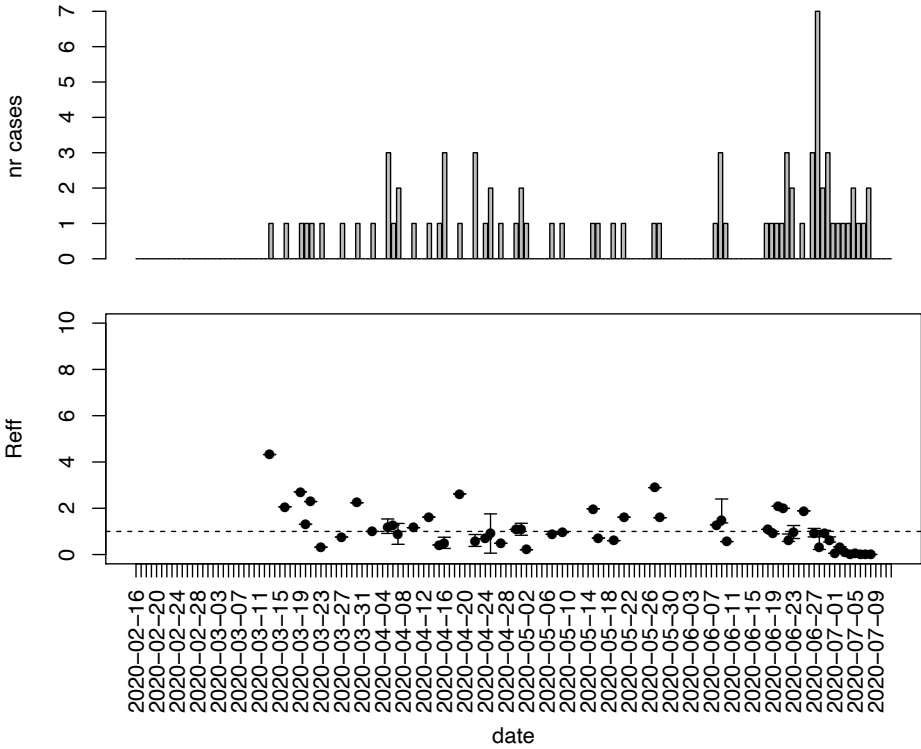
**MONTGOMERY, n=55**



Appendix Figure 113. Epidemic curves and reproduction number estimates until July 13th in Montgomery county.

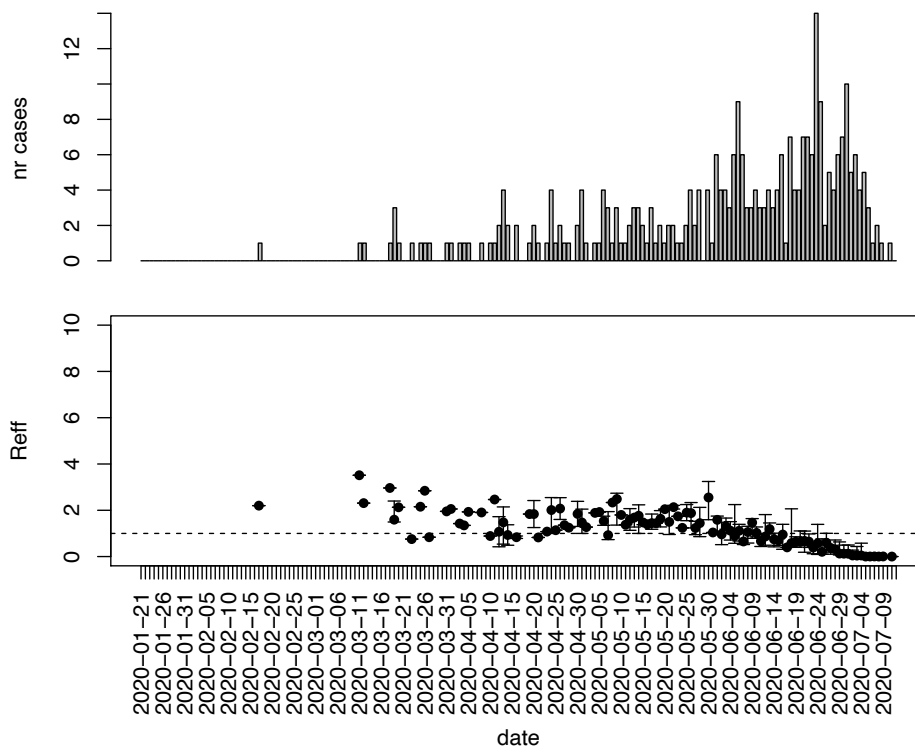


MORGAN, n=81



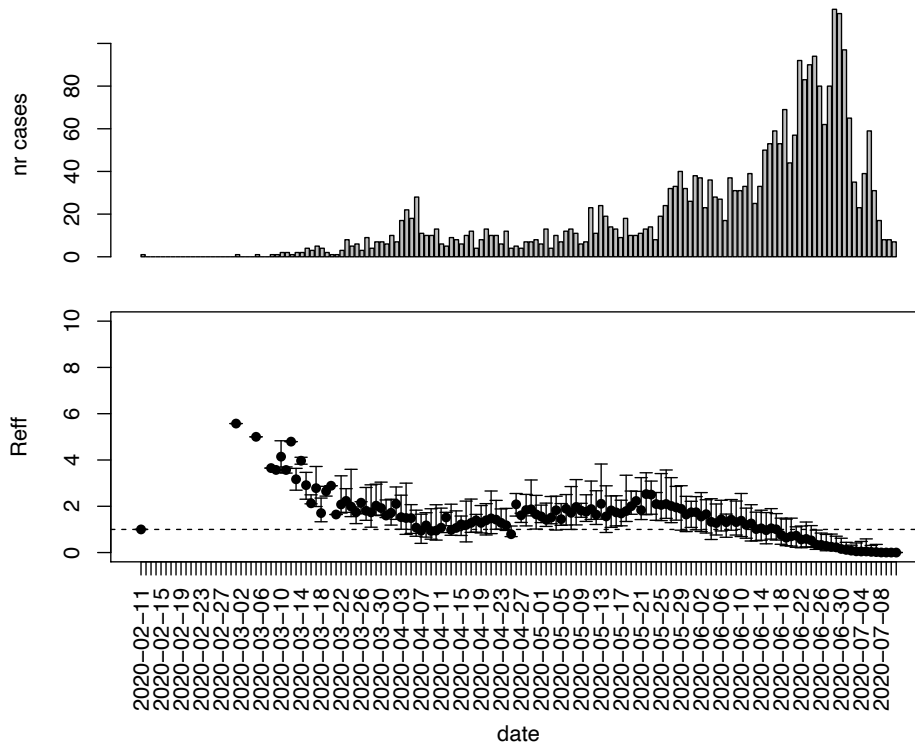
Appendix Figure 114. Epidemic curves and reproduction number estimates until July 13th in Morgan county.

MURRAY, n=299



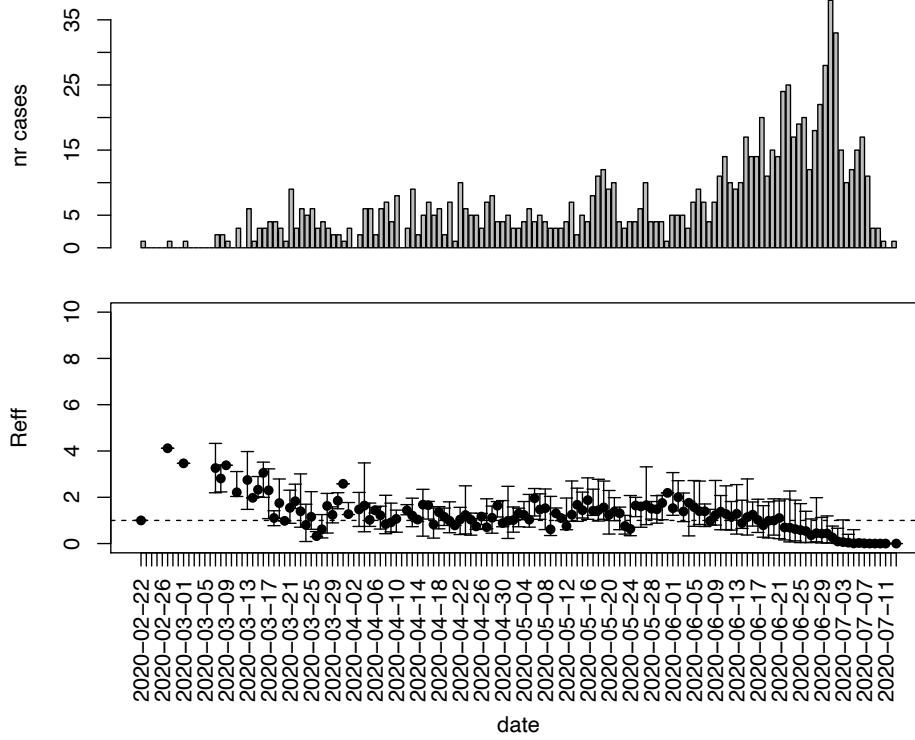
Appendix Figure 115. Epidemic curves and reproduction number estimates until July 13th in Murray county.

MUSCOGEE, n=2904



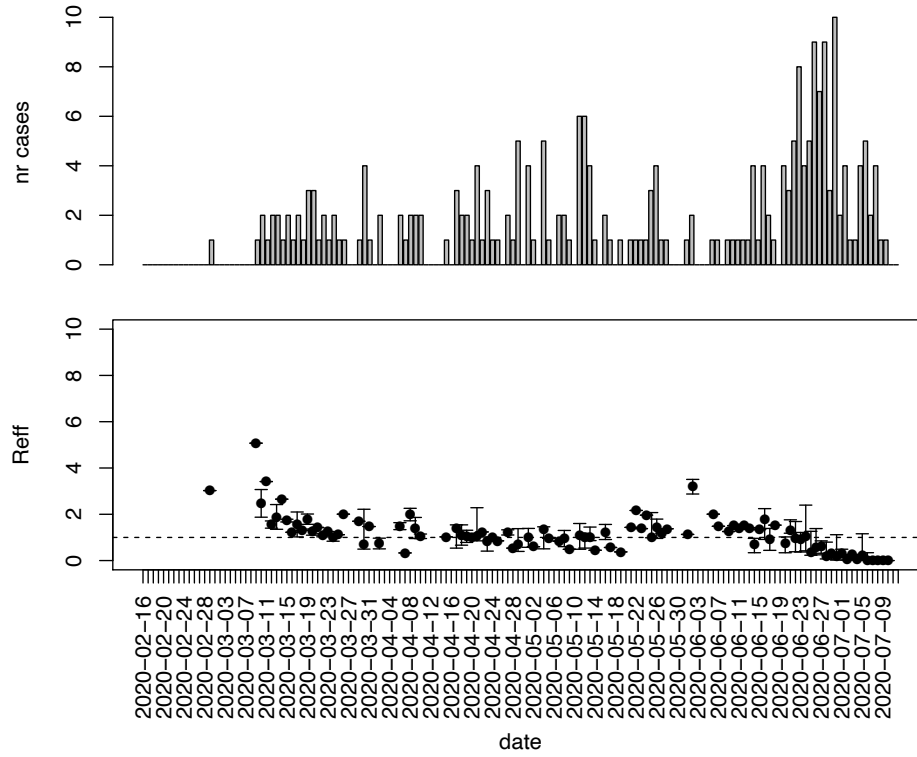
Appendix Figure 116. Epidemic curves and reproduction number estimates until July 13th in Muscogee county.

NEWTON, n=937



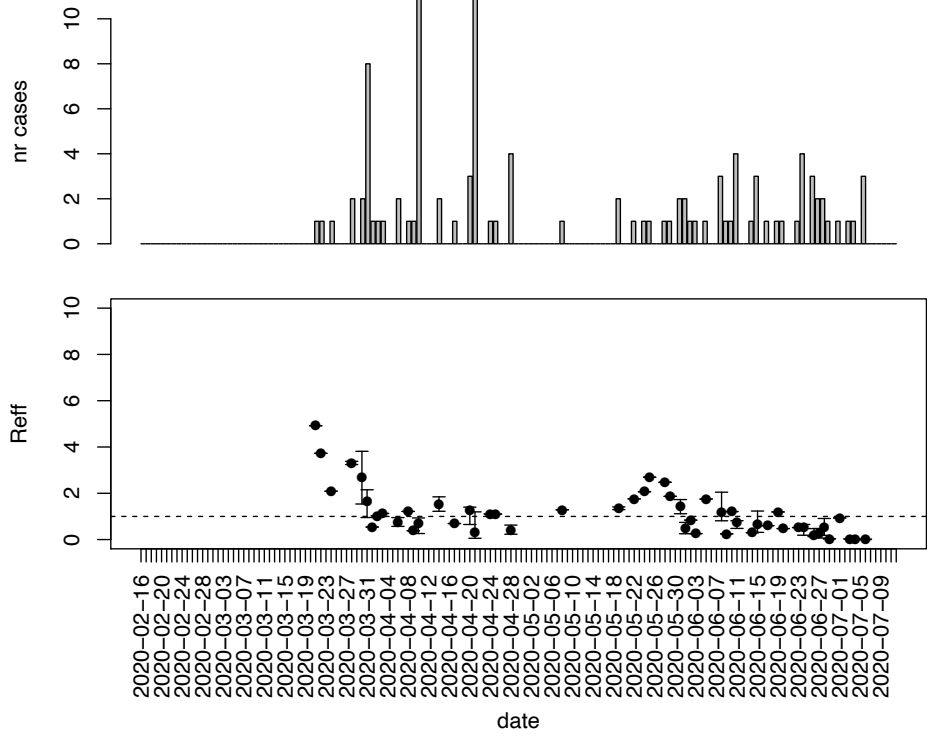
Appendix Figure 117. Epidemic curves and reproduction number estimates until July 13th in Newton county.

OCONEE, n=238



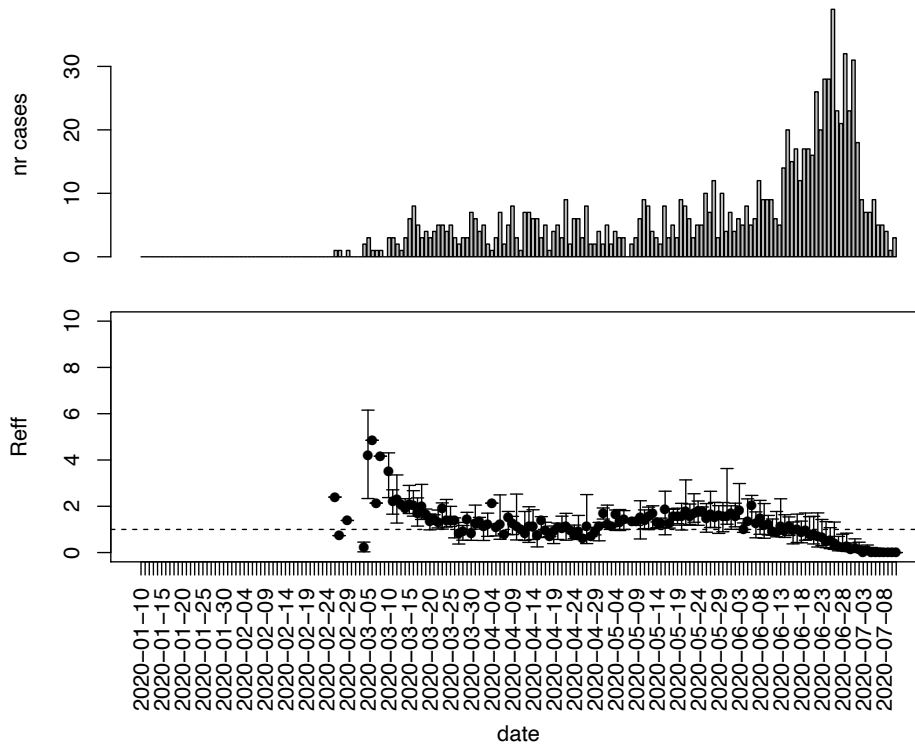
Appendix Figure 118. Epidemic curves and reproduction number estimates until July 13th in Oconee county.

OGLETHORPE, n=106



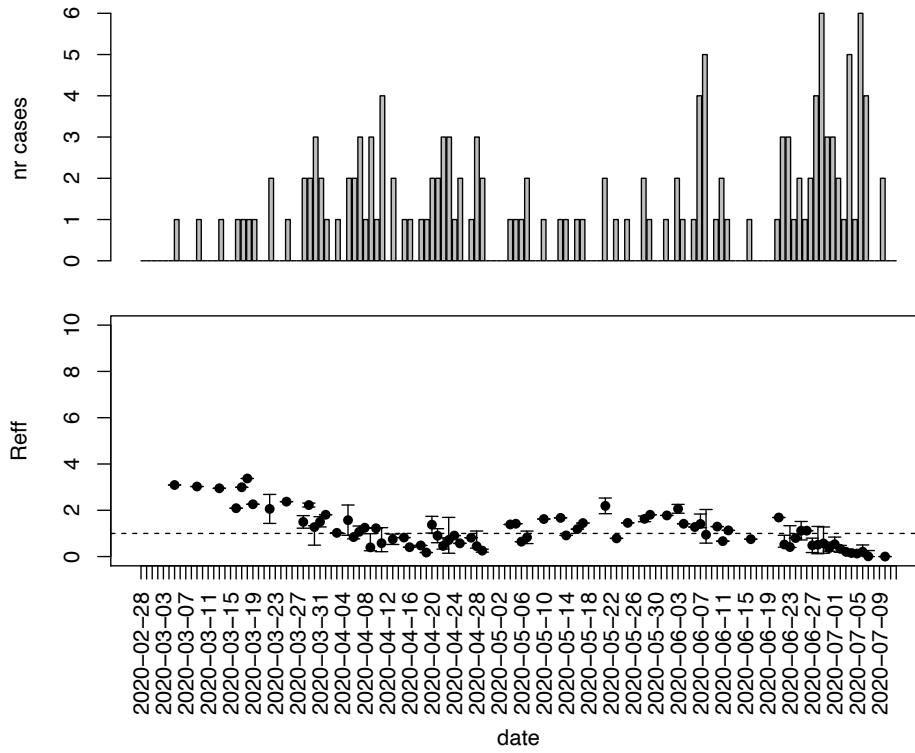
Appendix Figure 119. Epidemic curves and reproduction number estimates until July 13th in Oglethorpe county.

PAULDING, n=944



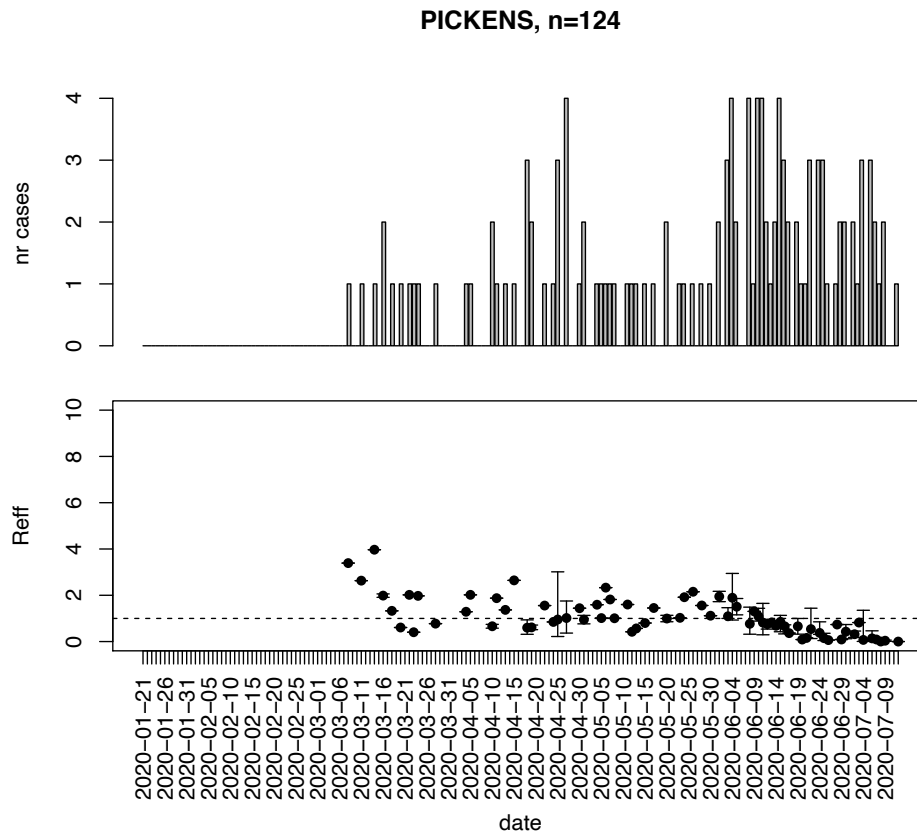
Appendix Figure 120. Epidemic curves and reproduction number estimates until July 13th in Paulding county.

PEACH, n=148



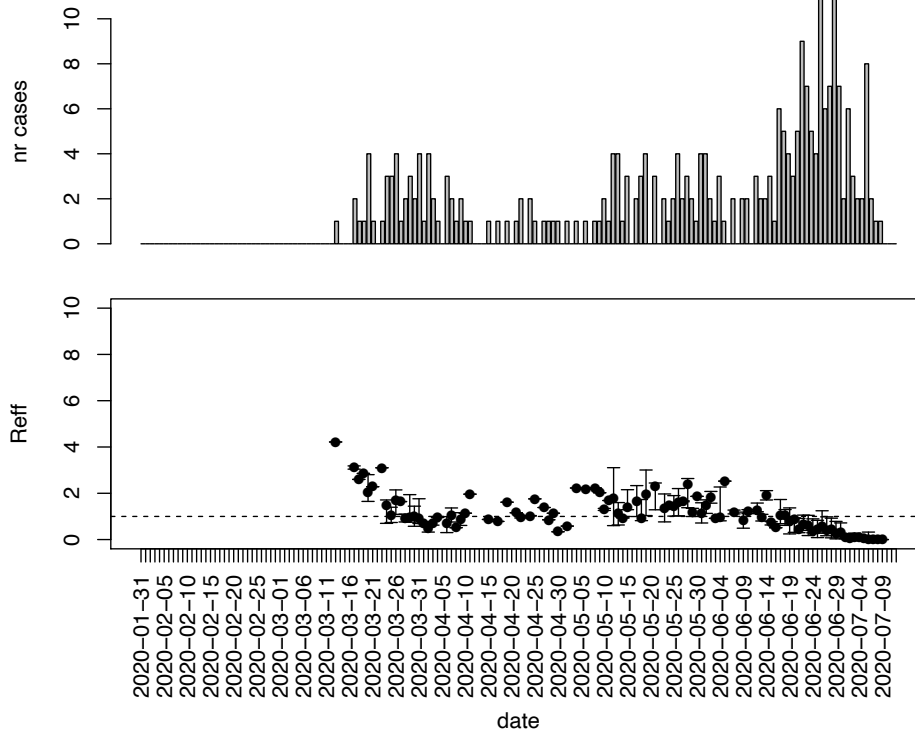
Appendix Figure 121. Epidemic curves and reproduction number estimates until July 13th in Peach county.



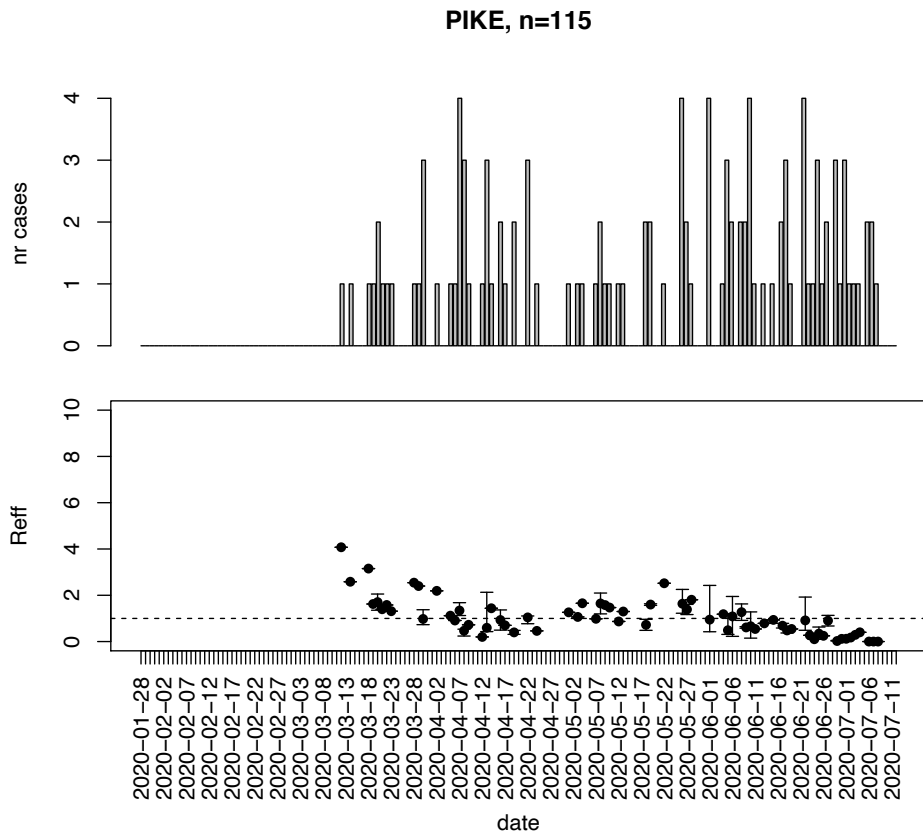


Appendix Figure 122. Epidemic curves and reproduction number estimates until July 13th in Pickens county.

PIERCE, n=262

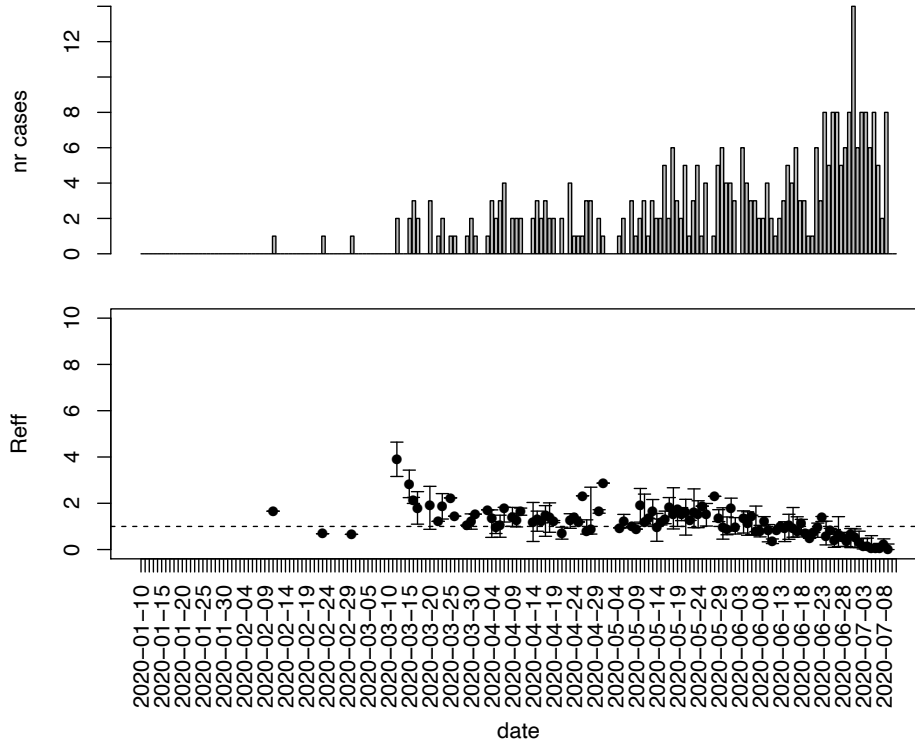


Appendix Figure 123. Epidemic curves and reproduction number estimates until July 13th in Pierce county.

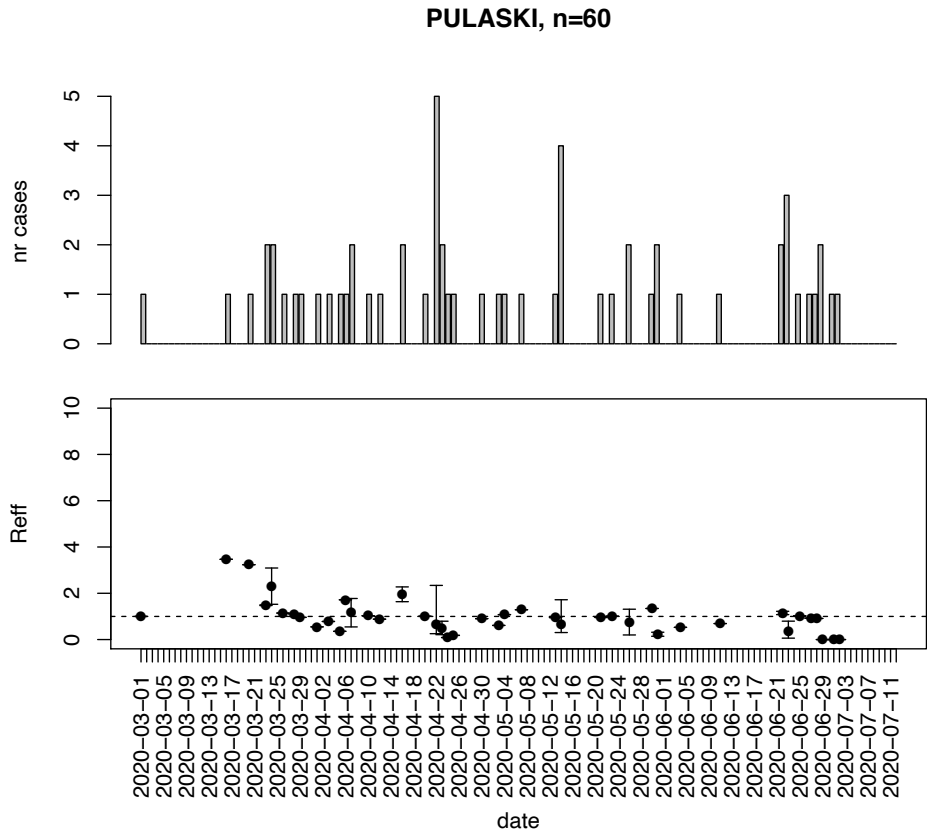


Appendix Figure 124. Epidemic curves and reproduction number estimates until July 13th in Pike county.

POLK, n=332

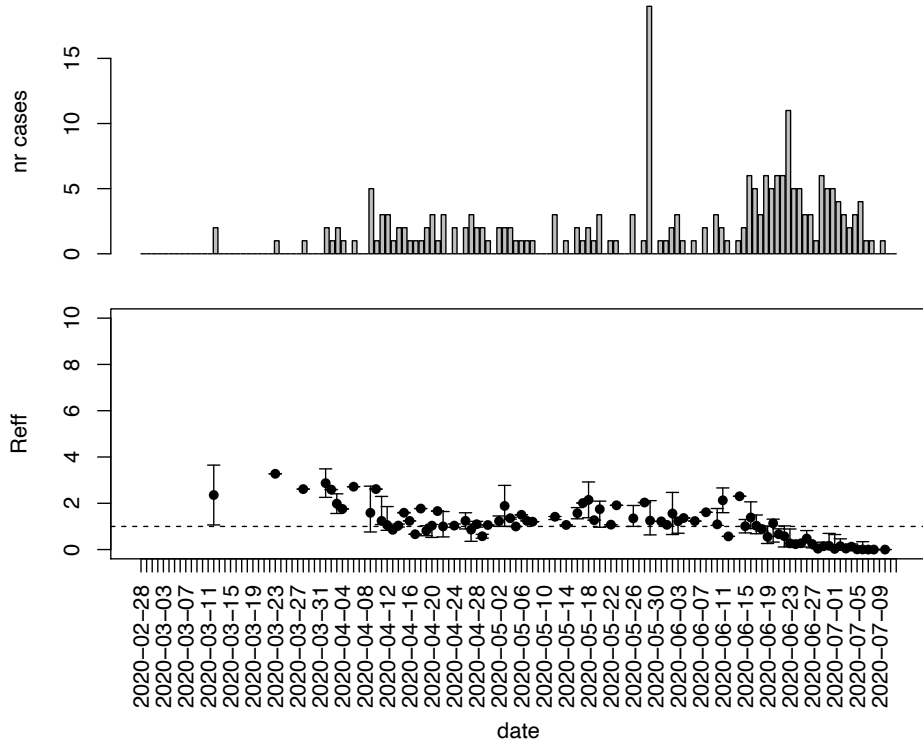


Appendix Figure 125. Epidemic curves and reproduction number estimates until July 13th in Polk county.

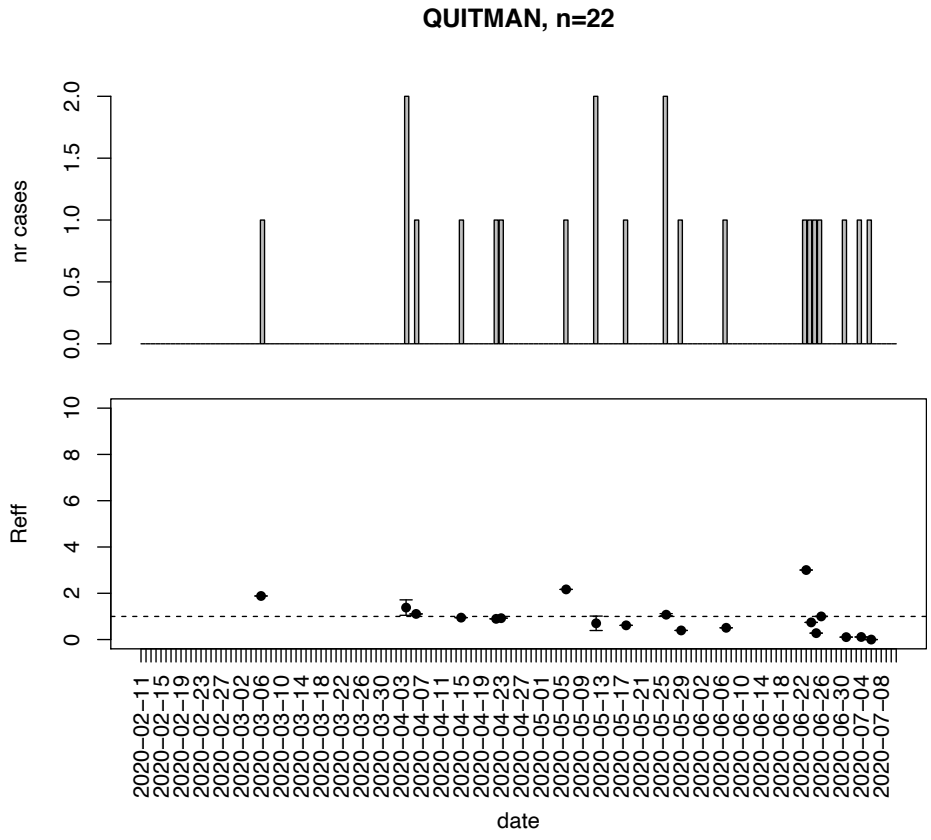


Appendix Figure 126. Epidemic curves and reproduction number estimates until July 13th in Pulaski county.

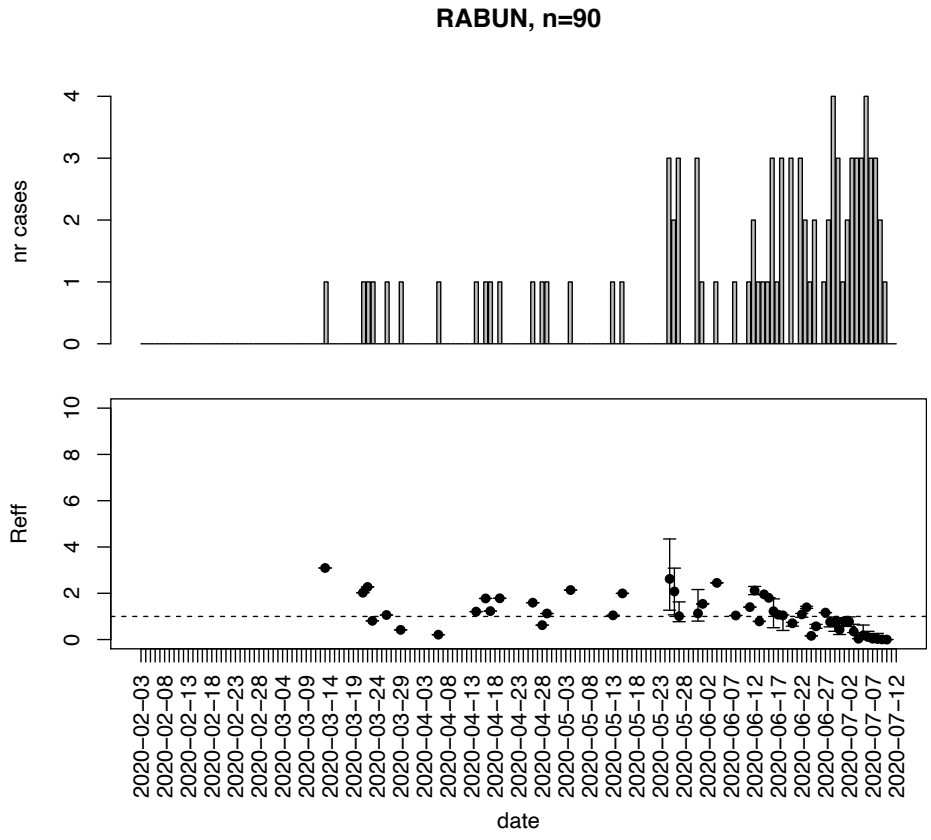
PUTNAM, n=220



Appendix Figure 127. Epidemic curves and reproduction number estimates until July 13th in Putnam county.



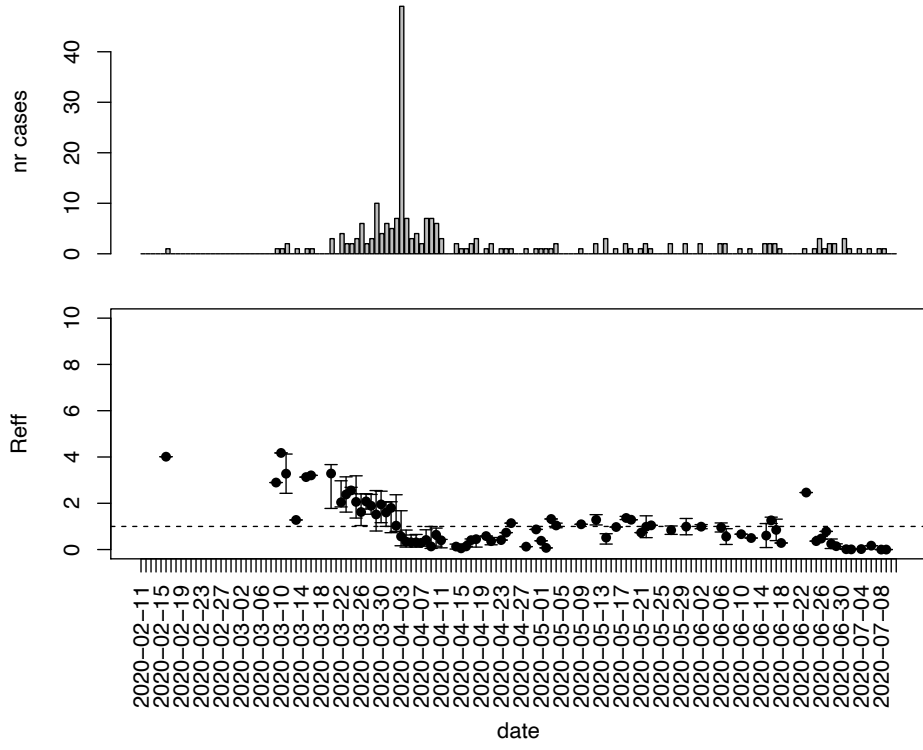
Appendix Figure 128. Epidemic curves and reproduction number estimates until July 13th in Quitman county.



Appendix Figure 129. Epidemic curves and reproduction number estimates until July 13th in Rabun county.

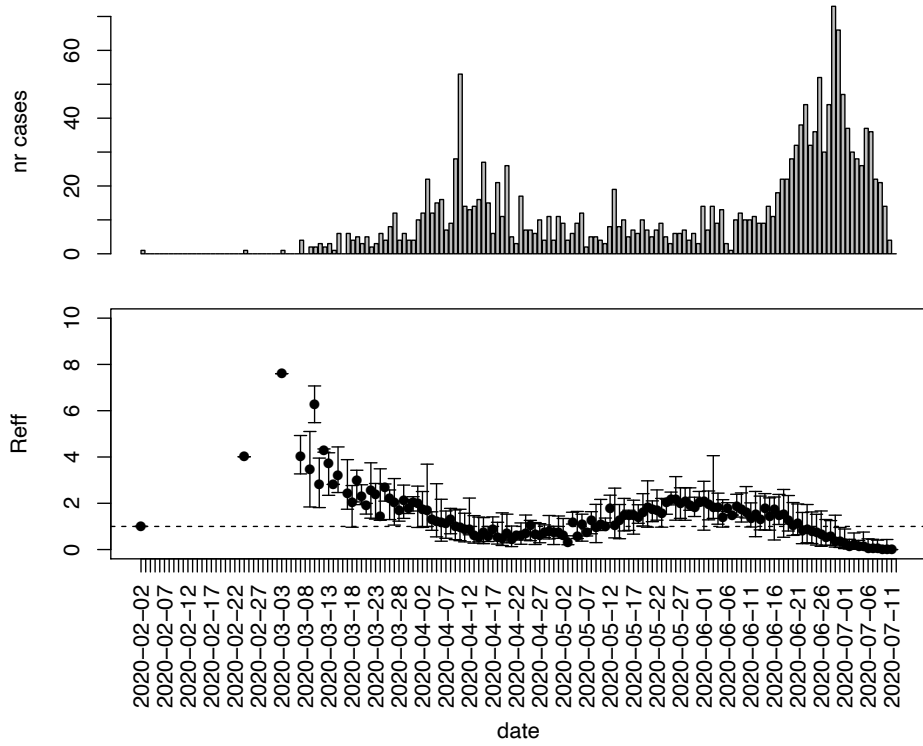


**RANDOLPH, n=226**



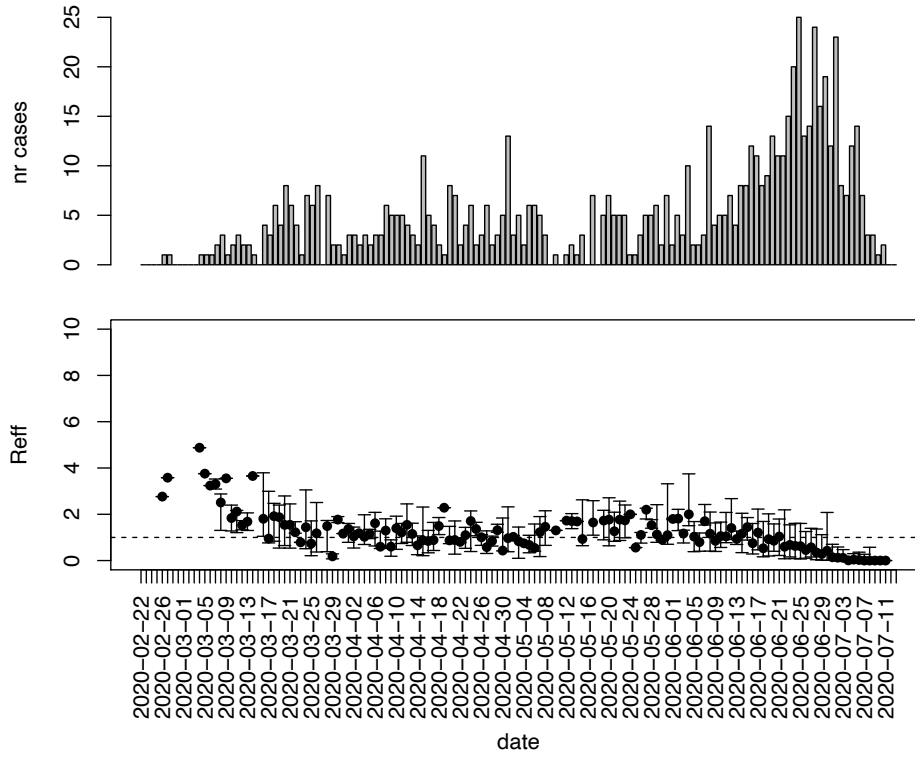
Appendix Figure 130. Epidemic curves and reproduction number estimates until July 13th in Randolph county.

**RICHMOND, n=1730**

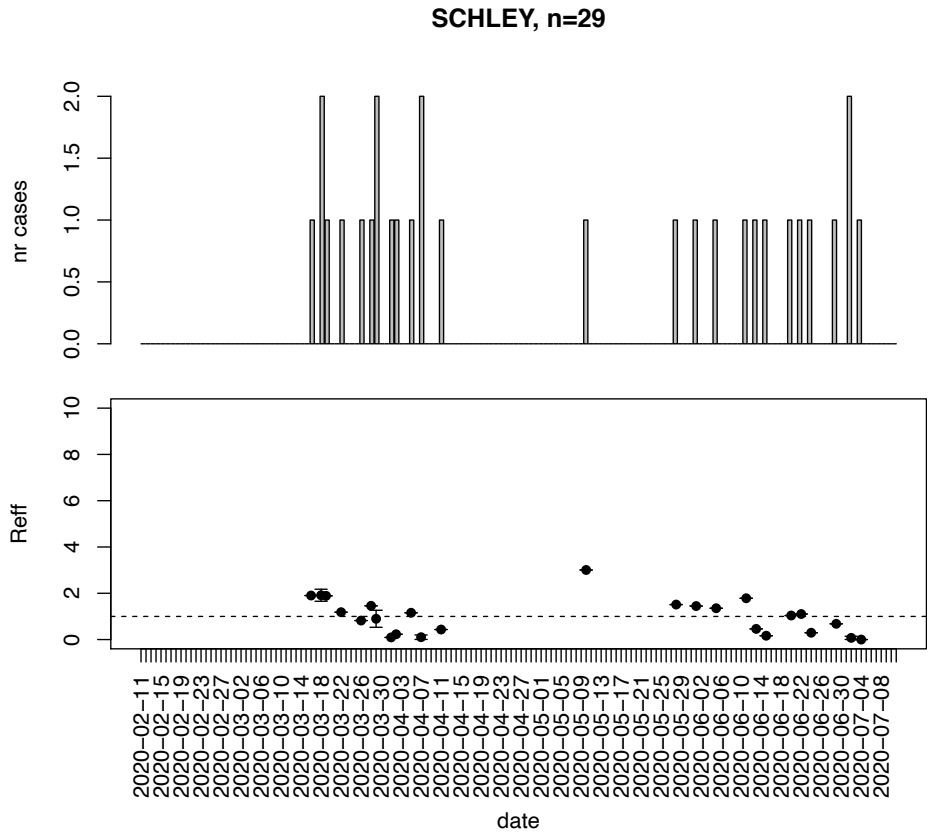


Appendix Figure 131. Epidemic curves and reproduction number estimates until July 13th in Richmond county.

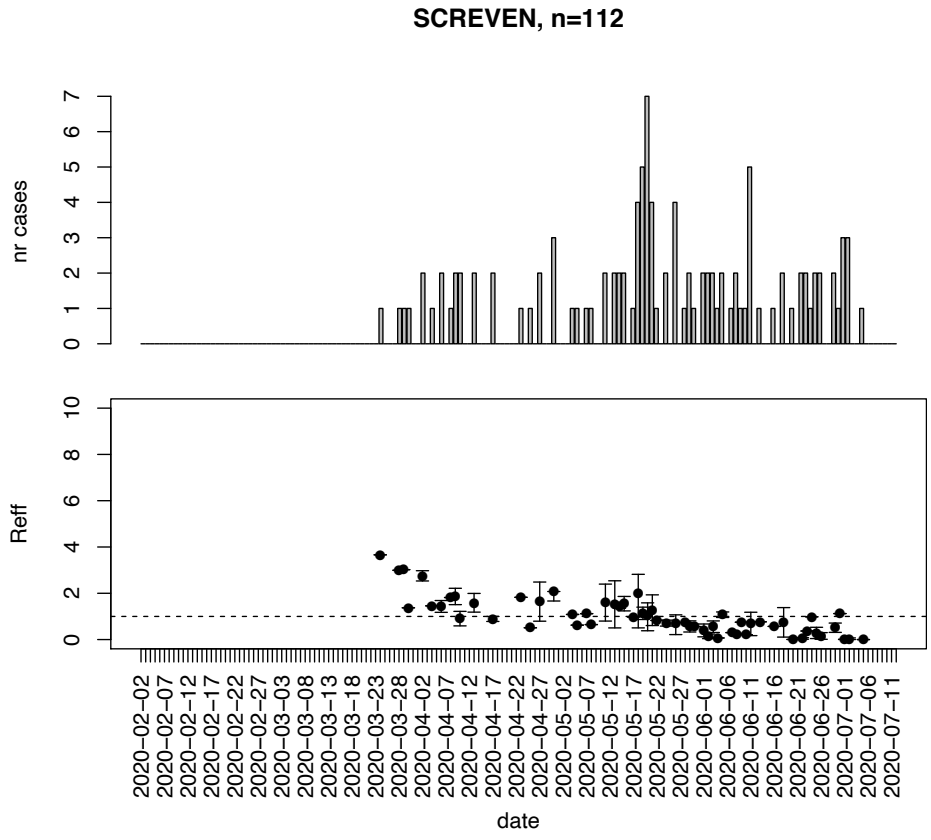
ROCKDALE, n=720



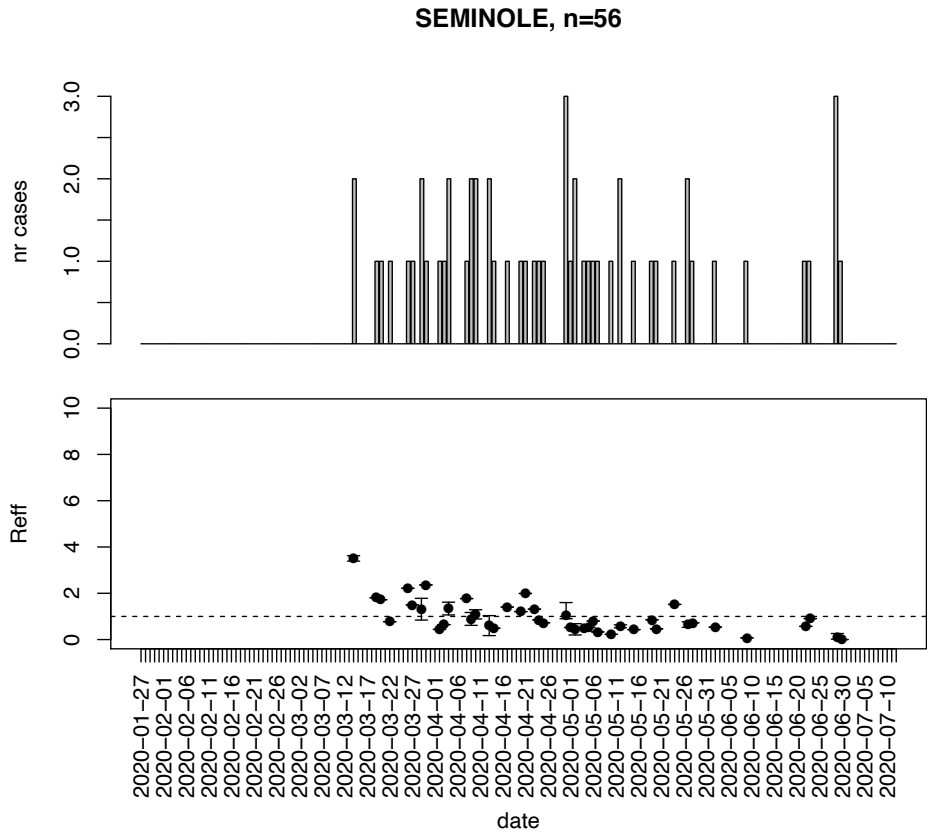
Appendix Figure 132. Epidemic curves and reproduction number estimates until July 13th in Rockdale county.



Appendix Figure 133. Epidemic curves and reproduction number estimates until July 13th in Schley county.

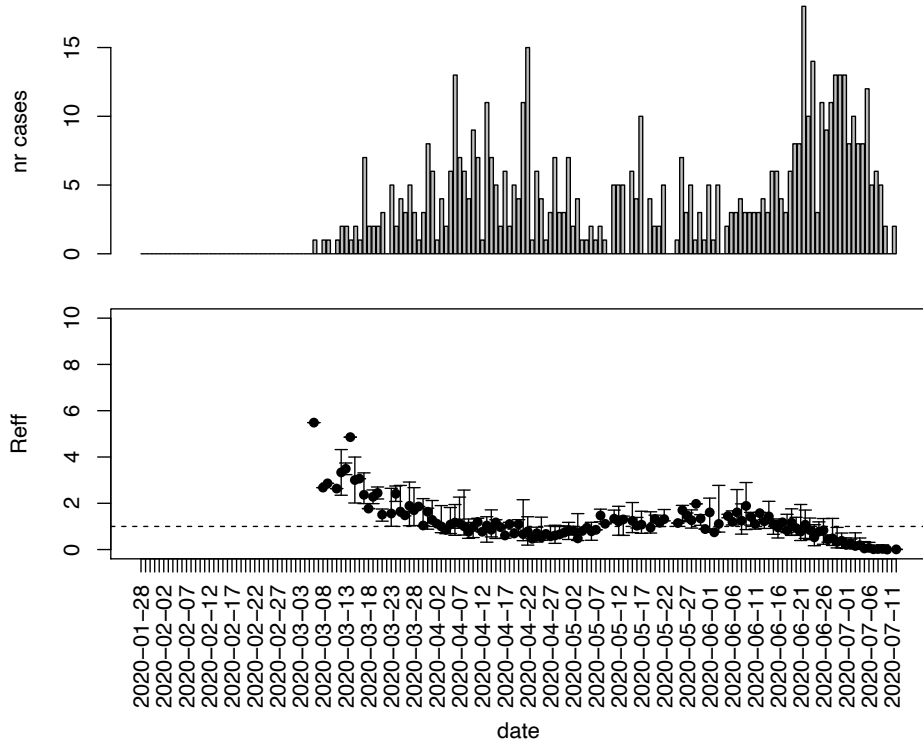


Appendix Figure 134. Epidemic curves and reproduction number estimates until July 13th in Screven county.



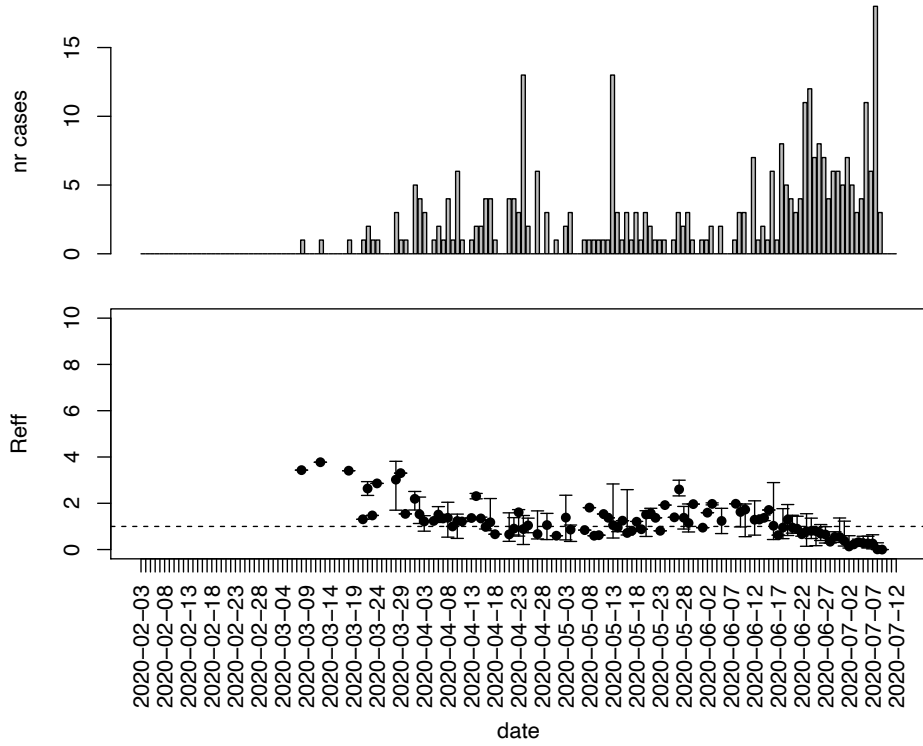
Appendix Figure 135. Epidemic curves and reproduction number estimates until July 13th in Seminole county.

SPALDING, n=578



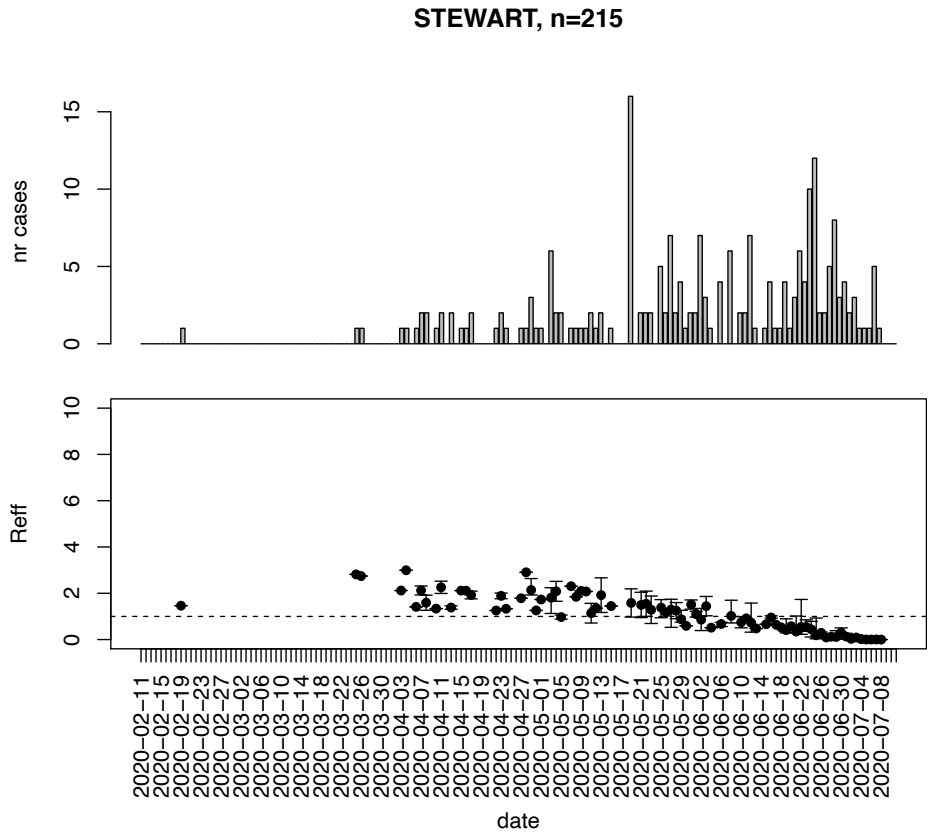
Appendix Figure 136. Epidemic curves and reproduction number estimates until July 13th in Spalding county.

STEPHENS, n=323



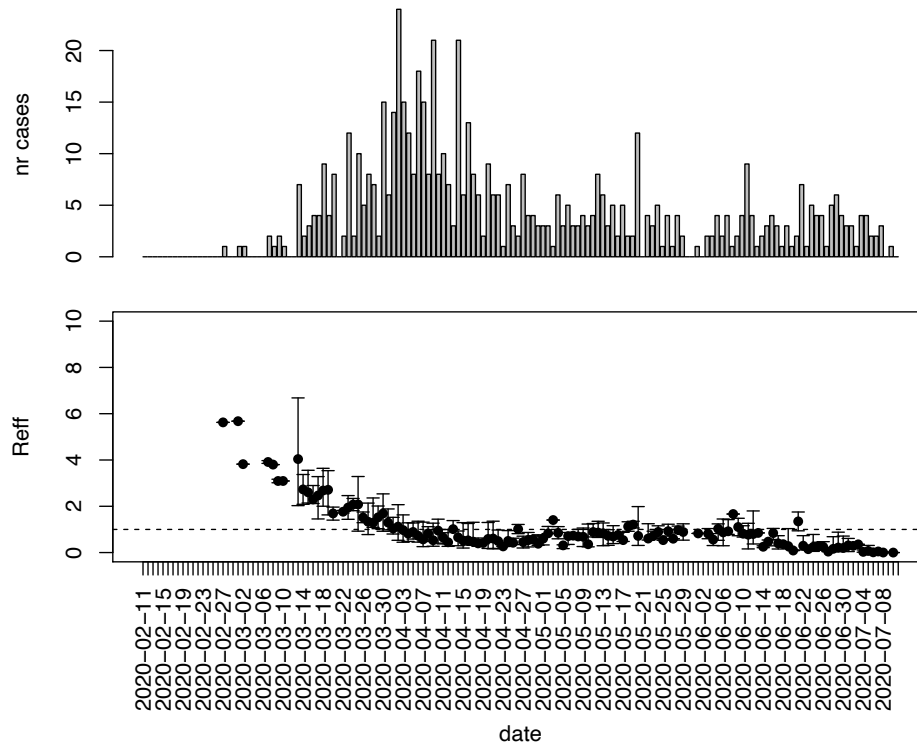
Appendix Figure 137. Epidemic curves and reproduction number estimates until July 13th in Stephens county.





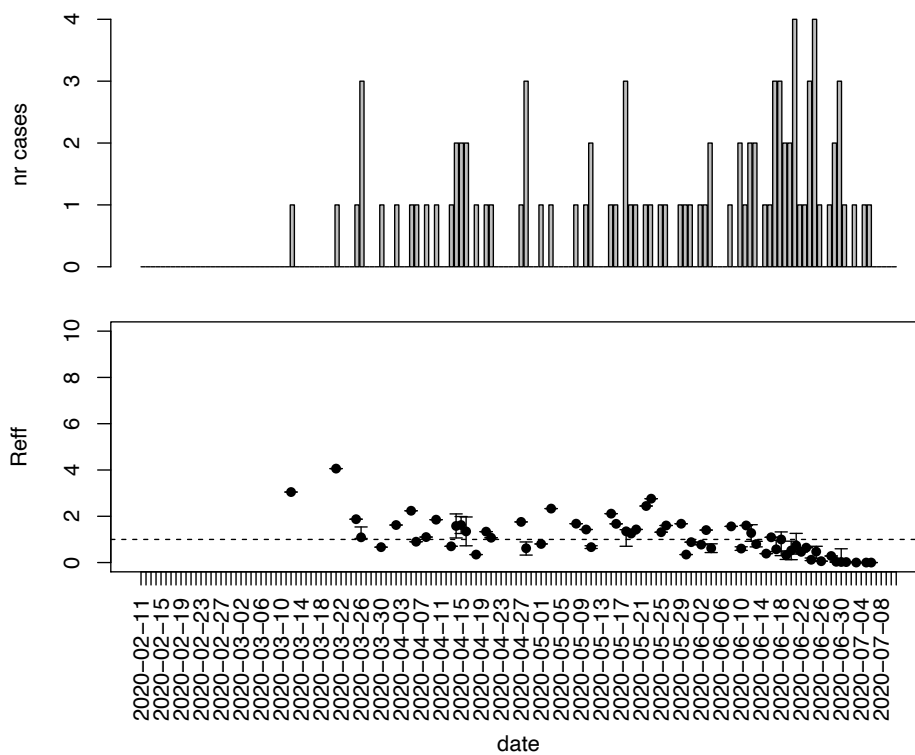
Appendix Figure 138. Epidemic curves and reproduction number estimates until July 13th in Stewart county.

SUMTER, n=613

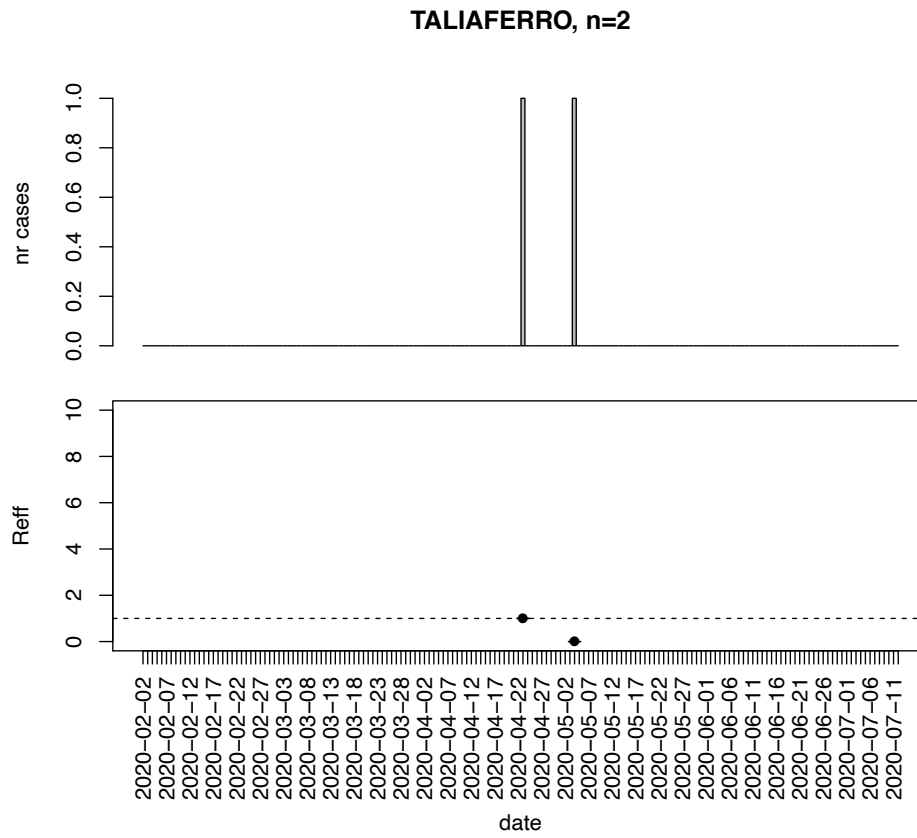


Appendix Figure 139. Epidemic curves and reproduction number estimates until July 13th in Sumter county.

TALBOT, n=94

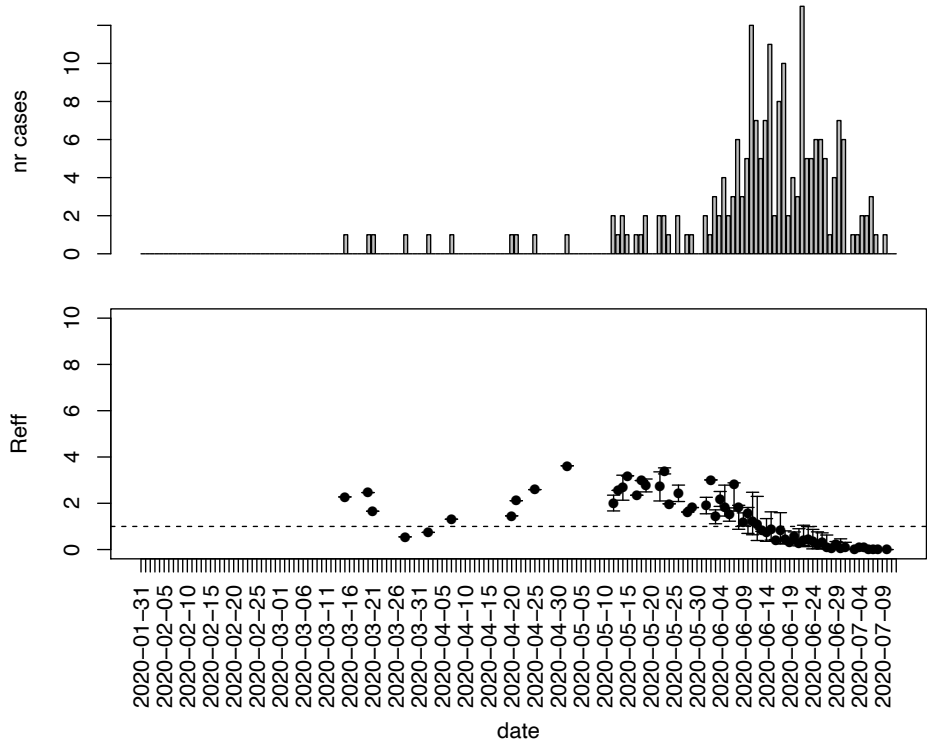


Appendix Figure 140. Epidemic curves and reproduction number estimates until July 13th in Talbot county.



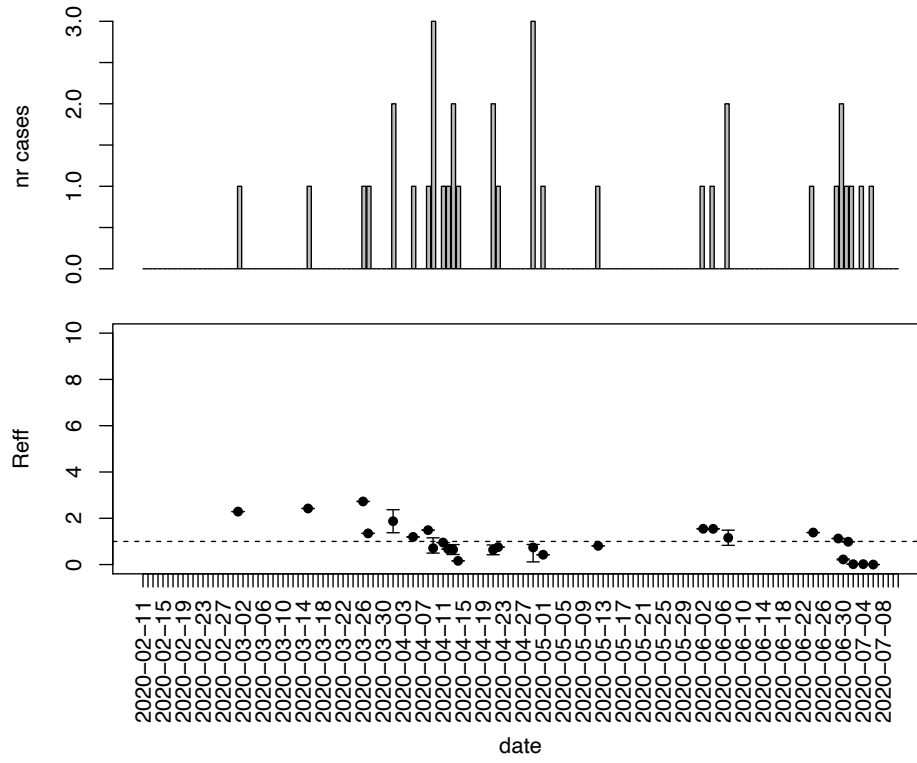
Appendix Figure 141. Epidemic curves and reproduction number estimates until July 13th in Taliaferro county.

TATTNALL, n=200



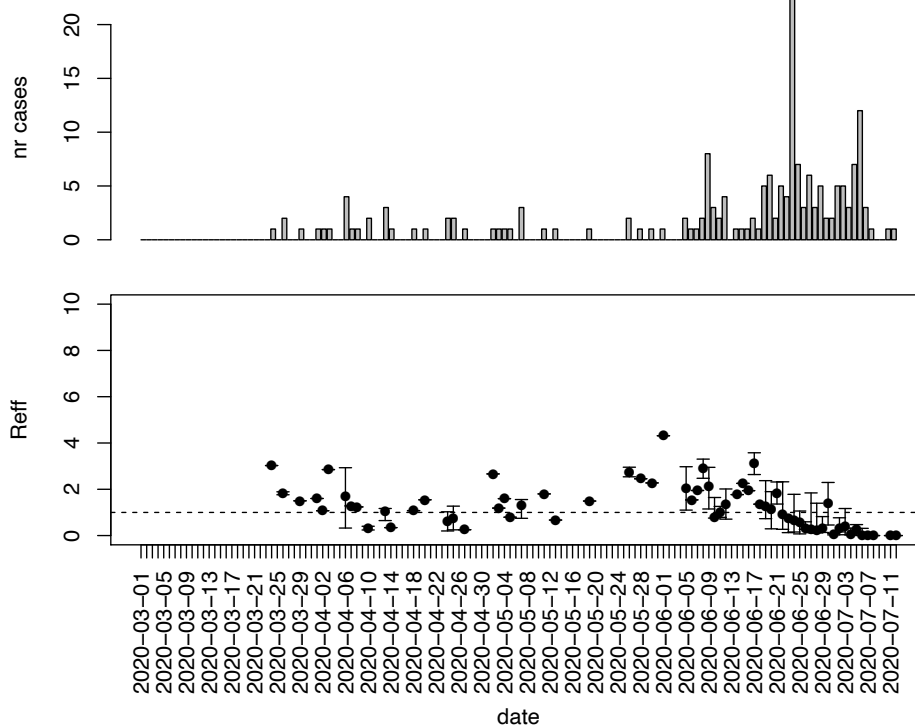
Appendix Figure 142. Epidemic curves and reproduction number estimates until July 13th in Tattnall county.

TAYLOR, n=36



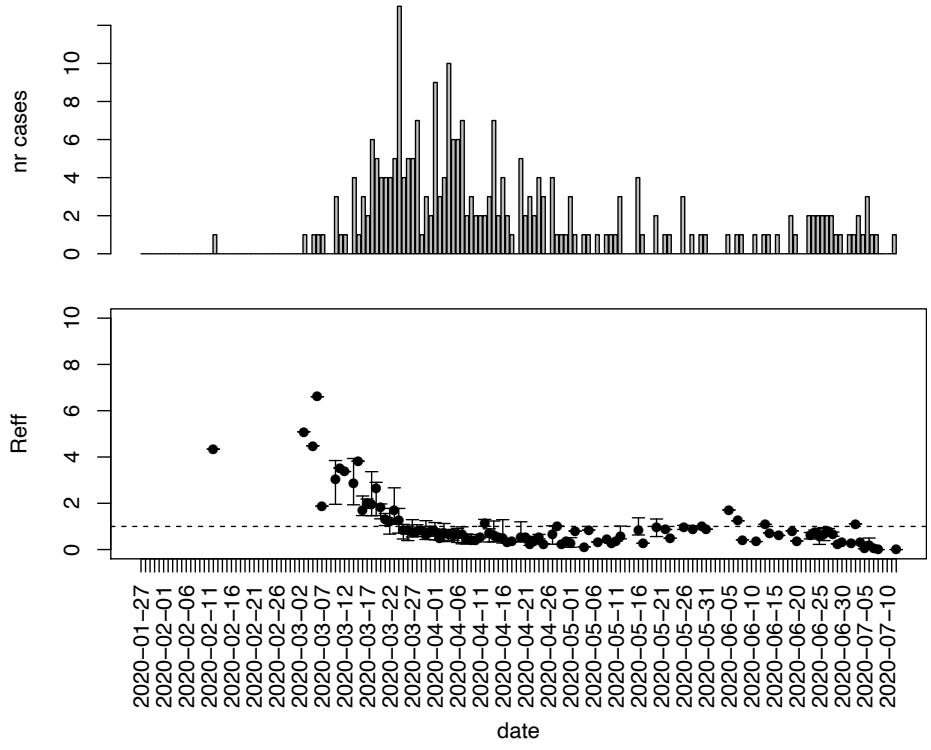
Appendix Figure 143. Epidemic curves and reproduction number estimates until July 13th in Taylor county.

TELFAIR, n=181



Appendix Figure 144. Epidemic curves and reproduction number estimates until July 13th in Telfair county.

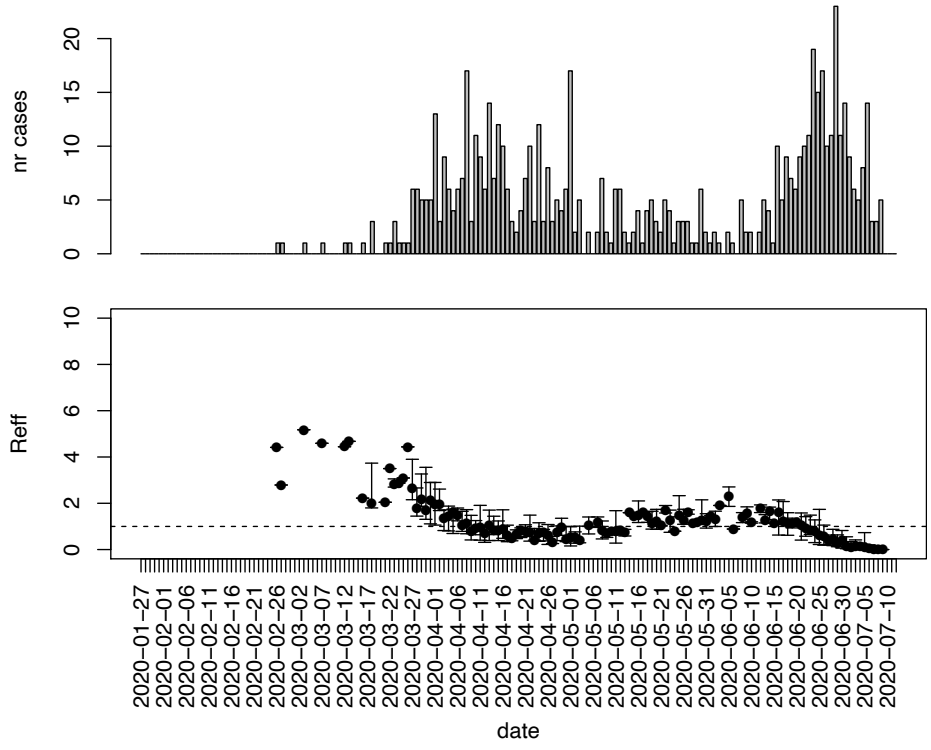
TERRELL, n=252



Appendix Figure 145. Epidemic curves and reproduction number estimates until July 13th in Terrell county.

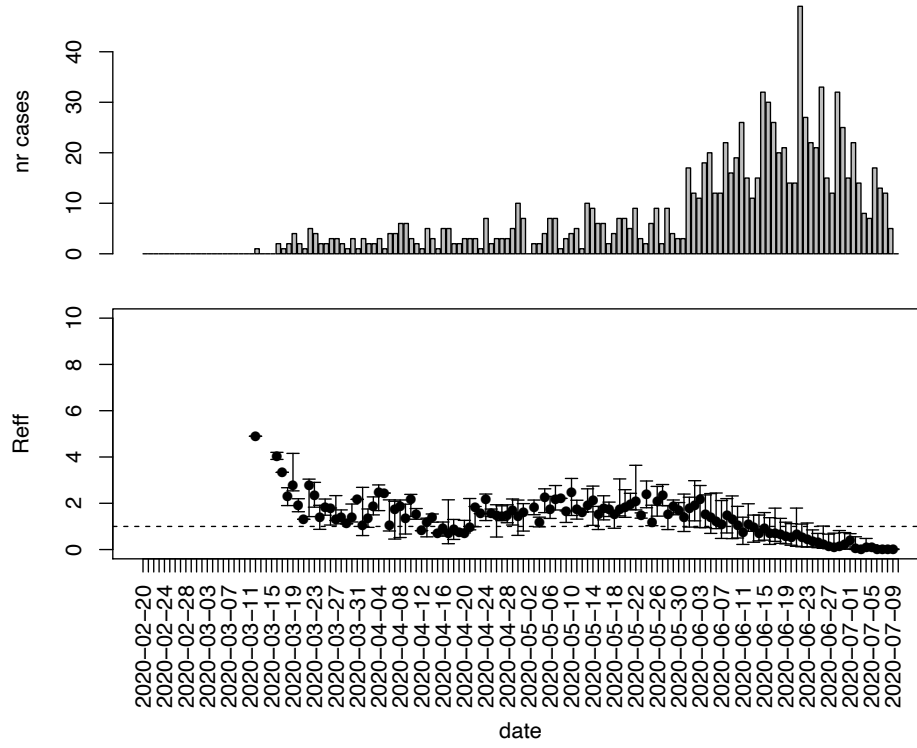


THOMAS, n=629



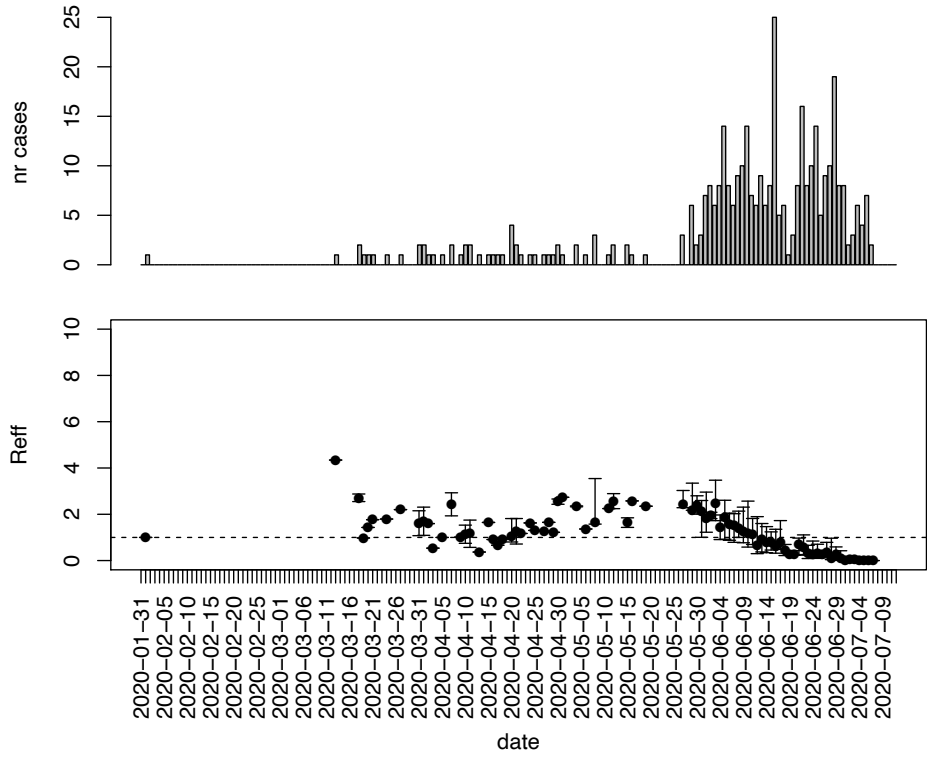
Appendix Figure 146. Epidemic curves and reproduction number estimates until July 13th in Thomas county.

TIFT, n=1023

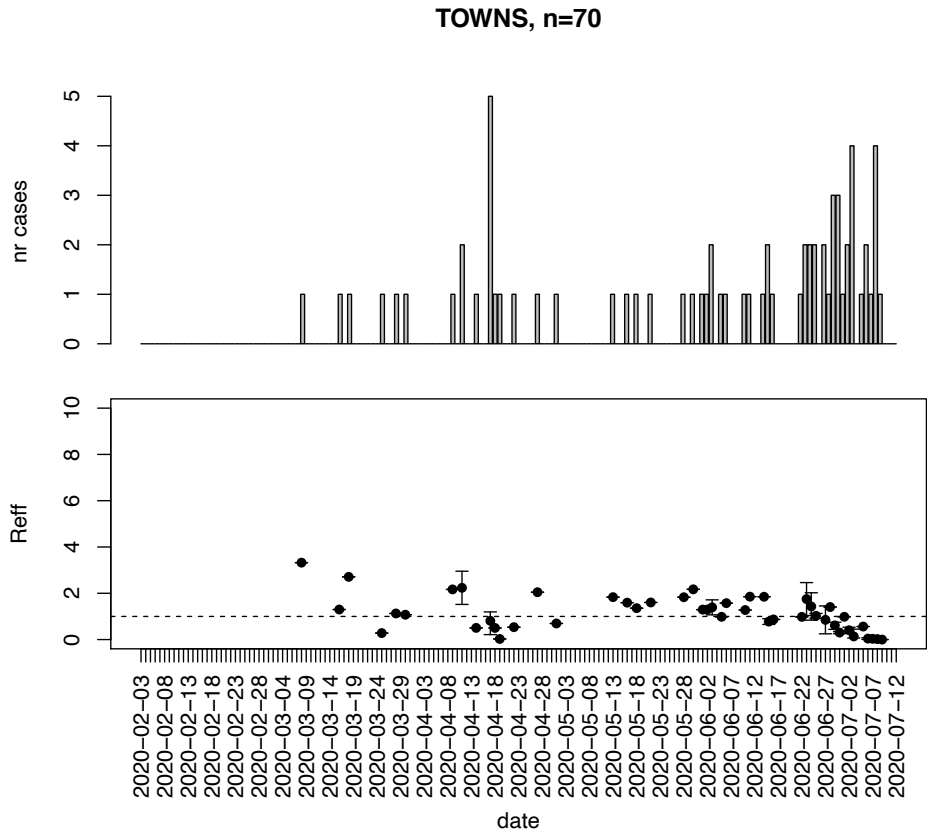


Appendix Figure 147. Epidemic curves and reproduction number estimates until July 13th in Tift county.

TOOMBS, n=375

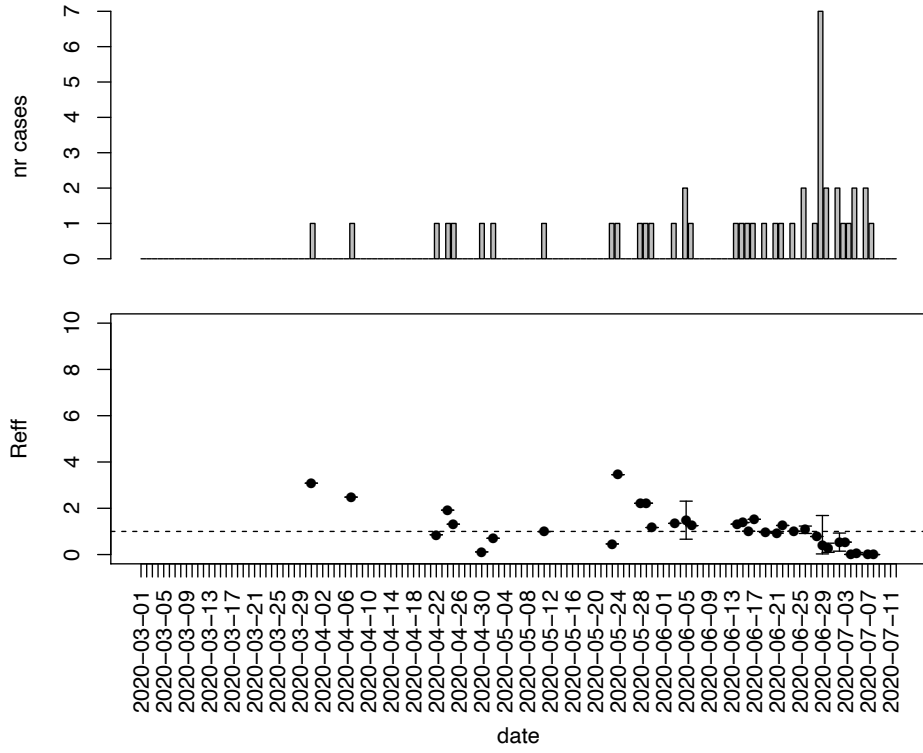


Appendix Figure 148. Epidemic curves and reproduction number estimates until July 13th in Toombs county.



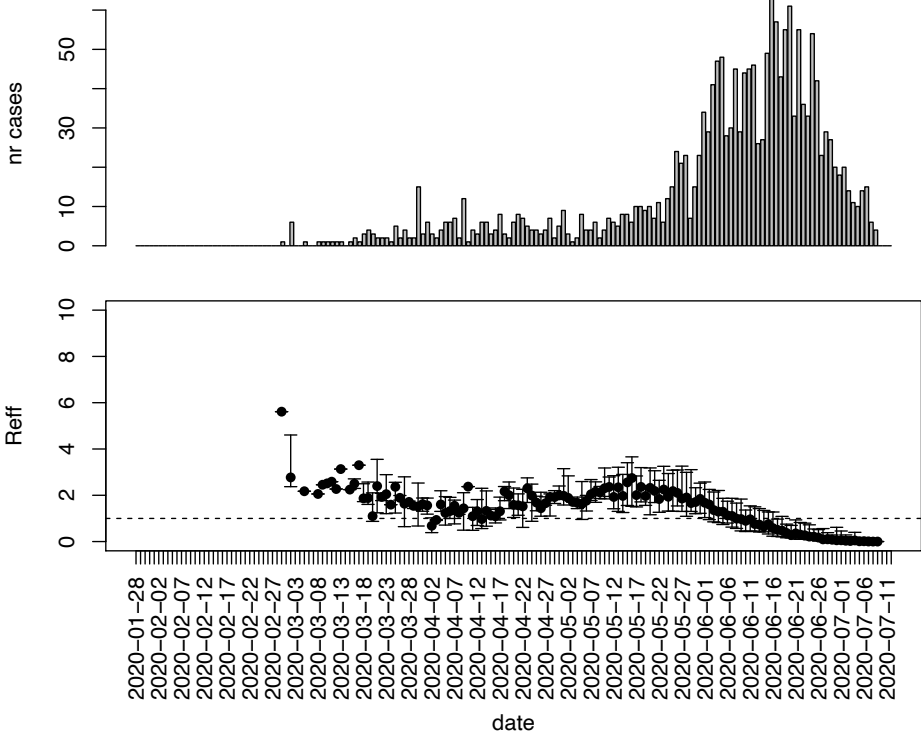
Appendix Figure 149. Epidemic curves and reproduction number estimates until July 13th in Towns county.

TREUTLEN, n=46



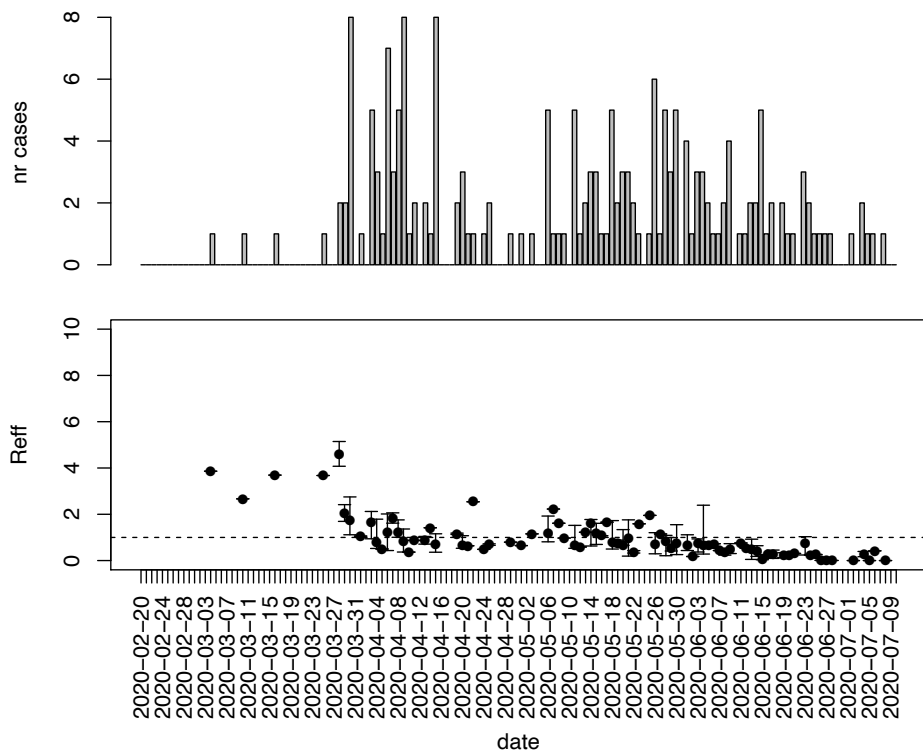
Appendix Figure 150. Epidemic curves and reproduction number estimates until July 13th in Treutlen county.

TROUP, n=1808

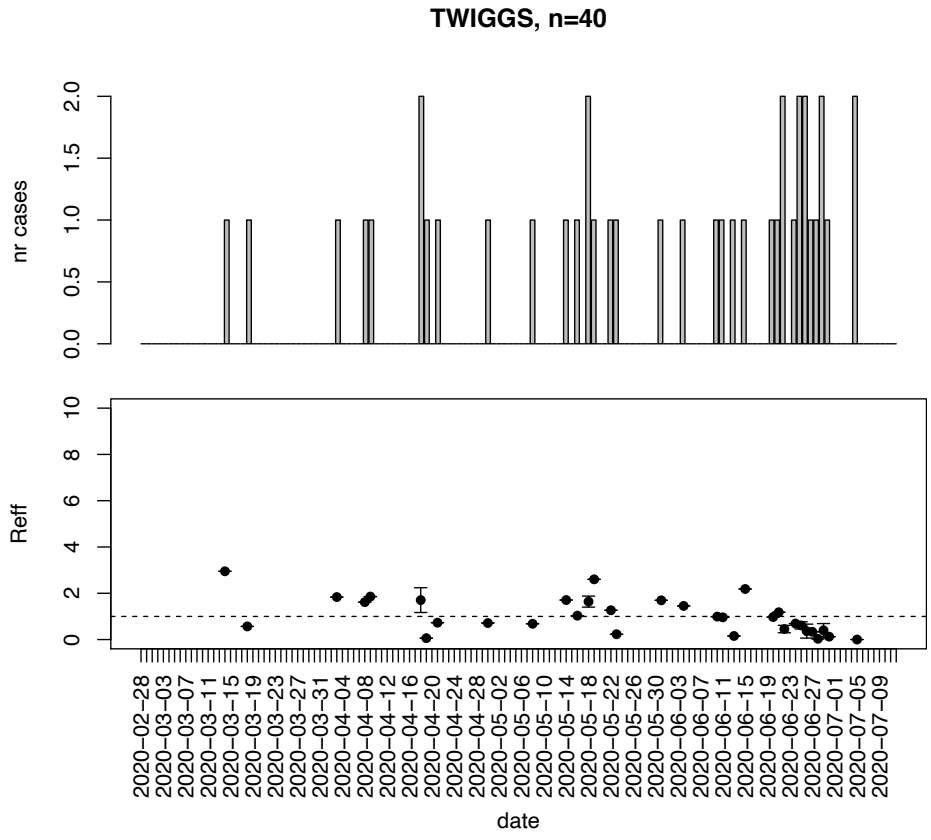


Appendix Figure 151. Epidemic curves and reproduction number estimates until July 13th in Troup county.

TURNER, n=191

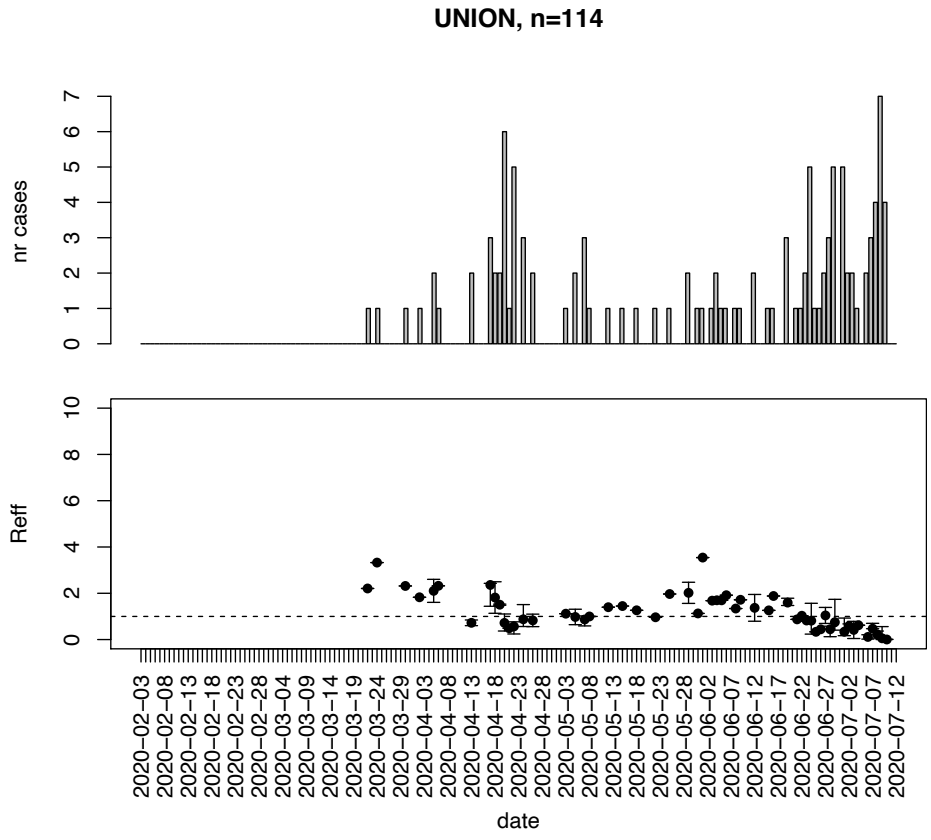


Appendix Figure 152. Epidemic curves and reproduction number estimates until July 13th in Turner county.



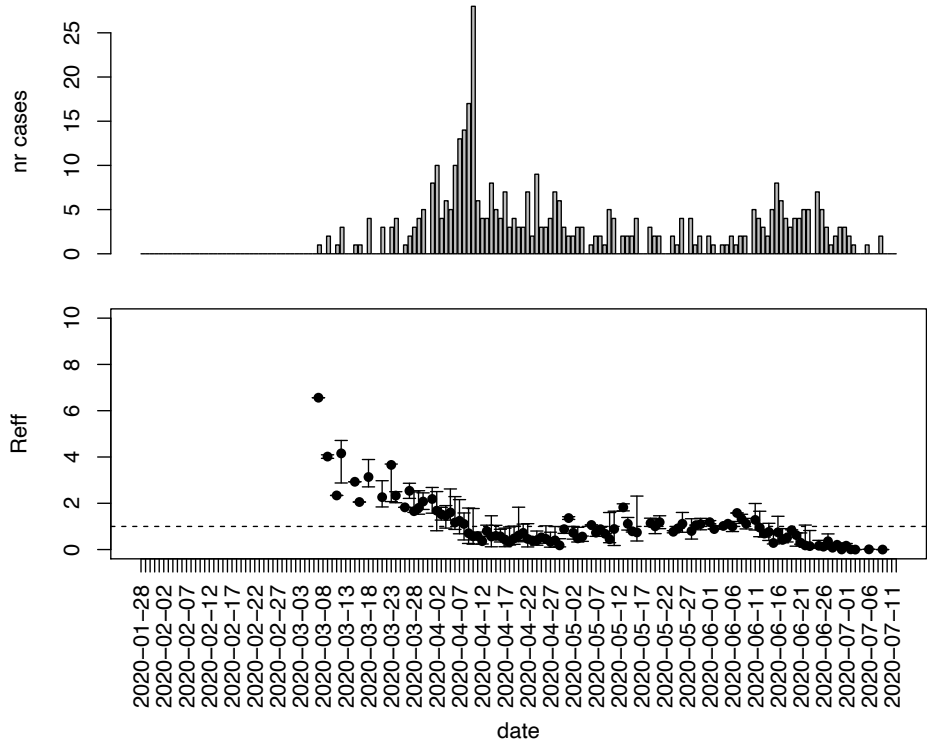
Appendix Figure 153. Epidemic curves and reproduction number estimates until July 13th in Twigg county.





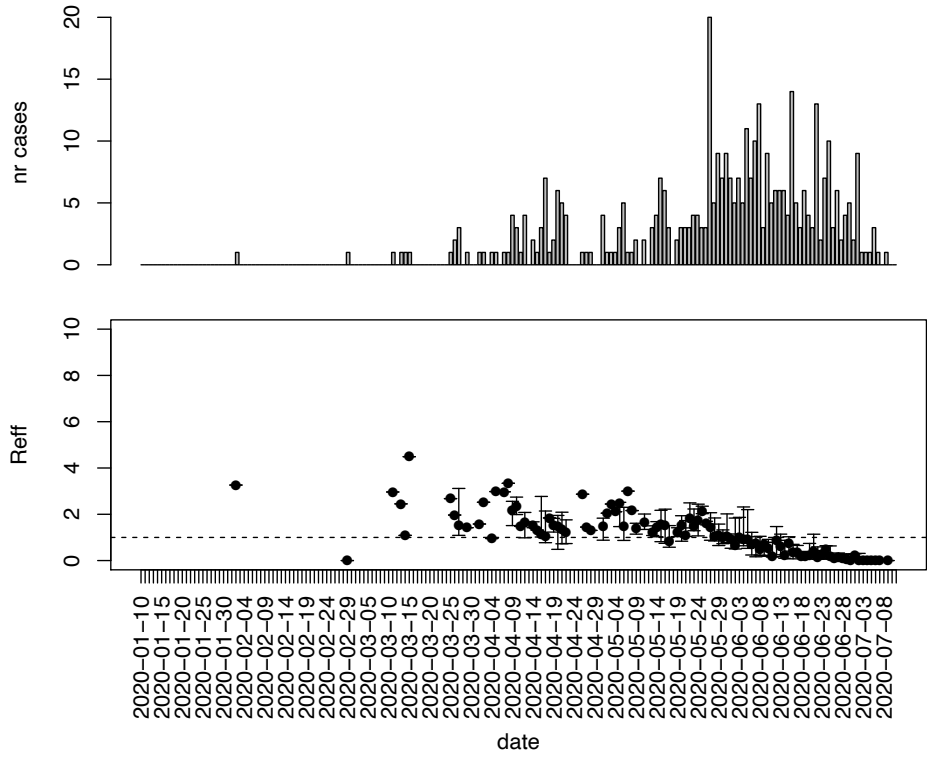
Appendix Figure 154. Epidemic curves and reproduction number estimates until July 13th in Union county.

UPSON, n=404



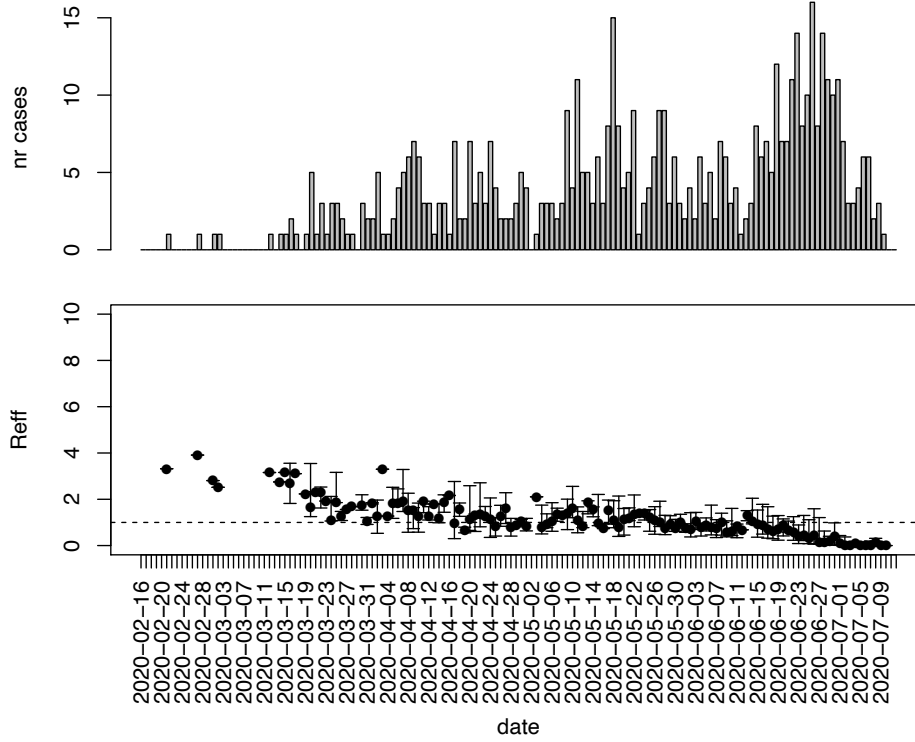
Appendix Figure 155. Epidemic curves and reproduction number estimates until July 13th in Upson county.

WALKER, n=394



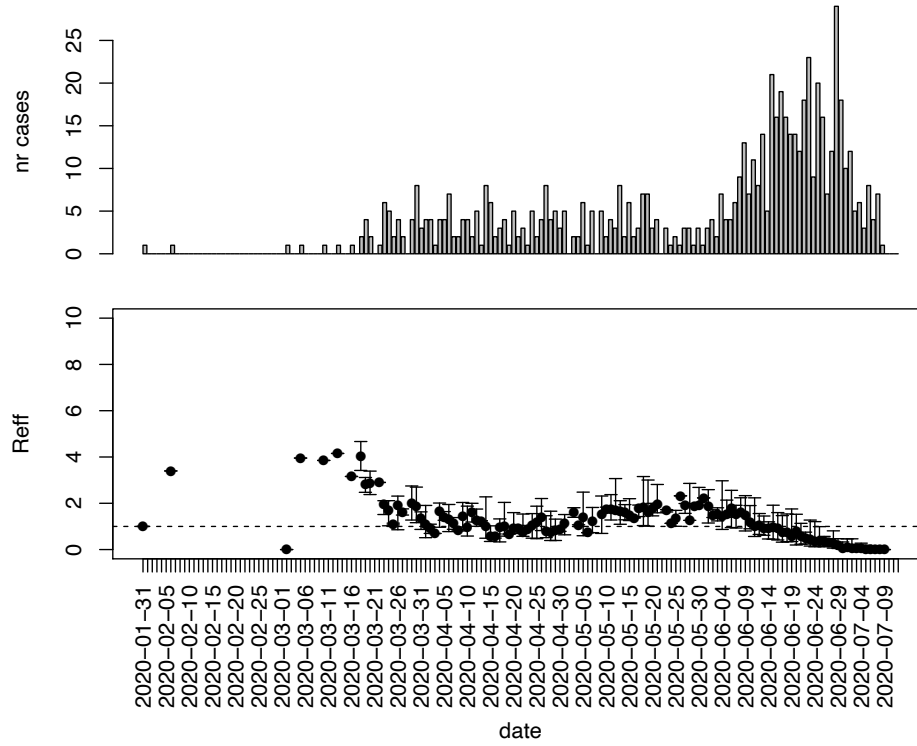
Appendix Figure 156. Epidemic curves and reproduction number estimates until July 13th in Walker county.

WALTON, n=551

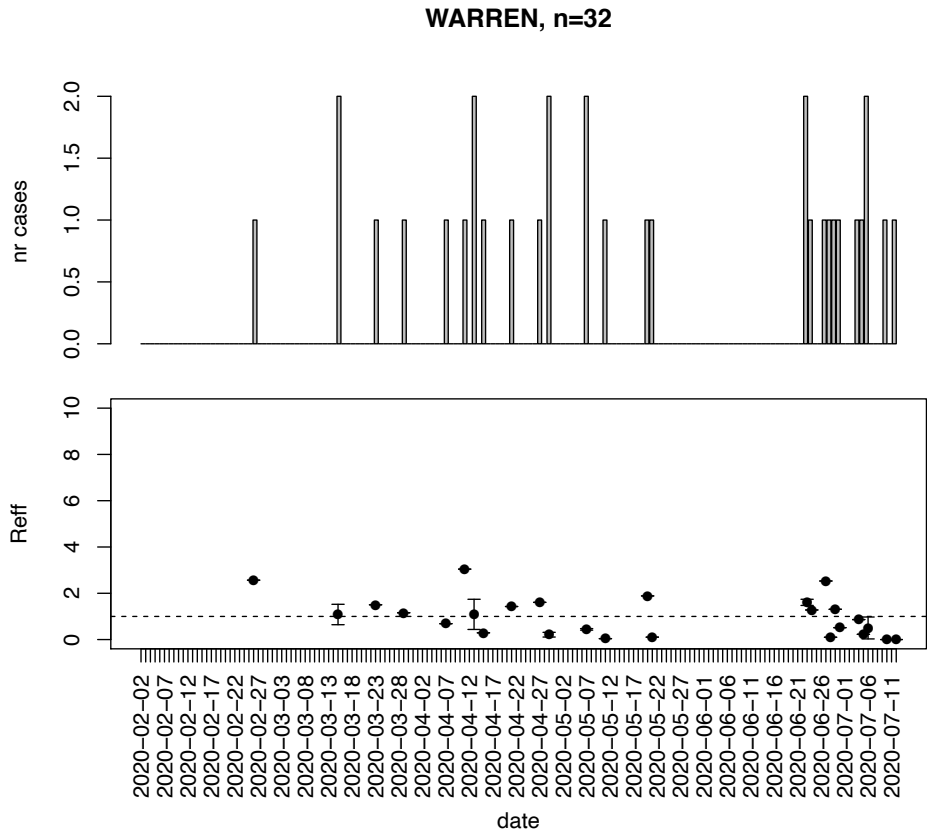


Appendix Figure 157. Epidemic curves and reproduction number estimates until July 13th in Walton county.

WARE, n=672

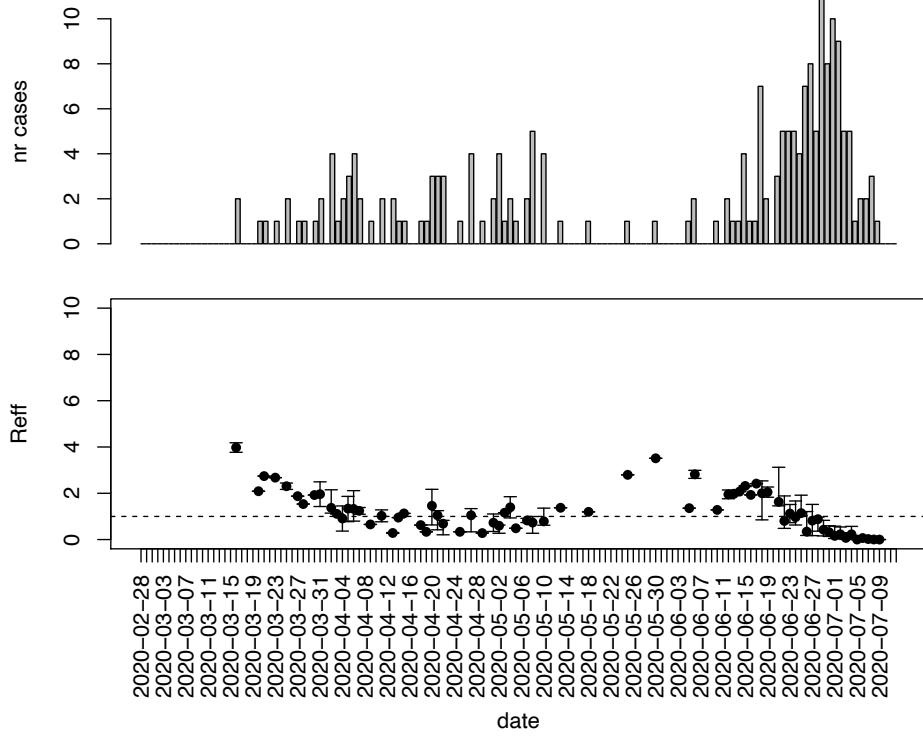


Appendix Figure 158. Epidemic curves and reproduction number estimates until July 13th in Ware county.



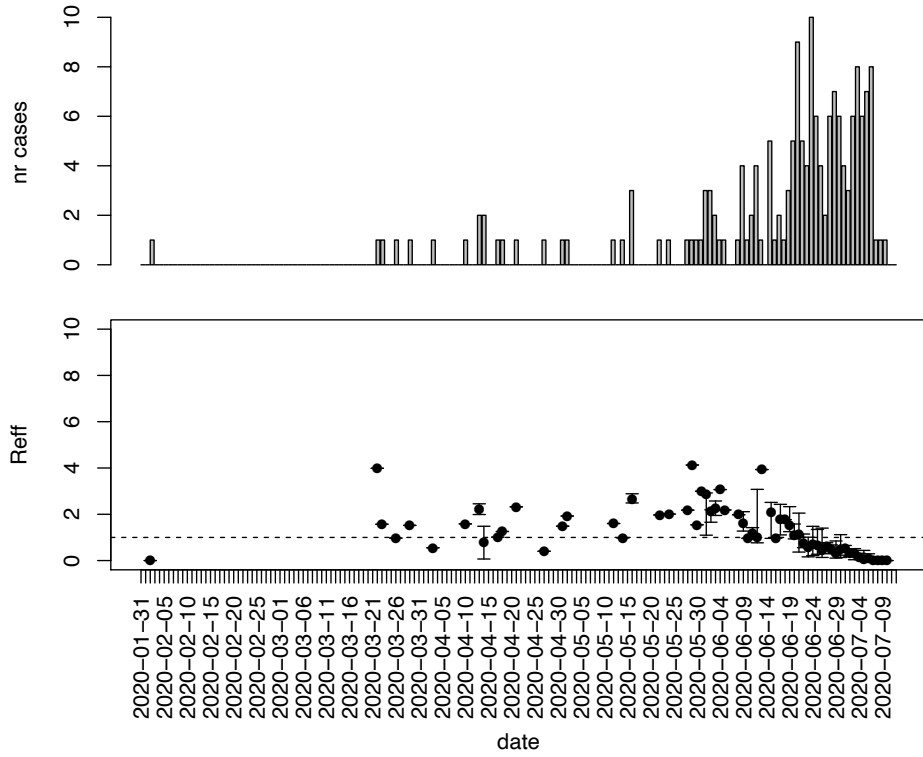
Appendix Figure 159. Epidemic curves and reproduction number estimates until July 13th in Warren county.

WASHINGTON, n=199



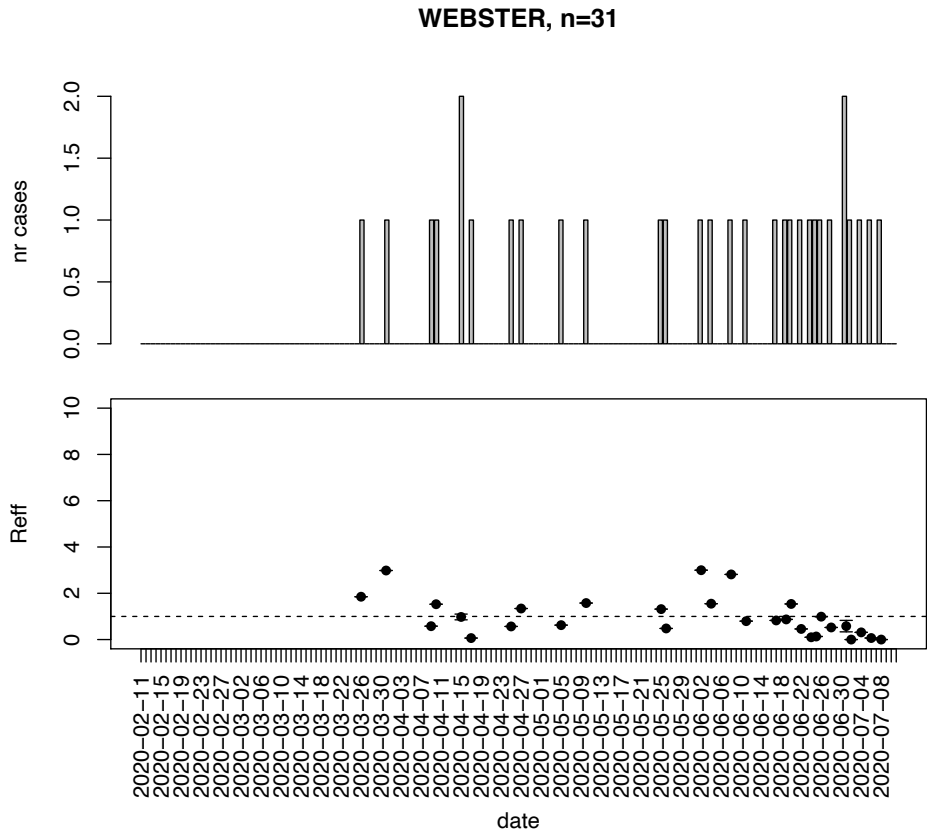
Appendix Figure 160. Epidemic curves and reproduction number estimates until July 13th in Washington county.

WAYNE, n=172



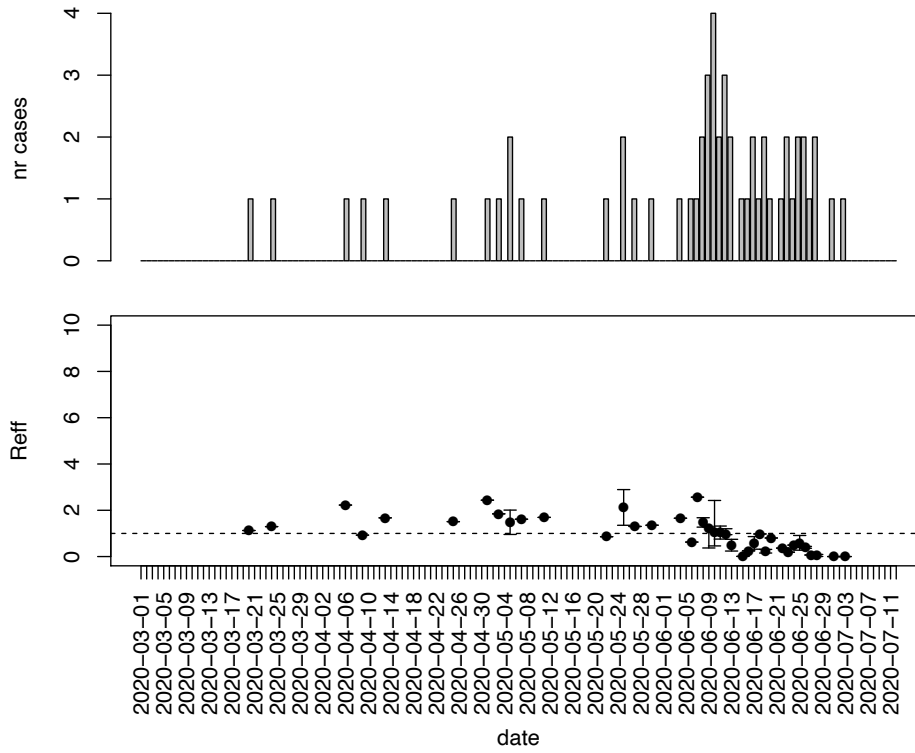
Appendix Figure 161. Epidemic curves and reproduction number estimates until July 13th in Wayne county.



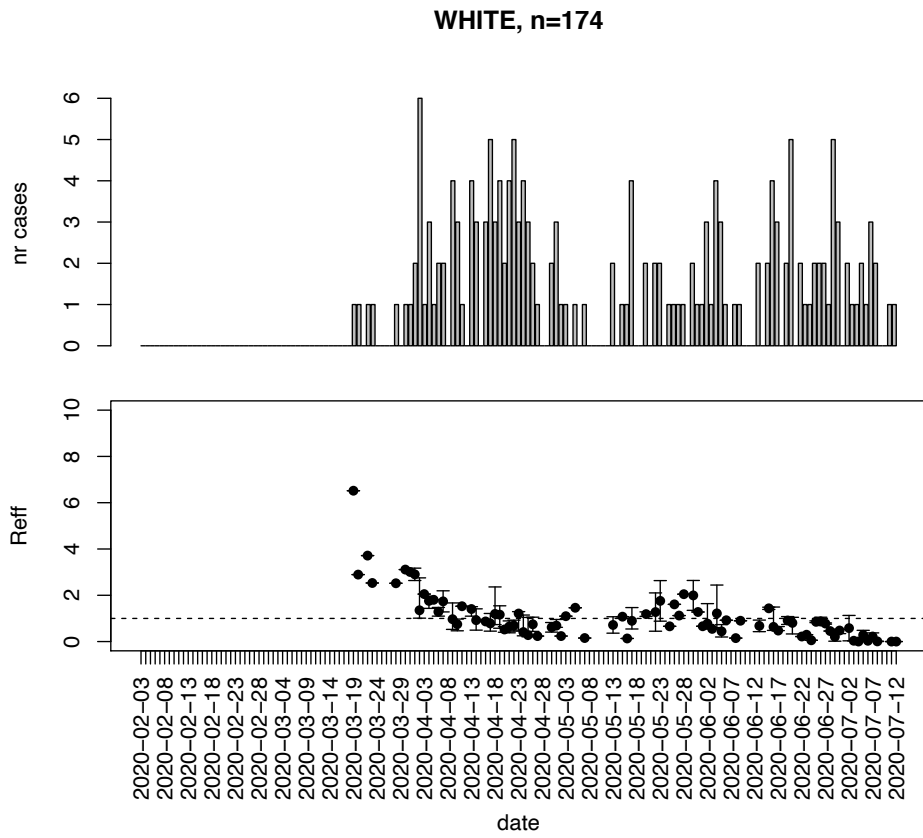


Appendix Figure 162. Epidemic curves and reproduction number estimates until July 13th in Webster county.

WHEELER, n=57

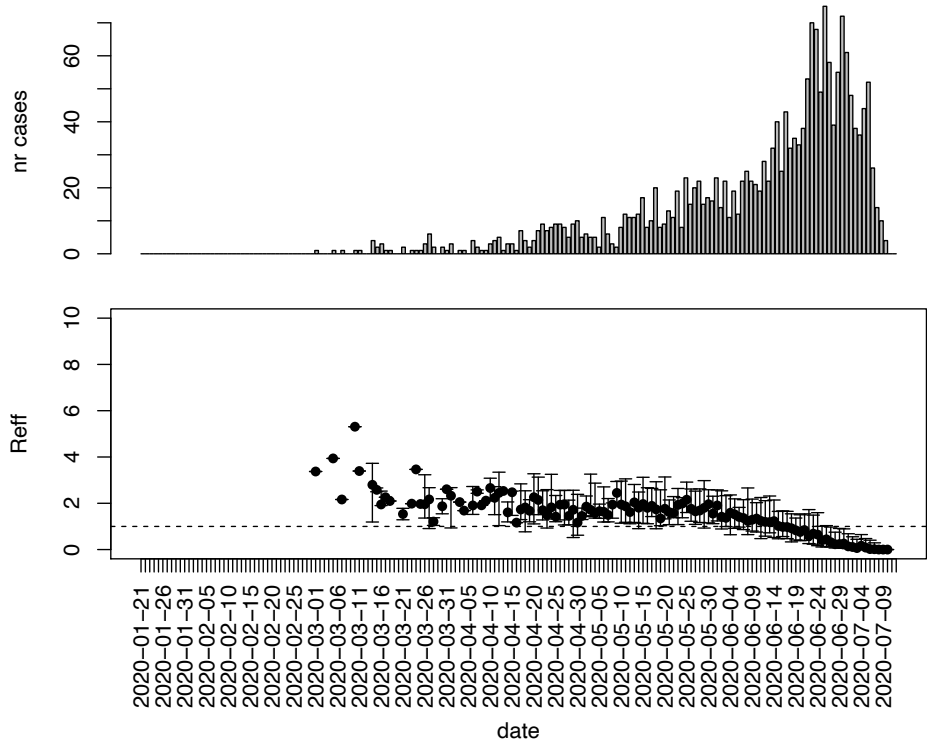


Appendix Figure 163. Epidemic curves and reproduction number estimates until July 13th in Wheeler county.



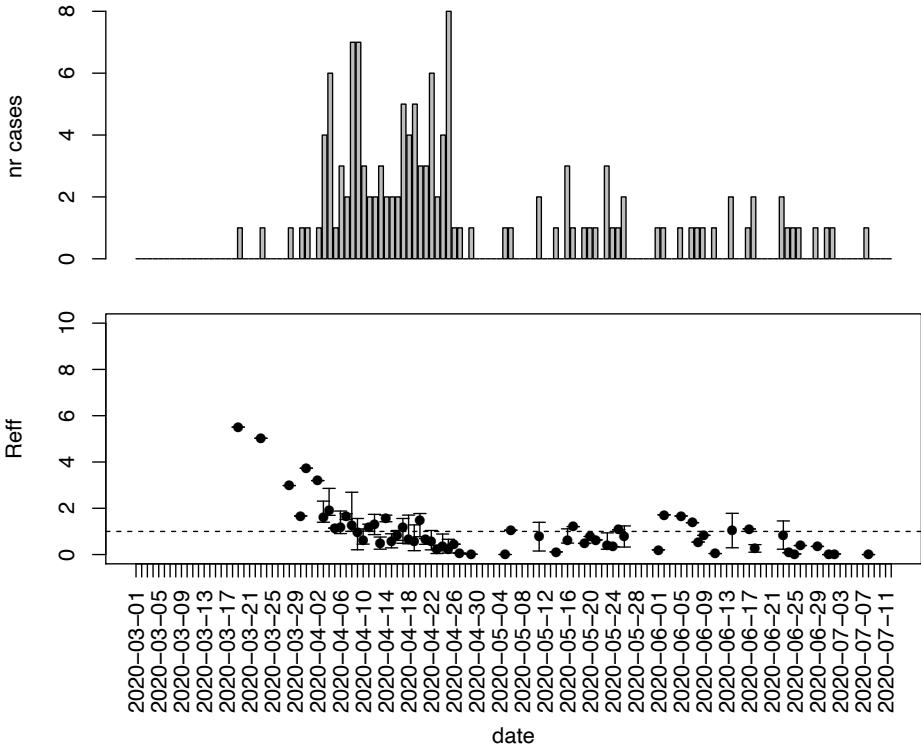
Appendix Figure 164. Epidemic curves and reproduction number estimates until July 13th in White county.

WHITFIELD, n=1926



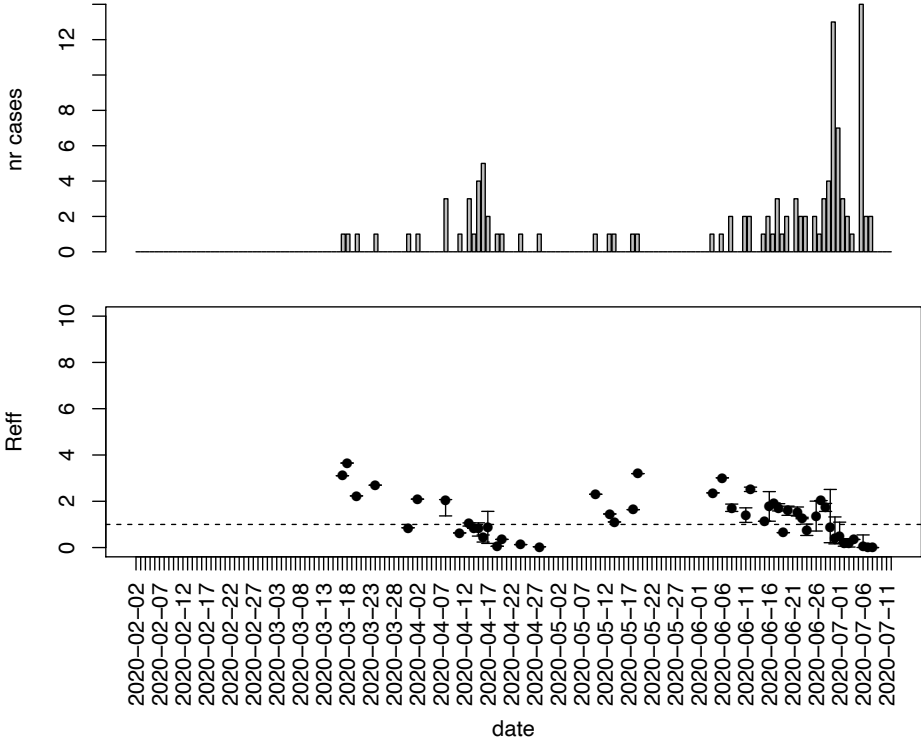
Appendix Figure 165. Epidemic curves and reproduction number estimates until July 13th in Whitfield county.

WILCOX, n=135



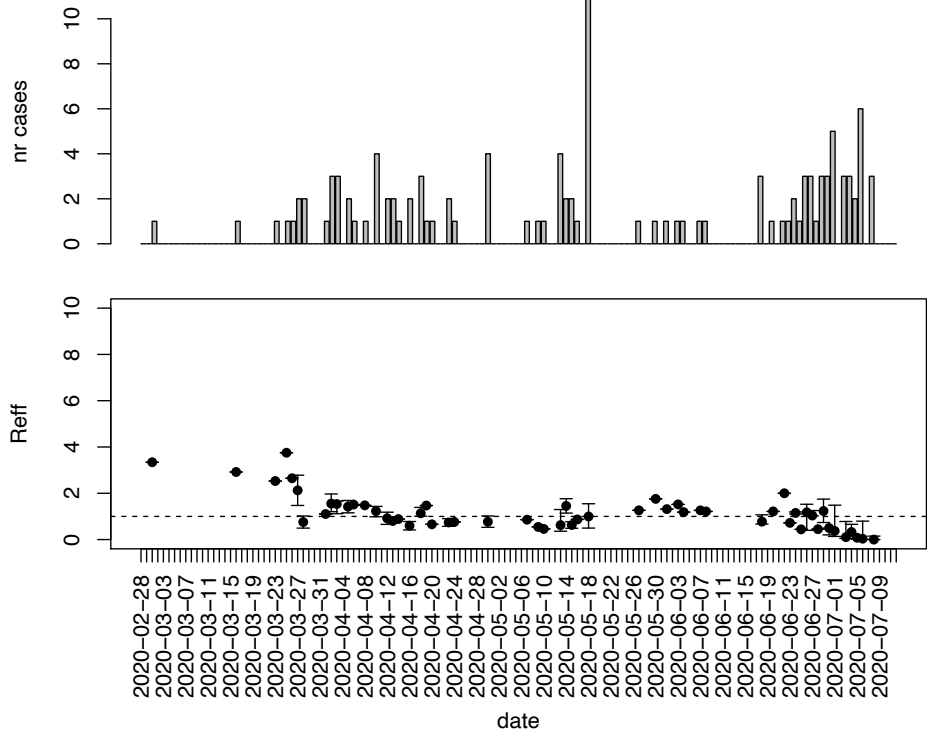
Appendix Figure 166. Epidemic curves and reproduction number estimates until July 13th in Wilcox county.

WILKES, n=113



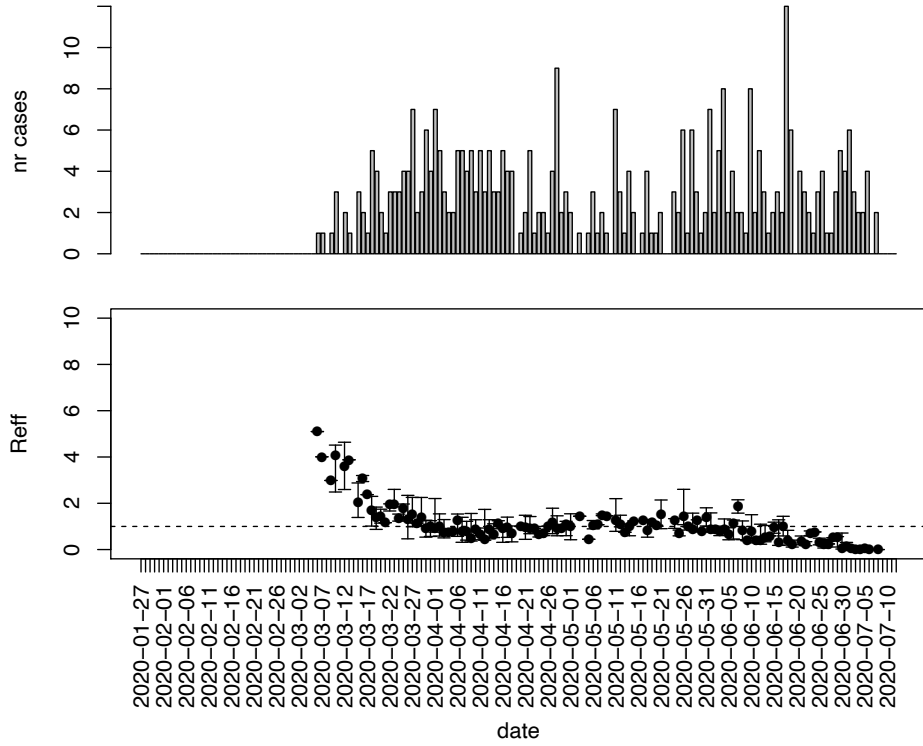
Appendix Figure 167. Epidemic curves and reproduction number estimates until July 13th in Wilkes county.

WILKINSON, n=117



Appendix Figure 168. Epidemic curves and reproduction number estimates until July 13th in Wilkinson county.

WORTH, n=359



Appendix Figure 169. Epidemic curves and reproduction number estimates until July 13th in Worth county.