

1 SARS-CoV-2 virus dynamics in recently infected people – data from a household transmission  
2 study

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13 Notes

14 **Author Note:** The findings and conclusions in this report are those of the authors and do  
15 not necessarily represent the official position of the US Centers for Disease Control and  
16 Prevention.

17 **Funding statement:** This study was supported by the Centers for Disease Control and  
18 Prevention, (cooperative agreements IP001078 and IP001083). Dr. Grijalva was supported in  
19 part by the National Institute for Allergy and Infectious Diseases (K24 AI148459). The work  
20 used REDCap, which is supported by CTSA award No. UL1 TR002243 from the National  
21 Center for Advancing Translational Sciences (NCATS) Clinical Translational Science Award  
22 (CTSA) Program, Award Number 5UL1TR002243-03.

23 **Conflict of interest statement:** Dr. Grijalva reports grants from Campbell  
24 Alliance/Syneos, the National Institutes of Health, the Food and Drug Administration, the

1 Agency for Health Care Research and Quality and Sanofi-Pasteur, and consultation fees from  
2 Pfizer, Merck, and Sanofi-Pasteur. Dr. Halasa reports grant support from Sanofi-Pasteur and  
3 Quidel.

4 **Ethics statement:** The study protocol was approved by Institutional Review Boards at  
5 Vanderbilt University Medical Center and Marshfield Clinic Research Institute. CDC determined  
6 this activity was conducted consistent with applicable federal law and CDC policy (see 45 C.F.R.  
7 part 46; 21 C.F.R. part 56).

8 **Acknowledgements:** We thank the following for their contributions to the study: Hannah  
9 Berger, Vicki Moon, Keegan Brighton, Gina Burbey, Deanna Cole, Leila Deering, Eric DeJarlais,  
10 Heather Dirxx, Sherri Guzinski, Joshua Hebert, Linda Heeren, Erin Higdon, Jacob Johnston,  
11 Chris Kadolph, Taylor Kent, Burney Kieke, Tamara Kronenwetter Koepel, Sarah Kohn, Diane  
12 Kohnhorst, Erik Kronholm, Stacey Kyle, Jim Linneman, Carrie Marcis, Karen McGreevey,  
13 Sudha Medabalimi, Nidhi Mehta, Nan Pan, Cory Pike, Rebecca Pilsner, DeeAnn Polacek,  
14 Martha Presson, Carla Rottscheit, Jacklyn Salzwedel, Kristin Seyfert, Tapan Sharma, Alyssa  
15 Spoerl, Sandy Strey, Krishna Chaitanya Upadhyay, Gail Weinand, and Benjamin Zimmerman at  
16 Marshfield Clinic Research Institute; Judy King, Dayna Wyatt, Robert Lyons, Carleigh Frazier,  
17 Emily Jookar, Karen Malone, Olivia Doak, Sarah Davis, Jorge Celedonio, Marcia Blair, Rendie  
18 McHenry, Claudia Guevara, Jennifer Luther, and Laura Short at Vanderbilt University Medical  
19 Center; Gaston Bonenfant and Bin Zhou at the Centers for Disease Control and Prevention; and  
20 all of the research participants.

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1 **Abstract**

2 We used daily real-time reverse-transcription polymerase chain reaction (rRT-PCR) results from  
3 67 cases of SARS-CoV-2 infection in a household transmission study, conducted April 2020--  
4 May 2021, to examine the trajectory of cycle threshold (Ct) values, an inverse correlate of viral  
5 RNA concentration. Ct values varied across RT-PCR platforms and by participant age.  
6 Specimens collected from children and adolescents had higher Ct values and adults aged  $\geq 50$   
7 years showed lower Ct values than adults aged 18-49 years. Ct values were lower on days when  
8 participants reported experiencing symptoms, with the lowest Ct value occurring 2-6 days after  
9 symptom onset.

10 *Keywords:* SARS-CoV-2, cycle threshold values, age, viral dynamics, RT-PCR

## Introduction

Cycle threshold (Ct) values, generated from real-time reverse-transcription polymerase chain reaction (RT-PCR) assays, represent the minimum number of amplification cycles needed to generate a signal for a specific target. Ct values are sometimes used as surrogate signals for SARS-CoV-2 viral loads[1], as they are inversely related to the amount of virus in the tested specimen. Widespread availability of RT-PCR has led to comparisons of Ct values at the patient and community levels to infer associations with illness severity and patient characteristics[2]. However, Ct values can vary by assay, specimen type and quality, and time during the infection course, especially complicating cross-sectional comparisons. Use of serial specimens collected from one individual over the course of infection on the same assay can partially mitigate these concerns, yet few investigations have used serial sampling to describe the natural history of SARS-CoV-2 infection[3-5] or included specimens from the general population with uncomplicated infection[6, 7].

We described SARS-CoV-2 RT-PCR Ct values in newly infected individuals who collected daily specimens as part of a prospective transmission study, and examined the impact of age and symptoms on Ct value trajectories.

## Methods

We conducted a household transmission study of SARS-CoV-2 in Tennessee and Wisconsin[8, 9] between April 2020 and May 2021. Non-hospitalized individuals (index participants) who had tested positive for SARS-CoV-2 by a provider-ordered nucleic acid amplification test, and resided with at least one other individual, were recruited into the study and consented and enrolled in the study, along with their household contacts, within 6 days of the index participant's symptom onset. Study procedures included daily swabbing and symptom

1 diaries (Supplementary Table 1), for 14 consecutive days. All participants completed  
2 demographic surveys and self-reported pre-existing conditions (asthma, chronic liver disease,  
3 premature birth, cardiac conditions, diabetes, cancer, immunocompromising conditions, extreme  
4 obesity, kidney disease, or pregnancy) and, after COVID-19 vaccines became available,  
5 vaccination status (verified against health records and immunization information systems).

6 Anterior nasal swabs were self-/parent-collected by study participants. Swabs were either  
7 placed in viral transport media (Remel MicroTest M4RT®, Lenexa, KS USA) and refrigerated  
8 by participants for 7-10 days before transport, or placed in inactivating viral transport media  
9 (Primestore®, Longhorn Vaccines & Diagnostics LLC, Bethesda, MD) and stored at room  
10 temperature by participants for 1-3 days before transport to local laboratories for processing and  
11 freezing at -80°C prior to testing. All specimens were tested by RT-PCR using either the CDC  
12 2019-Novel Coronavirus Real-Time RT-PCR Diagnostic Panel (EUA CDC-006-00019; with N1  
13 and N2 gene targets and RNaseP control; CDC assay) or the ThermoFisher TaqPath™ COVID-  
14 19 ComboKit (with S and N gene and ORF1ab targets and MS2 spike control; ThermoFisher  
15 assay). Only Ct values from tests interpreted as positive (at least two SARS-CoV-2 target Ct  
16 values <40) were analyzed. As an additional quality control measure for this analysis, we  
17 excluded Ct values from any test where the control (RNaseP or MS2) result was interpreted as  
18 negative or where the RNaseP control target had a Ct value >35 (though this exclusion did not  
19 change results).

20 Viral culture was conducted on positive specimens from a subset of participants tested  
21 using the CDC assay. Wells were seeded with Vero E6-TMPRSS2 cells, to which 100µl of  
22 participant specimen was added. Wells were monitored daily for culture positivity for five days  
23 after inoculation. If >20% of cells were detached in wells exhibiting viral cytopathic effect, the

1 specimen was interpreted as culture positive. Additional detail of culture methods and results are  
2 described elsewhere[10].

3 To examine trajectories of Ct values over the course of infection, we selected data from  
4 household contacts who met the following criteria: individuals' first study specimen was  
5 negative, they must have tested positive on  $\geq 3$  different days, and all specimens must have been  
6 tested using the same assay (Supplemental Figure 1). Days of lowest Ct values were defined per  
7 target (N1, N2, N, S, or ORF1ab). After exploring multiple model specifications (Supplementary  
8 methods), we described Ct values over time using generalized additive models examining the  
9 effect of age (representing age categorically, in groups 0-11, 12-17, or  $\geq 50$  years compared to 18-  
10 49 years), controlling for the target of each assay (which also differed by assay type), with a  
11 random effect spline for repeated measurements and a smoothing thin plate spline for time since  
12 first positive test. We also explored the effects of symptoms on each day of infection, controlling  
13 for age; symptoms were considered binary (symptom present/absent) for both the primary results  
14 (on impact of any symptom) and post-hoc analysis of individual symptoms (Supplemental Table  
15 1).

## 16 Results

17 A total of 577 household contacts from 302 households were enrolled in the parent study  
18 April 2020-May 2021. Sixty-seven contacts from 50 households met our criteria for “incident  
19 cases” (52.2% male; 82.1% non-Hispanic White; 19.4% with at least one underlying condition;  
20 92.5% symptomatic; 26.8% aged 0-11, 16.4% aged 12-17, 40.3% aged 18-49, 16.4% aged  $\geq 50$ ;  
21 10.4% having received one dose of an mRNA COVID-19 vaccine before enrollment; Table 1 and  
22 Supplemental Figure 1). Associations between other demographics and Ct values are presented

1 in Supplemental Table 2. A total of 544 specimens from incident cases were tested, including  
2 1384 Ct values against SARS-CoV-2 targets.

3 The median observed number of positive days among incident cases was 10 (interquartile  
4 range [IQR]: 8, 12 days), although 58% of participants' last specimen collected were still  
5 positive for SARS-CoV-2 and participants were tested for a median of 10 days following first  
6 positivity. The median observed duration of symptoms was 10 (IQR: 7, 13) days. The median  
7 time from symptom onset among incident cases to their first positive test was 0 (IQR: -1, 3)  
8 days, with symptom onset preceding first positivity in 48% of symptomatic cases (Supplemental  
9 Figure 2). The median time from symptom onset to lowest Ct value was 4 (IQR: 2, 6) days,  
10 indicating that symptom onset preceded lowest Ct value. The median time from first testing  
11 positive to lowest Ct values was 3 (IQR: 2, 4) days. Among symptomatic incident cases, the  
12 median time from symptom onset to lowest Ct value was 4 (IQR: 2, 6) days. Among 93  
13 specimens (from 13 incident cases, all culture positive at least once) that underwent attempted  
14 culture, Ct values were lower in culture-positive specimens (median N1 Ct value, 26.9 [IQR:  
15 25.0, 30.0]; median N2 Ct value, 28.3 [IQR: 26.0, 30.7] from 63 specimens) than in culture-  
16 negative specimens (median N1 Ct value, 35.6 [IQR: 34.1, 38.5]; median N2 Ct value, 38.0  
17 [IQR: 34.9, 39.0] from 30 specimens; Wilcox test  $p < 0.001$  for both targets).

18 Supplemental Table 3 reports Ct values by target and age, with sample sizes of  
19 participants and tests. On average, children aged 0-11 years had Ct values that were 3.5 units  
20 higher than adults aged 18-49 years (95% confidence interval [CI]: 2.8, 4.1;  $p < 0.001$ ).  
21 Adolescents aged 12-17 years also had higher average Ct values (absolute difference: 2.7; [CI:  
22 1.9, 3.4];  $p < 0.001$ ) and older adults, aged  $\geq 50$  years, had significantly lower Ct values (absolute

1 difference: -1.7; [CI: -2.4, -1.0];  $p < 0.001$ ) compared with adults aged 18-49 years (Figure 1). As  
2 expected, Ct values differed between assays (higher in the CDC assay).

3 Reporting symptoms on a given day was associated with lower Ct values, controlling for  
4 both target and age (absolute difference: -0.84 [CI: -1.0, -0.7],  $p < 0.001$ ). In post-hoc tests, Ct  
5 values were significantly lower on days incident cases reported fatigue, fever, aches, chills,  
6 diarrhea, cough, chest tightness/pain, shortness of breath, wheezing, nasal congestion, runny  
7 nose, sore throat, or headache (Supplemental Table 1). No significant difference in Ct values  
8 were noted on days the incident cases experienced abdominal pain, vomiting, or loss/change of  
9 taste/smell.

## 10 Discussion

11 Using data from incident cases from an intensive, prospective household study, this report  
12 contributes data on Ct values early in the infection period, which are difficult to capture using  
13 other designs. Compared to adults aged 18-49 years, we observed that Ct values were higher  
14 among children and adolescents (0-11 and 12-17 years; reflective of lower RNA levels), and  
15 lower among older adults ( $\geq 50$  years) in this largely wild-type-predominant period. These results  
16 are consistent with previous findings of variable Ct values by RT-PCR assay and time course of  
17 infection[11].

18 Other studies have reported differences in Ct values across individuals who were  
19 persistently asymptomatic[7, 12]. This analysis further contributes that daily symptom status  
20 (and not just overall symptom presentation) is associated with daily Ct values, with lower Ct  
21 values on days when participants experienced symptoms. While Ct values cannot be used to  
22 directly infer infectiousness, changes in Ct value within an individual may represent a signal of

1 viral proliferation or eventual clearance. We specifically observed that individuals may have  
2 higher viral RNA concentrations while symptomatic.

3 While other studies have reported significant differences in Ct values as a function of age,  
4 the direction and interpretation of these results has differed. Cross-sectional and retrospective  
5 studies examining Ct values among children have observed lower Ct values in children under the  
6 age of 5 compared to adults over age 18[13] and compared to older children between age 5 and  
7 14[14]. In this analysis of specimens collected daily since the first positive test result, Ct values  
8 among children and adolescents were higher than values among adults aged 18-49 years. The  
9 discrepancies between these findings and prior reports merit further investigation, and may have  
10 been driven by differences in the severity of illness, the time during infection, circulating  
11 variants, the particular age categories used, or the prospective versus cross-sectional study  
12 design.

13 Our observations of a median of 4 days from first positivity to peak viral RNA  
14 concentration are similar to prior reports[3, 7]. In this analysis, we observed that first positivity  
15 generally coincided with symptom onset, but that dates of symptom onset preceded dates of  
16 lowest Ct values by 2-6 days. One of the earliest reports on SARS-CoV-2 viral dynamics[5]  
17 observed that viral RNA concentrations were highest on the day of symptom onset, and fell  
18 thereafter (although no samples were collected prior to symptoms). A more recent model-based  
19 analysis of incident infections[7] found a median of 0.6 days from peak viral load to symptom  
20 onset among mildly symptomatic persons. Some of these differences may have emerged from the  
21 substantial heterogeneity we observed between timings of symptom onset and first positivity,  
22 which suggests that the natural history of infections can be variable. Our findings from this  
23 cohort with a broader range of ages and including only cases where date of first positivity is

1 known suggest relatively longer periods of rising viral RNA concentration following symptom  
2 onset. This supports the importance of following mitigation and infection control measures as  
3 symptoms develop and while ill to prevent onwards transmission.

4 Describing dynamics of Ct values based on frequent, systematic sampling of individuals  
5 over time ameliorates multiple concerns with the use of this data; however, these findings must  
6 still be interpreted with caution. Our selection of incident cases may have biased the sample  
7 towards those exhibiting delayed replication. Sample size and study period are also limitations,  
8 especially in our ability to assess the impact of vaccination status or dissociate vaccination or  
9 other demographics from age. Our incident cases, who were majority White, non-Hispanic, may  
10 not generalize to other populations. Ct values cannot be precisely converted to a quantitative  
11 representation of viral load, or used to directly infer differences in infectiousness. However,  
12 despite these limitations, clinical interpretation of Ct values (or their trajectories) may be  
13 “tempting” (*IDSIA and AMP joint statement on the use of SARS-CoV-2 PCR cycle threshold (Ct)*  
14 *values for clinical decision-making*, page 3) [15]. The present data are directly relevant to these  
15 interpretations. Specifically, specimens that were collected within 4 days of symptom onset may  
16 represent periods when Ct values are still declining.

17 These findings contribute to our understanding of RT-PCR Ct values during relatively  
18 mild, uncomplicated SARS-CoV-2 infections over a broad range of ages, in a community setting,  
19 and among individuals with a known date of first shedding. While these data were collected prior  
20 to Delta and Omicron circulation, and prior to widespread vaccination, they may provide context  
21 for interpreting trajectories in Ct values in similar populations during later SARS-CoV-2  
22 outbreaks.

## References

1. Tom MR, Mina MJ. To Interpret the SARS-CoV-2 Test, Consider the Cycle Threshold Value. *Clin Infect Dis* **2020**; 71:2252-4.
2. Magleby R, Westblade LF, Trzebucki A, et al. Impact of Severe Acute Respiratory Syndrome Coronavirus 2 Viral Load on Risk of Intubation and Mortality Among Hospitalized Patients With Coronavirus Disease 2019. *Clin Infect Dis* **2020**.
3. Kissler SM, Fauver JR, Mack C, et al. Viral dynamics of acute SARS-CoV-2 infection and applications to diagnostic and public health strategies. *PLoS Biol* **2021**; 19:e3001333-e.
4. Ke R, Martinez PP, Smith RL, et al. Longitudinal analysis of SARS-CoV-2 vaccine breakthrough infections reveal limited infectious virus shedding and restricted tissue distribution. *medRxiv* **2021**:2021.08.30.21262701.
5. He X, Lau EHY, Wu P, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nat Med* **2020**; 26:672-5.
6. Singanayagam A, Hakki S, Dunning J, et al. Community transmission and viral load kinetics of the SARS-CoV-2 delta (B.1.617.2) variant in vaccinated and unvaccinated individuals in the UK: a prospective, longitudinal, cohort study. *Lancet Infect Dis* **2021**.
7. Stankiewicz Karita HC, Dong TQ, Johnston C, et al. Trajectory of Viral RNA Load Among Persons With Incident SARS-CoV-2 G614 Infection (Wuhan Strain) in Association With COVID-19 Symptom Onset and Severity. *JAMA Netw Open* **2022**; 5:e2142796-e.
8. McLean HQ, Grijalva CG, Hanson KE, et al. Household Transmission and Clinical Features of SARS-CoV-2 Infections. *Pediatrics* **2022**; 149.
9. Grijalva CG, Rolfes MA, Zhu Y, et al. Transmission of SARS-COV-2 infections in households—Tennessee and Wisconsin, April–September 2020. *MMWR Morb Mortal Wkly Rep* **2020**; 69:1631.
10. Bonenfant G, Deyoe J, Wong T, et al. Surveillance and correlation of SARS-CoV-2 viral RNA, antigen, virus isolation, and self-reported symptoms in a longitudinal study with daily sampling. *Clin Infect Dis* **2022**:ciac282.
11. Rhoads D, Peaper DR, She RC, et al. College of American Pathologists (CAP) Microbiology Committee Perspective: Caution Must Be Used in Interpreting the Cycle Threshold (Ct) Value. *Clin Infect Dis* **2020**; 72:e685-e6.
12. Salvatore PP, Dawson P, Wadhwa A, et al. Epidemiological Correlates of Polymerase Chain Reaction Cycle Threshold Values in the Detection of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). *Clin Infect Dis* **2021**; 72:e761-e7.
13. Heald-Sargent T, Muller WJ, Zheng X, Rippe J, Patel AB, Kocielek LK. Age-Related Differences in Nasopharyngeal Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Levels in Patients With Mild to Moderate Coronavirus Disease 2019 (COVID-19). *JAMA Pediatr* **2020**; 174:902-3.
14. Strutner J, Ramchandrar N, Dubey S, et al. Comparison of Reverse-Transcription Polymerase Chain Reaction Cycle Threshold Values From Respiratory Specimens in Symptomatic and Asymptomatic Children With Severe Acute Respiratory Syndrome Coronavirus 2 Infection. *Clin Infect Dis* **2021**; 73:1790-4.
15. Infectious Diseases Society of America AfMP. IDSA and AMP joint statement on the use of SARS-CoV-2 PCR cycle threshold (Ct) values for clinical decision-making, **2021**:3.

Inserts

1

2 Table 1. Characteristics of 67 incident cases of SARS-CoV-2 infection participating in a prospective household transmission study –  
 3 Tennessee and Wisconsin, April 2020-May 2021

	Overall	Age 0-11	Age 12-17	Age 18-49	Age 50+	p value
n	67	18	11	27	11	
Partially vaccinated† (n, %)	7 (10.4)	0 (0.0)	1 (9.1)	4 (14.8)	2 (18.2)	0.337
Male (n, %)	35 (52.2)	9 (50.0)	5 (45.5)	16 (59.3)	5 (45.5)	0.807
Race-ethnicity (n, %)						0.754
Hispanic	10 (14.9)	3 (16.7)	2 (18.2)	3 (11.1)	2 (18.2)	
Non-white, non-Hispanic	2 (3.0)	0 (0.0)	0 (0.0)	2 (7.4)	0 (0.0)	
Non-Hispanic White	55 (82.1)	15 (83.3)	9 (81.8)	22 (81.5)	9 (81.8)	
Any underlying condition (n, %)	13 (19.4)	2 (11.1)	1 (9.1)	6 (22.2)	4 (36.4)	0.296
Number of household members, median [IQR]	6.0 [4.0, 6.0]	6.0 [6.0, 6.0]	6.0 [5.0, 7.0]	4.0 [3.8, 4.0]	2.0 [2.0, 3.0]	0.040
Days from first positive specimen to lowest Ct value, median [IQR]	3.0 [2.0, 4.0]	2.0 [1.0, 3.0]	3.0 [2.0, 3.0]	4.0 [3.0, 5.0]	3.0 [2.0, 3.3]	<0.001
Still positive at end of follow-up, n (%)	39 (58.2)	7 (38.9)	5 (45.5)	19 (70.4)	8 (72.3)	0.110
Duration of positivity in days*, median [IQR]	10.0 [8.0, 12.0]	8.0 [7.3, 9.8]	10.0 [5.5, 11.0]	10.0 [9.0, 12.0]	10.0 [8.0, 13.0]	-

Symptomatic (n, %)	62 (92.5)	16 (88.9)	10 (90.9)	26 (96.3)	10 (90.9)	0.805
Symptom duration in days*†‡, median [IQR]	10.0 [7.0, 13.0]	6.5 [4.5, 10.3]	9.0 [4.0, 13.0]	12.0 [9.3, 13.8]	11.5 [10.3, 13.0]	-
Days from symptom onset to first positive specimen‡, median [IQR]	0.0 [-1.0, 3.0]	0.0 [-2.0, 2.0]	0.0 [-1.0, 3.0]	1.0 [-1.0, 3.0]	0.0 [0.0, 4.0]	0.315
Days from symptom onset to lowest Ct‡, median [IQR]	4.0 [2.0, 6.0]	3.0 [0.0, 4.0]	3.0 [0.3, 6.0]	4.0 [3.0, 6.0]	3.5 [3.0, 7.0]	0.008

1 \*Comparison not performed due to censored data.

2 †Vaccination status defined at the time of study enrollment. Partial vaccination indicates having received one dose of a two-dose  
3 mRNA COVID-19 vaccine series. All other study participants had no vaccination documented.

4 §CDC assay indicates the CDC 2019-Novel Coronavirus Real-Time RT-PCR Diagnostic Panel. Remaining participants were tested  
5 with the ThermoFisher TaqPath™ COVID-19 ComboKit.

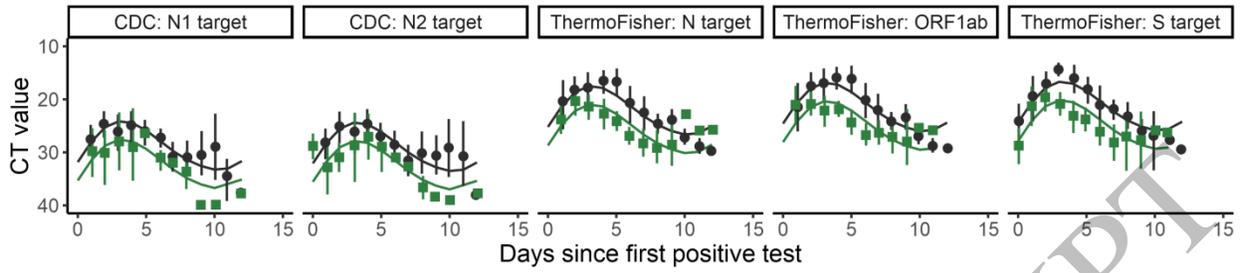
6 ‡The number of days of symptoms, days from symptom onset to first positive test, and symptom onset to peak Ct are calculated only  
7 among symptomatic incident cases. The time from symptom onset to first positive specimen and from symptom onset to lowest Ct  
8 value are calculated per target for the CDC assay N1 and N2 targets, and ThermoFisher assay N, S, and ORF1ab targets before taking  
9 the median of all time differences.

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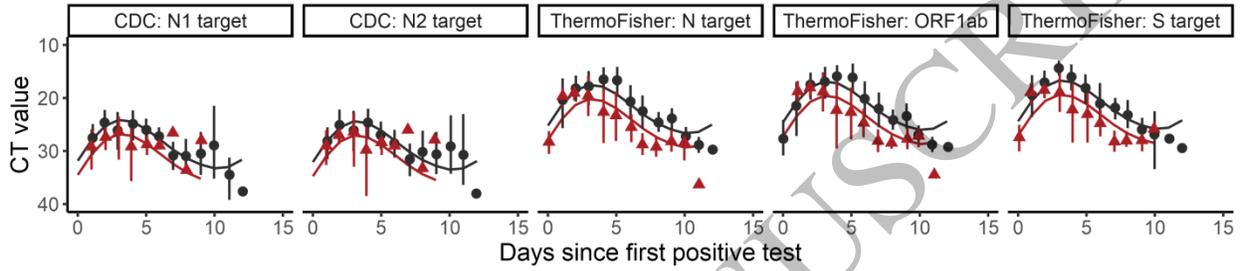
**Figure Legend**

Figure 1. Ct value curves over time since each participant first tested positive against each target, within age groups. Dots represent mean observed values within age groups, and vertical bars show bootstrapped 95% confidence intervals. Smooth lines represent predicted values from the Generalized Additive Model of Ct values over time, accounting for age and repeated measurements. Panel A shows results from participants age 0-11 (square) compared to the reference group, age 18-49 (circle); Panels B and C repeat this comparison with age 12-17 (triangle) or 50+ (diamond). Each plot from left to right represents a SARS-CoV-2 target from one of the two included testing platforms (CDC 2019-Novel Coronavirus Real-Time RT-PCR Diagnostic Panel or the ThermoFisher TaqPath™ COVID-19 ComboKit).

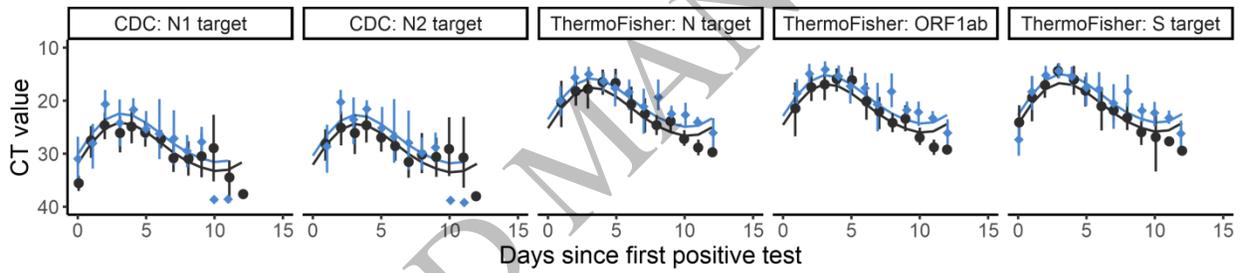
A. Participants aged 0-11 years, compared to 18-49 years



B. Participants aged 12-17 years, compared to 18-49 years



C. Participants aged 50+ years, compared to 18-49 years



Age Category ■ Age 00-11 ▲ Age 12-17 ● Age 18-49 ◆ Age 50+

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Figure 1  
206x165 mm (.86 x DPI)