What is important about the COVID-19 variants?

- Pandemic trajectory
- Double masks
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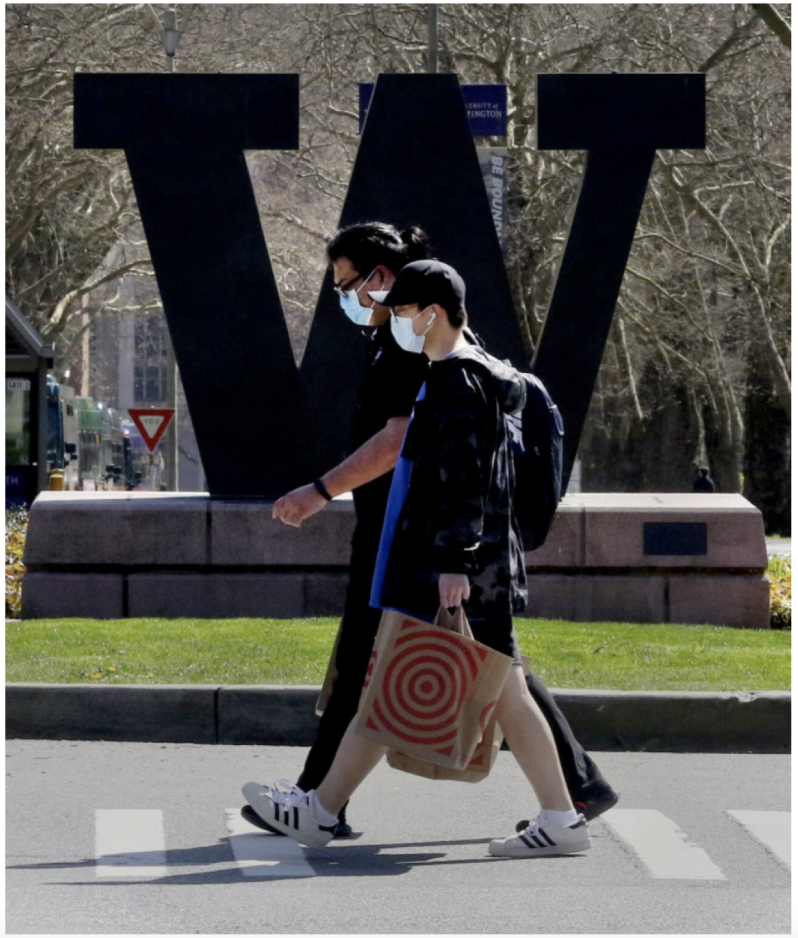
Variant of coronavirus from UK detected at UW, university says

The Seattle Times, 2/9/21

Feb. 9, 2021 at 7:31 pm



CDC: https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant.html

MMWR: https://www.cdc.gov/mmwr/volumes/70/wr/mm7003e2.htm

Medrxiv: https://www.medrxiv.org/content/10.1101/2021.02.06.21251159v1

https://www.medrxiv.org/content/10.1101/2021.02.02.21250985v1

Emerging SARS-CoV-2 Variants

- CDC site
- Variants of concern:
  - UK- VOC 202012/01, lineage B1.1.7, 20I/501Y.V1
  - SA- lineage B.1.351, 20H/501Y.V2, **E484K**
  - Brazil- lineage P.1, 20J/501Y.V3, **E484K**

VOC 202012/01, lineage B1.1.7, 20I/501Y.V1

- “Spike gene target failure” due to 6nt deletion
- First detected 10/12/20, represented 3% of sequences
- By 11/30/20, represented >90% of sequences and is now fixed
- Growth rate 40% to 70% higher, possibly due to better ACE2 binding
- Arrived in U.S. in November 2020, as of January in 30 states
- No evidence that variant impacts vaccine efficacy

Genomic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States

Nicole L. Washington[1,*,@], Karthik Gangavarapu[2,*,@], Mark Zeller[2], Alexandre Bolze[1], Elizabeth T. Cirulli[1], Kelly M. Schiabor Barrett[1], Brendan B. Larsen[3], Catelyn Anderson[2], Simon White[1], Tyler Cassens[1], Sharoni Jacobs[1], Geraint Levan[1], Jason Nguyen[1], Jimmy M. Ramirez III[1], Charlotte Rivera-Garcia[1], Efren Sandoval[1], Xueqing Wang[1], David Wong[1], Emily Spencer[2], Refugio Robles-Sikisaka[2], Ezra Kurzban[2], Laura D. Hughes[12], Xianding Deng[4], Candace Wang[4], Venice Servellita[4], Holly Valentine[5], Peter De Hoff[5], Phoebe Seaver[5], Shashank Sathe[5], Kimberly Gietzen[6], Brad Sickler[6], Jay Antico[6], Kelly Hoon[6], Jingtao Liu[6], Aaron Harding[7], Omid Bakhtar[7], Tracy Basler[8], Brett Austin[8], Magnus Isaksson[1], Phillip G. Febbo[6], David Becker[1], Marc Laurent[1], Eric McDonald[8], Gene W. Yeo[5], Rob Knight[5], Louise C. Laurent[5], Eileen de Feo[6], Michael Worobey[3], Charles Chiu[4,9], Marc A. Suchard[10], James T. Lu[1], William Lee[1,#], Kristian G. Andersen[2,11,#,@]

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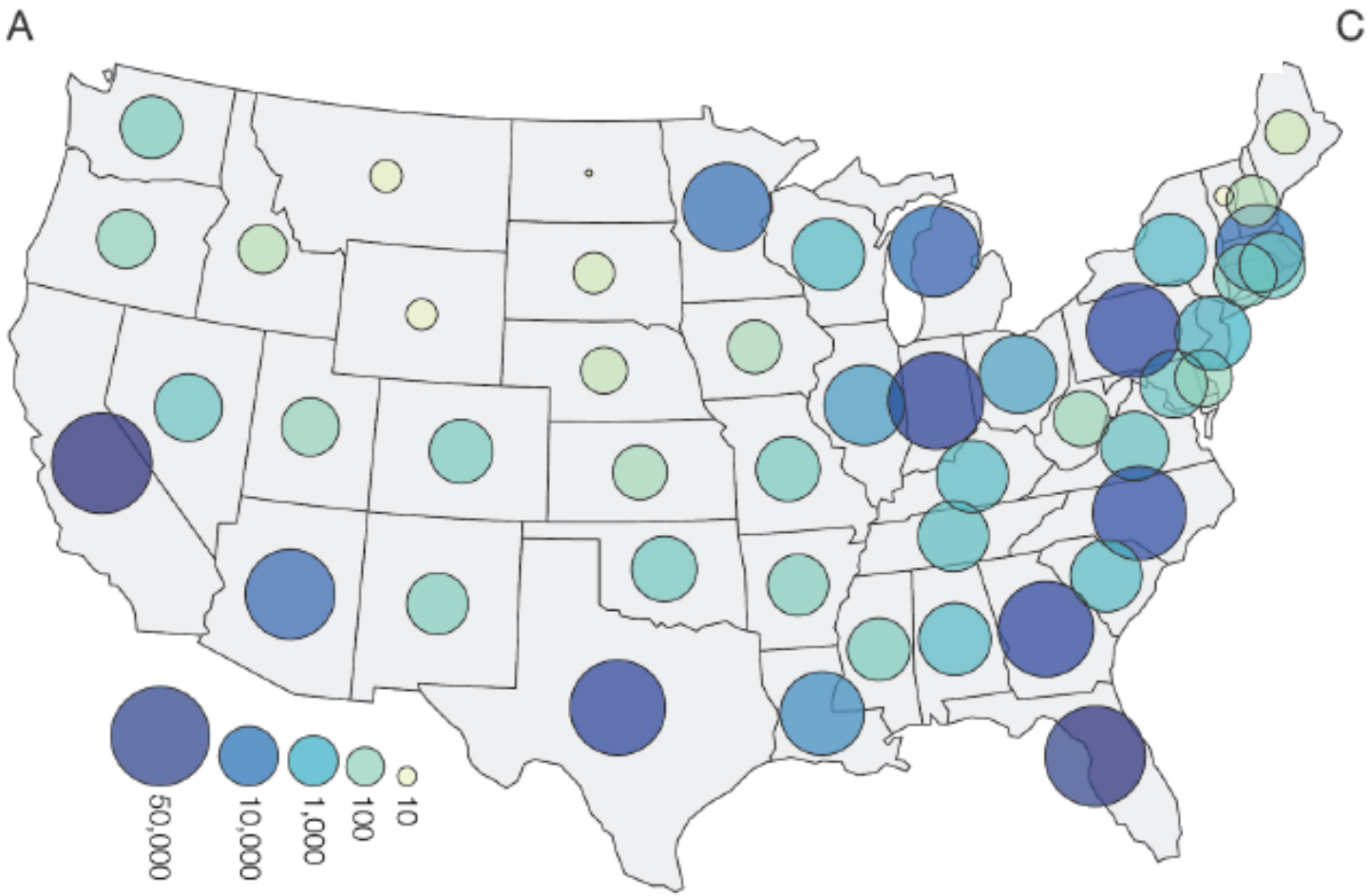

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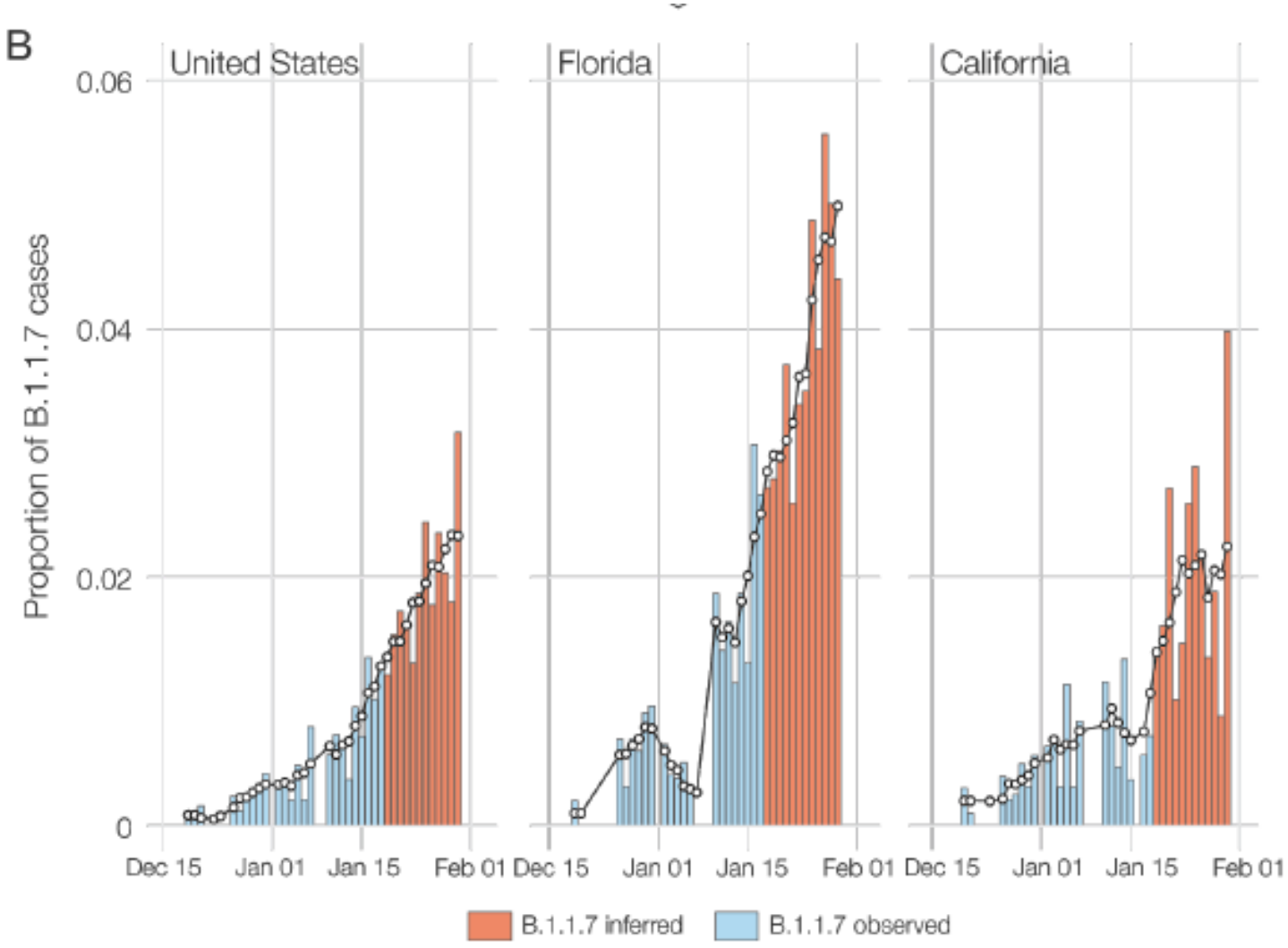

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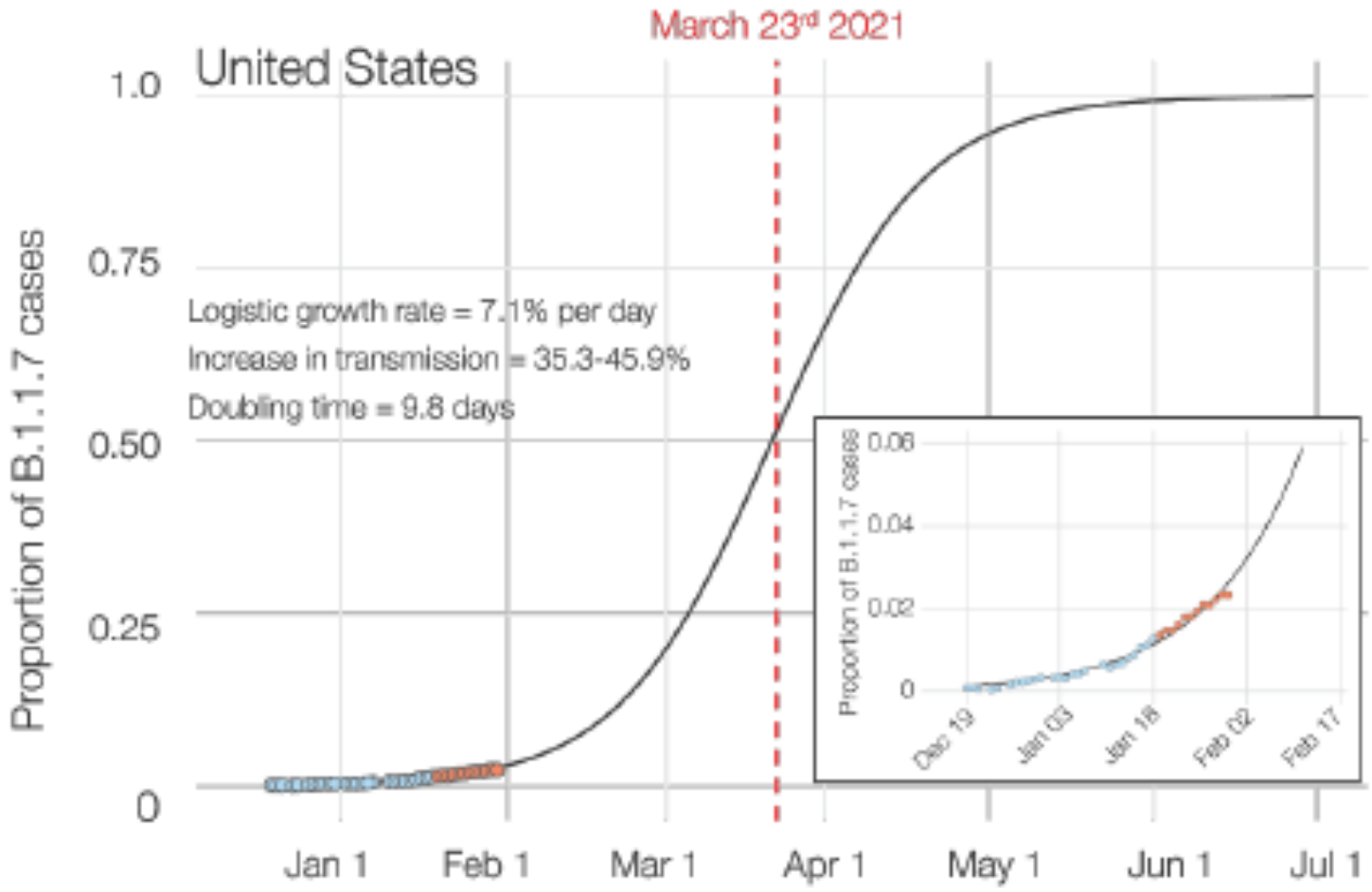
- ~35-45% more transmissible
- Doubling frequency ~1.5 weeks
- Potential dominant strain by March 2021
- If correct, anticipate increased surge in cases



PRELIMINARY – NOT PEER REVIEWED

Increased hazard of death in community-tested cases of SARS-CoV-2 Variant of Concern 202012/01

Nicholas G. Davies[1†], Christopher I. Jarvis[1], CMMID COVID-19 Working Group, W. John Edmunds[1], Nicholas P. Jewell[2,3], Karla Diaz-Ordaz[2,3*], Ruth H. Keogh[2,3*]

1. Centre for Mathematical Modelling of Infectious Diseases, London School of Hygiene and Tropical Medicine, London, UK.
2. Department of Medical Statistics, Faculty of Epidemiology and Population Health, London School of Hygiene and Tropical Medicine, London, UK.
3. Centre for Statistical Methodology, London School of Hygiene and Tropical Medicine, London, UK.

LINK:
https://www.medrxiv.org/content/10.1101/2021.02.01.21250959v1

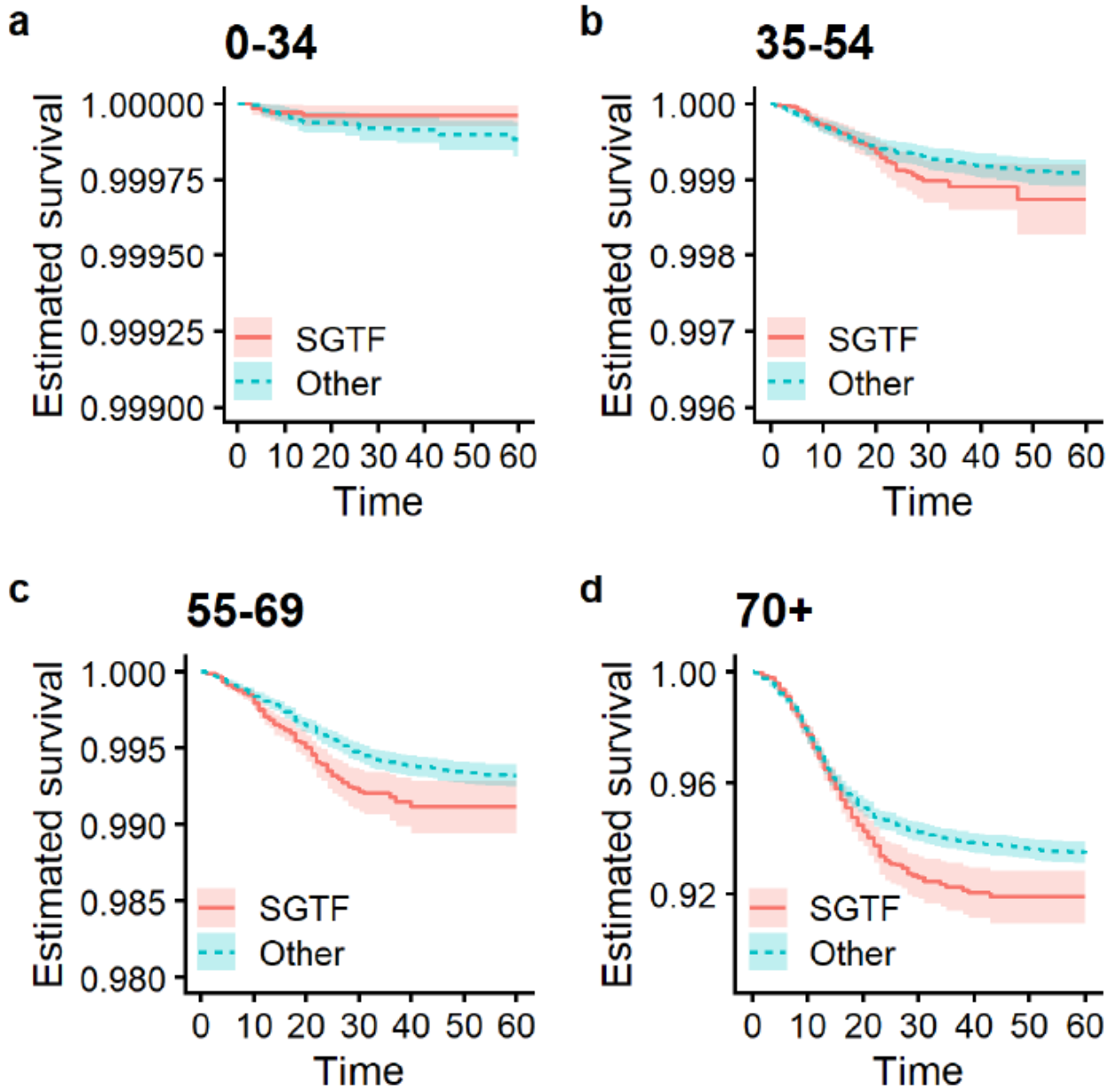


Fig. S2. Kaplan Meier plots of survival within 60 days of positive test for SGTF versus all other positive SARS-CoV-2 tests by age group. Note that the Y axis differs for each panel.

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