



Stonehill Biology Presents

Developing an integrative biological perspective to understand and combat COVID-19 Discussion Series

Tuesdays from 7 – 8pm EST

Hear the Stonehill Biology, Environmental Science, Health Science and Neuroscience Faculty give short lectures on SARS-CoV2 and COVID-19 from the perspectives of their expertise. Stay to ask questions!

- 5/5:** Series Introduction and Virology (Prof. Bleakley, Prof. Pan, and Prof. Hirst)
- 5/12:** Immunology and Physiology I (Prof. Maniero and Prof. Yu)
- 5/19:** Neuroscience/Physiology II and Patient Care (Prof. Cyr and Prof. Beatty)
- 5/26:** Epidemiology, Big Data & Biotechnology (Prof. Rosebrock, Prof. Harbert, and Prof. James-Pederson)
- 6/2:** Evolution and Ecology (Prof. Block and Prof. Hauff)
- 6/9:** Environmental Science and Conservation (Prof. Burkholder and Prof. LeFlore)

First in the series available now at:
<https://preview.tinyurl.com/y745nrhd>

Join us live at: <https://tinyurl.com/yak7sgey>

Epidemiology, Big-Data, and Biotechnology

Rob Harbert

Magdalena James-Pederson

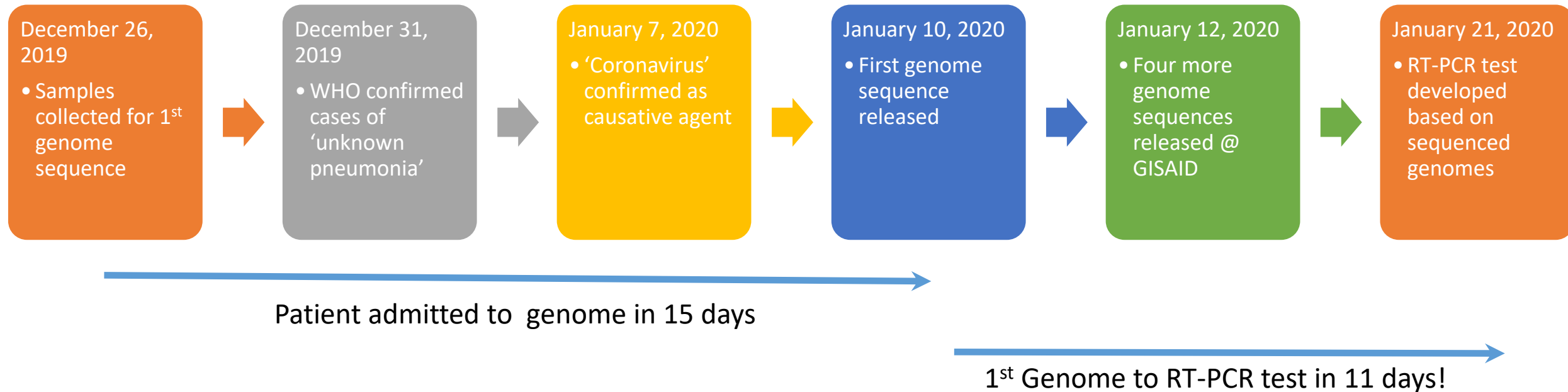
Tracy Rosebrock

Seminar Goals

- Explore the role that genome sequencing and analysis has played in the pandemic response
- Discuss ongoing genetic surveillance
- Look at the evidence for SARS-CoV-2 evolution
- The SARS-CoV-2 real-time RT-PCR diagnostic
- Existing serological tests to determine previous SARS-CoV-2 infection
- To connect the biological and social determinants of infection to the dynamics of viral transmission
- To gain a historical perspective on the second “wave” of epidemics and an understanding of the theoretical causes and possible means of prevention

The SARS-CoV-2 Genome

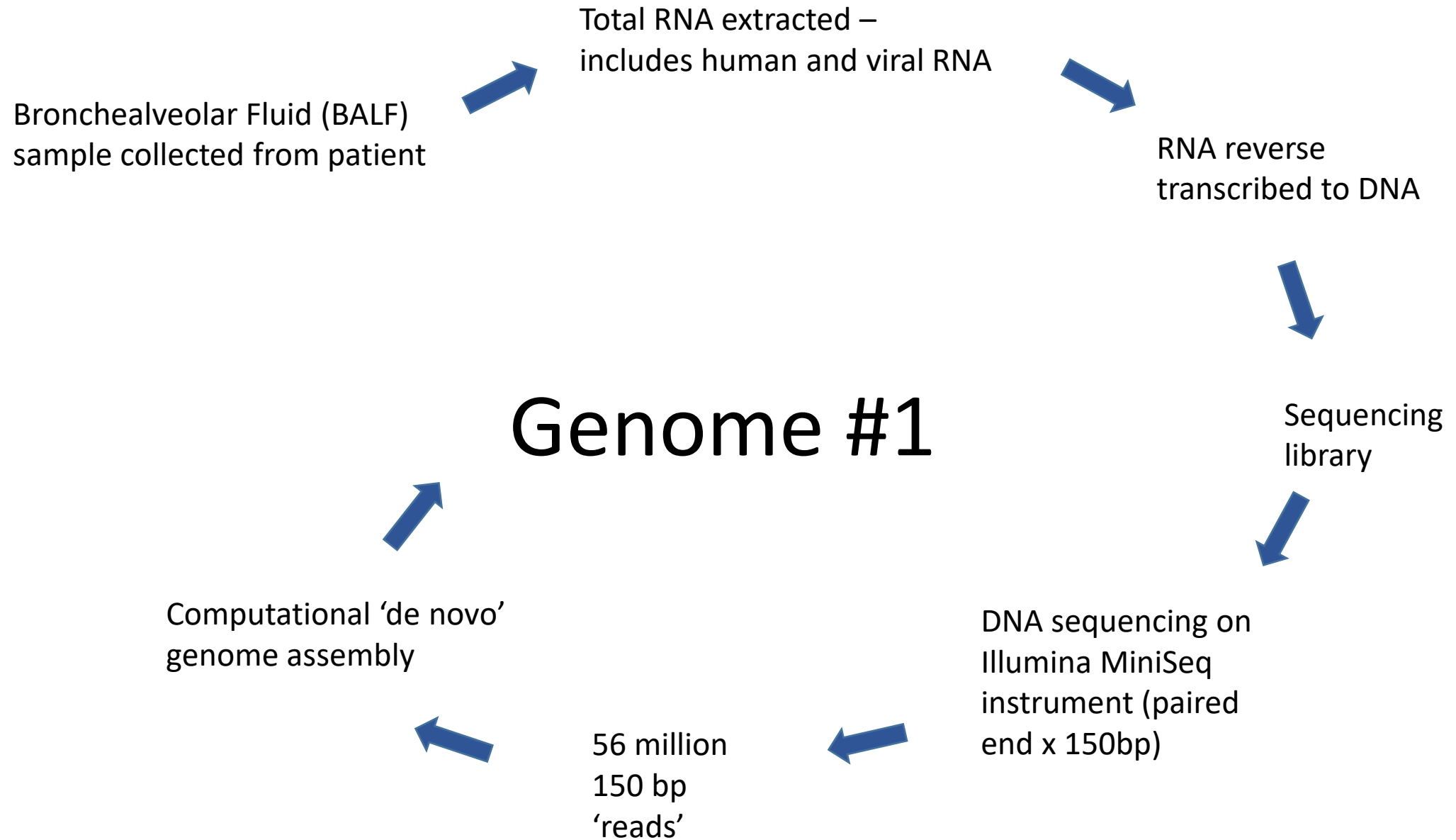
Rapid Response



Source:

<https://www.nature.com/articles/s41586-020-2008-3.pdf>
<https://doi.org/10.2807/1560-7917.ES.2020.25.3.2000045>

(First genome released as: [Genbank accession MN908947](https://www.ncbi.nlm.nih.gov/genbank/MN908947))



[illegible]

Map: Similar genome arrangement to other SARS related viruses

- ssRNA
- 29,903 nucleotides

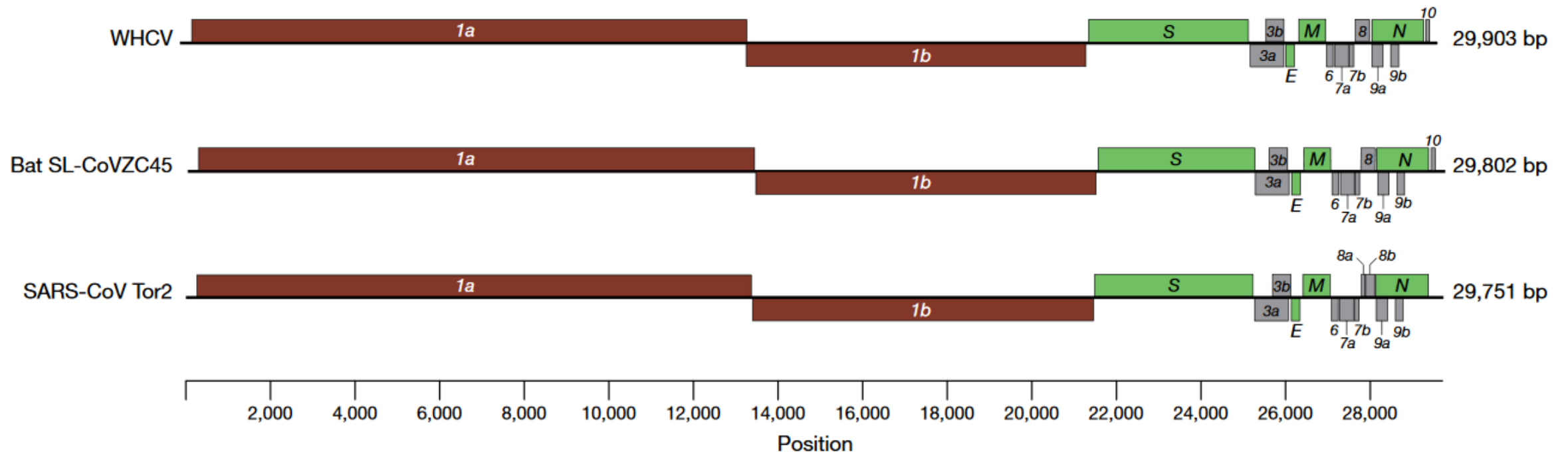


Fig. 1 | Genome organization of SARS and SARS-like CoVs. The organization of genes for WHCV, bat SL-CoVZC45 and SARS-CoV Tor2.

Genomic surveillance of SARS-CoV-2

Rapid genome sequencing

- >30,000 genomes sequenced (as of May 23, 2020)
- Contributions from thousands of scientists around the world
- Data mobilized by [GISAID](https://gisaid.org/)



Why do we need that many genomes!?

There is a lot to learn from the genome

MATTER

Most New York Coronavirus Cases Came From Europe, Genomes Show

Travelers seeded multiple cases starting as early as mid-February, genomes show.

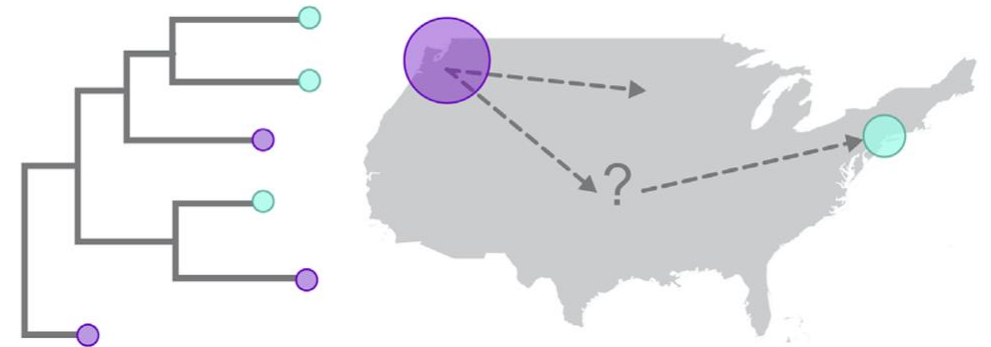
Significance of Pangolin Viruses in Human Pandemic Remains Murky

Scientists haven't found evidence that the new coronavirus jumped from pangolins to people, but they do host very similar viruses



Cell

Coast-to-coast SARS-CoV-2 spread



Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States

NEWS · 18 MAY 2020

Animal source of the coronavirus continues to elude scientists

Computational models, cell studies and animal experiments are being used to pinpoint the viral host that kicked off the pandemic.

Virology Coronavirus Insights OMICs Genomics

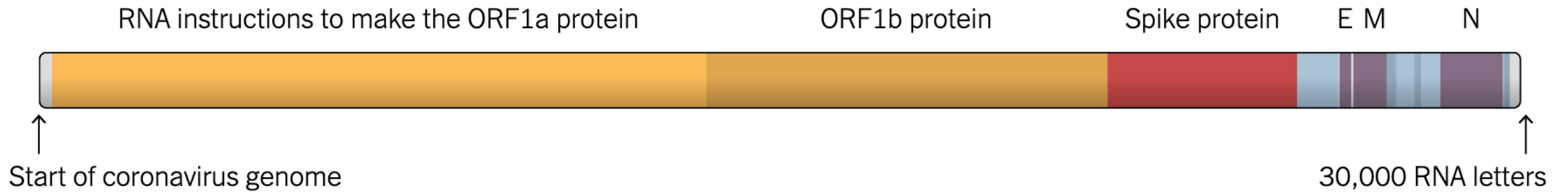
NYC Scientists Swab the Subway in Search of SARS-CoV-2

By Julianna LeMieux, PhD · April 1, 2020 · 0

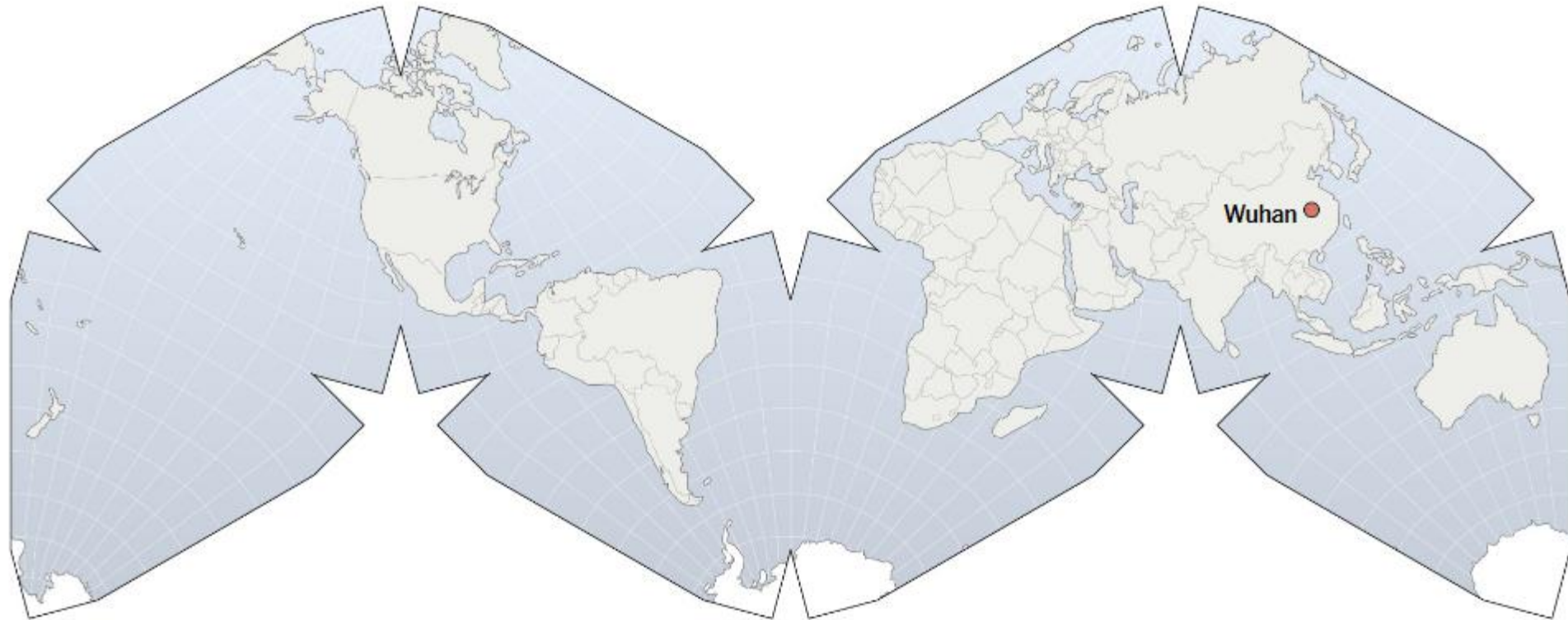
Inferring evolution

Building phylogenetic trees to track SARS-CoV-2 evolution and transmission

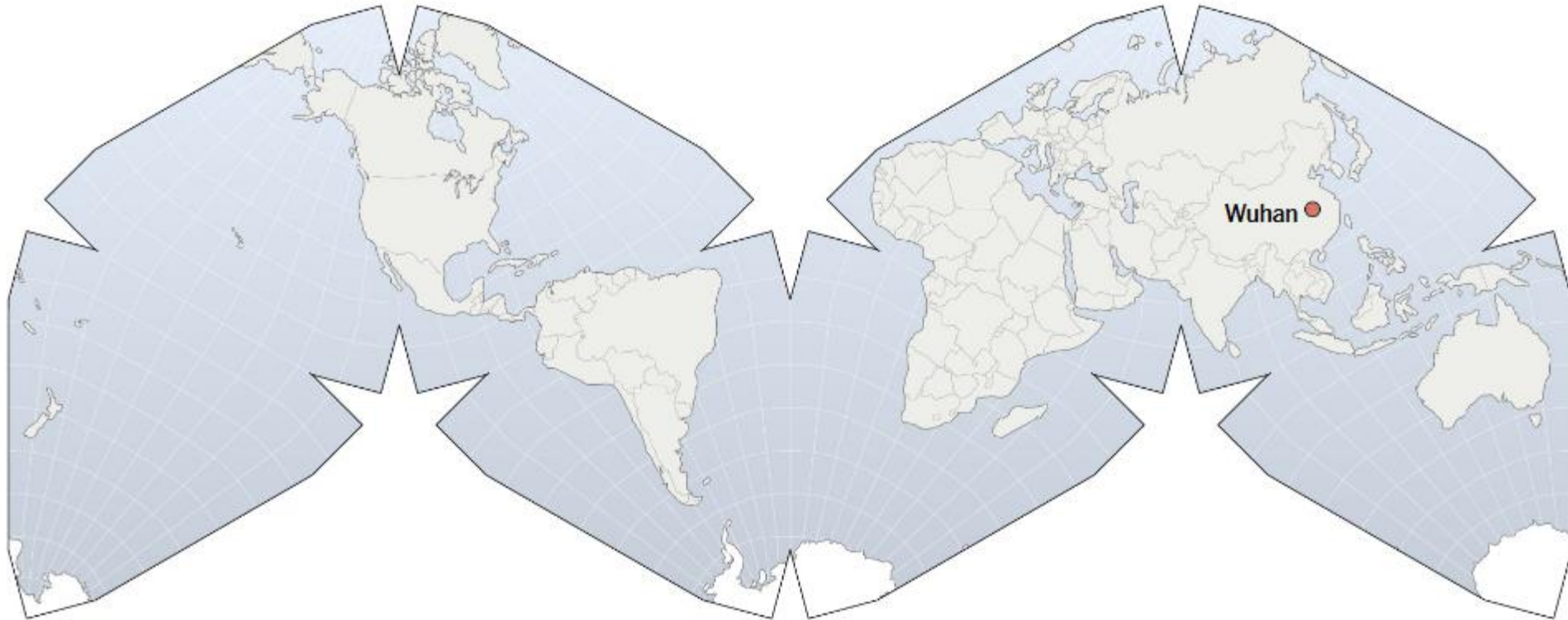
The SARS-CoV-2 Genome



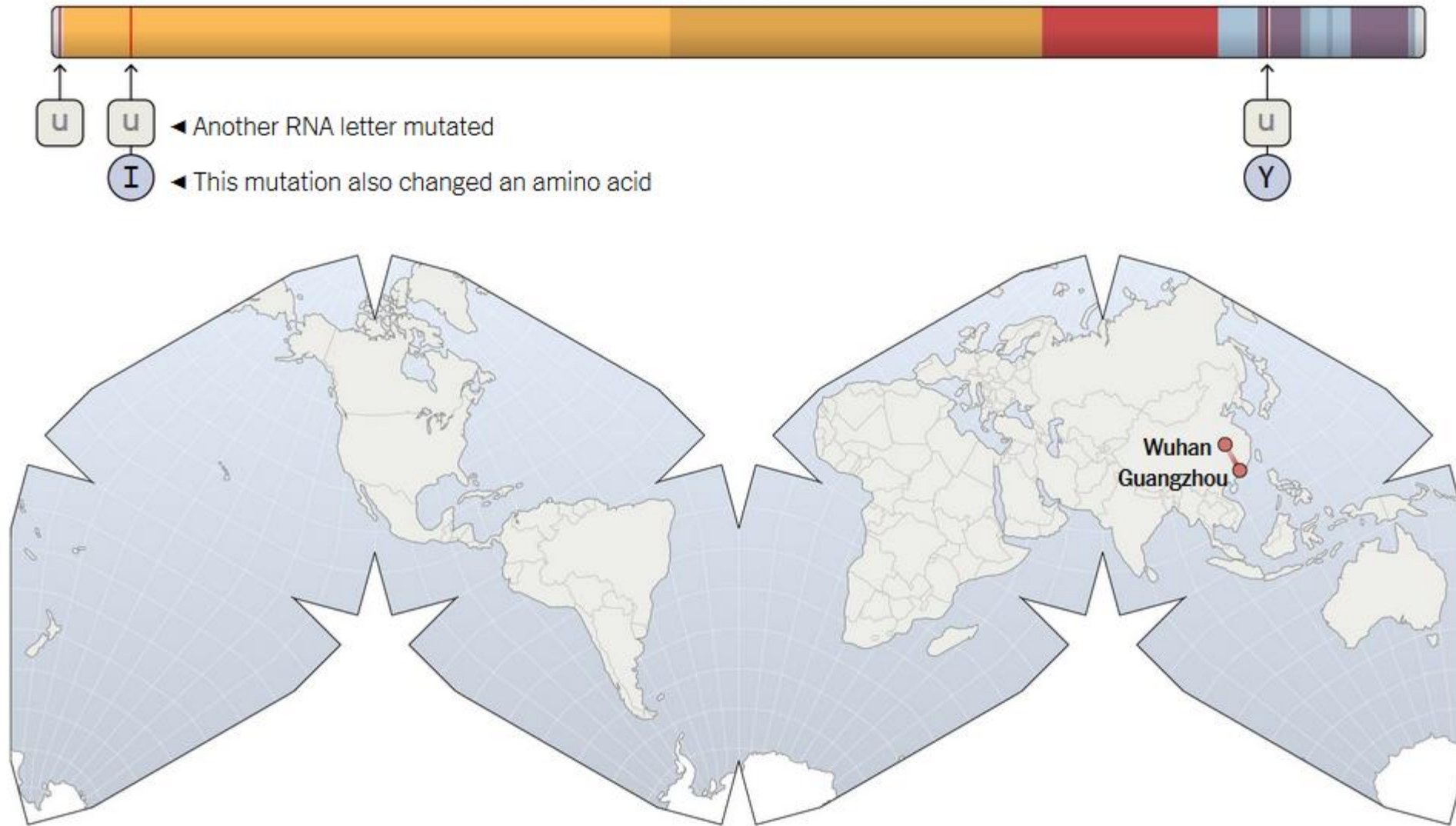
Genome **Wuhan-Hu-1**, collected on Dec. 26 from an early patient in Wuhan



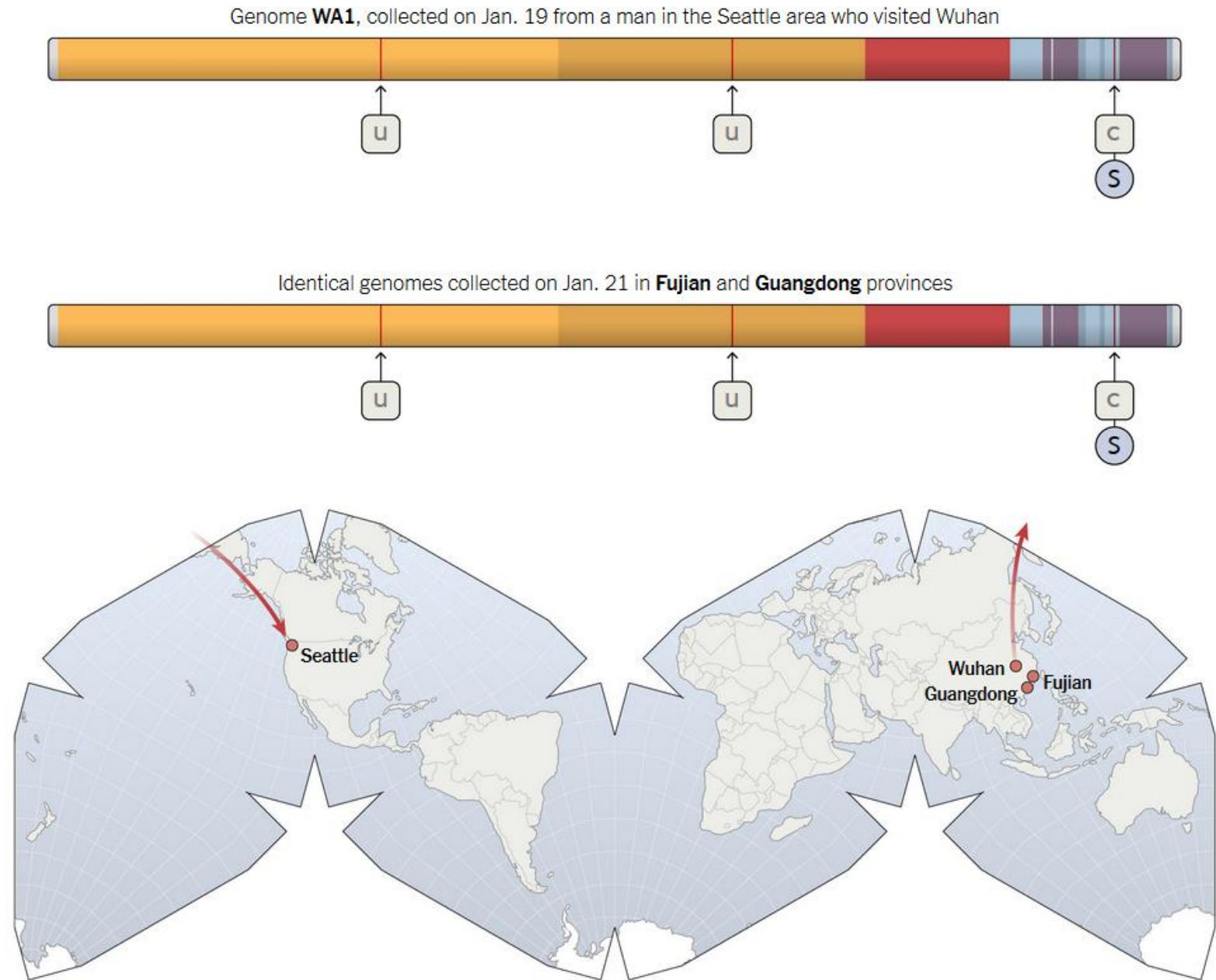
Genome **WH-09**, collected on Jan. 8 from another patient in Wuhan



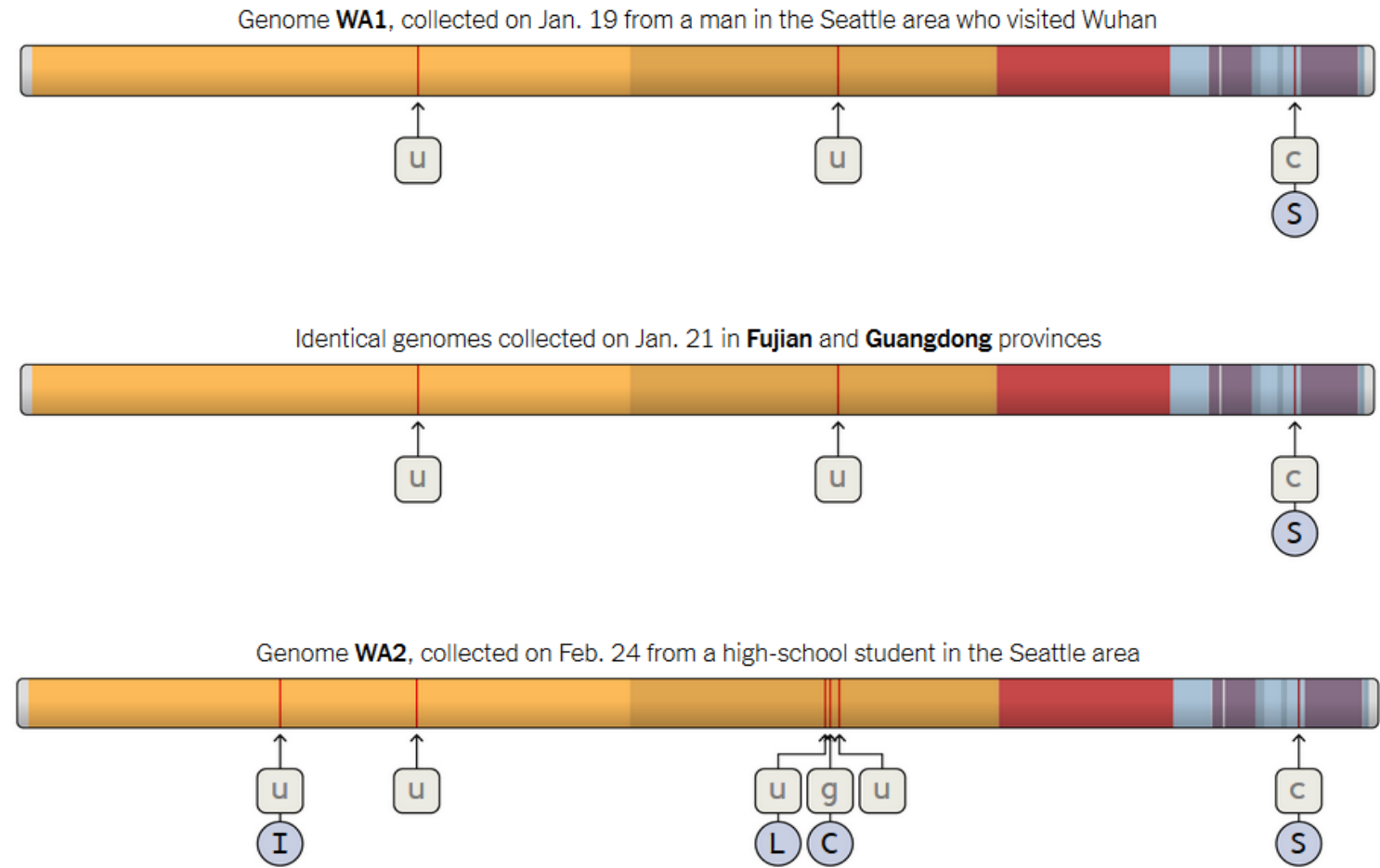
Genome **GZMU0030**, collected on Feb. 27 in Guangzhou



- First US genome from Seattle, WA
- Identical to two other documented genomes from China
- → Travel related transmission



- Second genome similar to first, but with more mutations
- → Suggests community spread for *weeks* before detection

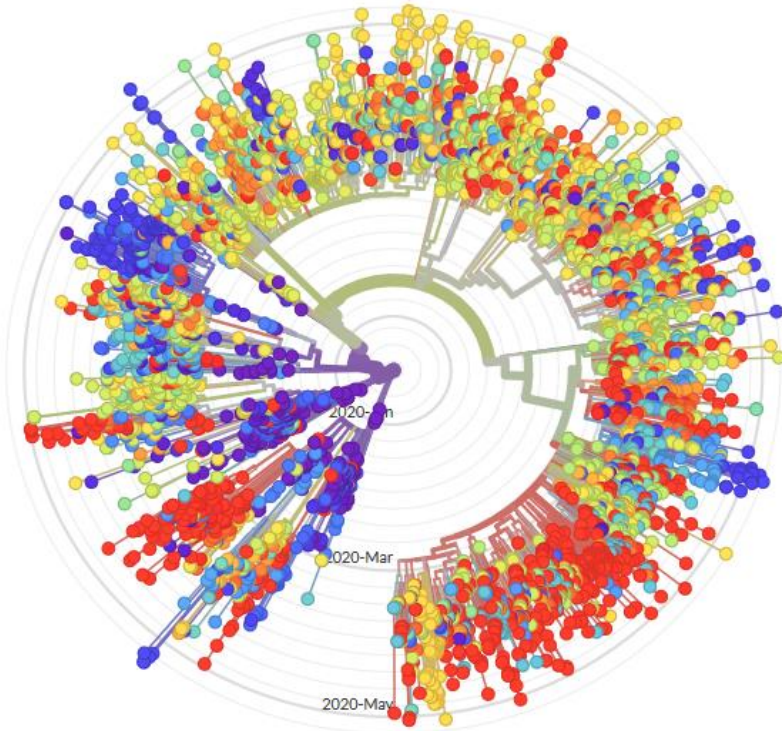


Four months of genomes:

<https://nextstrain.org/ncov/global?l=radial>

Phylogeny
Country ▼

RESET LAYOUT



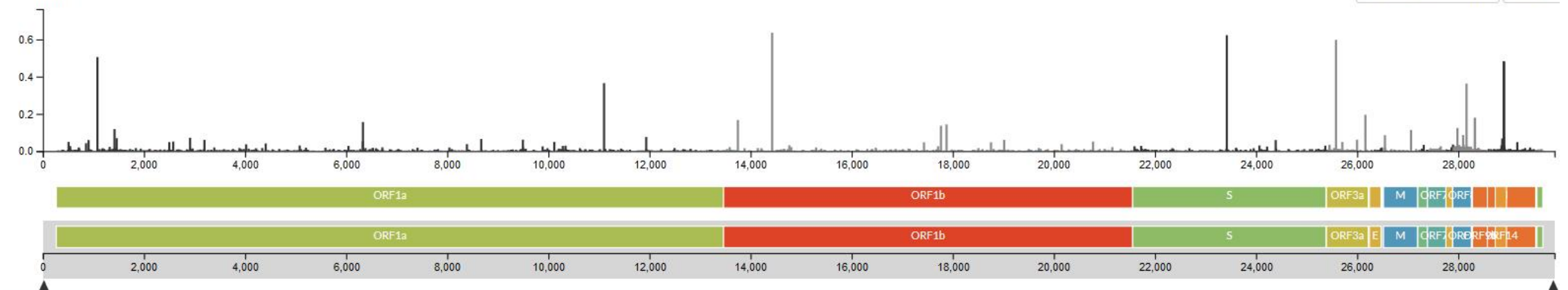
Transmissions

RESET ZOOM

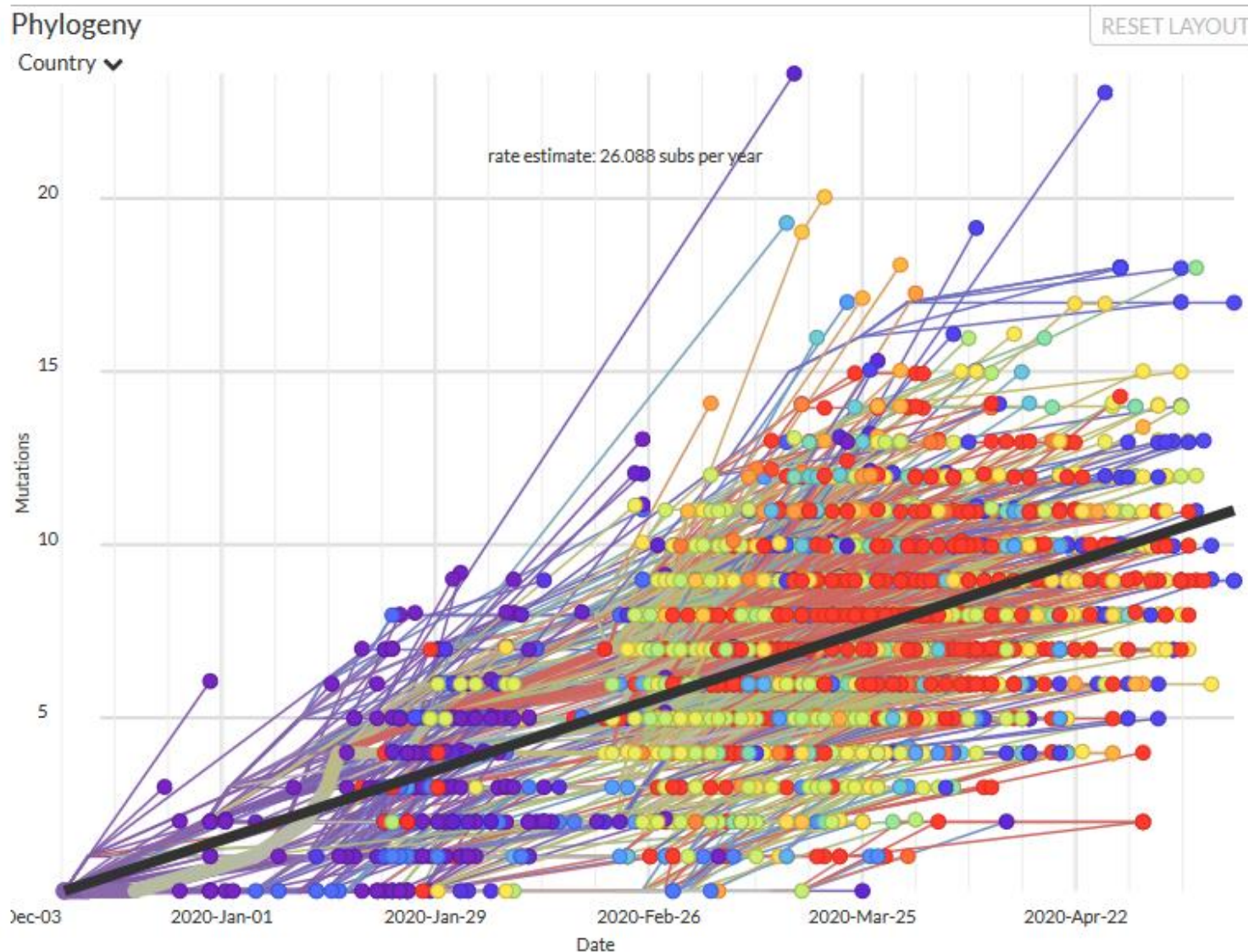


Diversity

ENTROPY EVENTS AA NT



Mutation rate places origin around late November 2019



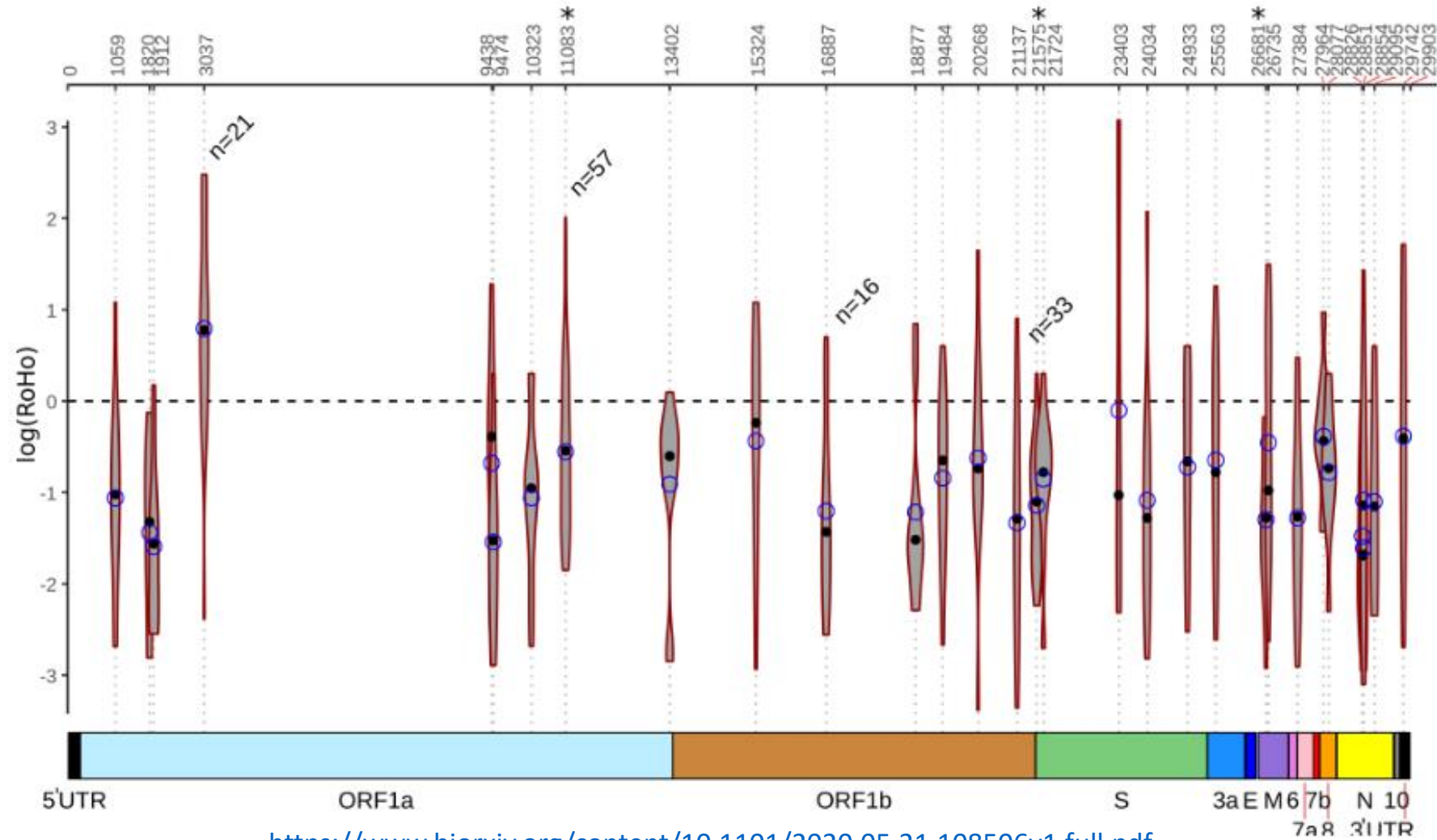
What have we learned from all those genomes?

- SARS-CoV-2 evolves slowly (~26 fixed mutations / year)
- There is no evidence of natural selection acting on the genome.
 - <https://www.biorxiv.org/content/10.1101/2020.04.27.064774v1.full.pdf>
- 7 of 9 genomes sequenced in late March at Yale cluster with the Seattle group → Domestic dispersal apparently more common than expected.
 - <https://doi.org/10.1016/j.cell.2020.04.021>
- Most NYC genomes from March are similar to those found in Europe
→ Travel restrictions to Europe came too late to stop initial dispersal
 - <https://www.medrxiv.org/content/10.1101/2020.04.08.20056929v2.full.pdf>

The virus is evolving

Is the virus *mutating* into a more virulent strain?

Recurrent Mutations are NOT associated with increased transmission



SARS-CoV-2 Origins

Evolutionary origins

- Phylogenetic analysis places the novel genome (WHCV) with two bat coronaviruses.
- In the Sarbecovirus genus with the 2003 SARS virus (SARS-CoV)

