

# United States Senate

WASHINGTON, DC 20510

February 16, 2021

The Honorable Charles Schumer  
Senate Majority Leader  
322 Hart Senate Office Building  
Washington, DC 20510

The Honorable Mitch McConnell  
Senate Minority Leader  
317 Russell Senate Office Building  
Washington, DC 20510

Leader Schumer and Leader McConnell:

As we continue our work on a COVID-19 relief package to provide additional essential relief to Americans, we must ensure that this package includes adequate resources for states and localities as they identify and respond to emerging variants of the SARS-CoV-2 virus. In particular, we must bolster the supply chain and improve data infrastructure to support widespread genomic-based surveillance of the virus, while ensuring that a diverse set of medical research institutions across the country have the funding needed to adapt their COVID-19-related projects to account for these variants.

In recent months, scientists have identified three new variants of the SARS-CoV-2 virus with concerning properties that could significantly increase the spread of COVID-19. All three variants are now present in the United States, with the B.1.1.7 variant rapidly surging.<sup>1</sup> Furthermore, the spread of these variants and continued high levels of COVID-19 cases increase the potential for future mutations with significant impacts on transmissibility or disease severity.

The United States lags far behind other countries in our genomic surveillance capabilities, even as this surveillance is increasingly becoming a key tool to track existing variants and identify new mutations.<sup>2</sup> These sequencing efforts remain uneven across the country, and are concentrated in areas with the most resources, leaving many communities without an accurate picture of the spread of the virus and its variants.<sup>3</sup> The CDC has taken steps to expand sequencing efforts, including implementing contracts with private partners and requesting samples from public health labs, but these actions are not sufficient to meet current or future needs. Congress must provide funding to expand genomic sequencing capacity across the country and particularly in vulnerable and medically underserved communities.

All public health measures in this package should include a focus on responding to the variants. We have heard from researchers in our home state of New Hampshire who are concerned that

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<sup>1</sup> <https://www.nytimes.com/2021/02/07/health/coronavirus-variant-us-spread.html>

<sup>2</sup> <https://www.nature.com/articles/d41586-021-00065-4>

<sup>3</sup> <https://www.sciencemag.org/news/2021/02/us-rushes-fill-void-viral-sequencing-worrisome-coronavirus-variants-spread>

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supply chain constraints could keep them from securing the supplies and materials needed for increased levels of genomic sequencing. Throughout the pandemic, labs around the country have experienced persistent shortages of COVID-19 testing supplies like reagents, testing instruments, and rapid tests,<sup>4</sup> an issue that has hampered our surveillance efforts for the past year. We must learn from these challenges and take this opportunity to prepare for the needed expansion in sequence-based surveillance. Funding for the COVID-19 testing supply chain should include specific support for manufacturing and procurement of the supplies used in genomic sequencing.

State and local public health labs and their partners also require a data infrastructure that can support the volume and complexity associated with sharing genetic sequence information. Across the country, including in New Hampshire, academic institutions have worked to support and expand the sequence-based surveillance capacity of state public health labs. However, the challenges associated with electronic transmittal of records containing a high volume of complex sequencing information has limited the ability of many facilities to take on this work, or scale it to meet the needs of their communities. We must provide additional support for data modernization to facilitate these partnerships and allow public health agencies to fully utilize the information gained from genetic sequencing of the virus.

Moving forward, there is a clear need for clinical research that incorporates our knowledge about these variants into our public health response and development of therapeutics and vaccines to fight COVID-19. Preliminary findings demonstrate that at least one of the variants shows resistance to existing COVID-19 monoclonal antibody treatments and vaccines, and another shares a mutation that likely gives it similar resistance.<sup>5</sup> In order to adapt these tools to respond to new and emerging variants, a geographically diverse set of research institutions must be able to participate in these efforts in order to reach the broadest range of COVID-19 patients. Congress has an opportunity to ensure that the \$5.2 billion allocated to support research and development of COVID-19 vaccines and therapeutics is distributed to a diverse set of institutions across the country, so they can adapt their COVID-19-related research to account for these variants and work collaboratively with public health infrastructure.

In order to turn the tide on the pandemic, we must combat the spread of these dangerous new variants in all communities within the United States. Building and supporting the supply chain and data infrastructure needed to conduct systematic sequencing-based surveillance must be prioritized in the upcoming relief package.

Sincerely,

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<sup>4</sup><https://www.gao.gov/reports/GAO-21-191/>

<sup>5</sup> <https://www.reuters.com/article/uk-health-coronavirus-science/south-african-virus-variant-may-resist-antibody-drugs-pfizer-biontech-vaccine-seems-to-work-vs-uk-variant-idINKBN29P2P1>;  
<https://www.nytimes.com/2021/02/07/world/south-africa-astrazeneca-vaccine.html>

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/s/ Margaret Wood Hassan

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Margaret Wood Hassan  
United States Senator

/s/ Jeanne Shaheen

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United States Senator