

primer-monitor.neb.com - Streaming Detection and Notification of New SARS-CoV-2 Variants

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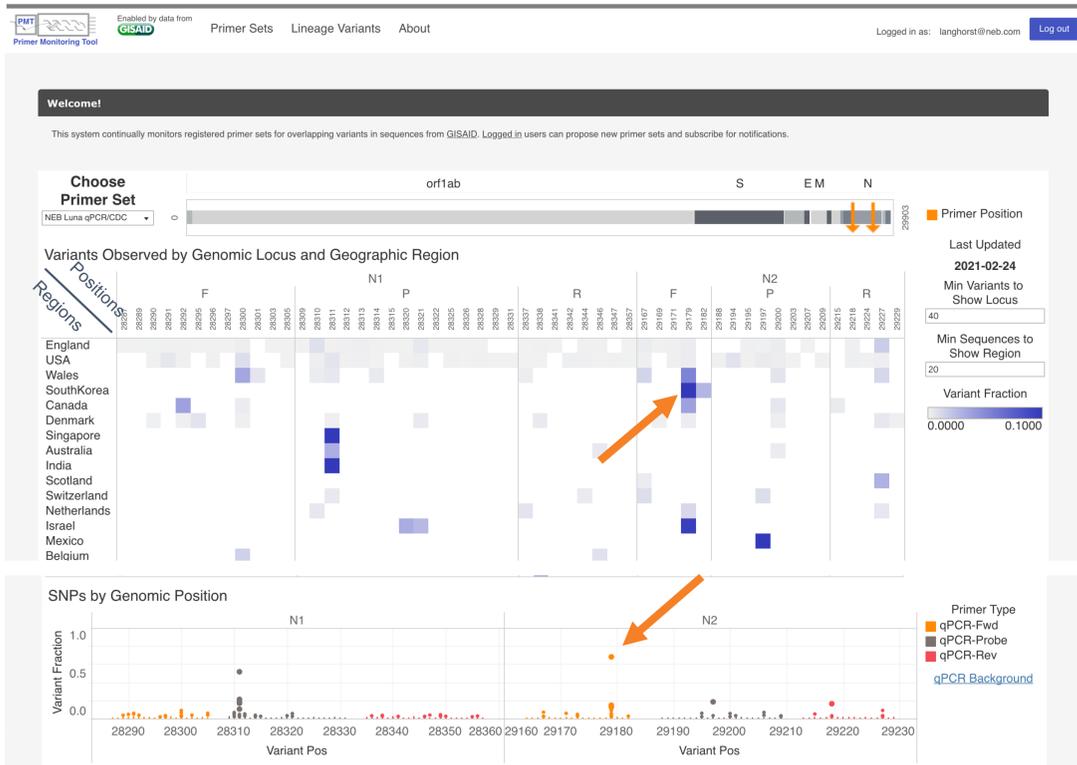
New England Biolabs, Inc.



Introduction

Nucleic acid diagnostic tests for SARS-CoV-2, whether based on RT-qPCR, RT-LAMP, RPA, or other amplification technology, all depend on primers. While the SARS-CoV-2 genome seems to be less variable [1] than some other retroviral genomes, variants with potential effects on amplification efficiency have arisen and become prevalent in local areas. Some regions (e.g. Brazil; Madera County, CA, USA [2]) report greater than 15% of observed sequences with variants in genomic loci commonly used by diagnostic tests. We developed a streaming analysis method to identify variants that may affect specific primers and a website to allow interested users to register primer loci. Users may subscribe to receive notification should variation cross a specified threshold in a geographic region of interest.

Geographic and Genomic Region Specificity

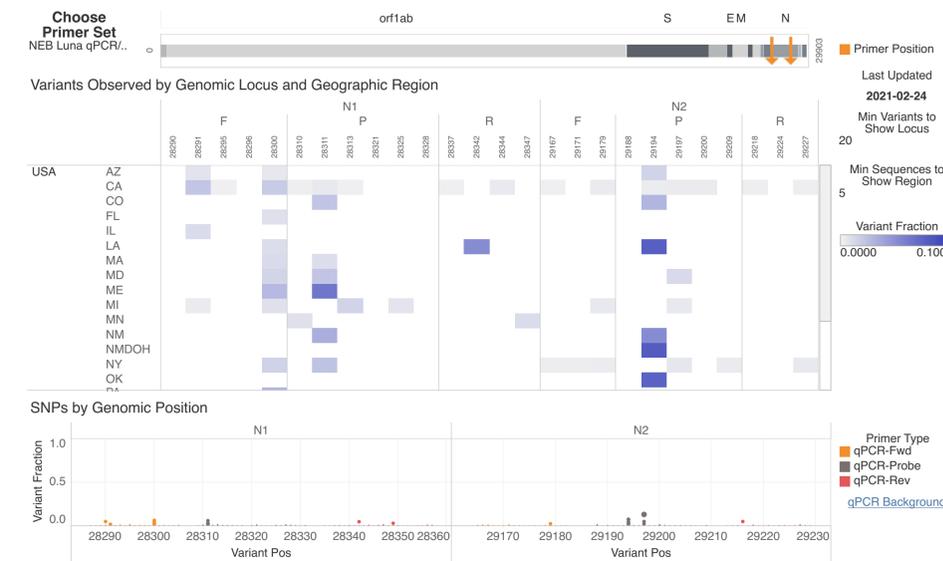
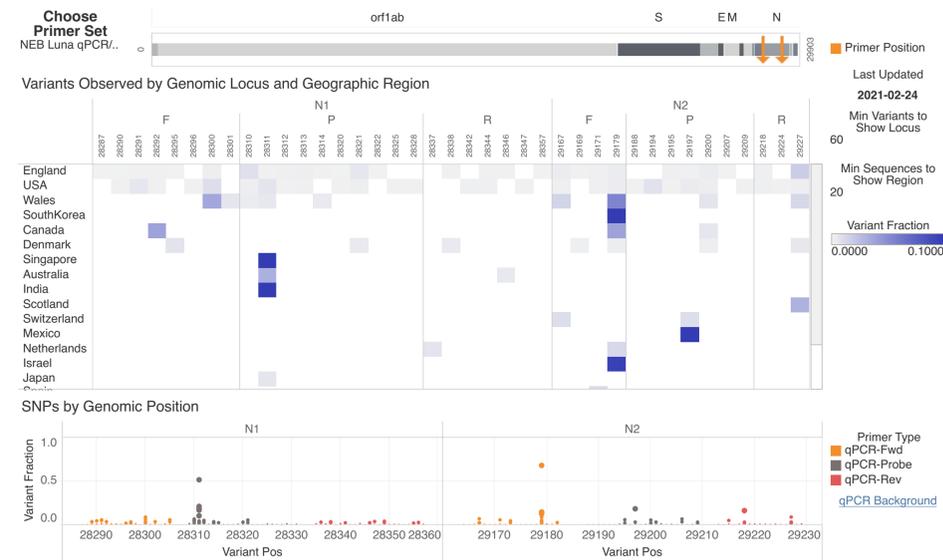


Selecting South Korea in the upper geographic pane highlights the relevant points in the lower genomic region view. The upper panel only displays sites with > 30 variants worldwide. The lower pane contains one point per geographic region at each genomic position (most are at or near 0 variant fraction).

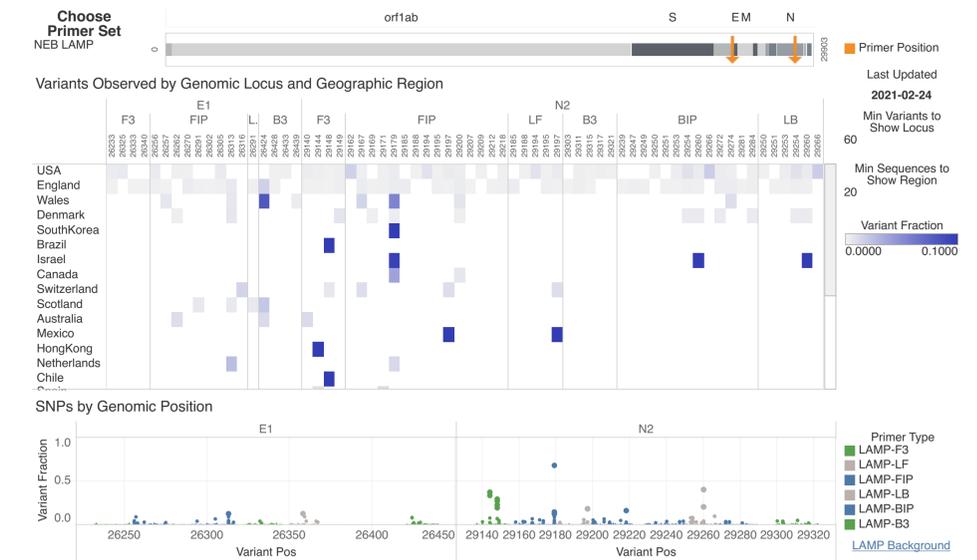
References

- 1 - Kupferschmidt, Kai. "The Pandemic Virus Is Slowly Mutating. But Does It Matter?" Science 369, no. 6501 (July 17, 2020): 238–39. <https://doi.org/10.1126/science.369.6501.238>.
- 2 - V Vanaerschot, Manu, Sabrina A. Mann, James T. Webber, Jack Kamm, Sidney M. Bell, John Bell, Si Noon Hong, et al. "Identification of a Polymorphism in the N Gene of SARS-CoV-2 That Adversely Impacts Detection by a Widely-Used RT-PCR Assay." BioRxiv, January 1, 2020, 2020.08.25.265074. <https://doi.org/10.1101/2020.08.25.265074>.

CDC/NEB Luna N1 and N2 qPCR Primers and Probes



NEB N2 and E1 LAMP Primers



Note: in LAMP primer sets, the LB/LF regions are contained within the BIP/FIP coordinates.

Conclusions

Evaluation of both geographic and genomic regional variation reveals specific hotspots where primer assessment might be warranted. Additional features including real-time assessment of user-specified primers, threshold-based notifications, time-course assessment, and primer-centric scoring are in progress or planned.