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 than 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) 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

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.

References
