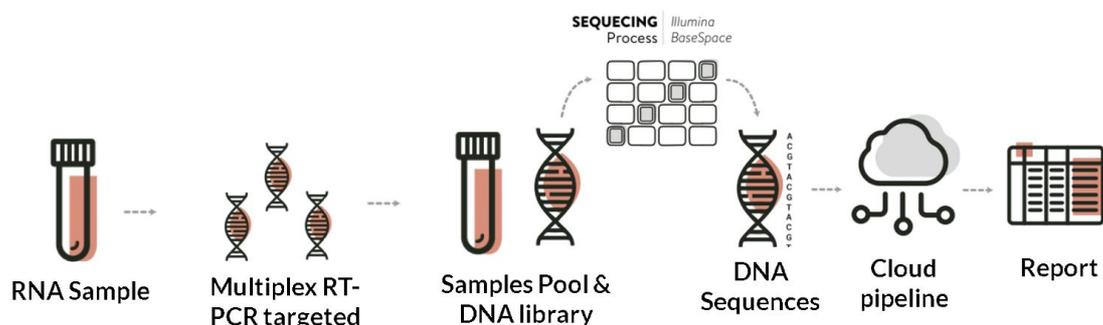


## High throughput workflow for detecting coronavirus using Biome Makers multiplex amplicon targeted sequencing approach

Sacramento, 20<sup>th</sup> April, 2020 – In the current COVID-19 pandemic the World Health Organization (WHO) has emphasized that mass testing is a key step to stop the spread of the virus. SARS-CoV-2 detection should include all the suspected cases as well as any asymptomatic people in contact with them. But efforts to identify COVID-19 have revealed deficiencies in the capacity to test millions of patient samples across the world quickly.

It is extremely difficult to simply scale up RT-qPCR assays to many thousands of patient samples per day; the supplies of these qPCR thermocyclers are limited and the technical staff needed to handle plates – even with automated liquid handlers – do not adequately scale to test millions of patients routinely. As a result, infected persons who are unknowingly transmitting COVID-19 and amplifying the pandemic conditions are continuously growing.

Biome Makers is a microbiome startup committed with societal challenges and believes it is our responsibility to share our know-how to respond to the pandemic outbreak, by enabling high-throughput testing of SARS-CoV-2 patients. This will allow identifying and limiting the transmission from asymptomatic persons and prevent the occurrence of follow-on waves of infection, especially after the social tactics to contain the initial disease spread are being suspended worldwide. For that reason, we have adapted our microbiome multiplex amplicon targeted sequencing to detect SARS-CoV-2 using the most common Next Generation Sequencer in the world: the Illumina's MiSeq. This device is now widely available across the world, including in-house availability in hospitals, clinics, research institutions and commercial service providers.



**The workflow** allows detection of COVID-19 viral RNA and increase 10X the current RT-qPCR assays, using a simple library preparation followed by Next-generation Sequencing (NGS). The method amplifies two SARS-CoV-2 genes and includes multiple controls to yield an accurate and quantitative report. Furthermore, we have adapted Biome Makers' microbiome computational pipeline to process the **sequencing** data, providing an end-to-end solution to identifying SARS-CoV-2 in biological samples. We recommend using this approach together with automatic viral RNA isolation and pipetting robots.

The whole workflow can be completed in hours, helping to scale and speed up the identification of COVID-19. With this development, we aim at contributing to the fight against this pandemic, which has already caused significant damage to our society, and could continue to do so if we do not have the right tools to control it.

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