

**To:** [REDACTED] [REDACTED] [REDACTED] [REDACTED]@rivm.nl]; [REDACTED] [REDACTED] [REDACTED] [REDACTED]@rivm.nl]; [REDACTED] [REDACTED] [REDACTED] [REDACTED]@rivm.nl]  
**From:** [REDACTED] [REDACTED]  
**Sent:** Wed 1/13/2021 10:01:30 AM  
**Subject:** FW: Contact regarding B.1.1.7 Variant  
**Received:** Wed 1/13/2021 10:01:31 AM

Ter info. Laat het graag aan jullie of we er iets mee willen?

**From:** [REDACTED] [REDACTED], [REDACTED] ([REDACTED]) <[REDACTED]@uu.nl>  
**Sent:** maandag 4 januari 2021 22:10  
**To:** [REDACTED] [REDACTED] [REDACTED] ([REDACTED]) <[REDACTED]@uu.nl>  
**Cc:** [REDACTED] [REDACTED] ([REDACTED]) <[REDACTED]@uu.nl>; [REDACTED] [REDACTED] ([REDACTED]) <[REDACTED]@uu.nl>  
**Subject:** Contact regarding B.1.1.7 Variant

Dear [REDACTED] [REDACTED] [REDACTED],

Hello, my name is [REDACTED] [REDACTED] and I work at the Pharmacology Department with [REDACTED] [REDACTED] and [REDACTED] [REDACTED]. I contact you, as you hold a position at RIVM too.

Our group has been working in the detection of different diseases and therefore we developed specific primers for SARS-CoV-2 and the results were 100% specific with detection accuracy as good as the ones suggested by GISAID. The information is in the following manuscript (accepted) :

<https://scientific-reports-under-consideration.nature.com/posts/classification-and-specific-primer-design-for-accurate-detection-of-sars-cov-2-using-deep-learning>

Right now, we developed a primer set for variant B.1.1.7 using the same methodology. We have already started communication with researchers from other countries, and we thought that RIVM will be interested in having a specific test for the variant as it has a higher transmission, as well as other concerning properties. You can find all the information below:

<https://www.biorxiv.org/content/10.1101/2020.12.29.424715v1>

### Design of Specific Primer Set for Detection of B.1.1.7 SARS-CoV-2 Variant using Deep Learning | bioRxiv

The SARS-CoV-2 variant B.1.1.7 lineage, also known as clade GR from Global Initiative on Sharing All Influenza Data (GISAID), Nextstrain clade 20B, or Variant Under Investigation in December 2020 (VUI – 202012/01), appears to have an increased transmissibility in comparison to other variants. Thus, to contain and study this variant of the SARS-CoV-2 virus, it is necessary to develop a ...

[www.biorxiv.org](https://www.biorxiv.org)

Looking forward to your answer,

[REDACTED]  
[REDACTED]

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