To: [redacted] [redacted] [[redacted]@rivm.nl]; [redacted] [redacted] [[redacted]@rivm.nl]; [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] and I work at the Pharmacology Department with [redacted]nd [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 transmissability 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

Looking forward to your answer,

[redacted]