To: [redacted] [redacted] [[redacted]@rivm.nl]; [redacted] [redacted] [[redacted]@rivm.nl]; [redacted] [redacted] [[redacted]@rivm.nl]
From: [redacted] [redacted]
Sent: Sun 1/10/2021 7:27:44 PM
Subject: Protocol for 501Y detection
Received: Sun 1/10/2021 7:27:44 PM
WHO Ref Centre Variant detection 20210107.pdf
ATT00001.htm
protocol_amplification_voc_20201201_uk_geneva-2.pdf
ATT00002.htm

Van: [redacted] [redacted] <[redacted]@hcuge.ch>
Datum: 10 januari 2021 om 18:39:30 CET
Aan: [redacted], [redacted] [redacted] <[redacted]@helsinki.fi>
CC: [redacted] [redacted] <[redacted]@rivm.nl>
Onderwerp: Re: share presentation

Hi [redacted]
Please find attached our PCR protocol that somehow saved us over Christmas (or spoilt our Christmas with the first cases being detected on 24th late afternoon, depends on how you look at it) :-) and the slides I presented at The Who lab meeting last Thursday.
Right now we use the TibMolBiol-Kit to screen all our positives detected on the Cobas system (the TibMolBiol assay is for N501Y, which means detection of B117 and B1.351 at the same time), while from private labs we still mostly received S-dropout samples from the Thermofisher assay or samples with a strong epidemiological link. We have found both variants in the meantime, and not only with epidemiological links to UK or SA, so my guess is that we have already community transmission ongoing, although right now there are still only a few. For S dropout, the majority we find are still other variants though with the 69-70 deletions, that are not B117. So I am careful to use this as a proxy for B117 unless there is confirmation.
Ultimately we still sequence the whole genome by NGS for all but this is more done for academic purposes and takes around 10 days, for the notification of our authorities we rely on the Sanger fragments.
Bw [redacted]