To: (10)(2e) [(10)(2e)@rivm.nl]
From: (10)(2e)
Sent: Mon 10/12/2020 1:02:35 PM
Subject: RE: ECDC EQA on molecular detection of SARS-CoV-2:
Received: Mon 10/12/2020 1:02:37 PM
SARS2_EQA_manuscript I.docx
Figure 1.jpg
Figure 2.tif
Supplementary material.docx

Beste (10)(2e),

Hartelijk dank voor jouw nuttige opmerkingen. We hebben nog een figure toegevoegd over de workflow.
Ik heb het aangepaste manuscript bij deze e-mail gevoegd.

Ik zal je laten weten wanneer er nieuws is.

Nogmaals bedankt.

Beste wensen,
(10)(2e)

From: (10)(2e) <(10)(2e)@rivm.nl>
Sent: dinsdag 29 september 2020 15:46
To: (10)(2e) ; (10)(2e) <(10)(2e)@rivm.nl>; (10)(2e)@charite.de' <(10)(2e)@charite.de>; (10)(2e)@charite.de' <(10)(2e)@charite.de>; (10)(2e)@rki.de' <(10)(2e)@rki.de>; (10)(2e)@rki.de' <(10)(2e)@rki.de>; (10)(2e)@charite.de' <(10)(2e)@charite.de>
Cc: (10)(2e) <(10)(2e)@rivm.nl>; (10)(2e) <(10)(2e)@charite.de>; (10)(2e) <(10)(2e)@charite.de>
Subject: RE: ECDC EQA on molecular detection of SARS-CoV-2: please provide comments before

Dear (10)(2e) et al.,

Sorry for my late response and raising issues that are probably difficult to address at this stage.

Table 1. Would be useful to indicate type Enterovirus and Rhinovirus. Was it indeed previous seasonal influenza virus A(H1N1) or actually A(H1N1)pdm09?

Table 2 Extraction method should always be seen in the context of the used PCR assay. Good performing extraction with bad performing assay would incorrectly indicate the extraction as less performing. To compare extraction methods each extract should be analyzed in exactly the same PCR assay. In addition volume sample in, volume extract, volume extract in PCR should be taken into account. To my opinion the study was not designed to analyze the impact of extraction methods. So, I think table 2 is kind of misleading. The design of the EQA allowed analysis of impact of workflows (extraction + PCR assay + volumes) and not separate components in the workflows.

Table 3 has a similar issue as it suggests that the PCR component on its own defines the outcome of the workflow. A bad performing extraction combined with good performing PCR assay would in this table indicate a bad performing PCR assay. If the PCR component on its own was meant to be analyzed RNA should have been distributed.

So, the piece of text in the manuscript connected with Tables 2 and 3 where the extraction and PCR components are analyzed separately should be interpreted with caution.

Workflow analysis is what can be done with the current setup. Something that we did in The Netherlands during the 2009 influenza pandemic: https://pubmed.ncbi.nlm.nih.gov/19540155/

Maybe a multivariate analysis of workflows would have been more appropriate. However, likely with similar conclusions.

Maybe this aspect should be highlighted in the discussion. Or repeat the analysis for workflows instead of extraction and PCR assay separately which might result in a reduction of 200 words in the text.

No further comments.

Best regards,

(10)(2e)

From: (10)(2e)) (10)(2e) < (10)(2e) @rivm.nl>
Sent: maandag 21 september 2020 17:13
To: (10)(2e) @charite.de' < (10)(2e) @charite.de>; (10)(2e) @charite.de' < (10)(2e) @charite.de>; (10)(2e) < (10)(2e) @rivm.nl>; (10)(2e) @rki.de' < (10)(2e) @rki.de>; (10)(2e) @rki.de' < (10)(2e) @rki.de>; (10)(2e) @charite.de' < (10)(2e) @charite.de>
Cc: (10)(2e) < (10)(2e) @rivm.nl>; (10)(2e) < (10)(2e) @charite.de>; (10)(2e) < (10)(2e) @charite.de>
Subject: ECDC EQA on molecular detection of SARS-CoV-2: please provide comments before

Dear all,

Please find attached the prefinal manuscript on the COVID-19 EQA.
Comments of ECDC have been taken into account. Suggestions to reduce with 200 words welcome.
Please provide your comments as soon as possible but no later than *25 September 2020.*

Best wishes (10)(2e) also on behalf of (10)(2e), (10)(2e) and (10)(2e).

@(10)(2e) : can you please forward this e-mail to (10)(2e)? Because I don't have his e-mail address.