

To: [redacted] [redacted] [redacted] @rivm.nl]; [redacted] [redacted] @isciii.es [redacted] [redacted] @isciii.es]
From: [redacted] [redacted]
Sent: Tue 9/1/2020 6:28:47 AM
Subject: Re: sequencing data I-MOVE 2019-2020 The Netherlands
Received: Tue 9/1/2020 6:28:52 AM

Dear [redacted]

Many thanks for the sequencing information. The sampling fraction is still impressive despite the COVID-19 burden.

With thanks and best wishes,

[redacted]

On 31/08/2020 13:02, [redacted] wrote:

Sorry [redacted]

2 corrections. I forgot to add 2 A(H1N1)pdm09 with very low viral load that were not sequenced. Now the numbers line up with those in the report that I will send later today.

Best regards,

[redacted]

From: [redacted]
Sent: maandag 31 augustus 2020 13:36
To: [redacted] <[redacted]@epiconcept.fr>; [redacted] [redacted]@isciii.es' <[redacted]@isciii.es>
Subject: sequencing data I-MOVE 2019-2020 The Netherlands

Dear [redacted]

Please find attached the updated Annex IV and V files with now our complete dataset for the season 2019-2020. Selection for sequencing not as systematic as before due to heavy workload with COVID-19. However, we were able to process a nice proportion of the total.

Best regards,

[redacted]

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