Study questions

1 message

Mon, May 30, 2022 at 16:21

To: mossk@mcmaster.ca

Dear Karen,

I hope you're doing well.

I have read your study "Isolation, Sequence, Infectivity, and Replication Kinetics of Severe Acute Respiratory Syndrome Coronavirus 2"

I have some questions:

1. Did you or your colleagues try to amplify, sequence and assemble (NGS approach) any other virus genome (other than sars-cov-2) from sars-cov-2 positive sample (PCR-positive)?

2. Did you or your colleagues try to extract RNA from uninfected supernatant and cells treated the same way as infected cells / supernatant but virus-free, and to generate the reads and implement "de novo" approach (de novo assembly) or to align (mapping assembly) the reads to sars-cov-2 genome? (extraction of RNA, library preparation, sequencing and assembly of sars-cov-2 genome)

Thank you for your answer and explanation.

Best regards,

Study questions

1 message

[redacted] Mon, May 30, 2022 at 16:40

To: samira.mubareka@sunnybrook.ca

Dear Samira,

I hope you're doing well.

[redacted]

I have read your study "Surface and Air Contamination With Severe Acute Respiratory Syndrome Coronavirus 2 From Hospitalized Coronavirus Disease 2019 Patients in Toronto, Canada, March – May 2020"

You are mentioned as corresponding author. I have some questions:

1. Did you or your colleagues try to assemble (NGS approach) any other virus genome (other than sars-cov-2) from sars-cov-2 positive sample (PCR-positive)?

2. Did you or your colleagues try to extract RNA from healthy controls (healthy persons or PCR-negative samples) or from uninfected supernatant and cells treated the same way as infected cells / supernatant but virus-free, and to generate the reads and implement "de novo" approach (de novo assembly) or to align (mapping assembly) the reads to sars-cov-2 genome? (extraction of RNA, library preparation, sequencing and assembly of sars-cov-2 genome)

Thank you for your answer and explanation.

Best regards,

[redacted]

Study questions

2 messages

Mon, May 30, 2022 at 17:32

To: mcarthua@mcmaster.ca

Dear Andrew,

I hope you're doing well.

I have read your study "A Comparison of Whole Genome Sequencing of SARS-CoV-2 Using Amplicon-Based Sequencing, Random Hexamers, and Bait Capture"

You are mentioned as corresponding author. I have some questions:

1. Did you or your colleagues try to assemble (NGS approach) any other virus genome (other than sars-cov-2) from sars-cov-2 positive sample (PCR-positive)?

2. Did you or your colleagues try to extract RNA from healthy controls (healthy persons or PCR-negative samples) or from uninfected supernatant and cells treated the same way as infected cells / supernatant but virus-free, and to generate the reads and implement "de novo" approach (de novo assembly) or to align (mapping assembly) the reads to sars-cov-2 genome? (extraction of RNA, library preparation, sequencing and assembly of sars-cov-2 genome)

Thank you for your answer and explanation.

Best regards,

McArthur, Andrew <mcarthua@mcmaster.ca> Thu, Jun 2, 2022 at 20:29

To:

Hi answers below:

> 1. Did you or your colleagues try to assemble (NGS approach) any other virus genome (other than sars-cov-2) from sars-cov-2 positive sample (PCR-positive)?

We did not. Read taxonomic analysis only found SARS-CoV-2 or human reads.

> 2. Did you or your colleagues try to extract RNA from healthy controls (healthy persons or PCR-negative samples) or from uninfected supernatant and cells treated the same way as infected cells / supernatant but virus-free, and to generate the reads and implement "de novo" approach (de novo assembly) or to align (mapping assembly) the reads to sars-cov-2 genome? (extraction of RNA, library preparation, sequencing and assembly of sars-cov-2 genome)

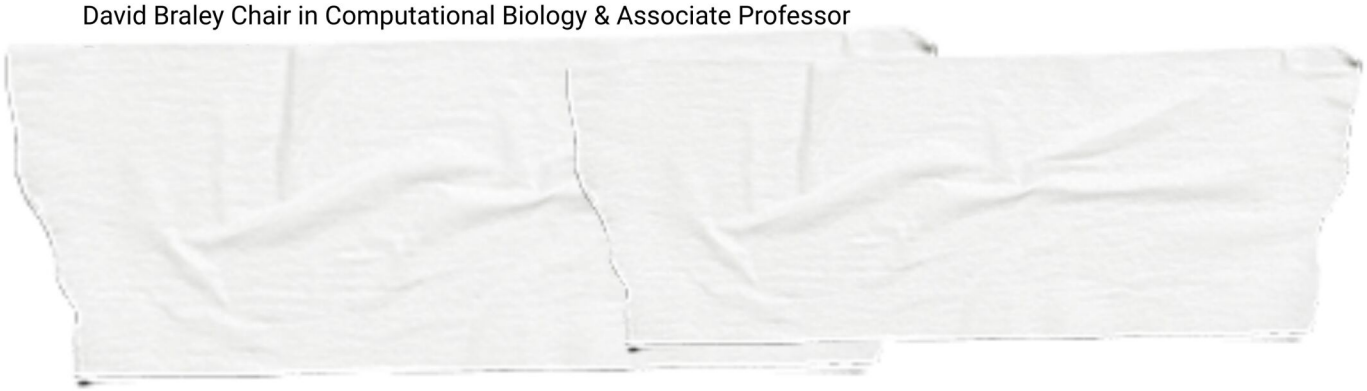
We used clinical swabs, and did not perform any cell culture. We did not have swabs from healthy controls but the study included negative controls for amplication/libraries, i.e. no sample RNA included. Results for the negative controls are included in the figures.

> Thank you for your answer and explanation.

My pleasure,

Andrew

Andrew G. McArthur, Ph.D.
David Braley Chair in Computational Biology & Associate Professor



Study questions

3 messages

Mon, May 30, 2022 at 17:19

To: christopher.kandel@tehn.ca

Dear Christopher,

I hope you're doing well.

I have read your study "Similar Duration of Viral Shedding of the Delta Variant of SARS-CoV-2 Between Vaccinated and Incompletely Vaccinated Individuals"

You are mentioned as corresponding author. I have some questions:

1. Did you or your colleagues try to assemble (NGS approach) any other virus genome (other than sars-cov-2) from sars-cov-2 positive sample (PCR-positive)?

2. Did you or your colleagues try to extract RNA from healthy controls (healthy persons or PCR-negative samples) or from uninfected supernatant and cells treated the same way as infected cells / supernatant but virus-free, and to generate the reads and implement "de novo" approach (de novo assembly) or to align (mapping assembly) the reads to sars-cov-2 genome? (extraction of RNA, library preparation, sequencing and assembly of sars-cov-2 genome)

Thank you for your answer and explanation.

Best regards,

Kandel MD, Christopher <Christopher.KandelMD@tehn.ca> Tue, May 31, 2022 at 03:32

Hi

Thanks for reading the paper.

Interesting questions, but unfortunately we did not sample healthy controls or sequence any

genomes aside from SARS-CoV-2.

All the best,
Chris

On May 30, 2022, at 11:19 AM, [redacted]<mail to[redacted]>> wrote:

EXTERNAL SENDER - BEWARE OF LINKS/CONTENT
[Quoted text hidden]

[redacted] Tue, May 31, 2022 at 03:35
To: Kandel MD, Christopher <Christopher.KandelMD@tehn.ca>

Hi Chris,

OK. Thanks for the quick response and answering my questions

Best regards,

[redacted]

On Tue, May 31, 2022, 03:32 Kandel MD, Christopher <Christopher.KandelMD@tehn.ca> wrote:
[Quoted text hidden]