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nCoV-2019 McGill Artic PCR Protocol, 5 ul RT and V3 only at 63C

Forked from nCoV-2019 McGill Artic PCR Protocol, 5 ul RT and V3 only + LA1 at 63C

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1 Works for me dx.doi.org/10.17504/protocols.io.bj9hkr36

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ABSTRACT

V3 only primers can be found here: https://github.com/sarahreiling/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019_V3only.scheme.bed

DOI

dx.doi.org/10.17504/protocols.io.bj9hkr36

PROTOCOL CITATION

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FORK NOTE

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MATERIALS TEXT

MATERIALS

Q5 High-Fidelity 2X Master Mix - 500 rxns **New England Biolabs Catalog #M0492L**

nuclease-free water **Contributed by users**

Fresh 80% Ethanol **Contributed by users**

Quant-iT™ PicoGreen™ dsDNA Assay Kit **Invitrogen - Thermo Fisher Catalog #P11496**

AmpureXP beads **Beckman Coulter Catalog #A63880**

ABSTRACT

V3 only primers can be found here: https://github.com/sarahreiling/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019_V3only.scheme.bed

Primer pool preparation

1 PRIMER POOL PREPARATION

If required resuspend lyophilised primers at a concentration of 100 µM each

V3 only primers for this protocol were designed using Primal Scheme and generate overlapping 400 nt amplicons. Primer names and dilutions are listed in the table below. https://github.com/sarahreiling/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019_V3only.scheme.bed

2 Generate primer pool stocks by adding **5 µl** of each primer pair to a **1.5 mL** Eppendorf labelled either “Pool 1 (100µM)” or “Pool 2 (100µM)”. Total volume should be **490 µl** for Pool 1 (100µM) and **490 µl** for Pool 2 (100µM). These are your 100µM stocks of each primer pool.

Primers should be diluted and pooled in the **mastermix cabinet** which should be cleaned with decontamination wipes and UV sterilised before and after use.

3 Dilute this primer pool 1:10 in molecular grade water, to generate 10 µM primer stocks. It is recommend that multiple aliquots of each primer pool are made to in case of degradation or contamination.

Primers need to be used at a final concentration of 0.015µM per primer. In this case both pools have 98 primers in so the requirement is 3.65µL primer pools (10uM) per 25µL reaction. For other schemes, adjust the volume added

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appropriately.

Multiplex PCR

4 ⚠

MULTIPLEX PCR

In the **extraction and sample addition cabinet** add **5 µl** RT product to each tube and mix well by pipetting.

The **extraction and sample addition cabinet** should should be cleaned with decontamination wipes and UV sterilised before and after use.

5 In the mastermix hood set up the multiplex PCR reactions as follows in 0.2mL 8-strip PCR tubes:

Component	Pool 1 [10 uM primer]	Pool 2 [10 uM]
Q5 Hot Start High-Fidelity 2X Master Mix	**12.5 µl**	**12.5 µl**
Primer Pool 1 or 2 (10µM pool 1+2)	**3.7 µl**	**3.7 µl**
Nuclease-free water	**3.8 µl**	**3.8 µl**
Total	**20 µl**	**20 µl**

Add 20ul of PCR mastermix to the **5 ul RT product** of step 10.

A PCR mastermix for each pool should be made up in the **mastermix cabinet** and aliquoted into PCR strip tubes. Tubes should be wiped down when entering and leaving the mastermix cabinet.

6 Pulse centrifuge the tubes to collect the contents at the bottom of the tube.

7 Set-up the following program on the thermal cycler:

Step	Temperature	Time	Cycles
Heat Activation	**98 °C**	**00:00:30**	1
Denaturation	**98 °C**	**00:00:15**	36
Annealing	**63 °C**	**00:05:00**	36
Hold	**4 °C**	Indefinite	1

Cycle number should be 25 for Ct 18-21 up to a maximum of 36 cycles for Ct 35

PCR clean-up

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8 ⚠

PCR CLEANUP

Combine the entire contents of “Pool 1” and “Pool 2” PCR reactions for each biological sample into to a single **1.5 mL** Eppendorf tube.

9 Clean-up the amplicons using the following protocol:

Add an equal volume (1:1) of AmpureXP beads to the sample tube and mix by pipetting.
Incubate for 5 min at room temperature.
Pellet on magnet for 5 min. Remove supernatant.
Add 200 ul of 80% ethanol to the pellet and wash twice.
Let the beads dry for 3 min.
Add 30 ul elution buffer and resuspend the beads. Incubate for 3 minutes.
Pellet on magnet for 5 min. Remove and keep eluate (30 ul).

Amplicon clean-up should be performed in the **post-PCR cabinet which** should should be cleaned with decontamination wipes and UV sterilised before and after use.

Amplicon Quantification and normalisation

10 ⚠

AMPLICON QUANTIFICATION AND NORMALIZATION

Quantify the amplicon pools using a fluorimetric dsDNA assay. (e.g: PicoGreen with a standard curve 0-200ng)

We expect following concentrations:

Pool 1+2 combined:
100-150 ng/ul for Ct 14-24
30-80 ng/ul for Ct 25-29
10-30 ng/ul for Ct 30-36

11 ⚠

Nextera Flex Library Prep:

After quantification of Pool 1+2, take a new plate and add 150 ng of Pool 1+2 and add up with nuclease-free water to a total volume of **30 ul (= 5 ng/ul).**

Nanopore Library Prep:

After quantification of Pool 1+2, take a new plate and add 200 ng of Pool 1+2 and add up with nuclease-free water to a total volume of **20 ul (= 10 ng/ul).**

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