

Jul 13, 2020

COVID-19 ARTIC v3 Illumina library construction and sequencing protocol - short amplicons (275bp)

 Forked from [COVID-19 ARTIC v3 Illumina library construction and sequencing protocol](#)

DOI

<https://dx.doi.org/10.17504/protocols.io.bh4zj8x6>

Emma Betteridge¹, Naomi Park¹, Keith James¹, Jillian Durham¹, Josh Quick²

¹Wellcome Sanger Institute; ²University of Birmingham

Coronavirus Method De...



Naomi Park

Wellcome Sanger Institute, Altos Labs



Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.bh4zj8x6>

External link: <https://doi.org/10.1038/s41467-023-37787-0>

Protocol Citation: Emma Betteridge, Naomi Park, Keith James, Jillian Durham, Josh Quick 2020. COVID-19 ARTIC v3 Illumina library construction and sequencing protocol - short amplicons (275bp). **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.bh4zj8x6>

Manuscript citation:

Taha, T.Y., Chen, I.P., Hayashi, J.M. *et al.* Rapid assembly of SARS-CoV-2 genomes reveals attenuation of the Omicron BA.1 variant through NSP6. *Nat Commun* **14**, 2308 (2023). <https://doi.org/10.1038/s41467-023-37787-0>

License: This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

We use this protocol and it's working

Created: July 01, 2020

Last Modified: July 13, 2020

Protocol Integer ID: 38777

Keywords: COVID-19, SARS-Cov-2, amplicon sequencing, ARTIC, Illumina library construction, coronavirus, cDNA from SAR, sequencing protocol, short amplicon, short amplicon method, viral nucleic acid extract, generating cDNA, producing 275nt amplicon, amplicon, key benefit of the short amplicon method, 275nt amplicon, illumina novaseq

Abstract

This SOP describes the procedure for generating cDNA from SARS-CoV-2 viral nucleic acid extracts and subsequently producing 275nt amplicons. This is followed by library construction, equivolume pooling of samples and quantitation, prior to sequencing on the Illumina NovaSeq.

A key benefit of the short amplicon method is that it can be utilised on any Illumina platform with a 300 cycle (or greater) kit.

It is an adaptation of the 400nt COVID-19 ARTIC v3 amplicon protocol which can be found here:

<https://www.protocols.io/view/covid-19-artic-v3-illumina-library-construction-an-bgxjjxkn>

Both the above protocols were adapted from the nCov-2019 sequencing protocol:

<https://www.protocols.io/view/ncov-2019-sequencing-protocol-bbmuik6w>

Guidelines

It is vital cDNA setup is performed in a laboratory in which post-PCR COVID-19 amplicons are not present, to minimise any risk of sample contamination.

Note: Throughout the protocol we have indicated the liquid handling automation in use at Sanger for specific parts of the process. However, these steps could be performed on alternative liquid handlers or manually.

Materials

MATERIALS

-  NEBNext Ultra II DNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7645L**
-  2x Kapa HiFi Hotstart Readymix **Kapa Biosystems Catalog #KK2602**
-  LunaScript RT SuperMix Kit **New England Biolabs Catalog # E3010L**
-  Illumina Library Quantitation Complete kit (Universal) **Kapa Biosystems Catalog #KK4824**
-  NEB Q5® Hot Start High-Fidelity 2X Master Mix **New England Biolabs Catalog #M0494L**
-  AccuClear® Ultra High Sensitivity dsDNA Quantitation Kit with DNA Standards **Biotium Catalog ##31028**

STEP MATERIALS

-  LunaScript RT SuperMix Kit **New England Biolabs Catalog # E3010L**
-  AccuClear® Ultra High Sensitivity dsDNA Quantitation Kit with DNA Standards **Biotium Catalog ##31028**
-  NEBNext Ultra II DNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7645L**
-  2x Kapa HiFi Hotstart Readymix **Kapa Biosystems Catalog #KK2602**
-  NEB Q5® Hot Start High-Fidelity 2X Master Mix **New England Biolabs Catalog #M0494L**

Primer pool sequences (v3) can be found here:

https://github.com/joshquick/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019.tsv

Protocol materials

-  NEBNext Ultra II DNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7645L**
-  2x Kapa HiFi Hotstart Readymix **Kapa Biosystems Catalog #KK2602**
-  LunaScript RT SuperMix Kit **New England Biolabs Catalog # E3010L**
-  AccuClear® Ultra High Sensitivity dsDNA Quantitation Kit with DNA Standards **Biotium Catalog ##31028**
-  NEB Q5® Hot Start High-Fidelity 2X Master Mix **New England Biolabs Catalog #M0494L**
-  Illumina Library Quantitation Complete kit (Universal) **Kapa Biosystems Catalog #KK4824**

cDNA generation

- 1 **Important!** This step must be performed in a RNase free, pre-PCR environment in which post PCR COVID-19 amplicons are not present, to minimise risk of sample contamination.

Decontaminate bench surfaces, pipettes and gloves with RNase ZAP before starting work. Keep reagents and samples chilled throughout the process.

- 2 Defrost PCR plate containing  10 µL extracted RNA  On ice .

3

 LunaScript RT SuperMix Kit **New England Biolabs Catalog # E3010L**

Prepare RT mastermix in a dedicated UV treated pre-PCR area to minimise contamination risk.

RT Master Mix	Vol / RXN (µL)	Vol/96 RXN (µL) inc. excess
LunaScript Super Mix	4	461
Nuclease-free water	6	691
Total	10	1152

Mix thoroughly by vortexing.

- 4 Use the SPT Labtech Dragonfly Discovery to dispense  10 µL of RT mastermix into the PCR plate containing  10 µL extracted RNA.

- 5 Seal and briefly centrifuge plate.

- 6 Place plate on a thermocycler and run the following program:

Temperature	Time
25°C	2 minutes
55°C	20 minutes



95°C	1 minute
4°C	∞
Lid temp: Tracking	

- 7 **PAUSE POINT** cDNA can be stored at 4°C (same day) or -20°C (up to a week).

cDNA amplification

8

If required, resuspend lyophilised primers in EB at a concentration of 100µM each.

Note

Primers for this protocol were designed by Josh Quick using **Primal Scheme** and generate overlapping 275nt amplicons. Primer sequences and additional information can be found here:



nCoV-2019_275.xlsx

Generate primer pool stocks by adding  5 µL of each odd region primer to a 1.5 mL Eppendorf labelled "Pool 1 (100µM)" and  5 µL of each even region primer to a 1.5 mL Eppendorf labelled "Pool 2 (100µM)". Mix thoroughly by vortexing.

Dilute each primer pool 1:6.25 in EB, to generate 16µM working stocks. Making single use aliquots of each primer pool is recommended to minimise the risk of contamination and degradation via freeze thaw cycles.

Note

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



NEB Q5® Hot Start High-Fidelity 2X Master Mix **New England**
Biolabs Catalog #M0494L

Prepare the following mastermixes:

PCR Primer Pool 1 Master Mix	Vol/PCR RXN (μl)	Vol/ 96 plate (μl) inc. exce ss
Q5 Hotstart 2X Master Mix	12.5	1440
Primer Pool 1 (16μM total)	3.6	415
Nuclease-free water	2.9	334
Total	19	218 9

Final concentration of each primer in the reaction is 0.015μM

PCR Primer Pool 2 Master Mix	Vol/PCR RXN (μl)	Vol/ 96 plate (μl) inc. exce ss
Q5 Hotstart 2X Master Mix	12.5	1440
Primer Pool 2 (16μM total)	3.6	415
Nuclease-free water	2.9	334
Total	19	218 9

Final concentration of each primer in the reaction is 0.015μM

Mix thoroughly by vortexing.

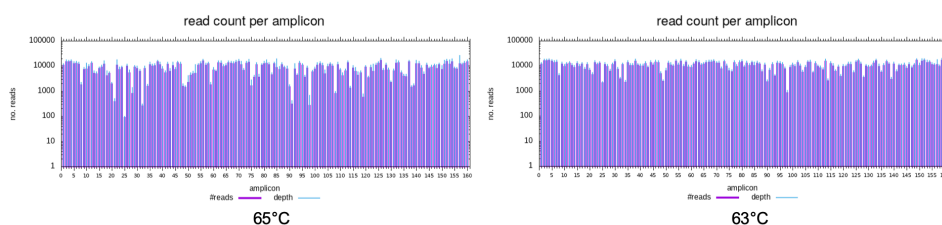
- 9 Use the SPT Labtech Dragonfly Discovery to dispense  19 μL mastermix per well into 2×96 well plates.
- 10 Use the Agilent Bravo to add  6 μL of cDNA template to each primer pool reaction and mix.

- 11 Heat seal and place the plates onto a thermocycler and run the following program.
Important! Heat seal to minimise evaporation.

Note: Amplification should ideally be performed in a different lab to minimise the risk of contaminating other samples.

Expected result

Critical step: We strongly recommend performing a gradient PCR to determine the optimal annealing temperature for your thermocycler. Subtle differences in thermocycler calibration can result in reduced coverage of specific amplicons. Reducing our annealing temperature from 65°C to 63°C for identical cDNA decreases variation in coverage depth across the genome.



	Step	Temperature	Time
	1	98°C	30 seconds
	2	95°C	15 seconds
	3	63°C	5 minutes



	4	Repeat steps 2 & 3 for a total of 35 cycles	
	5	4°C	∞

- 12 **PAUSE POINT** Amplified cDNA can be stored at 4°C (overnight) or -20°C (up to a week).

Amplified cDNA SPRI

- 13 Allow AMPure XP beads to equilibrate to room temperature (~30 minutes). Ensure solution is homogenous prior to use, mixing gently by inversion.
- 14 Centrifuge amplified cDNA plates.  1000 x g, 00:01:00
- 15 Use either the Agilent Bravo or Beckman Coulter NX with a 96 well multichannel head to perform the following steps:
- 15.1 Combine the entire volumes of primer 1 and primer 2 PCR reactions per sample into one PCR plate.
- 15.2 Add **0.8X** volume of SPRI beads per sample ( 40 µL SPRI :  50 µL amplified cDNA), mix well by pipetting.
- 15.3 Incubate for  00:05:00 at  Room temperature
- 15.4 Transfer the plate to the magnet, allow  00:02:00 for the beads to settle.
- 15.5 Carefully remove and discard the supernatant without disturbing the bead pellet.
- 15.6 Wash the beads with  180 µL 75% freshly prepared ethanol for  00:00:30 , then remove ethanol and discard.
(First wash)
- 15.7 Wash the beads with  180 µL 75% freshly prepared ethanol for  00:00:30 , then remove ethanol and discard.

(Second wash)

15.8 Allow beads to dry  00:05:00

15.9 Remove plate from magnet, add  20 μL nuclease-free water and resuspend by mixing well.

15.10 Incubate for  00:03:00 at  Room temperature

15.11 Transfer the plate to the magnet, allow  00:05:00 for the beads to settle.

15.12 Carefully transfer supernatant into a new plate, taking care not to disturb the bead pellet.

16 **PAUSE POINT** Purified amplified cDNA can be stored at -20°C for several weeks prior to library preparation.

Amplified cDNA quantification

17

Note

Purified amplified cDNA is quantified with a fluorescence based assay. We use the **AccuClear Ultra High Sensitivity dsDNA Quantitation kit with 7 DNA standards** (Biotium) according to manufacturer's instructions.

To streamline the workflow, we do not normalise sample input for library preparation. Instead we confirm samples are in the range of **50ng-1ug** per **20 μL sample** and take the entire volume into library preparation.



AccuClear® Ultra High Sensitivity dsDNA Quantitation Kit with DNA Standards **Biotium Catalog ##31028**

18 Pipette  20 μL of each DNA standard into wells A1 – G1 of a PCR plate. Add nuclease-free water to H1.

- 19 Dilute the AccuClear dye (100X) to working concentration by mixing  300 μL dye with  30 mL AccuClear buffer in a 50ml Falcon. Mix thoroughly by vortexing and transfer to a 384 well reservoir.
- 20 Use the SPT Labtech Mosquito LV to stamp 200nl of amplified cDNA and 1 μL of known standards in triplicate into a 384 assay plate. Immediately proceed to the next step.
- 21 Use the Agilent Bravo 384ST to add  50 μL 1X AccuClear dye from the reservoir to the assay plate, mix thoroughly by pipetting.
- 22 Measure fluorescence values on a BMG FLUOstar Omega plate reader calibrated for use with AccuClear dye.
- 23 Confirm known standards are performing as expected.
- 24 Dilute any samples >125ng/ μL with nuclease free water so they are in the range of 10 - 125ng/ μL and repeat quantitation.

Note

Note: We use **5X** the volume of standard vs sample in our assay setup, which should allow a quantitative range of 0.15ng/ μL – 125ng/ μL . This deviates from the standard kit SOP which has a stated range of 0.03ng/ μL – 25ng/ μL .

- 25 Ensure all samples (20 μL total volume) are in the range of 2.5-50ng/ μL prior to proceeding with library preparation.

Library preparation for Illumina sequencing

26

Note

We use the NEB NEBNext® Ultra™ II DNA Library Prep Kit for Illumina, which we have automated on the Agilent Bravo platform with some modifications. 200ng is our standard input for library preparation, an acceptable range is 50ng – 1ug per sample. We use a custom adapter set, however any TruSeq adapters are suitable.



NEBNext Ultra II DNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7645L**

27

Prepare end prep mastermix  On ice :

NEBNext End Prep	Vol/PCR RXN (μl)	Vol/96 plate (μl) inc. excess
NEBNext Ultra II End Prep Enzyme Mix	1.2	144
NEBNext Ultra II End Prep Reaction Buffer	2.8	336
Total	4	480

Mix well by pipetting.

28 The Bravo will combine  4 μL of end prep mastermix with  20 μL amplified cDNA and mix by pipetting.

29 Seal and transfer the plate to a thermocycler and run the following program:

Temperature	Time
20°C	30 minutes
65°C	30 minutes
4°C	∞

30 Prepare adapter ligation mastermix  On ice :

Adapter Ligation	Vol/PCR RXN (μl)	Vol/96 plate (μl) inc. excess
------------------	------------------	-------------------------------

	NEBNext Ultra II Ligation Master Mix	12	1440
	NEBNext Ligation Enhancer	0.4	48
	TruSeq adapter (10µM)	1	120
	Total	13.4	1608

Mix well by pipetting.

31 The Bravo will add  13.4 µL adapter ligation mastermix to each sample and mix by pipetting.

32 The plate is incubated on deck at  20 °C for  00:15:00 , however this step may also be performed on a thermocycler.

33

Note

Note: We use alternative TruSeq compatible adapters, which do not require the USER enzyme incubation step. If using NEBNext adapters, follow the steps in the NEB protocol to add USER enzyme to the ligation reaction.

34 A **0.8X** SPRI is performed post-ligation.

Ensure AMPure XP beads have been equilibrated to room temperature (~30 minutes) and the solution is homogenous prior to use.

The Bravo will perform a **0.8X** SPRI clean-up and elute sample in 25 µl nuclease-free water as follows:

34.1 Add 0.8X volume of SPRI beads per sample, mix well by pipetting.

34.2 Incubate for  00:05:00 at  Room temperature .

34.3 Transfer the plate to the magnet, allow  00:02:00 for the beads to settle.



- 34.4 Carefully remove and discard the supernatant without disturbing the bead pellet.
- 34.5 Wash the beads with  180 μL 75% freshly prepared ethanol for  00:00:30 , then remove ethanol and discard.
(First wash)
- 34.6 Wash the beads with  180 μL 75% freshly prepared ethanol for  00:00:30 , then remove ethanol and discard.
(Second wash)
- 34.7 Allow beads to dry for  00:05:00
- 34.8 Remove plate from magnet, add  25 μL nuclease free water and resuspend by mixing well.
- 34.9 Incubate for  00:03:00 at  Room temperature .
- 34.10 Transfer the plate to the magnet, allow  00:05:00 for the beads to settle.
- 34.11 Carefully transfer supernatant into a new plate, taking care not to disturb the bead pellet. Half of this eluate (**12.5 μL**) is used as input for library PCR.

Library PCR

35

Note

We use KAPA HiFi HotStart ReadyMix and unique dual indexed (UDI) tag plates for library PCR.

Note: this deviates from the standard NEB protocol which uses NEBNext Ultra II Q5 Master Mix and different cycling conditions.

 2x Kapa HiFi Hotstart Readymix **Kapa Biosystems Catalog #KK2602**

Prepare PCR mastermix  On ice :

	KAPA PCR Mastermix	Vol/PCR RXN (μl)	Vol/96 plate (μl) inc. excess
	KAPA HiFi HotStart ReadyMix	25	3000
	Water	12.5	1500
	Total	37.5	4500

Mix well by pipetting.

36 The Bravo will add  37.5 μL PCR mastermix and  12.5 μL sample into a lyophilised plate of UDIs and mix thoroughly by pipetting. The final concentration of each UDI in the PCR reaction is 2μM.

37 Seal and transfer the plate to a thermocycler and run the following program:

	Temperature	Time
	95°C	5 minutes
	98°C	30 seconds
	65°C	30 seconds
	72°C	2 minutes
	Repeat 4 times	
	72°C	5 minutes
	4°C	∞

Construct equivolume pool

38 In a post-PCR lab, combine **5μl** of each sample per plate to form an equivolume pool of 96 samples.

38.1 Using a multichannel pipette, transfer  5 μL of each sample in the PCR plate into a low volume reservoir.



38.2 Transfer the contents of the reservoir into an Eppendorf tube and mix well.

Equivolume pool SPRI

39 Allow AMPure XP beads to equilibrate to room temperature (~30 minutes). Ensure solution is homogenous prior to use, mixing gently by inversion.

39.1 Add **0.8X** volume of SPRI beads per pool tube, mix well by pipetting.

39.2 Incubate for  00:05:00 at  Room temperature .

39.3 Transfer the tube to a magnet, allow  00:05:00 for the beads to form a pellet.

39.4 Carefully remove and discard the supernatant, taking care not to disturb the bead pellet.

39.5 Wash the beads with  1 mL 75% ethanol for  00:00:30 then carefully remove ethanol and discard.
(First wash)

39.6 Wash the beads with  1 mL 75% ethanol for  00:00:30 then carefully remove ethanol and discard.
(Second wash)

39.7 Allow beads to dry for  00:05:00 .

39.8 Remove tube from magnet and resuspend beads in  1 mL elution buffer, mix well by pipetting.

39.9 Incubate for  00:03:00 at  Room temperature



39.10 Transfer tube to magnet, allow  00:05:00 for the beads to form a pellet.

39.11 Carefully transfer supernatant into a new tube, taking care not to disturb the bead pellet.

Equivolume pool quantification

40

Note

Equivolume pools may be quantified either by qPCR or on an Agilent Bioanalyzer. Pools are then diluted to 1nM for sequencing.

qPCR

Quantify samples in triplicate using the KAPA Complete kit (Universal) for Illumina (KK4824) plus the KAPA Library Quantification Dilution Control (KK4906).

We use the SPT Labtech Mosquito LV to stamp library pools in triplicate into a 384 assay plate, and the Agilent Bravo to setup the qPCR reactions (1:1600 dilution).

qPCR is performed on the Roche LightCycler 480.

Agilent Bioanalyzer

Prepare 3 dilutions of the equivolume pool (1:10, 1:100, 1:1000). Run 1µl of each dilution in triplicate using the High Sensitivity DNA assay kit.

Confirm size distribution is as expected, check there is no primer-dimer or adapter-dimer present.

Sequencing

41

Note

We currently sequence samples on an Illumina NovaSeq SP flow cell, using the XP workflow.

Alternatively, samples may be sequenced on any Illumina platform with a 300 cycle (or greater) kit. Loading concentration and sample plexing will need to be optimised per platform.

- 42 The following protocol is for loading a NovaSeq. We currently plex up to 384 samples per NovaSeq SP lane.
- 43 Steps must be performed within a given timeframe or data quality may be affected. Therefore, ensure the instrument is washed, waste containers emptied and ready for use prior to beginning step 46.
- 44 Defrost Illumina NovaSeq SP SBS and cluster reagent cartridges for 2-4 hours in a  Room temperature water bath. Use a lint free tissue to blot any water present on the foil seal. Gently mix cartridges 10X by inversion. Gently tap the bottom of the cartridges on the bench to reduce air bubbles.
- 45 Defrost components DPX1, DPX2 and DPX3 from a NovaSeq XP-2 lane kit, then keep  On ice
- 46 Bring flow cell to  Room temperature (~10 minutes) prior to use.
- 47  18 μL of each  1 nanomolar (nM) pool is required per SP lane. Denature pools by adding  4 μL 0.2N NaOH per 18 μL . Vortex briefly to mix.
- 48 Incubate at  Room temperature for  00:08:00
- 49 Add  5 μL 400mM Tris-HCl, pH8.0 to each tube to neutralise the reaction. Vortex briefly to mix, then keep  On ice .

**Note**

For the following steps, keep samples and mastermix  On ice until ready for loading onto the flow cell.

- 50 **Important!** Use mastermix within  01:00:00 of preparation for optimal sequencing performance.

Prepare ExAmp mastermix on ice:

ExAmp Master Mix	Volume per SP flow cell (μl)
DPX1	126
DPX2	18
DPX3	66
Total	210

Vortex  00:00:30 to mix, then centrifuge briefly up to  280 x g

- 51 Add  63 μL ExAmp mastermix to each denatured pool, mix well by pipetting.
- 52 Prepare the flowcell for sample loading by placing into the flow cell dock with the 2-lane manifold clamped in place.
- 53 Pipette  80 μL of library + ExAmp pool mix per manifold well. Wait for approximately 2 minutes to allow the solution to fill the lane.
- 54 **Important!** The sequencing run must be started within  00:30:00 of libraries being loaded onto the flow cell.



- 54.1 Unclamp the flow cell dock and discard the manifold. Load the flow cell onto the NovaSeq flow cell stage.
- 54.2 Load the SBS and cluster reagent cartridges.
- 54.3 Start sequencing run.