Version 5

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COVID-19 ARTIC v3 Illumina library construction and sequencing protocol V.5

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

Coronavirus Method Development Community COG-UK

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ABSTRACT

This SOP describes the procedure for generating cDNA from SARS-CoV-2 viral nucleic acid extracts and subsequently producing 400nt amplicons tiling the viral genome using V3 nCov-2019 primers (ARTIC). This is followed by library construction, equivolume pooling of samples and quantitation, prior to sequencing on the Illumina NovaSeq.

It is adapted from the nCov-2019 sequencing protocol which can be found here: https://www.protocols.io/view/ncov-2019-sequencing-protocol-bbmuik6w

DOI

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

PROTOCOL CITATION

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KEYWORDS

COVID-19, SARS-Cov-2, amplicon sequencing, ARTIC, Illumina library construction, coronavirus

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38995

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 TEXT

MATERIALS

NEBNext Ultra II DNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7645L** Step 26

2x Kapa HiFi Hotstart Readymix **Kapa Biosystems Catalog #KK2602** Step 35

LunaScript RT SuperMix Kit **New England Biolabs Catalog # E3010L** Step 3

Illumina Library Quantitation Complete kit (Universal) **Kapa Biosystems Catalog #KK4824**

NEB Q5® Hot Start High-Fidelity 2X Master Mix **New England Biolabs Catalog #M0494L** Step 8

AccuClear® Ultra High Sensitivity dsDNA Quantitation Kit with DNA Standards **Biotium Catalog ##31028** Step 17

Primer pool sequences (v3) can be found here:
https://github.com/joshquick/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019.tsv

ABSTRACT

This SOP describes the procedure for generating cDNA from SARS-CoV-2 viral nucleic acid extracts and subsequently producing 400nt amplicons tiling the viral genome using V3 nCov-2019 primers (ARTIC). This is followed by library construction, equivolume pooling of samples and quantitation, prior to sequencing on the Illumina NovaSeq.

It is adapted from the nCov-2019 sequencing protocol which can be found here:
https://www.protocols.io/view/ncov-2019-sequencing-protocol-bbmuik6w

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

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

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

Primer pool sequences (v3) can be found here:
https://github.com/joshquick/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019.tsv

Where an alt primer is available, the non alt version is omitted.

Achieving more even genome coverage

A hypothetical 'ideal' multiplex primer pool would generate the same number of reads from each amplicon, so the fraction of reads due to each amplicon would be 1/n, where n is the number of primer pairs in the

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multiplex pool. In reality this is not achievable, and the fraction of reads observed for each amplicon varies widely.

The ratio [actual observed read fraction/'ideal' read fraction] can be calculated for each individual amplicon, as indicated by the differently-coloured dots on the box-and-whisker plots below. This tells us whether a particular amplicon is under-represented (ratio <1x) or over-represented (>1x).

By changing the weights of each primer pair within the primer pool ('*rebalancing*') the number of reads obtained for each amplicon can be modified, and the effect of the process is illustrated below. The plots show the distribution per amplicon prior to rebalancing primer pair concentrations (above) and after (below). More amplicons cluster around 1x after rebalancing and the distance between the maximum and minimum ratios is also markedly reduced.

Weight to apply per primer pair

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

Pool1 primer pair	Weight (rounded to 1dp)		Pool2 primer pair	Weight (rounded to 1dp)
21L alt2 & 21R alt0	1		44L alt3 & 44R alt0	1
45L alt2 & 45R alt7	1.3		76L alt3 & 76R alt0	1.1
93L & 93R	1.4		14L alt4 & 14R alt2	1.4
47L & 47R	1.4		40L & 40R	1.7
77L & 77R	1.4		52L & 52R	1.8
37L & 37R	1.4		58L & 58R	1.8
43L & 43R	1.5		88L & 88R	1.8
53L & 53R	1.5		6L & 6R	1.9
49L & 49R	1.5		34L & 34R	1.9
15L alt1 & 15R alt3	1.5		42L & 42R	1.9
75L & 75R	1.5		62L & 62R	1.9
59L & 59R	1.5		72L & 72R	1.9
27L & 27R	1.6		82L & 82R	1.9
57L & 57R	1.6		84L & 84R	1.9
83L & 83R	1.6		90L & 90R	1.9
51L & 51R	1.7		2L & 2R	2
3L & 3R	1.7		16L & 16R	2
61L & 61R	1.7		30L & 30R	2
35L & 35R	1.7		32L & 32R	2
39L & 39R	1.7		56L & 56R	2
1L & 1R	1.7		92L & 92R	2
69L & 69R	1.7		46L alt1 & 46R alt2	2
87L & 87R	1.7		48L & 48R	2.1
11L & 11R	1.8		60L & 60R	2.1
79L & 79R	1.8		94L & 94R	2.1
41L & 41R	1.8		38L & 38R	2.2
65L & 65R	1.8		78L & 78R	2.2
63L & 63R	1.9		80L & 80R	2.2
25L & 25R	1.9		4L & 4R	2.3
7L alt0 & 7R alt5	1.9		28L & 28R	2.3
19L & 19R	2		8L & 8R	2.4
73L & 73R	2.1		10L & 10R	2.4
13L & 13R	2.2		22L & 22R	2.4
85L & 85R	2.2		98L & 98R	2.4
97L & 97R	2.3		20L & 20R	2.5
81L & 81R	2.3		96L & 96R	2.6
33L & 33R	2.4		18L alt2 & 18R alt1	3
95L & 95R	2.4		26L & 26R	3
29L & 29R	2.4		36L & 36R	3.1
31L & 31R	2.7		54L & 54R	3.1
89L alt2 & 89R alt4	2.8		66L & 66R	3.5
71L & 71R	3.1		68L & 68R	3.5
55L & 55R	3.2		24L & 24R	3.6
9L alt4 & 9R alt2	3.2		50L & 50R	4.1
5L & 5R	3.4		12L & 12R	4.4
17L & 17R	3.5		86L & 86R	5.7
23L & 23R	3.8		64L & 64R	6
91L & 91R	3.9		74L & 74R	6.7
67L & 67R	6.2		70L & 70R	7.8
mean weight	*2.1*		*mean weight*	*2.6*
cumulative weight	*104.3*		*cumulative weight*	*129.5*

A more detailed description of the process is provided in this document:

Improving the evenness of SARS-CoV-2 genome coverage by titration of primer concentrati

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

Prepare the following mastermixes:

Weighted PCR Primer Pool 1 Master Mix	**Vol/PCR RXN (µl)**	**Vol/96 plate (µl) inc. excess**
Q5 Hotstart 2X Master Mix	12.5	1440
Primer **Pool 1** (mean 102nM)	3.6	415
Nuclease-free water	2.9	334
Total	**19**	**2189**

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

Weighted PCR Primer Pool 2 Master Mix	Vol/PCR RXN (µl)	Vol/96 plate (µl) inc. excess
Q5 Hotstart 2X Master Mix	12.5	1440
Primer **Pool 2** (mean 102nM)	3.6	415
Nuclease-free water	2.9	334
Total	**19**	**2189**

The equivolume primer pools used in the standard protocol are of **[M]10 Micromolar (µM)** cumulative concentration, therefore each of the 98 primers in each pool is at **[M]102 Nanomolar (nM)** in the pool and at **[M]15 Nanomolar (nM)** in the final reaction. With the rebalanced primer pools, for equivalency we dilute them such that the **average** primer concentration is **[M]102 Nanomolar (nM)** , and therefore the **average** concentration of each primer in the final reaction is also **[M]15 Nanomolar (nM)** .

Mix thoroughly by vortexing.

9 Use the SPT Labtech Dragonfly Discovery to dispense **19 µl** mastermix per well into 2x96 well plates.

10 Use the Agilent Bravo to add **6 µl** of cDNA template to each primer pool reaction and mix.

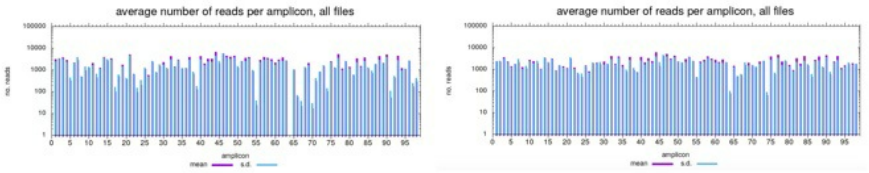
It is recommended to use filtered tips for this transfer to reduce risk of cross sample contamination via aerosolisation.

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.

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 specific amplicons dropping out. Reducing our annealing temperature from 65°C to 63°C for identical cDNA input recovered amplicon #64 as shown in the image below.

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann



65°C 63°C

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**

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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

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 **20µl sample** and take the entire volume into library preparation.

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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 1µl 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: 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 (20µl total volume) are in the range of 2.5-50ng/µl prior to proceeding with library preparation.

Library preparation for Illumina sequencing

26

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.

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

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

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

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.

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34.11 Carefully transfer supernatant into a new plate, taking care not to disturb the bead pellet. Half of this eluate **(12.5µl)** is used as input for library PCR.

Library PCR

35

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

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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.

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

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

Equivolume pool quantification

40

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

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

Alternatively, samples may be sequenced on an Illumina MiSeq using either v2 (500 cycle) or v3 (600 cycle) reagent kits. We have plexed up to 96 samples per run, this could be increased further depending on coverage requirements. Loading concentration will need to be optimised for MiSeq.
MiSeq run parameters: Read length 212 paired end + 16bp.

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

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

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 18µl. 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** .

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.

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann

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 (250PE).

Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad F Bronner, Louise Aigrain, Scott Goodwin, Scott Thurston, Stefanie Lensing, James Bonfield, Keith James, Nicholas Salmon, Charlotte Beaver, Rachel Nelson, David K. Jackson, Alex Alderton, Ian Johnston (11/04/2020). COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. https://dx.doi.org/10.17504/protocols.io.bibtkann