

Nov 04, 2020

Version 5

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

 [PLOS Global Public Health](#)

 In 1 collection

DOI

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

DNA Pipelines R&D¹, Benjamin Farr¹, Diana Rajan¹, Emma Betteridge¹, Lesley Shirley¹, Michael Quail¹, Naomi Park¹, Nicholas Redshaw¹, Iraad Bronner¹, Louise Aigrain¹, Scott Goodwin¹, Scott Thurston¹, Stefanie Lensing¹, James Bonfield¹, Keith James¹, Nicholas Salmon¹, Charlotte Beaver¹, Rachel Nelson¹, David K. Jackson¹, Alex Alderton¹, Ian Johnston¹

¹Wellcome Sanger Institute

Coronavirus Method De...

COG-UK



Diana Rajan

Wellcome Sanger Institute

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.bibt kann>

Protocol Citation: DNA Pipelines R&D, Benjamin Farr, Diana Rajan, Emma Betteridge, Lesley Shirley, Michael Quail, Naomi Park, Nicholas Redshaw, Iraad 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 2020. COVID-19 ARTIC v3 Illumina library construction and sequencing protocol. **protocols.io**

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

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 08, 2020

Last Modified: November 04, 2020

Protocol Integer ID: 38995

Keywords: COVID-19, SARS-Cov-2, amplicon sequencing, ARTIC, Illumina library construction, coronavirus, viral genome, sequencing protocol, viral nucleic acid extract, sequencing, cdna from sar, generating cdna, illumina novaseq

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>

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**

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**

 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**

Troubleshooting

cDNA generation

- 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.

- 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.

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

- Seal and briefly centrifuge plate.

- 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

Note

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

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

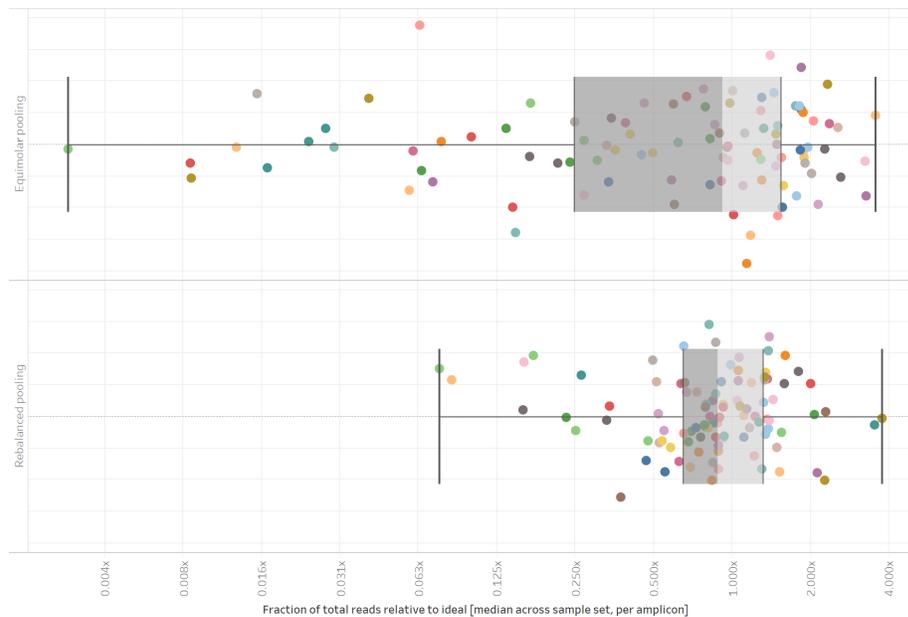
Expected result

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 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 ($>1x$).

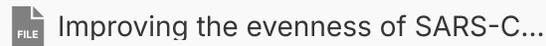
By changing the weights of each primer pair within the primer pool ('*rebalancing*') the number of reads obtained for each amplicon can be modified, and the effect of the process is illustrated below. The plots show the distribution per amplicon prior to rebalancing primer pair concentrations (above) 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

<i>Pool1 primer pair</i>	<i>Weight (rounded to 1dp)</i>		<i>Pool2 primer pair</i>	<i>Weight (rounded to 1dp)</i>
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
<i>mean weight</i>	<i>2.1</i>		<i>mean weight</i>	<i>2.6</i>
<i>cumulative weight</i>	<i>104.3</i>		<i>cumulative weight</i>	<i>129.5</i>

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



 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 plat
--	-------------------------	--------------------

		e (μl) inc. excess
	Q5 Hotstart 2X Master Mix	12.5
	Primer Pool 1 (mean 102nM)	3.6
	Nuclease-free water	2.9
	Total	19
		2189

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

Note

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 $19\ \mu\text{L}$ mastermix per well into 2×96 well plates.

10 Use the Agilent Bravo to add $6\ \mu\text{L}$ of cDNA template to each primer pool reaction and mix.

Note

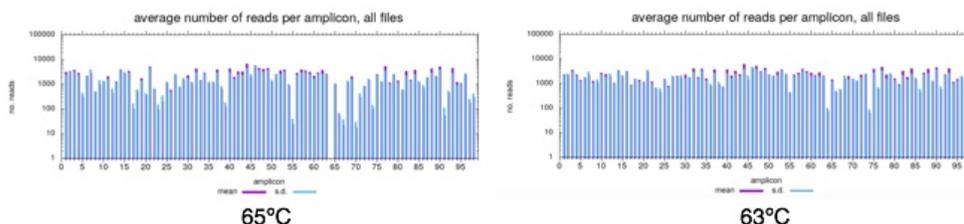
It is recommended to use filtered tips for this transfer to reduce risk of cross sample contamination via aerosolisation.

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.

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 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.



	Step	Temperature	Tim
--	-------------	--------------------	------------

		e
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 **20µl 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 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

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

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 (10 μM)	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 (**12.5µl**) 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 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 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 (250PE).