

Mar 03, 2020

Version 1

SARS-CoV-2 Enrichment Sequencing by Spiked Primer MSSPE method V.1

DOI

<https://dx.doi.org/10.17504/protocols.io.bc36iyre>

Jessica E. Manning¹, Jennifer Bohl², Sreyngim Lay¹, Sophana Chea¹, Vida Ahyong³, Erik Karlsson⁴

¹National Institute for Allergy and Infectious Diseases; ²National Institute of Allergy and Infectious Diseases;

³CZ Biohub; ⁴Institut Pasteur Cambodge

Chan Zuckerberg Biohub

Coronavirus Method De...



Vida Ahyong

CZ Biohub

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.bc36iyre>

Protocol Citation: Jessica E. Manning, Jennifer Bohl, Sreyngim Lay, Sophana Chea, Vida Ahyong, Erik Karlsson 2020. SARS-CoV-2 Enrichment Sequencing by Spiked Primer MSSPE method. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.bc36iyre>



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: February 28, 2020

Last Modified: March 03, 2020

Protocol Integer ID: 33630

Keywords: genome coverage on an iseq100, cov2 genome, spiked primer enrichment step, genome coverage, sequencing, genome, spiked primer msspe method, full genome, iseq100, spiked primer msspe method this protocol, spiked primer approach, cov2, nature microbiology

Abstract

This protocol was used to enrich for SARS-CoV2 sequencing reads from a confirmed COVID-19 swab sample and attain the full genome using an iSeq100. By using a spiked primer approach with 73 primers spanning the entire SARS-CoV2 genome, we were able to get an average of 15x genome coverage on an iSeq100 with 1.8 million paired end-reads. Here we overview all the steps, from sample extraction, library preparation with a spiked primer enrichment step, and sequencing on an iSeq100. The collaborative effort involved the Manning Lab, NIAID in Phnom Penh, Cambodia, Institut Pasteur Cambodge, Cambodia Ministry of Health, the Chan Zuckerberg Biohub, and the Chan Zuckerberg Initiative.

This approach was developed based on the work from Deng et al, Nature Microbiology, January 13, 2020.

<https://www.nature.com/articles/s41564-019-0637-9>



Materials

MATERIALS

☒ NEBNext Ultra II RNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7770L**

☒ NEBNext Adaptor for Illumina **New England Biolabs**

☒ Qubit dsDNA HS Assay kit **Thermo Fisher Scientific Catalog #Q32854**

☒ QIAamp Viral RNA Mini Kit **Qiagen Catalog #52904**

☒ NEBNext USER Enzyme **New England Biolabs Catalog #E7458**

☒ Capillary electrophoresis instrument (e.g. Agilent Tapestation 4200)

☒ High Sensitivity D5000 ScreenTape **Agilent Technologies Catalog #5067-5592**

☒ Qubit RNA HS Assay Kit **Thermo Fisher Scientific Catalog #Q32852**

☒ TruSeq i7/i5 Indexing Primers - Custom (or NEBNext® Multiplex Oligos for Illumina) **New England Biolabs Catalog #E7500L**

☒ ERCC RNA Spike-In Mix **Thermo Fisher Catalog #4456740**

☒ QIAseq FastSelect rRNA Removal Kit **Qiagen Catalog #333180**

☒ DNase I Set **Zymo Research Catalog #E1010**

STEP MATERIALS

☒ QIAamp® Viral RNA Mini **Qiagen Catalog #52906**

☒ DNase I Set **Zymo Research Catalog #E1010**

☒ Qubit RNA HS Assay Kit **Thermo Fisher Scientific Catalog #Q32852**

☒ High Sensitivity D5000 ScreenTape **Agilent Technologies Catalog #5067-5592**

☒ NEBNext Ultra II RNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7770L**

☒ ERCC RNA Spike-In Mix **Thermo Fisher Catalog #4456740**

☒ QIAseq FastSelect rRNA Removal Kit **Qiagen Catalog #333180**



Protocol materials

⊗ NEBNext Ultra II RNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7770L**

⊗ QIAamp® Viral RNA Mini **Qiagen Catalog #52906**

⊗ DNase I Set **Zymo Research Catalog #E1010**

⊗ Qubit dsDNA HS Assay kit **Thermo Fisher Scientific Catalog #Q32854**

⊗ QIAamp Viral RNA Mini Kit **Qiagen Catalog #52904**

⊗ Capillary electrophoresis instrument (e.g. Agilent Tapestation 4200)

⊗ ERCC RNA Spike-In Mix **Thermo Fisher Catalog #4456740**

⊗ NEBNext Adaptor for Illumina **New England Biolabs**

⊗ QIAseq FastSelect rRNA Removal Kit **Qiagen Catalog #333180**

⊗ Qubit RNA HS Assay Kit **Thermo Fisher Scientific Catalog #Q32852**

⊗ High Sensitivity D5000 ScreenTape **Agilent Technologies Catalog #5067-5592**

⊗ TruSeq i7/i5 Indexing Primers - Custom (or NEBNext® Multiplex Oligos for Illumina) **New England Biolabs Catalog #E7500L**

⊗ NEBNext USER Enzyme **New England Biolabs Catalog #E7458**

Sample Collection

- 1 Nasopharyngeal and oropharyngeal swabs (combined into one tube) were collected from a symptomatic patient meeting case definition for possible infection with SARS-CoV-2.

RNA extraction

- 2 Extraction of viral nucleic acids from clinical sample was performed with a QIAamp Viral RNA Mini Kit (Qiagen #52906) as described by manufacturer

 QIAamp® Viral RNA Mini **Qiagen Catalog #52906**

Extracted RNA samples were DNase-treated using the Zymo DNase I kit.

 DNase I Set **Zymo Research Catalog #E1010**

The nucleic acid was tested via real-time polymerase chain reaction for COVID-19 using both the Drosden and HKU protocols published by the World Health Organization and confirmed positive for COVID-19 on January 27th, 2020.

Ct values for PUI = 24.

RNA Quantification

- 3 RNA was quantified using the Qubit High Sensitivity RNA kit as described by the manufacturer.

 Qubit RNA HS Assay Kit **Thermo Fisher Scientific Catalog #Q32852**

Qubit input RNA concentration for PUI = 6.9 ng/uL

Library Preparation

- 4 **Library Preparation was performed with the NEBNext Ultra II non-directional RNA kit.**

 NEBNext Ultra II RNA Library Prep Kit for Illumina - 96 rxns **New England Biolabs Catalog #E7770L**



Fragmentation & SARS-CoV-2 primer spike in

Random primers at 1 μ M are mixed with a 10 μ M of SARS-CoV-2 primers (see below) at a 1:1 volume ratio.

		1 reac tion
	Reagent	vol stoc k (μ L)
	RNA (sample) (10ng – 100ng total)	3.5
	25pg ERCC Spike-in (50pg/ μ L stock) *	0.5
	(pink) First SS Reaction Buffer 5x	4
	(pink) Random Primers/Spiked primer mix	1
	QIAseq FastSelect (1:100) rRNA**	1
	Total volume	10
		μ L/r xn

* (optional) ERCCs are internal synthetic RNA controls comprised of 92 synthetic RNAs that do not match to any known microbe in the NCBI NR/NT databases.

 ERCC RNA Spike-In Mix **Thermo Fisher Catalog #4456740**

** (optional) FastSelect is designed for removing human rRNA, omit this reagent if not using human derived samples and only incubate at 94°C and then directly to 4°C (omit ramping down steps).

 QIAseq FastSelect rRNA Removal Kit **Qiagen Catalog #333180**

Thermocycler (heated lid set to 105°C):

- 8 min at 94°C (Adjust this fragmentation time depending on the quality of extracted RNA)

- 2 min 75°C
- 2 min 70°C
- 2 min 65°C
- 2 min 60°C
- 2 min 55°C
- 5 min 37°C
- 5 min 25°C

The 73 primers tile across the entire SARS-CoV2 genome at a spacing of ~400bp.
The PDF below shows the approximate location of the primer binding sites.

 enrichmentprimers.pdf

	Name	Sequence
	Primer_CoV1	GTGA CTTC CATGC CAATG
	Primer_CoV2	CTGAT TTTGG GGTC CATT TC
	Primer_CoV3	GAAAT GGTG AATTG CCCT C
	Primer_CoV4	GATAG CAATT CCAC CGGT G
	Primer_CoV5	CAGTA TAACC ACCA ATCTG
	Primer_CoV6	CATTA ATGCC AGAGA TGTC
	Primer_CoV7	GTATT TGTA TGCA GCAC



Primer_CoV 8	CTTCT GTGC AGTTA ACATC
Primer_CoV 9	GATTC TGTTG GTTG GAC
Primer_CoV1 0	GAATG TAAAA CTGA GGATC TG
Primer_CoV1 1	CAGC TGTAC CTGG TGCA AC
Primer_CoV1 2	CACTA CCTT CTGTA ATAAG
Primer_CoV1 3	CATAC AAAC TGCC ACCAT C
Primer_CoV1 4	GTCC TTTGT ACATA AGTG
Primer_CoV1 5	GAGC TGATT TGTCT TTATG TG
Primer_CoV1 6	CAGC ATCAC CATAG TCAC
Primer_CoV1 7	CGAA CCGT TCAAT CATAA G
Primer_CoV1 8	CACC ATAGA ATTTG CTTGT TC



Primer_CoV1 9	CTAGC TCTCT GAAG TGGTA TC
Primer_CoV 20	GTTTC TTCAT GTTG GTAG
Primer_CoV 21	CTAGC CCATT TCAAA TCCT G
Primer_CoV 22	GTTGT CCAG CATT CTTCA C
Primer_CoV 23	GACA AACTA GTATC AACC ATATC
Primer_CoV 24	CTGTC CTGG TTGAA TGCG AAC
Primer_CoV 25	CAGA GTACA GTGAA TGAC
Primer_CoV 26	GTAGA TGCTA TGTC CGAG
Primer_CoV 27	GAAC CTTTA GTGTT ATTAG
Primer_CoV 28	GTTCA AATAG CCTT CTCT G
Primer_CoV 29	CTTAA AAGA GGGT GTGTA G



Primer_CoV 30	CTCA CCTAC TGTCT TATTA C
Primer_CoV 31	CATTT AGATC GTAA GTGTG
Primer_CoV 32	GTGC GAAC AGTAT CTACA C
Primer_CoV 33	CACA ACACA GGCG AACT C
Primer_CoV 34	CACC TTCCT TAAAC TTCTC
Primer_CoV 35	CTTCT GAATT GTGA CATGC TG
Primer_CoV 36	GTCTC ACCA CTACG ACCG
Primer_CoV 37	GTTCA CGGC AGCA GTATA CACC
Primer_CoV 38	TCCA CAAA AGCA CTTGT GGAA GC
Primer_CoV 39	TGTG GGAA GTGTT TCTCC CTC
Primer_CoV 40	GTCTG AACA ACTG



		GTGTA AGTTC C
	Primer_CoV 41	ATTTC AGTAG TGCC ACCA GCC
	Primer_CoV 42	CATGT CCAC AACTT GCGT GTG
	Primer_CoV 43	AGCA CCGT CTATG CAATA CAAA G
	Primer_CoV 44	ACAG CAGC TAAAC CATGA GTAGC
	Primer_CoV 45	ACAA CCGT CTACA ACATG CAC
	Primer_CoV 46	GTCAC GGGG TGTCA TGTTT TC
	Primer_CoV 47	CGTGT GTCA GGGC GTAAA CTTTC
	Primer_CoV 48	GAGC CTTTG CGAG ATGAC AAC
	Primer_CoV 49	AACG GCAAT TCCA GTTTG AGC
	Primer_CoV 50	GCGG TTGAG TAAAC



		AAAA GAGG C
	Primer_CoV 51	GGGA ACAC AACC ATCTC TTGC
	Primer_CoV 52	ACGAT GCAC CACC AAAG GATTC
	Primer_CoV 53	AATAC CAGC ATTTC GCATG GCA
	Primer_CoV 54	TAGCA GCATT ACCAT CCTG AGC
	Primer_CoV 55	TGCAT TAACA TTGG CCGT GAC
	Primer_CoV 56	ACAA CCTG GAGC ATTGC AAAC
	Primer_CoV 57	TCACA TAGTG CATCA ACAG CGG
	Primer_CoV 58	TAAAG TTGC CACAT TCCTA CGTG G
	Primer_CoV 59	TAACA AAGC ACTC GTGG ACAG C



Primer_CoV 60	CCTG TTGTC CATCA AAGT GTCC C
Primer_CoV 61	GATGA ACCT GTTTG CGCA TCTG
Primer_CoV 62	CTATT TGTTC GCGT GGTTT GCC
Primer_CoV 63	ACCC TGTTT TCCTT CAAG GTCC
Primer_CoV 64	TGCTA CCGG CCTG ATAGA TTTC
Primer_CoV 65	TGCT GCATT CAGTT GAATC ACC
Primer_CoV 66	CAGA AGCT CTGAT TTCTG CAGC
Primer_CoV 67	TTGCA GTAGC GCGA ACAA AATC
Primer_CoV 68	ACGC ACAC AATCG AAGC GCAG
Primer_CoV 69	TGCC AATCC TGTA CGAC TGTAT GC



Primer_CoV 70	AGGA CACG GGTC ATCAA CTAC
Primer_CoV 71	TGCC AGCC ATTCT AGCA GGAG
Primer_CoV 72	TGTG GTGG CTCTT TCAA GTCC
Primer_CoV 73	TTTTG TCATT CTCC TAAGA AGC

Enrichment primer sequences for SARS-CoV-2 genome

5 First Strand Synthesis

Mix the following by pipetting up and down.

	1 rxn
Rea gent	vol stoc k (uL)
Frag men ted & prim ed RNA	10
Nucl ease -free wate r	8
(pin k) NEB Next	2



	First Strand Synthesis Enzyme Mix	
	Total volume	20 uL/rxn

Thermocycler (heated lid set to 105°C):

- 10 mins at 25°C
- 15 mins at 42°C
- 15 mins at 70°C
- Hold at 4°C

6 Second Strand Synthesis

		1 rxn
	Reagent	vol stock (uL)
	First strand synthesized DNA	20
	(orange) 2nd SS Reaction buffer (10X)	8

(orange) 2nd SS enzyme mix	4
Nuclease -free water	48
Total volume	80 uL/rxn

Thermocycler (heated lid off):

- 1 hour at 16°C
- Hold at 4°C

7 SPRI cleanup

*allow beads to sit in RT for 30 mins prior

- Use SPRI Beads 1.8x ratio of beads-to-total volume of sample. Prep 80% EtOH.
- Add 144uL of room temperature beads to 2nd Strand Synthesis Rxn. Mix well by pipetting gently.
- Pulse spin the tubes, but be sure not to spin down beads. Incubate for 5 mins at room temperature.
- Place samples on magnetic rack, and incubate for 5 mins on the rack.
- Remove supernatant.
- Add 200uL of 80% EtOH to samples while on the magnetic rack. Incubate at room temperature for 30s then remove the supernatant.
- Repeat EtOH wash step for a total of 2 times
- Air dry the beads for 5 mins while on the magnetic rack.
- Remove tube from magnetic rack. Elute DNA from beads into **53uL** of 0.1x TE Buffer, 10mM Tris-HCl, or Nuclease free water.
- Vortex to mix. Spin tubes and incubate for 2 mins at room temperature off the magnetic rack.
- Place on magnetic rack until solution is clear ~ 5 mins.
- Remove 50uL of the supernatant and transfer to a clean nuclease free PCR tube.

**Checkpoint: Samples can be stored frozen at -20 °C and library prep resumed the next day.

8 End Repair

Mix all the following by pipetting up and down

		1 rxn
	Rea gent	vol stoc k (uL)
	Purif ied ds- cDN A	50
	(gre en) Ultra II End Prep reac tion buff er (8.6 x)	7
	(gre en) Ultra II End Prep enzy me mix	3
	Total volu me	60 uL/r xn

Thermocycler (heated lid set to 105°C):

- 30 mins at 20°C
- 30 mins at 65°C
- Hold at 4°C

9 Adapter Ligation

- dilute adaptor to dilution prior to making master mix. Adaptor concentration depends on the amount of input; 1:100 dilution for samples <5ng, 1:25 for input of >5ng
- **Add adaptor separately after ligation master mix and ligation enhancer to avoid adaptor dimers.**

		1 rxn
	Rea gent	vol stoc k (uL)
	End Prep reac tion mixt ure	60
	(red) NEB Next Ultra II ligati on mast er mix	30
	(red) NEB Next ligati on enha ncer	1
	1:10 0 Ada ptor (Cat No. E73 37A A)	2.5
	Total volu me	93.5 uL/r xn

Thermocycler (heated lid off):

- 15 mins at 20°C with heated lid **off**



- Proceed immediately to Bead Purification.

10 SPRI Cleanup

*allow beads to sit in RT for 30 mins prior

- Use SPRI bead 0.9x ratio of beads-to-total volume of sample. Prep 80% EtOH.
- Add 87uL of room temperature beads (0.9x) to Adaptor Ligation reaction. Mix well.
- Pulse spin the tubes, but be sure not to spin down beads. Incubate for 5 mins at room temperature.
- Place samples on magnetic rack, and incubate for 5 mins on the rack.
- Remove supernatant.
- Add 200uL of 80% EtOH to samples while on the magnetic rack. Incubate at room temperature for 30s then remove the supernatant.
- Repeat EtOH wash step for a total of 2 times.
- Air dry the beads for 5 mins while on the magnetic rack.
- Remove tube from magnetic rack. Elute DNA from beads into 17uL of 0.1x TE Buffer, 10mM Tris-HCl, or Nuclease free water.
- Vortex to mix. Spin tubes and incubate for 2 mins at room temperature off the magnetic rack.
- Place on magnetic rack until solution is clear ~ 5 mins.
- Remove 15uL of the supernatant and transfer to a clean nuclease free PCR tube.

**Checkpoint: Samples can be stored frozen at -20 °C and library prep resumed the next day.

11 USER/Q5 Indexing PCR

Mix the following components by pipetting up and down.

		1 rxn
	Reagent	vol stock (ul)
	Purified, adaptor-ligated cDNA	15
	(white) USER Enzyme (Cat no.	3



M5505 L, 250uL)	
(blue) NEBNext Ultra II Q5 master mix	25
5uM i7 barcoded primer (NEB index primer/TruSeq /or similar)	5uL
5uM i5 barcoded primer (NEB Universal primer/TruSeq /or similar)	5uL
Total volume	53uL

Cycling conditions:

Thermocycler (heated lid at 105°C):	Cycles
37 °C for	1

15 mins	
98 °C for 30s	1
98 °C for 10s	6-15**
65 °C for 75s	
65 °C for 5 mins	1
Hold at 4 °C	

** PCR cycles are dependent on the input RNA. For libraries with <5ng input, perform 15-19 cycles of PCR. For 5-20ng input, perform 10-14 cycles of PCR. For >20ng input, perform 6-8 cycles of PCR.

12 SPRI Cleanup

*allow beads to sit in RT for 30 mins prior

- Use SPRI Beads at 0.8x ratio of beads-to-total volume of sample. Prep 80% EtOH.
- Add 43uL of room temperature Ampure Beads (0.8x) to barcoded DNA. Mix well.
- Pulse spin the tubes, but be sure not to spin down beads. Incubate for 5 mins at room temperature.
- Place samples on magnetic rack, and incubate for 5 mins on the rack.
- Remove supernatant.
- Add 200uL of 80% EtOH to samples while on the magnetic rack. Incubate at room temperature for 30s then remove the supernatant.
- Repeat EtOH wash step for a total of 2 times.
- Air dry the beads for 5 mins while on the magnetic rack.
- Remove tube from magnetic rack. Elute DNA from beads into **23uL** of 0.1x TE Buffer, 10mM Tris-HCL, or Nuclease free water.
- Vortex to mix. Spin tubes and incubate for 2 mins at room temperature off the magnetic rack.

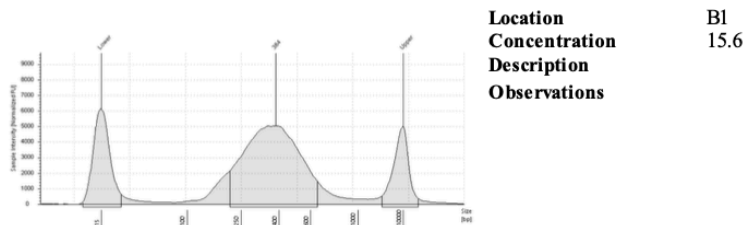
- Place on magnetic rack until solution is clear ~ 5 mins.
 - Remove 20uL of the supernatant and transfer to a clean nuclease free PCR tube.
- ** Checkpoint: Libraries are complete, samples can be stored frozen at -20 °C until ready for quantification and pooling.

Library Quality Control

- 13 Libraries were quantified by the Qubit High Sensitivity DNA kit and the Agilent High Sensitivity D500 DNA Tapestation assay. If adapter dimers are found, library should be size selected using a SPRI ratio of 0.8x.

 High Sensitivity D5000 ScreenTape **Agilent Technologies Catalog #5067-5592**

Expected result



Size [bp]	Calibrated Conc. [ng/ul]	Assigned Conc. [ng/ul]	PeakMolarity [nmol/l]	% IntegratedArea	PeakComment	Observations
15	4.84	-	497	-		Lower Marker
384	15.6	-	62.5	100.00		
10000	3.25	3.25	0.500	-		Upper Marker

Tapestation HS D5000 assay shows an average size library of 384bp at a concentration of 62.5 nM.

Quantified library is then diluted down to the loading concentration for the iSeq, 100pM. This value will vary depending on the type of sequencer.

iSeq Loading

- 14 The Illumina iSeq was loaded with 20uL of a 100pM library with a 5% PhiX spike in.



Analyses

- 15 Metagenomic sequencing results were uploaded onto IDseq.net directly from the Illumina Basespace Sequence Hub. The open-source cloud-based pipeline analyzed 1.8 million reads. The majority of reads mapped to the nasal and oral microbiome. Analyses of the viral components resulted in 3,077 single end reads aligning to the SARS-CoV2 taxon.

Expected result

▼ Betacoronavirus (2 viral species) ● 1	16,452,524	100.0	823.4	3,079	1	3,061	100.0	29,698.9	306.2
		100.0	830.6	3,106	3	3,071	99.2	4,341.7	304.1
Wuhan seafood market pneumonia virus	16,452,524	100.0	822.9	3,077	1	3,061	100.0	29,718.2	306.4
		100.0	822.4	3,075	1	3,061	99.8	4,385.1	307.1
Severe acute respiratory syndrome-related coronavirus	88,253	100.0	0.5	2	0	0	98.8	83.0	43.2
VALID PRIORITY: 1, C		100.0	8.3	31	2	10	35.5	39.3	9.7

Resulting reads from the Betacoronavirus genus were downloaded from IDseq and mapped to the NCBI genome accession number: MN908947.1. The geneious alignment displayed even coverage across the genome with an average coverage of 14.9x. One SNP was noted at position 25,654 in ORF3a resulting in a valine to leucine substitution when compared to NCBI accession MN908947.1.

Expected result

