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SARS-CoV-2 Whole Genome Amplicon Sequencing from Wastewater Solids or Liquid Wastewater V.2

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Wastewater-based epid...



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We use this protocol and it's working

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Abstract

This process instruction describes steps for whole genome amplicon sequencing of SARS-CoV-2 from wastewater, including two approaches for concentration and RNA extraction steps (using liquid wastewater, or wastewater solids), purification steps, reverse transcription and PCR with ARTIC primers, library construction, and Illumina sequencing. Sequencing data produced using this protocol may be used for a variety of analyses including estimation of variant and mutation abundance. The read lengths are sufficient for read merging and analysis of intact amplicons. This protocol has been used for sequencing activities as part of the WastewaterSCAN program.

Materials

- ARTIC v5.3.2 primers (IDT 10016495 or custom order based on https://github.com/quick-lab/SARS-CoV-2/tree/main/400/v5.3.2_400)
- ATCC Quantitative genomic RNA from Severe acute respiratory syndrome-related coronavirus 2 strain 2019-nCoV/USA-WA1/2020 (VR-1986D)
- Molecular biology grade ethanol
- Molecular biology grade water
- Qiagen elution buffer (19086)
- Ceres Nanotrap Microbiome A Particles (44202-30)
- Ceres Nanotrap Enhancement Reagent 1 Solution (10111-30)
- Thermo MagMAX Microbiome Lysis Solution (A42361)
- chemagic Viral DNA/RNA 300 Kit H96 (CMG-1033-S)
- Zymo OneStep PCR Inhibitor Removal Kit (D6035)
- Turbo DNase (AM2239)
- KAPA HyperPure (08963843001)
- NEB LunaScript MM (M3010E)
- NEB Q5 Hot Start High-Fidelity 2X Master Mix (M0494)
- NEBNext Ultra II DNA Library Prep Kit for Illumina (E7645L)
- NEBNext Indexing primers (E6440, E6442, E6444, E6446, E6448)
- KAPA Illumina Library Quantification Kit (KK4824)
- Rainin 1000 uL tips (30389213)
- Rainin 200 uL tips (30389240)
- Rainin 20 uL tips (30389226)
- Fisher scientific Reagent reservoirs (89094-662)
- Eppendorf Skirted Twin.Tec LoBind PCR plates (E0030129512)
- Centrifuge with 96-well PCR plate rotor attachment capable of generating ≥ 2000 rcf
- Thermal cycler capable of 2°C/s ramp rate
- Magnet for magnetic SPRI bead separation
- Optical cycler for library qPCR
- Illumina sequencer capable of ≥ 250 PE reads



Before start

Pool and dilute primers

1. ARTIC 5.3.2 primers can be purchased premixed from IDT (10016495) or custom ordered and mixed per the instructions provided by the Quick lab (https://github.com/quick-lab/SARS-CoV-2/tree/main/400/v5.3.2_400).
2. Make sufficient working stock of each primer mix at (on average) ~150 nM per primer by diluting the stock tubes or mixtures from ~1040 nM. For a full 96-well plate at the ARTIC PCR step, 150 µL of 150 nM working stock of each pool is sufficient.

Dilute gRNA

1. SARS-CoV-2 gRNA (ATCC VR-1986D) is used as a positive control. The positive control sample is 500 copies of the gRNA in 40 µL of water (12.5 copies / µL) added to the plate before the digestion of DNA. Dilute the stock gRNA in water according to the concentration provided by ATCC.



Select Sample Type

- 1 This protocol outlines procedures for the use of both wastewater solids and liquid wastewater for SARS-CoV-2 whole genome sequencing. Select Option 1 (Wastewater Solids  [go to step #2](#)) or Option 2 (Liquid Wastewater  [go to step #5](#)) to concentrate, extract RNA, and purify the sample and then  [go to step #29](#) to continue the procedure for either sample type.



Option 1: Preparation and RNA extraction from wastewater SOLIDS

- 2 For sequencing using wastewater solids, dewater wastewater and prepare solids for extraction as documented in the following protocol:

Protocol



NAME

High Throughput pre-analytical processing of wastewater settled solids for SARS-CoV-2 RNA analyses

CREATED BY

Alexandria B Boehm

[Preview](#)

- 3 After pre-analytical processing, extract and purify nucleic acids as documented in the following protocol:



Protocol



NAME

High Throughput RNA Extraction and PCR Inhibitor Removal of Settled Solids for Wastewater Surveillance of SARS-CoV-2 RNA

CREATED BY

Alexandria B Boehm

[Preview](#)

- 4 Following RNA extraction, diluted 1:4 in molecular grade water before proceeding to DNA digestion: [⇒ go to step #29 DNA digestion](#)

Option 2: Viral particle concentration and RNA extraction from LIQUID wastewater

5

Note

Viral particles are concentrated from 9.75 mL of clarified influent using **Ceres Nanotrap Microbiome A particles**. Note: include at least one concentration/extraction negative control (water instead of sample).

6

Spin down 50 mL of influent at 5,250 xg for 5 min to clarify the influent.

7

Add 4.875 mL of influent sample to one well (one well per sample) of a new KingFisher 24 Well Deep Well Plate.

8

Add another 4.875 mL of influent sample to the same well location on a second KingFisher 24 Well Deep Well Plate.

9

Add 50 µL of Nanotrap Enhancement Reagent 1 (ER1) Solution to each well used.



- 10 Add 75 μ L of Nanotrap Microbiome A Particles to each well used on the two KingFisher 24 Well Deep Well sample plates.
- 11 Prepare the "Lysis Plate": Add 350 μ L of MagMAX Microbiome Lysis Solution to each well of a new KingFisher 24 Well Deep Well Plate.
- 12 Run KF-008-WW-Nanotrap-24.bdz on the King Fisher Flex to concentrate the viral particles.
- 13 Once the protocol is completed, the "Lysis Plate" will contain ~350 μ L lysate that is ready to proceed to nucleic acid extraction.

14

Note

This total nucleic acid extraction is automated using the Chemagic 360 instrument using the **chemagic Viral DNA/RNA 300 Kit H96**.

- 15 Transfer 300 μ L of lysate to each well of the Chemagic Deepwell Plate
- 16 Add 300 μ L of Lysis Buffer to each well.
- 17 Add 10 μ L of Proteinase K to each well.
- 18 Add 60 μ L of Elution Buffer to each well of an Elution Plate.
- 19 Set up, load, and run the Chemagic for the Viral DNA/RNA 300 Kit H96.
- 20 Once the protocol is complete, the nucleic acid (~60 μ L) will be in the Elution Plate and ready to proceed to the inhibitor removal steps.

21

**Note**

Additional PCR inhibitors are removed from the extracted and purified nucleic acid using the **Zymo OneStep PCR Inhibitor Removal Kit**.

- 22 Mount a Zymo Silicon-A-HRC plate (included in kit) onto an Elution Plate (included in kit)
- 23 Add 150 μ L Prep Solution to the wells by piercing the cover foil in the middle with a pipette tip.
- 24 Incubate at room temperature for 5 min.
- 25 Centrifuge the plate at 3,500 xg for 5 min.
- 26 Transfer 60 μ L of eluate from the Chemagic Elution Plate into the wells of a prepared Silicon-A-HRC Plate mounted on a new Elution Plate.
- 27 Centrifuge the plate at 3,500 x g for 3 minutes.
- 28 The cleaned up nucleic acid is now in the Zymo Elution Plate. Proceed with next steps,

 [go to step #29 DNA Digestion](#)

DNA Digestion**1h 30m**

29

Note

DNA is digested from the total nucleic acid solution using Turbo DNase and then cleaned up and concentrated using KAPA HyperPure SPRI beads. Include at least one well of gRNA as a positive control and one of water as a negative control for the whole process after extraction.

- 30 Transfer 40 μ L of nucleic acid into a new plate.



31 To each sample add: 1 μ L Turbo DNase and 4 μ L 10X Turbo DNase Buffer

32 Incubate:

	A	B	C	D
	Table 1. Thermal Cycler Program for Turbo DNase			
	Steps	Cycles	Temp ($^{\circ}$ C)	Time
	1	1	37	30 min
	2	-	4	Hold

Lid Temp = 47 $^{\circ}$ C, Total Volume = 45 μ L

33 Add 90 μ L Kapa HyperPure Beads to each well.

34 Mix well by pipetting up and down at least 10 times.

35 Incubate at room temperature for 5 minutes.

36 Place the plate on a magnet to capture the beads.

37 Incubate until the liquid is clear.

38 Carefully remove and discard the supernatant.

39 Keeping the plate on the magnet, add 200 μ L of 80% ethanol.

40 Incubate the plate on the magnet at room temperature for 30 seconds.



- 41 Carefully remove and discard the ethanol.
- 42 Keeping the plate on the magnet, add 200 μ L of 80% ethanol.
- 43 Incubate the plate on the magnet at room temperature for 30 seconds.
- 44 Carefully remove and discard the ethanol. Try to remove all residual ethanol without disturbing the beads.
- 45 Dry the beads at room temperature for 3-5 minutes, or until all of the ethanol has evaporated.
- 46 Remove the plate from the magnet.
- 47 Resuspend the beads in 13 μ L of elution buffer.
- 48 Incubate the plate at room temperature for 2 minutes.
- 49 Place the plate on a magnet to capture the beads.
- 50 Incubate until the liquid is clear.
- 51 Transfer the 11 μ L of clear supernatant to a new plate for reverse transcription.

Reverse Transcription

1h 45m

52

**Note**

The remaining RNA is reverse transcribed into cDNA with the NEB LunaScript RT SuperMix then cleaned up and split in preparation for the two ARTIC PCRs.

53 Add 2.75 μ L LunaScript RT SuperMix to each well containing RNA.

54 Mix well by pipetting up and down at least 10 times.

55 Incubate:

	A	B	C	D
	Table 2. Thermal Cycler Program for LunaScript RT			
	Steps	Cycles	Temp ($^{\circ}$ C)	Time
	1	1	25	10 min
	2	1	50	50 min
	3	1	85	5 min
	4	-	4	Hold

Lid Temp = 95 $^{\circ}$ C, Total Volume = 14 μ L

56 Add 27.5 μ L Kapa HyperPure Beads to each well.

57 Mix well by pipetting up and down at least 10 times.

58 Incubate at room temperature for 5 minutes.

59 Place the plate on a magnet to capture the beads.



- 60 Incubate until the liquid is clear.
- 61 Carefully remove and discard the supernatant.
- 62 Keeping the plate on the magnet, add 200 μ L of 80% ethanol.
- 63 Incubate the plate on the magnet at room temperature for 30 seconds.
- 64 Carefully remove and discard the ethanol.
- 65 Keeping the plate on the magnet, add 200 μ L of 80% ethanol.
- 66 Incubate the plate on the magnet at room temperature for 30 seconds.
- 67 Carefully remove and discard the ethanol. Try to remove all residual ethanol without disturbing the beads.
- 68 Dry the beads at room temperature for 3-5 minutes, or until all of the ethanol has evaporated.
- 69 Remove the plate from the magnet.
- 70 Resuspend the beads in 12 μ L of elution buffer.
- 71 Incubate the plate at room temperature for 2 minutes.
- 72 Place the plate on a magnet to capture the beads.

- 73 Incubate until the liquid is clear.
- 74 Transfer the 5 μ L of clear supernatant to two new plates for the two ARTIC PCRs.

SARS-CoV-2 genome amplification with ARTIC PCR

4h 15m

75

Note

SARS-CoV-2 cDNA is amplified in two reactions using the ARTIC 5.3.2 primers (15 nM each primer in the PCR) and NEB Q5 Hot Start High-Fidelity 2X Master Mix then combined and cleaned up. Include at least one well on each plate as a negative control for the ARTIC PCR.

- 76 Make two master mixes, one for ARTIC Pool A and one for ARTIC Pool B. Per sample there should be: 6.25 μ L Q5 Hot Start High-Fidelity 2X Master Mix and 1.25 μ L of ARTIC PCR primer pool working stock (150 nM).
- 77 Add 7.5 μ L of Pool A master mix to each well of one plate containing 5 μ L cDNA.
- 78 Add 7.5 μ L of Pool B master mix to each well of the plate other containing 5 μ L cDNA.
- 79 Mix well by pipetting up and down at least 10 times.

80 Incubate:

	A	B	C	D
	Table 3. Thermal Cycler Program for ARTIC PCR			
	Steps	Cycles	Temp ($^{\circ}$ C)	Time
	1	1	98	30 sec
	2	35	95	15 sec
	3		63	5 min



	A	B	C	D
	4	-	4	Hold

Lid Temp = 105°C, Total Volume = 13 µL

- 81 Combine 12.5 µL of each of the Pool A and Pool B PCR reactions for a total of 25 µL.
- 82 Add 20 µL Kapa HyperPure Beads to each well.
- 83 Mix well by pipetting up and down at least 10 times.
- 84 Incubate at room temperature for 5 minutes.
- 85 Place the plate on a magnet to capture the beads.
- 86 Incubate until the liquid is clear.
- 87 Carefully remove and discard the supernatant.
- 88 Keeping the plate on the magnet, add 200 µL of 80% ethanol.
- 89 Incubate the plate on the magnet at room temperature for 30 seconds.
- 90 Carefully remove and discard the ethanol.
- 91 Keeping the plate on the magnet, add 200 µL of 80% ethanol.
- 92 Incubate the plate on the magnet at room temperature for 30 seconds.



- 93 Carefully remove and discard the ethanol. Try to remove all residual ethanol without disturbing the beads.
- 94 Dry the beads at room temperature for 3-5 minutes, or until all of the ethanol has evaporated.
- 95 Remove the plate from the magnet.
- 96 Resuspend the beads in 27 μL of elution buffer.
- 97 Incubate the plate at room temperature for 2 minutes.
- 98 Place the plate on a magnet to capture the beads.
- 99 Incubate until the liquid is clear.
- 100 Transfer the 25 μL of clear supernatant to a new plate.

Library Construction: End Prep

1h 10m

101

Note

The ends of the DNA amplicons are prepared for adapter ligation, this includes end repair, 5' phosphorylation and dA-tailing. This step uses the **NEBNext Ultra II DNA Library Prep Kit for Illumina**.

102 Add 1.5 μL NEBNext Ultra II End Prep Enzyme Mix to each well.

103 Add 3.5 μL NEBNext Ultra II End Prep Reaction Buffer to each well.

104 Mix well by pipetting up and down at least 10 times.

105 Incubate:

	A	B	C	D
Table 4. Thermal Cycler Program for End Prep				
Steps	Cycles	Temp (°C)	Time	
1	1	20	30 min	
2	1	65	30 min	
3	-	4	Hold	

Lid Temp = 75°C, Total Volume = 30 µL

Library Construction: Adaptor Ligation

45m

106

Note

NEBnext adapters are ligated to the end-repaired amplicons and then the uracil is excised via User enzyme incubation. This step uses the **NEBNext Ultra II DNA Library Prep Kit for Illumina**.

107 Add 1.25 µL NEBNext Adaptor for Illumina to each well. Do not premix adaptor with the Ligation Master Mix.

108 Add 15uL NEBNext Ultra II Ligation Master Mix to each well.

109 Mix well by pipetting up and down at least 10 times.

110 Incubate:



	A	B	C	D
Table 5. Thermal Cycler Program for Adaptor Ligation				
Steps	Cycles	Temp (°C)	Time	
1	1	20	15 min	
2	-	4	Hold	

Lid Temp = 30°C, Total Volume = 47 µL

111 Add 1.5 µL USER Enzyme to each well.

112 Mix well by pipetting up and down at least 10 times.

113 Incubate:

	A	B	C	D
	Table 6. Thermal Cycler Program for USER			
	Steps	Cycles	Temp (°C)	Time
	1	1	37	15 min
	2	-	4	Hold
	Lid Temp = 47°C, Total Volume = 48 µL			

Lid Temp = 47°C, Total Volume = 48 µL

Library Construction: Cleanup (0.9X SPRI)

45m

114

**Note**

Libraries are cleaned up using **KAPA HyperPure** SPRI beads to remove enzymes and salts in preparation for indexing PCR.

- 115 Add 43 μ L Kapa HyperPure Beads to each well.
- 116 Mix well by pipetting up and down at least 10 times.
- 117 Incubate at room temperature for 5 minutes.
- 118 Place the plate on a magnet to capture the beads.
- 119 Incubate until the liquid is clear.
- 120 Carefully remove and discard the supernatant.
- 121 Keeping the plate on the magnet, add 200 μ L of 80% ethanol.
- 122 Incubate the plate on the magnet at room temperature for 30 seconds.
- 123 Carefully remove and discard the ethanol.
- 124 Keeping the plate on the magnet, add 200 μ L of 80% ethanol.
- 125 Incubate the plate on the magnet at room temperature for 30 seconds.



- 126 Carefully remove and discard the ethanol. Try to remove all residual ethanol without disturbing the beads.
- 127 Dry the beads at room temperature for 3-5 minutes, or until all of the ethanol has evaporated.
- 128 Remove the plate from the magnet.
- 129 Resuspend the beads in 12 μ L of elution buffer.
- 130 Incubate the plate at room temperature for 2 minutes.
- 131 Place the plate on a magnet to capture the beads.
- 132 Incubate until the liquid is clear.
- 133 Transfer the 10 μ L of clear supernatant to a new plate.

Library Construction: Indexing by PCR

1h

134

Note

The uniquely dual-indexed forward and reverse (i7 and i5) primer pairs are added to the adapter ligated DNA via PCR, this enables high throughput sample multiplexing. This step uses the **NEBNext Ultra II DNA Library Prep Kit for Illumina** and one of the sets of **NEBNext® Multiplex Oligos for Illumina® (96 Unique Dual Index Primer Pairs)**.

135 Add 12.5 μ L Q5 NEBNext Library PCR Master Mix to each well.

136 Add 2.5 μ L Index Primer Mix to each well.

137 Mix well by pipetting up and down at least 10 times.

138 Incubate:

	A	B	C	D
Table 7. Thermal Cycler Program for Indexing PCR				
Steps	Cycles	Temp (°C)	Time	
1	1	98	30 sec	
2	4	98	10 sec	
3		65	75 sec	
4	1	65	5 min	
5	-	4	Hold	

Lid Temp = 105°C, Total Volume = 25 µL

139 Add 22.5 µL Kapa HyperPure Beads to each well.

140 Mix well by pipetting up and down at least 10 times.

141 Incubate at room temperature for 5 minutes.

142 Place the plate on a magnet to capture the beads.

143 Incubate until the liquid is clear.

144 Carefully remove and discard the supernatant.

145 Keeping the plate on the magnet, add 200 µL of 80% ethanol.

- 146 Incubate the plate on the magnet at room temperature for 30 seconds.
- 147 Carefully remove and discard the ethanol.
- 148 Keeping the plate on the magnet, add 200 μ L of 80% ethanol.
- 149 Incubate the plate on the magnet at room temperature for 30 seconds.
- 150 Carefully remove and discard the ethanol. Try to remove all residual ethanol without disturbing the beads.
- 151 Dry the beads at room temperature for 3-5 minutes, or until all of the ethanol has evaporated.
- 152 Remove the plate from the magnet.
- 153 Resuspend the beads in 27 μ L of elution buffer.
- 154 Incubate the plate at room temperature for 2 minutes.
- 155 Place the plate on a magnet to capture the beads.
- 156 Incubate until the liquid is clear.
- 157 Transfer the 25 μ L of clear supernatant to a new plate. Libraries are ready for pooling and sequencing.

Library Pooling

- 158 Measure the library concentration by qPCR using the KAPA Illumina Library Quantification kit.



- 159 Pool samples, aiming for equimolar amounts of each. Negative control libraries may not yield enough material to be pooled in the same quantity as actual samples.

Sequencing and Analysis

- 160 Sequence the pool on an Illumina system using a kit that will yield ≥ 250 PE reads.
- 161 The resulting sequences can be used for various analyses, including estimation of variant and mutation abundance. The read lengths are sufficient for read merging and analysis of intact amplicons.

Our pipelines for mutation and variant abundance estimation rely on:

- viralrecon for processing and mutation abundance (<https://github.com/nf-core/viralrecon>),
- VLQ for variant abundance (<https://genomebiology.biomedcentral.com/articles/10.1186/s13059-022-02805-9> and https://github.com/baymlab/wastewater_analysis), and
- Freyja for variant abundance (<https://www.nature.com/articles/s41586-022-05049-6> and <https://github.com/andersen-lab/Freyja>).