

Jun 10, 2025 Version 1

Miniaturized and Automatized Whole-Genome Amplification of SARS-CoV 2 Virus using Illumina CovidSeq reagents for Next-Generation Sequencing V.1 V.1



DOI

dx.doi.org/10.17504/protocols.io.14egn3zpzl5d/v1

Quentin Semanas^{1,2}, christophe GINEVRA^{1,2}, Richard Chalvignac^{1,2}

¹Hospices Civils de Lyon; ²genEPII

GENEPII Sequencing Pla...



Quentin Semanas

Hospices Civils de Lyon, GenEPII

OPEN  ACCESS



DOI: dx.doi.org/10.17504/protocols.io.14egn3zpzl5d/v1

Protocol Citation: Quentin Semanas, christophe GINEVRA, Richard Chalvignac 2025. Miniaturized and Automatized Whole-Genome Amplification of SARS-CoV 2 Virus using Illumina CovidSeq reagents for Next-Generation Sequencing V.1. **protocols.io** <https://dx.doi.org/10.17504/protocols.io.14egn3zpzl5d/v1>

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 19, 2023

Last Modified: June 10, 2025

Protocol Integer ID: 85227



Abstract

Since December 2019, the rapid spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) around the world has necessitated to drastically scale-up the viral genomic surveillance to track the emergence of variant of concern. To scope with large-scale surveillance studies, various Next Generation Sequencing (NGS) methods have been reported and one of the main limitation has been the complexity of workflow in terms of turnaround time and cost effectiveness, limiting yield. By optimizing the ARTIC v4.1 sequencing strategy, we set-up automatization and miniaturization of SARS-CoV-2 whole genome sequencing protocol for monitoring emergence of new variants, applicable to a large workflow in a rapid and cost-effective manner.

Materials

 Illumina CovidSeq Assay **Illumina, Inc.**

 MGI Nucleic Acid Extraction Kit **MGI Tech Co Catalog #1000021043**

Abstract

- 1 Since December 2019, the rapid spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) worldwide has necessitated to drastically scale-up the viral genomic surveillance to track the emergence of variant of concern.

The limitations of NGS workflow for increasing the genomic surveillance includes the cost effectiveness and the lack of automation of the techniques used. By optimizing the ARTIC v4.1 sequencing strategy, we developed automatization and miniaturization of SARS-CoV-2 whole genome sequencing protocol for monitoring emergence of new variants, applicable to a large workflow in a rapid and cost-effective manner.

RNA extraction from nasopharyngeal swab was performed with the MGISP-960 workstation using MGI Easy Magnetic Beads Virus DNA/RNA Extraction Kit (MGI Tech, Marupe, Latvia).

The automatized and miniaturized method (Pre and Post PCR part) was performed with the Mosquito HV and Dragonfly® Discovery platforms (SPT Labtech, Melbourne, UK). Each reagent distribution being performed with the Dragonfly and each pipetting step with the Mosquito HV excepted for the last Library Clean Up part of the process.

- 2 This protocol is suitable for miniaturized and automatized CovidSeq Illumina protocol on 384 samples (SARS-CoV 2). All reagents used are parts of Illumina COVIDSeq Assay (RUO) Kit excepted Amplification Primers (IDT ARTIC V4.1), UDI Indexes (IDT Indexes Illumina compatible).

Nucleic acids extraction

3h

- 3 Clinical SARS-CoV2 positive samples were extracted using MGI Nucleic Acid Extraction Kit (Catalog #1000021043) on MGISP 960 following manufacturer recommendations. It will provide a workflow of up to 192 samples in 1 hour and 20 minutes resulting in four 96 well RNA plates in 2 hours and 40 minutes.

3h

Pre-PCR - Annealing - cDNA Synthesis - Amplification

5h

- 4 Pre-PCR was prepared using Illumina COVIDSeq Assay (RUO) kit with a miniaturized and automatized protocol using SPT Labtech automatons (Mosquito and Dragonfly).

Equipment

Mosquito HV

NAME

High Volume 16-Channel Robotic Liquid Handler

TYPE

SPT LabTech

BRAND

3097-01057

SKU

<https://www.sptlabtech.com/products/liquid-handling/mosquito-hv/>^{LINK}

Equipment

Dragonfly

NAME

Low volume liquid dispensing automaton

TYPE

SPT Labtech

BRAND

SU-0185

SKU

<https://www.sptlabtech.com/products/dragonfly/dragonfly-discovery/>^{LINK}

5 PRE-PCR ASSAY

Prepare following mixes for each steps of Pre-PCR part (Annealing, RT, Amplification). Volumes are edited for 384 samples including reagent overage required by SPT automatons.

Reagents	Volume for 384 samples (μL)
EPH3 HT	1500

Premix 1 - Annealing

Reagents	Volume for 384 samples (μL)
FSM HT	1890
RVT HT	210
TOTAL	2100

Premix 2 - RT

Reagents	Volume for 384 samples (μL)
IPM HT	3600
Primer Pool 1 or 2 (1/10)	1032
NUCLEASE FREE WATER	1128
TOTAL	5760

Premix 3 - Amplification (Do twice for each primer pool)

5.1 Annealing - Preparation

- Using Dragonfly, distribute 3.57μL of EPH3 per well of an "Annealing" Eppendorf LoBind 384 Well Plate.

 3.57 μL EPH3

5.2 RNA Extract Pool

- Using Mosquito HV 9mm, pool the four 96 Well RNA Plates into the "Annealing" Eppendorf LoBind 384 Well Plate.

 3.57 μL RNA **per Well**

5.3 Annealing

- Seal, briefly vortex the "Annealing" Eppendorf LoBind 384 Well Plate and centrifuge.
- Place the plate in a thermocycler and run the following program :




Temperature	Duration
65°C	5 min
4°C	Infinite


Annealing Program - Indicate 7 µL as volume and heat lid at 75°C.

5.4 RT-PCR - Preparation

- When the thermal cycler program RT displays 5 min remaining, engage *Premix 3 - RT* distribution using the Dragonfly into a new Eppendorf LoBind 384 Well Plate ("RT" Eppendorf LoBind 384 Well Plate).

 4.706 µL RT Premix ***per Well***

- When the thermal cycler program Annealing is done, briefly centrifuge the plate. Proceed to Mosquito HV 9mm transfer of Annealed RNA into the "RT" Eppendorf LoBind 384 Well Plate.

 5 µL Annealed RNA ***per Well***

5.5 RT-PCR

- Seal, briefly vortex the "RT" Eppendorf LoBind 384 Well Plate and centrifuge.
- Place the plate in a thermocycler and run the following program :

Temperature	Duration
25°C	5 min
50°C	10 min
80°C	5 min
4°C	Infinite

RT Program - Indicate 10 µL as volume and heat lid at 99°C.

5.6 Amplification - Preparation

- When the thermal cycler program RT displays 1 min remaining, engage *Premix 2 - Amplification* distribution for Primer Pool 1 and 2 using the Dragonfly into two new Eppendorf LoBind 384 Well Plate identifiante :



- "POOL 1" Eppendorf LoBind 384 Well Plate
- "POOL 2" Eppendorf LoBind 384 Well Plate.

 14 µL Amplification Premix ***per Well for Primer Pool 1 and 2***

- When the thermal cycler program RT is done, briefly centrifuge the plate.
- Proceed to Mosquito HV 9mm transfer of cDNA into the two Amplification Eppendorf LoBind 384 Well Plate.

 3.5 µL cDNA ***per Well for the two amplification plates***

5.7 Amplification

- Seal, briefly vortex the two Amplification Eppendorf LoBind 384 Well Plates and centrifuge.
- Place the plate in a thermocycler and run the following program :

Temperature	Duration	Cycles
98°C	3 min	-
98°C	15 sec	32
63°C	5 min	
4°C	Infinite	-

Amplification Program - Indicate 17.5 µL as volume and heat lid at 100°C.

Post-PCR - Library Preparation

3h

- 6 Sequencing library was prepared using Illumina COVIDSeq Assay (RUO) kit with a miniturized and automatized protocol using SPT Labtech automatons (Mosquito and Dragonfly).



Equipment

Mosquito HV

NAME

High Volume 16-Channel Robotic Liquid Handler

TYPE

SPT LabTech

BRAND

3097-01057

SKU

<https://www.sptlabtech.com/products/liquid-handling/mosquito-hv/>^{LINK}

Equipment

Dragonfly

NAME

Low volume liquid dispensing automaton

TYPE

SPT Labtech

BRAND

SU-0185

SKU

<https://www.sptlabtech.com/products/dragonfly/dragonfly-discovery/>^{LINK}

7 POST-PCR ASSAY

- Prepare following mixes for each steps of Post-PCR part (Tagmentation, Indexing PCR).

Volumes are edited for 384 samples including reagent overage required by SPT automatons.

- Washes and Tagmentation Stop steps reagents will be distributed directly into an new LVSD 384 well Plate using Dragonfly.

Reagents	Volume for 384 samples (µL)
ELBTs	160.4
TB1	481.3
NUCLEASE FREE WATER	802.1
TOTAL	1443.8

Premix 1 - Tagmentation

Reagents	Volume for 384 samples (µL)
EPM	1200
NUCLEASE FREE WATER	1200
TOTAL	2400

Premix 2 - Amplification / Indexing PCR

7.1 Amplification POOL 1 and POOL 2 Eppendorf LoBind 384 Well Plates Pool

- Following Amplification program, briefly centrifuge the two Amplification POOL 1 and POOL 2 Eppendorf LoBind 384 Well Plates and place them on Mosquito HV 4.5mm board in order to proceed to Pool step :
- Identify a new Eppendorf LoBind 384 Well Plates as " Library Pool Plate" and place it on Moquito HV 4.5mm board with the two Amplification Eppendorf LoBind 384 Well Plates.
- Proceed to transfer :

 5 µL from each Pool plates (POOL 1 and 2) **into the *Library Pool Plate***

- It will result of **10µL POOL 1/2 per well for 384 samples.**

7.2 Tagmentation

- Prepare two different new plates for mix distribution :
 1. Eppendorf LoBind 384 Well Plates labelled "**Tagmentation Plate**"
 2. LVSD 384 well Plate labelled "**Reagent / Trash Plate**" (Half of this plate will be used for distribution of TWB and ST2 reagents; the other half will be used as trash for

washes steps)

- Using Dragonfly, proceed to :

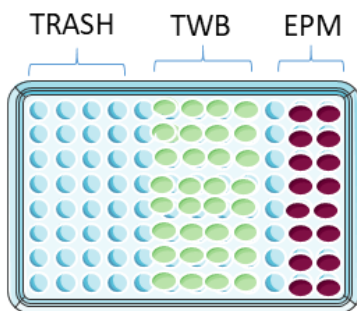
1- Premix 1 distribution on **"Tagmentation Plate"**

🧪 3 μ L of ELBTs per well

2- Premix 2 distribution on **"Reagent / Trash Plate"** organized as follow :

🧪 50 μ L per well for TWB **on green columns**

🧪 40 μ L per well for EPM **on red columns**



LVSD 384 Well Plate

"Reagent / Trash Plate" Organization

When distribution is done, place Plates on Mosquito HV 4.5mm board and proceed to transfer of Amplicons from "Library Pool Plate" to the "Tagmentation Plate".

🧪 2 μ L of SARS-CoV2 amplicons **into *Tagmentation Plate***

7.3 **Tagmentation incubation / Stop**

- When Mosquito tranfer is done, directly proceed to Tagmentation step.
- Place the plate in a thermocycler and run the following program :

Temperature	Duration
55°C	5 min

5m






Temperature	Duration
10°C	Infinite

Tagmentation Program - Indicate 5 µL as volume and heat lid at 80°C - Proceed to thermal cycler pre heat before to launch.

- When Tagmentation is done, directly proceed to Stop step using Dragonfly :

 1 µL of ST2 per well **directly into the Tagmentation Plate**

- Seal, briefly vortex and centrifuge the plate. Incubate :

 00:05:00 Room Temperature

7.4 Post Tagmentation Clean Up

2m

- When Tagmentation is stopped, proceed to washes steps using Mosquito :
- Place "Tagmentation Plate" on Mosquito 384 Magnetic Block
- Incubate 384 Magnetic Block

 00:02:00 384 Magnetic Block

- Remove supernatant and transfer it to "Reagent / Trash Plate"

 4 µL removed from "Tagmentation Plate" and transfer to "Reagent / Trash Plate"

- Add TWB in each well of the "Tagmentation Plate"

 5 µL of TWB into "Tagmentation Plate"

- Seal the plate, vortex and briefly centrifuge.
- **Proceed to Wash Step once again until last supernatant removing**

7.5 Amplify and Index Tagmented Amplicons

When washes steps are done :

- Removed supernatant
- Proceed to Mosquito transfer of Premix 2 (EPM) AND indexes :

🧪 4 μL of Premix 2 into "Tagmentation Plate"

🧪 1 μL of Indexes into "Tagmentation Plate"

- Seal, briefly vortex and centrifuge the plate.
- Place the plate in a thermocycler and run the following program :

Temperature	Duration	Cycles
72°C	3 min	-
98°C	3 min	-
98°C	20 sec	7
60°C	30 sec	
72°C	1 min	
72°C	3 min	-
10°C	Infinite	-

Amplification / Indexing Program - Indicate 7 μL as volume and heat lid at 100°C.

7.6 Library Pool and Manual Clean Up

7m

- When Amplification/Indexing Program is done, proceed to Pool of the 384 wells of "Tagmentation Plate" into a new Eppendorf LoBind 384 Well Plate labelled "Library Pool Plate" :

🧪 1 μL of the 384 wells into **one column** of the new "Library Pool Plate"

- Pool **12 μL of the 16 wells** of the "Library Pool Plate" column into one Eppendorf LoBind 1.5mL Tube. It will result of a final volume :

🧪 192 μL Pool Library


- Proceed to Manual Clean Up using Illumina Tune Beads (ITB) at 0.9x. Add :

🧪 172.8 μL of ITB into the Eppendorf LoBind 1.5mL containing the 192 μL Final Pool.

Be careful to hardly vortex ITB before use.

- Vortex to mix and incubate :




 00:05:00 at Room Temperature

- Centrifuge briefly and place the Tube on magnetic stand until liquid is clear.
- Remove supernatant and proceed to two EtOH 80% washes steps (30 sec contact, remove supernatant X2)
- Let beads dry 1min after last supernatant removing
- Add RSB to proceed to Elution :

 55 μ L of RSB

- Vortex and centrifuge briefly. Incubate :

 00:02:00 at Room Temperature

- Place the Tube on magnetic stand until liquid is clear.
- Transfer 50 μ L of supernatant into a new Eppendorf LoBind 1.5mL labelled "Final Library Pool"

Store on ice or at +4°C until Quantification Process following Illumina COVIDSeq Assay (RUO) Kit recommendations.

Protocol references

https://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/Illumina-COVIDSeq-Test/illumina-covidseq-ruo-kits-reference-guide-1000000126053-08.pdf