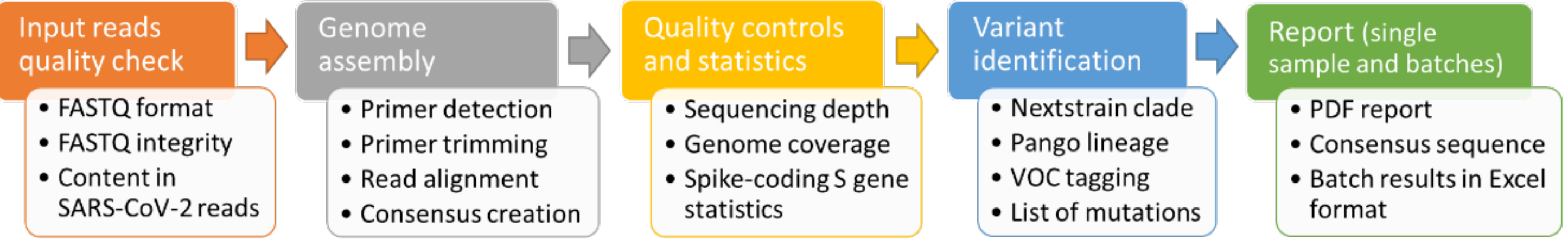


(a)



(b)

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UploadSample analysis

QC	Sample ID	Nextstrain clade	Pango lineage	Spike mutations	Coverage	Other mutations
✓	Sample40	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	99.55 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...
✓	Sample39	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	99.51 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...
✓	Sample38	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	99.72 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...
✓	Sample37	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	98.62 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...
✓	Sample35	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	99.67 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...
✓	Sample34	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	99.58 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...
✓	Sample33	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	99.59 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...
✓	Sample32	21L (Omicron) VOC	BA.2 VOC	T19I, L24-, P25-, P26-, A27S, G...	98.72 %	E:T9I, M:Q19E, M:A63T, N:P13L, N:E...

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(c)

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Sample Analysis Report

Sample ID: Sample25

Status: Valid sample for SARS-CoV-2 variant identification and good quality genome.

RESULTS

SARS-COV-2 variant:

Nextstrain clade	21K (Omicron) VOC
Pango lineage	BA.1 VOC

Variant of concern detected

SARS-COV-2 Spike mutations (amino acid changes):

A67V
H69-
V70-
T95I
G142-
V143-
Y144-
Y145D
N211-
L212I
G339D
S371L
S373P
S375F
K417N
N440K
G446S
S477N

SAMPLE DATA

Sequencing:

Technology	Illumina (paired-end)
Uploaded files	BS11001_S25_L001_R1_001.fastq.gz BS11001_S25_L001_R2_001.fastq.gz
Number of reads	929970
Number of sequenced base pairs	60.93 Mb

Genome:

Quality	Good
File name	Sample25.consensus.fa
Length	29871 bp
Coverage	99.84%
Sequencing depth	1755.40 x (downsampled)
Number of ACGT bases	29858

S gene (Spike)

Percent of ACGT bases	100.0 %
Number of N bases	0
Longest stretch of N bases	0

Mutations in other genes:

Gene	Mutation
E	T9I
M	D3G
M	Q19E
M	A63T
N	P13L
N	E31-
N	R32-
N	S33-
N	R203K
N	G204R
ORF1a	K856R
ORF1a	S2083-
ORF1a	L2084I
ORF1a	A2710T
ORF1a	T3255I
ORF1a	P3395H

METHODS

EPISEQ[®] SARS-COV-2 release 1.1.0

Pipeline version 2022-07-08

Reference genome and third-party tool versions

Reference genome for assembly	MN908947.3
pangolin	4.1.1
pangoLEARN	1.11
Nextclade	nextclade 2.2.0

APPENDIX

Variant of Concern (VOC)

If a VOC is detected in the sample, it is highlighted in the result table, page 1. The definition of the VOC is based on:

the CDC: <https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html>

the WHO: <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>

Pango lineage	Nextstrain clade	WHO label	First Detected	Earliest sample date
B.1.1.7 / Q*	20I (Alpha, V1)	Alpha	United Kingdom	September 2020
B.1.351*	20H (Beta, V2)	Beta	South Africa	May 2020
P.1*	20J (Gamma, V3)	Gamma	Brazil	November 2020
B.1.617.2 / AY*	21A (Delta)	Delta	India	October 2020
B.1.617.2 / AY*	21I (Delta)	Delta	India	October 2020
B.1.617.2 / AY*	21J (Delta)	Delta	India	October 2020
B.1.1.529 / BA*	21K (Omicron)	Omicron	Multiple Countries	November 2021
B.1.1.529 / BA*	21L (Omicron)	Omicron	Multiple Countries	November 2021
B.1.1.529 / BA*	21M (Omicron)	Omicron	Multiple Countries	November 2021
B.1.1.529 / BA*	22A (Omicron)	Omicron	Multiple Countries	November 2021
B.1.1.529 / BA*	22B (Omicron)	Omicron	Multiple Countries	November 2021
B.1.1.529 / BA*	22C (Omicron)	Omicron	Multiple Countries	November 2021

*Includes all descendent lineages.

Figure S1: Description of EPISEQ SARS-COV-2 pipeline workflow (a), result display (b) and sample report (c)