DATA SHEET

Illumina COVIDSeq™ Assay (96 samples)

- Streamlined, integrated workflow for SARS-CoV-2 sequencing and characterization
- Uniform coverage across the SARS-CoV-2 genome for accurate detection of sequence variants
- Low- to mid-throughput assay that supports a low number of samples sequenced on benchtop instruments

illumina®

Introduction

As the COVID-19 pandemic continues to rage across the world,[1] variants, including Alpha B117, Beta, Delta, Gamma, and Omicron, continue to emerge. These and possibly other new SARS-CoV-2 strains have the potential to be more contagious or serious, raising concerns about public health efforts, certain diagnostic tests, and vaccines developed to combat the pandemic.[2] This highlights the need for genomic surveillance to identify and monitor new SARS-CoV-2 variants. The Illumina COVIDSeq Assay (96 samples) is a low- to mid-throughput amplicon-based next-generation sequencing (NGS) assay that enables labs to identify and track the emergence and prevalence of new SARS-CoV-2 variants and lineages.

Illumina COVIDSeq workflow

Illumina COVIDSeq Assay (96 samples) is part of a streamlined, integrated workflow that spans isolation of genetic material through sequencing and data analysis for detection and characterization of SARS-CoV-2 (Figure 1).

Library preparation

Illumina COVIDSeq Assay (96 samples) kit includes all reagents necessary for cDNA conversion, amplification, and library preparation. The kit includes the ARTIC v3 primer pool, based on the validated, publicly available ARTIC multiplex PCR protocol, to detect and characterize SARS-CoV-2 RNA. A modified, optimized ARTIC v4 primer pool that improves viral genome coverage and variant calling and is available as an accessory product.

Sequencing

Prepared libraries can be sequenced on any Illumina sequencing system; however, the low-throughput configuration of Illumina COVIDSeq Assay (96 samples) makes it ideal for benchtop platforms, including the iSeq™ 100, MiniSeq™, MiSeq™, NextSeq™ 550, NextSeq 1000, and NextSeq 2000 Systems. Read lengths of 2 × 101 bp and 2 × 151 bp are recommended.

Data analysis

The Illumina DRAGEN™ COVID Lineage App is freely available in BaseSpace™ Sequence Hub. The easy-to-use app performs SARS-CoV-2 detection, aligns reads to a reference genome, calls variants, and generates a consensus genome sequence. In conjunction with Pangolin and NextClade, the Dragen COVID Lineage App also provides lineage and clade calls needed for most surveillance applications.

Uniform SARS-CoV-2 genome coverage

The Illumina COVIDSeq Assay (96 samples) provides uniform coverage across the SARS-CoV-2 genome, particularly in the spike protein locus, a critical region of the SARS-CoV-2 genome[3-5] (Figure 2). For labs that need to perform detailed SARS-CoV-2 sequencing, the ARTIC v4 primer pool delivers improved coverage in the spike protein locus for in-depth characterization of new variants (Figure 2).

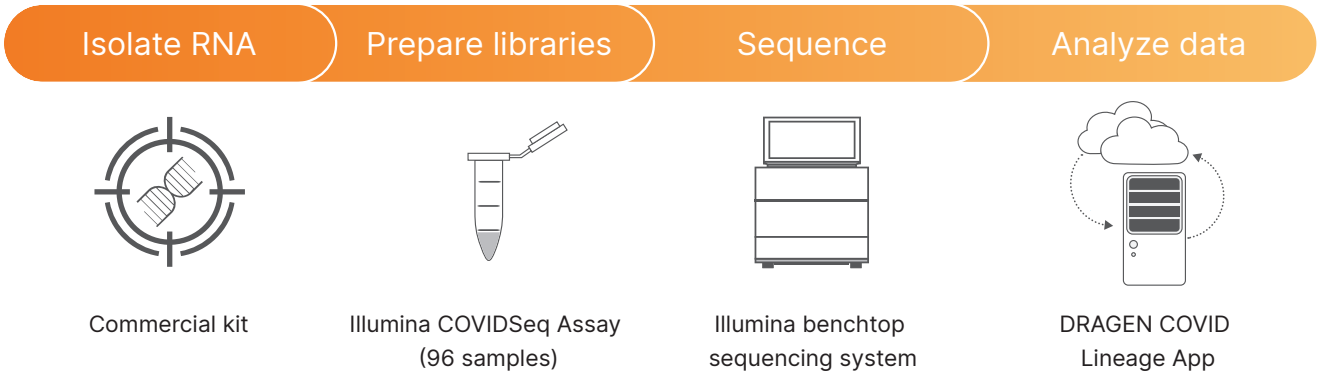

Figure 1: Illumina COVIDSeq workflow—In a streamlined, comprehensive workflow, SARS-CoV-2 libraries are prepared using the Illumina COVIDSeq Assay (96 samples), sequenced on any Illumina benchtop sequencing system, and analyzed in the DRAGEN COVID Lineage App for viral detection, variant calling, and strain typing.

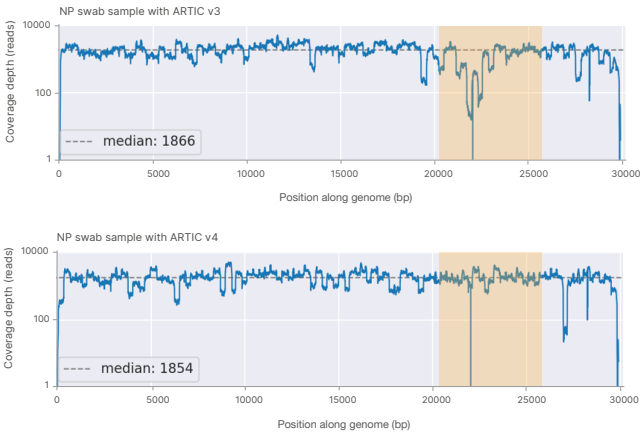

Figure 2: Uniform genome coverage in B.1.617.2 (Delta) variant SARS-CoV-2—Illumina COVIDSeq Assay (96 samples) provides uniform viral genome coverage across the spike protein locus (highlighted region) with ARTIC v3 (top) and ARTIC v4 (bottom) primer pools. The ARTIC v3 pool includes primers for 11 human control genes; the ARTIC v4 pool does not. Note, sharp coverage drop seen with both primer pools at ~22K bp is not a dropout but a true six-base deletion.

Summary

The emergence and spread of new SARS-CoV-2 variants during the COVID-19 pandemic highlights the need for sequencing-based viral surveillance. Illumina COVIDSeq Assay (96 samples) accommodates small sample batch sizes to enable decentralized surveillance for the emergence and prevalence of new SARS-CoV-2 variants and lineages.

Learn more

Illumina COVIDSeq Assay (96 samples), illumina.com/products/by-type/clinical-research-products/covidseq-assay.html

Improved performance using the Illumina COVIDSeq Assay (96 samples) technical note, illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/illumina-covidseq-tech-note-m-gl-00408/illumina-covidseq-tech-note-m-gl-00408.pdf

Ordering information

Product	Catalog no.
COVIDSeq Assay (96 samples) index 1	20049393
COVIDSeq Assay (96 samples) index 2	20051772
Accessory product	
COVIDSeq Positive Control (96 reactions)	20051775
Illumina COVIDSeq v4 Primer Pools, 384 Samples RUO	20065135

References

1. World Health Organization. WHO Director-General's statement on IHR Emergency Committee on Novel Coronavirus (2019-nCoV). 30 January 2020.
2. Baric, RS. Emergence of a highly fit SARS-CoV-2 variant. *N Engl J Med*. 2020;383:2684–2686.
3. McCarthy KR, Rennick LJ, Nambulli S, et al. Recurrent deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape. *Science*. 2021; doi:10.1126/science.abf6950.
4. Addetia A, Xie H, Roychoudhury P, et al. Identification of multiple large deletions in ORF7a resulting in in-frame gene fusions in clinical SARS-CoV-2 isolates. *J Clin Virol*. 2020; 129:104523.
5. Rosenthal SH, Kagan RM, Gerasimova A, et al. Identification of eight SARS-CoV-2 ORF7a deletion variants in 2,726 clinical specimens. *bioRxiv*. 2020; doi.org/10.1101/2020.12.10.418855.

illumina®

1.800.809.4566 toll-free (US) | +1.858.202.4566 tel
techsupport@illumina.com | www.illumina.com

M-GL-00243 v1.0