

Illumina Microbial Amplicon Prep

Versatile library preparation solution for public health surveillance and microbiology research

- Supports user-designed primers to sequence pathogens of public health concern
- Enables high-quality genome-wide coverage across multiple microbial species
- Accommodates DNA and RNA inputs from a range of sample sources and types



Introduction

The COVID-19 pandemic underscored the importance of having effective viral surveillance systems in place to identify, monitor, and control disease outbreaks. Population-scale genomic surveillance of endemic and newly emerging infectious diseases, including those caused by SARS-CoV-2,¹⁻³ Zika,^{4,5} Ebola,⁶ and M pox⁷ (formerly Monkeypox) viruses, is now possible as a result of next-generation sequencing (NGS) technology.

The Illumina Microbial Amplicon Prep kit is a low- to mid-throughput sequencing-based assay that expands the discovery power of microbiology and infectious disease research. With this kit, which leverages the proven Illumina COVIDSeq™ Assay workflow, researchers can use lab-designed or commercially available primers for targeted sequencing of viruses and select regions from various larger microbial species, including bacteria or parasites. This versatile library preparation solution supports a broad range of public health research applications, including tracking pathogens over time and geographies, detecting variants, classifying pathogen strains, identifying microbial resistance markers, and more.

Excellent performance across microbial species

Illumina Microbial Amplicon Prep can be combined with well-designed primers to provide sequence coverage across viral genomes, including both RNA and DNA viruses (Figure 1). This kit enables targeted sequencing of either whole genomes or select regions of viruses, depending on the application. For microbial species with larger genomes, primers against select regions may be used.

Illumina Microbial Amplicon Prep can be used with RNA or DNA extracted from a variety of sources such as microbial cultures, nasopharyngeal swabs, skin swabs, nasal swabs, wastewater samples, and others. Using high-quality input DNA or RNA, with additional cleanup and purification steps after extraction, is recommended for successful library preparation.

Streamlined workflow

Illumina Microbial Amplicon Prep is a highly multiplexed PCR-based library preparation solution for use with microbial targets. This kit is based on the robust Illumina COVIDSeq Assay workflow, spanning isolation of genetic material through sequencing and data analysis for detection and characterization of microbial species (Figure 2).

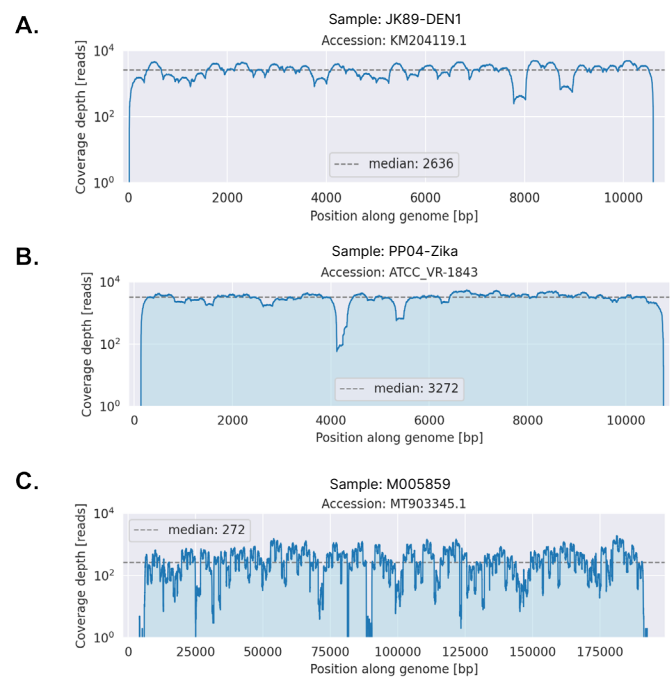


Figure 1: Genome-wide coverage for RNA and DNA viruses— Illumina Microbial Amplicon Prep provides genome coverage exceeding 95% for (A) Dengue and (B) Zika RNA viruses. (C) Coverage plot for M pox virus demonstrates compatibility with DNA viruses.

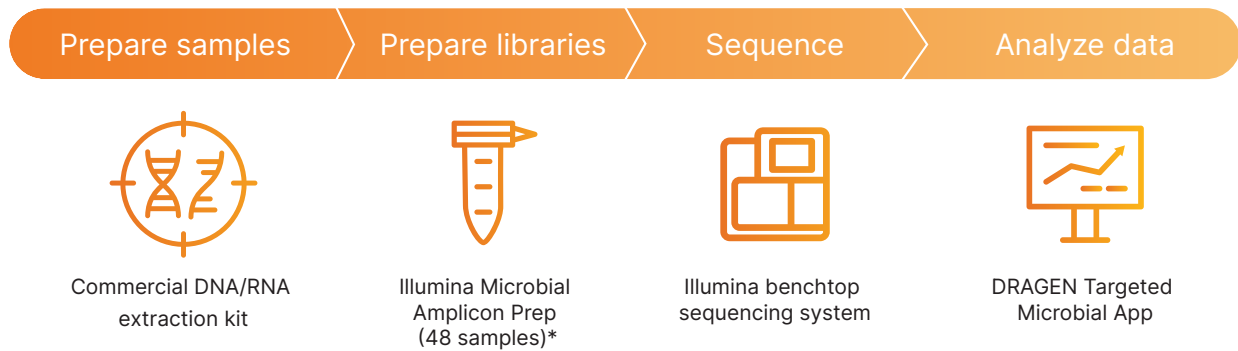


Figure 2: Illumina Microbial Amplicon Prep workflow— In a streamlined workflow, microbial libraries are prepared using the Illumina Microbial Amplicon Prep kit, sequenced on any Illumina benchtop sequencing system, and analyzed in the DRAGEN Targeted Microbial App for detection, variant calling, and strain typing. *Kit includes indexes for library preparation. Primer oligos are purchased separately.

Library preparation

Illumina Microbial Amplicon Prep kit includes reagents necessary for cDNA conversion, amplification, and library preparation. The kit is compatible with lab-designed primers or commercially available primer sets, which are purchased separately. Amplicon lengths of 400 base pairs are recommended, but longer amplicons may be necessary with some targets.

Sequencing

Prepared libraries can be sequenced on any Illumina sequencing system; however, the low-throughput configuration of Illumina Microbial Amplicon Prep makes it ideal for benchtop platforms, including the iSeq™ 100, MiniSeq™, MiSeq™, NextSeq™ 500, 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™ Targeted Microbial App is freely available in BaseSpace™ Sequence Hub. The easy-to-use app aligns reads to reference genomes, calls variants, and generates a consensus genome sequence representing the population of nucleic acid species in the sample (Figure 3). When available, external curated databases are accessed for additional lineage analysis.

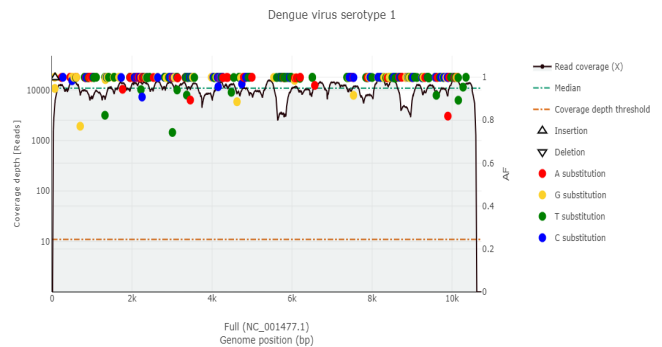


Figure 3: Coverage plot of the Dengue virus genome generated using the Illumina DRAGEN Targeted Microbial App—The coverage plot output from the DRAGEN Targeted Microbial App is interactive, with the ability to toggle between log-scale, include or exclude the median coverage lines, and/or the substitution/deletion information. Each circle represents a SNP that varies from the reference genome. Each color indicates whether it is an A, G, T, or C substitution. Insertions and deletions are also indicated by triangles. The coverage plot shows a single genome consensus mapped to the best hit from the reference database (NC_001477.1). Interactive plots can be downloaded as PNG files as shown above.

Summary

The Illumina Microbial Amplicon Prep kit empowers public health researchers to protect the health of their communities by providing an integrated solution for microbial library preparation. This flexible assay is compatible with user-designed primers and supports RNA or DNA inputs extracted from a broad range of sample sources. Integration with innovative NGS platforms delivers exceptional data quality, flexibility, and scalability for highly effective public health surveillance.

Learn more

[Illumina Microbial Amplicon Prep](#)

[Microbial genomics](#)

Ordering information

Product	Catalog no.
Illumina Microbial Amplicon Prep (48 samples)	20097857

References

1. Chen Z, Azman AS, Chen X, et al. [Global landscape of SARS-CoV-2 genomic surveillance and data sharing.](#) *Nat Genet.* 2022;54(4):499-507. doi:10.1038/s41588-022-01033-y
2. Hodcroft EB, Zuber M, Nadeau S, et al. [Spread of a SARS-CoV-2 variant through Europe in the summer of 2020.](#) *Nature.* 2021;595(7869):707-712. doi:10.1038/s41586-021-03677-y
3. Wilkinson E, Giovanetti M, Tegally H, et al. [A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa.](#) *Science.* 2021;374(6566):423-431. doi:10.1126/science.abj4336
4. Faria NR, Sabino EC, Nunes MRT, Alcantara LCJ, Loman NJ, Pybus OG. [Mobile real-time surveillance of Zika virus in Brazil.](#) *Genome Med.* 2016;8(1):97. doi:10.1186/s13073-016-0356-2
5. Giovanetti M, Faria NR, Lourenço J, et al. [Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region.](#) *Cell Rep.* 2020;30(7):2275-2283.e7. doi:10.1016/j.celrep.2020.01.085
6. Gire SK, Goba A, Andersen KG, et al. [Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak.](#) *Science.* 2014;345(6202):1369-1372. doi:10.1126/science.1259657
7. Tiwari A, Adhikari S, Kaya D, et al. [Monkeypox outbreak: Wastewater and environmental surveillance perspective.](#) *Sci Total Environ.* 2023;856(Pt 2):159166. doi:10.1016/j.scitotenv.2022.159166



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

© 2023 Illumina, Inc. All rights reserved. All trademarks are the property of Illumina, Inc. or their respective owners. For specific trademark information, see www.illumina.com/company/legal.html.
 M-GL-01788 v1.1