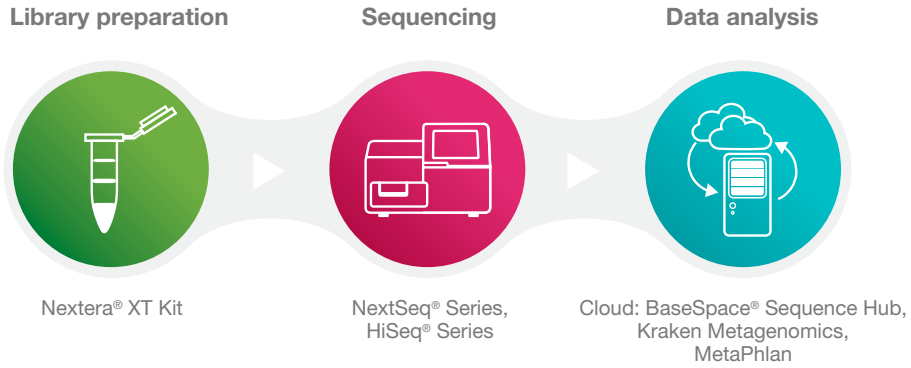
illumina®

# Illumina virology solutions

Detect low-frequency variants and subtypes within a viral population with Illumina next-generation sequencing (NGS) solutions for virology. With NGS, you can see a more complete picture not only of viruses and host interaction, but also other phages specific to microbes.

Determine the source of infection, route of transmission, and molecular pathway. Perform drug resistance testing, molecular epidemiology of viral pathogens, vaccine development, viral-host transcriptome interactions, viral surveillance, quality control/ contamination of biologics, and virus discovery with our comprehensive solutions.

## Workflow




# Bioinformatics solutions

BaseSpace® Sequencing Hub is the Illumina cloud-based genomics computing environment for NGS data management and analysis. Access BaseSpace Hub via the intuitive web-based interface or linux-based command line tool for simple data storage and sharing.

### Targeted Re-sequencing

Genotyping software which is an integrated sequencing solutions for HIV, HCV and HBV drug resistance determination.

### Whole RNA-Seq

Kraken software is aligning k-mers and then classifying with a bacterial, archaeal, and viral database

## Recent virology articles using Illumina MiSeq technology:


da Silva F. R., Cibulski S. P., Daudt C., Weber M. N., Guimaraes L. L., et al. (2016) Novel Bovine Papillomavirus Type Discovered by Rolling-Circle Amplification Coupled with Next-Generation Sequencing. PLoS One 11: e0162345

El-Shamy A., Pendleton M., Eng F. J., Doyle E. H., Bashir A., et al. (2016) Impact of HCV core gene quasispecies on hepatocellular carcinoma risk among HALT-C trial patients. Sci Rep 6: 27025

Kok Y. L., Vongrad V., Shilaih M., Di Giallonardo F., Kuster H., et al. (2016) Monocyte-derived macrophages exhibit distinct and more restricted HIV-1 integration site repertoire than CD4(+) T cells. Sci Rep 6: 24157

Lee H. K., Lee C. K., Tang J. W., Loh T. P. and Koay E. S. (2016) Contamination-controlled high-throughput whole genome sequencing for influenza A viruses using the MiSeq sequencer. Sci Rep 6: 33318

Li Y., Wang H., Nie K., Zhang C., Zhang Y., et al. (2016) VIP: an integrated pipeline for metagenomics of virus identification and discovery. Sci Rep 6: 23774

Russier M., Yang G., Rehg J. E., Wong S. S., Mostafa H. H., et al. (2016) Molecular requirements for a pandemic influenza virus: An acid-stable hemagglutinin protein. Proc Natl Acad Sci U S A 113: 1636-1641

Schobel S. A., Stucker K. M., Moore M. L., Anderson L. J., Larkin E. K., et al. (2016) Respiratory Syncytial Virus whole-genome sequencing identifies convergent evolution of sequence duplication in the C-terminus of the G gene. Sci Rep 6: 26311

Stewart H., Bingham R. J., White S. J., Dykeman E. C., Zothner C., et al. (2016) Identification of novel RNA secondary structures within the hepatitis C virus genome reveals a cooperative involvement in genome packaging. Sci Rep 6: 22952

van Diemen F. R., Kruse E. M., Hooykaas M. J., Bruggeling C. E., Schurch A. C., et al. (2016) CRISPR/Cas9-Mediated Genome Editing of Herpesviruses Limits Productive and Latent Infections. PLoS Pathog 12: e1005701

Wang Z., Pan Q., Gendron P., Zhu W., Guo F., et al. (2016) CRISPR/Cas9-Derived Mutations Both Inhibit HIV-1 Replication and Accelerate Viral Escape. Cell Rep 15: 481-489

Xu Y., Bailey E., Spackman E., Li T., Wang H., et al. (2016) Limited Antigenic Diversity in Contemporary H7 Avian-Origin Influenza A Viruses from North America. Sci Rep 6: 20688

Zhao J., Liu J., Vemula S. V., Lin C., Tan J., et al. (2016) Sensitive Detection and Simultaneous Discrimination of Influenza A and B Viruses in Nasopharyngeal Swabs in a Single Assay Using Next-Generation Sequencing-Based Diagnostics. PLoS One 11: e0163175

Dedkov V. G., Lukashev A. N., Deviatkin A. A., Kuleshov K. V., Safonova M. V., et al. (2016) Retrospective diagnosis of two rabies cases in humans by high throughput sequencing. J Clin Virol 78: 74-81

Kolehmainen P., Siponen A., Smura T., Kallio-Kokko H., Vapalahti O., et al. (2017) Intertypic recombination of human parechovirus 4 isolated from infants with sepsis-like disease. J Clin Virol 88: 1-7

McGinnis J., Laplante J., Shudt M. and George K. S. (2016) Next generation sequencing for whole genome analysis and surveillance of influenza A viruses. J Clin Virol 79: 44-50

Parker J. and Chen J. (2017) Application of next generation sequencing for the detection of human viral pathogens in clinical specimens. J Clin Virol 86: 20-26

Sato M., Kuroda M., Kasai M., Matsui H., Fukuyama T., et al. (2016) Acute encephalopathy in an immunocompromised boy with astrovirus-MLB1 infection detected by next generation sequencing. J Clin Viro


Explore the exciting discoveries our NGS solutions are enabling.
Visit www.illumina.com/MicroStories and www.illumina.com/MicroWebinars.

www.illumina.com

illumina®