Infectious Disease Portfolio:
Global Challenges & Illumina Solutions

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OUR MISSION

Improve human health by unlocking the power of the genome

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Whom we serve

KEY MARKETS

Reproductive health

Genetic disease

Oncology

Research / Applied genomics

Infectious disease

Drug discovery

Multiomics

CUSTOMERS

Universities and academic research centers

Pharmaceutical companies

Genome centers

Biotechnology companies

Hospitals

Consumer genetics companies

Government agencies

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The sequencing workflow

1. Library preparation

A sequencing library contains the DNA of interest to the experiment.

Adapters are added to both ends of the molecules to uniquely identify them.

Many libraries may be pooled together for a single sequencing run.

2. Cluster growth/generation

Libraries are loaded into a flow cell, a glass slide where sequencing chemistry occurs.

Each DNA fragment is amplified into distinct clonal clusters through bridge amplification.

3. Sequencing

Fluorescently labeled nucleotides are incorporated with complementary DNA bases of interest.

The instrument excites the fluorescent labels and captures an image of the flow cell, allowing identification.

4. Data analysis

Primary analysis, on the instrument, converts the images into base calls.

Secondary analysis generates alignments and variant detection.

Tertiary analysis allows for annotation, filtering, and interpretation.

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More than 21,000 systems installed around the world*

Our sequencing and array instruments

High-throughput			Mid-throughput		
NovaSeq™ X / NovaSeq™ X Plus	NovaSeq™ 6000	iScan™ System	NextSeq™ 1000 / NextSeq™ 2000	NextSeq™ 550	NextSeq™ 500

Low-throughput			IVD instruments		
iSeq™ 100	MiniSeq™	MiSeq™	NovaSeq™ 6000Dx†	NextSeq™ 550Dx†	MiSeq™Dx†

*Net installed base as of fiscal year 2023

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Sequencing systems and key applications overview

		Large whole-genome sequencing (WGS) (human, plant, animal)	Small WGS (microbe, virus)	Exome sequencing	Targeted gene sequencing	Whole-transcriptome sequencing	Gene expression profiling with mRNA-Seq	Targeted gene expression profiling
High-throughput	**NovaSeq X / NovaSeq X Plus** • Our most powerful sequencer, equipped with XLEAP-SBS chemistry	■	■	■	■	■	■	
	NovaSeq 6000 • Scalable throughput for broad, deep sequencing	■	■	■	■	■	■	
Mid-throughput	**NextSeq 1000/2000** • Flexibility, affordability, and scalability	■	■	■	■	■	■	
	NextSeq 500/550 • Tunable output with sequencing and array capabilities		■	■	■	■	■	
Low-throughput	**MiSeq** • Our first benchtop sequencer		■		■			■
	MiniSeq • < 1 day turnaround time		■		■			■
	iSeq 100 • Our most affordable sequencer		■		■			■

Note: Only key applications are highlighted, which does not reflect each system's entire set of capabilities.

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Global Challenges in Infectious Disease

Outbreak, Pandemic, Epidemic Disease Management

Spread of Antimicrobial Resistance 'AMR'

Diagnostic for Patient Management

Many new factors contribute to an increase in the transmissibility and severity of infectious diseases

Increased threat due to multi-drug resistant organisms through the environment

Access to low cost, accurate IVD's is still a major challenge in many under-developed countries

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Infectious Diseases by the Numbers

770M — Cumulative cases of **COVID-19**[1]

400K — Respiratory deaths each year caused by **influenza virus**[2]

10.6M — People that fell ill from **tuberculosis** in 2021[3]

39M — People living with **HIV** in 2022[4]

3.8% — Global GDP lost due to **antimicrobial resistance** by 2050[5]

247M — **Malaria** cases in 84 malaria-endemic countries in 2021[3]

1.5M — New **hepatitis B** infections globally in 2019[3]

$28-45B — Direct annual cost of treating **healthcare associated infections** in the US[6]

1. https://covid19.who.int/ (Accessed Sept. 7, 2023); 2. https://ourworldindata.org/influenza; 3. World health statistics 2023: monitoring health for the SDGs, Sustainable Development Goals. Geneva: World Health Organization; 2023.; 4. https://www.unaids.org/en/resources/fact-sheet; 5. Global antimicrobial resistance and use surveillance system (GLASS) report 2022. Geneva: World Health Organization; 2022.; 6. Gidey K, et al. Clinical and economic burden of healthcare-associated infections: A prospective cohort study. PLoS One. 2023 Feb 23;18(2):e0282141.

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Infectious diseases impact human health and economics

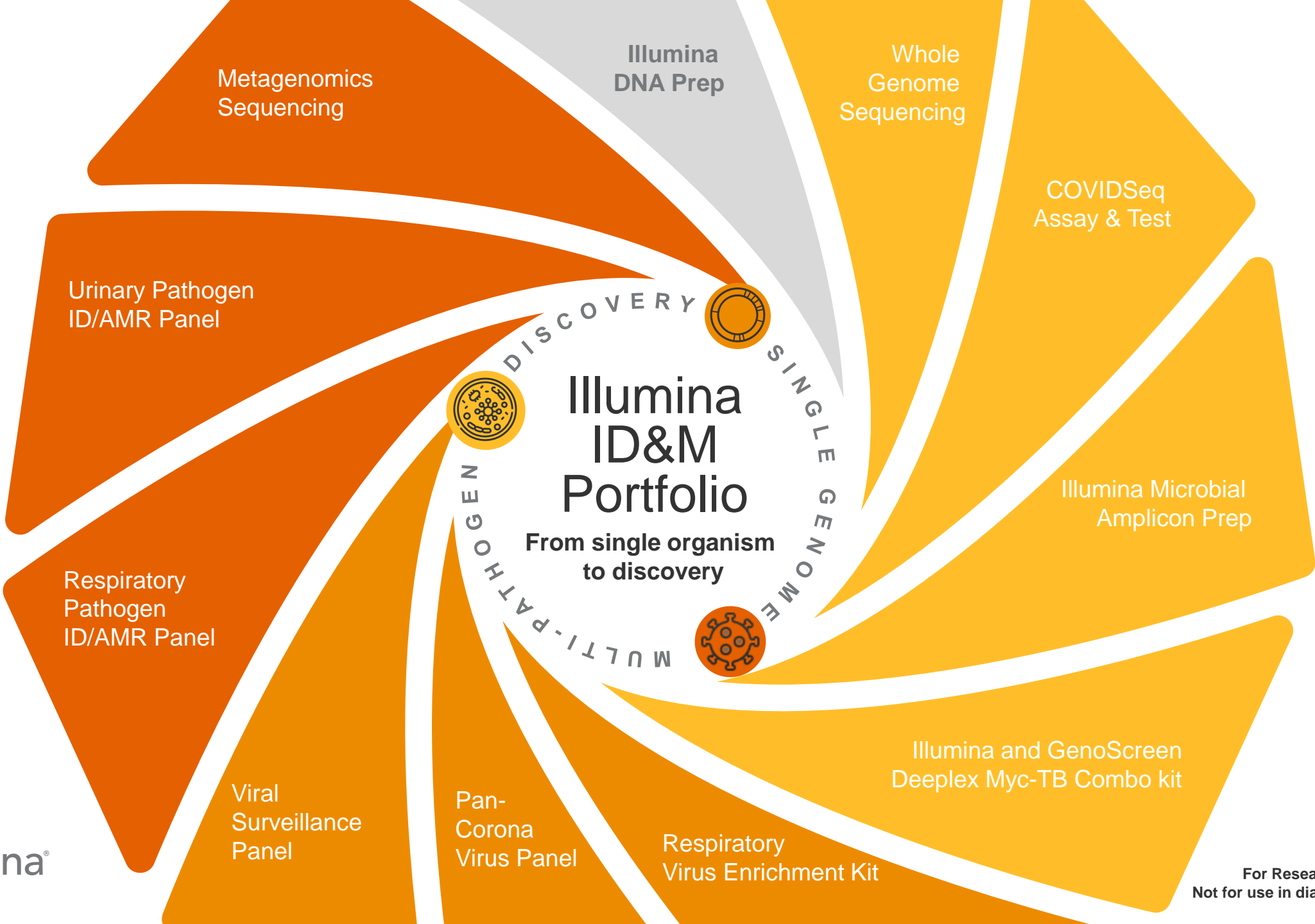# Illumina technologies – a unique advantage against infectious diseases

Flexible and scalable solutions to enable accessibility worldwide

- ✓ Novel pathogen ID and drug resistance characterization
- ✓ Insights for clinical assay development
- ✓ Pathogen monitoring and genomic surveillance
- ✓ Host genetics and immune response
- ✓ Drug and vaccine development
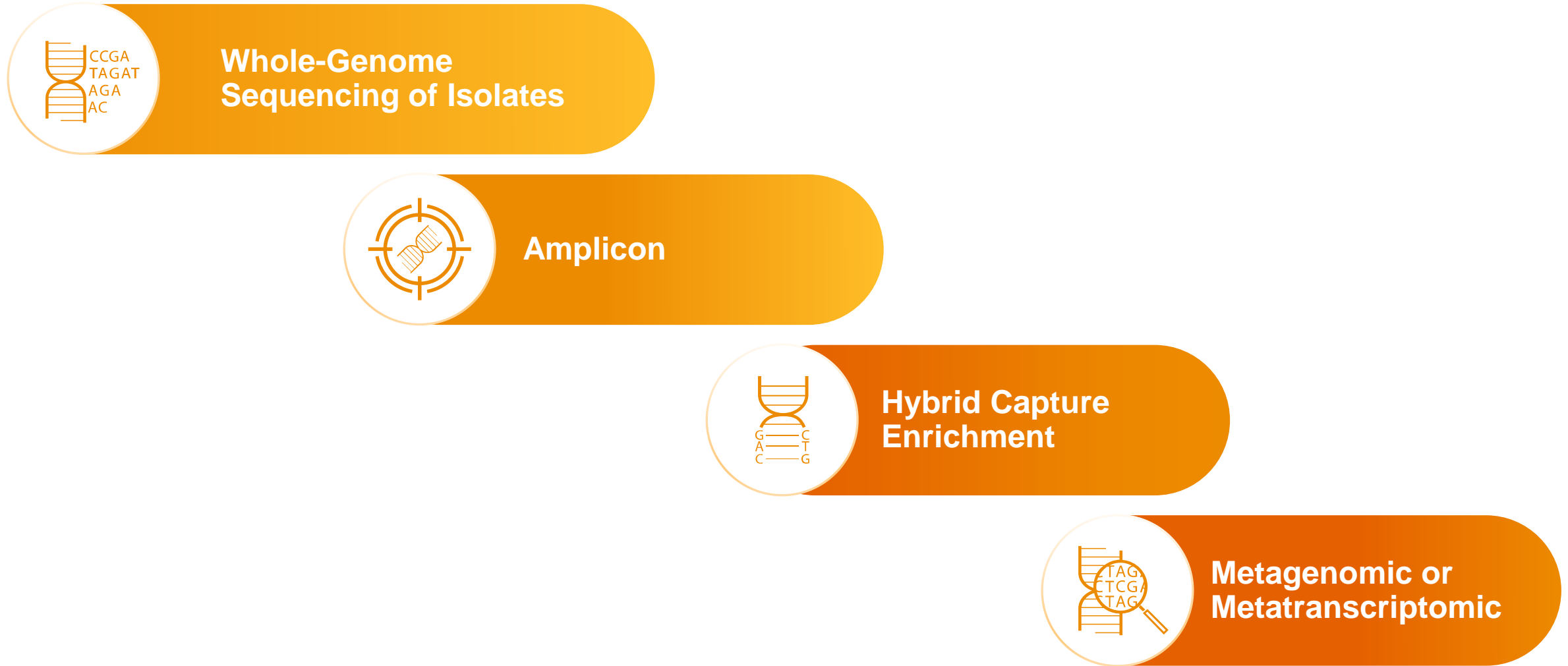
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Portfolio & Methods Introduction

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Illumina
ID&M
Portfolio

From single organism to discovery

DISCOVERY
SINGLE GENOME
MULTI-PATHOGEN

Metagenomics Sequencing

Illumina DNA Prep

Whole Genome Sequencing

COVIDSeq Assay & Test

Urinary Pathogen ID/AMR Panel

Illumina Microbial Amplicon Prep

Respiratory Pathogen ID/AMR Panel

Illumina and GenoScreen Deeplex Myc-TB Combo kit

Viral Surveillance Panel

Pan-Corona Virus Panel

Respiratory Virus Enrichment Kit

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Enabling the ID&M Portfolio with End-to-End Workflows

Library Prep/Panel	Systems	Current Software- on BSSH
Illumina DNA Prep		DRAGEN™ Metagenomics & SRST2
COVIDSeq		DRAGEN™ COVID Lineage
Illumina and GenoScreen Deeplex Myc-TB Combo Kit		Deeplex Web App
Illumina Microbial Amplicon Prep (IMAP) Illumina Microbial Amplicon Prep – Influenza		DRAGEN™ Targeted Microbial
Respiratory Virus Enrichment Kit (RVEK, formerly RVOP)		DRAGEN™ RNA Pathogen Detection
Viral Surveillance Panel (VSP) Pan-Coronavirus Panel		DRAGEN™ Microbial Enrichment
Respiratory Pathogen ID/AMR Panel (RPIP) Urinary Pathogen ID/AMR Panel (UPIP)		Explify™
Ribo-Zero Plus Microbiome		Microbiome Metatranscriptomics

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NGS Methods Enable Genomic Investigation

Whole-Genome Sequencing of Isolates

Amplicon

Hybrid Capture Enrichment

Metagenomic or Metatranscriptomic

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Single Pathogen
"I know what I am looking for…"

1

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Illumina DNA Prep

Illumina library prep with the flexibility for whole-genome sequencing, amplicon & shotgun metagenomics methods for nucleotide resolution.

Applications

Genomic surveillance (HAI, Foodborne pathogens), gene-specific amplicons (16S, AMR genes), pathogen discovery, microbiome analysis & host/pathogen studies and more

Methods

Whole genome sequencing, amplicon & shotgun metagenomics or metatranscriptomics

Other technologies

Microbial culture, Sanger sequencing, qPCR (presence/absence), pulse field electrophoresis (PFGE)

Features

Fastest Illumina library prep workflow, with ~3.5 hours total time

Flexibility to accommodate variations in sample types (gDNA, blood, saliva, dried blood spots, and direct from culture), DNA input amount (1-500 ng), and methods (WGS, amplicon or metagenomics)

Optimized library prep performance; delivers consistent insert sizes, uniform coverage, and optimized performance, regardless of DNA input amount or genome size.

The bead-based technology minimizes bias and opportunities for error, resulting in highly reproducible sequencing data.

Compatible with all Illumina platforms

Automatable through our many partners

Current users:

- Researchers, Academic labs
- Public health labs
- Clinical research
- Applied Microbiology Labs
  (Pharma, manufacturing, direct-to-consumer)
- Service providers

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Amplicon Targeted Assays

01
Amplicon is faster and
easier than hybrid capture

02
Amplicon-based COVIDSeq™
familiar to many customers

03
Risk of mutations causing low coverage,
primer design may need updating over time

GenoScreen Deeplex Myc-TB	Identification of MTBC, 15 anti-TB drugs, and >100 non-TB mycobacteria
COVIDSeq	Full genome SARS-CoV-2
Illumina Microbial Amplicon Prep – Influenza (IMAP-Flu)	Full genome Influenza A&B
Illumina Microbial Amplicon Prep (IMAP)	Open platform for ID&M research & surveillance applications

Illumina and GenoScreen Deeplex Myc-TB Combo Kit

Culture-free amplification of *Mycobacterium tuberculosis* drug targets with strain identification, as well as Nontuberculous Mycobacteria species identification

*Detection of heteroresistance down to 1-3% will depend on coverage depth

Applications

- Tuberculosis genomic surveillance
- Anti-tuberculosis drug resistance
- Mycobacterium tuberculosis characterization
- Non-Mycobacterium tuberculosis identification

Methods

Amplicon Sequencing (tNGS)

Other technologies

Microbial culture,
qPCR (presence/absence),
Line Probe Assay

Features

Culture-free or cultured isolates

Prediction of resistance to 15 anti-TB drugs in 24-48h

Detection of minority variants potentially conferring heteroresistance down to 1-3%

MTBC strain typing (spoligotyping and SNP typing)

Identification of more than 100 Nontuberculous Mycobacteria (NTM)

Secure and automated analysis and easy interpretation of results via Deeplex Web App

Compatible with iSeq™ 100, MiniSeq™, MiSeq™, and NextSeq™ 550 platforms

Current users:

- National TB Programs, Public health or Ministry of Health labs
- Clinical research
- Applied Microbiology Labs (Pharma, manufacturing, direct to consumer)
- Researchers, Academic labs
- Service providers

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WHO guidance of products that meet tNGS class-based performance criteria

3 tNGS solutions that met the inclusion criteria for WHO evaluation

Where a product has not yet met the requirements for a specific drug (i.e. no check mark below), further improvements to the product and WHO review of the evidence will be necessary before clinical use.

Drug class	TB Drug	GenoSreen Deeplex Myc-TB Combo kit	Company O	Company S	Company A
First-line	rifampicin	✔	✔		
First-line	isoniazid	✔	✔		**Company A Assay** did not meet the inclusion criteria and as such, is currently not WHO endorsed until further data can be reviewed by WHO
First-line	fluoroquiolones	✔	✔		
First-line	ethambutol	✔		✔	
First-line	pyrazinamide	✔			
Second-line	bedaquiline	✔			
Second-line	linezolid	✔	✔		
Second-line	clofazimine	✔			
Second-line	amikacin	✔	✔		
Second-line	streptomycin	✔	✔		

WHO Rapid Communication: Use of targeted next-generation sequencing to detect drug-resistant tuberculosis. July 2023 https://www.who.int/publications/i/item/9789240076372

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COVIDSeq Assay and COVIDSeq Test

Whole genome amplicon design for the detection and characterization of the SAR-CoV-2 RNA virus

Applications

- SARS-CoV-2 identification
- Novel mutations
- SARS-CoV-2 Surveillance
- Vaccine efficacy

Methods

Amplicon Sequencing (WGS)

Other technologies

Sanger sequencing, qPCR (presence/absence), lateral flow assays, shotgun metagenomics

Features

Full genome design of SARS-CoV-2 with 99 targets including S-genes, for highly accurate detection.

Flexible input for both nasal swabs and wastewater samples

Analysis powered by DRAGEN™ COVID Lineage App

Compatible with all Illumina Systems

COVIDSeq Assay (96 samples)

COVIDSeq Test (3072 samples)

Current user:

- Public health labs
- Researchers, Academic labs
- Clinical research
- Applied Microbiology Labs (Pharma, manufacturing, direct to consumer)
- Service providers

*not tested on NovaSeqX

Illumina Microbial Amplicon Prep Influenza (IMAP-Flu)

Whole genome amplicon design for the detection and characterization of Influenza A/B RNA virus

Applications

- Genomic surveillance
- Influenza virus identification
- Seasonal virus characterization

Methods

Amplicon Sequencing

Other technologies

Sanger sequencing, qPCR (presence/absence), PCR.

Features
Amplicon-based library preparation kit with reagents and indexes for 48 samples with data analysis included

Flexibility to support multiple sample types (including nasal swabs and isolates)

>98% coverage for both influenza A and B viruses

Works with multiple subtypes including H1N1, H3N2, and H5N1 (highly pathogenic avian influenza)

Streamlined workflow, 9 hours from extracted RNA to library

Analysis powered by DRAGEN Targeted Microbial App

Compatible with all Illumina Systems*, ideal for benchtop systems

Current users:

- Researchers, Academic labs
- Public health labs
- Clinical research
- Applied Microbiology Labs (Pharma, manufacturing, direct-to-consumer)
- Service providers

*not tested on NovaSeqX

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Illumina Microbial Amplicon Prep (IMAP)

Unique and flexible amplicon library prep solution allowing researchers to use lab designed or commercially available primers for targeted sequencing of viruses and select markers from larger microbial species

Applications

- Genomic surveillance
- Viral surveillance
- Functional Genomics
- Recombinant virus sequencing
- Vaccine efficacy and development
- Wastewater surveillance

Methods

Amplicon Sequencing

Other technologies

Amplicon Sequencing Sanger sequencing, qPCR (presence/absence), PCR.

Features

Amplicon-based library preparation kit with reagents and indexes for 48 samples with data analysis included

Based on COVIDSeq Assay chemistry and protocol

Use with lab-designed primers, published primers, or commercially available primer sets

Starting from extracted RNA, DNA, or total nucleic acid inputs

Flexibility to accommodate variations in sample types (e.g. swabs, wastewater, culture)

Analysis powered by DRAGEN Targeted Microbial App

Compatible with all Illumina Systems*, ideal for benchtop systems

Current users:

- Researchers, Academic labs
- Public health labs
- Clinical research
- Applied Microbiology Labs (Pharma, manufacturing, direct to consumer)
- Service providers

*not tested on NovaSeqX

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Illumina Microbial Amplicon Prep

Tested & Demonstrated Protocols

Illumina Tested[1]	Customer Demonstrated
Chikungunya	Dengue I-IV[2]
RSV	Lumpy skin disease[3]
SARS-CoV-2: ARTIC v4	Mpox[4]
Zika	RSV[5]
	SARS-CoV-2: ARTIC v4.1[6] & v5.3.2[7]

* The list is for informational purposes only and does
  not imply the protocols are validated or supported by Illumina.

1. Data on file
2. https://dx.doi.org/10.17504/protocols.io.kqdg39xxeg25/v2
3. https://doi.org/10.1101/2022.09.15.508131
4. https://dx.doi.org/10.17504/protocols.io.5qpvob1nbl4o/v4
5. https://dx.doi.org/10.17504/protocols.io.eq2lyjzbrlx9/v2
6. https://community.artic.network/t/sars-cov-2-v4-1-update-for-omicron-variant/342
7. https://community.artic.network/t/sars-cov-2-version-5-3-2-scheme-release/462

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Multi-pathogen & Syndromic Panels
"I think I know…"

2

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Hybrid Capture Enrichment Panels

01
Hybrid capture enables detection of a large range of potential pathogens and possible co-infections

02
More cost effective and sensitive than non-enriched shotgun metagenomic approaches[1]

03
Robust method can tolerate sequence differences and mismatches, allowing for successful enrichment of divergent sequences and variants.[2]

Panel	What it does
Viral Surveillance Panel (VSP)	Full genome of >60 viruses of high public health concern
Pan Coronavirus Panel (Pan CoV)	Full genome >200 coronaviruses and variants
Respiratory Virus Enrichment Kit (RVEK) (formerly RVOP)	Full genome of >40 common respiratory viruses
Respiratory Pathogen ID/AMR Panel (RPIP)	>280 respiratory pathogens (bacteria, viruses, fungi); >1200 AMR alleles; whole genome of SARS-CoV-2 and influenza
Urinary Pathogen ID/AMR Panel (UPIP)	>170 urogenital pathogens (bacteria, viruses, fungi, parasites) including STIs; >3700 AMR markers

1 Bierstedt et al. Broad genomic AMR surveillance with an efficient, probe-captured NGS Panel. 2023 APHL poster
2 Nagy-Szakal et al. Targeted hybridization capture of SARS-CoV-2 and metagenomics enables genetic variant discovery and nasal microbiome insights. https://journals.asm.org/doi/10.1128/spectrum.00197-21

Importance of wastewater surveillance for public health

Community monitoring enables early detection of pathogens, threats and resistance profiles
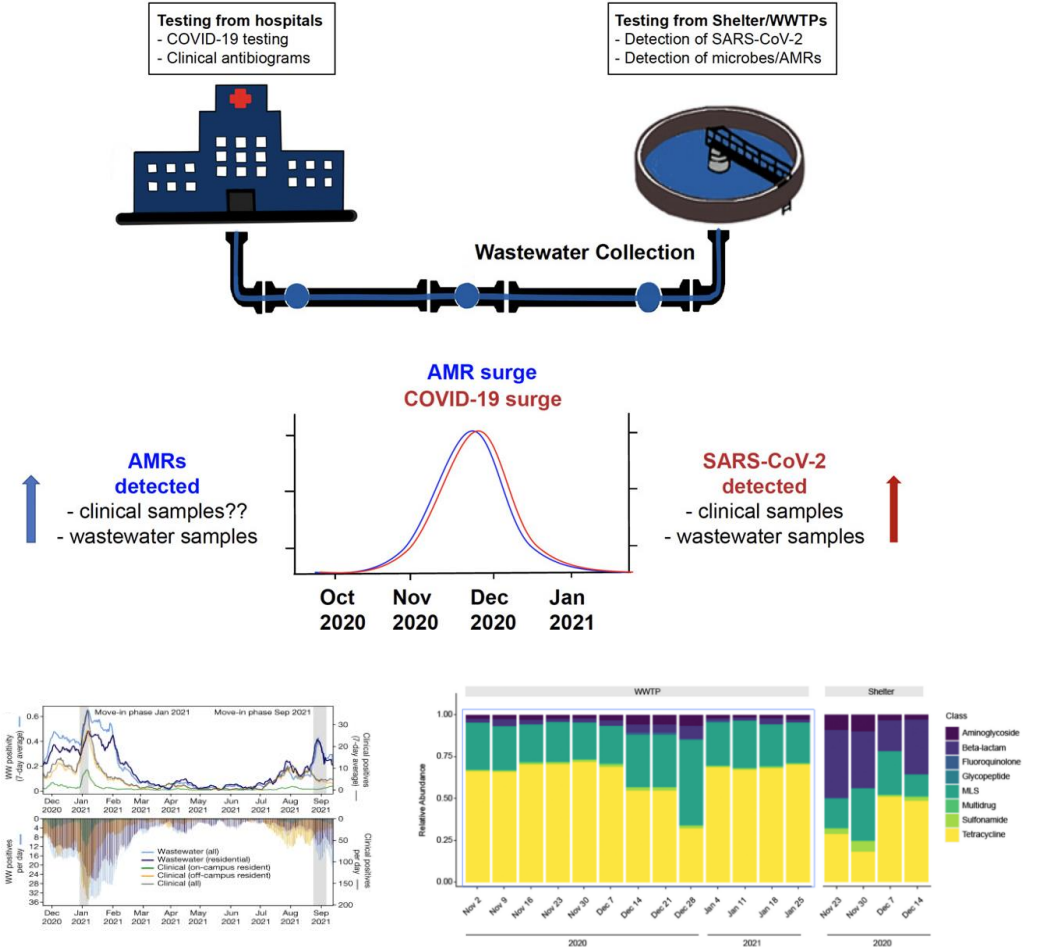
Discover emerging microbes in entire populations irrespective of access to care

Detect & track pathogens, variants, and antimicrobial resistance (AMR) genes in communities early

Karthikeyan et al. 2021. Nature, https://doi.org/10.1038/s41586-022-05049-6
Harrington et a. 2022. Science of The Total Environment, https://doi.org/10.1016/j.scitotenv.2022.158577

Urban monitoring of antimicrobial resistance during a COVID-19 surge through wastewater surveillance

Comprehensive NGS approach for surveillance of viral and bacterial pathogens in wastewater

Research Insights

Illumina's hybrid capture based Viral Surveillance Panel (VSP) and Urinary Pathogen ID/AMR Panel (UPIP) were evaluated on wastewater samples against traditional shotgun metagenomics

In the two extraction methods used, there was negligible difference in coverage and # of viral genomes

VSP enrichment of wastewater samples enhances (2x) the number of DNA and RNA viruses observed and allows for more granular strain identification

UPIP enrichment enhances detection, coverage and depth of urinary pathogens and AMR markers

AMR gene family coverage in UPIP enriched samples is 2.19X higher at 20X fewer reads

Broad surveillance of viral pathogens and AMR markers in wastewater, a complex environmental sample, at low sequencing depth
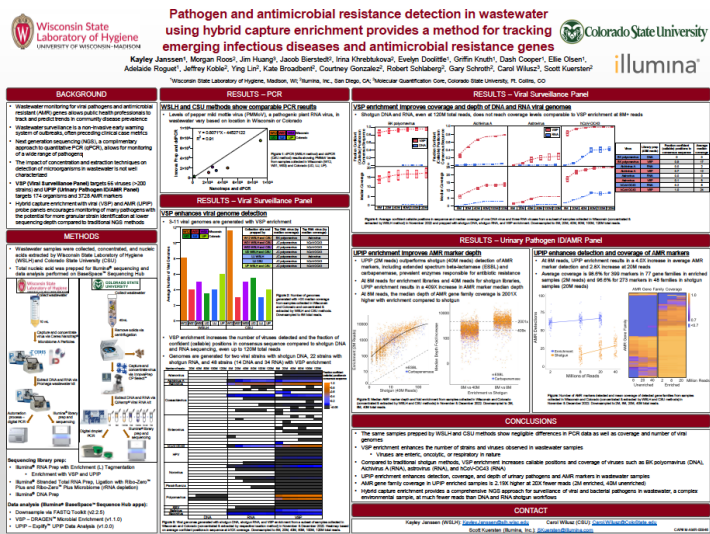
Janssen K, et al. Pathogen and antimicrobial resistance detection in wastewater using hybrid capture enrichment provides a method for tracking emerging infectious diseases and antimicrobial resistance genes. Poster presented at: Association of Public Health Laboratories Annual Conference; May 22-25, 2023; Sacramento, CA.

Illumina Viral Surveillance Panel (VSP)

Culture-free panel for the detection and characterization of the most critical viral public health threats.

Applications

- Genomic Surveillance
- Seasonal Virus monitoring
- Emerging Virus Surveillance
- Wastewater Surveillance

Methods

Probe-enhanced DNA and RNA Sequencing

Other technologies

Sanger sequencing, qPCR (presence/absence), ELISA, pulse field electrophoresis (PFGE), Cell culture

Features

Culture-free method

Broad viral surveillance panel including full genome design of 66 most critical viruses in Public Health, including, but not limited to; Mpox, SARS-CoV-2, Poliovirus, Influenza A/B, RSV, human parainfluenza viruses, and human adenoviruses.

Probe-enhanced panel, combined with Illumina RNA Prep with Enrichment Kit, generating reliable results

Analysis powered by DRAGEN Targeted Microbial App

Compatible with all Illumina platforms

Current users:

- Researchers, Academic labs
- Public health labs
- Service providers

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Illumina Viral Surveillance Panel

Arthropod transmitted / febrile tropical

Arbovirus
Chikungunya
Dengue Virus 1
Dengue Virus 2
Dengue Virus 3
Dengue Virus 4
West Nile Virus
Yellow fever virus
Zika

Bloodborne

Hepatitis A
Hepatitis B
Hepatitis C
Hepatitis E
HIV 1
HIV 2
Torque Teno virus

Encephalitis

Eastern equine encephalitis virus
Hendra henipavirus
Japanese encephalitis virus
Nipah virus
Tick-borne encephalitis virus
Venezuelan equine encephalitis virus
Western equine encephalitis virus

Respiratory / Cardiopulmonary

Adenovirus
Coronavirus -229E
Coronavirus -HKU1
Coronavirus- OC43
Coronavirus-NL63
Influenza A
Influenza B
Hantavirus
MERS-CoV
Metapneumovirus
Parainfluenza
Parechovirus
Respiratory syncytial virus
Rhinovirus
SARS-COV
SARS-COV-2

Hemorrhagic fever

Chapare virus
Crimean-congo hemorrhagic fever virus
Ebola
Guanarito Virus
Rift Valley Fever Virus
Junin Virus
Kyasanur Forest disease virus
Lassa fever virus
Lujo hemorrhagic fever virus
Machupo Virus
Marburg Virus
Omsk hemorrhagic fever virus
Sabia virus

Enteric

Aichivirus
Astrovirus
Coxsackievirus
Enterovirus
Norovirus
Poliovirus
Rotavirus
Salivirus
Sapovirus

Oncolytic

Oncolytic HPV
Polyomavirus

Rash/Lesion

Mpox
Parvovirus
Rubella
Variola virus

*Sample types and sensitivity not validated by ILMN

Pan-Coronavirus Panel (Pan-CoV)

Culture-free panel for the detection of known and closely related novel coronaviruses, for surveillance of animal reservoirs and human coronaviruses.

Applications

- Coronavirus surveillance
- Virus evolution & monitoring
- Coronavirus Identification
- Zoonotic, Spillover viral monitoring
- Wastewater surveillance

Methods

Probe-enhanced (Hybrid-capture) Viral RNA

Other technologies

Classic Microbiology Techniques, Sanger sequencing, qPCR (presence/absence), pulse field electrophoresis (PFGE)

Features

Culture-free method

Whole-genome Sequencing of 203 known coronaviruses and over 370 strains of animal and closely related novel coronaviruses.

Enrichment panel allow for variation in viral genome, allowing for mutations and novel strains to be detected

Probe-enhanced panel for combining with Illumina RNA Prep with Enrichment Kit

Analysis powered by DRAGEN Targeted Microbial App

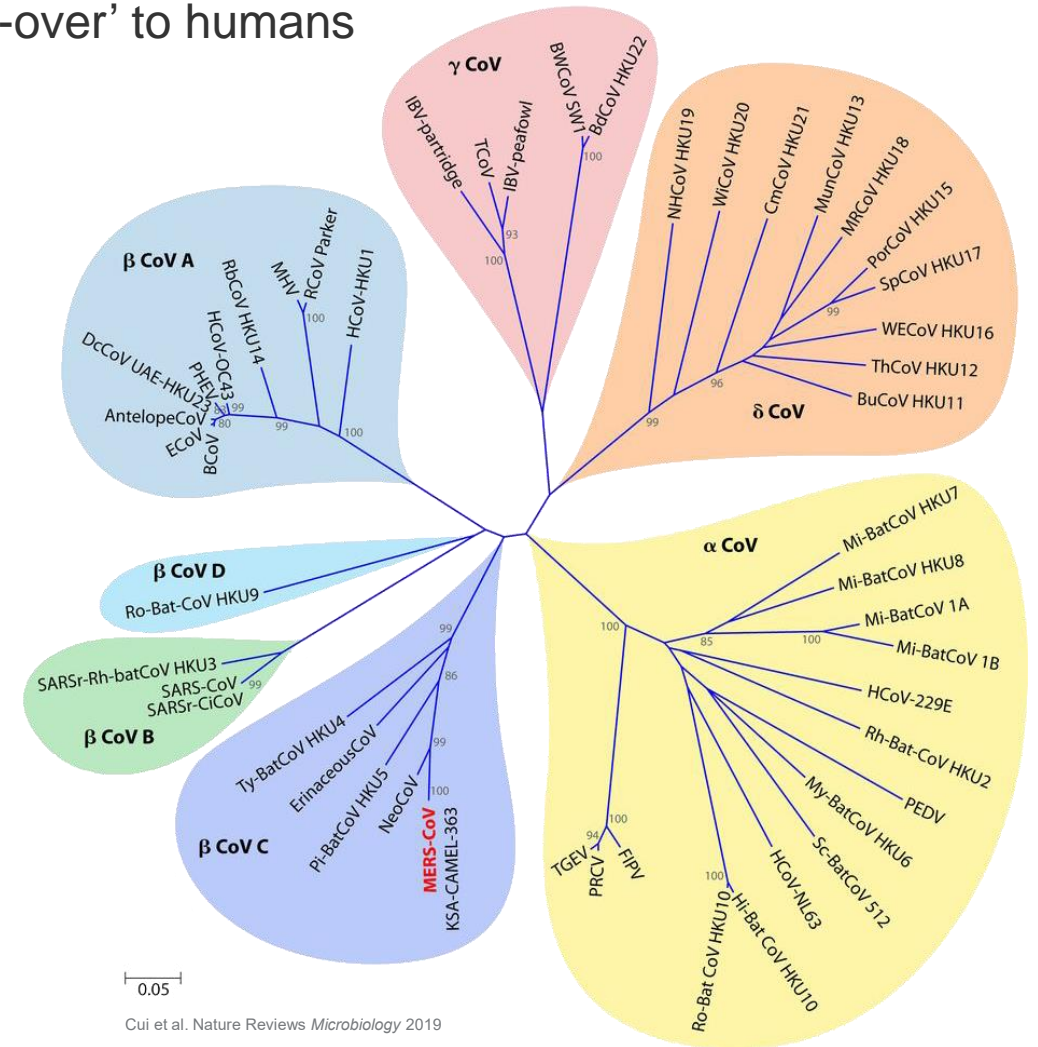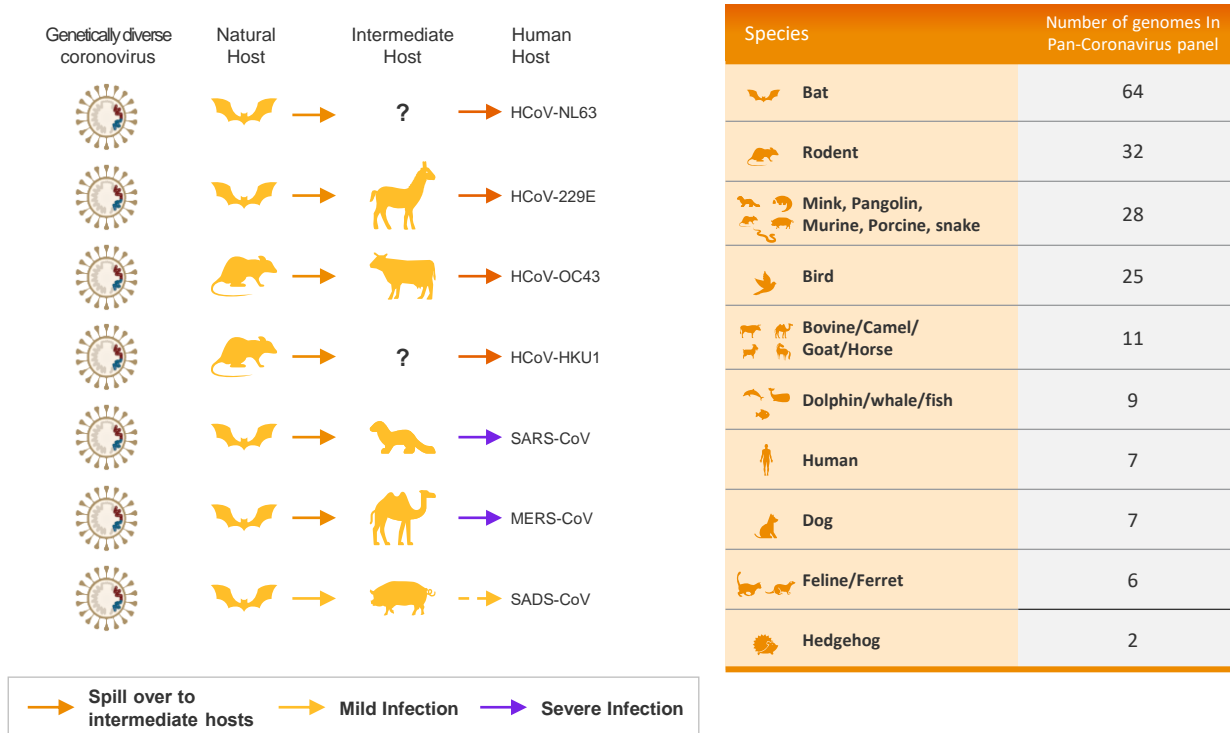Compatible with all Illumina platforms

Current users:

- Researchers, Academic labs
- Public health and Zoonotic labs
- Service providers

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Pan-Coronavirus Panel (Pan-CoV)

Monitor the environment and animal reservoirs to detect 'spill-over' to humans

Illumina Pan-Coronavirus Panel (>200 coronaviruses)

Species	Number of genomes In Pan-Coronavirus panel
Bat	64
Rodent	32
Mink, Pangolin, Murine, Porcine, snake	28
Bird	25
Bovine/Camel/Goat/Horse	11
Dolphin/whale/fish	9
Human	7
Dog	7
Feline/Ferret	6
Hedgehog	2

Cui et al. Nature Reviews *Microbiology* 2019

Illumina Respiratory Virus Enrichment Kit (RVEK)

A culture-free comprehensive respiratory viral panel to detect and characterize common respiratory viruses

Applications

- Genomic surveillance
- Seasonal Virus monitoring
- Respiratory Virus Identification
- Wastewater surveillance

Methods

Probe-enhanced metagenomics (Precision Metagenomics)

Other technologies

Classic virology techniques,

Sanger sequencing,

qPCR (presence/absence)

Features

Culture-free method

Broad viral pathogen panel, including full genome design of >40 viruses

Robust method that remains effective with mutational changes that can render amplicon approaches or PCR ineffective

Includes human probes for positive internal control

Can detect as low as 2 genome copies per reaction

Analysis powered by DRAGEN Targeted Microbial App

Compatible with all Illumina platforms

Current users:

- Researchers, Academic labs
- Applied Microbiology Labs
- (Pharma, Biotechs)
- Service providers.

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Illumina Respiratory Virus Enrichment Kit

Human adenovirus

Human adenovirus B1

Human adenovirus C2

Human adenovirus E4

Human bocavirus

Human bocavirus 1 (Primate bocaparvovirus 1 isolate st2)

Human bocavirus 2c PK isolate PK-5510

Human bocavirus 3

Human bocavirus 4 NI strain HBoV4-NI-385

Human coronavirus

Human coronavirus 229E

Human coronavirus HKU1

Human coronavirus NL63

Human coronavirus OC43

Human coronavirus SARS-CoV-2

Human enterovirus

Human enterovirus C104 strain: AK11

Human enterovirus C109 isolate NICA08-4327

Human metapneumovirus

Human metapneumovirus (CAN97-83)

Human parainfluenza virus

Human parainfluenza virus 1

Human parainfluenza virus 2

Human parainfluenza virus 3

Human parainfluenza virus 4a

Human parechovirus

Human parechovirus 6

Human parechovirus type 1 PicoBank/HPev1/a

Human respiratory syncytial virus

Human Respiratory syncytial virus (type A)

Human Respiratory syncytial virus 9320 (type B)

Human rhinovirus

Human rhinovirus A89

Human rhinovirus B14

Human rhinovirus C (strain 024)

Influenza A

Influenza A virus (A/Hong Kong/1073/99(H9N2))

Influenza A virus (A/Korea/426/1968(H2N2))

Influenza A virus (A/Michigan/45/2015(H1N1))

Influenza A virus (A/New York/392/2004(H3N2))

Influenza A virus (A/Puerto Rico/8/1934(H1N1))

Influenza A virus (A/Texas/50/2012(H3N2))

Influenza A virus (A/Zhejiang/DTID-ZJU01/2013(H7N9))

Influenza A virus (AA/goose/Guangdong/1/1996(H5N1))

Influenza B

Influenza B virus (B/Brisbane/60/2008)

Influenza B virus (B/Colorado/06/2017)

Influenza B virus (B/Lee/1940)

Influenza B virus (B/Wisconsin/01/2010)

Influenza B virus (B/Washington/02/2019)

Polyomavirus

KI polyomavirus Stockholm 60

WU Polyomavirus

Human control genes

Human control genes

Respiratory Pathogen ID/AMR Enrichment Panel Kit (RPIP)

Culture-free panel for identification, characterization, and quantitation of organisms associated with lower respiratory tract infections and genomic surveillance

Applications

- Antimicrobial Resistance
- Seasonal Virus monitoring
- Respiratory Pathogen Identification
- Genomic surveillance
- Wastewater surveillance

Methods

hybrid capture enrichment (Precision Metagenomics)

Other technologies

Classic Microbiology Techniques, Sanger sequencing, qPCR (presence/absence)

Features

Culture-free method

Identify more than 282 pathogens associated with Lower Respiratory Tract Infection (52 Fungi, 42 Viruses, 182 Bacteria)

2,097 Antimicrobial Resistance Markers associated to 26 Antimicrobial Classes

Designed for the Identification of coinfections or hard-to-grow pathogens

Flexibility to accommodate a variety of sample types (e.g. sputum, bronchoalveolar lavage, wastewater, etc.)

Analysis powered by Explify RPIP Data Analysis

Compatible with all Illumina platforms

Current user:

- Researchers, Academic labs
- Public health labs
- Clinical research
- Service providers

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Urinary Pathogen ID/AMR Enrichment Panel Kit (UPIP)

Culture-free identification and quantification of both common and underrecognized uropathogens that can cause urinary tract infections and sexually transmitted Infections.

Applications

- Antimicrobial Resistance
- Urinary Pathogen Identification
- Genomic surveillance
- Wastewater surveillance

Methods

hybrid capture enrichment (Precision Metagenomics)

Other technologies

Microbiology culture, Sanger sequencing, qPCR (presence/absence), STI Ag/Ab rapid test, shotgun metagenomics

Features

Culture-free method

Identify more than 174 pathogens associated with Urinary Tract Infection (14 Fungi, 4 Parasites, 35 Viruses, 121 Bacteria)

Comprehensive Antimicrobial Resistance characterization of 3,761 Antimicrobial Resistance Markers associated to 18 Antimicrobial Classes

Flexibility to accommodate variations in sample types (e.g., urine, swab, isolated organisms, cell culture and wastewater samples) and applications

Optimized library prep performance, generating reliable results

Automated analysis powered by Explify UPIP Data Analysis

Compatible with all Illumina platforms

Current users:

- Researchers, Academic labs
- Public health labs
- Clinical research
- Service providers

Illumina Infectious Disease Hybrid Capture Panel Comparison

	Illumina Viral Surveillance Panel VSP	Illumina Respiratory Oligo Virus Panel RVOP	Illumina Pan-Coronavirus Panel PCP	Illumina Respiratory Pathogen ID/AMR Panel RPIP	Illumina Urinary Pathogen ID/AMR Panel UPIP
Target(s)	66 viral pathogens, 203 strains	40 common respiratory viruses	225 Coronaviruses, over 370 strains	282 Respiratory pathogens (viral, bacteria, fungi) and 2108 antimicrobial resistance markers	174 Urinary pathogens (virus, bacteria, fungi, parasite) and 3728 antimicrobial resistance markers
Whole Genome vs. Detection	Whole Genome	Whole genome of common respiratory viruses, including recent flu strains and SARS-CoV-2. Includes human probes as a quality feature, human probes are included in every sample	Whole Genome	Detection of pathogens and AMR markers Whole genome: SARS-CoV-2, Influenza A/B	Detection of pathogens and AMR markers
Library Prep	RNA Prep with Enrichment	RNA Prep with Enrichment	RNA Prep with Enrichment	RNA Prep with Enrichment	DNA Prep with Enrichment
Software	DRAGEN Targeted Microbial App	DRAGEN Targeted Microbial App	DRAGEN Targeted Microbial App	Explify RPIP	Explify UPIP
Configuration	Standalone panel (96 reactions) Panel, Library Prep and Indexes Set A or B	Standalone panel	Standalone panel (96 reactions)	Panel, Library Prep, Indexes Set A, B , C, or D	Panel, Library Prep, Indexes Set A, B , C, or D

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Discovery
Hypothesis-free

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Pathogen discovery and whole-genome sequencing enables vaccine development driven by synthetic vaccinology

SARS-CoV-2 Full Discovery

Shotgun sequencing for the discovery of the pathogen
Clinical assay designed created once genome published

SARS-CoV-2 Full Genome Sequence

The sequence was publicly available 31 days after the first case
Vaccine development started immediately without isolation of viral particles

Epitope & Vaccine Candidates

Bioinformatics screening for epitope candidates
Package into vectors for animal test screening
Worldwide Pharma, startups, and universities joined the race

Clinical Trials

ModeRna mRNA-based vaccine mRNA-1273 started
clinical testing just 2 months after sequence identification

DISCOVERY TO WGS AND ANALYSIS IS THE FIRST STEP TO DISCOVER VACCINE ANTIGEN

Illumina DNA Prep

Illumina library prep with the flexibility for whole-genome sequencing,
amplicon & shotgun metagenomics applications for nucleotide resolution.

Applications

Genomic surveillance (HAI, Foodborne pathogens), gene-specific amplicons (16S, AMR genes), pathogen discovery, microbiome analysis & host/pathogen studies
and more

Methods

Whole genome sequencing, amplicon & shotgun metagenomics
or metatranscriptomics

Other technologies

Whole Transcriptome, qPCR.

Features

Fastest Illumina library prep workflow, with ~3.5 hours total time

Flexibility to accommodate variations in sample types (gDNA, blood, saliva, dried blood spots, and direct from culture), DNA input amount (1-500 ng), and methods (WGS, amplicon or metagenomics)

Optimized library prep performance; delivers consistent insert sizes, uniform coverage, and optimized performance, regardless of DNA input amount or genome size.

The bead-based technology minimizes bias and opportunities for error, resulting in highly reproducible sequencing data.

Compatible with all Illumina platforms

Automatable through our many partners

Current users:
- Researchers, Academic labs
- Public health labs
- Clinical research
- Applied Microbiology Labs
  (Pharma, manufacturing, direct to consumer)
- Service providers

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Ribo-Zero Plus Microbiome rRNA Depletion Kit

Fast, efficient depletion of undesirable host and pan-bacterial rRNA from complex microbial samples for metatranscriptomics research.

Applications

- Gut Metatranscriptomics
- Metatranscriptomics

Methods

Metatranscriptomics,

rRNA depletion

Other technologies

Whole Transcriptome, qPCR.

Features

Eliminate unwanted rRNA from bacteria common complex microbial samples, validated in adult and infant stool samples.

Optimized library prep performance, generating reliable results

Includes access to simplified data analysis and visualization with BaseSpace Microbiome Metatranscriptomics App

Compatible with MiSeq, NextSeq 550, NextSeq 1000, NextSeq 2000 and NovaSeq 6000.

Current users

- Researchers, Academic labs
- Applied Microbiology Labs
- (Pharma, Biotechs)
- Service providers

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Infectious Diseases by the Numbers

		Illumina Solution – building blocks to impact human health
770M	Cumulative cases of **COVID-19**[1]	**COVIDSeq or IMAP**
400K	Respiratory deaths each year caused by **influenza virus**[2]	**RVEK / RPIP or IMAP-Flu**
10.6M	People that fell ill from **tuberculosis** in 2021[3]	**Illumina and GenoScreen Deeplex Myc-TB Combo Kit**
39M	People living with **HIV** in 2022[4]	**VSP or IMAP**
3.8%	Global GDP lost due to **antimicrobial resistance** by 2050[5]	**RPIP and UPIP**
247M	**Malaria** cases in 84 malaria-endemic countries in 2021[3]	**IMAP**
1.5M	New **hepatitis B** infections globally in 2019[3]	**VSP**
$28-45B	Direct annual cost of treating **healthcare associated infections** in the US[6]	**IDP**

1. https://covid19.who.int/ (Accessed Sept. 7, 2023); 2. https://ourworldindata.org/influenza; 3. World health statistics 2023: monitoring health for the SDGs, Sustainable Development Goals. Geneva: World Health Organization; 2023.; 4. https://www.unaids.org/en/resources/fact-sheet; 5. Global antimicrobial resistance and use surveillance system (GLASS) report 2022. Geneva: World Health Organization; 2022.; 6. Gidey K, et al. Clinical and economic burden of healthcare-associated infections: A prospective cohort study. PLoS One. 2023 Feb 23;18(2):e0282141.

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Thank you

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