Pathogen ID & Surveillance: Sequencing Roadmap Beyond COVID-19 at illumina

Let’s Discuss!!!

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AMR East & LATAM; Microbial and Infectious Disease Sales Specialist

Genome Trakr Meeting – Technology Talk
College Park, MD
10.20.2022

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illuminá Infectious Disease & Microbiology Specialist Team

- **Chris Detter** (505-699-1996; cdetter@illumina.com)
  - **ID&M Specialist – US East and LATAM**
    - DoE Joint Genome Institute & Livermore National Lab
      - Part of Human Genome Program… R&D
    - Los Alamos National Lab – Genome Center Director
      - Focus on Infectious Disease Genomics….and SFAF
    - Defense Threat Reduction Agency (DTRA)
      - Built Genome centers abroad
    - MRIGlobal
      - Chief Scientist R&D for Biosurveillance and Infectious Disease
      - Applied development of Biosurveillance using Genomics

- **Jason Smith** (858-531-8182; jsmith6@illumina.com)
  - **ID&M Specialist – US West and Canada**
    - Illumina: Sequencing Specialist – US-West
    - Past Companies: PacBio, Ion Torrent, Applied Bio, LLNL
    - Location: Reno, NV
    - Expertise: Microbiology (UCSB) , Computer Science (CSU Chico), Next-Generation-Sequencing (Field Sales/Support)

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Emerging and Reemerging Infectious Diseases
List of priority infectious diseases that threaten global health security

**Viral infections**
- Pandemic influenza
- COVID-19
- Middle East respiratory syndrome
- Severe acute respiratory syndrome
- Marburg
- Ebola
- Lassa fever
- Viral hemorrhagic fevers
- Rift Valley fever
- West Nile fever
- Dengue
- Polio
- Zika
- Nipah and henipavirus diseases
- Chikungunya
- Measles
- Yellow fever
- Viral hepatitis

**Bacterial infections**
- Tuberculosis
- Invasive meningococcal disease
- Invasive pneumococcal disease
- Cholera
- Typhoid
- Diphtheria
- Pertussis (whooping cough)

**Drug-resistance**
- Drug-resistant bacterial, viral, and protozoal infections
- Drug-resistant malaria
- Antiretroviral-resistant human immunodeficiency virus/AIDS

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1 - WHO Blueprint priority disease.

2022 Infectious Disease & Microbial Focus at Illumina

Infectious Disease Testing  Public Health  Microbiology Research

Illumina Developed

Partnerships  Commercial Enablement

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Next-Generation Sequencing Unlocking the Power of the Microbial Genome

> APPLICATIONS

- Healthcare Associated Infections
- Disease of unknown Etiology
- Antibiotic Resistance
- Respiratory Pathogens
- Wastewater Surveillance
- Foodborne Pathogens
- Clinical
Illumina technology has been used in the fight against COVID-19 at all stages of the pandemic

**JANUARY 2020**
Identification of new virus causing COVID-19 with Illumina platform

**SINCE LATE 2020**
Public health and research institutions use Illumina technology to characterize novel SARS-CoV-2 variants COVIDSeq, RVOP, RPIP, etc.

**JUNE 2020**
Illumina develops first sequencing based COVID-19 diagnostic test COVIDSeq™

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Beyond Positive Detection of Sars-CoV-2 by RT-qPCR or NGS

Are there mutations in the viral sequence?
- Guidance for PCR-based testing revision
- Guidance for vaccine targets

What was the route of transmission?
- Guidance for public health policy decisions

How fast is the virus mutating?

Are there any co-infections?

Source: GISAID
## The Spectrum of Molecular Identification & Diagnostics

<table>
<thead>
<tr>
<th>Method</th>
<th>Characteristics</th>
</tr>
</thead>
</table>
| **PCR** | • Sensitive, Specific  
         • Fast and Cheap  
         • Very limited scope  
         • Low/No Mismatch Tolerance |
| **Multiplex PCR** | • Sensitive, Specific  
         • Fast and Cheap  
         • Limited scope  
         • Low/No Mismatch Tolerance |
| **Amplicon Sequencing** | • Amplicon panels  
                                • Marker genes  
                                • Limited breadth  
                                • Primer interactions  
                                • Amplicon dropout |
| **Precision Metagenomics** | • Very broad  
                                • All pathogen types detected  
                                • Modest depth  
                                • Very sensitive-specific  
                                • Reliable AMR |
| **Shotgun Metagenomics** | • Broadest  
                                • All pathogen types detected  
                                • Deep sequencing  
                                • Variable sensitivity  
                                • Variable AMR detection |

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The Illumina RNA (DNA) Prep with Enrichment Workflow

Leveraging BLT technology to achieve rapid turnaround time without compromising quality

- **cDNA Synthesis**
- **Tagmentation**
- **Capture**
- **Quant & Norm**

**Library Preparation***

- **9.5 (6.5) hours**
- Comparable to Illumina DNA Prep w/ Enrichment + cDNA Synthesis

**MiniSeq Rapid 100-cycles kit**
- <5h
- 1x100
- 18 samples

**MiSeq V3 150-cycles kit**
- ~12h
- 1x75
- 24 samples
- 21h
- 2x75

**NextSeq 550 Mid-Output 150-cycles kit**
- ~9h
- 1x75
- 96 samples
- 15h
- 2x75

*Approximate time for manual processing of 24 samples with 3-plex enrichment is ~9.5 from Total RNA to library with ~2 hours of hands-on time.

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Respiratory Viral Oligo Panel (RVOP)

**Comprehensive Detection of 40+ Respiratory Viral Whole Genomes**

- 7,800 probes (80bp) tiling the **full genome** of common respiratory viruses, recent flu strains, and SARS-CoV-2
- Includes probes that target human mRNAs to act as positive controls

**Respiratory Viruses Detected by Respiratory Virus Oligo Panel**

- Human coronavirus 229E
- Human coronavirus NL63
- Human coronavirus OC43
- Human coronavirus HKU1
  - **SARS-CoV-2**
- Human adenovirus B1
- Human adenovirus C2
- Human adenovirus E4
- Human bocavirus 1 (Primate bocaparvovirus 1 isolate st2)
- Human bocavirus 2c PK isolate PK-5510
- Human bocavirus 3
- Human parainfluenza virus 1
- Human parainfluenza virus 2
- Human parainfluenza virus 3
- Human parainfluenza virus 4a
- Human metapneumovirus (CAN97-83)
- Respiratory syncytial virus (type A)
- Human Respiratory syncytial virus 9320 (type B)
- Influenza A virus (A/Puerto Rico/8/1934[H1N1])
- Influenza A virus (A/Korea/426/1968[H2N2])
- Influenza A virus (A/New York/392/2004[H3N2])
- Influenza A virus (A/goose/Guangdong/1/1996[H5N1])
- Human bocavirus 4 Ni strain HBoV4-NI-385
- KI polymavirus Stockholm 60
- WU Polyomavirus
- Human parechovirus type 1 PicovBank/HPeV1/a
- Human parechovirus 6
- Human rhinovirus A89
- Human rhinovirus C (strain O24)
- Human rhinovirus B14
- Human enterovirus C104 strain: AK11
- Human enterovirus C109 isolate NCP09-4327
- Influenza A virus (A/Zhejiang/DTID-ZJ01/2013[H7N9])
- Influenza A virus (A/Hong Kong/1073/99[H9N2])
- Influenza A virus (A/Texas/50/2012[H3N2])
- Influenza A virus (A/Michigan/45/2015[H1N1])
- Influenza B virus (B/Lee/1940)
- Influenza B virus (B/Wisconsin/01/2010)
- Influenza B virus (B/Brisbane/60/2008)
- Influenza B virus (B/Colorado/06/2017)
- Influenza B virus (B/Washington/02/2019)
- Human control genes

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## Respiratory Pathogen ID/AMR Panel (RPIP)

### Comprehensive Detection of Respiratory Pathogens and Antimicrobial Resistance Genes

<table>
<thead>
<tr>
<th>Pathogens</th>
<th>Quantities</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bacteria</td>
<td>180+</td>
</tr>
<tr>
<td>Viruses*</td>
<td>40+</td>
</tr>
<tr>
<td>Fungi</td>
<td>50+</td>
</tr>
<tr>
<td>Antimicrobial Resistant Genes</td>
<td>50+</td>
</tr>
<tr>
<td>Antimicrobial Resistance Alleles</td>
<td>1200+</td>
</tr>
</tbody>
</table>

*full genome coverage available for SARS-CoV-2 and flu viruses

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**Introducing Viral Surveillance Panel (VSP)**

- **66 Viral species** with 216 strains total (numbers in parenthesis)
- Oligo Hybrid Capture-80 bp oligos tiles across each genome for WGS Sequencing in **full-length**
- Flexible to mutations/strain variation of 20% due to hybrid capture technology
- Free to use DRAGEN Microbial Enrichment BaseSpace® app for analysis- including, consensus sequences, contig assembly, genome coverage and read counts
- Designed for **broad viral genomic surveillance for a variety of sample types*** including wastewater, environmental and post-clinical for public health

<table>
<thead>
<tr>
<th>Arthropod transmitted / febrile tropical</th>
<th>Bloodborne</th>
<th>Encephalitis</th>
<th>Respiratory/Cardiopulmonary</th>
<th>Hemorrhagic fever</th>
<th>Enteric</th>
<th>Oncolytic</th>
<th>Rash/Lesion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chikungunya(1)</td>
<td>Hepatitis A(1)</td>
<td>Eastern equine encephalitis virus(1)</td>
<td>Adenovirus(3)</td>
<td>Chapare virus(1)</td>
<td>Aichivirus (3)</td>
<td>Oncolytic HPV(14)</td>
<td>Monkeypox(2 - both clades)</td>
</tr>
<tr>
<td>Dengue Virus 1(1)</td>
<td>Hepatitis B (1)</td>
<td>Hendra encephalitis virus(1)</td>
<td>Coronavirus -229E(1)</td>
<td>Crimean-congo haemorrhagic fever virus(1)</td>
<td>Astrovirus(1)</td>
<td>Polyomavirus(9)</td>
<td>Parvovirus(1)</td>
</tr>
<tr>
<td>Dengue Virus 2(1)</td>
<td>Hepatitis C(7)</td>
<td>Japanese encephalitis Virus(1)</td>
<td>Coronavirus -HKU1(1)</td>
<td>Ebolavirus(1)</td>
<td>Coxsackieviruses(28)</td>
<td>Rubella(1)</td>
<td></td>
</tr>
<tr>
<td>Dengue Virus 3(1)</td>
<td>Hepatitis E(1)</td>
<td>Nipah Virus(1)</td>
<td>Coronavirus- OC43(1)</td>
<td>Rift Valley Fever Virus(3)</td>
<td>Enterovirus(28)</td>
<td>Norovirus(14)</td>
<td></td>
</tr>
<tr>
<td>Dengue Virus 4(1)</td>
<td>HIV 1(1)</td>
<td>Tick-borne encephalitis virus(1)</td>
<td>Coronavirus-NL63(1)</td>
<td>Junin Virus(1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>West Nile Virus(2)</td>
<td>HIV 2(1)</td>
<td>Venezuelan equine encephalitis virus(1)</td>
<td>Influenza A(7)</td>
<td>Kyasanur Forest disease virus(1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yellow fever virus(1)</td>
<td>Torque Teno virus(1)</td>
<td>Western equine encephalitis virus(1)</td>
<td>Influenza B(1)</td>
<td>Lassa fever virus(2)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Zika(2)</td>
<td></td>
<td></td>
<td>Hantavirus(33)</td>
<td>Lujo Hemorrhagic Fever Virus(1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>MERS-CoV(1)</td>
<td>Machupo Virus(1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Metapneumovirus(1)</td>
<td>Marburg Virus(1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Parainfluenza(4)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Parechovirus(1)</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>Respiratory syncytial virus(1)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Rhinovirus(3)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>SARS-CoV(1)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>SARS-COV-2(1)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* *Note: Red Box indicates recent public health outbreaks world-wide*
Viral Surveillance Panel - Applications

* Sample Type: Wastewater, Surfaces, Soil, Air, Clinical, Zoonotic, etc.
* We recommend ~1M reads for simple samples & ~5-10M reads for complex samples

Environmental Surveillance
- Emerging
- Outbreaks
- Public Health
- USDA
- FDA
- BioDefense
- Customs Boarder Patrol
- Academic
- etc

Clinical Surveillance
- Outbreaks
- Emerging
- Reflex
- Public Health Labs
- Service Labs
- Government Labs
- Clinical Hospital Labs
- Academic Medical Centers
- etc

Viral Metagenomics
- Research
- WGS
- Academic
- Government
- etc

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Pan-Corona

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Introducing Pan-Coronavirus (Pan-CoV) Panel

- The Pan-CoV Panel allows for detection and WGS of 203 known coronaviruses and over 370 strains of animal and closely related novel coronaviruses, for surveillance of animal reservoir and sequencing of known human coronaviruses.

- Hybrid capture panels allow for up to 20% variation in viral genome, allowing for mutations and novel strains to be detected.

- At least one reference genome for each "branch" in the coronavirus phylogenetic tree is captured on the panel.

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**Illumina Pan-Coronavirus Panel (Pan-Cov Panel)**

<table>
<thead>
<tr>
<th>Species</th>
<th>Number of genomes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bat</td>
<td>64</td>
</tr>
<tr>
<td>Rodent</td>
<td>32</td>
</tr>
<tr>
<td>Mink, Pangolin, Murine, Porcine, snake</td>
<td>28</td>
</tr>
<tr>
<td>Bird</td>
<td>25</td>
</tr>
<tr>
<td>Bovine/Camel/Goat/Horse</td>
<td>11</td>
</tr>
<tr>
<td>Dolphin/whale/fish</td>
<td>9</td>
</tr>
<tr>
<td>Human</td>
<td>7</td>
</tr>
<tr>
<td>Dog</td>
<td>7</td>
</tr>
<tr>
<td>Feline/Ferret</td>
<td>6</td>
</tr>
<tr>
<td>Hedgehog</td>
<td>2</td>
</tr>
</tbody>
</table>

**Genetically diverse coronaviruses**

- Natural Host
- Intermediate Host
- Human Host

**Species**

- HCoV-229E
- HCoV-OC43
- SARS-CoV
- MERS-CoV
- HCoV-HKU1
- HCoV-NL63
- SADS-CoV

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Pan-Coronavirus Panel - Applications

* Sample Type: Zoonotic, Wastewater, Surfaces, Air, etc.
* We recommend ~5-10M reads for complex samples

Environmental Surveillance

• Emerging
• Outbreaks

• Zoonotic Researchers
• Public Health
• BioDefense
• Academic
• etc

Viral Metagenomics

• Research
• WGS
• Discovery

• Zoonotic Researchers
• Academic
• Government
• etc

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COMING SOON

UPIP

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Urinary Pathogen Identification Panel (UPIP)

174 Pathogens
- 14 fungi
- 35 viruses
- 4 parasites
- 121 bacteria

46 Antibiotics

3,728 Antimicrobial Resistance Markers

Bonus: Simultaneous detection of STI pathogens

27 sexually transmitted pathogens detectable within the same urine specimen & workflow

Exact numbers of pathogens and AMR markers may change with product updates/improvements.

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Urinary Pathogen Identification Panel - Applications

* Sample Type: Urine, Swabs, Blood, Wastewater, etc.

* We recommend ~1M reads for simple samples & ~5-10M reads for complex samples

- UPIP provides **highly sensitive, culture-free identification and quantification** of both common and underrecognized uropathogens that can cause urinary tract infections.

- Also provides **Extensive antimicrobial resistance** information.

**Clinical ID**

- Chronic
- Undiagnosed
- Outbreaks

- **Public Health Labs**
- **Long Term Care Facilities**
- **Academic Medical Centers**
- **Commercial Service Labs**
- **Government Labs**
- **etc**

**Clinical Surveillance**

- Outbreaks
- Emerging
- Research
- Antimicrobial Resistance Monitoring (AMR)

- **Public Health Labs**
- **Government Labs**
- **Academic Research Centers**
- **etc**

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<table>
<thead>
<tr>
<th></th>
<th><strong>Illumina Respiratory Oligo Virus Panel (RVOP)</strong></th>
<th><strong>Illumina Respiratory Pathogen ID/AMR Panel (RPIP)</strong></th>
<th><strong>Illumina Urinary Pathogen ID/AMR Panel (UPIP)</strong></th>
<th><strong>Illumina Pan-Coronavirus Panel (Pan-CoV)</strong></th>
<th><strong>Illumina Viral Surveillance Panel (VSP)</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Target(s)</strong></td>
<td>40 common respiratory viruses</td>
<td>282 Respiratory pathogens (viral, bacteria, fungi) and 2108 antimicrobial resistance markers</td>
<td>174 Urinary pathogens (virus, bacteria, fungi, parasite) and 3728 antimicrobial resistance markers</td>
<td>225 Coronavirus, over 370 strains</td>
<td>66 viral pathogens, 216 strains</td>
</tr>
<tr>
<td><strong>Whole Genome vs. Detection</strong></td>
<td>Whole Genome</td>
<td>Detection of pathogens and AMR markers Whole genome: SARS-CoV-2, Influenza A/B</td>
<td>Detection of pathogens and AMR markers</td>
<td>Whole Genome</td>
<td>Whole Genome</td>
</tr>
<tr>
<td><strong>Library Prep</strong></td>
<td>RNA Prep with Enrichment</td>
<td>RNA Prep with Enrichment</td>
<td>DNA Prep with Enrichment</td>
<td>RNA Prep with Enrichment</td>
<td>RNA Prep with Enrichment</td>
</tr>
<tr>
<td><strong>Software</strong></td>
<td>RNA Pathogen App</td>
<td>Explify RPIP</td>
<td>Explify UPIP</td>
<td>DRAGEN Microbial Enrichment App</td>
<td>DRAGEN Microbial Enrichment App</td>
</tr>
<tr>
<td><strong>Configuration</strong></td>
<td>Standalone panel</td>
<td>Panel, Library Prep, Indexes Set A, B, C, or D</td>
<td>Panel, Library Prep, Indexes Set A, B, C, or D</td>
<td>Standalone panel (96 reactions)</td>
<td>Standalone panel (96 reactions)</td>
</tr>
</tbody>
</table>

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Apps Galore!

1) Plug & Play, 2) Easy to Share & Collaborate, 3) Simple Push-Button Analysis, 4) Automation & Integration, 5) Secure

**Illumina Core Apps**
- 16S Metagenomics
- Kraken Metagenomics
- Prokka Genome Annotation
- SRST2
- Velvet de novo Assembly
- String Graph Metagenomics

**BaseSpace Labs Apps**
- DRAGEN Metagenomics Pipeline
- MetaPhlAn
- SPA des Genome Assembler
- DNA Star
- EzBioCloud 16S-based MTP
- SEAR
- GENIUS Metagenomics: Know Now

**BaseSpace 3rd Party Apps**
- DRAGEN RNA Pathogen Detection
- DeepChek-HBV, HCV, HIV
- Explify RPIP Analysis
- CosmosID Metagenomics

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https://illumina.box.com/Metagenomics
Antimicrobial resistance: Microbial sequencing, by NGS, is well established in research and public health settings and is emerging as a component that can be used to predict antimicrobial resistance. (Ranson E., 2020)

Early detection: NGS has been used in a vast array of analyses for infectious disease research of public health relevance to identify outbreak origins, track transmissions, investigate epidemic dynamics, determine etiological agents of a disease, and discover novel human pathogens (Berry, I. M., 2020)

Endemic Disease Surveillance: NGS is a great tool for vector control programs and public health environmental surveillance (Junqueira, A.C.M., 2017). That technology and bioinformatics tools offer new opportunities for Emerging Infectious Diseases surveillance in quality and in scale. (Kwok, K.T.T., 2020)

Wastewater: NGS can provide a comprehensive insight into microbial communities and their functional capacities in water and wastewater systems, thus eliminating the need to develop a new assay for each target organism or gene. (The Water Research Foundation, 2020)

Foodborne: Whole-Genome Sequencing provides information beyond the identity and relationship of strains; it can also help public health by improving the safety, quality, and shelf life of foods. (Brown, E., 2019)
Applying Genomics in Surveillance of Pathogens

Transmission Vectors

Environmental / Clinical Monitoring

Zoonotic Reservoirs

Antimicrobial Resistance
Importance of Wastewater Surveillance for Public Health

Community-level monitoring of infectious diseases and detection of emerging pathogens

- Asymptomatic population is included despite not seeking medical care/getting clinically tested
- Track which variants are dominant in a community
- Whole community-level view of infectious diseases regardless of access to healthcare
- Discover emerging microbes in a population
- Detect pathogens in community before hospitals can detect surges (pandemic preparedness)
- Find antimicrobial resistance (AMR) genes

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Wastewater Surveillance with Illumina NGS - Workflow


Sample Collection

24 hour wastewater influent collected from various treatment plants across the USA

RNA Extraction + Quantification

RNA was extracted using a Qiagen RNAEasy protocol. qPCR according to the N1 CDC protocol

Library Prep-in Duplicates

- COVIDSeq™ Assay (included v3 Primers)
- COVIDSeq™ Assay with v4 Primers
- Illumina RNA Prep with Enrichment Kit + Respiratory Virus Oligo Panel v2

Data Analysis

- BaseSpace DRAGEN™ RNA Pathogen App
- Kallisto pipeline: Not available on BaseSpace
- Nature Biotechnology 34, 525–527 (2016), doi:10.1038/nbt.3519
- BaseSpace DRAGEN™ COVID Lineage app

Sequencing

- 2 × 150 bp read length on the MiSeq, 1M reads/sample
- 2 × 150 bp read length on the NextSeq, 10 M reads/sample

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3rd Party Solutions

- Health Care Acquired Infections
- TB - GenoScreen
Enablement through 3rd party solutions

Healthcare Acquired Infections (HAI)

- Web based software solution to process bacterial whole genome sequence data (WGS).
- Detailed genetic characterization to accurately determine and track 13 of the most common bacteria found in healthcare settings.
- Uses illumina’s WGS pipeline!

Mycobacterium tuberculosis (mtb)

- An all-in-one assay based on targeted sequencing
- DIRECT from Clinical Samples....no culture required!
- IDs more than 140 mycobacterial species
- Prediction of resistance to 15 anti-TB drugs
- Uses illumina’s Library Prep and Sequencers!
Enablement of our Solutions

- MiSeq
- NextSeq 1000/2000
- Infinity Long Reads
- New SBS Chemistry
MiSeq

Key Applications

- Bacterial & viral (small) genomes
- 16S profiling
- Targeted regions, amplicon panels

# paired reads

<table>
<thead>
<tr>
<th>Kit</th>
<th># reads</th>
<th>Cycles</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nano</td>
<td>1</td>
<td>300-500</td>
</tr>
<tr>
<td>Micro</td>
<td>4</td>
<td>300</td>
</tr>
<tr>
<td>v2</td>
<td>15</td>
<td>50-300-500</td>
</tr>
<tr>
<td>v3</td>
<td>25</td>
<td>150-600</td>
</tr>
</tbody>
</table>

kits available

- Foodborne Pathogen Outbreaks
- Public Health Genomic Epidemiology
- Genomic Epidemiology

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NextSeq 1000/2000 - will enable a broader range of applications and cost savings

**Key Applications**

- Larger genomes (i.e. fungal)
- Metagenomics
- Whole Genome Sequencing at Scale
- Multiplexing many genomes
- Cost reduction via multiplexing

**NEW**

- P1 and P2 with 600 cycle this year
  - ~35hrs vs 65hrs (MiSeq)
  - ~same price, but 4x more data
- P4 coming 2023/4 with new SBS Chemistry.
  - Patterned flow cell like NovaSeq….future proof
- NO Washes. Single, disposable cassette
- DRAGEN on-board for 6x faster secondary analysis

<table>
<thead>
<tr>
<th># paired reads</th>
<th>kits available</th>
<th>Cycles</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>P1</strong></td>
<td>100</td>
<td>300</td>
</tr>
<tr>
<td><strong>P2</strong></td>
<td>400</td>
<td>300</td>
</tr>
<tr>
<td><strong>P3 (2000 only)</strong></td>
<td>1200</td>
<td>300</td>
</tr>
</tbody>
</table>

For Research Use Only. Not for use in diagnostic procedures.
Thank You!

Questions?