

Integrating Next Generation Sequencing Results into the Laboratory Information Management System to Improve Reporting for Surveillance and Outbreak Investigation

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Introduction/Project Overview

- Wadsworth Center (WC), the New York State Department of Health (NYSDOH) public health laboratory, has implemented Next Generation Sequencing (NGS) for clinical, surveillance and outbreak testing applications over the last 10 years.
- NGS testing presents new challenges, including complicated analyses, data storage requirements, reporting and regulatory compliance. WC has been constrained by the large amount of data generated, data integration and reporting in the Laboratory Information Management System (LIMS).
- Over the past year, WC has developed a LIMS solution to allow groups of accession numbers to be reported together in an "investigation module" to enhance reporting and communication of NGS data.
- The investigation module has been developed for use with several clinical and surveillance reports including carbapenemase-producing organisms, tuberculosis and other bacteria of public health importance such as healthcare associated infections, vaccine preventable diseases, *Legionella* and food and waterborne associated pathogens.

CLIMS Overview

CLIMS (Clinical Laboratory Management System)

- Sample tracking and lab information management
- Collect, report, and maintain sample data
- Developed in-house to meet custom needs of Wadsworth Center
- Supports all Clinical and Environmental Labs at Wadsworth Center (except Newborn Screening)
- Allows Wadsworth Center to
 - Electronically centralize data collected
 - Distribute data to external users and systems
 - Respond quickly to public health emergencies
 - Interface seamlessly with other NYSDOH systems
- NGS analysis is performed outside of CLIMS
- Key findings imported into CLIMS for tracking and reporting

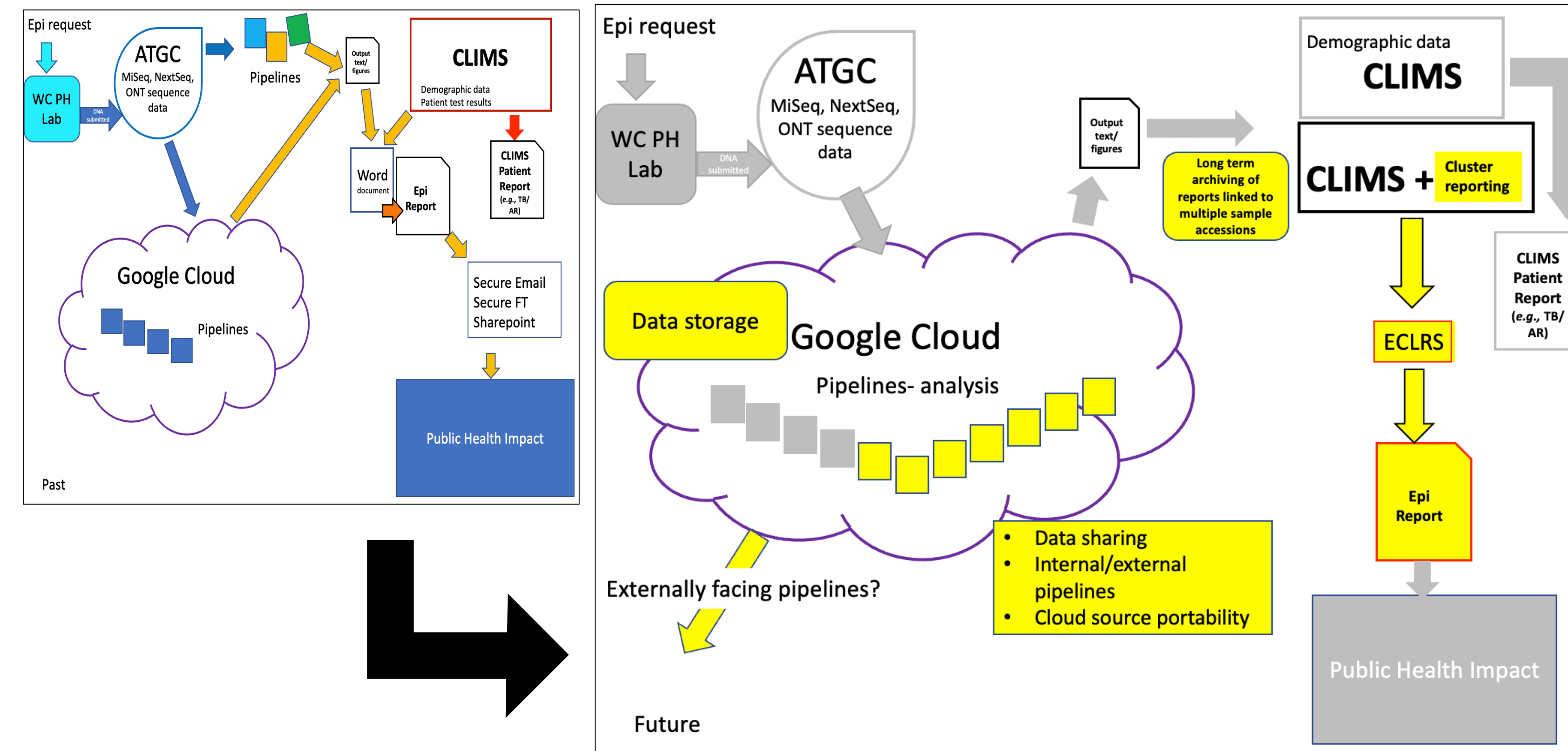
Test Ordering

- Electronic ordering (via data entry in Web Portal)
- Electronic ordering (via Excel, CSV, or HL7 files in Web Portal)
- HL7 Messaging (via UPHN)
- Paper (via Fillable PDF)

Result Reporting

- HTML or PDF (via Web Portal)
- HL7 Messaging (via UPHN and PHINMS)
- PDF Messaging (via UPHN)
- Paper (via USPS)
- Includes Communicable Disease reporting, EIP, Rabies, HIV, Food, TB, *C. auris*, Zika, and other outbreaks, etc.

CLIMS and Surveillance Reporting Vision



- An investigation report includes a description, summary information, and a list of included accessions along with preselected demographic data fields and select results (combining data and results from the LIMS with information generated via bioinformatics analyses).
- Attachments can be added to the report such as a SNP matrix, phylogenetic tree and any additional observations that are not able to be generated automatically.
- The report can continue to be manipulated when new accessions are added over time.
- All reporting is electronic through the LIMS and can be securely accessed through a web browser and downloaded by the requestor.
- Future enhancements will include the ability to generate SNP matrices and phylogenetic trees directly from the LIMS.

Previous Investigation Reports

Table 1: Isolates submitted for Whole Genome Sequencing

NYS IDR	Collection Date	Specimens Source	Carbapenemase Gene Variant	MLST	Secondary
IDR20001322-01-02	5/8/2022	Rectal swab	NDM-1/OXA-58	866	1436
IDR200013409-01-02	7/6/2022	Rectal swab	NDM-1/OXA-58	866	1436
IDR200013423-01-02	7/6/2022	Rectal swab	NDM-1/OXA-58	866	1436
IDR200013468-01-02	8/21/2022	Rectal swab	NDM-1/OXA-58	866	1436

Whole Genome Sequencing Analysis
Whole genome sequencing indicates that IDR2000021322 differs by 20 mutation events (ME) from IDR2000031395 and by 6 and 7 MEs from IDR2000031409 and IDR2000031425, respectively. The loss of one or more plasmids in IDR2000031395 may explain the differences in the number of MEs. Comparing the latter three isolates with each other shows only a difference of 1 or 2 MEs (Figure 1). All 4 isolates are considered related.

Reports sent to requesting epidemiologist through: **encrypted email, not audited and saved in various locations**

New Investigation Reports

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Reports sent to requesting epidemiologist through: **LIMS with auditing and saved long-term in this system**

Investigation Module

- Development Approach: iterative development and deployment with several phases**
- Load NGS generated results into CLIMS and produce reports (2016)
 - Allow users to create, manage, and report investigations (2022)
 - Streamline investigation workflow (iterative; improvements Q1 2023)
 - Increase amount of NGS data managed in CLIMS and automate loading (in progress)
 - Create processes to review and manage the NGS data (future)
 - Create tools to assist in the building of SNP matrix and phylogenetic tree (future)
 - Generate more complete and comprehensive Investigation Reports directly from CLIMS (iterative/in progress)

NGS Bioinformatic Pipeline Overview

Clinical NGS Pipelines:

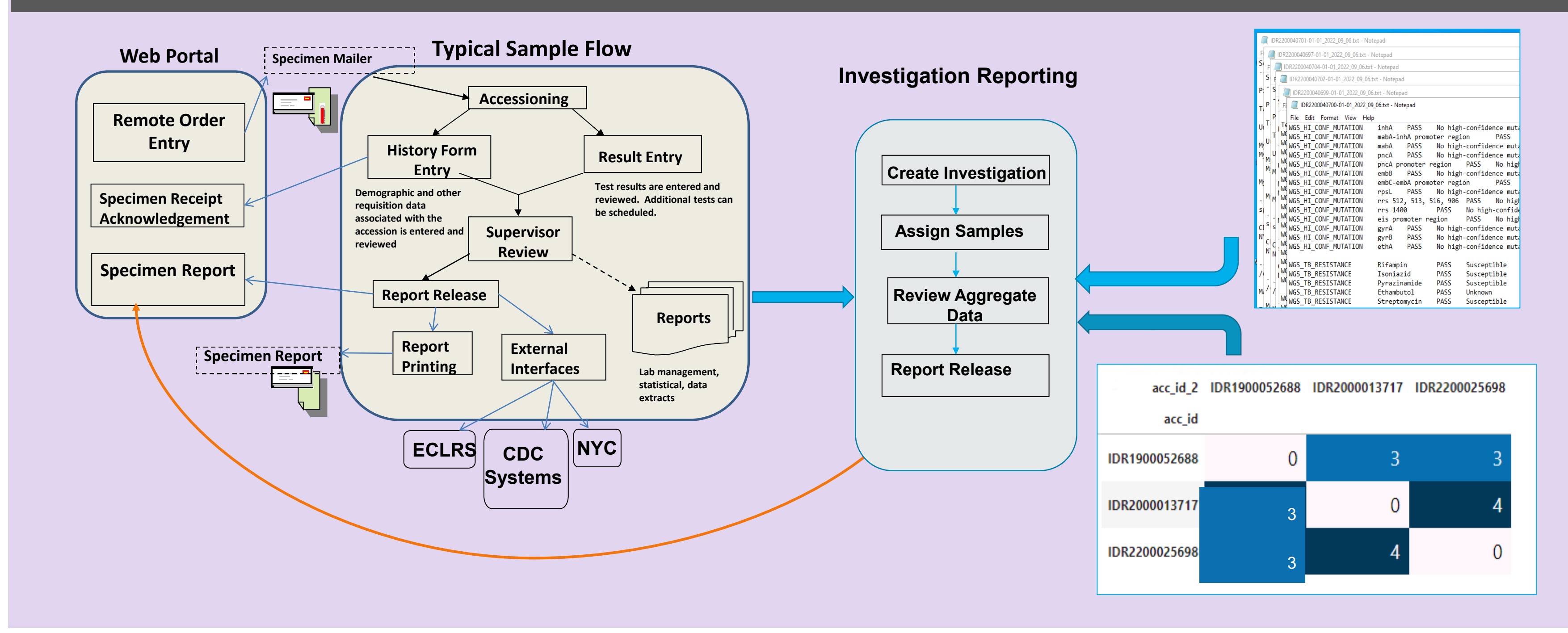
- M. tuberculosis* drug resistance
- AR WGS- MLST and gene variant
- Streptococcus pneumoniae* typing
- Group A *Streptococcus emm* gene typing

Surveillance NGS Pipelines:

- LegioCluster- Mutation event relatedness
- M. tuberculosis* -TB phylogeny, nearest neighbor, wgSNP cluster analysis

*An investigation consists of any number of accessions to be added; an accession can be associated with multiple investigations.
*Each original sample accession contains the bioinformatic pipeline outputs, quality control data associated with NGS metrics, pipeline details including version, and NCBI sequence identifiers.

CLIMS Architecture



Definitions:
 AR- Antimicrobial resistance
 MLST- Multilocus sequence typing
 EIP- Emerging Infections Program
 CSV-Comma separated values
 HL7- Health level 7
 UPHN- Universal public health node
 HTML- Hypertext markup language
 PDF- Portable document format

1. Create a New Investigation

The screenshot shows the 'Manage Investigation' window in the LIMS. It includes fields for 'Investigation Details', 'Submitter Information', 'Specimens', and 'Investigation'. A 'New Investigation' button is highlighted with a red arrow.

2. Add Samples to Investigation

The screenshot shows the 'Add Samples' window in the LIMS. It displays a table of samples with columns for 'Acc ID', 'Sample ID', and 'Status'. A red arrow points to the 'Add Samples' button.

3. Manage Investigation Reporting

The screenshot shows the 'Manage Investigation Reporting' window in the LIMS. It displays a table of reports with columns for 'Acc ID', 'Report ID', and 'Status'. A red arrow points to the 'Manage Investigation Reporting' button.

Conclusions

- The long-term impact of having NGS reporting consistently maintained, audited and available in our LIMS with direct connection to patient demographics represents a major improvement, particularly as WC plans to continue to expand its NGS offerings for both clinical and surveillance applications.
- These updates are critically important to ensure NGS data integration into our reports in order to provide the most actionable data to our epidemiologists and clinicians.

