

Analytical Validation Case Study: Exatype for Multi-Target Respiratory Virus Panels

Executive Summary

The COVID-19 pandemic underscored the global need for **fast, accurate, and scalable pathogen identification**. As respiratory-virus testing expands beyond single-target assays, the combination of **multiplexed amplification panels** and **next-generation sequencing (NGS)** has emerged as a powerful approach for comprehensive respiratory pathogen surveillance and identification. At the center of this evolution, [Hyrax Biosciences](#)' **cloud-based genomic analysis platform, Exatype**, provides a **platform-agnostic analysis** environment capable of transforming raw sequencing data into actionable genomic insights.

In this **analytical validation study**, **Exatype** was used to analyse datasets generated from **multiple respiratory virus panels** across a **range of sequencing platforms**.

Exatype's Key Capabilities:

- **Identification of the infecting virus or co-infections** with high confidence,
 - Generation of **consensus sequences**, foundational for novel assay design and continuous lineage tracking,
 - **Analysis and visualisation of coverage** across each target region to assess sequencing performance, and
 - Quantification of **amino acid and nucleotide variant prevalences**, providing insight into potential changes in viral fitness, transmissibility, or treatment resistance.
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Background & Rationale

The emergence of SARS-CoV-2 highlighted the limitations of traditional diagnostic approaches. During the COVID-19 pandemic, timely identification of pathogens - and their evolving variants - became critical to both **clinical decision-making** and **public health response**. **Exatype played a pivotal role** - processing approximately 42% of all SARS-CoV-2 genomes generated across the African continent (>72,000 genomes). This contribution established **Hyrax Biosciences** as a trusted analytical partner in large-scale genomic surveillance and rapid outbreak response.

Building on this foundation, we present an **analytical validation study demonstrating Exatype's capability for processing multi-target respiratory virus panels**. These assays, which amplify a wide range of pathogens from a single sample, have transformed respiratory testing. When combined with NGS and an analysis solution like Exatype, these assays enable

comprehensive and rapid identification of viruses such as **SARS-CoV-2**, **Influenza A/B** and **Respiratory Syncytial Virus (RSV)**.

Validation Results

Study Design

Exatype was used to analyse raw sequencing data from twenty respiratory virus samples obtained from public (n=16)^{1, 2, 3} and collaborator (n=4) sources. The data were generated with **different multi-target assays** (including the Illumina Respiratory Virus Oligo Panel (RVOP), Thermo Fisher Ion AmpliSeq FluAB Research Panel, and Twist Bioscience Respiratory Virus Panel)) across **Illumina**, **Ion Torrent**, and **Oxford Nanopore Technologies** platforms, using standardised, platform-specific workflows.

Quantitative Outcomes

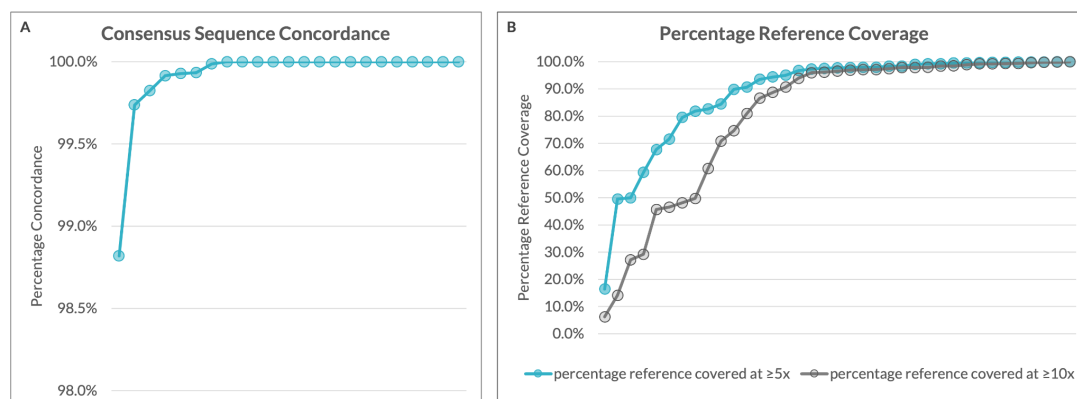


Figure 1: Consensus Sequence Concordance^{} and Reference Sequence Coverage**

Table 1: Key Outcomes Summary

Analytical Metric	Validation Result	Notes
Pathogen Identification	100% match to expected respiratory viruses*	Accurate identification of all viruses present, including mixed infections
Consensus Sequences	≥98.8% concordance ^{**} (Fig. 1A)	High reproducibility confirms analytical robustness
Coverage Depth	≥95% of reference covered at ≥5x; ≥85% covered at ≥10x across samples and platforms (Fig. 1B)	Coverage varied across samples and platforms but consistently met analytical thresholds
Sensitivity Threshold	Detection of minor variants ≥10%	Enables monitoring of within-sample diversity and emerging mutations

*for samples and/or regions with sufficient coverage (≥20x for Illumina paired-end reads, ≥30x for Illumina single-end reads, Ion Torrent and Nanopore)

[#]where comparator consensus sequences were available



Exatype: Analytical Validation and Real-World Genomic Insight

Analytical Insights: Precision Through Integration

Exatype provides a comprehensive analytical framework for **multi-target respiratory virus sequencing**, delivering precision and depth beyond standard pathogen identification. Each analysis produces **complete consensus sequences**, **coverage profiles** across all target regions, and **quantitative amino acid and nucleotide variant prevalences**, all generated within a single, integrated workflow. These results enable laboratories and assay developers to **evaluate assay performance**, **confirm amplification success**, and **monitor emerging mutations** with implications for viral fitness, transmissibility, or therapeutic response. By consolidating these functions into one validated platform, **Exatype** ensures **analytical consistency** and **reproducibility** across sequencing technologies and assay formats.

Practical Value: From Analysis to Application

The analytical capabilities of **Exatype** extend beyond assay-specific performance, supporting **standardisation**, **reproducibility**, and **transparent data interpretation** across sequencing technologies. By integrating **Exatype**, laboratories and assay developers gain a unified framework for **comparative analysis**, **performance benchmarking**, and **variant tracking**. This interoperability strengthens data integrity, accelerates research translation, and supports surveillance initiatives where consistent, high-quality results are essential.

Conclusion

This analytical validation confirms that the **Exatype** platform provides **accurate, reproducible, and biologically meaningful** analysis of multi-target respiratory virus panels. Across **three leading sequencing technologies** and **multiple commercial assays**, **Exatype** consistently reproduced expected results with high concordance - while providing enhanced visibility into viral genome coverage and variation.

As respiratory virus testing evolves beyond simple detection, **Exatype** enables laboratories to extract deeper genomic insight from their data - supporting not only identification but also **surveillance, variant tracking, and public health preparedness**. In doing so, **Exatype** establishes an analytical standard for precision, scalability, and insight in pathogen genomics.



References

1. [Mu et al., 2023, The combined effect of oseltamivir and favipiravir on influenza A virus evolution in patients hospitalized with severe influenza, Antiviral Research, 216: 105657](#)
2. [Goya et al., 2023, Genomic Characterization of Respiratory Syncytial Virus during 2022-23 Outbreak, Washington, USA, Emerging Infectious Diseases, 29 \(4\): 865-868](#)
3. [Mehta et al., 2021, Respiratory Co-Infections: Modulators of SARS-CoV-2 Patients' Clinical Sub-Phenotype, Frontiers in Microbiology, 12: 653399](#)

