



Enrich SURVEILLANCE



Advancing SARS-CoV-2 surveillance

The COVID-19 pandemic has strongly highlighted the importance of viral surveillance. Sequencing is now broadly used to monitor the viral genome and its evolution in the population, as well as to detect new emerging variants and study their impact on antiviral drugs and vaccine efficacy. High-performing sample prep workflows are needed to unlock the information from every sample. After sequencing, a reliable analytics solution is needed to accurately analyze the data. Roche is partnering with Hyrax Biosciences to provide a software solution that turns raw sequence data into meaningful results.

Enrich, sequence, and report with confidence

High-quality results

Achieve uniform and broad genome coverage with the KAPA RNA HyperCap workflow—Confidently detect and report variants with the Exatype platform

Minimize time

Save valuable time and maintain data quality by 1-hour hybridization with the KAPA HyperCap SARS-CoV-2 panel—Report your findings faster by on-cloud parallel processing using the intuitive interface of the Exatype platform

Scalability

Scale up with ease using the streamlined, automation friendly, KAPA HyperCap workflow and Hyrax Biosciences' secure, cloud-based IT infrastructure

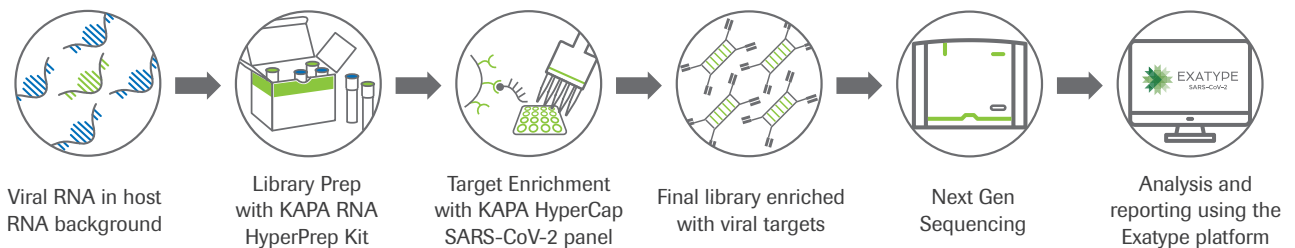
Proven technology

Hybrid capture based methods may better detect relatively divergent SARS-CoV-2 sequences of new emerging variants¹

Proven expertise

Roche and Hyrax Biosciences combine their proven expertise in sample prep and reporting to offer a complete, end-to-end solution for SARS-CoV-2 surveillance

From sample preparation to meaningful results



¹Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health. 8 Jan 2021 | COVID-19: Laboratory and diagnosis. World Health Organization.

Rely on proven expertise in viral genome sequence analysis



Hyrax Biosciences is driven by one overriding goal: to automate the analysis and interpretation of pathogen DNA-sequence data. Exatype—their DNA analysis platform—delivers consistently accurate and clear reporting at scale, without the need for human intervention. The read mapping and alignment algorithms are the foundation of Exatype and are designed to enable analysis of any disease through customizable applications in the near future.

Enjoy a user-friendly experience

- Detect emerging variants with confidence with the KAPA HyperCap SARS-CoV-2 panel and the Exatype platform
- Experience an intuitive interface with five simple steps to data analysis at hpr.exatype.com
- Review and download variant reports, coverage plots, sequencing metrics, consensus sequences for GISAID upload



EXATYPE™
SARS-CoV-2



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Create job

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Create a new job **SARS-CoV-2**

Job name

Job details (Optional - for your reference)

Next

01 Job details | 02 Data format | 03 Select data | 04 Sample details | 05 Review & submit



View results

Sample name

Results

Completed Samples

Sample name: Sample_001

Sequencing platform: Illumina

Sample ID: d3482a2b-dc01-4099-b484-c1ec6b92136a

Sample status: **Completed**

Sample coverage plot

Lineage/Clade typing

Sample	Pangolin (2.4.2 - 2021-04-28) ¹	Nextstrain clade (0.14.2) ²	Nextstrain AA substitutions (0.14.2) ²	Nextstrain AA deletions (0.14.2) ²
Sample_001	B.1.1.7	20I/501Y.V1	ORF1a: T100L, A1708D, L2230T ORF1b: P218L, P314L, P1975S, K2557R S: N501Y, A570D, D614G, A653V, P681H, T716I, S982A, D1118H, M1229I ORF8: Q27, R52L, K68, Y73C N: M1X, D3L, R203K, G204R, S235F	ORF1a: S367S, G367E, F367T S: H69, V70, Y144-

Download as CSV ¹<https://github.com/cov-lineages/pangolin> ²<https://clades.nextstrain.org/>

Sequence file downloads

Amino acid mutations

Nucleotide mutations

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