

Accukit™ SARS-CoV-2 RNA

Standardized Nucleic Acid Quantitation for Sequencing (SNAQ-SEQ) is an innovative QC method that uses mixtures of synthetic DNA or RNA as internal standards (IS) for NGS-based assays. The IS mixtures are identical to the sequencing target regions that are added to each sample prior to NGS library prep and will covary with the sample to provide an ideal run control approach for systemic and technical sequencing errors.

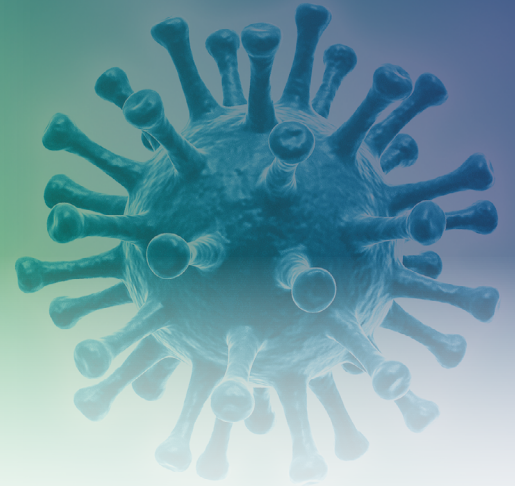
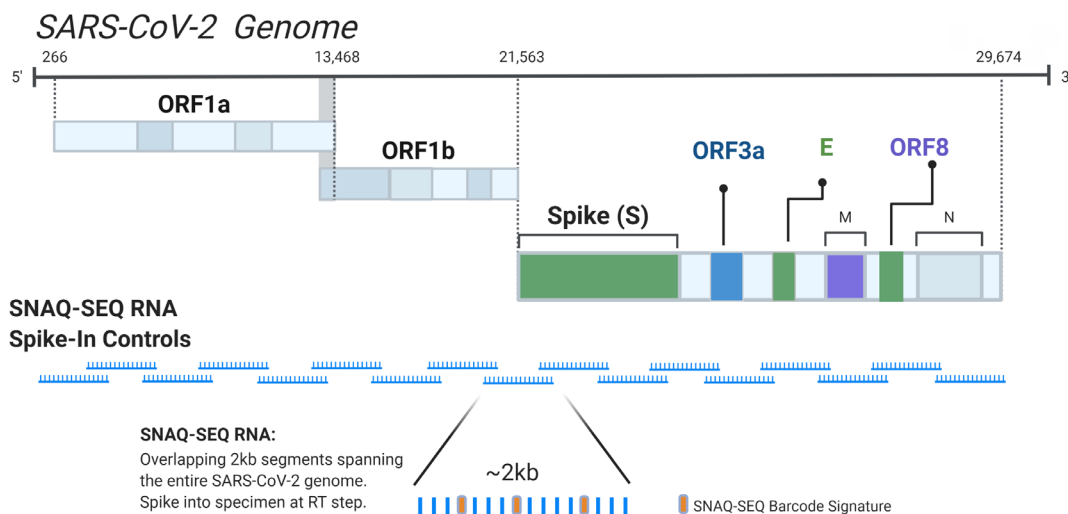
SARS-CoV-2

The rapid emergence of the COVID-19 pandemic has thrust tools like next generation sequencing (NGS) applications to the forefront of the global public health response. NGS is a sensitive and specific tool that is being used to detect the presence of the SARS-CoV-2 virus from a variety of sample types both clinical and environmental.

Tracking SARS-CoV-2 viral strain evolution is critical for monitoring new regional outbreaks, contact tracing, infection control and verifying the performance of front-line RT-PCR diagnostic assays. Being able to report accurate sequence variations confidently, is critically important.

The Accukit SARS-CoV-2 RNA standard is a mixture of 17 synthetic RNA overlapping constructs spanning the entire SARS-CoV-2 genome. When added to the RNA from the extracted sample prior to the reverse transcription (RT) step, will control for systemic and technical errors through the entire workflow. It also contains a complexity control (65k unique molecules) to estimate library preparation and bioinformatic impact on complexity capture for each sample.

Accukit™ SARS-CoV-2 RNA Standards



Applications

SEQUENCE ACCURACY (LIMIT OF BLANK)

Accukit SARS-CoV-2 RNA standards co-located with the target sample measure background error due to library prep, sequencing, or other factors. The input sequence of the SARS-CoV-2 standards are known so any output variation would have arisen from process error. Thus, the standards provide a limit of blank (LOB) for every position measured and help to eliminate variant caller error, particularly with low frequency alleles. The complexity control provides an independent quantitative measure of each sample's molecular diversity yield in support of assessing reagent quality and performance drift.

LIMIT OF DETECTION (LOD)

When added in a limiting amount to every sample, Accukit SARS-CoV-2 provides LOD control for qualitative detection assays. By virtue of being in each sample, it assures the assay met its sensitivity performance threshold, even in the absence of a positive target. A positive control for a negative result.

QUANTIFICATION OF VIRAL LOADS

The sequencing read ratio between Internal standard and viral genome can be used to measure the viral abundance. The abundance reporting range varies by library preparation, but protocols like Arctic have supported accurate viral measurements for samples ranging from CT22 to CT35.

PIPELINE INDEPENDENT QC

Standardize intra- and inter-lab testing, across platforms, operators, assays and geographies to improve the quality of the result and ensure optimal reagent performance with every run.

Feature	Specifications		
Catalog Number	1270	1269	1231
Design Coverage	Covers 99% (29,852 bases of 29,870 bases of the SARS-Cov-2 genome)		
Internal Standards Mixtures (ISM)	17 overlapping constructs; ~2kb construct size		
Complexity Control Included	Yes, 65,536 potential unique molecules (input)		
Nominal Input Amount	1,000 copies of ISM	250 copies of ISM	1,000 copies of ISM
Format and Concentration	RNA Mixture, 1,000 copies per ul	RNA Mixture, 250 copies per ul	RNA Mixture, 1,000 copies per ul
Volume	8 - 50 ul vials	8 - 50 ul vials	2 - 50 ul vials
SARS-CoV-2 Assay Compatibility	ARTIC amplicon primers v3 + Illumina/Oxford Nanopore	POLAR amplicon primers v3 + Illumina	Ion Ampliseq SARS-CoV-2 Panel + Ion S5 + Genexus

For more information: info@accugenomics.com