AccuGenomics
A higher standard of accuracy

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 native target (NT) 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.
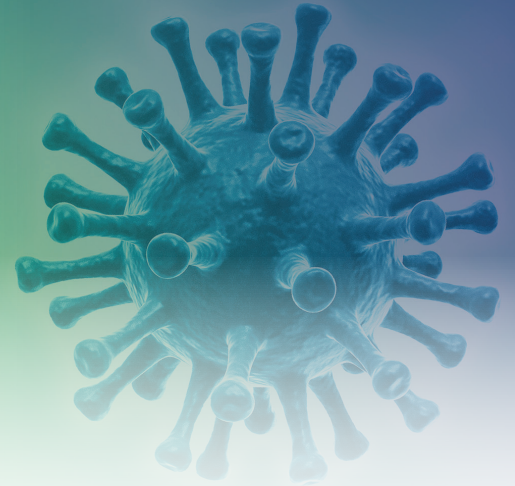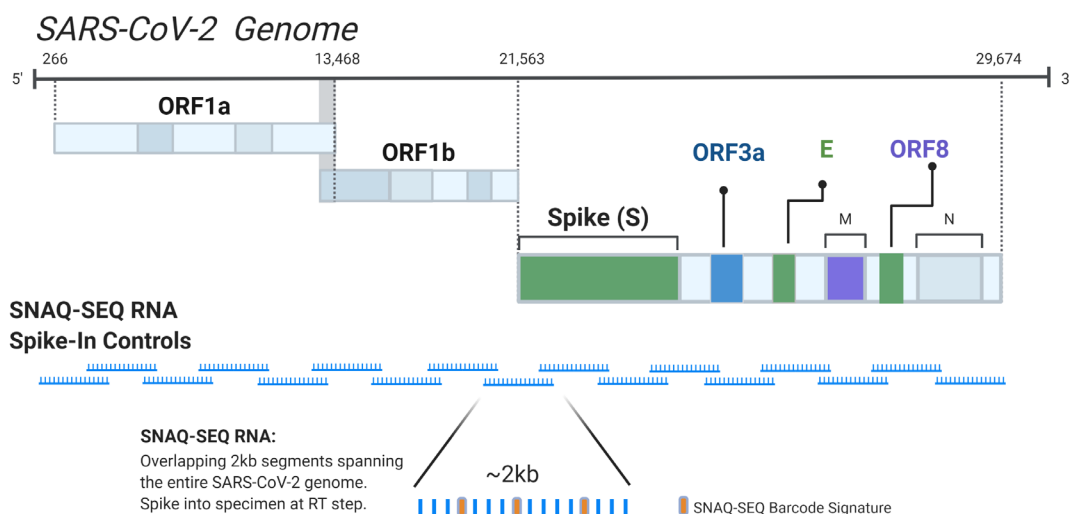
SARS-CoV-2

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 (and track the emergence of new variants) from a variety of sample types (clinical and wastewater).

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 confidently report accurate sequence variations is also critically important. SARS-CoV-2 Accukits are used for diagnostic and surveillance (wastewater) applications.

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

Accukit™ SARS-CoV-2 RNA Standards

SARS-CoV-2 Genome
266 13,468 21,563 29,674
5' 3'
ORF1a
ORF1b
Spike (S)
ORF3a E ORF8
M N

SNAQ-SEQ RNA Spike-In Controls

SNAQ-SEQ RNA:
Overlapping 2kb segments spanning the entire SARS-CoV-2 genome. Spike into specimen at RT step.

~2kb

SNAQ-SEQ Barcode Signature

Applications

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 that each assay has met its sensitivity performance threshold, even in the absence of a positive target signal. The Accukit serves as an internal positive control, even for a negative result.

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.

QUANTIFICATION OF VIRAL LOADS

The sequencing read ratio between Internal standard (IS) and native template (NT) 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	#1851: (Artic v3/v4/v4.1 Omicron)	#1881: (Midnight)
Internal Standards Mixtures (ISM)	33 overlapping constructs; with Complexity Control	29 overlapping constructs; with Complexity Control
Nominal Input Amount	2,000 copies of ISM (assuming complexity capture > 10%)	2,000 copies of ISM (assuming complexity capture >2%)
Format, Volume and Concentration	ssRNA Mixture; provided in 8 x 50 ul vials (2,000 copies/ul), 400 reactions	ssRNA Mixture; provided in 2 x 50 ul vial (10,000 copies/ul), 500 reactions
Design Coverage	Covers >99% (29,852 bases of 29,870 bases of the SARS-Cov-2 genome), full panel coverage for each Accukit	
Complexity Control Included	Yes, >65,000 unique molecules (input)	
SARS-CoV-2 Assay Compatibility	Illumina/TMO/Oxford Nanopore (Amplicon or hybrid capture)	

For more information: info@accugenomics.com

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