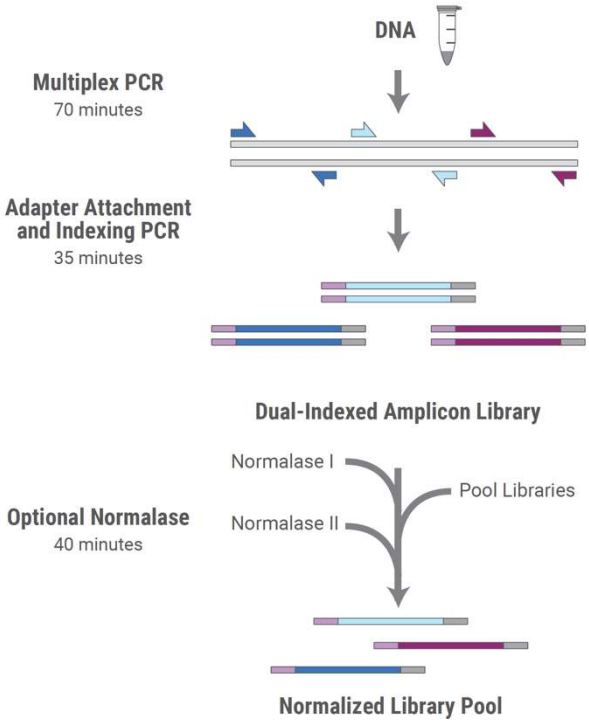
SWIFT NORMALASE™ AMPLICON SARS-CoV-2 PANEL

Whole viral genome single-tube NGS assay with 2-hour workflow

Description

The Swift Normalase Amplicon Panel (SNAP) for SARS-CoV-2 offers a robust NGS workflow that provides optimal coverage and data quality on Illumina® sequencing platforms. This kit leverages Swift's multiplex PCR technology, enabling library construction from cDNA using tiled primer pairs to target the full-length 29.9 kb viral genome with a single pool of multiplexed primer pairs. Primers were designed against the NCBI Reference Sequence NC_045512.2 (Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome).

SNAP kits utilize multiple overlapping amplicons in a single tube, using a rapid, 2-hour workflow to prepare ready-to-sequence libraries. The PCR1+PCR2 workflow generates robust libraries, even from low input quantities. The libraries may be quantified with conventional methods such as Qubit® or Agilent Bioanalyzer and normalized by manual pooling or normalized enzymatically with the included Swift Normalase reagents.



Specifications

Feature	Specification
Design Coverage*	98% (29,313 of 29,903 total bases)
Panel Information	341 amplicons, sized 116-255 bp (average 150 bp)
Input Material	1st or 2nd strand cDNA Minimum 10-100+ viral copies (qRT-PCR Ct value 30-40)
Time	2 hours cDNA-to-Library or 3 hours cDNA-to-Normalized-Library-Pool
Components Provided	Target-specific multiplex primer pool • PCR and library prep reagents Swift Normalase • Combinatorial Dual Indexed Adapters Note: kits do not include RT module or magnetic beads
Multiplexing Capability	Up to 384 CDI • Inquire for custom indexing and UDIs
Recommended Depth	50K reads/library (+/- detection); 1M reads per library (variant calling)

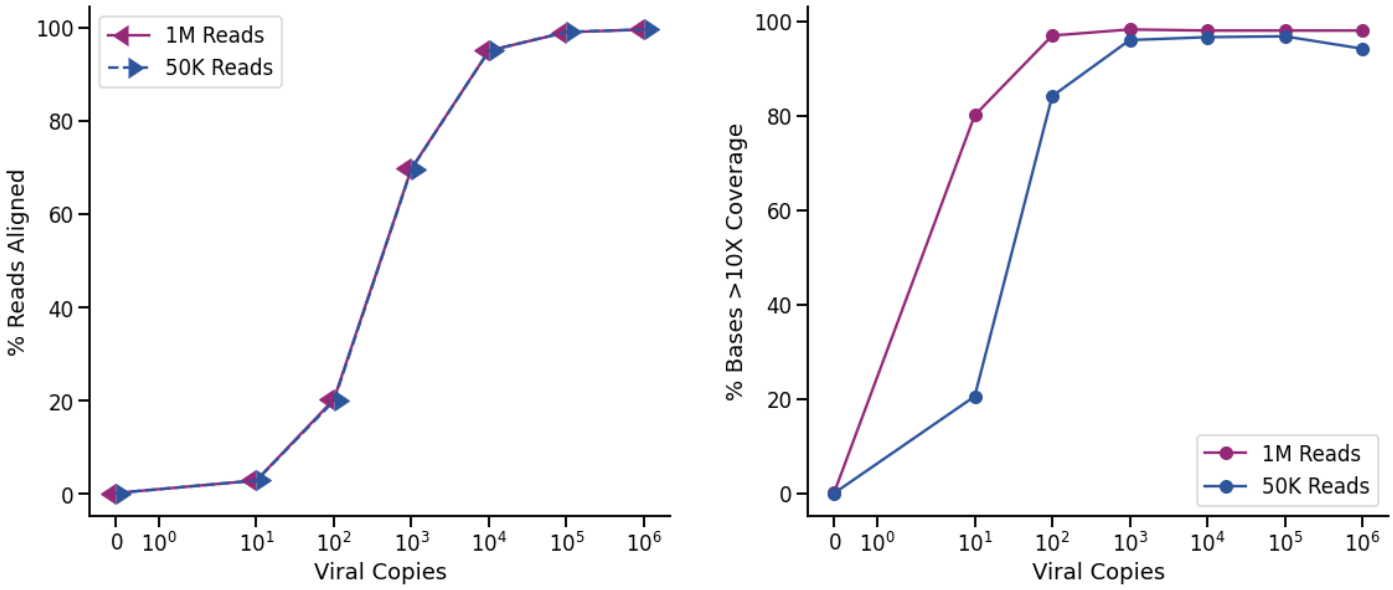
* Please inquire with your Swift sales representative or distributor to review a copy of the primer design file.

Applications and Sample Types

- Applications: Detection, Variant Calling, Screening, Epidemiological Studies, Public Health Surveillance
- Sample Types: nasopharyngeal/oropharyngeal swabs, sputa, bronchoalveolar lavage (BAL), stool

High Performance Over a Wide Range of Viral Copy Number

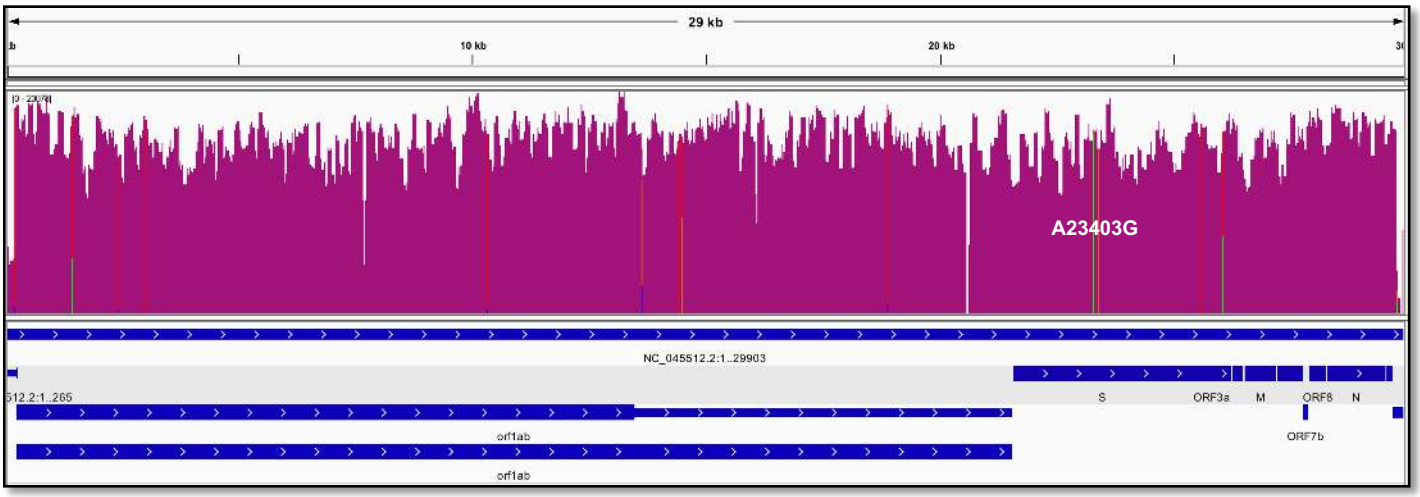
The SNAP SARS-CoV-2 Kit was tested with inputs ranging from zero to 1 million viral genome copies mixed with 50 ng of Universal Human Reference (UHR) RNA to simulate host background. Mixed RNA samples were converted into first-strand cDNA and used as input into the SNAP SARS-CoV-2 kit. Libraries were enzymatically normalized to 4nM using the Normalase workflow provided in the SNAP protocol prior to sequencing.



SARS-CoV-2 synthetic template material (Twist Bioscience Cat. No. 102024) was mixed with UHR RNA (Agilent 740000) and converted into first-strand cDNA using the Superscript® IV First-Strand Synthesis System (Thermo Fisher 18091050). cDNA was processed with the Swift SNAP SARS-CoV-2 Kit, sequenced with Illumina® MiniSeq® 2 x 150 bp chemistry and downsampled to 50,000 or 1 million reads per sample. These plots illustrate the percentage of reads aligned to the NC_045512.2 reference (left) and the percentage of SARS-CoV-2 genomic bases covered at >10X depth (right) vs. viral copy number.

Complete Coverage Enables Detection of Key Variants

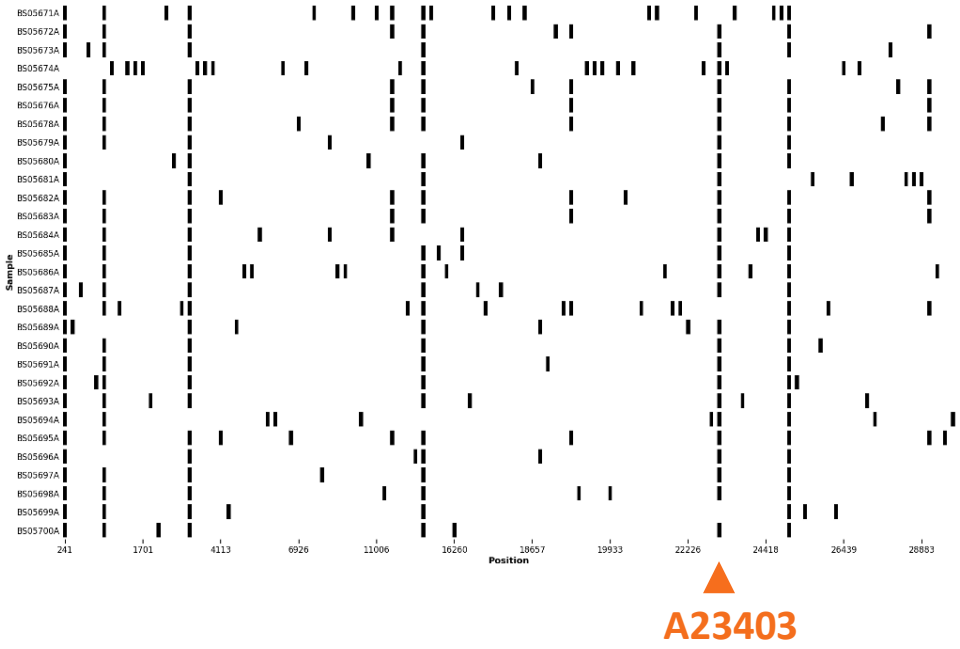
The SNAP SARS-CoV-2 Kit uses a single-tube multiplex primer pool to generate amplicons along the length of the 29.9 kb viral genome. Sequencing the full-length SARS-CoV-2 genome is important as it enables detection of known key variants of interest as well as discovery of novel mutations. Confident mutation detection is crucial for tracking nucleotide variants and improving our understanding of virus evolution, transmission, and pathogenesis.



A nasopharyngeal swab specimen processed with the Swift SNAP SARS-CoV-2 Kit and sequenced with Illumina® MiSeq® to 50,000 reads demonstrates coverage across the 29.9 kb genome. The A23403G/D614G mutation was detected in this sample, which affects the viral spike protein and is a key variant of interest for its hypothesized role in transmissibility of COVID-19.

Establish Comprehensive Mutation Profiles from Challenging Specimens

Department of Pathology investigators at NYU Grossman School of Medicine are using Swift's SNAP SARS-CoV-2 Kit to identify mutation profiles from specimens with qRT-PCR Ct values ranging from 16 to 42. Following presence/absence assessment using qRT-PCR, excess cDNA was used as input into the Swift SNAP workflow to establish an NGS-based mutation profile for public health surveillance.



"Swift has been a valued research partner, and we look forward to working with them to continually improve the ability of amplicon-based methods to achieve greater coverage in fewer reads, which would enable us to achieve good genome coverage for low viral load samples."

– Adriana Heguy, PhD, Professor of Pathology at NYU Langone Health, NYU Grossman School of Medicine

A total of 29 nasopharyngeal swab specimens were processed with the Swift SNAP SARS-CoV-2 Kit by NYU Langone Health and sequenced with Illumina® MiSeq® to 50,000 reads. Sequencing data was aligned to the NC_045512.2 reference using BWA and variants were called using GATK Haplotype Caller. Variants with allele fractions of 0.5 or greater are shown. The location of the A23403G/D614G mutation, a key variant of interest, is highlighted and was detected in 26 of the 29 sequenced libraries.

Ordering Information

Workflow Component	Product Name	Catalog Number
Primer Pool	SARS-CoV-2 Panel (96 rxns)	COVG1-96
SNAP Core	Swift Normalase Amplicon Protocol SNAP Core (96 rxns, no indexing)	SN-5X296
Indexing Primers*	SNAP Combinatorial Dual Index Primer Kit (Set 1A, 96 rxns)	SN-5S1A96
	SNAP Combinatorial Dual Index Primer Kit (Set 1B, 96 rxns)	SN-5S1B96
	SNAP Combinatorial Dual Index Primer Kit (Set 2A, 96 rxns)	SN-5S2A96
	SNAP Combinatorial Dual Index Primer Kit (Set 2B, 96 rxns)	SN-5S2B96

**Please inquire for custom index primer compatibility (UDIs, etc.).*

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