



# SWIFT NORMALASE® AMPLICON PANELS (SNAP)

## 16S v2 Panel and ITS1 Panel

Single pool high complexity NGS microbial enrichment assays

### Highlights

- Two multiplexed assays cover all variable regions of the 16S v2 rRNA and ITS1 regions
- Integrated library normalization enables streamlined library balancing and pooling process without the need to quantify samples
- 16S and ITS1 regions separated into two assays to enable independent balancing of sequencing read depth for each region
- Improved coverage uniformity of the 16S variable regions for increased data quality
- ITS1 primer re-design to increase data output from PE 150 sequencing

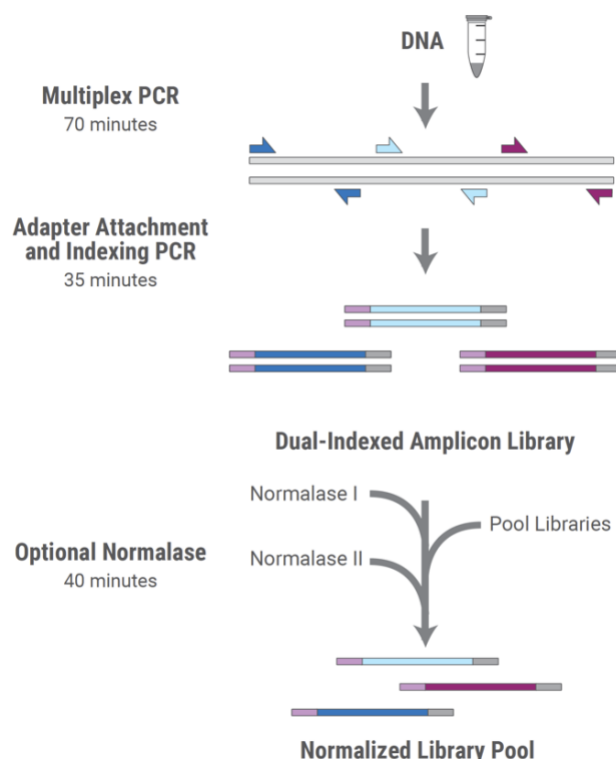


### Introduction

The Swift Normalase Amplicon Panels (SNAP) for 16S v2 and ITS1 offers a robust NGS workflow that provides optimal coverage and NGS data quality on Illumina® sequencing platforms. These kits leverage Swift's multiplex PCR technology, enabling library construction from DNA using tiled primer pairs to target all V1-V9 variable rRNA regions and the ITS1 region, each with a single pool of multiplexed primer pairs.

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.

In addition, the SNAP 16S v2 and ITS1 panels facilitate NGS analysis of complex microbial communities (e.g. bacteria, archaea, fungi) using single primer pools that target the 16S rRNA gene (variable regions 1-9) and ITS1 region. These panels can be customized with additional targets including antibiotic resistance or virulence genes, allowing sub-genera level identification and functional analysis.



# Supported Applications

Metagenomics, Microbiome, Environmental studies Agricultural and soil microbial health studies, detection and characterization of bacterial and fungal structure in complex samples, custom targets including functional genes like ARGs/AMRs (please inquire).

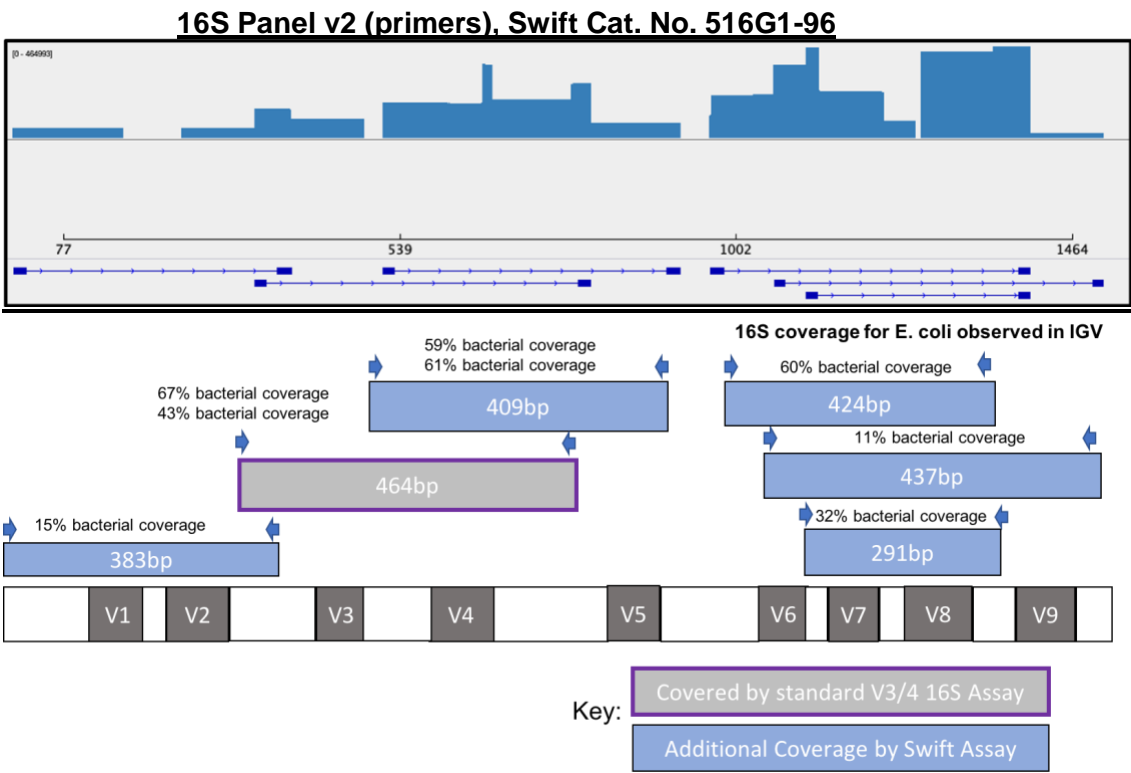
# Specifications

Feature	SNAP 16S v2 Panel and ITS1 Panel
Panel Information*	16S V2 (23 primers); Average 425 bp amplicon size ITS1 (15 primers); Amplicon size 145-695 bp
Input Material	10 pg for microbial isolates; 1-50 ng for metagenomic samples
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 magnetic beads
Multiplexing Capability	Up to 1536 CDI • Inquire for custom indexing and UDIs
Recommended Depth	16S v2: 100K reads per library ITS1: 25K reads per library

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

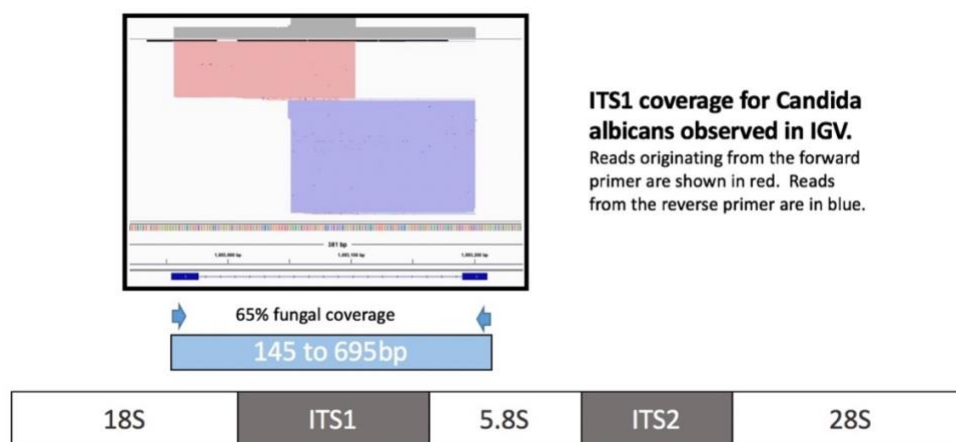
# Coverage of All Variable Regions of the 16S rRNA Gene and ITS1 Region

The SNAP 16S v2 and ITS1 Panels facilitate NGS analysis of complex microbial communities (e.g. bacteria, archaea, fungi) using primer pools that target the 16S rRNA gene (variable regions 1-9) and ITS1 region. In addition, these panels can be customized with additional targets including antibiotic resistance or virulence genes, allowing sub-genera level identification and functional analysis.



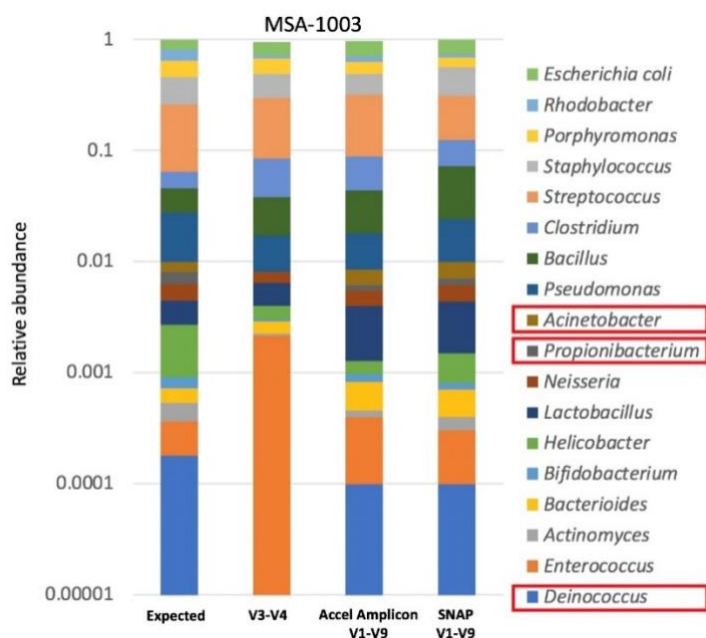
Sequencing read coverage (IGV Sashimi plot) and illustration of multiplexed primer coverage of all nine variable regions of 16S rRNA.

## ITS1 Panel (primers), Swift Cat. No. 517G1-96



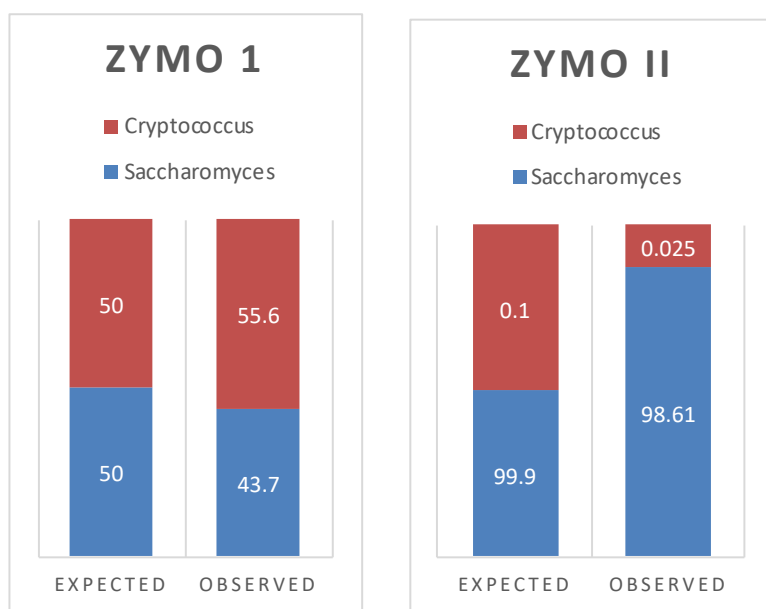
Sequencing read coverage (IGV) and illustration of multiplexed primer coverage of ITS1 region from *C. albicans*.

## Panels Provide Superior Representation of Diverse Microbial Communities

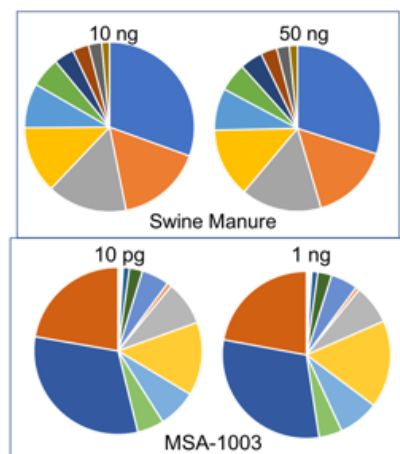


The 16S v2 panel covering V1-V9 regions of 16S rRNA (Swift Cat. No. 516G1-96) provides accurate representation of each genus in a commercially available standard (MSA-1003) compared to libraries interrogating the V3-V4 region alone. The Swift Accel-Amplicon and 16S v2 SNAP panels performed equally. Strains were present at levels from 0.02% to 18% in MSA-1003. Organisms marked in red were not detected with sole use of the V3-V4 region.

The panel covering the ITS1 region (Swift Cat. No. 517G1-96) provides accurate representation of each genus in two commercially available standards (Zymo I- ZymoBIOMICS Microbial Community standard and Zymo II- ZymoBIOMICS Microbial Community standard II (Log distribution)). Fungal strains were present at levels from 0.1% to 99.9% in Zymo II. The ITS1 SNAP panel performance resulted in expected representation of the fungal species in a bacterial background.



## Consistent Performance with Varying Biomass, Sample Type, & Read Length



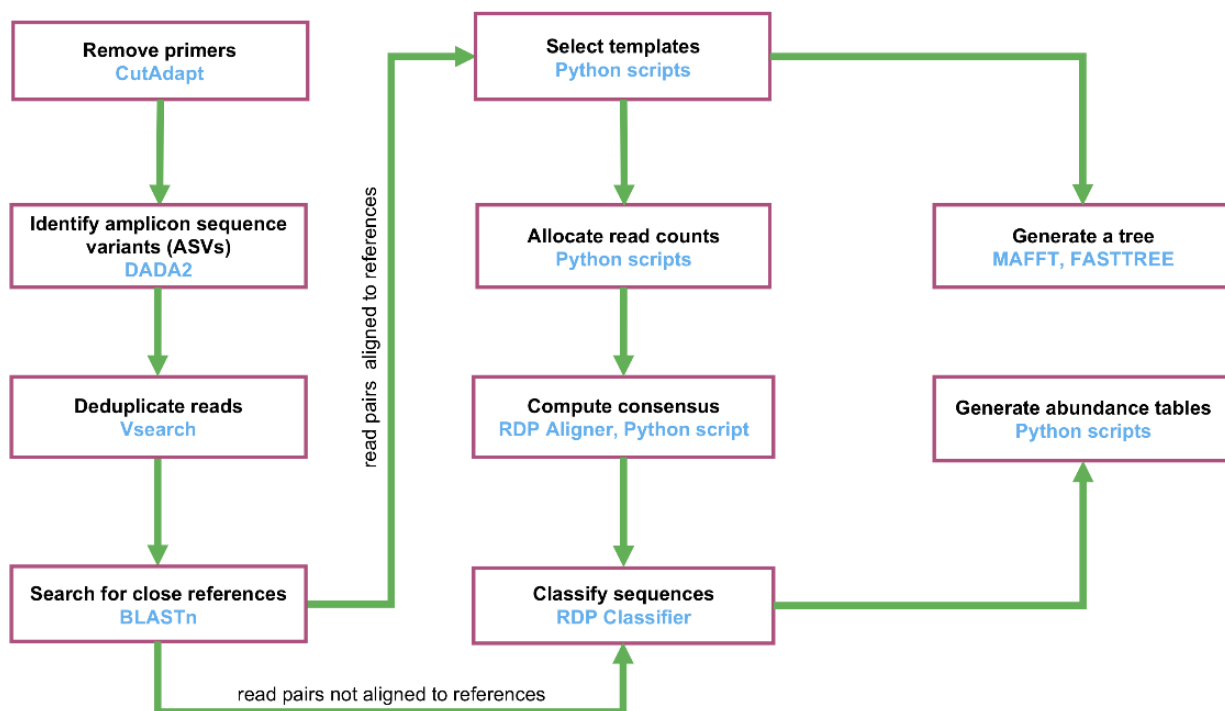
Sample	Accel-Amplicon V1-V9 2x150 PE sequencing		16S SNAP V1-V9 2x150 PE sequencing		Accel-Amplicon V1-V9 2x300 PE sequencing	
	Shannon Species Diversity	% Reads PF Classified to Genus	Shannon Species Diversity	% Reads PF Classified to Genus	Shannon Species Diversity	% Reads PF Classified to Genus
Manure 1	2.84	94.1%	2.72	95.2%	2.84	92.5%
Manure 2	2.87	94.6%	2.80	92.2%	2.85	92.8%
Manure 3	2.71	94.6%	2.92	92.5%	2.69	92.6%
Manure 4	2.74	95.0%	2.98	93.8%	2.70	93.6%

Using the same protocol and cycling conditions, input quantities of 10 pg to 50 ng with both MSA-1003 (bottom left) and swine manure (top left) gave consistent and expected sequencing results in terms of sensitivity and relative abundance. The Accel-Amplicon 16S+ITS and 16S v2 SNAP products gave similar results (top). When comparing 2x150 and 2x300 PE reads, a comparable number of species were identified from swine manure samples (right).

## 16S SNAP APP: Multiple Variable-Region Aware Read Classification Tool

Multi V-region 16S NGS data generated with the 16S Panels may be processed and analyzed by an open-source tool, the 16S SNAP APP, published by Swift Biosciences at <https://github.com/swiftbiosciences/snapp>. Details for Fastq read processing using 16S SNAP APP can be found in the README file included at the Github repository and in the Technical Note. For ITS1 data analysis support, please contact us at [techsupport@swiftbio.com](mailto:techsupport@swiftbio.com)

### SNAP-APP for 16S multi-amplicon analysis



## Ordering Information

Workflow Component	Product Name	Catalog Number
<b>Primer Pools</b>	16S v2 Panel (96 rxns)	516G1-96
	ITS1 Panel (96 rxns)	517G1-96
<b>SNAP Core</b>	Swift Normalase Amplicon Panels (SNAP) Core Kit (96 rxns)	SN-5X296
	Swift Normalase Amplicon Panels (SNAP) Core Kit (4x96 rxns Bundle)	SN-5X384
<b>CD Indexing Primers*</b>	SNAP Set 1A Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S1A96
	SNAP Set 1B Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S1B96
	SNAP Set 2A Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S2A96
	SNAP Set 2B Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S2B96
	SNAP Set S1AB-S2AB Combinatorial Dual Indexing Primers (384-plex, 4x96 rxns Bundle)	SN-5S0384
<b>UD Indexing Primers*</b>	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns SU001-SU096)	SN91096-1-PLATE
	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns SU097-SU192)	SN91096-2-PLATE
	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns SU193-SU288)	SN91096-3-PLATE
	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns SU289-SU384)	SN91096-4-PLATE
	SNAP Unique Dual Indexing Primer Plate (384-plex, 4x96 rxns Bundle)	SN91384-PLATES
	SNAP Unique Dual Indexing Primer Plate (1536-plex, 16x96 rxns Bundle)	Please inquire

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

Visit [www.swiftbiosci.com](http://www.swiftbiosci.com) to order.



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