



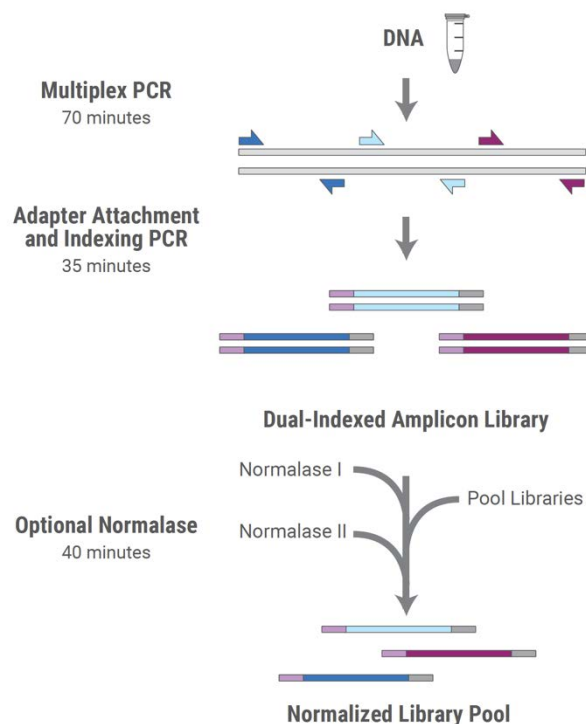
# SWIFT NORMALASE® AMPLICON 16S & ITS1 PANELS

## Single pool high complexity NGS microbial enrichment assays

### Description

The Swift Normalase Amplicon Panels (SNAP) for 16S and ITS1 offers a robust NGS workflow that provides optimal coverage and NGS data quality on Illumina® sequencing platforms. This kit leverages Swift's multiplex PCR technology, enabling library construction from DNA using tiled primer pairs to target either (a) all V1-V9 variable regions or (b) ITS1, 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.



### Highlights

- Profiles complex metagenomic samples: Multiplexed assay covers all variable regions of the 16S rRNA or ITS1 genes in a single primer pool
- Integrated library normalization: Swift's unique Normalase chemistry enables streamlined library balancing and pooling without the expense of quantification kits
- Solves sequencing complexity problems: Unique amplicon chemistry generates diverse clusters without PhiX or phased primers, recovering >20% of reads
- Saves costs: Flexibility with Illumina® sequencers and read lengths
- Fast workflow, high quality data: From DNA to Illumina® compatible libraries within 2 hours

### Specifications

Feature	SNAP 16S Panel or ITS1 Panel
<b>Panel Information</b>	17 primers (16S) or 15 primers (ITS1); Average 425 bp amplicon size
<b>Input Material</b>	1 ng bacterial or fungal template DNA
<b>Time</b>	2 hours cDNA-to-Library or 3 hours cDNA-to-Normalized-Library-Pool
<b>Components Provided</b>	Target-specific multiplex primer pool • PCR and library prep reagents Swift Normalase • Combinatorial Dual Indexed Adapters Note: kits do not include magnetic beads
<b>Multiplexing Capability</b>	Up to 384 CDI • Inquire for custom indexing and UDIs
<b>Recommended Depth</b>	100K reads per library

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

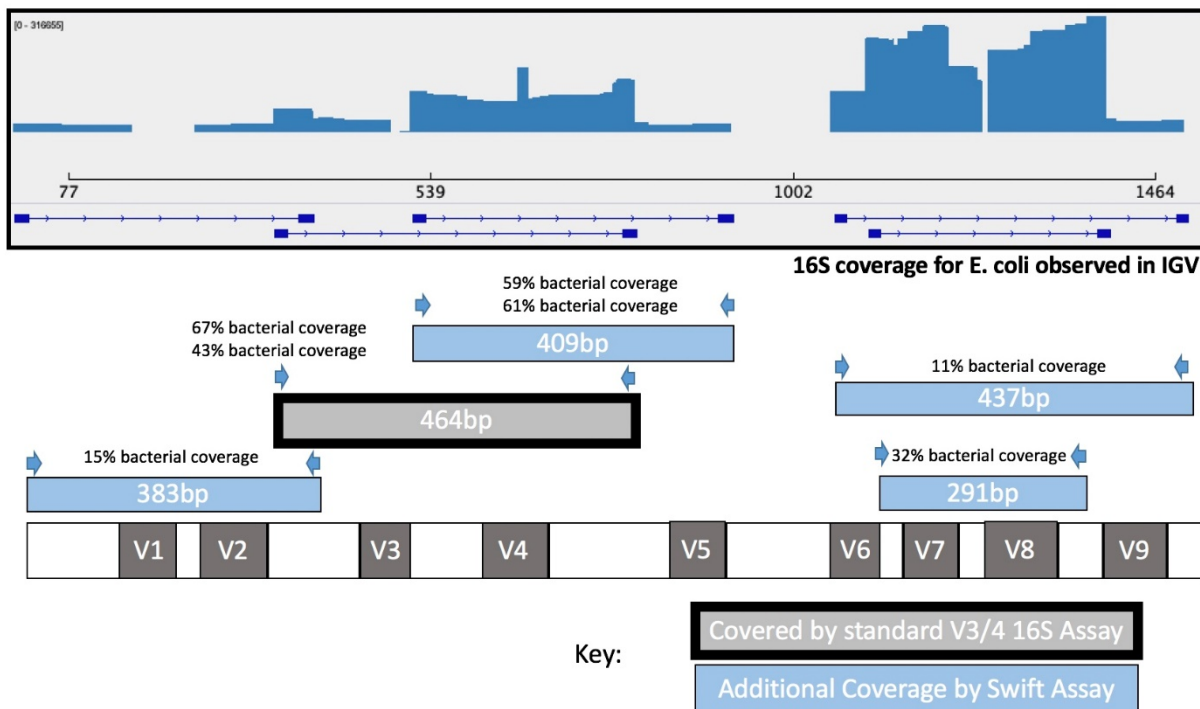
## Supported Applications

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).

## Coverage of All Variable Regions in a Single PCR Reaction

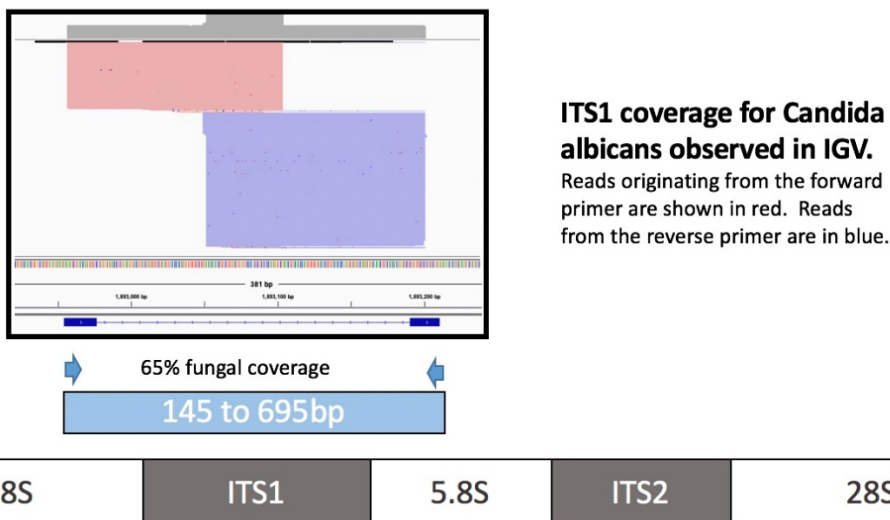
The Swift SNAP 16S and ITS1 Panels facilitate NGS analysis of complex microbial communities (e.g. bacteria, archaea, fungi) using a single primer pool targeting the 16S rRNA gene (variable regions 1-9) or ITS1 genes. In addition, these panels can be customized with additional targets including antibiotic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

### 16S Panel v2 (primers), Swift Cat. No. 516G1-96



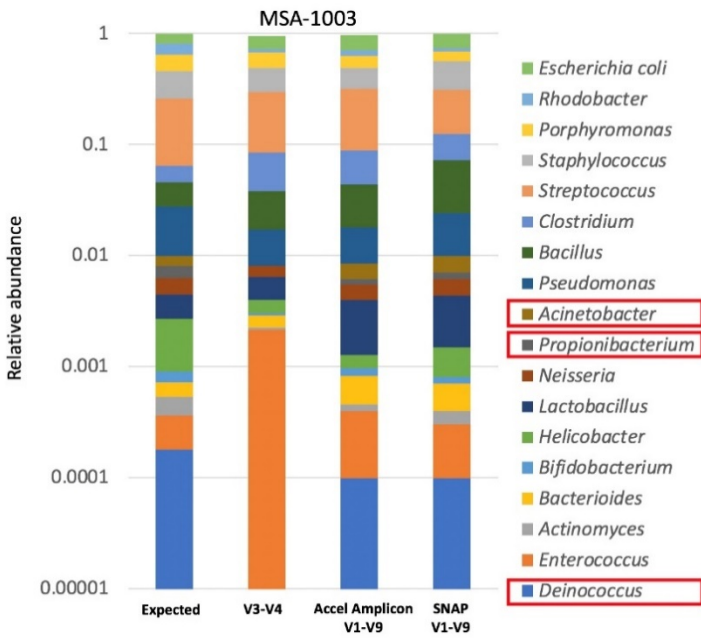
Sequencing read coverage (IGV Sashimi plot) and illustration of multiplexed primer coverage of all nine variable regions of 16S rRNA.

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



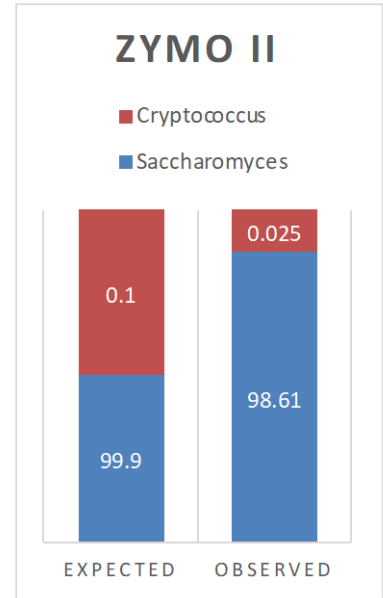
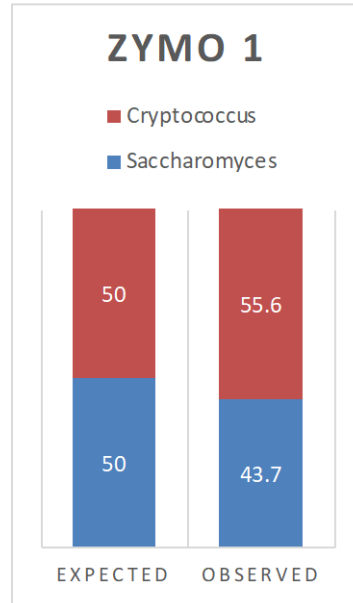
Sequencing read coverage (IGV) and illustration of multiplexed primer coverage of ITS1 region from C. albicans.

# Provides Superior Representation of Diverse Microbial Communities

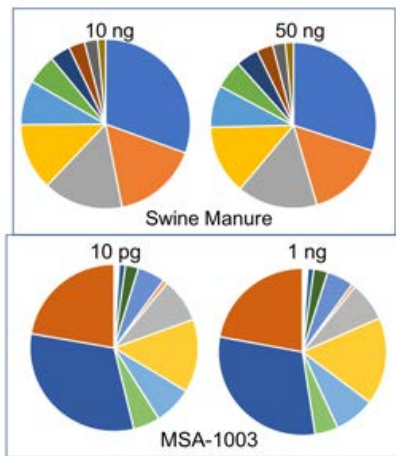


Panels covering V1-V9 regions of 16S rRNA (Swift Cat. No. 516G1-96) provide accurate representation of each genus in a commercially available standard (MSA-1003) compared to libraries interrogating the V3-V4 region alone. The Swift Accel-Amplicon panel and Swift 16S SNAP panels performed equally. Strains 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 standard (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 ITS SNAP panel performed well, resulting in expected representation of the fungal species in a bacterial background.



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

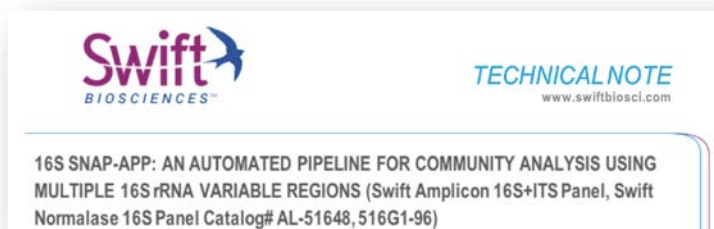


Sample	Accel-Amplicon V1-V9 2x150 PE sequencing		16S SNAP V1-V9 2x150 PE sequencing		Accel-Amplicon V1-V9 2x300 PE sequencing	
	Shannon Species Diversity	% Reads PF Classified to Genus	Shannon Species Diversity	% Reads PF Classified to Genus	Shannon Species Diversity	% Reads PF Classified to Genus
Manure 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%

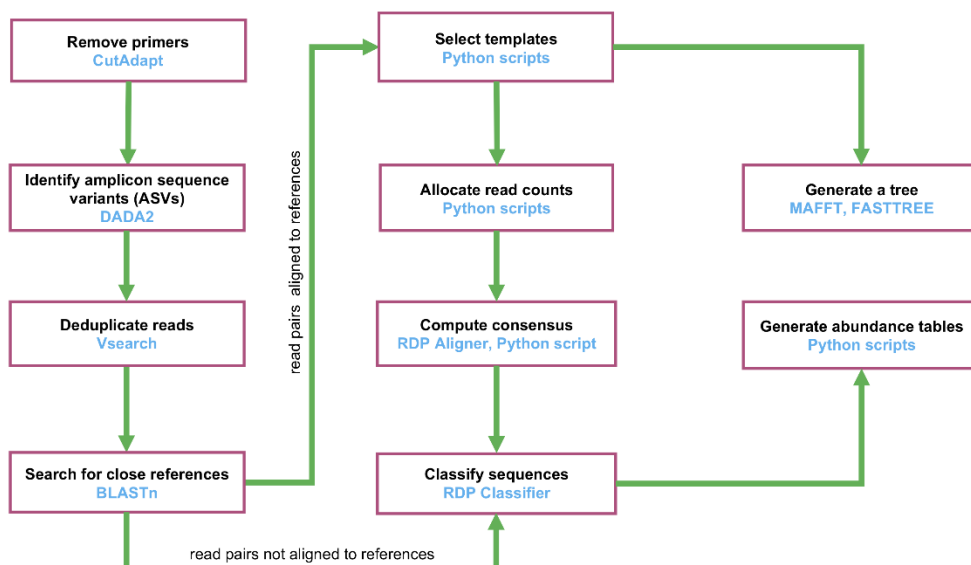
Using the same protocol and cycling conditions, input quantities of 10 pg to 50 ng with both MSA-1003 (bottom left) and swine manure (top left) gave consistent and expected sequencing results in terms of sensitivity and relative abundance. The Accel-Amplicon 16S+ITS and 16S SNAP products gave similar 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 SNAP 16S Panel v2 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 SNAPP can be found in the README file included at the Github repository and in the Technical Note.



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



## Ordering Information

Workflow Component	Product Name	Catalog Number
Primer Pool	16S Panel v2 (primers only)	516G1-96
	ITS1 Panel (primers only)	517G1-96
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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