

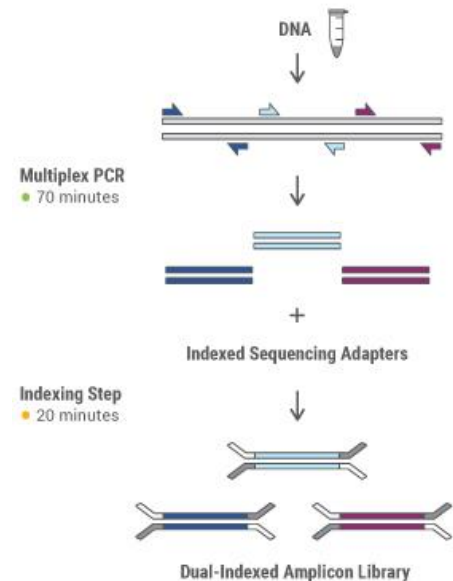


SWIFT AMPLICON 16S+ITS PANEL

Single tube comprehensive NGS microbial detection assay

Highlights

- Profiles complex metagenomic samples**
 Multiplexed assay covers all variable regions of the 16S rRNA, ITS1 and ITS2 genes in a single primer pool
- 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



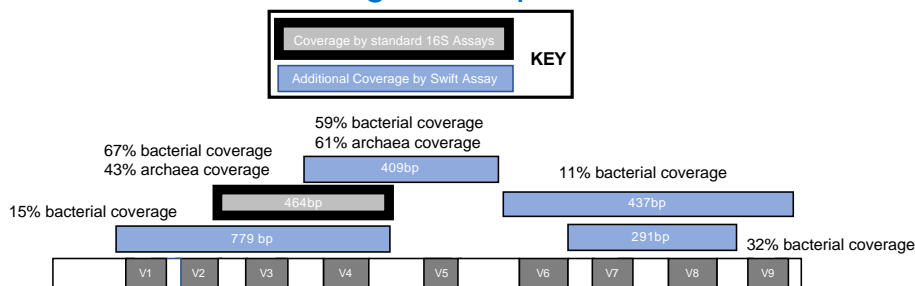
The Swift Amplicon 16S+ITS Panel facilitates NGS analysis of complex microbial communities (e.g. bacteria, archaea, fungi) using a single multiplexed primer pool targeting the 16S rRNA (variable regions 1-9) and ITS genes.

Applications and Sample Types

- Metagenomics: Bacteria, Archaea, Fungi
- Environmental: Air, Water, Wastewater
- Agriculture: Plant microbiome, Soil – ITS for fungal
- Microbiome: Human – skin, GI tract, stool, vagina, Plant – surface, roots and soil
- Forensics: Microbiome to establish time of death
- Detection and characterization of bacterial and fungal structure in complex samples

Complete Coverage of Variable Regions for Bacteria, Archaea, and Fungal Identification

16S rRNA gene amplicons



ITS1 and ITS2 amplicons (fungal)

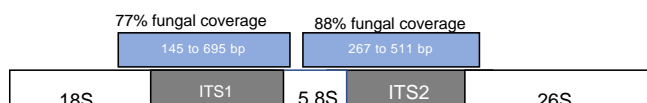


Figure 1. The Swift Amplicon 16S+ITS panel generates libraries covering all variable regions of 16S and fungal ITS1/ITS2 targets, unlike conventional 16S rRNA gene assays that target only V3-V4, or region-specific single-plex primers that require phased reverse primers and result in low complexity libraries with limited sensitivity and low-quality sequencing.

Provides Superior Representation of a Diverse Microbial Community Versus V3-V4 Only

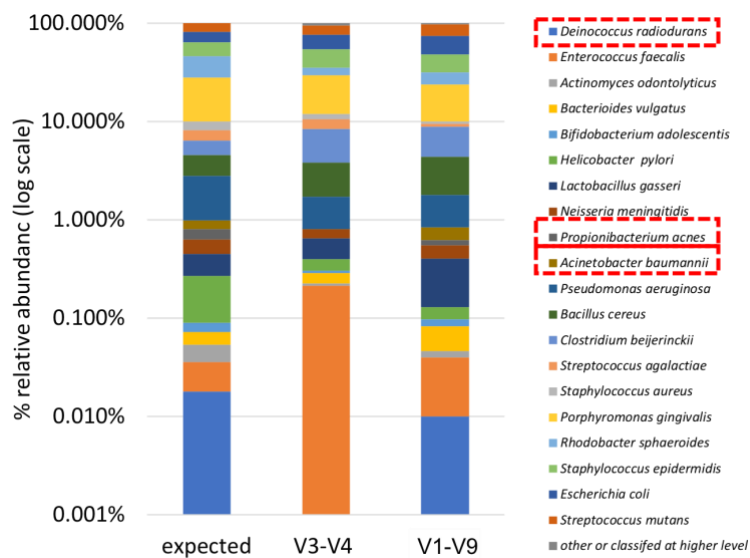
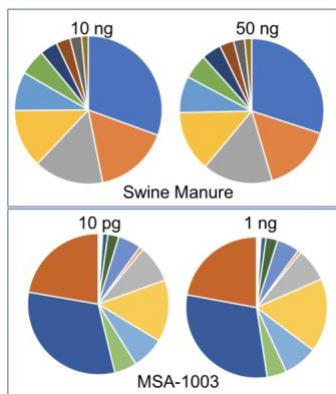


Figure 2. The Swift Amplicon 16S+ITS Panel covering all V1-V9 regions provides sensitive detection and accurate representation of each species in the sample compared to standard methods interrogating the V3-V4 region alone. Organisms marked in red were underrepresented by V3-V4 only method. Input DNA was a mix of 20 bacterial species (ATCC MSA-1003) tested with the Swift Amplicon 16S+ITS Panel, sequenced with Illumina® MiSeq® V3 (2x300bp reads).

Consistent Performance with Varying DNA Input, Sample Type, and Read Length



Sample	V1-V9, 2x150 PE sequencing		V1-V9, 2x300 PE sequencing	
	Shannon Species Diversity	% Reads PF Classified to Genus	Shannon Species Diversity	% Reads PF Classified to Genus
Manure 1	2.84	94.1%	2.84	92.5%
Manure 2	2.87	94.6%	2.85	92.8%
Manure 3	2.71	94.6%	2.69	92.6%
Manure 4	2.74	95.0%	2.70	93.6%

Figure 3. (Left) Using the same protocol and cycling conditions, input quantities of 10 pg to 50 ng with both ATCC MSA-1003 (bottom left) and swine manure (top left) gave consistent and expected sequencing results in terms of sensitivity and relative abundance. (Right) When comparing 2x150 and 2x300 PE reads, the Swift 16S+ITS Panel identified a comparable number of species from swine manure samples.

Specifications

Feature	Swift Amplicon 16S+ITS Panel
Input DNA (tested range)	1 ng (tested with 10 pg to 50 ng)
Amplicons	7 total: 5 (16S rRNA) + 2 (fungal ITS)
Average Amplicon Size	475 bp
Genes Covered	16S rRNA (V1-V9), Fungal ITS1+ITS2
Assay Format	Single tube multiplex PCR; 2 hours DNA-to-Library
Components Provided	Target specific primer pool, PCR and library preparation reagents, including indexed adapters
Depth Recommendations	100-300K reads per sample
Multiplexing Capability	96 or more libraries on Illumina® MiSeq® v2
Compatible Platforms	Illumina MiSeq, MiniSeq

Ordering Information

Product Name	Reactions	Catalog Number
Swift Amplicon 16S+ITS Panel	48	AL-51648

Visit www.swiftbiosci.com for easy ordering.