# Microbiome & Mycobiome Sequencing with LoopSeq™

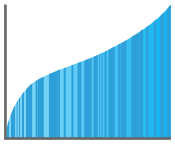
## Kits to conquer microbial metagenomics challenges

As researchers explore the complexity of microbial communities for basic research, food safety and quality testing, pathogen detection, soil health monitoring, diagnostics development, and more, next generation sequencing (NGS) has become the method of choice. But conventional short-read NGS technology can only identify a fraction of the organisms in a microbial population at the species level, and cannot provide information on microbe abundance. Alternative long-read sequencing approaches have the potential for more accurate species identification and abundance measurements, but the high error-rate of current long-read technologies leads to less reliable results.

**10x**
Less hands-on time

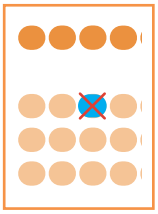
**<96**
Samples in a single tube

**Hi-Res**
Species and strain-level resolution



**20x**
Better quantitation (no PCR bias)

To help researchers overcome these challenges and develop accurate and comprehensive data on the composition of microbial communities, **Loop Genomics** has developed a range of affordable, easy-to-implement **Microbiome & Mycobiome Metagenomics Kits** and **Sequencing Services**. Leveraging **Loop's** synthetic long read technology, every kit delivers the advantages of long-read sequencing from the convenience of your existing sequencing infrastructure. Turn the page to see our available microbiome and mycobiome kits or go straight to the back page to see how LoopSeq technology works.



**5-7x** Lower error rate than Illumina MySeq v3 and PacBio SMRT

**7,500x** Lower error rate than Nanopore sequencing

**0** False positive species assignments with LoopSeq

**23** False positive species assignments with Illumina

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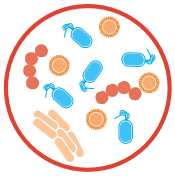
# Microbial Metagenomics Kits for a range of applications



## LoopSeq 16S Microbiome 24-plex Kit and 96-plex Kit

**APPLICATIONS: Samples with ≥10 ng of genomic DNA**

Gain a more in-depth understanding of microbial populations with the LoopSeq 16S Microbiome Kit.

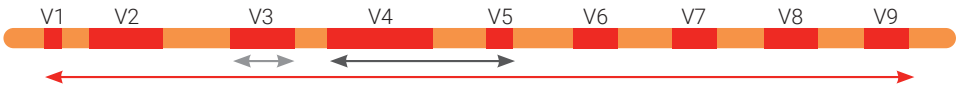



*Figure 1. **LoopSeq 16S Microbiome Kits sequence the entire variable region of the 16S rRNA gene.***

Unlike short-read sequencing approaches which provide information on just a few of the variable regions in the 16S ribosomal RNA gene—typically V3 and/or V4-V5 —the long reads generated by the LoopSeq 16S Microbiome Kit provide sequence information for the complete 16S variable region (**Figure 1**). As a result, the majority of organism assignments are at the species or even strain level (**Figure 2**).

*Learn more about all of our LoopSeq Kits and get more information about the technology by visiting* ***loopgenomics.com***

In addition, because barcoding happens before PCR amplification*, quantitation is highly accurate, provides absolute rather than relative measurements, and is free from PCR bias (**Figure 3**).

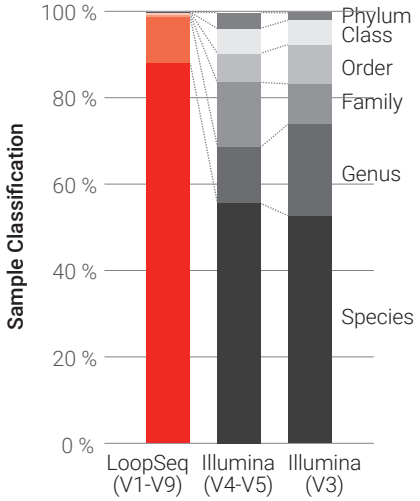



*Figure 2. **LoopSeq Microbiome Kits enable more comprehensive classification than short-read NGS approaches (data shown for a complex environmental sample).***

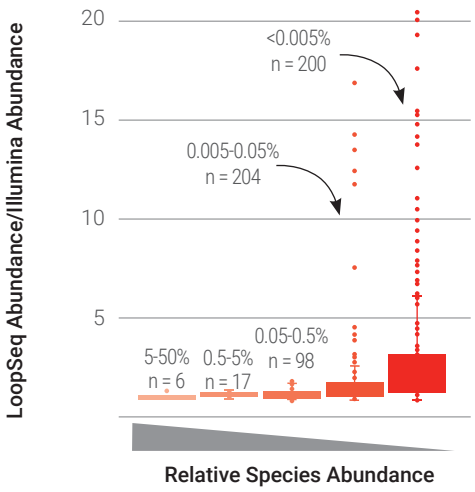



*Figure 3. **LoopSeq Complete more accurately measures low-abundance species due to pre-amplification, single molecule counting.** We simulated a standard NGS approach by estimating species abundance based only on the frequency of short-reads, and then compared those estimates with the LoopSeq-calculated values. Higher values indicate a larger discrepancy between LoopSeq and Illumina measurements, and demonstrate the poor ability of short-read sequencing approaches to measure species abundance..*

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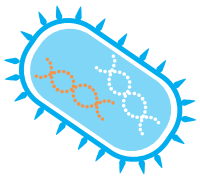
** Except for the 16S Low Biomass Kit, which includes a few PCR amplification cycles prior to barcoding.*



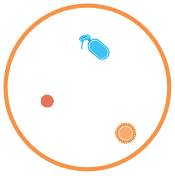
## LoopSeq 16S & 18S Microbiome 24-plex Kit and 96-plex Kit

**APPLICATIONS: Identify both prokaryotic and eukaryotic microbes**

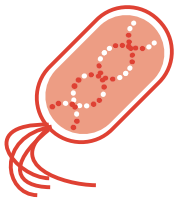
With the LoopSeq 16S & 18S Microbiome Kit, you can expand microbial identification to include eukaryotic microorganisms in addition to bacteria. This kit delivers all the same advantages as the LoopSeq 16S Microbiome Kit including easy workflow, low error rate, and highly accurate species identification and quantitation.

## LoopSeq Low Biomass Microbiome Kit

**APPLICATIONS: Microbiome studies of skin, water, hard surfaces, and even air**



The addition of a few PCR amplification cycles before the barcoding step enables studies of even low biomass microbial communities. Compatible with picogram amounts of input DNA, such as from microbiomes found on skin, water, hard surfaces, and even air, use of this kit in a recent human skin microbiome study resulted in ***zero*** background signal from human DNA.



## LoopSeq 16S Read Cloud Microbiome Kit

**APPLICATIONS: Projects that prioritize quantitative measurement and affordability over identification down to the species-level**

Even more affordable than our standard LoopSeq 16S Microbiome Kit, the 16S Read Cloud Kit delivers the same single-molecule counting and phased long reads as the standard kit, but at a lower read density. Thus, quantitation is accurate and reliable but error rates are slightly higher and fewer full-length V1-V9 synthetic long reads are achieved, leading to a lower percentage of the community identified at the species level.

# Achieve unprecedented insight into the *mycobiome*

## LoopSeq 18S-ITS1-ITS2 Mycobiome Kit

**APPLICATIONS: Fungal metagenomics**

With the ability to capture the full-length sequence of the ~2,500 bp 18S-ITS1-ITS2 region (Figure 4), fungal researchers can gain species-level identification and quantitation of organisms in a complex fungal community. The result is a view into the mycobiome that is not available with any other technology.

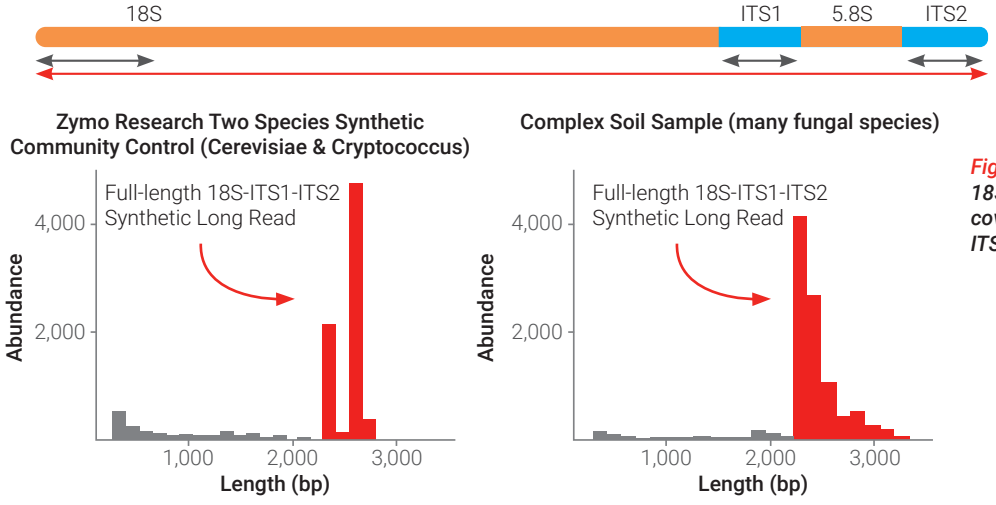
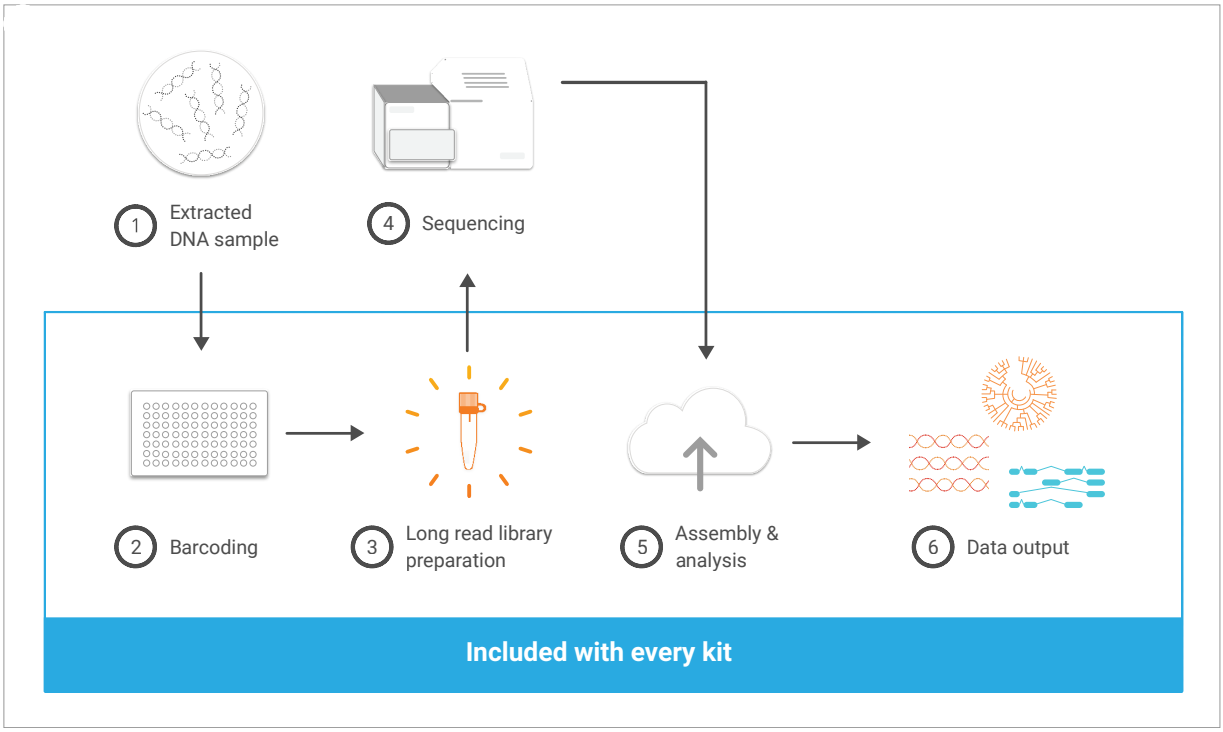



*Figure 4. The LoopSeq 18S-ITS1-ITS2 Mycobiome Kit covers the entire 18S-ITS1-ITS2 region.*

# The easy LoopSeq workflow




The power of the **LoopSeq** approach stems from our unique, proprietary barcoding technology and implementation. The key steps of the workflow are as follows:

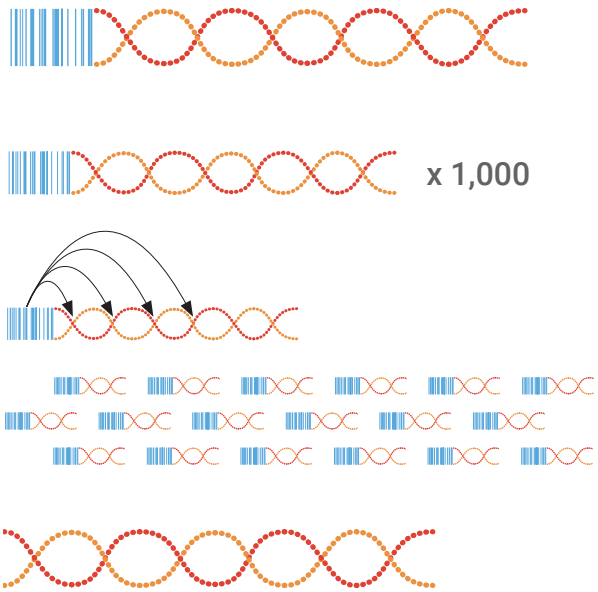
**Barcoding.**
Every sample is exposed to millions of unique barcodes, but only one barcode attaches per strand of DNA.

**Amplification.**
Every molecule, along with its unique barcode, is amplified using PCR.

**Distribution.**
Each copy of the amplified DNA has the barcode randomly distributed to a different location.

**Sequencing.**
Sequence the segment next to each barcode.

**Assembly.**
Short reads that share the same barcode are combined algorithmically into a full-length molecule using linked-read *de novo* assembly.

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