

LoopSeq™ 16S Long Read Kit
LoopSeq™ 16S & 18S Long Read Kit
LoopSeq™ 18S - ITS Mycobiome Kit

Genome Amplification Oligonucleotide Sequences
Version 1.0



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LoopSeq Targeted Sequencing Overview

For targeted biomarker sequencing, the first step when using a LoopSeq™ kit is to amplify the target region from genomes using oligonucleotides that are specific to the biomarker of interest. The oligonucleotide sequences used vary depending on the application and the target organism(s). After LoopSeq library construction and sequencing, if the reconstructed long reads span the entire target region, the long read sequences would include sequences in the primer regions. Since the sequences in the primer region originate from the oligonucleotides used during PCR, the error rates in the primer region compared to the reference would be significantly higher than the rest of the reconstructed long reads. This does not reflect a higher error rates at the end of the long read molecules, but rather the use of degenerate primer sequences and oligonucleotide synthesis errors.

LoopSeq Oligonucleotide Sequences

A list of the oligonucleotide sequences used to amplify different biomarkers from genomes is provided below.

Kit name	Forward sequence	Reverse sequence	Target organism(s)
LoopSeq™ 16S Long Read	AGAGTTTGATCMTGGCTCAG	TACCTTGTTACGACTT	Bacteria
LoopSeq™ 16S & 18S Long Read	AGAGTTTGATCMTGGCTCAG GATTAAGCCATGCAAGTS GGTTGATYCTGCCRGRG TCYGGTTGATCCTGCC	GMWACCTTGTTACGACTT TACCTTGTTACGACTT	Bacteria, archaea, eukarya
LoopSeq™ 18S - ITS Mycobioime	TACCTGGTTGATYCTGCCAGT	CTBTTVCCKCTTCACTCG GGTTGGTTTCTTTTCCT TAAATTACAACCTCGGAC TCCTCCGCTTWTTGWTWTGC	Fungus

Revision History

Version	Date	Description of Change
1.0	Nov 2019	<ul style="list-style-type: none">Initial release

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