

## ACCEL-NGS® 1S PLUS DNA LIBRARY KIT

The Accel-NGS 1S Plus DNA Library Kit is designed for Illumina® platforms. Utilizing Swift Biosciences' innovative technology, this kit allows DNA library construction from single-stranded DNA (ssDNA), as well as double-stranded DNA (dsDNA), which is nicked, damaged, or contains short fragments.



### Features

- Does not require intact dsDNA
- Highly efficient adapter ligation
- Inputs as low as 10 pg
- Simple, 2-hour workflow
- High sequence quality and even coverage

### Applications

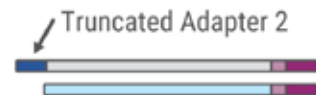
- ssDNA samples
- Damaged samples, including nicked DNA
- Metagenomics
- Viromics
- Difficult-to-extract organisms
- Heat-denatured pathogenic samples

### Simple Workflow

#### Adaptase™

⌚ 17 minutes

#### ssDNA Fragment



#### Indexed Library

#### Extension

⌚ 8 minutes

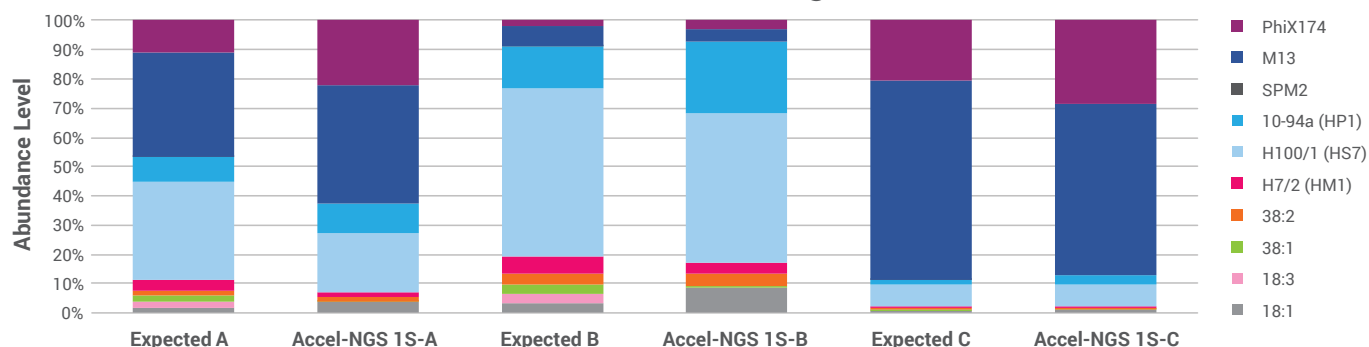
#### Ligation

⌚ 15 minutes

#### Indexing PCR

⌚ Time varies

## Accurate Detection of Both ssDNA and dsDNA Phage



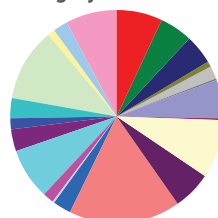
The Accel-NGS 1S Plus DNA Library Kit was used to prepare and sequence three artificial viromes containing different proportions of the ssDNA phage PhiX174 and M13 mixed with dsDNA phage. In all cases, the proportions were preserved when sequenced with the Accel-NGS 1S Plus Kit without any prior whole genome amplification for detection of ssDNA phage.

## DNA Extraction and Sequencing of a Hard-to-Extract Microbe

Extraction Method	Qubit® (ng/μl)	NanoDrop® (ng/μl)
Bead Beating	3.1	5.5
NaOH Boiling	< 2.0	107.3

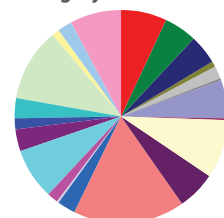
<i>Facklamia sp.</i> HGF4	Bead Beating	NaOH Boiling
Fold-coverage	65.5x	52.9x
Number of Contigs	42	46
Total Consensus	1,896,447	1,892,667
Largest Contig	190,702	190,844
N <sub>50</sub> Contig Size	85,449	86,622

**Bead Beating**  
Sub-system  
Category Distribution



**Sub-system Coverage**  
51% In sub-system  
52% Not in sub-system

**NaOH Boiling**  
Sub-system  
Category Distribution



**Sub-system Coverage**  
51% In sub-system  
52% Not in sub-system

Colors in pie charts represent different *Facklamia sp.* sub-system categories as annotated by the RAST server.

- DNA extraction by NaOH boiling produced higher DNA yields from *Facklamia sp.* than bead beating, and in less time.
- Sequencing of the NaOH extracted DNA produced a high quality *de novo* assembled genome sequence that was indistinguishable from that produced from bead beating extracted DNA.

## Ordering Information

Product Name	Reactions	Catalog No.
Accel-NGS 1S Plus DNA Library Kit	24	10024
Accel-NGS 1S Plus DNA Library Kit	96	10096

An Accel-NGS 1S Plus Indexing Adapter Kit is required for complete functionality of the library kit.

Visit [www.swiftbiosci.com](http://www.swiftbiosci.com) for easy ordering.



**Swift Biosciences, Inc.**

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