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

1. **Adaptase™**
   - **Time:** 17 minutes
   - **Steps:**
     - Add Adapase
     - Tail Truncated Adapter 1

2. **Extension**
   - **Time:** 8 minutes
   - **Steps:**
     - Add Truncated Adapter 1’ Primer
     - Truncated Adapter 1’

3. **Ligation**
   - **Time:** 15 minutes
   - **Steps:**
     - Add Truncated Adapter 2

4. **Indexing PCR**
   - **Time:** Varies
   - **Steps:**
     - PCR Full-length Adapters

**Indexed Library**
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

<table>
<thead>
<tr>
<th>Extraction Method</th>
<th>Qubit® (ng/µl)</th>
<th>NanoDrop® (ng/µl)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bead Beating</td>
<td>3.1</td>
<td>5.5</td>
</tr>
<tr>
<td>NaOH Boiling</td>
<td>&lt; 2.0</td>
<td>107.3</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Facklamia sp. HGF4</th>
<th>Bead Beating</th>
<th>NaOH Boiling</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fold-coverage</td>
<td>65.5x</td>
<td>52.9x</td>
</tr>
<tr>
<td>Number of Contigs</td>
<td>42</td>
<td>46</td>
</tr>
<tr>
<td>Total Consensus</td>
<td>1,896,447</td>
<td>1,892,667</td>
</tr>
<tr>
<td>Largest Contig</td>
<td>190,702</td>
<td>190,844</td>
</tr>
<tr>
<td>N50 Contig Size</td>
<td>85,449</td>
<td>86,622</td>
</tr>
</tbody>
</table>

- 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

<table>
<thead>
<tr>
<th>Product Name</th>
<th>Reactions</th>
<th>Catalog No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accel-NGS 1S Plus DNA Library Kit</td>
<td>24</td>
<td>10024</td>
</tr>
<tr>
<td>Accel-NGS 1S Plus DNA Library Kit</td>
<td>96</td>
<td>10096</td>
</tr>
</tbody>
</table>

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.