ACCEL-NGS® 2S PLUS & 2S PCR-FREE DNA LIBRARY KITS

The Accel-NGS 2S Plus and 2S PCR-free DNA Library Kits utilize a proprietary adapter ligation chemistry which provides complex libraries from low abundance inputs and delivers excellent genomic coverage across a range of inputs.

Features

- Broad input range: 10 pg to 1 µg
- PCR-free libraries from 10 ng
- Sequential repair and ligation steps
- Increased library complexity
- Balanced coverage of AT-/GC-rich genomes

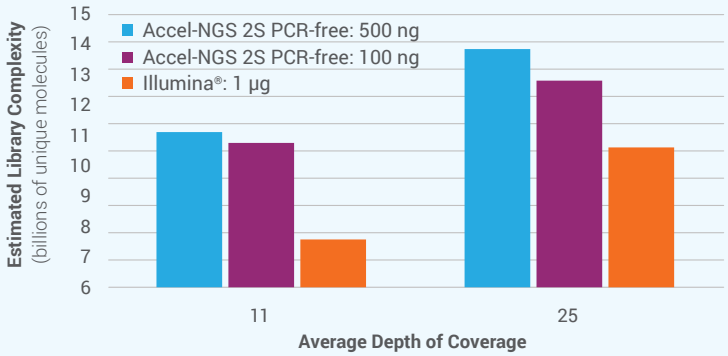
Applications

- Whole genome sequencing
- ChIP-seq
- Metagenomics
- Cell-free DNA (cfDNA)
- PCR-free sequencing

Simple Workflow

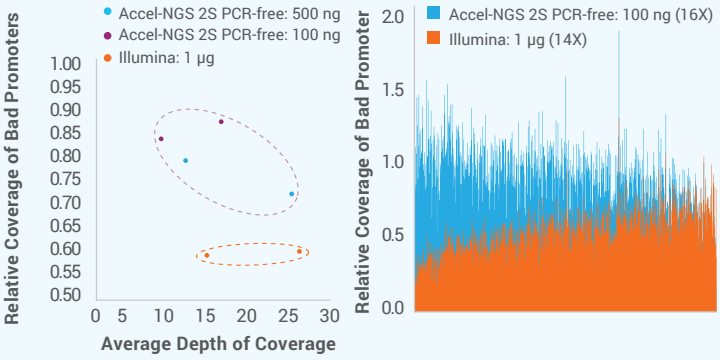
Performance Data

Generate Higher Complexity Libraries Than the Leading Kit



Library complexity was obtained at various sequencing depths for Accel-NGS 2S PCR-free libraries compared to libraries made with the leading kit.

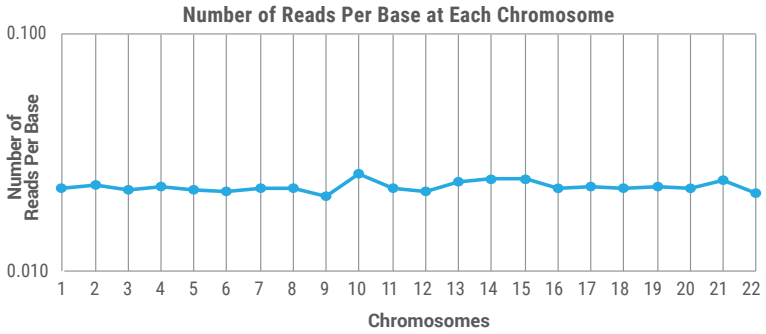
Cover Extreme Base Composition Regions Better



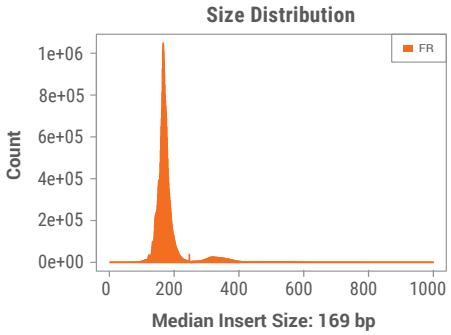
Relative coverage of the GC-rich 1000 bad promoters obtained at various sequencing depths of Accel-NGS 2S PCR-free libraries compared to libraries made with the leading kit.

PCR-Free Prep from 10 ng of Cell-Free DNA

# Reads	% Mapped to Human Genome	Estimated LibRARY Size	Chimera	Dimers
69,853,401	99.5	1.2 x 10^9	2.6%	0.02%



Even at low sequencing depth, the minimal sequence-dependent bias of the Accel-NGS 2S adapter attachment results in even coverage across the genome. Data was normalized to mappable chromosome content.



The inherently narrow size distribution of cfDNA, centering around 165 bp, reduces loss of DNA during library prep size selection steps.

Increased Coverage at Low Inputs

	1 ng					100 pg				
	PCR Cycles	Yield (nM)	Reads (Millions)	Average Coverage	Duplication Rate	PCR Cycles	Yield (nM)	Reads (Millions)	Average Coverage	Duplication Rate
Swift	9	58.0	11.3	16X	0.4%	12	45	14.5	20X	1.2%
Kapa	12	21.0	11.3	14X	7.9%	16	47	14.5	14X	10.4%
NEB	14	134.0	11.3	15X	1.2%	17	86	14.5	14X	10.4%
Nextera	12	9.6	11.3	13X	3.4%	—	—	—	—	—

A sample representing a broad range of base compositions (19-71% GC) was constructed using an equal mixture of six microbial genomes: B. pertussis *(68% GC),* R. sphaeroides *(69% GC),* S. avermitilis *(71% GC),* P. falciparum *(19% GC),* S. aureus *(32% GC), and* E. coli *(50% GC). NGS libraries were constructed from 1 ng and 100 pg of this sample, and sequencing metrics were compared across four commercially-available library kits: Swift Biosciences' Accel-NGS 2S Plus, Kapa Biosystems' Hyper, New England BioLabs® NEBNext® Ultra™, and Illumina's Nextera. Data shown is the average of duplicate libraries. Nextera chemistry restricts library construction to only 1 ng of input DNA.*

Ordering Information

Product Name	Reactions	Catalog No.
Accel-NGS 2S PCR-free DNA Library Kit	24	20024
Accel-NGS 2S PCR-free DNA Library Kit	96	20096
Accel-NGS 2S Plus DNA Library Kit	24	21024
Accel-NGS 2S Plus DNA Library Kit	96	21096

An Accel-NGS 2S Indexing Adapter Kit is required for complete functionality of the library kit.

Visit **www.swiftbiosci.com** for easy ordering.

Swift Biosciences, Inc.
58 Parkland Plaza, Suite 100 • Ann Arbor, MI 48103 • 734.330.2568 • www.swiftbiosci.com