Unison™

Ultralow DNA NGS Library Preparation Kit

CAT#: NLK-01-008 (8 Reactions)
NLK-01-048 (48 Reactions)

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Datasheet (MB-BD-DS002,V1.0)

Unison™ Ultralow DNA NGS Library Preparation Kit

Micronbrane

A fast, simple NGS library construction workflow specifically optimized for ultralow DNA inputs as low as 10pg DNA. Ideal for various NGS applications dealing with scarce sample input, such as host-depleted DNA obtained by Micronbrane's Devin™ Microbial DNA Enrichment Kit (MEK-01-024).

Introduction

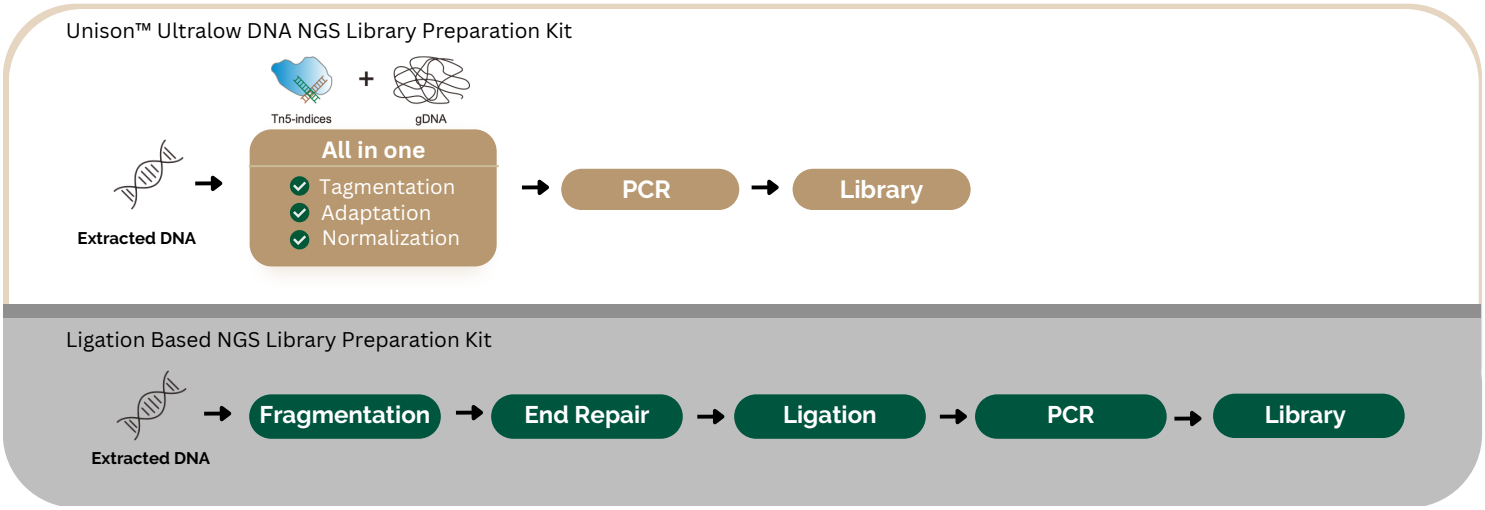
Next-generation sequencing (NGS) technology has been introduced into genomic research for more than 15 years now. More researchers are doing more applications using NGS as a regular tool to solve their research questions. With the maturation and standardization of the sequencing quality, the quality of overall sequencing data is more determined by the quality of the NGS library constructed. An easy-to-repeat NGS library preparation workflow with uniform performance is crucial to researchers, especially those dealing with scarce and precious samples.

Micronbrane's Unison™ Ultralow DNA NGS Library Prep Kit is based on well-studied transposase based tagmentation of the DNA, with no or minimal manipulation of the low input DNA itself before the PCR amplification step. The enzyme concentration is carefully titrated and optimized for low input DNA. Hence the kit can not only construct NGS library successfully from ultralow DNA input as low as 10pg of DNA, but also ensure that the sequencing profile of the amplified library is a true presentation of the input DNA sample.

Highlights

- **Fast library prep workflow**
  Minimal 45 minutes hands-on time with proprietar ultralow (UL-tagmentation) reduces total library prep time to < 3 hours
- **Optimised for ultralow DNA inputs**
  Standard recommended input is 1-5ng DNA. Successful NGS library can be achieved for as low as 10pg of DNA
- **Consistent library preparation performance**
  UL-tagmentation enables generation of uniform insert sizes (350 – 550 bp) across a broad range of input DNA
- **DNA background in the reagents carefully monitored** and transparently communicated with customer to ensure the true positive amplification of the DNA targeted by customers
- **Easily automatable**

Figure 1: Unison™ is a proprietary transposome-based library prep workflow optimised for ultra-low DNA inputs. Comparing to the ligation-based method, it only takes one step before PCR



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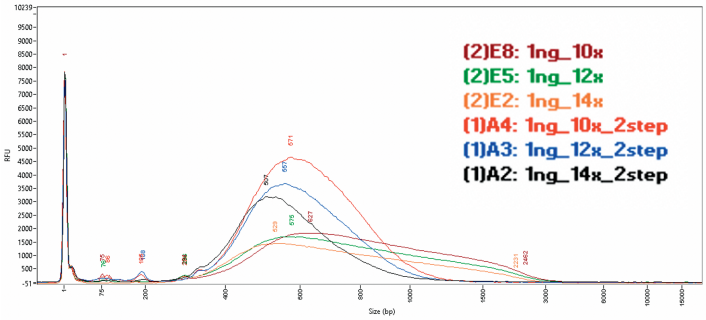
Fast, simple library preparation workflow with ultralow DNA input

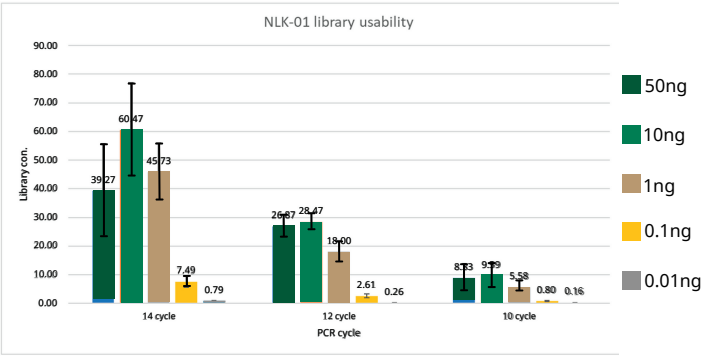
The Unison™ Ultralow DNA Library Prep Kit is one of the fastest library preparation workflows developed for Illumina sequencing platforms.

Its ultralow tagmentation (UL-tagmentation) chemistry is developed for ultralow DNA inputs and enables a highly uniform saturation-based normalization process. The whole workflow as illustrated in Figure 1, is comprised of 3 steps including tagmentation, amplification and purification with 45 minutes hands on time and a total workflow time less than 3 hours. Transposome-based tagmentation eliminates the need for separate mechanical or enzymatic DNA fragmentation steps, saving time and costs associated with shearing instruments or enzymatic kits. More importantly to low input samples, one-step tagmentation method of library preparation eliminates multiple manipulations of the scarce DNA samples comparing to ligation-based library construction methods illustrated in Figure 1.

Figure 2: Performance of Unison™ Ultralow DNA NGS Library Preparation Kit.



A. Uniform fragment size of libraries using one-step and two-step magnetic-beads purifications.



B. Unison™ kit can generate NGS library for DNA as low as 10pg with additional PCR cycles. Furthermore, for DNA input more than 1 ng, it can generate relatively normalized libraries, making it easy for NGS libraries pooling before sequencing.

Optimized library preparation performance

UL-tagmentation enables generation of uniform insert sizes (350 – 550 bp) across a broad range of input DNA, eliminating the need for careful transposome:DNA ratio optimization as a means of controlling fragment length. In addition to uniform insert sizes (Figure 2A), the Unison™ Kit has also been optimized to deliver relatively uniform and consistent library yields when the input DNA is more than 1-5 ng as shown in Figure 2B. This feature is extremely useful as NGS libraries are often pooled before loading as a single pooled sample on the sequencing platforms. Relatively normalized NGS libraries enable an easier library pooling process and more uniform coverage for each sample in the library pool.

Furthermore, the Unison™ Kit has been optimized for ultralow DNA input such as microorganisms' genomic DNA isolated from scarce biofluid samples. As a demonstration, we tested the kit with ZymoBIOMICS Microbial Community standards (D6331, Zymo Research) which comprises 21 different microorganisms at known percentage. Various amount of Zymo standards DNA were tested as input DNA and amplified at 10, 12 and 14 PCR cycles. Libraries were sequenced on Illumina platform and analysed. Although the percentage of one species is different from the percentage provided by Zymo Research, the percentage of all 21 microorganisms were consistent among different conditions of DNA input and PCR cycles shown in Figure 3, suggesting that Unison™ ultralow DNA NGS library preparation Kit poses minimal PCR bias towards the DNA of low input and has a good representation of the original DNA samples before NGS library preparation.

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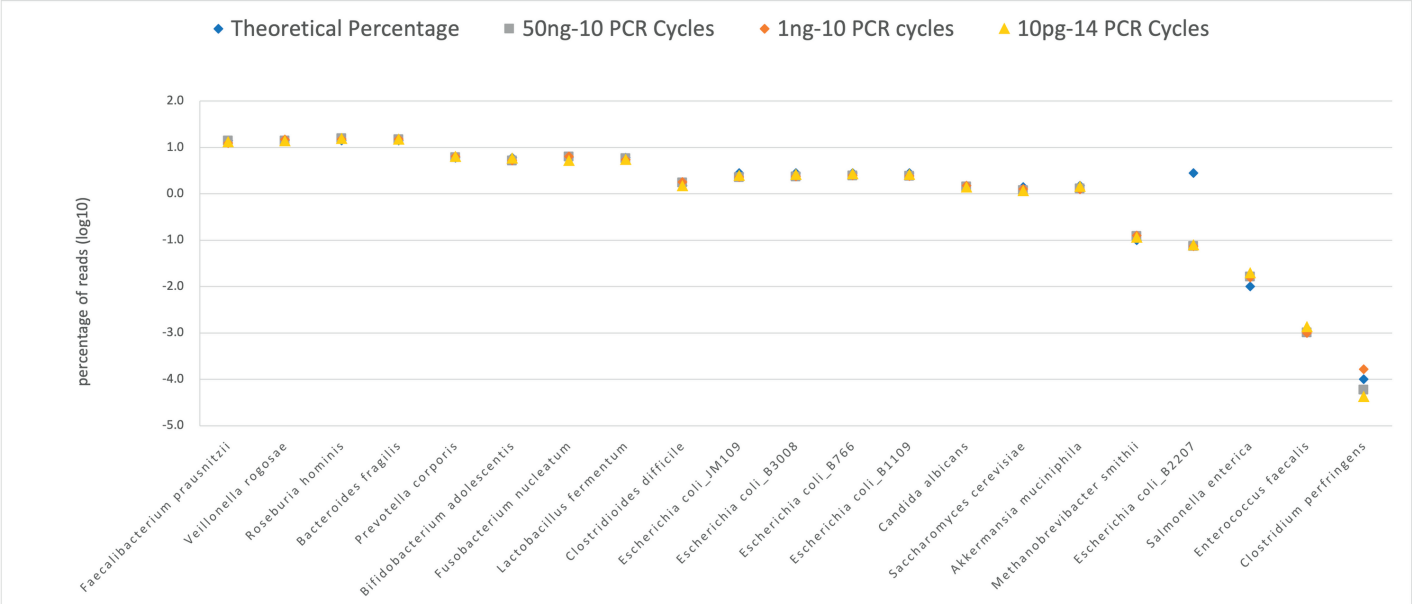
Figure 3. Consistent percentage of 21 microorganisms in ZymoBIOMICS Microbial Community Standards (Zymo Research) in various NGS libraries prepared by Unison™ Ultralow DNA NGS Library Prep kit with different DNA input and PCR cycles.



Summary

Unison™ Ultralow DNA NGS Library Prep kit used an efficient Tn5 based NGS library preparation method. It is specifically optimized for high molecular weight DNA of ultralow input and generates NGS library of fragment size optimal for Illumina platforms with relatively normalized concentration. The specifications of the kit are listed in Table 1. The kit allows users to prepare NGS libraries using DNA from various sources including human, animal and microorganisms without requiring much DNA input. It can be widely used for various applications such as whole genome sequencing, targeted sequencing by capture and metagenomic sequencing. The workflow can also be easily automated on various automation systems, making it ideal for the laboratories need scale and minimize the human error in the NGS library preparation process.

Table 1: Unison™ Ultralow DNA NGS Library Prep kit specifications

Parameter	Unison™ Ultralow DNA NGS Library Preparation
DNA input type	Double-stranded DNA (>1Kb)
DNA input amount	1-5 ng recommended, as low as 10 pg
Sample multiplexing	24 single indexes, 382 dual indexes
Supported sequencing systems	All Illumina systems
Total library prep workflow time (gDNA)	3 hours
Reagents not included in the kit	Indexes for Illumina platforms, Magnetic beads for library DNA purification

Learn more / Contact us

Currently, Unison™ Ultralow DNA NGS Library Prep kit can be used independently for DNA samples for research. It can also be used together with Micronbrane's Devin™ Microbial DNA enrichment kit for metagenomic sequencing of various clinical sample types. For more information, please check micronbrane.com or contact us at info@micronbrane.com.

References

1.Illumina DNA Prep datasheet (Pub. No. 770-2020-009-A)
2.Chen et al (2022) Poster presented at EECMID 2022

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