DeCodiFi™ Long&Complex

Maximizing assembly contiguity in ultra-low input workflows

When working with ultra-low DNA inputs, traditional polymerases force a critical compromise: sacrifice library yield or suffer fragment length compression. DeCodiFi™ Long&Complex High-Fidelity Polymerase eliminates this bottleneck, **preserving high-molecular-weight architectures across both major long-read sequencing platforms**.

PERFORMANCE DATA

Evidence-based performance

1. Superior library preparation

Higher yields, longer fragments & specific amplification

DeCodiFi™ Long&Complex establishes a superior fragment distribution baseline. While other polymerases library compression or non-specific amplification (LongAmp), Long&Complex maintains high processivity to efficiently shift the molecular population toward higher molecular weights.

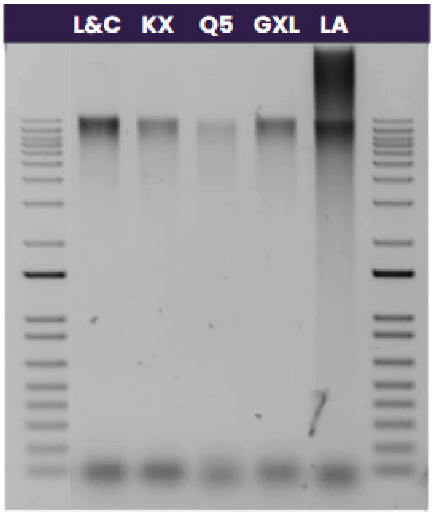

Figure 1: Library amplification QC. Comparison of *E. coli* library yields using five polymerases: DeCodiFi™ Long&Complex (L&C), KOD Xtreme™ Hot Start DNA Polymerase (KX), Q5® Hot Start High-Fidelity DNA Polymerase (Q5), PrimeSTAR® GXL DNA Polymerase (GXL), and LongAmp® Taq DNA Polymerase (LA). Libraries were generated using the PacBio's Ampli-Fi protocol with 1 ng of DNA input per 50 µL reaction and a standardized 14-cycle amplification program. Samples were analyzed via agarose gel electrophoresis to characterize size distribution and yield prior to PacBio® sequencing.

Key Insight: DeCodiFi™ Long&Complex produced the highest yield with a distinct distribution shift toward higher molecular weight fragments.

2. PacBio® Ampli-Fi Workflow

The PacBio® Ampli-Fi™ protocol enables the sequencing of limited-biomass samples, but its true success depends on generating long HiFi reads. DeCodiFi™ Long&Complex prevents fragment compression during amplification, delivering the optimal read lengths necessary to bridge complex regions and maximize final contiguity.

Table 1: Sequencing and assembly metrics for *E. coli* library.

Escherichia coli	*>Q30(%)*	*N50*	*Gene completeness*
KOD Xtreme™	97	3,539 kb	92.47%
DeCodiFi™ Long&Complex	97	**4,585 kb**	92.40%
Q5®	98	1,610 kb	92.37%
PrimeSTAR® GXL	97	4,585 kb	92.43%

Gene completeness was assessed using BUSCO with the enterobacterales_odb12 dataset for *E. coli*. To ensure compatibility, *E. coli* samples were normalized to a uniform depth of 63X corresponding to the lowest coverage sample for each genome.

MEAN LENGTH

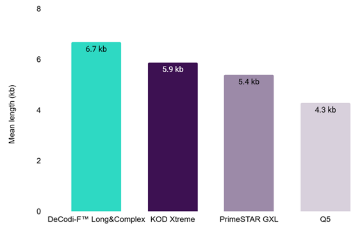

Figure 2: Read Mean Lengths. Comparison of *E. coli* mean lengths using four polymerases: DeCodiFi™ Long&Complex (L&C), KOD Xtreme™ Hot Start DNA Polymerase (KX), Q5® Hot Start High-Fidelity DNA Polymerase (Q5 &, PrimeSTAR® GXL DNA Polymerase (GXL). Libraries were generated using the PacBio's Ampli-Fi protocol with 1 ng of DNA input per 50 µL reaction and a standardized 14-cycle amplification program.

Key Insight: DeCodiFi™ reaches maximum N50 values supported by a robust mean read length, providing the ideal framework for unbiased structural variant detection.

DeCodiFi™ Long&Complex is now a PacBio®-recommended polymerase in the Ampli-Fi HiFi protocol.

Independently evaluated by PacBio®'s AppsLab on the HG002 human reference genome, DeCodiFi™ Long&Complex delivers strong performance in read length (10.15 kb mean) and assembly contiguity, and joins PacBio®'s updated Ampli-Fi protocol as a tested and recommended polymerase for HiFi library preparation. As a direct manufacturer with stable supply chains and consistent QC, Kura Biotech offers PacBio® users a validated option with continuity of supply and regional technical support. DeCodiFi™ Long&Complex is also designed to be cost-competitive within the validated options for the protocol.

3. OXFORD NANOPORE™ Workflows

In ONT workflows, read length is the primary driver of assembly contiguity. DeCodiFi™ Long&Complex optimizes Oxford Nanopore™ library preparation from 1 ng of input by capturing ultra-long fragments up to 47.1 kb. This extended reach translates directly into a 65% increase in Contig N50, reducing genomic fragmentation and lowering overall sequencing costs.

Table 1: Sequencing and assembly metrics for *S. epidermis* library.

Staphylococcus epidermidis	***Max length***	***Mean mapped length***	***Assembly size***
KOD Xtreme™	31.9 kb	5.8 kb	2.5 Mb
DeCodiFi™ Long&Complex	**47.1 kb**	**6.0 kb**	2.5 Mb

CONTIG N50

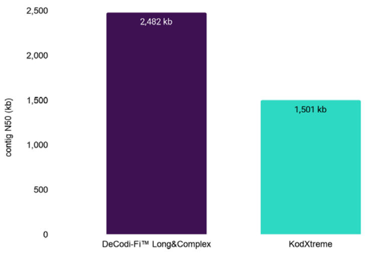

Figure 1: Library amplification QC. Comparison of *S. Epidermidis* Contig N50 using two polymerases: DeCodiFi™ Long&Complex (L&C) and KOD Xtreme™ Hot Start DNA Polymerase (KX). Libraries were generated with 1 ng of DNA input per 50 µL reaction and a standardized 14-cycle amplification program.

Key Insight: Libraries amplified with DeCodiFi™ Long&Complex close complex genomic gaps, drastically reducing the number of independent contigs.

CONCLUSION

The new standard for long-read prep

Why settle for fragmented data? **DeCodiFi™ Long&Complex** provides the processivity required for:

- Maximum read lengths across all long-read platforms (PacBio® & ONT).
- Highest assembly contiguity (N50) to resolve complex genomes.
- Ultra-low input compatibility (starting at 1 ng) without coverage bias.
- Uncompromised specificity to eliminate short-fragment smears.

From library prep to final assembly, ensure your results are Long & Complex.

Ready to evaluate DeCodiFi™ Long&Complex?

Request product information or connect with our team to discuss your challenging DNA amplification workflow.

Contact us at **sales@kurabiotech.com**

Know more about Kura Biotech

We are a global biotechnology company specialized in sample preparation and testing for laboratories. We develop advanced enzymatic solutions for toxicology, food safety, and genomics, fully designed and produced in-house to streamline complex workflows and enhance analytical efficiency.

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