Telomere Sequencing

Oxford Nanopore Technologies Services

Summary

Renew Biotechnologies (Renew), a certified Oxford Nanopore Technologies (ONT) sequencing service provider, offers Telomere Sequencing for high-resolution characterization of telomere length and chromosome-end biology from native, high-molecular-weight genomic DNA. This long-read sequencing workflow measures chromosome arm-specific telomere lengths while preserving subtelomeric sequence context, structural variation, and DNA methylation in a single assay. Designed for translational research and comprehensive telomere biology studies, the service offers the following key features and benefits.

Key Features & Benefits

- **Chromosome Arm Resolution:** Measures telomere length for individual chromosome arms rather than genome-wide averages.
- **Native Long-Read Sequencing:** Preserves subtelomeric sequence context, structural variation, and DNA methylation.
- **Integrated Multiomic Analysis:** Generates telomere, genomic, and epigenetic information from a single sequencing workflow.
- **No Live Cell Requirement:** Uses extracted genomic DNA, eliminating the need for viable cells required by some conventional telomere assays.

Ideal Applications

- Telomere biology research
- Aging and longevity studies
- Oncology and genomic instability
- Cell therapy and regenerative medicine
- Longitudinal translational studies
- Chromosome-end biology

Protocol Overview

ONT Kit: Oxford Nanopore Telo-Seq Kit

Sequencing Platform: Oxford Nanopore PromethION

Workflow

1. **gDNA Extraction:** High-molecular-weight genomic DNA is isolated from biological samples.
2. **Library Preperation:** Samples undergo telomere-specific adapter ligation, chromosome-end enrichment, and sequencing adapter ligation using ONT's Telo-Seq workflow.
3. **Native Long-Read Sequencing:** Prepared libraries are sequenced on the Oxford Nanopore PromethION platform.
4. **Bioinformatic Processing:** Sequencing data are processed to estimate chromosome arm-specific telomere lengths and characterize subtelomeric regions.
5. **Data Delivery:** Sequencing results and quality reports are delivered through the Renew customer portal.

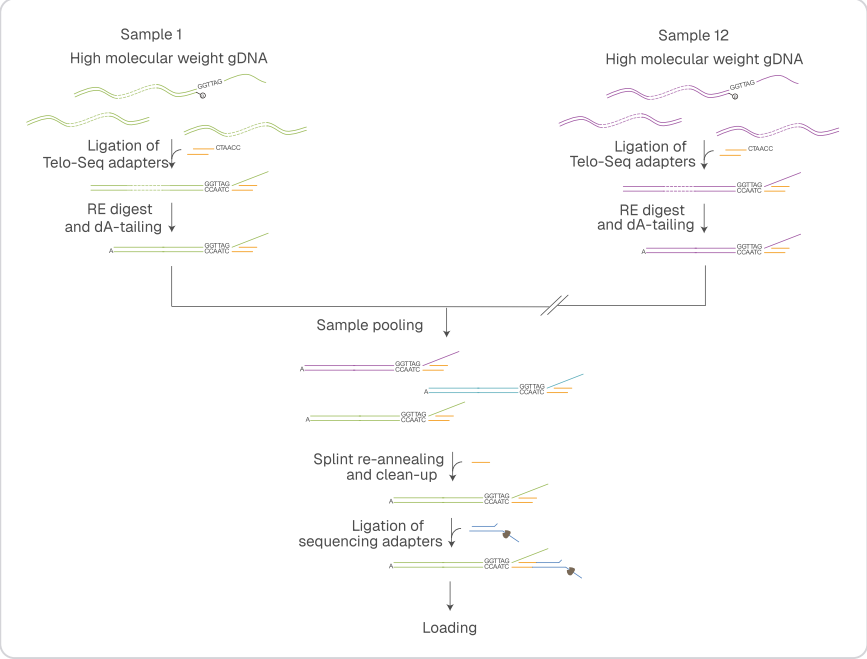

Figure 1. ONT Telo-Seq Library Preparation Workflow. This schematic illustrates the key steps involved in preparing high-molecular-weight genomic DNA for telomere sequencing with Oxford Nanopore Technologies' Telo-Seq workflow. The process includes telomere-specific adapter ligation, enzymatic processing to enrich chromosome-end molecules, sequencing adapter ligation, and long-read sequencing. This figure was adapted from ONT.

Sample Requirements

Parameter	Requirement
Sample Type	High-Molecular-Weight (HMW) Genomic DNA
Minimum Input DNA	1 µg
Recommended Input	2 µg
Quality Control (QC)	260/280 ratio: 1.8–2.0 260/230 ratio: 1.9–2.5
DNA Integrity	>90% of starting DNA fragments >10 kb

Throughput and Capacity

Parameter	Requirement
Sample Type	N50 >10Kb
Sequencing Yield per Sample	Approximately 1–5 Gb*
Samples per Flow Cell	Up to 12 samples per PromethION flow cell

*Dependent on sample input and multiplex level

Turnaround Time

Results appear in Renew's client portal within 14-21 days from sample receipt**.

**May vary with project scope, sample quality, and sequencing depth and bioinformatic requirements.

Data Output

File Format

Renew provides standard sequencing files, quality reports, and analysis outputs for downstream review and interpretation.

File	Description
POD5	Raw nanopore sequencing data, available upon request for an additional fee.
BAM	Aligned sequencing reads used for downstream telomere, methylation, and variant-aware analysis.

File	Description
CH3	Renew's base modification output format, designed to organize methylation and other epigenetic calls for downstream use.
QC Report	Summary of sequencing metrics, run statistics, sample-level performance, and quality indicators.

Bioinformatics Outputs

Renew supports downstream analysis using widely adopted long-read bioinformatics tools and workflows.

Analysis Type	Recommended Package(s)
Probe Design	**Epi2Me** supports general nanopore sequencing analysis workflows and provides accessible pipelines for ONT data exploration.
Epigenetic Analysis	**ModSeqR** and **ModKit** support methylation and base modification analysis from nanopore sequencing data.
SNV Calling	**Clair3** is commonly used for small variant calling from long-read sequencing data.
STR Detection	**LongTR** and Straglr support short tandem repeat detection and repeat expansion analysis from long-read data.
Taxonomic Classification	**Kraken** enables taxonomic classification of sequencing reads for contamination assessment or metagenomic-style analysis.
Long-Read Genome Assembly	**Flye** and **Hifiasm** are used for long-read assembly workflows when project goals require de novo assembly or structural reconstruction.
Basecalling and Aligning	**Dorado** performs ONT basecalling, while **Minimap2** supports long-read alignment to reference genomes.
BAM File Manipulation	**Samtools** supports common BAM operations including sorting, indexing, filtering, and file inspection.
FASTQ Manipulation	**SeqTK** provides lightweight FASTQ processing, filtering, and format manipulation for sequencing reads.

Custom Bioinformatics Services

For project-specific analyses beyond standard deliverables, Renew offers custom bioinformatics support tailored to individual study objectives.

Data Delivery

Delivery Option	Description
Client Web Portal	Secure browser-based access for manual download on Mac, Linux, or Windows.
AWS S3 Transfer	Automated AWS-to-AWS transfer option for teams managing large datasets in cloud environments.
Command Line Script	Manual command-line download option for Mac and Linux users who prefer scripted file retrieval.

Service Inclusions

Each project is supported by cross-functional expertise spanning library preparation, sequencing, bioinformatics, quality control, and project management.

Common Challenges & Solutions

Concern	Renew's Solution
Live-Cell Workflow Constraints	Telo-Seq uses extracted HMW gDNA, reducing dependence on viable cells, tight shipping windows, and site-specific Flow-FISH workflows.
Global Averages Masking Biology	Reports global and chromosome arm-specific telomere lengths to identify shortening that may be obscured in bulk measurements.
Subtelomeric Context	Long reads extend into subtelomeric regions, enabling methylation and structural analysis alongside telomere length.
Sample Quality Variability	Renew performs input QC and can provide HMW gDNA extraction to improve consistency for long-read telomere analysis.

Contact and Pricing

Contact us for more information or request a quote

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