Direct Whole Methylome Sequencing (dWMS)

Renew Biotechnologies Service

Summary

Direct Whole Methylome Sequencing (dWMS) is Renew's low-pass whole-genome sequencing service optimized for native DNA methylation analysis. Combining proprietary library preparation with native Oxford Nanopore sequencing, dWMS enables genome-wide methylation profiling without bisulfite conversion or PCR amplification while simultaneously capturing native sequence information from the same dataset.

Designed for scalable methylome characterization, dWMS provides a flexible alternative to methylation arrays for translational research, regional methylation analysis, and non-model species epigenomics.

Key Features & Benefits

- **Native Methylation Profiling:** Characterize native 5mC, 5hmC, and 6mA methylation without bisulfite conversion or PCR amplification.
- **Integrated Multiomic Analysis:** Generate sequence variation and methylation information from the same dataset.
- **Species-Agnostic Workflow:** Analyze human, animal, plant, microbial, and non-model organisms without array or CpG target limitations.
- **Scalable Low-Pass Sequencing:** Optimize throughput and cost for genome-wide regional methylation studies.

Ideal Applications

- Methylation array replacement
- Biomarker research and development
- Population-scale epigenomic studies
- Cross-species methylome analysis

Platform and Core Technology

Library Prep: Proprietary Renew Direct Whole Methylome Sequencing workflow

Platform: PromethION

Protocol Overview

1. **Genomic DNA (gDNA) Extraction:** Genomic DNA is isolated from biological samples.
2. **Library Preparation:** Samples undergo Renew's proprietary native dWMS library preparation and adapter ligation.
3. **Native Long-Read Sequencing:** Libraries are sequenced on the Oxford Nanopore PromethION platform.
4. **Bioinformatic Processing:** Sequencing data are processed through automated methylation analysis workflows.
5. **Data Delivery:** Results are delivered through the customer portal.

Sample Requirements

Parameter	Requirement
Sample Type	Genomic DNA
Minimum Input DNA	0.5 µg
Quality Control (QC)	1 µg

Sequencing Performance

Coverage and sequencing yield depend on genome size.

Metric	Typical Performance
Minimum Coverage	5x
Average Read Length	~10 kb N50
CpG Coverage	>95% CpG coverage
Epigenetic Signals	5mC, 5hmC, 6mA, non-CpG methylation

Data Output

File Format

Data is delivered via the Renew client portal, including sequencing files, methylation calls, variant outputs, and quality control reports. Optional services (available for an additional fee) include POD5 file delivery, alignment to client-supplied reference genomes, and custom bioinformatics analyses.

File	Description
POD5	Raw sequencing data
BAM	Sequencing reads + base modifications

File	Description
CH3	Base modification output format
QC Report	Sequencing metrics and run statistics

QC Reports

For each batch of samples, we provide Quality Control Reports that include read length distribution, base quality, and yield, along with summary statistics such as total number of reads, average read length, and error rates.

Bioinformatics Outputs

Renew delivers methylation outputs in CH3 format, reducing storage requirements by more than 95% while preserving base-resolution methylation information.

For researchers transitioning from array workflows, ModSeqR converts ONT methylation outputs into array-compatible formats supporting minfi, DMRcate, and chAMP.

Throughput & Capacity

Coverage scales with genome size and multiplexing strategy.

Standard Methylation Analysis

- **modkit extract:** read-level CpG methylation calls
- **modkit pileup:** aggregated methylation levels per CpG site

Turnaround Time

Typical turnaround: 14–21 days

Varies based on project scope, sample quality, sequencing depth, and bioinformatic requirements.

Choosing the Right Whole-Genome Workflow

Direct Whole Methylome Sequencing vs. Standard Whole-Genome Sequencing

Both services use Oxford Nanopore native long-read sequencing but are optimized for different research goals.

Choose Direct Whole Methylome Sequencing (dWMS) when your primary objective is genome-wide methylation profiling. dWMS uses Renew's proprietary library preparation workflow and low-pass sequencing strategy to maximize native methylation analysis while simultaneously providing native sequence information from the same dataset. It is well-suited for biomarker research, methylation array replacement, regional methylation analysis, and translational epigenomics.

Choose Standard Whole-Genome Sequencing (WGS) when comprehensive genome characterization, higher sequencing depth, structural variant discovery, de novo assembly, or detailed variant analysis is the primary objective. WGS provides greater genome coverage while still preserving native epigenetic information.

Service Inclusions

Each project includes dedicated scientific and project management support spanning study design through data delivery.

- Data delivery through Renew client portal
- Post-project technical consultation
- Live project tracking
- Flexible data delivery
- Experimental design consultation
- Proprietary library preparation
- Standardized sequencing QC

Contact and Pricing

Contact us for more information or request a quote

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