

# NEGEDIA Whole Genome Methylation Seq (WGMS)

Code NGD0500R

Code NGD0501R

Code NGD0502R

Code NGD0503R

**NEGEDIA** Whole Genome Methylation Seq (WGMS) service delivers ultra-high resolution, base-level mapping of DNA methylation. The service converts **5-methylcytosine (5mC)** and **5-hydroxymethylcytosine (5hmC)** into detectable bases while maintaining the original DNA structure, improving mapping efficiency and overall sequencing performance. Applicable to mammals, plants, and other organisms with 5-mC and 5hmC, this service analyzes the entire genome, covering all regulatory regions and uncovering key epigenetic modifications vital for gene regulation, complex disease research, and biomarker discovery.

## AVAILABLE OPTIONS

WGMS 30x Illumina  
(NGD0500R)

Estimated output per sample is ≈ **400 million reads**.

WGMS 20x Illumina  
(NGD0501R)

Estimated output per sample is ≈ **300 million reads**.

WGMS 30x MGI  
(NGD0502R)

Estimated output per sample is ≈ **400 million reads**.

WGMS 20x MGI  
(NGD0503R)

Estimated output per sample is ≈ **300 million reads**.

## OUR SERVICE INCLUDES

STEP 1



Fluorometric  
quantification  
of starting  
material

STEP 2



Library  
preparation

STEP 3



Library  
QC

STEP 4



Sequencing  
(PE - 2x150 bp)

TAT



35 working  
days

## STARTING MATERIALS

### SERVICE CODE

NGD0500R - NGD0501R - NGD0502R - NGD0503R

### STARTING MATERIAL

500 ng DNA (10 µl / concentration > 50 ng/µl) per sample (Qubit quantified), (NanoDrop quantified > 500 ng recommended)

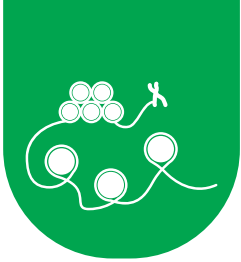
### QUALITY REQUIREMENTS

- RNase treatment to minimize contamination through RNA
- Quantification: fluorescence-based methods like e.g., Qubit or PicoGreen
- Qualitative assessment: agarose gel 0.8 % and / or capillary electrophoresis-based methods

### STORAGE & SHIPPING

- Storage: short term storage: refrigerated (4 °C) / long term storage: - 20 °C
- Shipping: can be sent at room temperature / recommended: refrigerated (4 °C)
- Samples have to be sent in 1.5 ml snap cap tubes. Tubes of different size, or tubes that have screw caps may not be used.

For low cells quantity please contact our Customer Service at [service@negedia.com](mailto:service@negedia.com)



### SERVICE HIGHLIGHTS

- **Reliable Results:** The enzymatic method avoids excessive DNA damage, leading to higher-quality sequencing data and better detection of methylation patterns.
- **Low Sample Degradation:** Since it doesn't rely on harsh bisulfite conversion, the DNA remains more intact, allowing for better coverage and reduced errors.
- **High Sensitivity:** It detects both major DNA methylation markers—5-methylcytosine (5mC) and 5-hydroxymethylcytosine (5hmC)—with high accuracy.

### APPLICATION NOTES

Negedia Whole Genome Methylation Seq (WGMS) is a molecular biology technique that determines the methylation status of an entire genome at single-cytosine resolution.

This service is based on a high-performance enzyme-based alternative to bisulfite conversion for the identification of 5mC and 5hmC. Unlike bisulfite conversion, this highly efficient service minimizes DNA damage, resulting in superior detection of methylated cytosines, with fewer sequencing reads.

#### Key Applications:

- Detailed mapping of DNA methylation at single-base resolution.
- Elucidating the mechanisms underlying cell fate commitment, reprogramming, and gene regulation.
- Identifying novel epigenetic markers and potential therapeutic targets for various diseases.

**NEGEDIA®** is a cutting-edge NGS laboratory built on the Telethon Foundation's 30 years of expertise in rare genetic disease research. We are committed to making genomics accessible across the Life Sciences, providing high-precision sequencing and bioinformatics solutions for both research and clinical applications.

» **Clinical Services:** Supporting laboratories, clinics, and hospitals in leveraging NGS for clinical research and diagnostic advancements.

» **Research Services:** Supporting research institutes and universities at every stage, from experimental planning to advanced bioinformatics analysis.

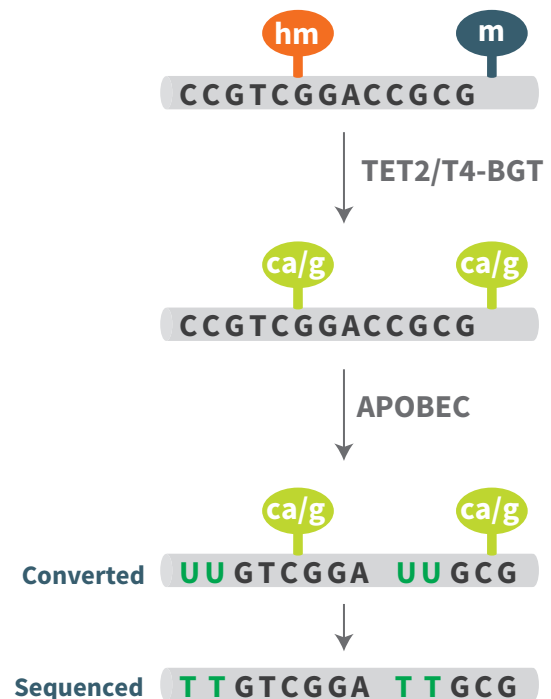
For more information or to discuss a project, contact us at [info@negedia.com](mailto:info@negedia.com)

### BIOINFORMATICS ANALYSIS

**STANDARD BIOINFORMATIC ANALYSIS (INCLUDED IN NGD0500R - NGD0501R NGD0502R - NGD0503R)**



- FastQ files
- Quality report



# GENOMICS AND BEYOND

CERTIFIED  
UNI EN ISO 9001:2015

