

Whole Genome Methylation Sequencing (WGMS) Service

Research Use Only



Almac WGMS data generation service

A high quality, robust Next Generation Sequencing (NGS) solution built on New England Biolab's enzymatic methylation sequencing platform (EM-seq). Almac's wet lab optimised workflow generates comprehensive WGMS data from fresh frozen (FF) samples. The platform covers coding and non-coding regions, generating raw sequencing data for use in biomarker discovery and retrospective clinical investigation. Optional bioinformatics services include processing of raw sequencing data to generate readily interpretable CpG site methylation profiles, and fully customised downstream analysis and reporting solutions.

Platform	
Intended Use	Research Use Only (RUO) for biomarker discovery and retrospective clinical investigation.
Technology	NGS Technology - Illumina sequencing platforms.
Type	Core laboratory service offering for whole genome methylation sequencing (WGMS) data generation with associated QC report.
Genomic feature	Whole genome CpG site methylation profiling (5-mC and 5-hmC).
Sample requirements	
Tissue type	Optimised for Fresh Frozen (FF) samples.
Input material requirements	200ng DNA from FF samples.
Workflow	
Library preparation	NEBNext Enzymatic Methyl-seq (EM-seq™).
Platform performance	
Coverage	30X average on target coverage across cohort (sample quality dependent).
Read length	2 x 150 bp.
Quality control (QC)	
QC assessment	Comprehensive QC assessment of data including: <ul style="list-style-type: none">· Sample & Library QC: DNA input, post-library preparation quality & quantity.· Sequencing Run QC.· Post Sequencing & Alignment QC: Including coverage QC and duplication rate.
Turnaround time	
TAT	For batch retrospective testing - turnaround time (TAT) agreed on a per project basis.
Reporting	
Raw data provided	FASTQ and/or BAM files.
QC Report	Excel compatible report, detailing sample and pre/post alignment sequence QC.
Bioinformatics services	<ul style="list-style-type: none">· Scalable WGMS pipeline hosted on DNAnexus cloud platform enabling:<ul style="list-style-type: none">· Pre/post sequence alignment QC.· CpG site methylation profiling delivered in bedGraph format (optional).· Custom downstream analysis & reporting can be facilitated by Almac Diagnostic Services Bioinformatics Team if required, at an additional cost.

Key benefits:

- **QC guarantee of 30X mean target coverage** across sample cohort enables comprehensive downstream analysis and data interpretation.
- **EM-Seq methodology allows for more uniform coverage of CpG site methylation sites.**
- Protocol **optimised for fresh frozen tissue samples.**
- **Interactive QC report** enables rapid and comprehensive sample quality interrogation across the cohort.
- **Raw Sequence data** delivered in FASTQ format, compatible with the majority of bioinformatics pipelines for processing and interpreting Em-Seq data.
- Optional bioinformatics services to generate **readily interpretable CpG site methylation profiles, and fully customised downstream analysis and reporting solutions.**

Performance validation:

To assess the robustness and performance of Almac's whole genome methylation sequencing (WGMS) Data Generation Platform, Almac performed a number of studies including input, accuracy, and repeatability & reproducibility assessments.

1. Input & Accuracy study

The quality of WGMS data generated at Almac using a range of high-quality DNA derived from fresh frozen samples across a range of disease indications was assessed. Methylation profiles from samples sequenced using 200ng input achieved a Pearson correlation greater than 0.90 at 10X coverage against the same samples orthogonally sequenced using 800ng input (Table 1).

Table 1: Methylation profile concordance between 200ng and 800ng inputs

Coverage (X)	Mean Pearson Correlation
1	0.843
5	0.882
10	0.906
15	0.923
20	0.935

Conclusion – Minimum recommended input is 200ng DNA

2. Repeatability & Reproducibility study

The repeatability and reproducibility of the WGMS platform was assessed using DNA isolated from fresh frozen tissue samples. Across all samples and comparisons made in the reproducibility and repeatability studies, a mean Pearson correlation of greater 0.90 was achieved between methylation profiles at 1X coverage (Table 2).

Table 2: Methylation profile concordance across repeatability/reproducibility studies

Analysis	Coverage (X)	Mean Pearson Correlation
Repeatability	1	0.901
Repeatability	5	0.911
Repeatability	10	0.919
Repeatability	15	0.931
Repeatability	20	0.942
Reproducibility	1	0.906
Reproducibility	5	0.915
Reproducibility	10	0.921
Reproducibility	15	0.931
Reproducibility	20	0.939

Conclusion - Highly repeatable and reproducible WGMS data generation

Almac Diagnostics Services Expertise:

- More than 15 years' experience in working with challenging sample types.
- High quality service with robust quality control and data assurance.
- Data analysis and interpretation services available for customised investigation of data.
- Your study designed, managed & performed by PhD level scientists in our CLIA & CAP accredited laboratory.

For Research Use Only.

Not for use in diagnostic procedures.

Find out more:

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