

Methylation Sequencing with EMSeq or TAPS+ Library Prep

Service Overview

The NGS Core Facility offers a comprehensive TAPS (TET-assisted pyridine borane sequencing) service based on TAPS+ positive-readout chemistry. Unlike bisulfite- or enzymatic-conversion approaches, TAPS+ directly converts methylated cytosines (5mC) to thymines while preserving unmethylated cytosines, thereby maintaining full base complexity (ATCG). This enables simultaneous detection of DNA methylation, single-nucleotide variants (SNVs), insertions/deletions (indels), and copy-number variations (CNVs) from a single library. This document summarises the key technical parameters, deliverables, and sample input requirements

Technical Specifications

Parameter	Specification
Library Preparation	Watchmaker DNA Library Prep Kit with TAPS+ or NEBNext® Enzymatic Methyl-seq Kit
Sequencing Platform	Illumina NovaSeq X Plus
Run Type	Paired-end, 2 × 150 bp
Data Output	Approx. 125 Gb raw data per package (≈40× coverage); multiple data packages can be booked
Quality Target	> 75% of bases ≥ Q30
Deliverables	FASTQ files (sequences and base quality scores)
Turnaround Time	6–8 weeks after sample receipt, depending on the number of samples processed and provided all samples meet the specified input requirements
Expedited Processing	Faster turnaround times are available upon request and may incur additional costs; please contact us in advance

Starting Material

Please ensure your samples meet the following input requirements.

Material	Amount	Concentration	Volume	DNA quality
Genomic DNA (gDNA)	500 ng – 1 µg	> 20 ng/µL	up to 25 µL	DINe value ≥8

Notes

- The stated data output of approx. 125 Gb (≈40× coverage) refers to a single data package. Additional packages can be ordered for deeper coverage.
- For high sample purity, the A260/A280 ratio should be 1.8–2.1 and the A260/A230 ratio 2.0–2.2. Reduced ratios indicate contamination (e.g. salts, phenol) which may influence the efficiency of library preparation. Processing of samples with reduced purity is the responsibility of the customer.
- After receipt of the samples, the DNA quality is determined in the NGS CF on the TapeStation. Only samples with a DINe value ≥ 8 will be processed. Lower values can indicate degradation of the sample material, which can ultimately be reflected in the sequencing data.
- Please refer to our [Sample Requirements & Submission Guidelines](#) for information on quality control, data storage, liability, confidentiality and general sample preparation and shipping instructions.

Contact

For questions and pricing information, please contact:

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