

Panel-based Targeted Enrichment

Service Overview

The NGS Core Facility offers a comprehensive Panel-based Targeted Enrichment service covering library preparation, hybridisation-based target enrichment, sequencing, and primary data delivery. This document summarises the key technical parameters, deliverables, and sample input requirements.

Technical Specifications

Parameter	Specification
Library Preparation	Twist Library Preparation EF Kit 2.0 with unique dual indexing (UDI), followed by the Twist Target Enrichment Standard Hybridisation V1 protocol using a Target Enrichment Panel (e.g. such as Mitochondrial Panel, Mouse Exome Panel, Comprehensive Viral Research Panel)
Sequencing Platform	Element Biosciences AVITI24 or Illumina NovaSeq X Plus
Run Type	Paired-end, 2 × 150 bp
Data Output	Depending on the selected panel. For example, approx. >150x (~2.5 Mb) raw data per package for Mitochondrial Panel
Quality Target	> 75% of bases ≥ Q30
Deliverables	FASTQ files (sequences and base quality scores)
Turnaround Time	6–8 weeks after sample receipt, 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)	200 ng	> 10 ng/μL	20 μL	DINe value ≥8

Notes

- Coverage values are approximate and depend on selected panel, library complexity, GC content, and target region characteristics.
- Sequencing Platform (NovaSeq X plus or AVITI24) and FlowCell assignment is determined by the facility based on availability and project requirements.
- 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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