

RNA Sequencing (mRNA-Seq or total RNA with rRNA/Globin Depletion [Polaris])

Service Overview

The NGS Core Facility offers a comprehensive RNA sequencing (mRNA-Seq or rRNA/Globin Depletion [Polaris]) service covering library preparation, sequencing, and primary data delivery. This document summarises the key technical parameters, deliverables, and sample input requirements.

Technical Specifications

Parameter	Specification
Library Preparation	Watchmaker mRNA Library Prep Kit or with Polaris Depletion. Both with Twist Universal Adapters and Twist UDI Primers
Sequencing Platform	Illumina NovaSeq X Plus
Run Type	Paired-end, 2 × 100 bp
Data Output	mRNA-Seq -> on average 15 M (low coverage) or 30 M (standard) reads per package; raw data (> 75% bases ≥ Q30) total RNA-Seq with rRNA/Globin Depletion [Polaris] -> on average 50 M reads per package; raw data (> 75% bases ≥ Q30)
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	RNA quality
RNA (total, DNA-free)	20–200 ng	> 5 ng/μL (Qubit measured)	25–50 μl	RINe value ≥7

Notes

- The stated read counts (low-pass: 15 M; standard: 30 M; total RNA: 50 M) refer to raw reads per package. The appropriate coverage tier should be selected based on experimental design and downstream analysis requirements.
- After receipt of the samples, the RNA quality is determined in the NGS CF on the TapeStation. Only samples with a RINe value ≥ 7 will be processed. Lower values can indicate degradation of the sample material, which can affect library quality and ultimately be reflected in the sequencing data.
- 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) that may impair the efficiency of library preparation. Processing of samples with reduced purity is at the customer's own risk.
- 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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