

Gene
expressionTotal
transcriptome

Ultra low-input

Small RNA
sequencing

FFPE tissue

Single cell
sequencing

Gene-expression profiling in FFPE cohorts

Robust RNA sequencing of (partly) degraded samples

Biobanks harbor a wealth of gene-expression data of patients with various clinical conditions. The effects of treatment are documented and can be followed over time on the molecular level. These biobanks generally consist of Formalin Fixed Paraffin Embedded (FFPE) tissue. A high degree of RNA degradation within such FFPE cohorts is often

hampering analyses by, leading to exclusion of key samples and/or essential time points.

GenomeScan offers a ISO/IEC 17025 accredited service for expression profiling of FFPE or (partly) degraded samples. Optionally, our bioinformatics experts can generate a comprehensive report with presentation-ready figures.

Input material

Sample

- Optimal total RNA amount for standard workflow: ≥ 250 ng up to 1000 ng
- Optimal total RNA amount for low input workflow: 1 ng up to 10 ng
- Degraded RNA fragments >200 bp (DV200 $> 50\%$)

Sequencing on Illumina NovaSeq 6000

- Paired-end 150 bp (PE150)
- Reads: 60 million/sample

Deliverables

- FastQ file
- Quality score (Q30) $\geq 80\%$

* After validation, new projects start with a pilot experiment to assess the quality of the FFPE material of your cohort.



Factors that affect RNA quality are e.g. age of the blocks, treatment of the material before fixation, storage conditions. Also, formalin fixation damages RNA, causing extensive shredding and modification of nucleotides.

Committed to your project

What we agree is what you get: The best transcriptomics results

- Guidance in optimizing experimental design
- Quality control measurements at various stages to monitor sample performance

Providing additional services:

Extensive expertise in sample preparation

- RNA isolation from FFPE blocks
- Tumor microdissection performed by pathologists from the Leiden University Medical Center (LUMC)

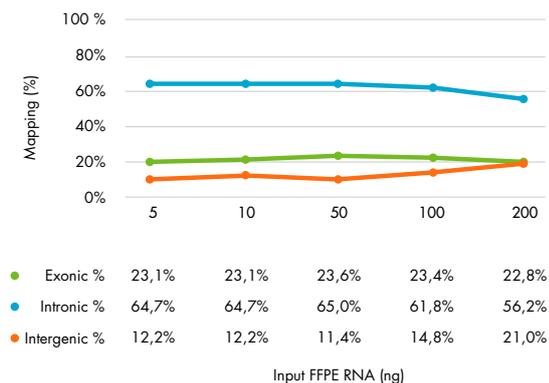
Publication ready results

Laboratory and data-analysis pipelines provide the optimal means for generating results that are suitable for publication

Discover new biomarkers or prognostic markers for disease

Over the years, we have gained extensive expertise in generating reproducible datasets from FFPE blocks. In the study described below, RNA was obtained from a pool of multiple FFPE blocks (Isolation method: Qiagen All Prep DNA/RNA FFPE. Avg. insert size 318 bp ±22).

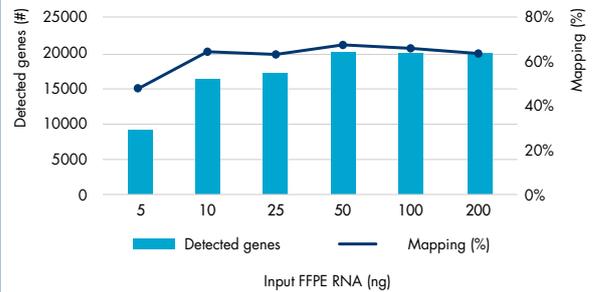
Gene-expression profiling on FFPE RNA is reproducible in a wide range of input amounts



Effect of the amount of FFPE RNA on mapping of the reads to exons, introns and intragenic regions.

A high concordance between results is a measure of robustness and reliability of the workflow.

Optimal input helps maximize the number of detected genes and mapping percentage



Effect of the amount of FFPE RNA input on number of detected genes and percentage mapping

The optimum input is essential to maximize the number of detected genes and mapping percentage and will guarantee dependable results.

Our laboratory and data-analysis pipelines provide the optimal means for generating results that are biologically relevant. However, every FFPE cohort is different. Any new project will start with a pilot to explore the quality of the FFPE material of your cohort. This will reduce the chance of suboptimal data quality and quantity. We provide you data and guidance to make an informed decision before proceeding with the main study.

About GenomeScan

As an ISO-accredited leading Dutch Next Generation Sequencing service provider, GenomeScan develops customizable NGS solutions for pharmaceutical and biotech companies, healthcare providers and academic institutions. By providing state-of-the-art tools to analyze genetic disorders fast, affordably, and effectively, GenomeScan fosters innovation through partnership with medical centers and research laboratories.