Product Specification Sheet

Genome Scan

Gene Expression | **Total Transcriptome** | Ultra low input | Small RNA Sequencing | FFPE Tissue | Single Cell Sequencing

# Total Transcriptome

## Identify all RNA species, including partially degraded RNAs

Total transcriptomic sequencing is not restricted to messenger RNA, but involves sequencing of most RNA species, including long non-coding RNA (lncRNA). A ribosomal RNA (rRNA) depletion step is performed to remove the 18S and 28S ribosomal subunits that make up 60-90% of all RNA species present in your sample, allowing for deeper sequencing of your RNAs of interest.

This approach also tolerates the use of lower quality RNA (degraded RNA) for sequencing. Known causes for RNA degradation include FFPE-fixation and laser-capture methods. Our scientists have set up validated procedures to analyze these challenging samples. This includes clinical-grade sample isolation from FFPE material and tailored data-analysis.

### Input material

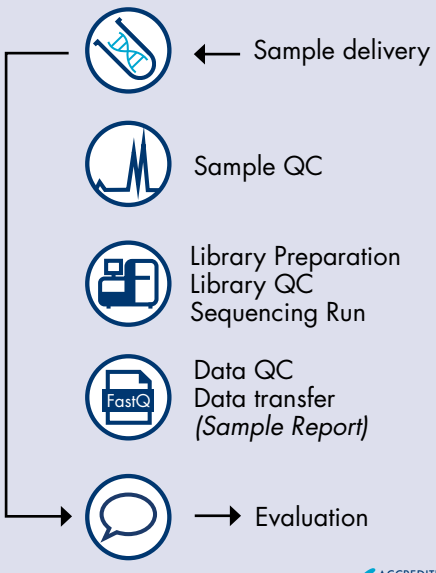
Validated for fresh tissues, whole blood and biopsies. Ribosomal RNA (rRNA) depletion step is mandatory. (Globin reduction possible).

**Isolated Sample**
- Optimal total RNA amount: ≥ 30 ng / sample
- Validated input range from: 10 ng
- Minimal volume of 15 µl / sample
- Quality: all RIN / RQN

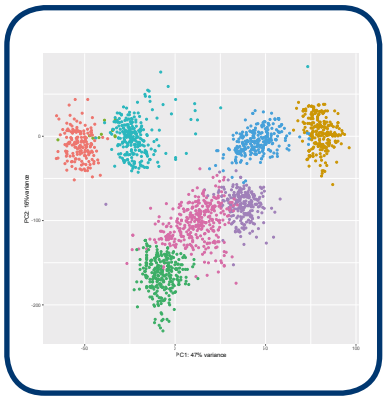
**Sequencing on Illumina NovaSeq 6000 (PE 150)**
- Standard read depth 40M / sample
- Unique Molecular Identifier tags

**Deliverables**
- FastQ files of rRNA depleted transcripts
- Quality score (Q30) ≥ 80%
- **Data delivery 3 weeks after successful sample QC**

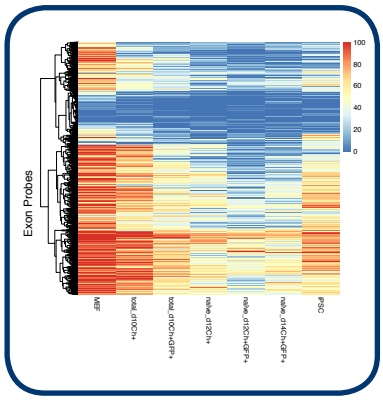
### NGS Laboratory workflow



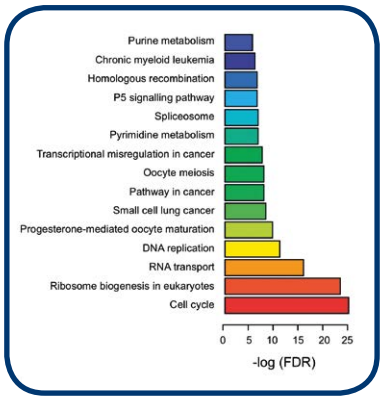

ACCREDITED ISO/IEC 17025 L518 By RvA



Principal components analysis




Heatmap




Pathway analysis

## Committed to your project

### Data quality guarantee

Depth of coverage, base quality and data quality are essential metrics to evaluate the quality of your NGS data. Our average score for 2018 was Q30 ≥ 90%.

### Reads of unique transcripts

A known challenge of NGS sample prep is the formation of PCR duplicates (inversely related to the amount of sample input). Our RNA NGS service includes Unique Molecular Identifiers (UMIs) that ensure the ability to identify these PCR-artifacts and hence allow the read representation of truly unique transcripts.

### Publication ready results

We have dedicated data-analysis pipelines to provide you with the output figures to best represent your data. For every option from microRNA's to long non-coding RNA's and from high-throughput screening methods to delicate single-cell sequencing.

## Data analysis options

Our data analysis report provides multiple visualization options (see frame above) to make data easily comprehensible and useable for decision makers.
The report summarizes the most relevant information, with additional technical details in appendices or individual sample reports. It is based on many years of experience working with customers and a stringent quality system.
Robust industry-standard methods are used to determine gene expression levels and identify differentially expressed genes between biological conditions.
Results can be viewed as summary table, individual gene lists, or heatmap.

Read mappings can be visualized using many intuitive graphical user interfaces that are available in the public domain. Multiple levels of quality controls ensure read integrity and biological plausibility of the results.

## Biological Insights

- *de novo* transcriptome assembly
- Discovery of transcripts and variants
- Differential expression analysis of genes,transcript variants, and exons (alternative splicing)
- Analysis of gene fusions and trans-splicing events
- Analysis of non-coding RNAs
- Gene regulatory networks, signaling pathways and networks, and gene enrichments
- Host/pathogen interactions or xenografts

## Custom analysis

Custom bioinformatics can be performed allowing more in depth mining of your data set. Functional gene information mining, gene enrichment set, gene ontologies may be additionally provided when required.

## About GenomeScan

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

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