



Gene expression



Total transcriptome



Ultra low-input



Small RNA sequencing



FFPE tissue



Single cell sequencing

# Small RNA Sequencing

Discovery and expression profiling of small RNAs in any organism

In the world of non-coding RNAs, the small RNAs play a regulatory role. GenomeScan offers a robust method for the discovery and quantification of RNA species of up to 120 nucleotides in length, for efficient measurement of RNA species.

Size selection is the most challenging part of the procedure, directly affecting the representation of the small RNAs in your sample. Our R&D team has developed an ISO/IEC 17025 accredited method

using the BluePippin system, allowing for precise size selection of the transcripts of interest. With minimal input, samples showed a technical concordance ( $R^2$ ) of 0.99 in our validation study.

In certain samples or disease states, the abundance of specific small RNA's can mask the detection of other small RNAs. Our scientists can design custom blocking oligos to remove any uninformative RNAs from the library, so less sequencing-space is required.

## Input material

Isolated total RNA or small RNA fraction

### Isolated sample requirements

- Preferred minimal input for total RNA:  $\geq 250$  ng / sample
- Preferred minimal input for small RNA:  $\geq 2$  ng / sample
- Minimal volume of 20  $\mu$ l / sample
- Quality applies only to total RNA: RIN  $\geq 7$  / RQN  $\geq 6$

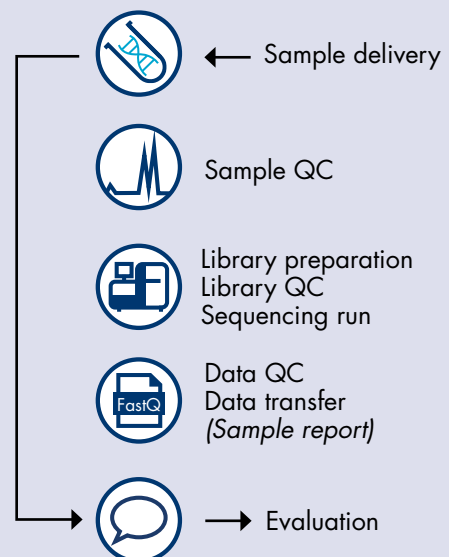
### Sequencing on Illumina NovaSeq (PE 150)

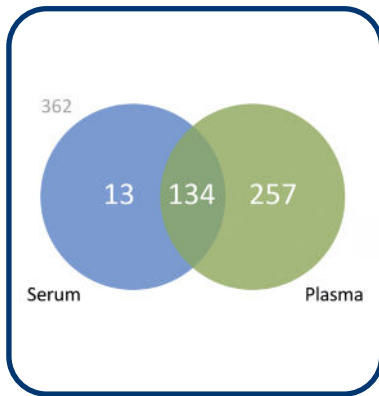
- Standard read depth 15M / sample

### Deliverables

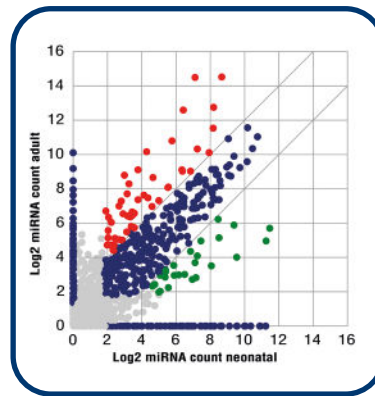
- FastQ files
- Quality score (Q30)  $\geq 80\%$
- Optional data analysis with comprehensive report

## NGS Laboratory workflow

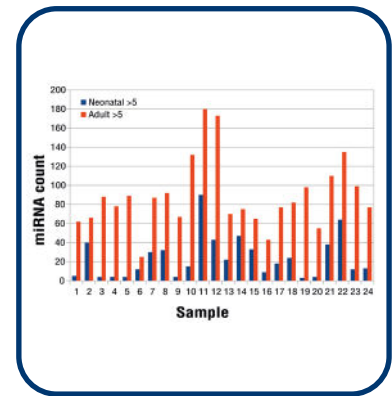




Venn diagram analysis



Correlation analysis



Quantitative expression 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 is generally Q30  $\geq$  90%.

### Publication ready results

Our IT team has developed validated pipelines to find the biological meaning in your samples. IT experts provide you intuitive output to fast-track data-interpretation.

## Dependable data-analysis and visualization

You receive reliable and easily understandable data, suitable for publication or visualization in your project meetings. The data analysis report provides multiple tables and graphs to assist you in testing your hypotheses, discovering new biomarkers, or understanding biological mechanisms. The report summarizes the most relevant information, such as quantification tables, gene lists, or data mining, with additional technical details included in appendices or individual sample reports. It is based on extensive experience working with customers and adhering to a strict quality system. To determine expression levels and identify differentially expressed small RNAs between biological conditions, we employ robust industry-standard methods. The results can be viewed as summary tables, individual gene lists, or heatmaps.

Read mappings can be visualized using various intuitive graphical user interfaces available in the public domain. Multiple levels of quality control ensure the integrity of reads and the biological plausibility of the results.

## Biological insights

- Analysis of non-coding RNAs
- Gene set enrichment analysis (GSEA) adapted for microRNAs

## 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, 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.