Product Specification Sheet

Genome Scan

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 RNA's play a regulatory role. GenomeScan offers a robust method for the discovery and quantification of RNA species of up to 350 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 oligo's to remove any uninformative RNAs from the library, so lees sequencing-space is required.

Input material

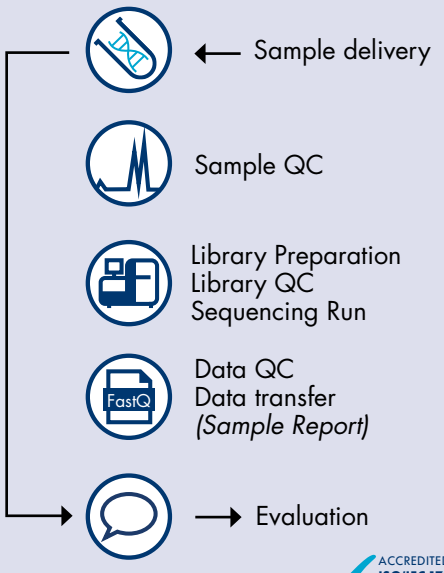
Validated for fresh tissues, whole blood and biopsies.

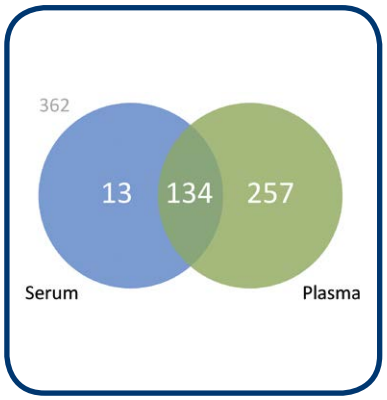
Isolated Sample
- Optimal total RNA amount: ≥ 250 ng / sample
- Validated input range from: 100 ng / sample
- Quality: all RIN / RQN ≥ 7

Sequencing on Illumina NovaSeq 6000 (PE 150)
- Standard read depth 15M / sample
- Unique Molecular Identifier tags

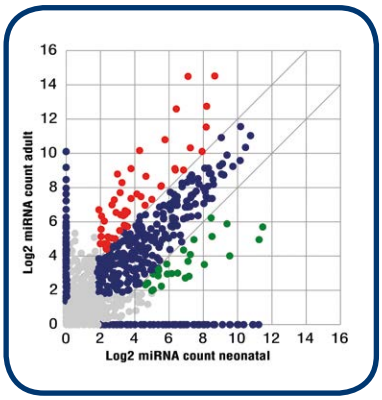
Deliverables
- FastQ files of poly-A containing transcripts
- Quality score (Q30) ≥ 80%
- **Data delivery 3 weeks after successful sample QC**

NGS Laboratory workflow

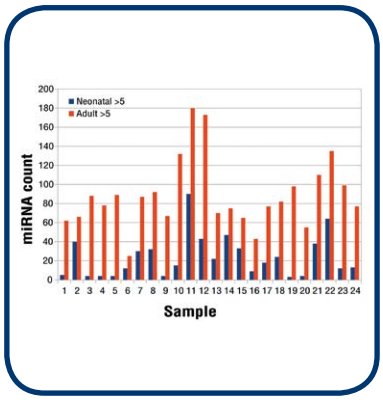




Venn diagram analysis



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 for 2018 was Q30 ≥ 90%.

Reads of unique transcripts

A known challenge of NGS sample prep is the formation of PCR duplicates. Our services include Unique Molecular Identifiers (UMIs) for identification and removal of these PCR-artifacts. Your research will only contain truly unique transcripts.

Publication ready results

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

Dependable data-analysis and visualization

You can rely on comprehensible data, ready for publication or visualization in your project meeting. The data-analysis reports provide multiple tables and graphs to test your hypothesis, discover new biomarkers or understand biological mechanisms. The report summarizes the most relevant information such as quantification tables, gene lists or data mining with additional technical details in appendices or individual sample reports. It is based on many years of experience working with customers and operating under a stringent quality system.
To determine gene expression levels and identify differentially expressed genes between biological conditions, we use robust industry-standard methods. Results can be viewed as summary table, individual gene lists, or heatmaps.

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.

genomescan.nl

+31 71 5681050

info@genomescan.nl