Your expert NGS partner
Exiqon Sequencing Services

Exiqon offers a complete package for Next Generation Sequencing:

- Thorough QC of RNA samples and libraries
- RNA isolation from various samples
- High quality library preparation and enrichment for your RNA of choice
- Scientific consultation by our PhD level staff before and after the project
- Comprehensive data analysis with report including publication-ready figures and tables
- 4-6 weeks turnaround time for a project

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Sample-to-answer NGS Service

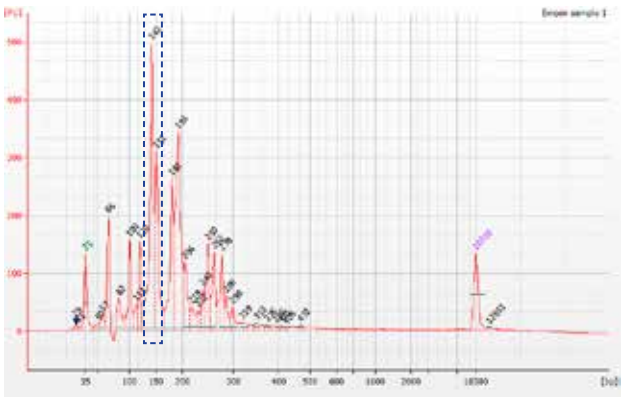
Exiqon's NGS services include all the steps in a sequencing project, from initial consultation with our RNA experts to a comprehensive final report. We perform RNA isolation, library preparation, sequencing, data analysis and quality control adapted to your needs. All analyses are performed by PhD-level scientists with extensive sequencing experience to ensure that you get the best service throughout the project.

We currently offer four RNA sequencing solutions:
- microRNA sequencing
- Small RNA sequencing
- mRNA sequencing
- Whole transcriptome sequencing

Exiqon Services provide outstanding data analysis, interpretation and visualization of your results. Our superior bioinformatics pipeline is based on solid biological expertise. As our experimental and bioinformatics pipelines are closely integrated, we can offer a market leading product adapted to your needs. Data and results from your microRNA profiling project are delivered in an easy-to-read report.

microRNA sequencing

Take advantage of Exiqon's vast experience in microRNA profiling. Use our microRNA Sequencing Service for accurate quantification and discovery of microRNAs.



Accurate selection of microRNAs. Exiqon's microRNA Sequencing Services use an RNA fraction of 15-30 nt in length ensuring that all microRNAs are included in sequencing.

We help you find new microRNAs using the advanced miRPara software tool specifically adapted for Next Generation Sequencing. We offer powerful data analysis adapted to your project. We perform advanced differential expression analysis between sample groups to identify differentially expressed microRNAs. We can accommodate specific customer requests.

At the end of the service project you will receive a comprehensive report containing the data analysis results and biological interpretation of the data. We also offer validation of the results using Exiqon's class-leading microRNA qPCR platform.

microRNA sequencing key specifications	
Minimum RNA input amount	250ng + 60ng for QC
Sequenced RNA species	microRNAs
Recommended product	1x50bp, 7.5M reads
Enrichment method	Size selection, 15-30 bases

Small RNA sequencing

Find out what small RNAs are in your sample and get an insight into the regulation of small non-coding RNAs such as snRNAs, snoRNAs and tRNAs.

We take advantage of our excellent bioinformatics pipeline in setting up and analyzing your samples. Data is compared to a comprehensive reference database of small RNAs constructed from a broad range of reference sources, ensuring a relevant and in depth interpretation of the sequencing experiment. To get the most out of your sample, we recommend that you choose a size range of the RNAs you would like to have sequenced in order to optimize read depth.

At the end of the service project you will receive a comprehensive report containing the data analysis results and biological interpretation of the data. PCR validation of your results is available.

Small RNA sequencing key specifications	
Minimum RNA input amount	250ng + 60ng for QC
Sequenced RNA species	Small RNA 30-200nt
Recommended product	1x50-200bp, 7.5M reads
Enrichment method	Size selection

mRNA sequencing

Use our mRNA Sequencing Service to sequence all polyadenylated (poly-A) mRNA transcripts - the protein coding portion of the transcriptome. By focusing on just the polyadenylated RNA, which represents only a fraction of the whole transcriptome, we increase the sensitivity of the experiment which allows us to identify transcripts expressed at very low levels.

We offer mRNA sequencing for human, mouse or rat samples and any other species where a reference genome is available. Please contact us for further details.

Take advantage of our excellent bioinformatics and QC pipeline and get accurate mRNA expression profiles and information on transcripts that are differentially expressed between sample groups. We recommend paired-end sequencing as this allows for alignment of reads with greater confidence and generates data on splice variants.

The final report contains all the data analysis results and a biological interpretation of the data.

mRNA sequencing key specifications	
Minimum RNA input amount	100ng + 60ng for QC
Sequenced RNA species	mRNA >170nt
Recommended product	2x50bp, 50M reads
Enrichment method	PolyA enrichment

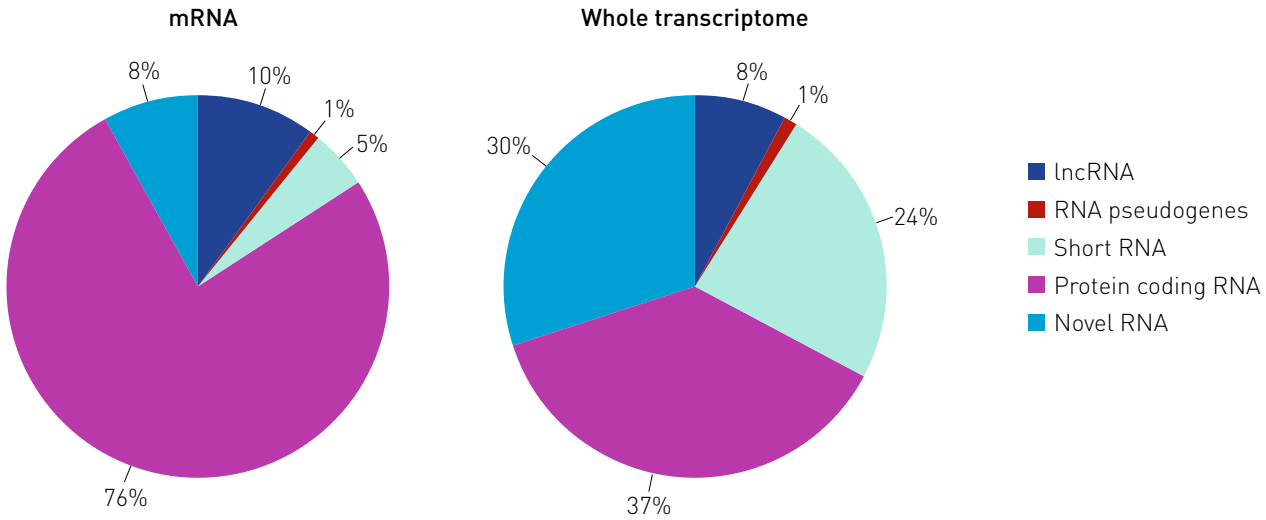
Whole transcriptome sequencing

Whole transcriptome sequencing allows us to sequence all coding and non-coding RNAs in your samples after depletion of ribosomal RNA. Our RNA experts can help you discover new transcripts or perform differential expression analysis on the entire transcriptome. We can also help you identify splice variants by using paired-end sequencing.

Each project can be tailored to your individual needs by using different combinations of read lengths (50, 75 or 100bp), using single- or paired-end sequencing or setting read depths.

Just like our other sequencing services, you will receive a comprehensive final report at the end of the project, complete with data analysis results and biological interpretation of the data.

Whole transcriptome sequencing key specifications	
Minimum RNA input amount	100ng + 60ng for QC
Sequenced RNA species	mRNA + LncRNA >170nt
Recommended product	2x50bp, 50M reads
Enrichment method	Ribosomal RNA depletion



Distribution of known and novel RNA isoform biotypes obtained from subjecting an RNA sample for mRNA and totalRNA sequencing, respectively, at Exiqon NGS Services. Sequencing was performed on an Illumina NextSeq 500. The reads for each sample were filtered to remove remnants of mitochondrial RNA and rRNA followed by alignment to the human genome using the Ensembl transcript annotation (GRCh37) as a guide. Genes not possible to map to a specific RNA biotypes are displayed as Novel, while the mapped RNA biotypes contain both known and novel isoforms.

Sequencing project workflow

Consultation on experimental design - Tailored experimental design to suit your project and budget

RNA sample submission
Minimum 100-250ng of isolated RNA + 60ng for QC needed for RNA sequencing

Sample submission
Cells, tissue, FFPE, whole blood or other

Sample isolation
Samples are isolated by Exiqon for optimal yield

RNA sample quality control - Quality control of samples to identify potential outliers and sample bias

Library preparation - Targeting RNA of interest

Library quality control - Quality control and quantification (Bioanalyzer and qPCR)

Next Generation sequencing
Sequencing of RNA of interest using Illumina NextSeq 500 og HiSeq 2500 allowing maximum flexibility by accommodating different sized projects and ensuring fast delivery times

Data analysis and interpretation
Filtering, mapping, normalization, differential expression analysis (including statistics), GO enrichment analysis and biological interpretation

Delivery of report and final consulting
An extensive report is generated and accompanied by a followup scientific discussion with our NGS experts

Delivery of RAW data

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13-0111 - 923031 - v1.0 - 07/2014

Data analysis

We use a high-quality automated data analysis pipeline optimized to achieve the highest possible yield of annotated reads. This pipeline includes numerous intermediate QC steps to ensure that you receive reliable high quality data.

We can adapt the pipeline to fit your project to ensure that you get the most out of your samples.

All data is analyzed and interpreted by our PhD level scientists and delivered in a report that includes publication-ready figures and tables.

Raw sequencing data

Sequencing QC

Alignment and Filtering

Mapping QC

Transcript assembly: Identification of known and novel transcripts

Differential expression analysis of all identified transcripts

Gene ontology analysis / miRSearch

Visualization of results

Data analysis report

Post-support with PhD-level scientist

Seamless integration with products for validation and functional analysis

NGS instruments

Sequencing by market leading Illumina NextSeq and HiSeq technology

First class reports

The result of your sequencing project is presented in an easy-to-read summary report. It contains a description of the project, assessments of the sample and data quality and an overview of the results of the data analysis with publication-grade illustrations.

Our experimental and bioinformatics pipelines are closely integrated, which enables us to offer you a market leading product.

Download a report example from:
exiqon.com/ngs-services

Read more at: exiqon.com/ngs-services