



# Gene expression analysis with Gubra

## Gene expression analysis using mRNA sequencing

mRNA sequencing using RNAseq is a powerful addition to your preclinical study. RNAseq will highlight molecular mechanisms of a treatment and is very sensitive and highly reproducible across experiments. Everything from sample collection to analysis are done in-house to ensure high quality data.

### Designated laboratory and staff

Samples are processed in a designated molecular biology laboratory staffed with highly trained specialists. The workflow from RNA isolation to sample preparation and sequencing are automated to secure high throughput and consistent results. NGS are carried out using the Illumina technology.

### Bioinformatic analysis

Bioinformatic analysis are performed by Gubra bioinformaticians. The analysis includes extensive quality control, mapping of sequencing reads, unbiased cluster analysis and differential expression analysis across different treatment groups. Furthermore, Gubra maintains relevant gene-set tables for relevant pathologies.

### Key gene expression services

- Explore all details of data through personal and secure access to our interactive data presenter GubraView.
- Data downloadable in ready-to-present PowerPoint format.
- Walk-through of data with a Gubra bioinformatic scientist.
- Custom analyses to answer specific research questions.

### Custom analysis and scientific counselling

On top of the standard analysis Gubra bioinformaticians are available for discussions of study design and walk-through of data. Additional analysis can be included and our bioinformaticians are experts within the metabolic space and can provide value insights to the data and the perspectives.

### Sample flow

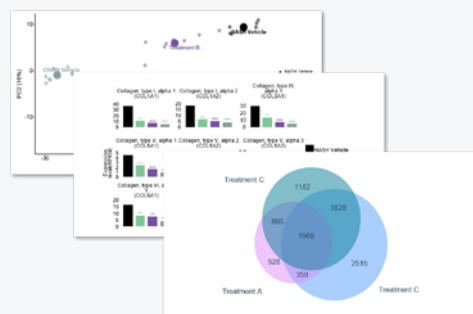
Illustration of the sample flow from sample collection and preparation to sequencing and data analysis. Everything is performed on site at Gubra.

1. Samples are collected in house.



3. Extensive bioinformatic analysis of the data.

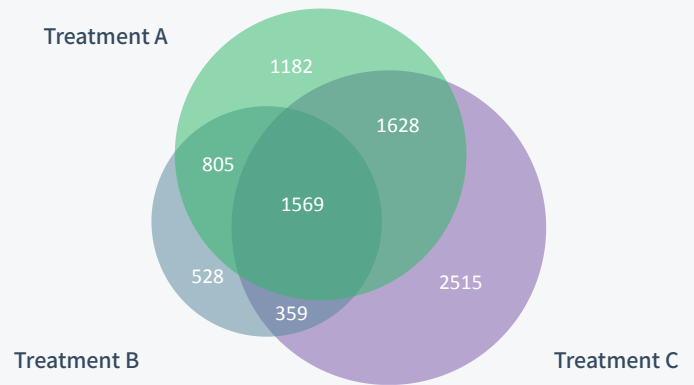
2. RNA are isolated from samples and sequenced.



## Data presentation

High-level results are presented in PowerPoint format providing an overview of the experiment. The presentation includes Venn diagrams of overlapping differentially expressed genes, PCA analysis and pathway summaries.

[View data presentation example](#)



## Data online in GubraView

Due to the size and complexity of RNAseq datasets, results cannot be captured fully in a PowerPoint data presentation. Therefore, all RNAseq experiments are available in GubraView. GubraView presents data with high resolution and enables researchers and professionals with biological insight to raise specific queries to the data - without the need for a bioinformatician.

[See our introduction video to GubraView](#)



## Pathways and Gene panels

Gubra maintains a selection of manually curated gene-sets for relevant pathologies. These are available from GubraView. Additional gene-sets and pathways can be analysed using the Reactome pathway catalogue and the genes associated with a disease can easily be obtained.

Plot display Color palette Treatment statistics

Study endpoint  
Select the data endpoint to plot  
Gene expression

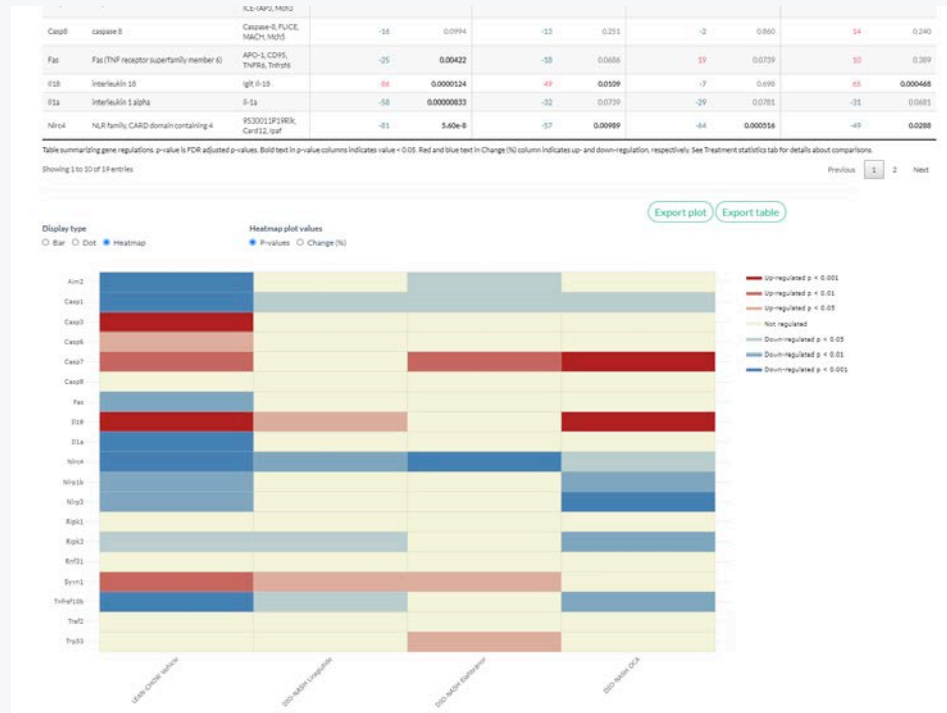
Gene table subsets  
 All genes  
 Regulation overlap  
 Disease association  
 Pathway membership  
 Gubra curated gene panels

Search

Uniform Medical Language System Disease  
 Hemorrhagiconia  
 Metabolic Diseases  
 Streptococcal pneumonia  
 Sepsis

Click row in table below to plot expression of gene  
 Show 10 entries

Name	Description	Synonyms
Gna13	guanine nucleotide binding protein (G protein), alpha inhibiting 3	Galpha13
Pbsn	probasin	PB
Cdc45	cell division cycle 45	Cdc45l
Scm12	sex comb on midleg like 2 (Drosophila)	4932420G07Rik
ApoH	apolipoprotein H	B2GPI, beta-2-glycoprotein 1, beta-2-GPI
Narf	nuclear prelamin A recognition factor	4430402O11Rik
Cav2	caveolin 2	BCD1, Copeb, CFBP, FM2, FM6, lerepo1, lerepo3, Zfp



## Compare expression from multiple genes in heatmaps

Heatmaps can be produced in GubraView to compare the regulation of multiple genes and treatments into a single figure.

## Try it yourself

Heatmaps can be produced in GubraView to compare the regulation of multiple genes and treatments into a single figure.

[Explore RNAseq in GubraView](#)

Plot display Color palette Treatment statistics

Study endpoint  
Select the data endpoint to plot  
Gene expression

Gene table subsets  
 All genes  
 Regulation overlap  
 Disease association  
 Pathway membership  
 Gubra curated gene panels

Click row in table below to plot expression of gene  
 Show 10 entries

Name	Description	Synonyms	LEAN-CHOW Vehicle	
			Change (%)	p-value
Gna13	guanine nucleotide binding protein (G protein), alpha inhibiting 3	Galpha13	3	0.72
Pbsn	probasin	PB		
Cdc45	cell division cycle 45	Cdc45l	-30	0.097
Scm12	sex comb on midleg like 2 (Drosophila)	4932420G07Rik	-21	0.48
ApoH	apolipoprotein H	B2GPI, beta-2-glycoprotein 1, beta-2-GPI	109	<b>3.07e-1</b>
Narf	nuclear prelamin A recognition factor	4430402O11Rik	69	<b>9.30e-</b>
Cav2	caveolin 2	BCD1, Copeb, CFBP, FM2, FM6, lerepo1, lerepo3, Zfp	-49	<b>0.0000031</b>
Klf6	Kruppel-like factor 6		-72	<b>1.20e-1</b>
Scmh1	sex comb on midleg homolog 1	Scm13	-16	0.051
Cox5a	cytochrome c oxidase subunit Va	CcOX	24	<b>0.026</b>

Table summarizing gene regulations. p-value is FDR adjusted p-values. Bold text in p-value columns indicates value < 0.05. Red and blue

Showing 1 to 10 of 21,755 entries