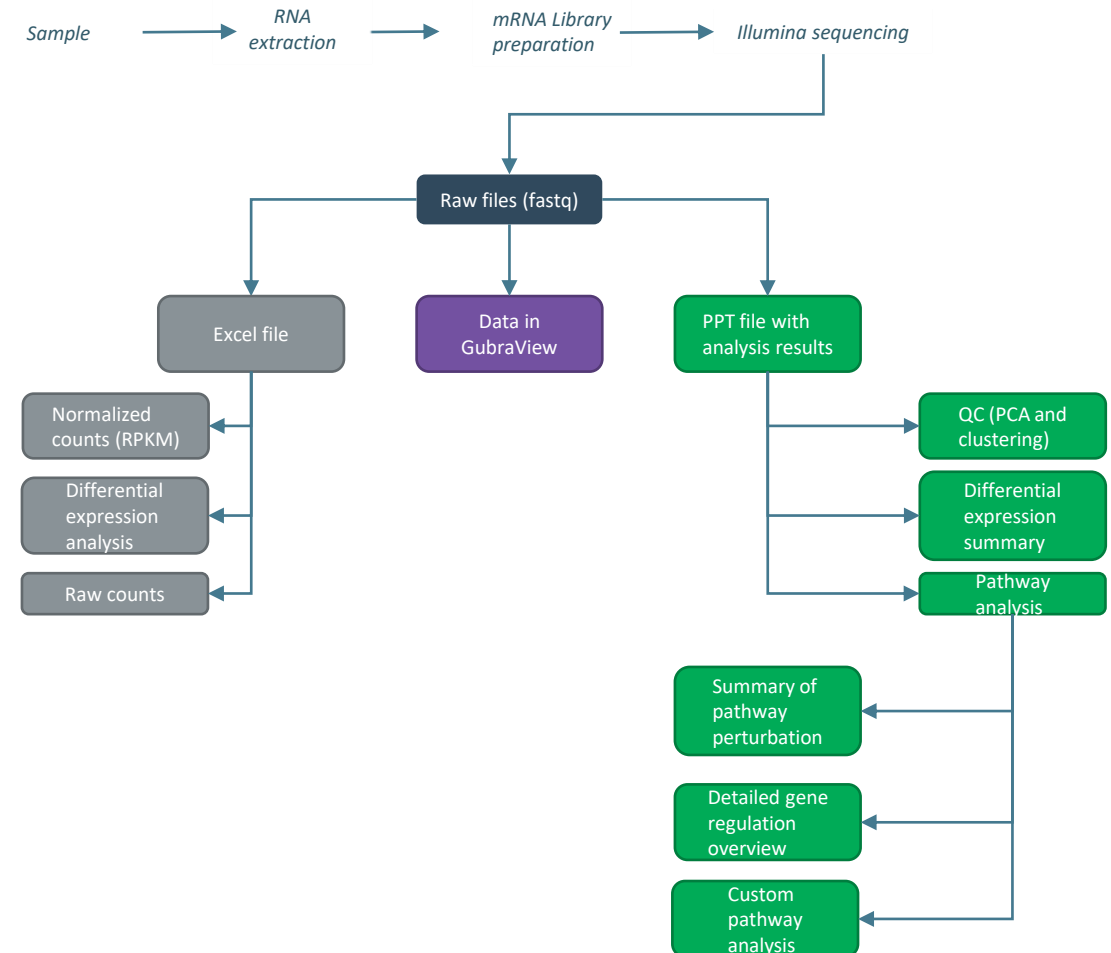


Gubra RNAseq overview

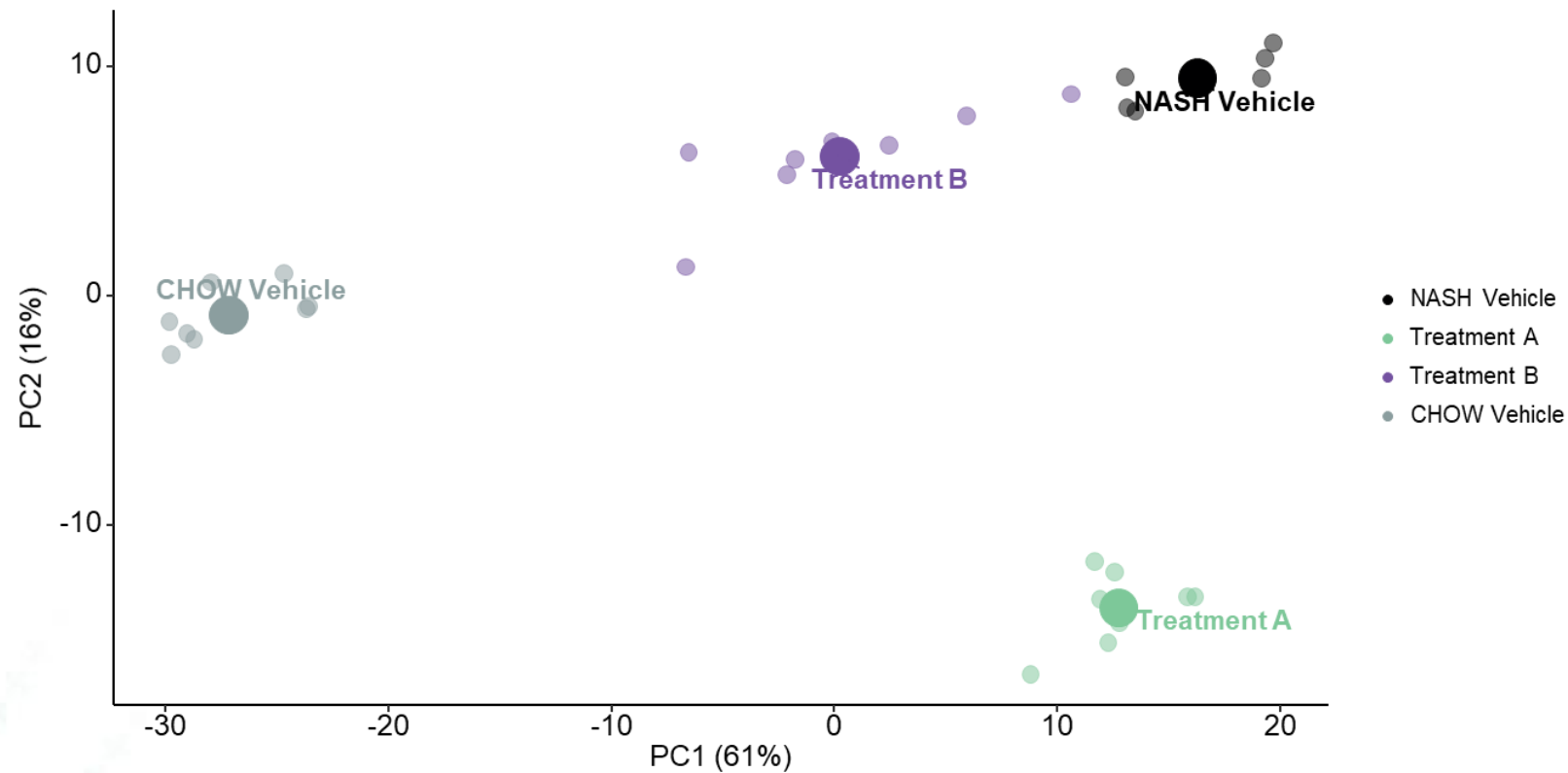
- + Sample collection, RNA extraction, library build and sequencing using Illumina technology
- + Data delivered in a ready-to-present PowerPoint® presentation containing:
 - Sample and group clustering based on gene expression using PCA analysis
 - Overview of up- and downregulated genes in the different treatment groups compared to control group
 - Overview of gene regulation overlaps between the different treatment groups.
 - Each pathway contains a defined number of genes presented in a graphical overview.
 - Expression level of each genes in pathway grouped by treatment.
 - Volcano plots illustrating the relationship between fold regulation and statistically significance comparing treatment group to control.
- + Analysed data delivered in spreadsheet format including statistics and can be accessed through GubraView
- + Walk-through of data with a Gubra scientist

Following slides contains examples from our data presentations

Example of standard RNAseq data package:

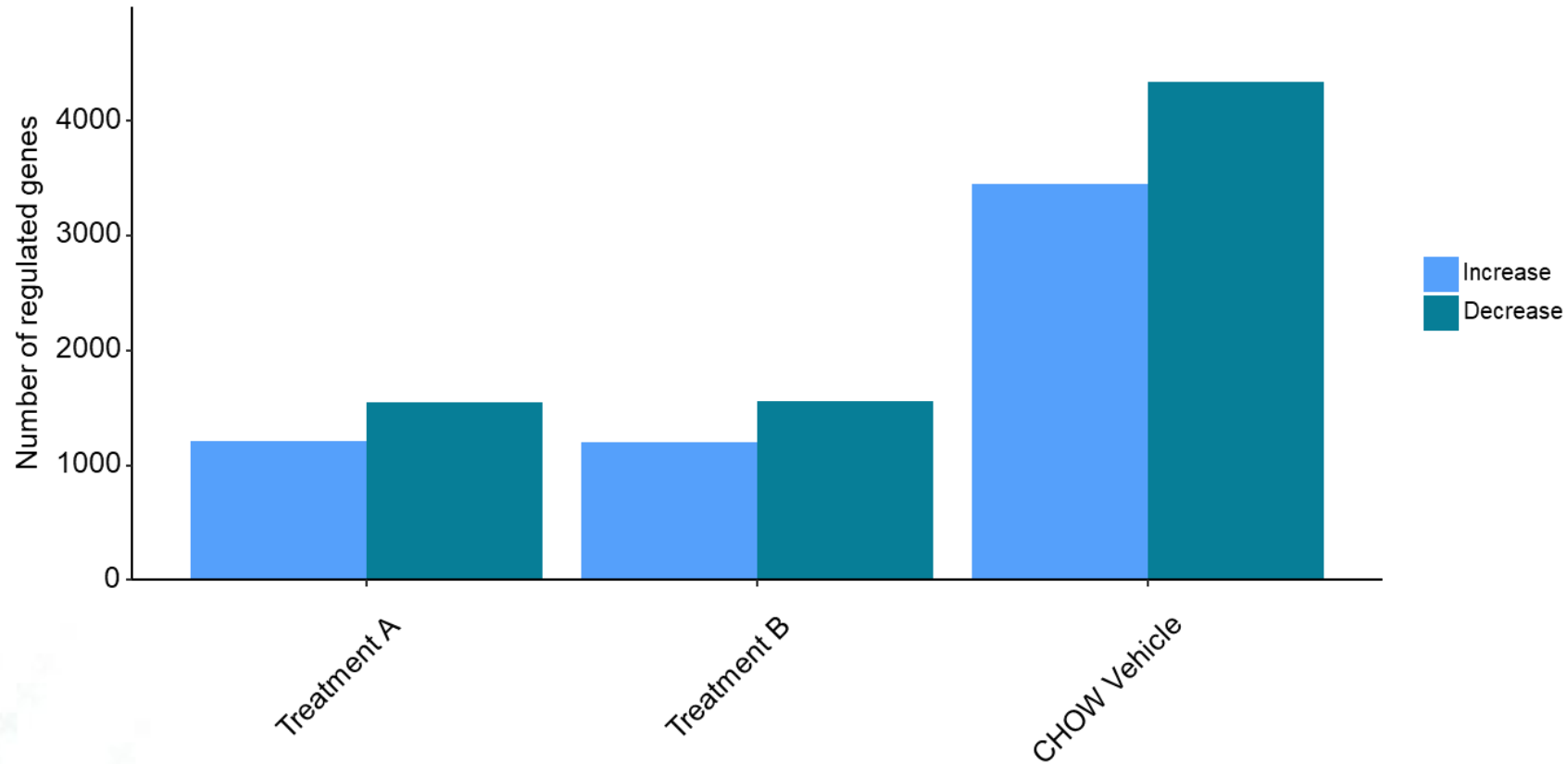


Sample transcriptomic profiling using PCA



Overview of gene expression between control and treatment groups, with close proximity of samples indicating high similarity.

Differentially gene expression analysis



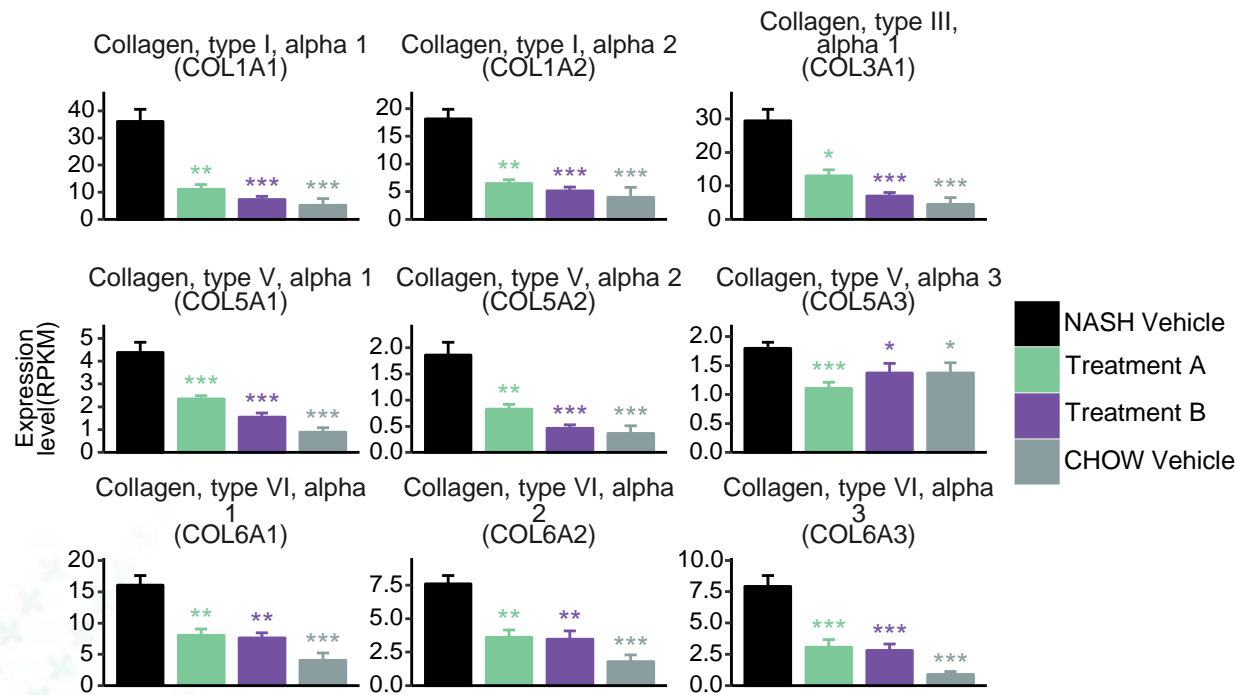
Overview of up- and downregulated genes based on differential expression analysis using DESeq2. Grouped by treatment compared to a control group. Colour indicates up or down regulation.

Included signalling pathways and genes

Lipid metabolism	Inflammation signaling	Monocyte recruitment	Stellate cell activation	Hepatocellular cell death	Insulin signaling	FXR signaling	Custom
CD36	MAP3K5	CCR1	ACTA2	AIM2	AKT1	APOA1	Available upon request
CD36	FOS	CCR1	MCAM	CASP1	ELK1	APOA5	Contact Gubra
CPT1A	CHUK	CCR2	COL1A1	CASP3	FOXO1	APOC2	
CYP7A1	MAPK8	CD14	COL1A2	CASP6	G6PC	APOC3	
CYP8B1	JUN	CD163	COL1A2	CASP6	GK3P	SLC27A5	
FASN	NFKB1	CD68	COL3A1	CASP7	SLC2A4	CYP7A1	
NR1H4	MAPK11	CD86	COL5A1	CASP8	GRB2	CYP8B1	
GPAT2	SMAD2	ADGRE1	COL5A2	IL18	GYS2	FASN	
GPAT4	SMAD3	IL10	COL5A3	IL1A	INSR	G6PC	
HMGCR	SMAD4	IL1A	COL6A1	NLRC4	IRS1	SLC2A4	
HMGCS1	TGFB1	IL1B	COL6A2	NLRP1	IRS2	ABCB4	
HMGCS2	TGFBR1	LGALS3	COL6A3	NLRP3	MAPK1	NFKB1	
LDLR	TGFBR1	CCL2	EGF	RIPK1	MAPK3	SLC22A7	
LRP1	TLR4	CCL5	EGF	RIPK3	MAP2K1	SLC51B	
PPARA	TNF	CCL5	GFAP		MAP2K2	PCK1	
PPARD	TNF	TGFB1	MMP13		PCK1	PPARA	
SCARB1	TNF	TNF	MMP2		PRKCI	NR0B2	
SCD	TNFRSF1A		MMP9		PRKCZ	SREBF1	
SQLE	TRAF2		PDGFA		PYGL	UGT2B10	
SREBF2	TRAF6		TGFB1		SREBF1	VLDLR	
SREBF1			TIMP1				
			TIMP2				
			TIMP3				
			TIMP4				

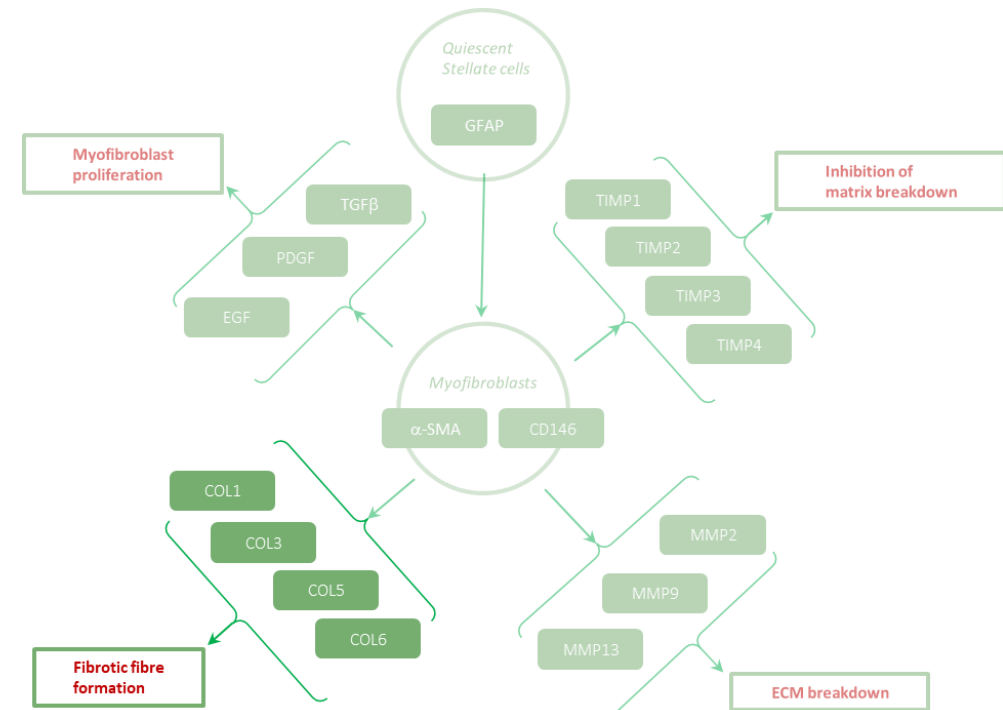
Pathway analysis - example

Stellate cell activation - Fibrotic fibre formation



(Average + SEM of expression levels of pathway subset genes. *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$ compared to NASH Vehicle after correction for gene-wise multiple testing. (right) Pathway subset highlighted.

Expression level of each genes included in pathway grouped by treatment. Statistical differences in expression levels are indicated on figures.



Each pathway contains a defined number of genes presented in a graphical overview. We offer a variety of pre-defined pathways