

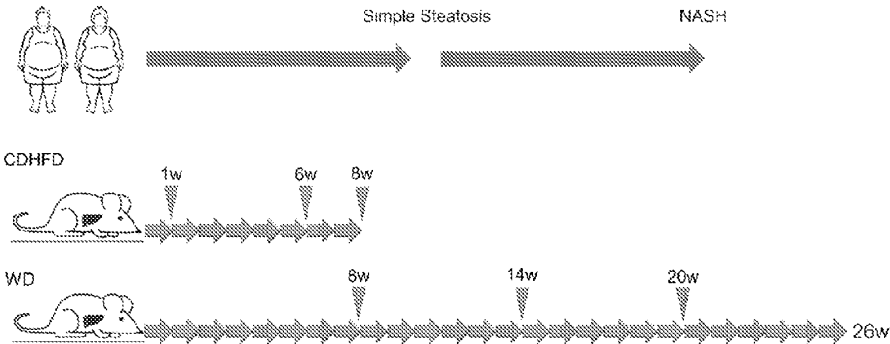


Figure 1

Mouse Models of NAFLD & NASH

Model	Obesity	Insulin Resistance	Steatosis	Inflammation	NASH	Fibrosis	HCC
HFD	✓✓	✓✓	✓✓	✓	X	X	X
CD	X	X	✓✓	✓	✓✓	✓✓	X
WD	✓✓	✓✓	✓✓	✓	X	X	X
DIAMOND	✓✓	✓✓	✓✓	✓✓	✓✓	✓✓	✓✓
CDHFD	✓✓	✓✓	✓✓	✓✓	✓✓	✓✓	✓
WD + Fructose	✓✓	✓✓	✓✓	✓✓	✓✓	✓✓	✓✓

Figure 2

(a)

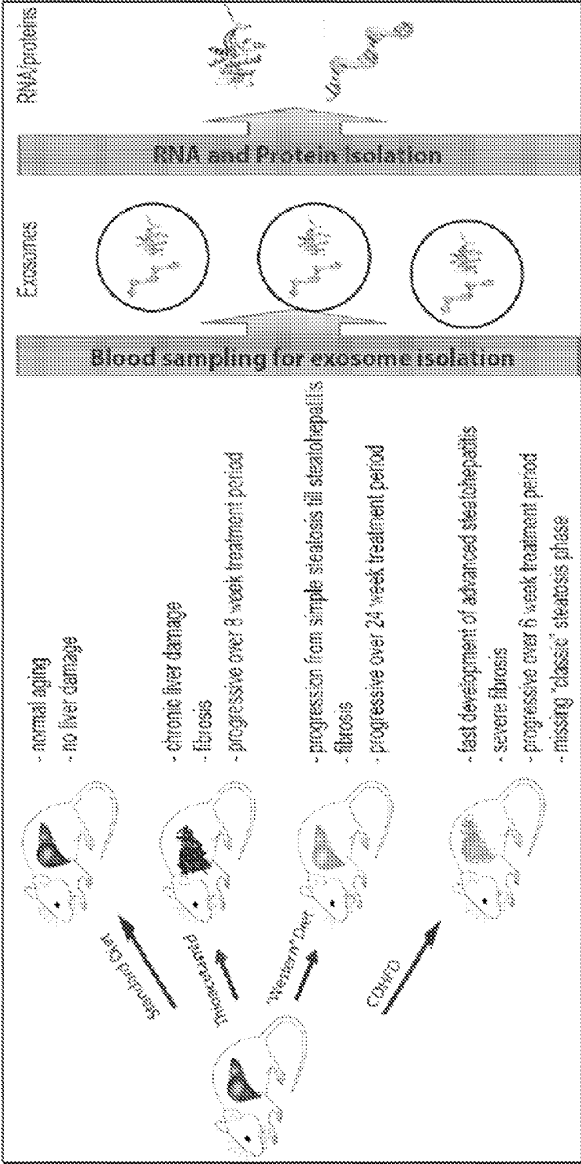


Figure 3(a) (continued)

(b)



(c)

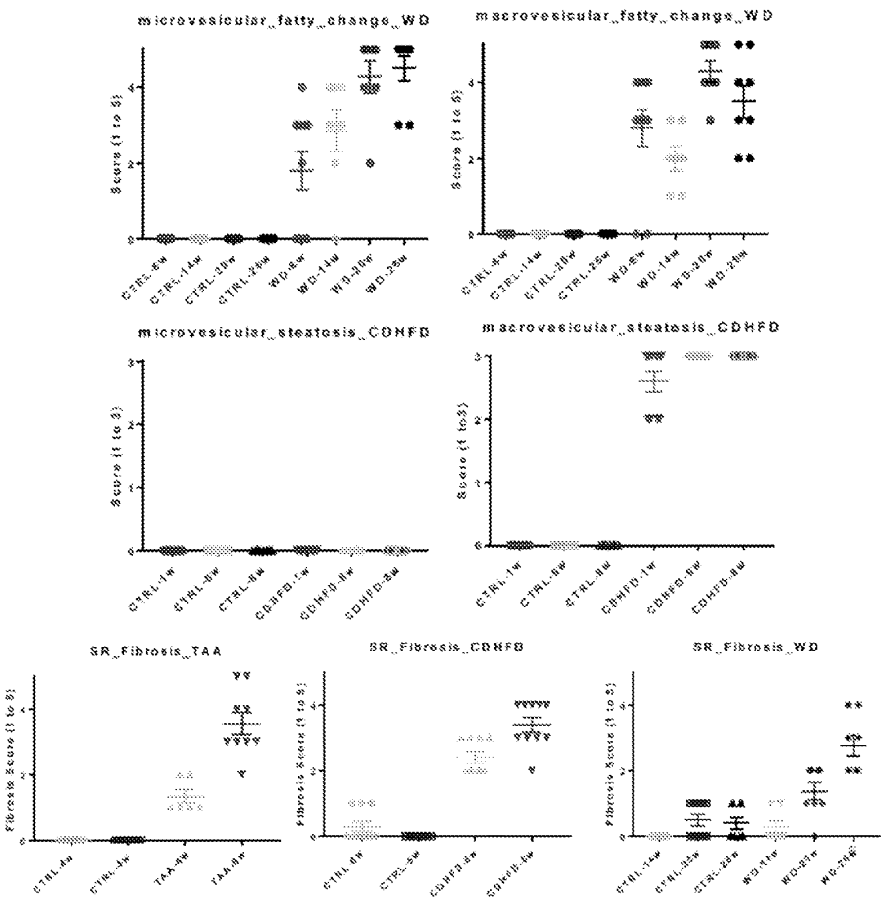


Figure 3(b)-(c) (end)

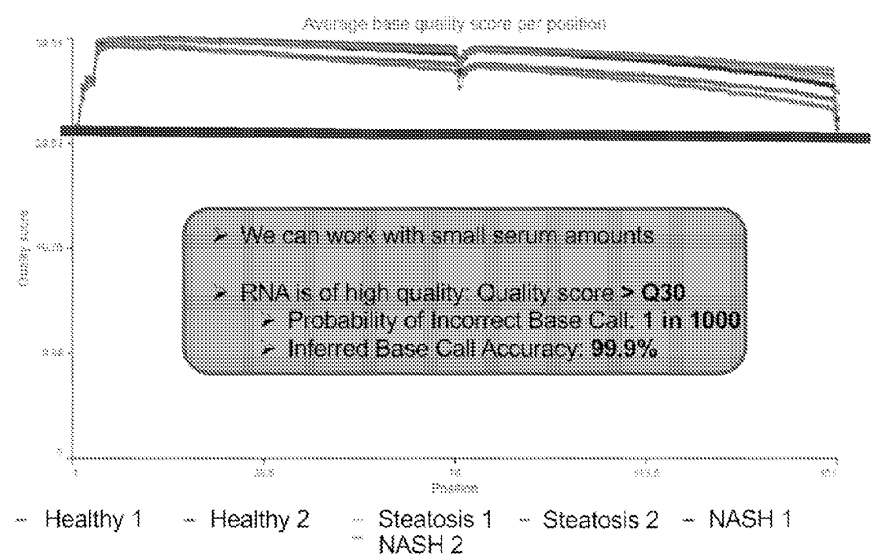


Figure 4

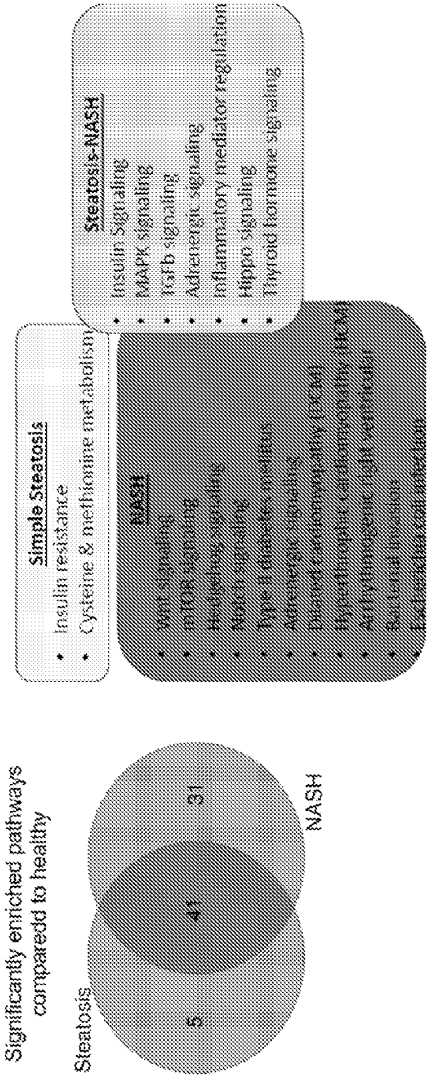


Figure 5

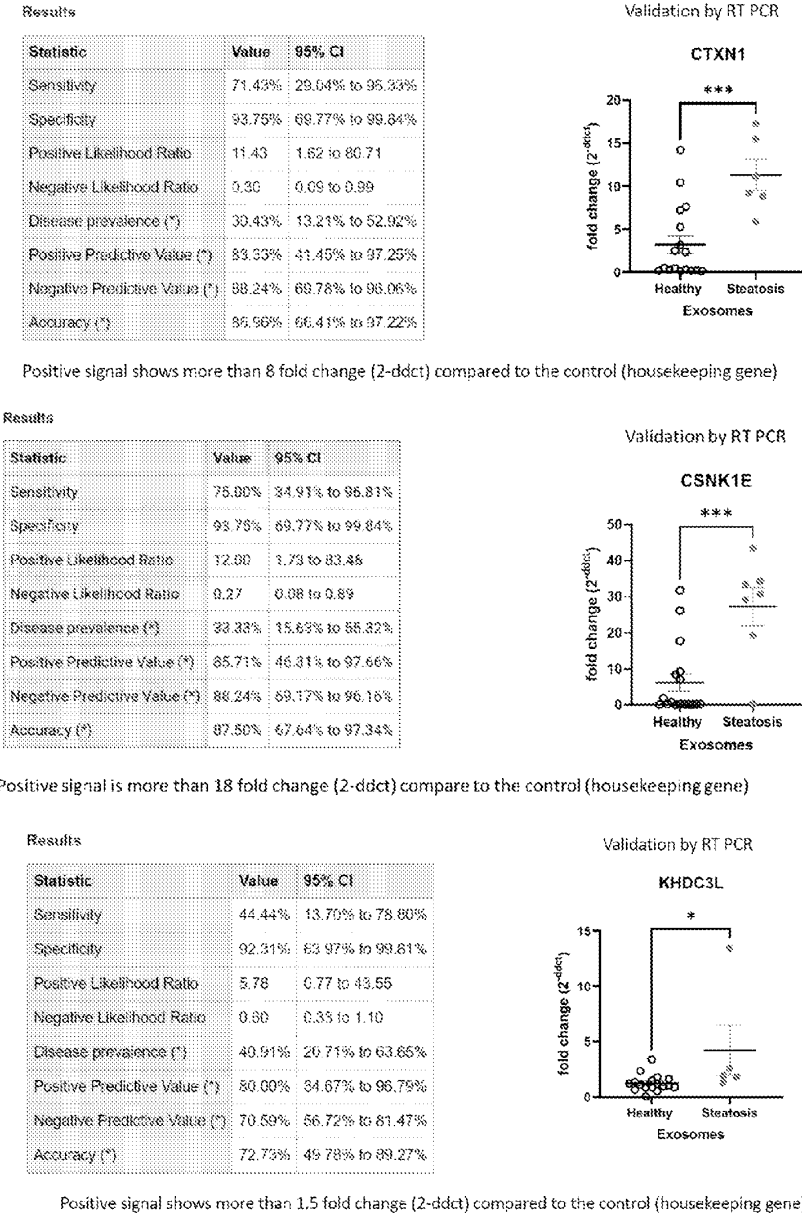


Figure 6

Validation by RT-PCR, human serum

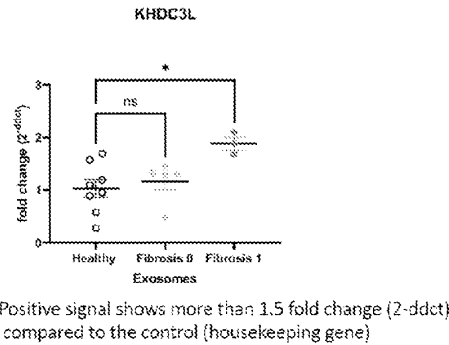
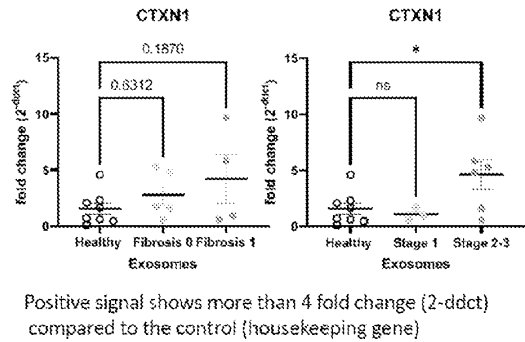
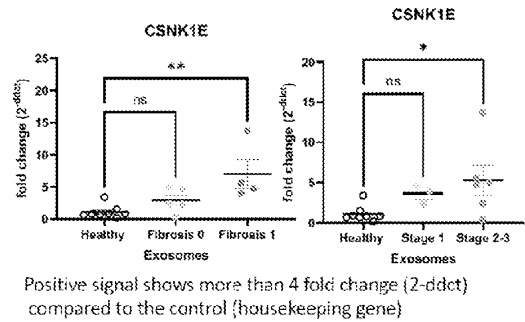


Figure 7

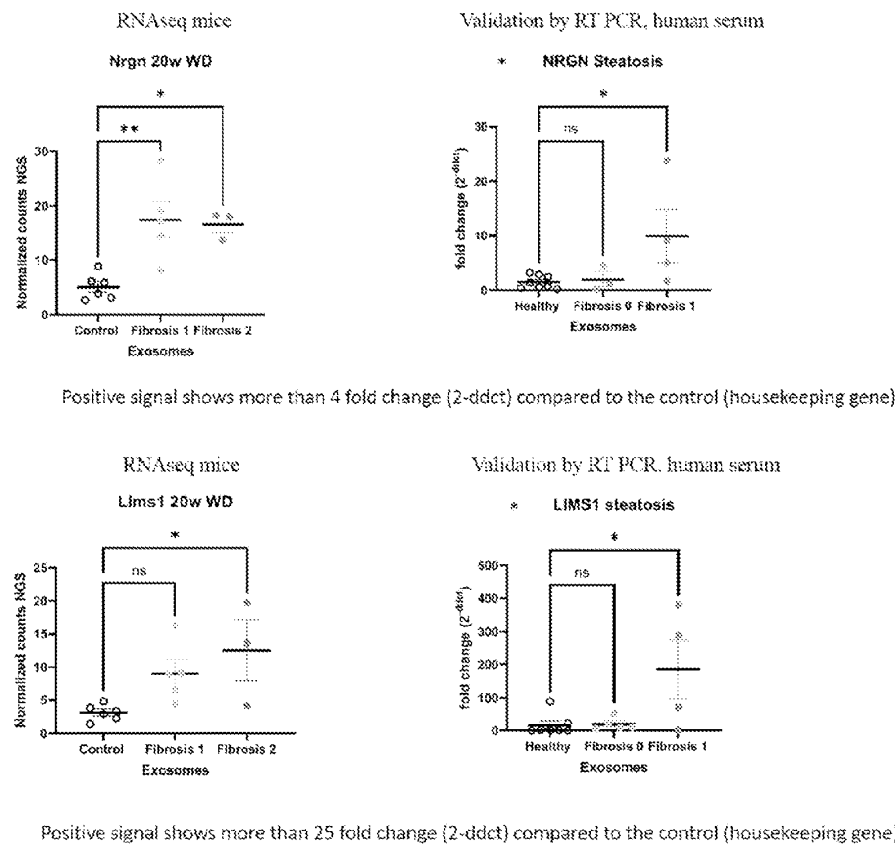
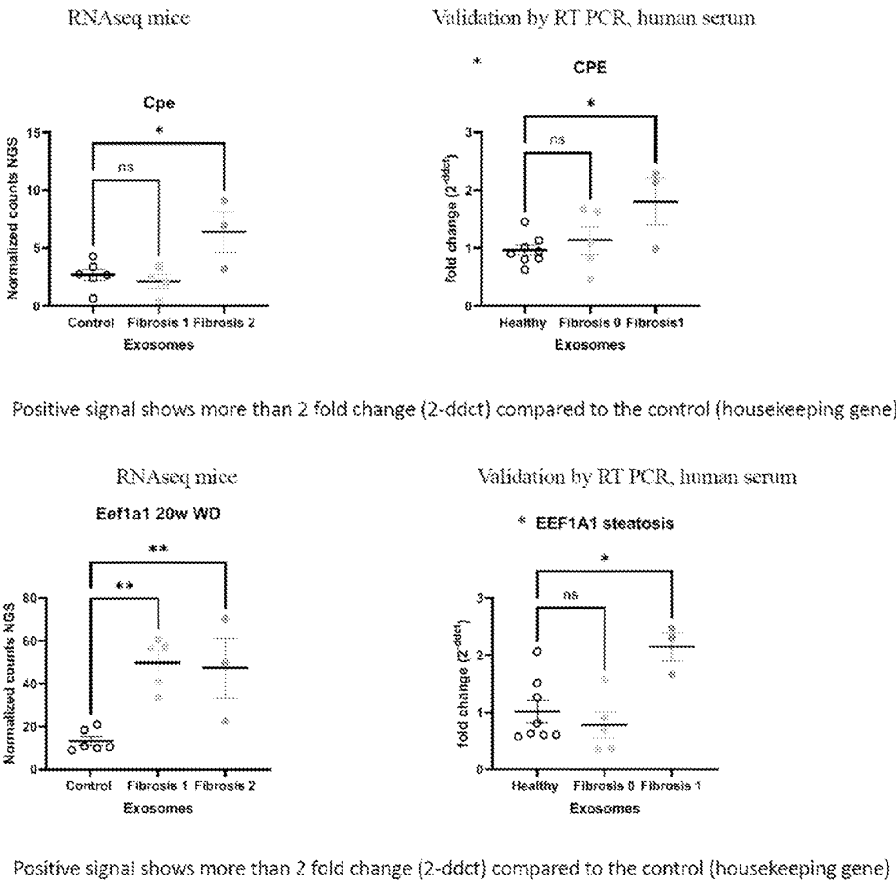


Figure 8



RNAseq mice

Validation by RT PCR, human serum

Eef1a1 20w WD

* EEF1A1 steatosis

Figure 9

Validation of previous steatosis genes and new genes from the NGS mouse data using additional steatosis samples (cDNA synthesis was done using Oligo (dT))

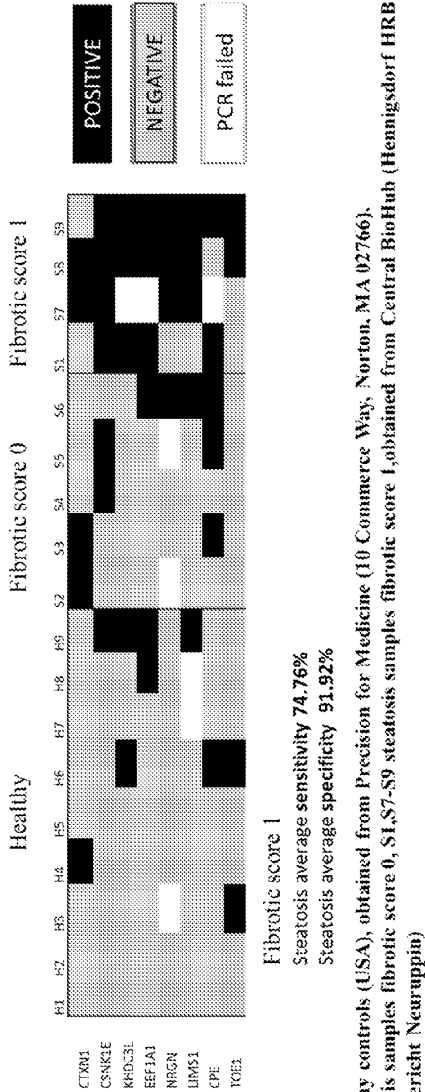


Figure 10

NASH exosome expression signature

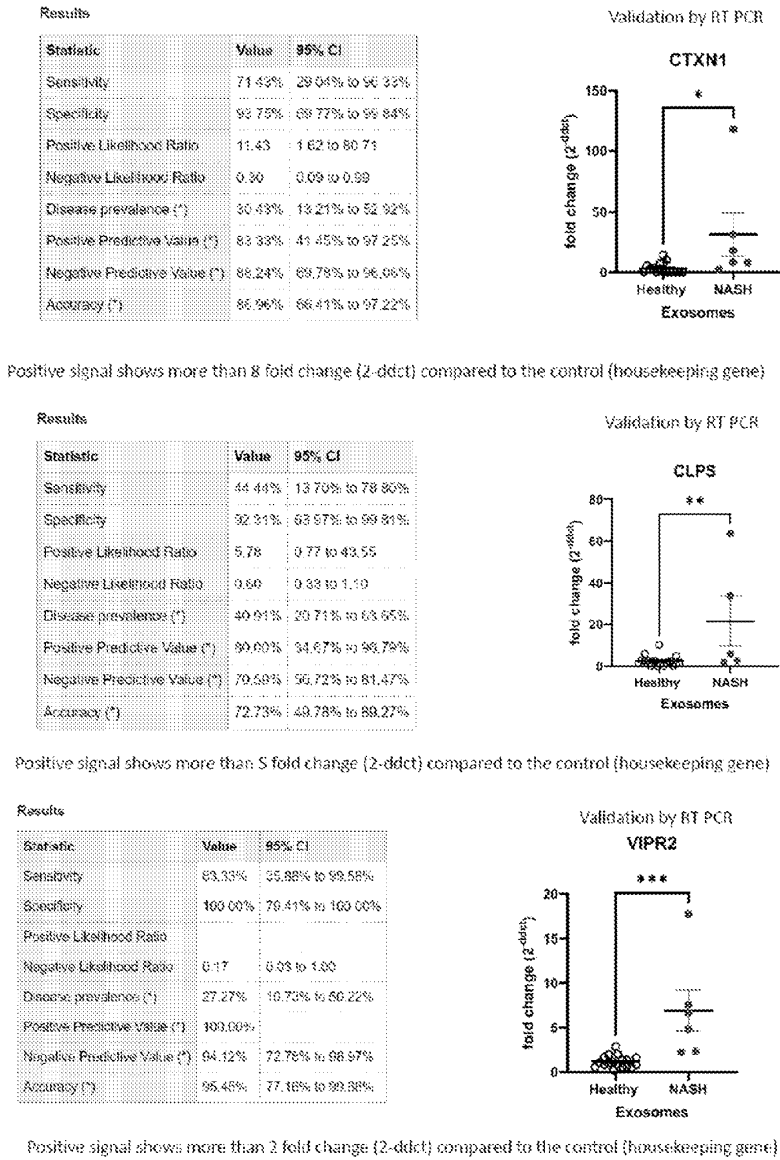


Figure 11

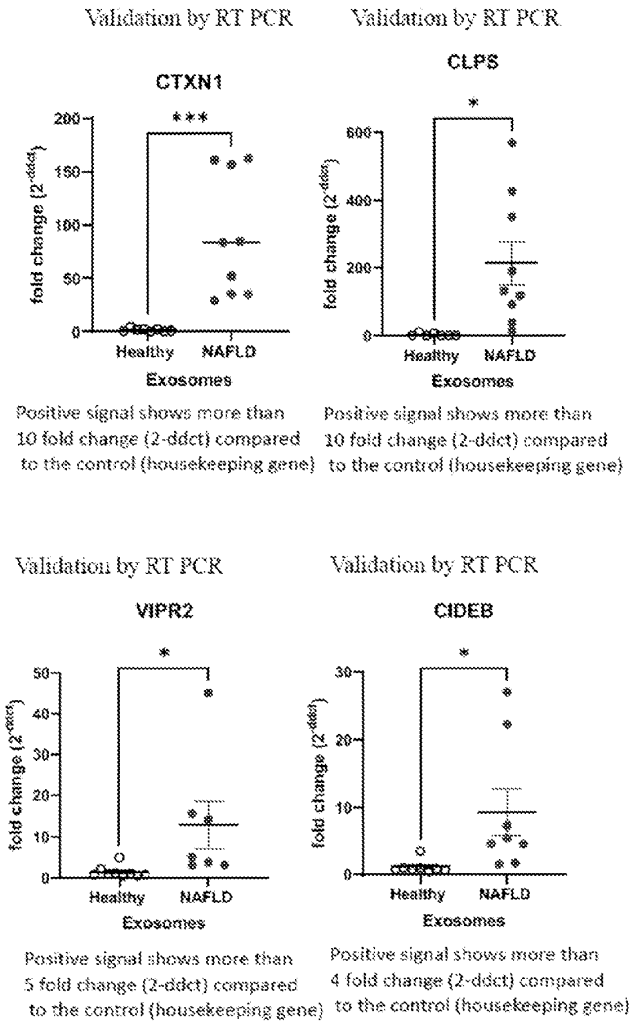


Figure 12

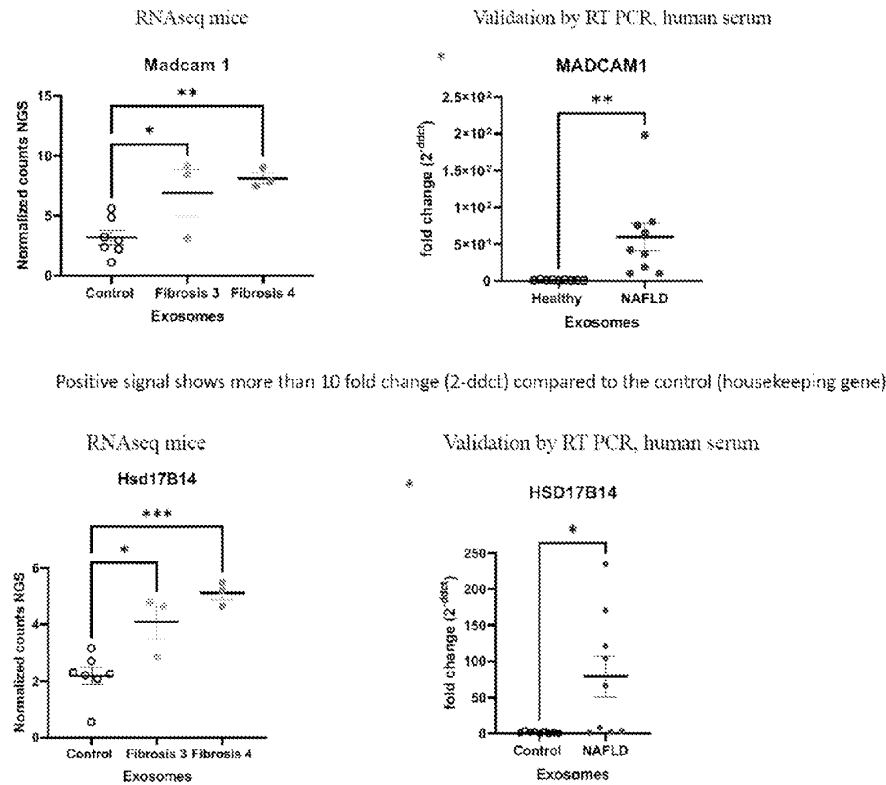
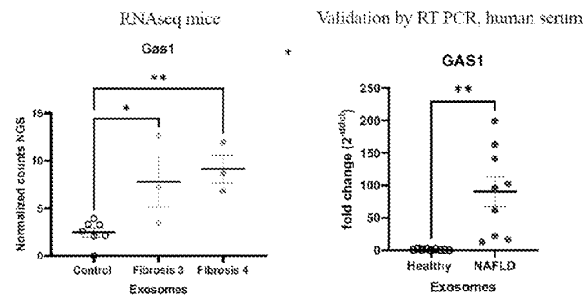
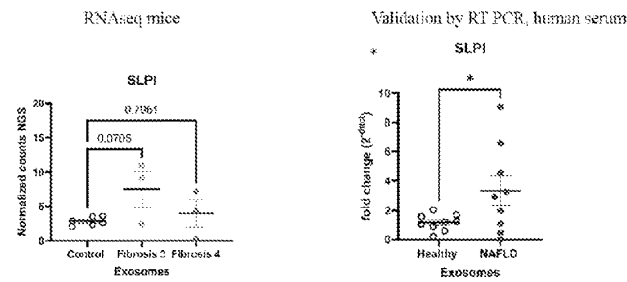


Figure 13



Positive signal shows more than 10 fold change (2^{-delta delta ct}) compared to the control (housekeeping gene)



Positive signal shows more than 2.5 fold change (2^{-delta delta ct}) compared to the control (housekeeping gene)

Figure 14

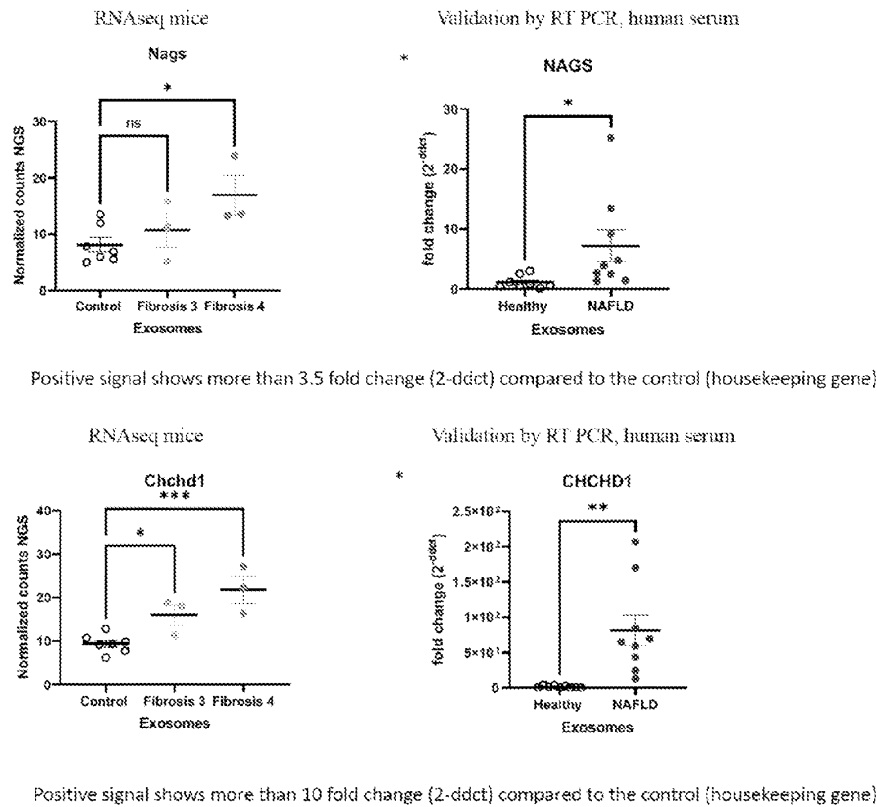


Figure 15

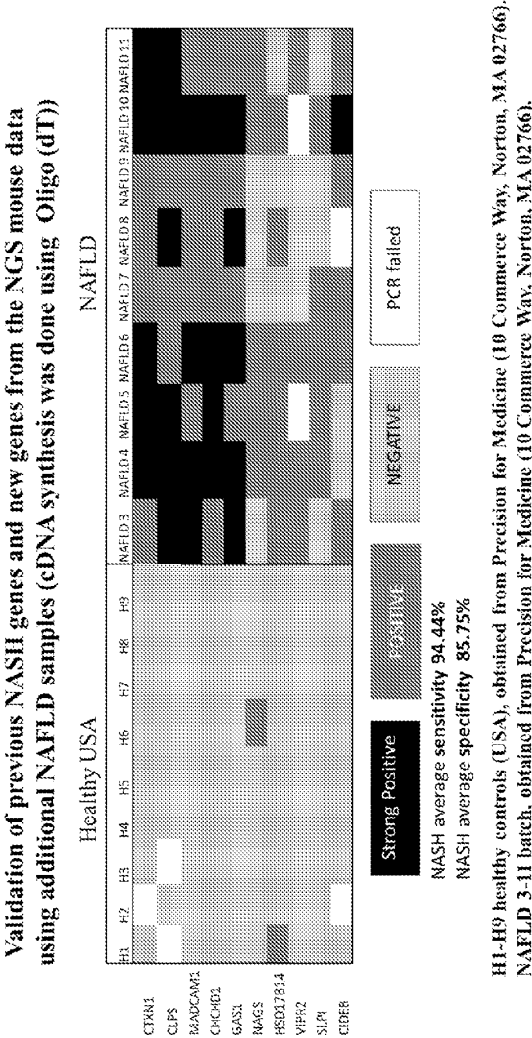


Figure 16

	Steatosis	NASH
CTXN1		
CSNK1E		
EEF1A1		
NRGN		
CPE		
KHDC3L		
LIMS1		
MADCAM1		
CHCHD1		
CLPS		
HSD17B14		
SLPI		
CIDEB		
NAG5		
VIPR2		
GAS1		

Candidate genes fit the criteria

- Protein Coding genes
 - Passed qPCR validation
- cDNA synthesis was done using Oligo (dT)

Fibrotic score 1

Steatosis average sensitivity 75.95%
Steatosis average specificity 91.92%

NASH average sensitivity 94.44%
NASH average specificity 85.75%

Figure 17

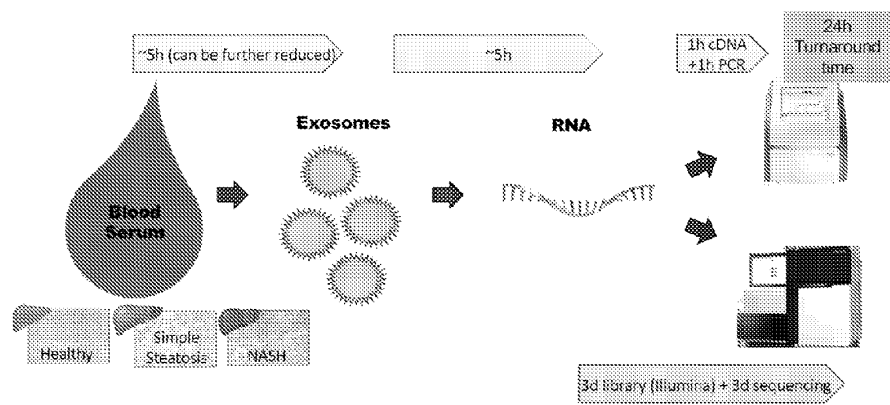


Figure 18