SUPPLEMENTARY

Table S1. Anthropometric and biochemical variables.
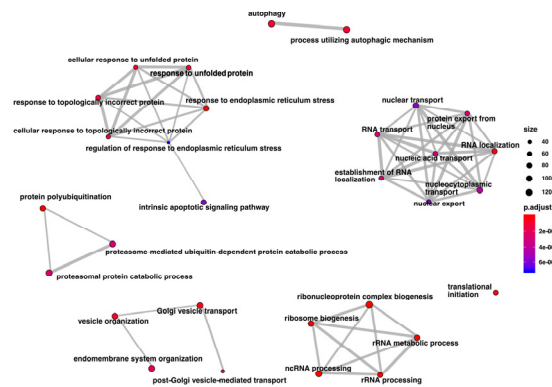
	NOb	Ob.LIR	Ob.HIR
Age	49.75±7.93	45.75±9.35	48.00±10.73
Gender (M/F)	2 / 2	0/4	3 / 1
Diabetes	0	0	1
Statins	0	0	1
Metformin	0	0	1
Waist	85.75±8.84 [a]	133.75±11.61 [b]	154.00±18.20 [b]
BMI	24.04±2.09 [a]	51.34±0.00 [b]	52.6±0.50 [b]
Glucose	104.75±9.57	99.5±12.87	122.75±26.31
Insulin	12.73±7.88 [a]	14.27±3.28 [a]	36.657±7.57 [b]
HOMA-IR	3.30±2.06 [a]	3.53±1.11 [a]	10.80±1.55 [b]
Tg	123.25±45.96	147.75±39.81	112±25.78
Chol	229.25±36.48	209±42.24	174.5±39.06
HDL-Cho	55.25±23.30	42.75±8.26	45.50±5.80
LDL-Cho	156.25±47.89	133.85±44.82	105.80±33.72

Abbreviations: Body mass index (BMI); Homeostatic model assessment of insulin resistance (HOMA-IR); triglycerides (Tg); total cholesterol (Chol); high-density lipoprotein cholesterol (HDL-Cho); low-density lipoprotein cholesterol (LDL-Cho). Different letters mean differences among groups (pval<0.05).
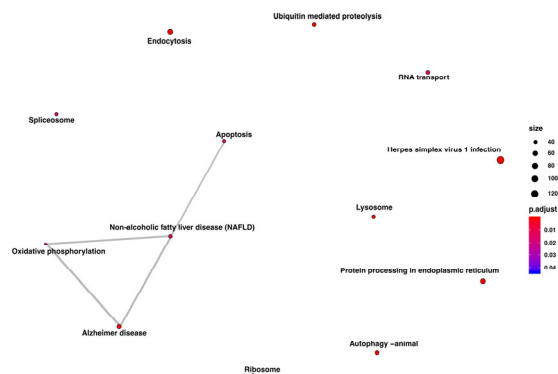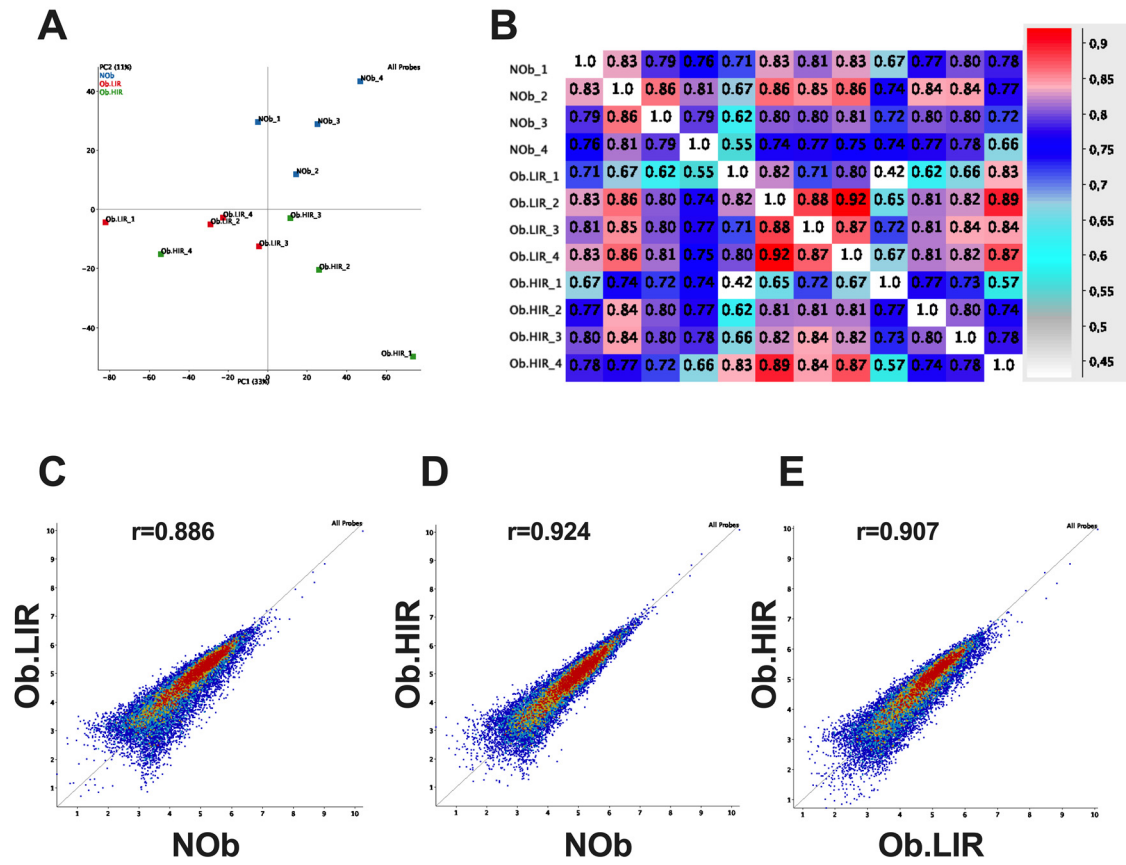
A Reactome

Infectious disease

SUMOylation of DNA replication proteins
SUMOylation of SUMOylation proteins
Transport of the SLBP Dependant Mature mRNA
Major pathway of rRNA processing in the nucleolus and cytosol
Influenza Viral RNA Transcription and Replication
Transport of Mature mRNAs Derived from Intronless Transcripts
ISG15 antiviral mechanism
Influenza Life Cycle
rRNA processing in the nucleus and cytosol
The citric acid (TCA) cycle and respiratory electron transport
Processing of Capped Intron-Containing Pre-mRNA
Influenza infection
Transport of Mature mRNA Derived from an Intronless Transcript
rRNA processing
Antiviral mechanism by IFN-stimulated genes
SUMOylation of ubiquitinylation proteins
size
Translation
Unfolded Protein Response (UPR)
Antigen processing: Ubiquitination & Proteasome degradation
p.adjust
Class I MHC mediated antigen processing & presentation
Transcriptional Regulation by TP63
Asparagine N-linked glycosylation
Metabolism of carbohydrates
Transport to the Golgi and subsequent modification
G2/M Transition
Mitotic G2-G2/M phases
ER to Golgi Anterograde Transport
Regulation of PLK1 Activity at G2/M Transition
Organelle biogenesis and maintenance

B GO

autophagy
process utilizing autophagic mechanism
cellular response to unfolded protein
response to unfolded protein
nuclear transport
response to topologically incorrect protein
response to endoplasmic reticulum stress
protein export from nucleus
cellular response to topologically incorrect protein
RNA transport
RNA localization
regulation of response to endoplasmic reticulum stress
nucleic acid transport
size
establishment of RNA localization
nucleocytoplasmic transport
protein polyubiquitination
nuclear export
intrinsic apoptotic signaling pathway
p.adjust
proteasome mediated ubiquitin dependent protein catabolic process
proteasomal protein catabolic process
translational initiation
ribonucleoprotein complex biogenesis
Golgi vesicle transport
ribosome biogenesis
vesicle organization
rRNA metabolic process
endomembrane system organization
ncRNA processing
post-Golgi vesicle-mediated transport
rRNA processing

C KEGG

Ubiquitin mediated proteolysis
Endocytosis
RNA transport
Spliceosome
Apoptosis
size
Herpes simplex virus 1 infection
Lysosome
Non-alcoholic fatty liver disease (NAFLD)
p.adjust
Oxidative phosphorylation
Protein processing in endoplasmic reticulum
Alzheimer disease
Autophagy –animal
Ribosome

Figure S1. The top significantly H3K4me3 enriched pathways analyzed by Reactome (A), GO biological function (B) and KEGG (C) databases.

2

Figure S2. Store similarity for H3K4me3 enrichment among study participants. PCA plot (A) and correlation matrix (B). H3K4m3 store similarity among the 3 groups (C, D and E).

RNA seq in groups

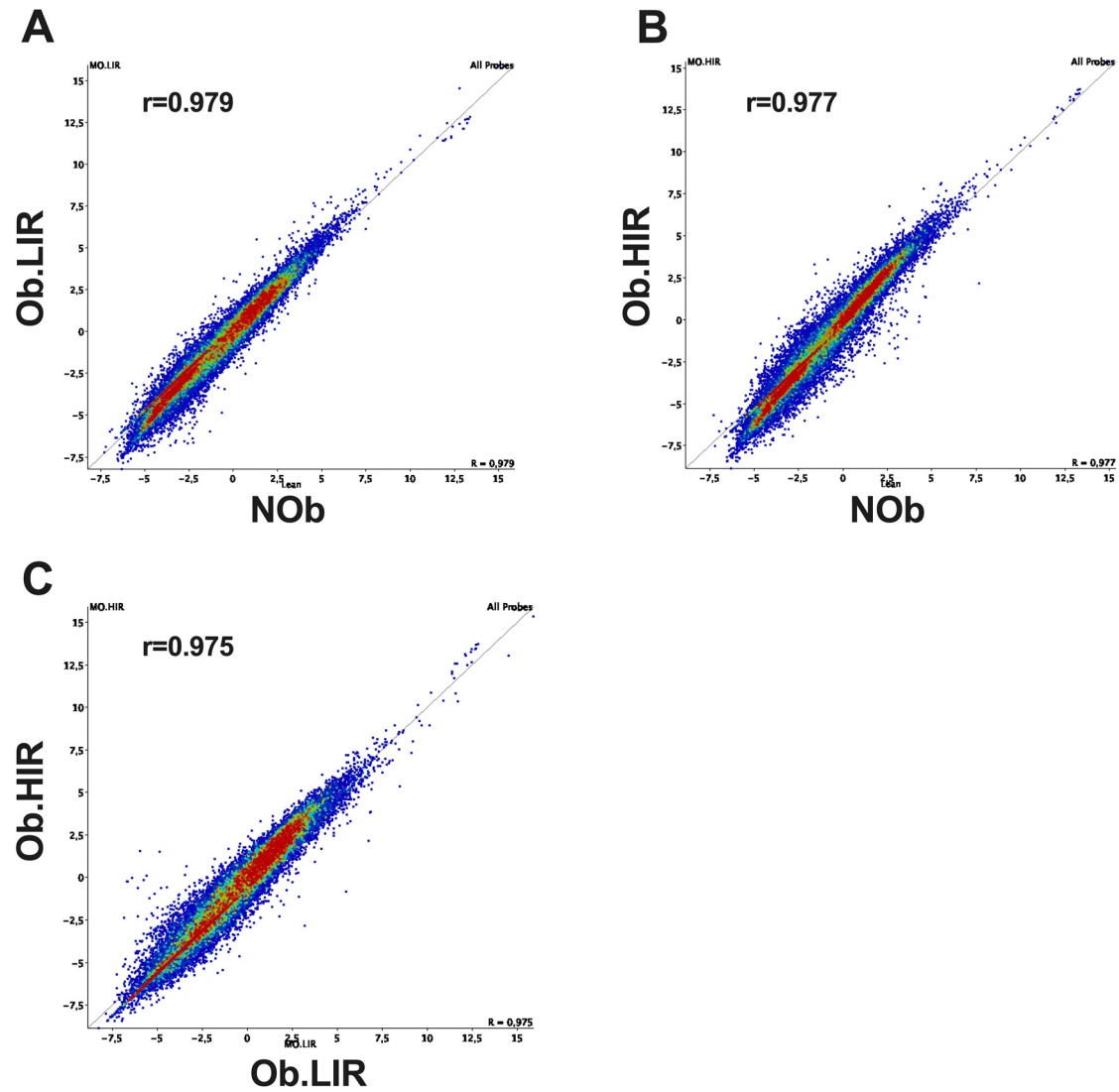**A**

r=0.979

B

r=0.977

C

r=0.975

Figure S3. Store similarity for mRNA expression among study groups.