SUPPLEMENTARY TABLES

Supplementary Table 1. Characteristics of the study participants.

Variables	Controls ($n = 32$)	Nonalcoholic hepatic steatosis ($n = 59$)	P
Sex (male/female)	(12/20)	(40/19)	$P < 0.05$
age	45.84 ± 13.83	49.15 ± 11.22	$P > 0.05$
BMI	22.68 ± 2.45	26.62 ± 3.02	$P < 0.05$
TG	1.00 ± 0.29	2.24 ± 1.32	$P < 0.05$
TC	4.78 ± 0.60	5.19 ± 1.18	$P < 0.05$
HDL-C	1.73 ± 0.45	1.43 ± 0.39	$P < 0.05$
LDL-C	2.91 ± 0.60	3.34 ± 0.89	$P < 0.05$
fasting blood-glucose	4.63 ± 0.43	4.99 ± 0.56	$P < 0.05$
ALT	15.15 ± 9.00	30.49 ± 32.00	$P < 0.05$
AST	18.17 ± 6.00	23.00 ± 10.00	$P < 0.05$
GGT	18.95 ± 17.00	31.15 ± 39.00	$P < 0.05$
uric acid	267.08 ± 73.08	350.23 ± 81.48	$P < 0.05$

Supplementary Table 2. Logistic regression analyses with steatosis as dependent variable.

Variables	B	SE	P
Coriobacteriaceae	61.17	26.68	$P < 0.05$
Collinsella	55.46	28.15	$P < 0.05$
Acinetobacter	7690.89	3551.86	$P < 0.05$
Lachnospira	−1551.01	592.79	$P < 0.05$

All gut microbiota (log10 (1+phylum/family/genus)) are analyzed. These models were adjusting for age, sex and BMI.