

Reference	Medium for BA analysis	Nutritional state	N	BMI (kg/m ²)	HOMA-IR	FPG (mg/dL)	HbA1c (%)	Results
Dasarathy 2011 [40]	Plasma	ND	Control: 38 NASH: 36	ND	ND	ND	ND	BA s: ↑GCA ↑TCA ↑TCDC in NASH vs controls. Other : ↑FGF21 in NASH vs controls.
Kalhan 2011 [31]	Plasma	Fasting	Control: 25 NAFL: 11 NASH: 24	Control: 24.5±2.6 NAFL: 34±4* NASH: 34.8±4.7*	Control: 0.96±0.4 NAFL 2.6±1.1* NASH 3.26±1.6*	Control: 84.6±9 NAFL: 88.2±10.8 NASH: 95.4±16.2*	ND	BA s: ↑GCA ↑TCA ↑GCDC in NASH vs controls. ↑TCA in NAFL vs controls.
Bechmann 2013 [34]	Plasma	ND	Control: 10 NAFL: 39 NASH: 59	Control: 22.4±2.46 NAFL: 51.3±1.5 NASH: 53.5±1.3	ND	Control: ND NAFL: 95.5±8.5 NASH: 122.9±11*	Control: ND NAFL: 5.54±0.16 NASH: 16.92±4.59*	BA s: Total BAs positively correlated with NAS. Other : No ≠ in C4 between NAFL, NASH and controls. Serum adiponectin negatively correlated with serum BAs and NAS. Hepatic mRNA levels: ↓NTCP, ↓BSEP, ↓EPHX1 in NASH vs controls.
Ferslew 2015 [32]	Serum, urine.	Fasting, Postprandial.	Control: 15 NASH: 7	Control: 25±2.7 NASH: 32±5.2*	Control: 1.6±0.6 NASH: 13±8.7*	Control: 86±8 NASH: 124±16*	ND	BA s: Fasting plasma: ↑Conjugated BAs in NASH vs controls. Postprandial plasma: ↑Total BAs in NASH vs controls. Postprandial urine: ↑GCA ↑TCA ↑GCDC ↑DCA in NASH vs controls. Other : MCA are majoritary BA species in urine.
Jiao 2017 [38]	Serum	ND	Control: 11 NASH: 16	Control: 19.2±3.4 NASH: 33.8±7.7*	Control: ND NASH: 4.28±2.83	ND	ND	BA s: ↑Total BAs ↑CA ↑CDCA ↑DCA ↑UDCA in NASH vs controls. ↑2dary/1ary BA ratio, ↓CDCA ↑DCA proportions in NASH vs controls. Other : ↓FGF19 in NASH vs Control. Microbiota: ↑Glycine and Taurine metabolizing bacteria. Hepatic mRNA levels: ↑CYP7A1 ↑CYP27A1 ↑CYP8B1 ↑BACS ↑NTCP ↑OATP1B1 ↑OATP1B3 ↑HNF4A ↑FGFR4 ↑KLB in NASH vs controls
Puri 2017 [30]	Plasma	Fasting	Control: 24 NAFL: 25 NASH: 37	Control: 27.3±5.8 NAFL: 32.6±5.4 NASH: 34.4±4.2*	ND	ND	ND	BA s: ↑1ary BAs ↑UDCA in NASH vs Controls. ↑GCA ↑TCA in NASH vs NAFL. ↑TCA ↓CDCA in NAFLD associated with severe steatosis. ↑GCA associated with severe lobular inflammation. ↓TUDCA and ↑TLCA associated with portal inflammation. ↑GCA, ↑TCA, ↑GCDC, ↑DCA, ↑GLCA associated with hepatocyte ballooning. ↑Conjugated CA associated with NAS>4. Other : No ≠ in C4 or FGF19. Hepatic mRNA levels: ↑CYP7A1 in NASH vs controls and NAFL.
Legry 2017 [39]	Plasma	Fasting	Control: 26 NASH: 32	Control: 39.4±5.9 NASH: 40.2±5.8	Control: 3.25±2.05 NASH: 4.05±2.65	Control: 82.3±11.8 NASH: 85.8±8.4	ND	BA s: No ≠ in BAs in NASH vs controls. No correlation of BAs and necro-inflammatory lesions of NASH Other : No ≠ in C4. Hepatic mRNA levels: ↓PPARA ↓CYP3A4 ↓BSEP ↑CYP7A1 ↑ATP8B1 in NASH vs controls.
Caussy 2019 [33]	Plasma	Fasting	Cohort 1 Non-NAFLD by MRI: 120 NAFLD by MRI: 36 Cohort 2 Biopsy-proven NAFLD: 156	Cohort 1 Non-NAFLD by MRI: 25±5.2 NAFLD by MRI: 31.8±5.9* Cohort 2 Biopsy-proven NAFLD: 32±6	Cohort 1 Non-NAFLD by MRI: 1.7±1 NAFLD by MRI: 6.6±11.4* Cohort 2 Biopsy-proven NAFLD: 8.5±17.3	Cohort 1 Non-NAFLD by MRI: 88.4±9.6 NAFLD by MRI: 102.5±27.5* Cohort 2 Biopsy-proven NAFLD: 106.2±33.1	Cohort 1 Non-NAFLD by MRI: 5.7±0.4 NAFLD by MRI: 6.1±0.7* Cohort 2 Biopsy-proven NAFLD: 6±0.9	Cohort 1 : BA s: No ≠ in BA concentrations in NAFLD vs Non-NAFLD. ↑CA ↑CDCA ↓GHCA proportions in NAFLD vs Non-NAFLD. Cohort 2 : BA s: No ≠ in BA concentrations among NAFLD patients classified on NAFL vs NASH. ↑BAs associated with ↑fibrosis stages. Lobular inflammation positively correlated with free CA. Ballooning positively correlated with free CA and CDCA but negatively correlated with conjugated CA and DCA. NAS positively correlated with free CA and CDCA but negatively correlated with conjugated CA.
Aranha 2008 [37]	Liver	ND	Control: 8 NASH: 15	Control: ND NASH 26.6±2.5	ND	ND	ND	BA s: ↑CDCA ↑DCA in NASH vs controls. ↑DCA in NASH vs controls. CA correlated with inflammation and CDCA with fibrosis in NASH.
Lake 2013 [36]	Liver	ND	Control: 17 NAFL: 4 NASH: 16	ND	ND	ND	ND	BA s: ↓CA ↑TCA ↑GCDC ↓GDCA ↑TDCA in NASH vs controls. ↓GDCA ↑TDCA ↑GCDC in NASH vs NAFL. Other : CA, DCA, CDCA, and GDCA negatively correlated with CYP7B1 gene expression. GDCA positively correlated with CYP8B1 gene expression. Hepatic mRNA levels: ↓CYP27A1 ↑CYP7B1 ↓HSD3B7 ↓CYP8B1 ↑BAAT in NASH vs controls. Protein levels: ↑CYP7B1 in NASH vs controls and NAFL.

Mouzaki 2016 [35]	Feces	ND	Control: 25 NAFL: 12 NASH: 16	Control: 27 (20-35) NAFL: 28 (25-44) NASH: 33 (24-50)*	Control: 1.3 (0.5-7.6) NAFL: 1.6 (0.6-15.6) NASH: 4.3 (1.2-40)*	Control: 88.2 (72-117) NAFL: 95.4 (82.2-205.2) NASH: 102.6 (73.8-135)	Control: 5.1 (4.4-7.2) NAFL: 5.3 (0.1-5.8)* NASH: 5.9 (5.3-7.3)*	<p>BAs: In feces: ↑Total BAs, ↑CA, ↑CDCA in NASH vs controls. ↑Conjugated LCA in NASH vs NAFL. 1 ary fecal BAs positively correlated with ALT, NAS and serum TG.</p> <p>Other: ↑C4 in NASH vs controls. Gut microbiota: ↓<i>Bacteroidetes</i>, <i>C. leptum</i> negatively correlated with CA and LCA.</p>
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