Figure S1. Identification of T-α/β/ωMCA by fragmentation profiles and RTs. (A) TIC chromatogram of m/z 514.284 in the mouse serum sample. (B) MS/MS spectra of the peak with a RT of 9.283 in the mouse serum in part A. (C) TIC chromatogram of authentic T-αMCA when fragmentation was performed at m/z 514.284. (D) MS/MS spectra of the peak, with a RT of 9.25 in panel C. (E) TIC chromatogram of authentic T-βMCA when the fragmentation was performed at m/z 514.284. (F) MS/MS spectra of the peak, with a RT of 9.32 in part E. (G) TIC chromatogram of authentic T-ωMCA when the fragmentation was performed at m/z 514.2796. (H) MS/MS spectra of the peak, with a RT of 9.21 in part G. T-αMCA, tauro-α-muricholic acid; T-βMCA, tauro-β-muricholic acid; T-ωMCA, tauro-ω-muricholic acid; TIC, total ion count; RT, retention time.

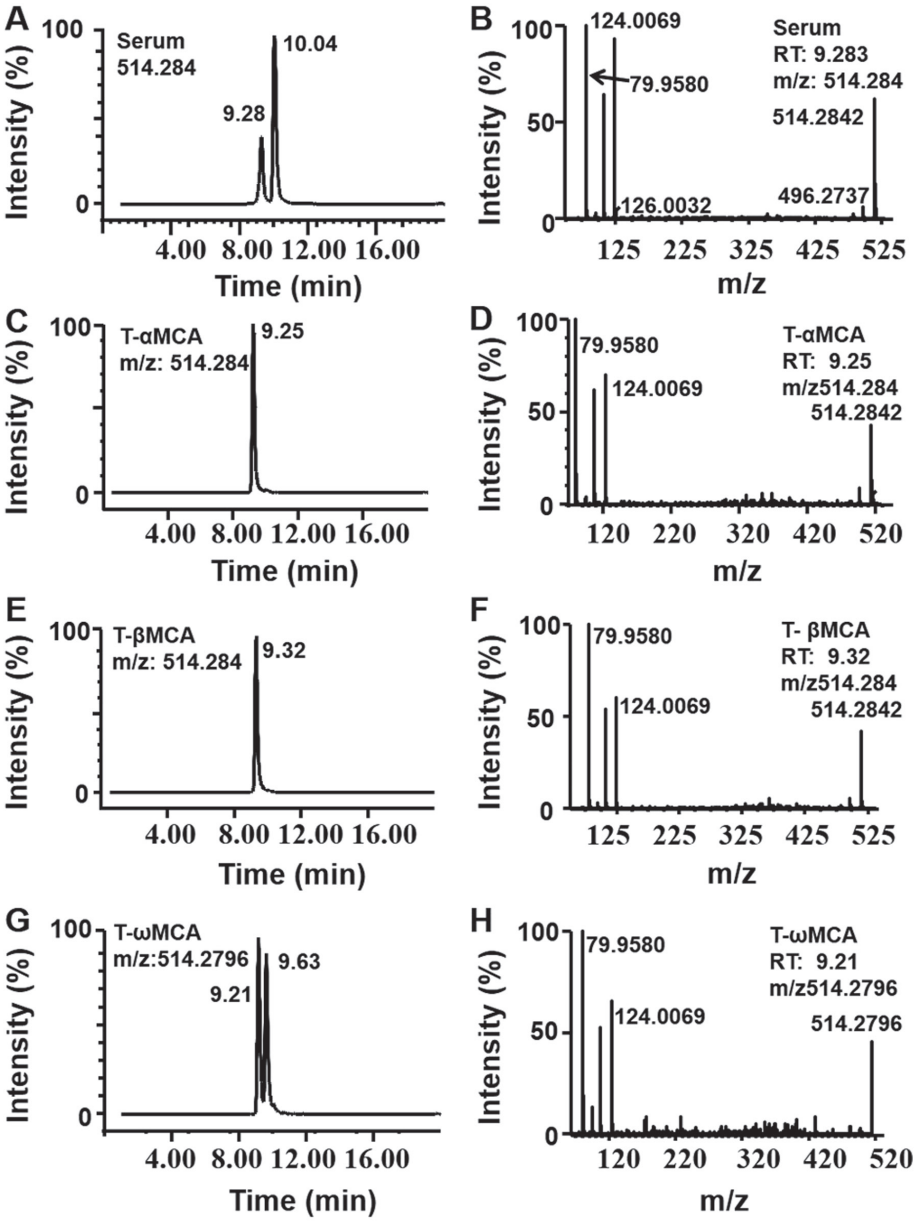

Figure S2. Identification of TCDCA by fragmentation profiles and RTs. (A) TIC chromatogram of m/z 498.278 in the mouse serum sample. (B) MS/MS spectra of the peak with a RT of 10.950 in the mouse serum in part A. (C) TIC chromatogram of authentic TCA when the fragmentation was performed at m/z 498.287. (D) MS/MS spectra of the peak, with RT 10.693 in part C. TCDCA, taurochenodeoxycholic acid; TIC, total ion count; RT, retention time.

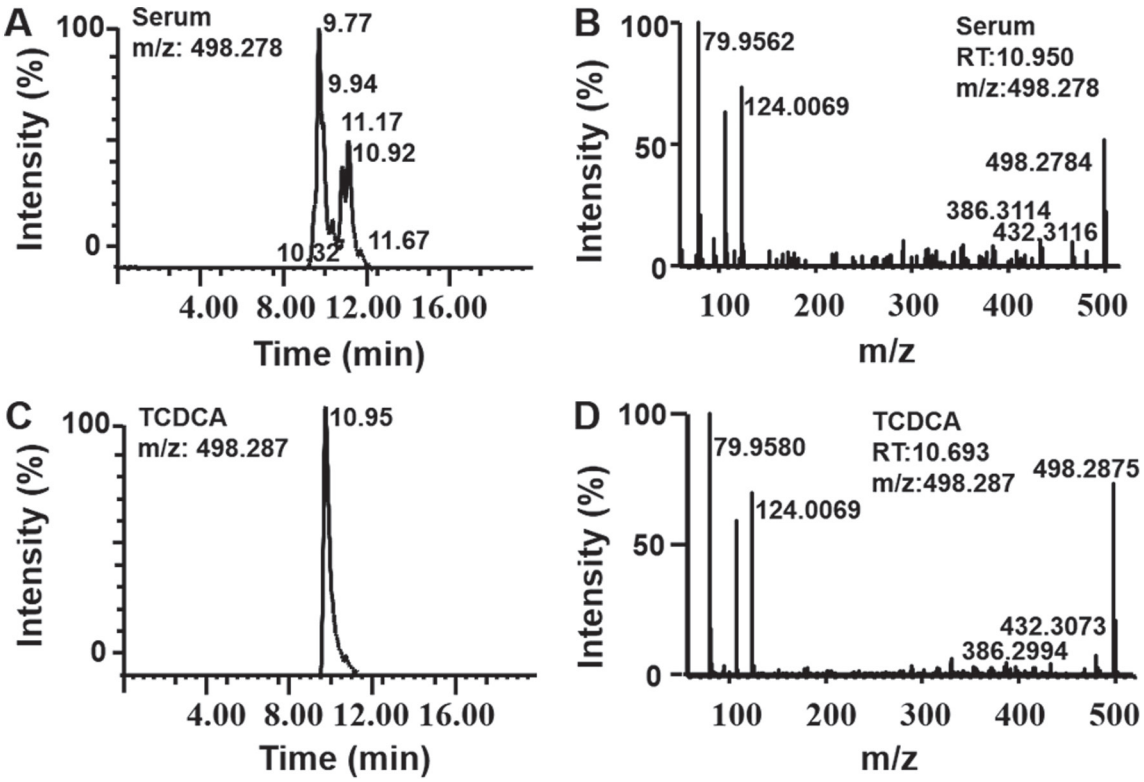

Figure S3. Identification of TUDCA by fragmentation profiles and RTs. (A) TIC chromatogram of m/z 498.288 in the mouse serum sample. (B) MS/MS spectra of the peak with a RT of 10.02 in the mouse serum in part A. (C) TIC chromatogram of authentic TCA when the fragmentation was performed at m/z 498.287. (D) MS/MS spectra of the peak, with a RT of 10.03 in part C. TUDCA, tauroursodeoxycholic acid; TIC, total ion count; RT, retention time.

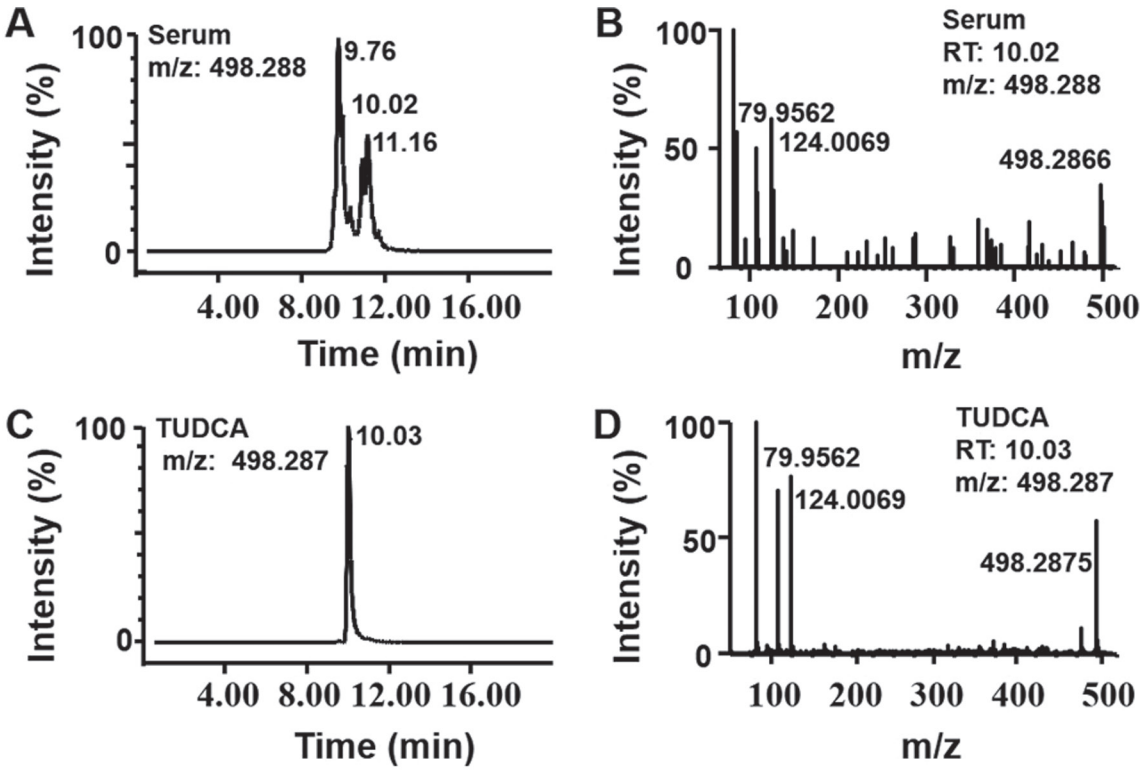

Figure S4. Identification of TDCA by fragmentation profiles and RTs. (A) TIC chromatogram of m/z 498.287 in the mouse serum sample. (B) MS/MS spectra of the peak with a RT of 11.16 in the mouse serum in part A. (C) TIC chromatogram of authentic TCA when the fragmentation was performed at m/z 489.287. (D) MS/MS spectra of the peak, with a RT of 11.18 in panel C. TDCA, taurodeoxycholic acid; TIC, total ion count; RT, retention time.

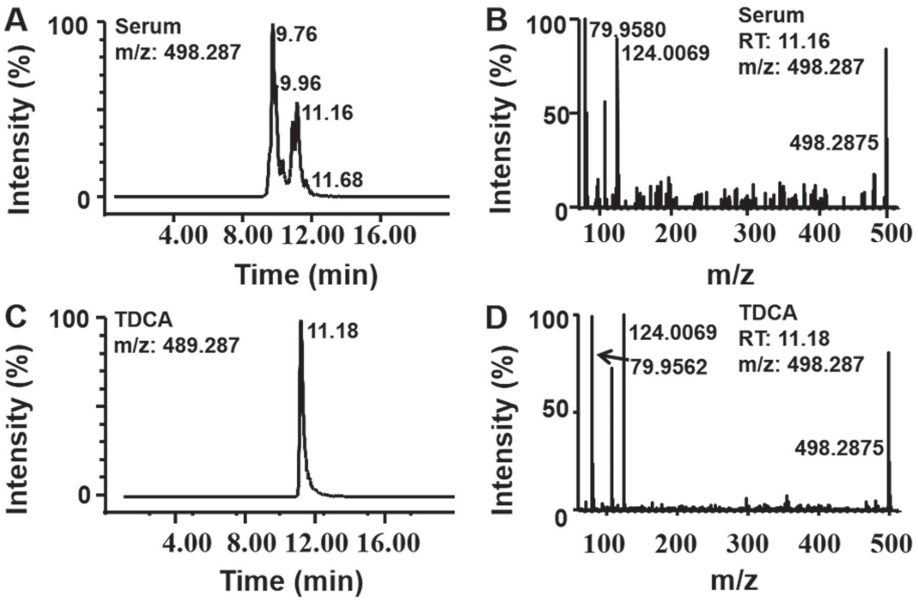

Table SI. Primer sequences used in the reverse transcription-quantitative PCR.

Gene	Primer sequence (5'→3')	Product (bp)
Cholesterol 7α-hydroxylase	F: GTCCGGATATTCAAGGATGC R: GGGAATGCCATTTACTTGGA	107
Sterol 12α-hydroxylase	F: GATAGGGGAAGAGAGCCACC R: TCCTCAGGGTGGTACAGGAG	96
Multidrug resistance-related protein 4	F: TTAGATGGGCCTCTGGTTCT R: GCCCACAATTCCAACCTTT	102
Multidrug resistance protein 1a	F: CTCTATTGGACAAGTGCTCACTG R: CTCCTCGTGCATTGGCGAA	104
Organic solute transporter-β	F: CCAGGACCAGGATGGAATAA R: AGAGAAAGCTGCAGCCAATG	110
Oatp1	F: TAATCGGGCCAACAATCTTC R: ACTCCCATAATGCCCTTGG	109
Oatp2	F: TAGCTGAATGAGAGGGCTGC R: ACCAAACTCAGCATCCAAGC	103
Multidrug resistance protein 2	F: ACGGGCTCTTGACTTACCAC R: CTACGACCCCACAGAGGGTA	105
c-Fos	F: TGGCACTAGAGACGGACAGA R: TCCTACTACCATTCCCCAGC	94
c-Jun	F: GGGACACAGCTTTCACCCTA R: GAAAAGTAGCCCCCAACCTC	104
Il10	F: TGTCAAATTCATTCATGGCCT R: ATCGATTTCTCCCCTGTGAA	108
Il6	F: ACCAGAGGAAATTTTCAATAGC R: TGATGCACTTGCAGAAAACA	109
Tumor necrosis factor α	F: AGGGTCTGGGCCATAGAACT R: CCACCACGCTCTTCTGTCTAC	103
Fibrinogen a chain	F: CAACTCTTGGGCCACGTACT R: GGGTCACCTGCCTCATCTT	108
Fibrinogen β chain	F: AGGAGGCTCTTCCTTTCTCC R: CAAGCTGCCGATGATGACTA	90
Suppressor of cytokine signaling 3	F: AACTTGCTGTGGGTGACCAT R: CGGCTACCACATCCAAGGAA	136
18S ribosomal RNA	F: ATTGGAGCTGGAATTACCGC R: AAGGCCGGAGATTTCGCT	102

Il, interleukin; *Oatp*, organic anion transporting polypeptide; F, forward; R, reverse.