

1 **SUPPORTING INFORMATION**

2
3 Emily C. Gentry^{1,2}, Stephanie L. Collins¹⁵, Morgan Panitchpakdi^{1,2}, Pedro Belda-Ferre^{3,11}, Allison
4 K. Stewart⁸, Mingxun Wang^{1,2}, Alan K. Jarmusch^{1,2,14}, Julian Avila-Pacheco⁴, Damian R. Plichta⁴,
5 Allegra T. Aron^{1,2}, Hera Vlamakis^{4,5}, Ashwin N. Ananthakrishnan¹⁶, Clary B. Clish⁴, Ramnik J.
6 Xavier,^{4,5,6,7}, Erin S. Baker^{8,9}, Andrew D. Patterson¹⁰, Rob Knight^{3,11-13}, Dionicio Siegel¹, Pieter C.
7 Dorrestein^{1,2*}

8
9 ¹ Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego,
10 La Jolla, San Diego, CA, USA

11 ² Collaborative Mass Spectrometry Innovation Center, Skaggs School of Pharmacy and
12 Pharmaceutical Sciences, University of California San Diego, La Jolla, CA, USA

13 ³ Department of Pediatrics, University of California San Diego, La Jolla, CA, USA

14 ⁴ Broad Institute of MIT and Harvard, Cambridge, Massachusetts, USA

15 ⁵ Center for Microbiome Informatics and Therapeutics, Massachusetts Institute of Technology,
16 Cambridge, MA 02139, USA

17 ⁶ Center for Computational and Integrative Biology Massachusetts General Hospital and
18 Harvard Medical School, Boston, MA 02114, USA

19 ⁷ Department of Molecular Biology, Massachusetts General Hospital and Harvard Medical
20 School, Boston, MA 02114, USA

21 ⁸ Department of Chemistry, North Carolina State University, Raleigh, NC, USA

22 ⁹ Comparative Medicine Institute, North Carolina State University, Raleigh, NC, USA

23 ¹⁰ Center for Molecular Toxicology and Carcinogenesis, Department of Veterinary and
24 Biomedical Sciences, The Pennsylvania State University, University Park, PA, USA

25 ¹¹ Department of Computer Science, Jacobs School of Engineering, University of California, San
26 Diego, California, USA

27 ¹² Center for Microbiome Innovation, Jacobs School of Engineering, University of California, San
28 Diego, California, USA

29 ¹³ Department of Bioengineering, University of California, San Diego, California, USA

30 ¹⁴ Immunity, Inflammation, and Disease Laboratory, Division of Intramural Research, National
31 Institute of Environmental Health Sciences, National Institutes of Health, Research Triangle
32 Park, NC 27709, USA

33 ¹⁵ Department of Biochemistry and Molecular Biology, The Pennsylvania State University,
34 University Park, PA, USA

35 ¹⁶ Division of Gastroenterology, Massachusetts General Hospital, Boston, MA, USA

36 * Corresponding author; email: pdorrestein@health.ucsd.edu

37
38 **TABLE OF CONTENTS**

39 **S1-S4: Supplementary Methods**

40 **S5-S8: Supplementary Tables**

41 **S8-S28: Supplementary Figures**

42 **S29-S38: Supplementary Data**

43 **S39: Supplementary References**

45 **Supplementary Methods**

46

47 **Media preparation**

48 Fecal culture medium (FCM) was prepared according to a protocol by McDonald *et al.*¹
49 autoclaving for 20 min at 121 °C. The media was brought into an anaerobic chamber and left
50 overnight with the lid slightly ajar to remove any remaining oxygen from the media. Then, an
51 aqueous solution of L-cysteine was pushed through a 0.2uM syringe filter into the media solution
52 for a concentration of 0.5% L-Cysteine (w/v) to maintain anoxic solution.

53

54 **Data analysis of HMP culture extracts**

55 MS1 feature detection and MS/MS pairing was performed using MZmine
56 2.37corr17.7_kai_merge2^{2,3}. An intensity threshold of 1E3 and 50 were set for MS1 and MS2
57 detection, respectively, with centroid data. MS1 chromatogram construction was performed using
58 the ADAP chromatogram builder, where the minimum group size was set to 3, group intensity
59 threshold was 1E3, minimum highest intensity was 3E3, and mass tolerance was 0.01 *m/z* or
60 20ppm. Chromatogram deconvolution was then performed using a local minimum search
61 algorithm with a chromatographic threshold of 90%, a search minimum in retention time (RT)
62 range of 0.2 min, minimum relative height of 1%, minimum absolute threshold height of 3E3,
63 minimum ratio for top/edge of 1, and a peak duration of 0.01-2 min. Pairing between MS1 and
64 MS2 was performed with a mass tolerance of 0.01 *m/z* or 20ppm and RT range of 0.3 min. Isotope
65 peaks were grouped, then features from different samples were aligned using the same mass
66 and RT tolerances; alignment was performed by placing a weight of 75 on *m/z* and 25 on RT. A
67 peak area feature table was exported as a .csv file and consensus MS/MS spectral data were
68 exported in .mgf format.

69

70 **Synthesis of pure conjugated bile acids**

71 Materials: Organic solutions were concentrated under reduced pressure on a Büchi rotary
72 evaporator using a water bath. Chromatographic purification of products was accomplished by
73 flash chromatography on Silicycle F60 silica gel. All reactions were carried out in well ventilated
74 fume hoods. Thin-layer chromatography (TLC) was performed on Silicycle 250 μ m silica gel
75 plates. Visualization of the developed chromatogram was performed by irradiation with 254 nm
76 UV light or treatment with a solution of ceric ammonium molybdate stain followed by heating.
77 Yields refer to purified compounds unless otherwise noted.

78 Instrumentation: ^1H and ^{13}C NMR spectra were recorded on a Bruker 600 (600 and 151 MHz for
79 ^1H and ^{13}C , respectively) instrument, and are internally referenced to residual protiosolvent signals
80 of CD_3OD at δ 3.31 and 49.0 ppm and $(\text{CD}_3)_2\text{SO}$ at δ 2.50 and 39.51 ppm. Data for ^1H NMR are
81 reported as follows: chemical shift (δ ppm), integration, multiplicity (s = singlet, br s = broad singlet,
82 d = doublet, t = triplet, q = quartet, m = multiplet), and coupling constant (Hz). Data for ^{13}C NMR
83 are reported in terms of chemical shift and no special nomenclature is used for equivalent
84 carbons.

85

86 Glutamate conjugated cholic acid (Glu-CA): NaHCO_3 was used as the inorganic base. Product
87 was purified using 6-18% CH_3OH in CH_2Cl_2 with 1% acetic acid to obtain a 21% isolated yield as
88 an off-white amorphous solid. ^1H NMR (600 MHz, CD_3OD) δ 4.37 (dd, *J* = 8.8, 5.0 Hz, 1H), 3.96

89 (t, J = 3.0 Hz, 1H), 3.80 (q, J = 3.0 Hz, 1H), 3.37 (tt, J = 11.2, 4.4 Hz, 1H), 2.38 (t, J = 7.7 Hz, 2H),
90 2.37 – 2.22 (m, 3H), 2.18 (ddd, J = 13.4, 9.3, 6.6 Hz, 2H), 2.05 – 1.78 (m, 6H), 1.79 – 1.70 (m,
91 1H), 1.69 – 1.62 (m, 1H), 1.63 – 1.50 (m, 5H), 1.49 – 1.29 (m, 6H), 1.12 (qd, J = 11.8, 5.7 Hz,
92 1H), 1.04 (d, J = 6.5 Hz, 3H), 0.98 (td, J = 14.2, 3.5 Hz, 1H), 0.92 (s, 3H), 0.72 (s, 3H); ^{13}C NMR
93 (151 MHz, $(\text{CD}_3)_2\text{SO}$) δ 174.41, 172.68, 71.17, 70.57, 66.38, 51.74, 46.31, 45.86, 41.61, 41.46,
94 35.40, 35.29, 34.97, 34.49, 32.55, 31.82, 31.04, 31.00, 30.47, 28.63, 27.43, 27.24, 26.30, 22.93,
95 22.72, 17.23, 12.45; HRMS (ESI) exact mass calculated for $[\text{M}+\text{H}]^+$ ($\text{C}_{29}\text{H}_{48}\text{NO}_8$) requires m/z
96 538.3375, found 538.3376 with a difference of 0.19 ppm.

97

98 Glutamate conjugated chenodeoxycholic acid (Glu-CDCA): NaHCO_3 was used as the inorganic
99 base. Product was purified using 6-12% CH_3OH in CH_2Cl_2 with 1% acetic acid to obtain a 50%
100 yield as an off-white amorphous solid. ^1H NMR (600 MHz, CD_3OD) δ 4.37 (t, J = 6.7 Hz, 1H), 3.79
101 (t, J = 3.3 Hz, 1H), 3.37 (tt, J = 10.5, 4.2 Hz, 1H), 2.38 (t, J = 7.5 Hz, 2H), 2.35 – 2.22 (m, 2H),
102 2.21 – 2.12 (m, 2H), 2.03 – 1.99 (m, 1H), 1.97 – 1.80 (m, 5H), 1.74 (dt, J = 13.3, 8.0 Hz, 1H), 1.69
103 – 1.58 (m, 2H), 1.54 – 1.45 (m, 5H), 1.39 – 1.27 (m, 7H), 1.23 – 1.15 (m, 2H), 1.15 – 1.06 (m,
104 1H), 0.99 (d, J = 6.1 Hz, 3H), 0.93 (s, 3H), 0.70 (s, 3H); ^{13}C NMR (151 MHz, $(\text{CD}_3)_2\text{SO}$) δ 174.34,
105 172.57, 70.43, 66.27, 55.71, 51.68, 50.08, 42.00, 41.49, 40.82, 35.37, 35.11, 34.88, 34.81, 32.37,
106 32.32, 31.67, 30.87, 30.59, 27.89, 27.13, 23.25, 22.79, 20.33, 18.43, 11.73; HRMS (ESI) exact
107 mass calculated for $[\text{M}+\text{H}]^+$ ($\text{C}_{29}\text{H}_{48}\text{NO}_7$) requires m/z 522.3426, found 522.3423 with a difference of
108 0.57 ppm.

109

110 Glutamate conjugated deoxycholic acid (Glu-DCA): NaHCO_3 was used as the inorganic base.
111 Product was purified using 6-12% CH_3OH in CH_2Cl_2 with 1% acetic acid to obtain a 55% yield as
112 an off-white amorphous solid. ^1H NMR (600 MHz, CD_3OD) δ 4.37 (dd, J = 8.4, 4.8 Hz, 1H), 3.96
113 (t, J = 3.1 Hz, 1H), 3.57 – 3.48 (m, 1H), 2.38 (t, J = 7.6 Hz, 2H), 2.35 – 2.29 (m, 1H), 2.21 – 2.12
114 (m, 2H), 1.96 – 1.75 (m, 8H), 1.66 – 1.57 (m, 3H), 1.55 – 1.50 (m, 2H), 1.48 – 1.23 (m, 9H), 1.17
115 (qd, J = 13.0, 3.9 Hz, 1H), 1.09 (dd, J = 12.1, 5.8 Hz, 1H), 1.03 (d, J = 6.5 Hz, 3H), 0.98 (td, J =
116 14.1, 3.4 Hz, 1H), 0.93 (s, 3H), 0.71 (s, 3H); ^{13}C NMR (151 MHz, $(\text{CD}_3)_2\text{SO}$) δ 174.36, 174.08,
117 172.70, 71.16, 70.07, 51.71, 47.55, 46.35, 46.08, 41.70, 36.34, 35.75, 35.22, 35.18, 33.91, 33.02,
118 32.48, 31.76, 30.84, 30.28, 28.68, 27.32, 27.08, 27.08, 26.20, 23.61, 23.18, 17.18, 12.54; HRMS
119 (ESI) exact mass calculated for $[\text{M}+\text{H}]^+$ ($\text{C}_{29}\text{H}_{48}\text{NO}_7$) requires m/z 522.3426, found 522.3427 with
120 a difference of 0.19 ppm.

121

122 Isoleucine conjugated cholic acid (Ile-CA): Purified according to literature procedure⁴ and
123 characterization data is consistent with reported data.

124

125 Leucine conjugated cholic acid (Leu-CA): Purified according to literature procedure⁴ and
126 characterization data is consistent with reported data.

127

128 Methionine conjugated chenodeoxycholic acid (Met-CDCA): NaHCO_3 was used as the inorganic
129 base. Product was purified using 3-6% CH_3OH in CH_2Cl_2 with 1% acetic acid to obtain a 79%
130 yield as a white amorphous solid. ^1H NMR 600 MHz, CD_3OD) δ 4.53 (dd, J = 9.3, 4.6 Hz, 1H),
131 3.79 (q, J = 2.9 Hz, 1H), 3.37 (tt, J = 10.9, 4.2 Hz, 1H), 2.62 – 2.47 (m, 2H), 2.36 – 2.23 (m, 2H),
132 2.21 – 2.10 (m, 2H), 2.09 (s, 3H), 2.05 – 1.79 (m, 7H), 1.78 – 1.70 (m, 1H), 1.68 – 1.59 (m, 2H),

133 1.56 – 1.42 (m, 5H), 1.40 – 1.27 (m, 5H), 1.24 – 1.15 (m, 2H), 1.14-1.06 (m, 1H), 1.03 – 0.94 (m,
134 4H), 0.93 (s, 3H), 0.69 (s, 3H); ^{13}C NMR (151 MHz, CD_3OD) δ 176.93, 175.25, 72.83, 69.05,
135 57.34, 52.54, 51.50, 43.66, 43.12, 41.02, 40.73, 40.41, 36.80, 36.54, 36.19, 35.86, 34.01, 33.81,
136 33.21, 32.10, 31.32, 31.29, 29.28, 24.62, 23.42, 21.78, 18.94, 15.24, 12.23; HRMS (ESI) exact
137 mass calculated for $[\text{M}+\text{H}]^+$ ($\text{C}_{29}\text{H}_{50}\text{NO}_5\text{S}$) requires m/z 524.3404, found 524.3406 with a
138 difference of 0.38 ppm.

139

140 Methionine conjugated deoxycholic acid (Met-DCA): NaHCO_3 was used as the inorganic base.
141 Product was purified using 3-6% CH_3OH in CH_2Cl_2 with 1% acetic acid to obtain a 76% yield as
142 a white amorphous solid. ^1H NMR (600 MHz, CD_3OD) δ 4.53 (dd, J = 9.3, 4.6 Hz, 1H), 3.96 (t, J
143 = 3.0 Hz, 1H), 3.53 (tt, J = 11.2, 4.6 Hz, 1H), 2.62 – 2.55 (m, 1H), 2.55 – 2.48 (m, 1H), 2.37 – 2.28
144 (m, 1H), 2.24 – 2.10 (m, 2H), 2.09 (s, 3H), 1.99 – 1.93 (m, 1H), 1.93 – 1.73 (m, 7H), 1.65 – 1.57
145 (m, 3H), 1.57 – 1.49 (m, 2H), 1.49 – 1.37 (m, 6H), 1.36 – 1.30 (m, 1H), 1.30 – 1.25 (m, 2H), 1.22
146 – 1.06 (m, 2H), 1.03 (d, J = 6.5 Hz, 3H), 0.98 (td, J = 14.2, 3.2 Hz, 1H), 0.93 (s, 3H), 0.71 (s, 3H).
147 ^{13}C NMR (151 MHz, CD_3OD) δ 177.0099, 175.27, 74.06, 72.52, 52.54, 49.24, 48.11, 47.54, 43.58,
148 37.42, 37.15, 36.72, 36.41, 35.27, 34.78, 33.80, 33.17, 32.11, 31.27, 31.01, 29.86, 28.67, 28.38,
149 27.43, 24.86, 23.72, 17.68, 15.22, 13.24; HRMS (ESI) exact mass calculated for $[\text{M}+\text{H}]^+$
150 ($\text{C}_{29}\text{H}_{50}\text{NO}_5\text{S}$) requires m/z 524.3404, found 524.3405 with a difference of 0.19 ppm.

151

152 Phenylalanine conjugated cholic acid (Phe-CA): Purified according to literature procedure⁴ and
153 characterization data is consistent with reported data.

154

155 Phenylalanine conjugated chenodeoxycholic acid (Phe-CDCA): NaHCO_3 was used as the
156 inorganic base. Product was purified using 3-6% CH_3OH in CH_2Cl_2 with 1% acetic acid to obtain
157 a 94% yield as a white amorphous solid. ^1H NMR (600 MHz, CD_3OD) δ 7.29 – 7.17 (m, 5H), 4.64
158 (dd, J = 9.5, 4.9 Hz, 1H), 3.79 (q, J = 2.9 Hz, 1H), 3.41 – 3.33 (m, 1H), 3.22 (dd, J = 14.0, 4.8 Hz,
159 1H), 2.93 (dd, J = 13.9, 9.5 Hz, 1H), 2.27 (q, J = 11.7 Hz, 1H), 2.23 – 2.17 (m, 1H), 2.10 – 2.03
160 (m, 1H), 1.98 – 1.94 (m, 1H), 1.90 – 1.81 (m, 3H), 1.76 – 1.59 (m, 4H), 1.55 – 1.43 (m, 4H), 1.40
161 – 1.27 (m, 5H), 1.26 – 1.04 (m, 5H), 1.02 – 0.94 (m, 1H), 0.94 – 0.91 (m, 6H), 0.66 (s, 3H); ^{13}C
162 NMR (151 MHz, $(\text{CD}_3)_2\text{SO}$) δ 173.41, 172.64, 137.99, 129.15, 128.10, 126.32, 70.41, 66.23,
163 55.60, 53.59, 50.05, 41.94, 41.47, 36.87, 35.36, 35.01, 34.87, 34.78, 32.34, 32.15, 31.54, 30.59,
164 27.79, 23.22, 22.77, 20.31, 18.35, 11.70; HRMS (ESI) exact mass calculated for $[\text{M}+\text{H}]^+$
165 ($\text{C}_{33}\text{H}_{50}\text{NO}_5$) requires m/z 540.3684, found 540.3683 with a difference of 0.19 ppm.

166

167 Phenylalanine conjugated deoxycholic acid (Phe-DCA): NaHCO_3 was used as the inorganic base.
168 Product was purified using 3-6% CH_3OH in CH_2Cl_2 with 1% acetic acid to obtain a 99% yield as
169 a white amorphous solid. ^1H NMR (600 MHz, CD_3OD) δ 7.30 – 7.17 (m, 5H), 4.65 (dd, J = 9.3,
170 4.9 Hz, 1H), 3.94 (t, J = 3.0 Hz, 1H), 3.57 – 3.48 (m, 1H), 3.21 (dd, J = 13.9, 4.9 Hz, 1H), 2.94
171 (dd, J = 13.9, 9.3 Hz, 1H), 2.25 – 2.17 (m, 1H), 2.11 – 2.03 (m, 1H), 1.95 – 1.84 (m, 2H), 1.85 –
172 1.74 (m, 4H), 1.71 – 1.62 (m, 1H), 1.64 – 1.55 (m, 3H), 1.54 – 1.48 (m, 2H), 1.50 – 1.32 (m, 6H),
173 1.31 – 1.24 (m, 1H), 1.24 – 1.11 (m, 3H), 1.12 – 1.01 (m, 1H), 1.02 – 0.93 (m, 4H), 0.93 (s, 3H),
174 0.67 (s, 3H); ^{13}C NMR (151 MHz, $(\text{CD}_3)_2\text{SO}$) δ 173.42, 172.74, 137.97, 129.15, 128.11, 126.33,
175 71.11, 70.04, 53.56, 48.66, 47.52, 46.22, 46.01, 41.68, 36.86, 36.33, 35.72, 35.21, 35.08, 33.87,
176 32.98, 32.27, 31.63, 30.27, 28.66, 27.21, 27.05, 26.18, 23.57, 23.14, 21.14, 17.10, 12.49; HRMS

177 (ESI) exact mass calculated for [M+H]⁺ (C₃₃H₅₀NO₅) requires m/z 540.3684, found 540.3684 with
178 a difference of 0.00 ppm.

179
180 Threonine conjugated cholic acid (Thr-CA): NaHCO₃ was used as the inorganic base. Product
181 was purified using 6-12% CH₃OH in CH₂Cl₂ with 1% acetic acid to obtain a 97% yield as a white
182 amorphous solid. ¹H NMR (600 MHz, CD₃OD) δ 4.37 (s, 1H), 4.28 (s, 1H), 3.96 (t, J = 3.0 Hz,
183 1H), 3.80 (q, J = 3.0 Hz, 1H), 3.37 (tt, J = 11.4, 4.5 Hz, 1H), 2.39 (ddd, J = 14.7, 10.1, 5.1 Hz, 1H),
184 2.33 – 2.19 (m, 3H), 2.04 – 1.96 (m, 2H), 1.96 – 1.79 (m, 4H), 1.78 – 1.71 (m, 1H), 1.68 – 1.63
185 (m, 1H), 1.63 – 1.51 (m, 5H), 1.48 – 1.28 (m, 5H), 1.18 (d, J = 6.3 Hz, 3H), 1.16 – 1.07 (m, 1H),
186 1.05 (d, J = 6.5 Hz, 3H), 0.98 (td, J = 14.2, 3.5 Hz, 1H), 0.92 (s, 3H), 0.72 (s, 3H). ¹³C NMR (151
187 MHz, CD₃OD) δ 176.98, 74.04, 72.86, 69.08, 68.75, 48.08, 47.48, 43.15, 42.96, 40.97, 40.42,
188 36.91, 36.46, 35.87, 35.82, 34.08, 33.21, 31.14, 29.52, 28.68, 27.84, 24.22, 23.14, 20.26, 17.77,
189 13.00; ¹³C NMR (151 MHz, (CD₃)₂SO) δ 173.13, 71.28, 70.66, 66.73, 66.47, 46.41, 45.93, 41.67,
190 41.52, 35.46, 35.43, 35.02, 34.55, 32.72, 31.97, 30.50, 28.67, 27.51, 26.36, 23.01, 22.77, 19.92,
191 17.29, 12.52; HRMS (ESI) exact mass calculated for [M+H]⁺ (C₂₈H₄₈NO₇) requires m/z 510.3426,
192 found 510.3424 with a difference of 0.39 ppm.

193
194 Tyrosine conjugated cholic acid (Tyr-CA): Purified according to literature procedure⁴ and
195 characterization data is consistent with reported data.

196
197 Tyrosine conjugated chenodeoxycholic acid (Tyr-CDCA): NaOH was used as the inorganic base.
198 Product was purified using 3-12% CH₃OH in CH₂Cl₂ with 1% acetic acid to obtain a 74% yield as
199 a white amorphous solid. ¹H NMR (600 MHz, CD₃OD) δ 7.03 (d, J = 8.5 Hz, 2H), 6.69 (d, J = 8.5
200 Hz, 2H), 4.58 (dd, J = 9.3, 4.9 Hz, 1H), 3.80 (q, J = 3.0 Hz, 1H), 3.41 – 3.33 (m, 1H), 3.11 (dd, J
201 = 14.0, 4.9 Hz, 1H), 2.84 (dd, J = 14.0, 9.3 Hz, 1H), 2.31 – 2.17 (m, 2H), 2.11 – 2.02 (m, 1H), 2.02
202 – 1.93 (m, 2H), 1.91 – 1.81 (m, 3H), 1.77 – 1.58 (m, 4H), 1.55 – 1.43 (m, 4H), 1.43 – 1.04 (m,
203 9H), 0.98 (td, J = 14.2, 3.4 Hz, 1H), 0.93 (t, J = 3.3 Hz, 6H), 0.67 (s, 3H). ¹³C NMR (151 MHz,
204 CD₃OD) δ 176.67, 175.21, 157.21, 131.22, 129.19, 116.15, 72.85, 69.10, 57.31, 55.23, 51.49,
205 43.64, 43.13, 41.01, 40.72, 40.43, 37.62, 36.80, 36.52, 36.19, 35.85, 34.02, 33.84, 33.23, 31.32,
206 29.20, 24.61, 23.38, 21.76, 18.85, 12.17; HRMS (ESI) exact mass calculated for [M+H]⁺
207 (C₃₃H₅₀NO₆) requires m/z 556.3633, found 556.3634 with a difference of 0.18 ppm.

208
209
210
211
212
213
214
215
216
217
218
219
220

221 **Supplementary Tables**

222

223 **Supplementary Table 1: Number of unique spectral matches per compound for Q-ToF data**
224 **in positive ionization mode.**

	aMCA	bMCA	CA	CDCA	DCA	gMCA	HDCA	UDCA
Ala	241	4	342	418	420	74	264	40
Arg	180	101	409	38	38	103	44	72
Asn	152	159	55	2	35	159	0	2
Asp	39	36	39	0	8	39	2	0
Cit	33	33	64	224	226	33	224	224
Cys	0	N/A	4	0	0	0	0	0
DOPA	0	0	0	0	0	0	0	0
Gln	13	8	20	4	4	11	4	4
Glu	77	48	181	164	170	76	137	N/A
His	720	673	605	242	239	724	244	244
Ile/Leu	982	601	757	1563	1590	920	1376	1420
Lys	1181	963	1250	551	579	672	548	626
Met	115	115	10	204	214	115	217	207
Orn	305	199	215	80	83	203	73	84
Phe	1658	1453	1507	2629	2629	1544	2517	2624
Pro	0	0	0	0	0	0	0	0
Ser	1	3	44	30	32	24	30	30
Thr	349	328	139	7	22	340	0	0
Trp	446	420	518	1286	1286	502	1283	1283
Tyr	568	465	563	431	431	534	412	436
Val	0	0	48	8	4	0	4	4

225

226

227

228
229
230

Supplementary Table 2: Number of unique spectral matches per compound for QE data in positive ionization mode.

	aMCA	bMCA	CA	CDCA	DCA	gMCA	HDCA	UDCA
Ala	27	27	68	139	301	27	165	45
Arg	217	235	366	46	51	217	46	48
Asn	152	152	28	6	4	152	4	4
Asp	36	36	3	2	8	36	2	2
Cit	2	2	34	188	187	2	188	188
Cys	N/A	N/A	N/A	N/A	0	N/A	N/A	N/A
DOPA	0	0	0	0	0	0	0	0
Gln	8	2	15	2	2	8	2	2
Glu	51	36	113	149	178	111	136	N/A
His	595	591	595	244	244	595	244	225
Ile/Leu	595	574	712	1476	1548	584	1434	1414
Lys	517	464	856	548	570	141	542	548
Met	115	97	10	199	198	115	198	198
Orn	203	196	422	80	83	23	36	83
Phe	1509	639	1407	2513	2513	1274	2450	2526
Pro	0	0	0	0	0	0	0	0
Ser	8	4	37	36	32	11	28	30
Thr	231	235	108	5	35	229	5	10
Trp	499	471	506	1283	1284	495	1268	1283
Tyr	486	361	563	333	324	355	310	333
Val	0	15	16	26	42	0	4	4

231
232
233
234

235 **Supplementary Table 3: Number of unique spectral matches per compound for Q-ToF data**
 236 **in negative ionization mode.** There is very little negative mode data in the public domain
 237 resulting in very few matches.

	aMCA	bMCA	CA	CDCA	DCA	gMCA	HDCA	UDCA
Ala	0	0	0	0	0	0	0	0
Arg	0	0	0	0	0	0	0	0
Asn	0	0	0	0	2	0	0	0
Asp	0	0	0	0	0	0	0	0
Cit	0	0	0	0	0	0	0	0
Cys	0	0	0	0	0	0	0	0
DOPA	0	0	0	0	0	0	0	0
Gln	0	0	0	0	0	0	0	0
Glu	0	0	0	0	0	0	0	0
His	0	0	0	0	0	0	0	0
Ile/Leu	0	0	0	0	0	0	0	0
Lys	0	0	0	0	0	0	0	0
Met	0	0	0	0	0	0	0	0
Orn	0	0	0	0	0	0	0	0
Phe	0	0	0	0	0	0	0	4
Pro	0	0	0	0	0	0	0	0
Ser	0	0	0	0	0	0	0	0
Thr	0	0	0	0	0	0	0	0
Trp	0	0	0	0	0	0	0	0
Tyr	0	0	0	0	0	0	0	2
Val	0	0	0	0	0	0	0	0

238
 239
 240
 241

242 **Supplementary Table 4: Organisms, bile acids and intensities. Provided in separate**
243 **extended tables.**

244

245 **Supplementary Table 5: Universal spectrum identifiers and MASST job links for all**
246 **conjugated BAs in synthetic mixtures. Provided in separate extended tables.**

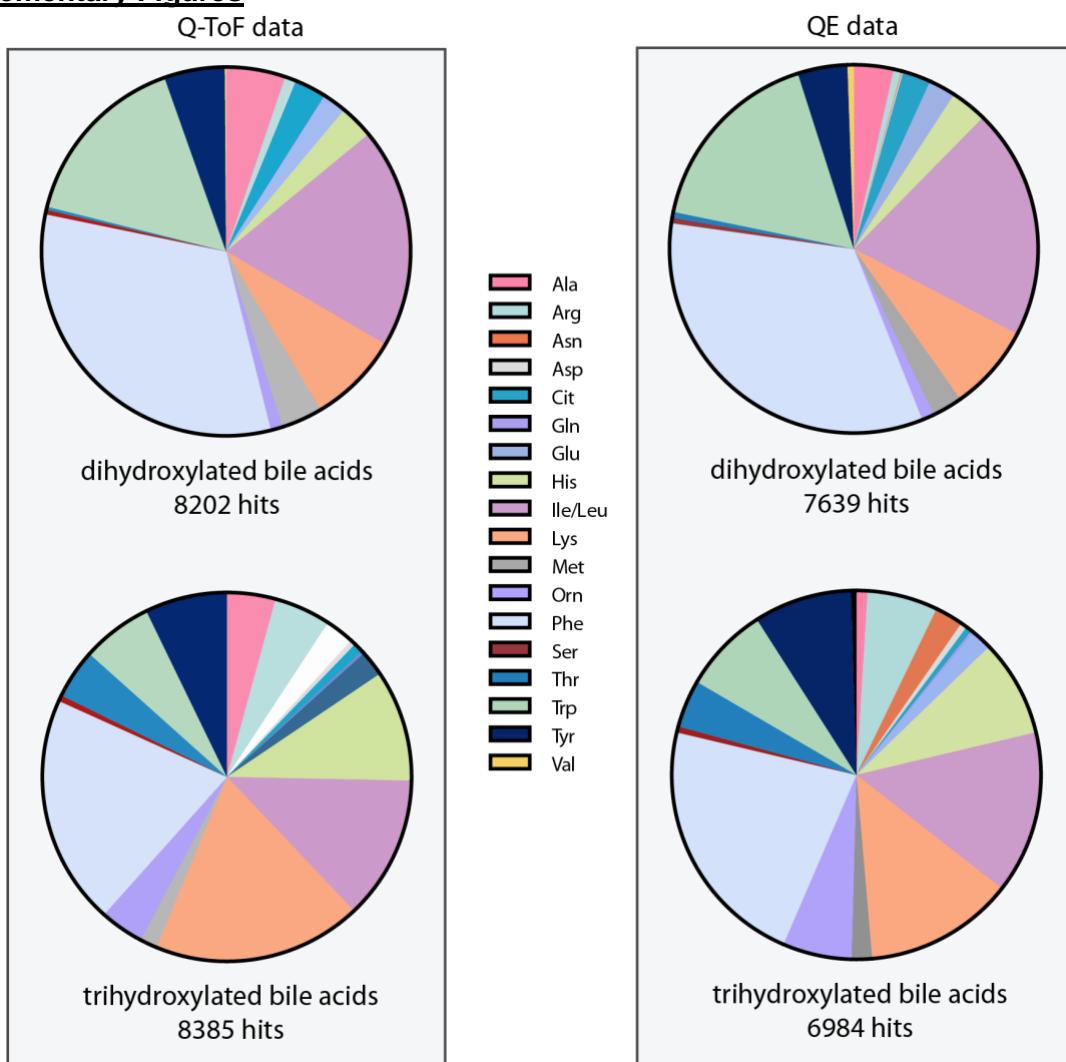
247

248

249

250

251 **Supplementary Figures**



252
253 **Supplementary Fig. 1: Comparison of amino acid distributions for MASST searches of**
254 **Orbitrap (Thermo QE) vs. Q-ToF (Bruker MaXis) data in positive ionization mode.**

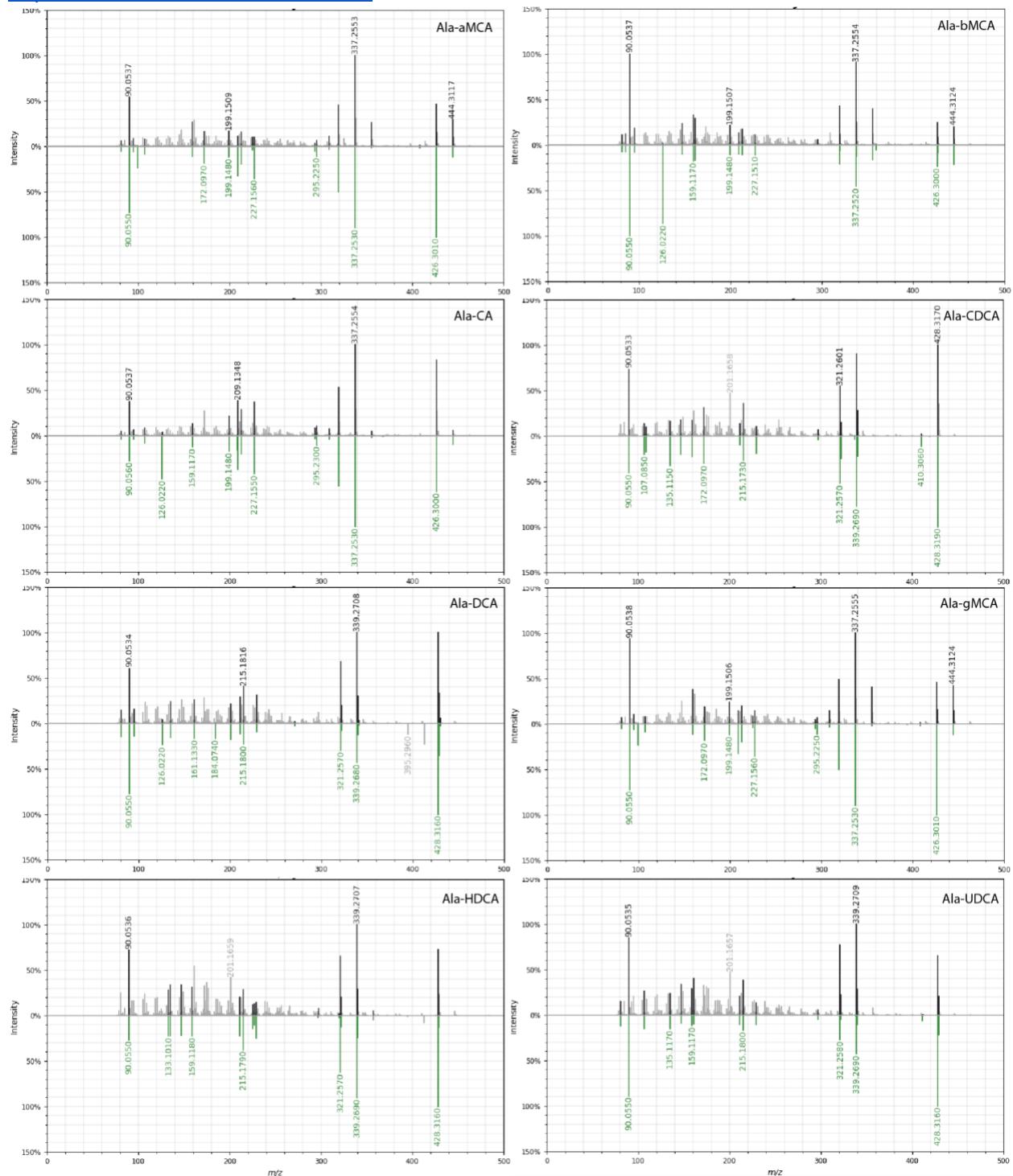
255

256

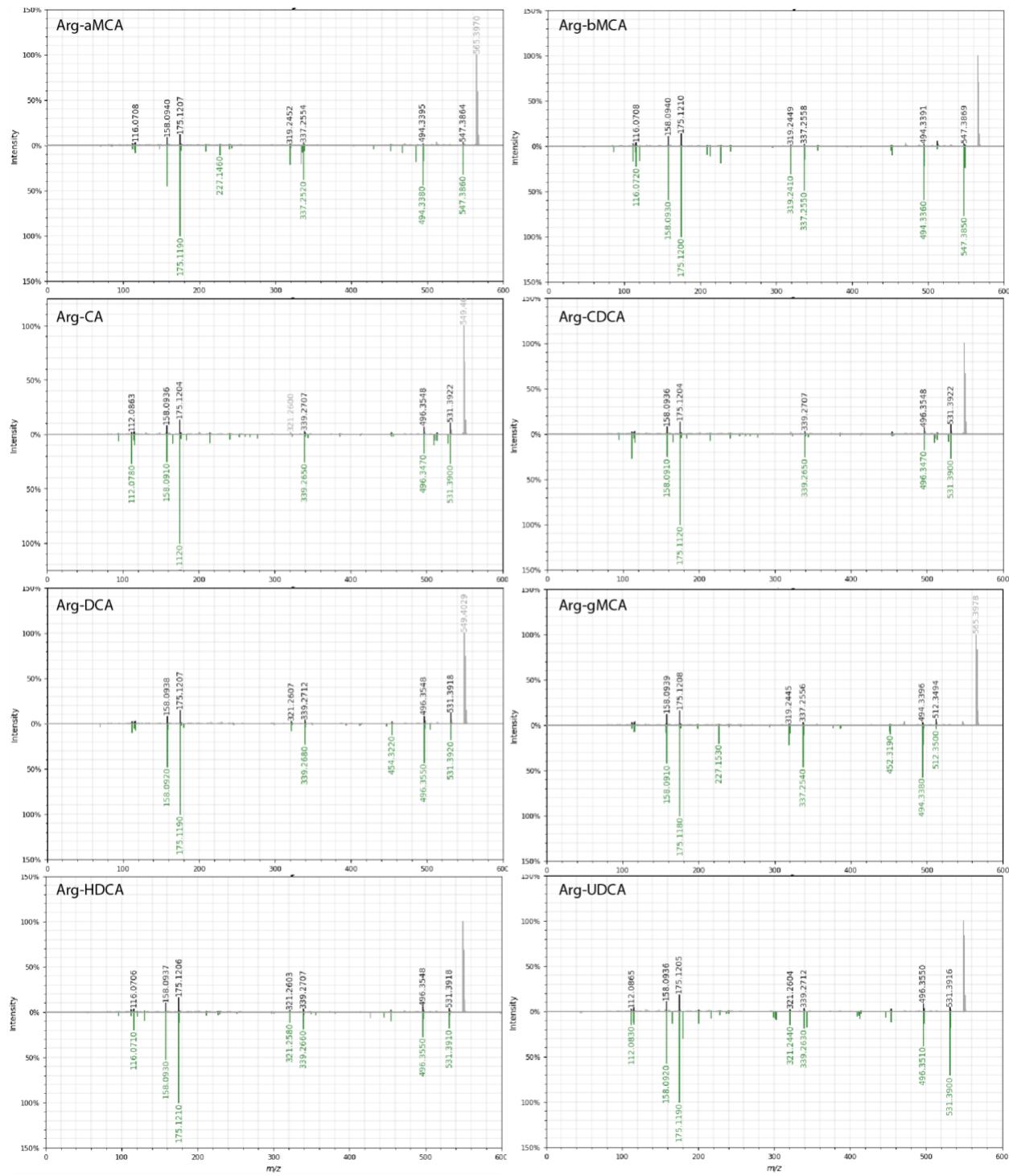
257

258

259 All mirror plots were produced with Metabolomics Spectral Resolver available at
 260 <https://metabolomics-usi.ucsd.edu/>⁵.

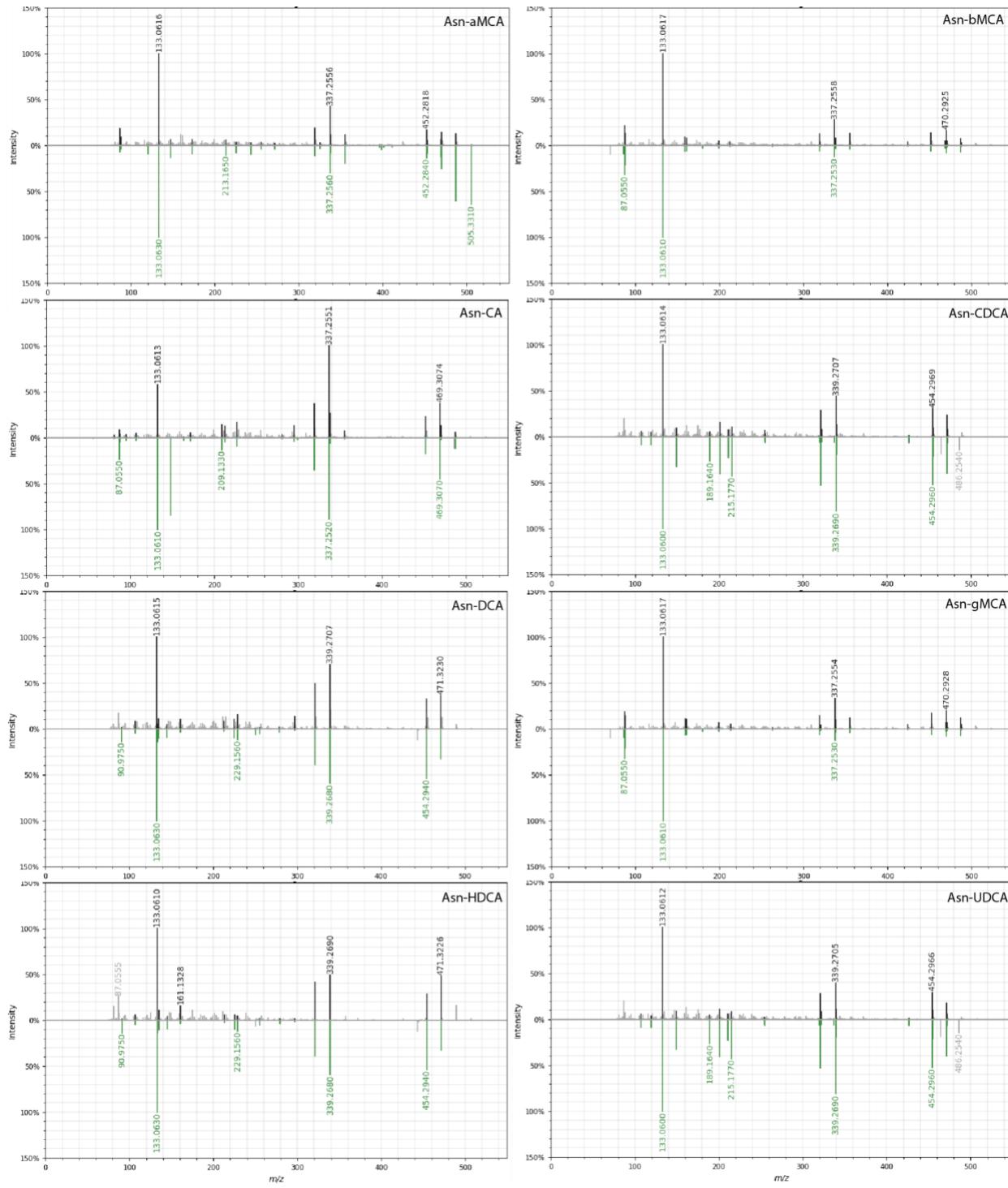


261
 262 **Supplementary Fig. 2: Mirror plots for MS/MS matches to Ala conjugated bile acids.**
 263



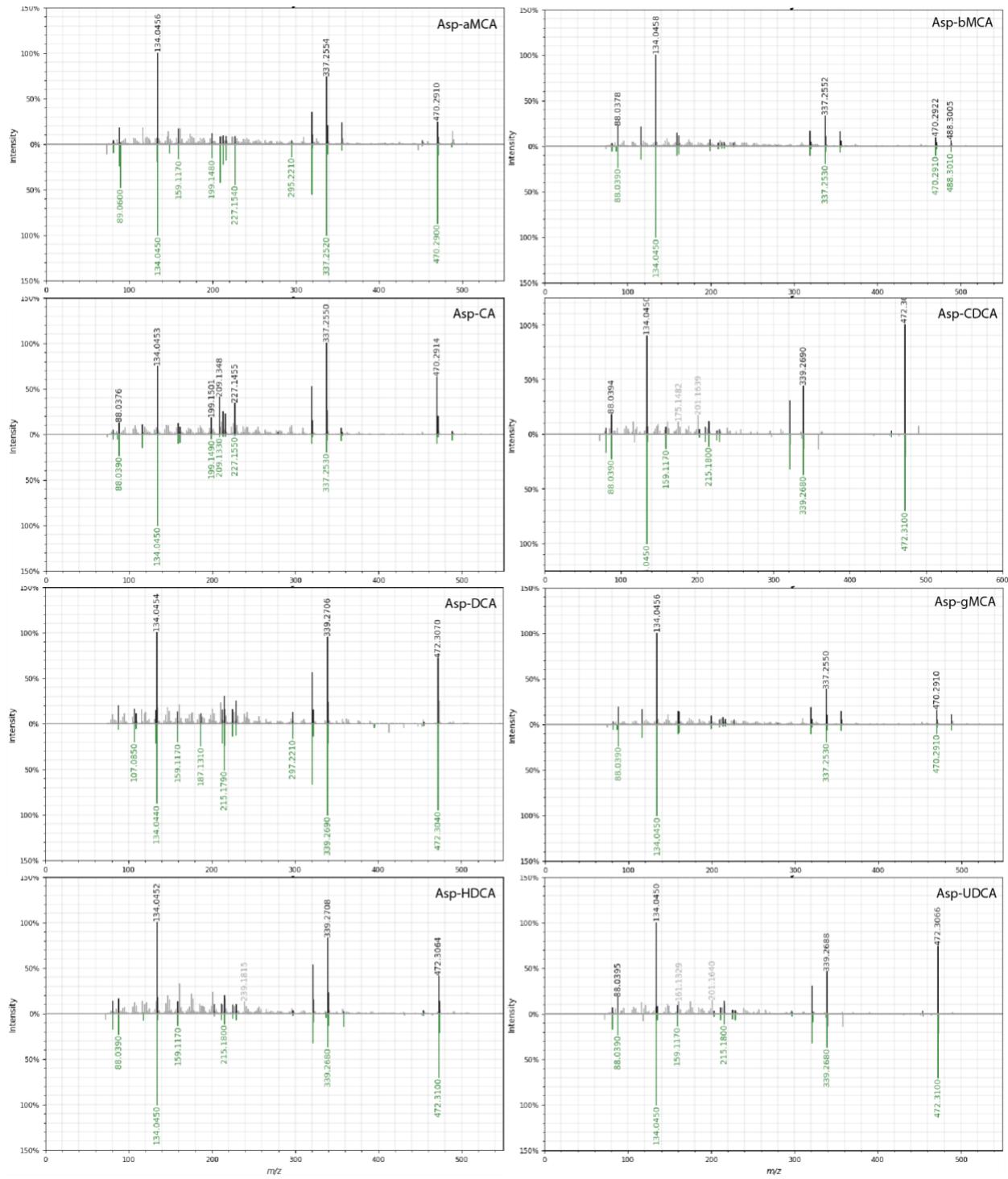
264
265
266

Supplementary Fig. 3: Mirror plots for MS/MS matches to Arg conjugated bile acids.



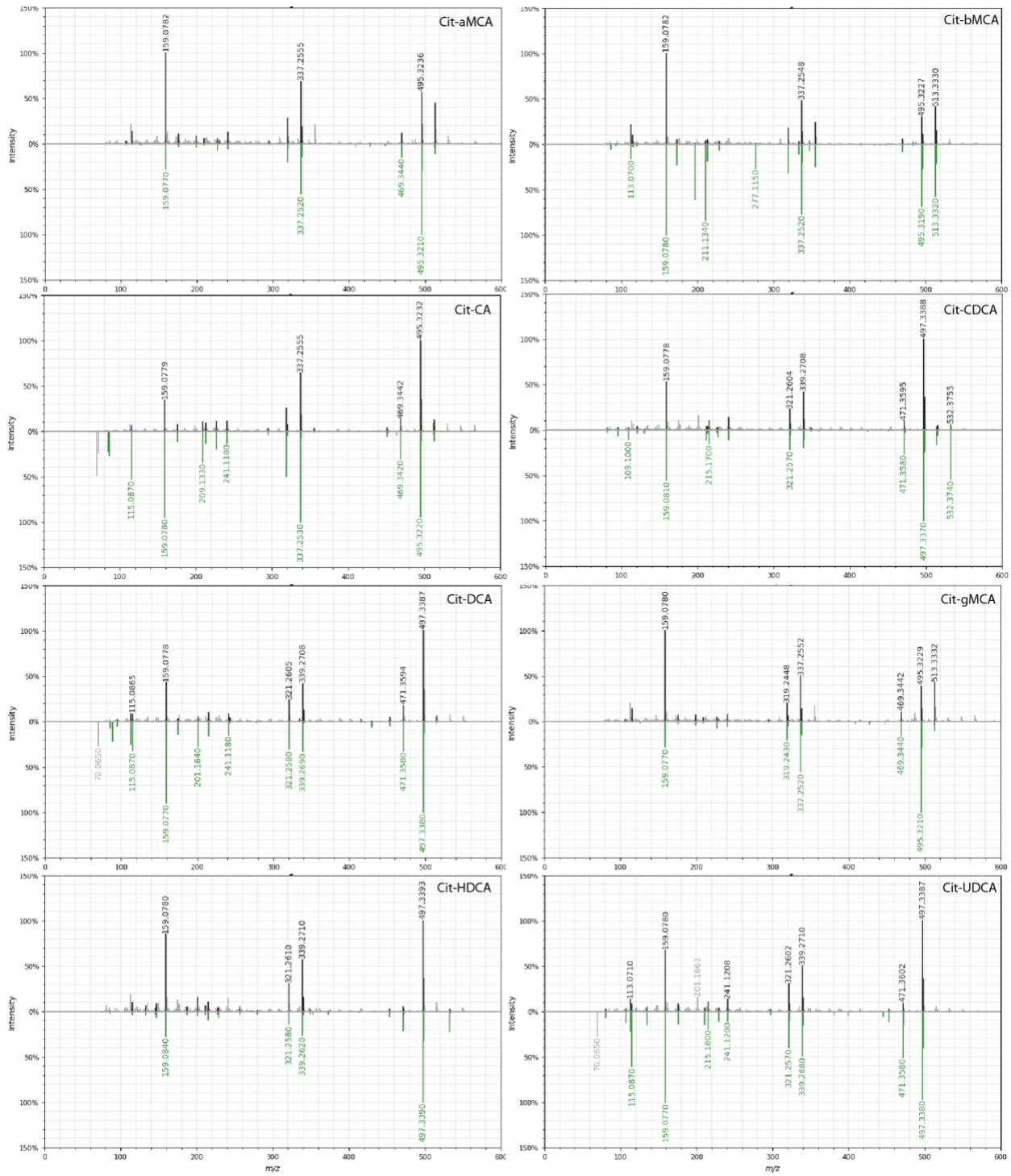
267
268
269

Supplementary Fig. 4: Mirror plots for MS/MS matches to Asn conjugated bile acids.

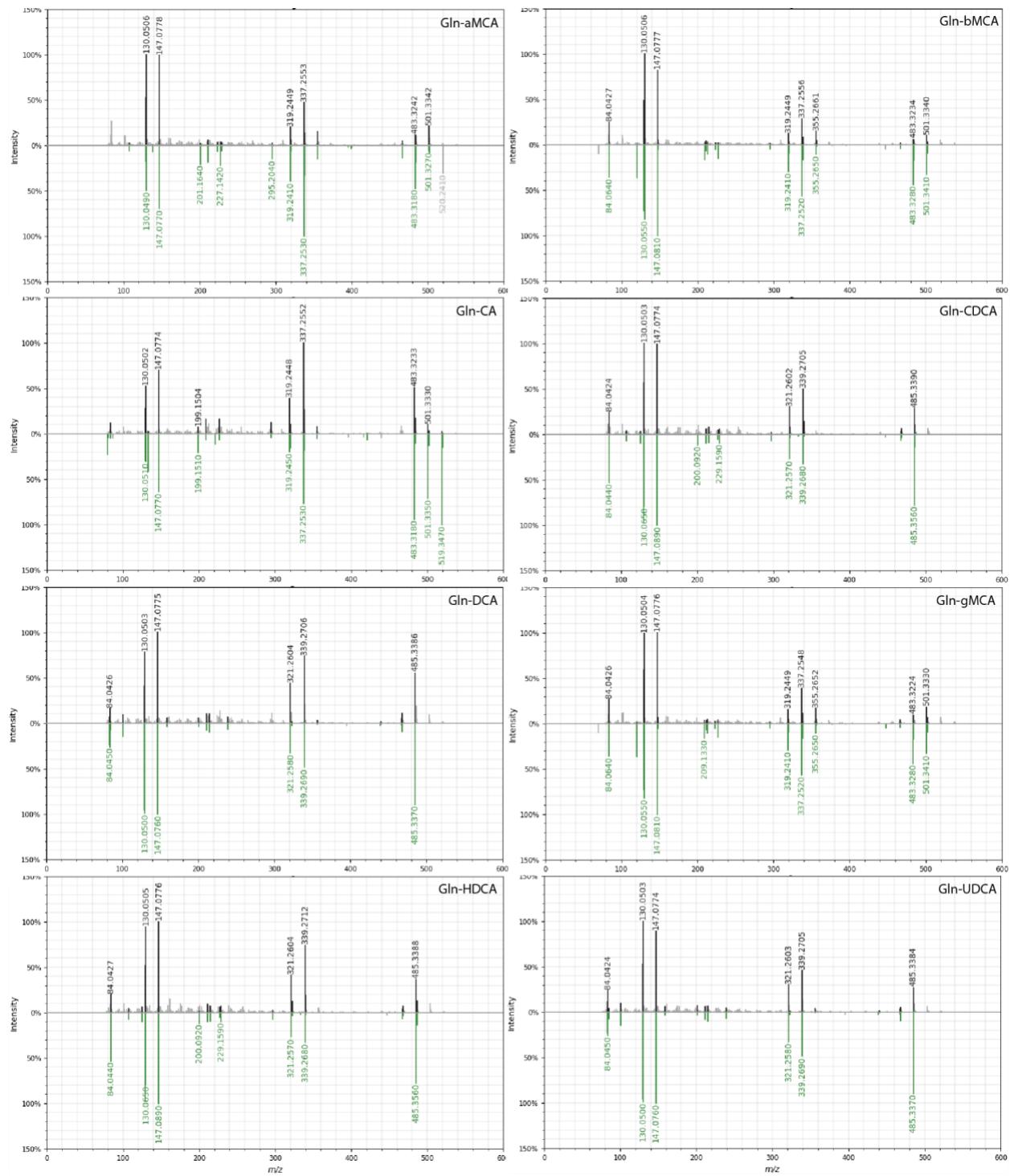


270
271
272

Supplementary Fig. 5: Mirror plots for MS/MS matches to Asp conjugated bile acids.

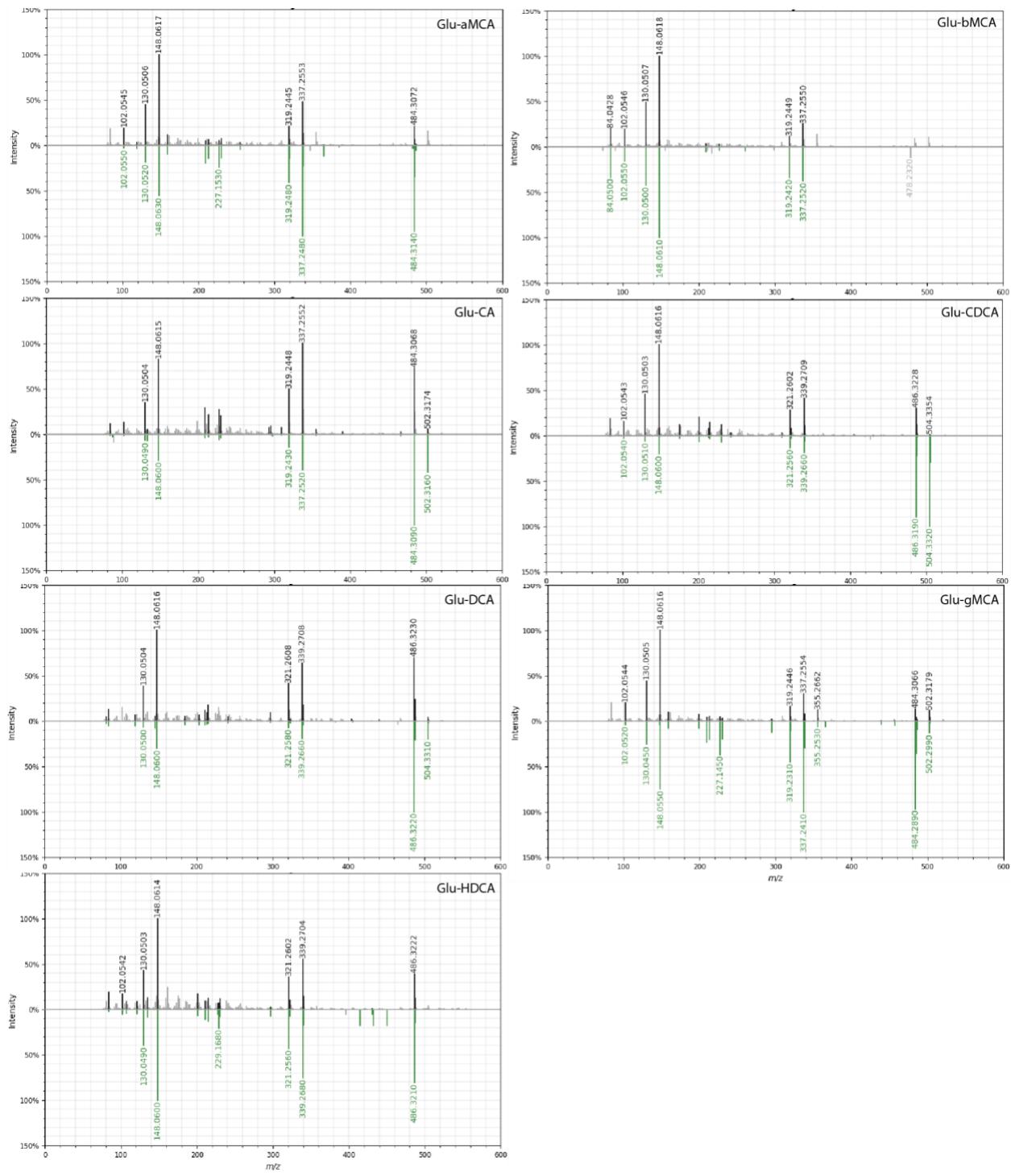


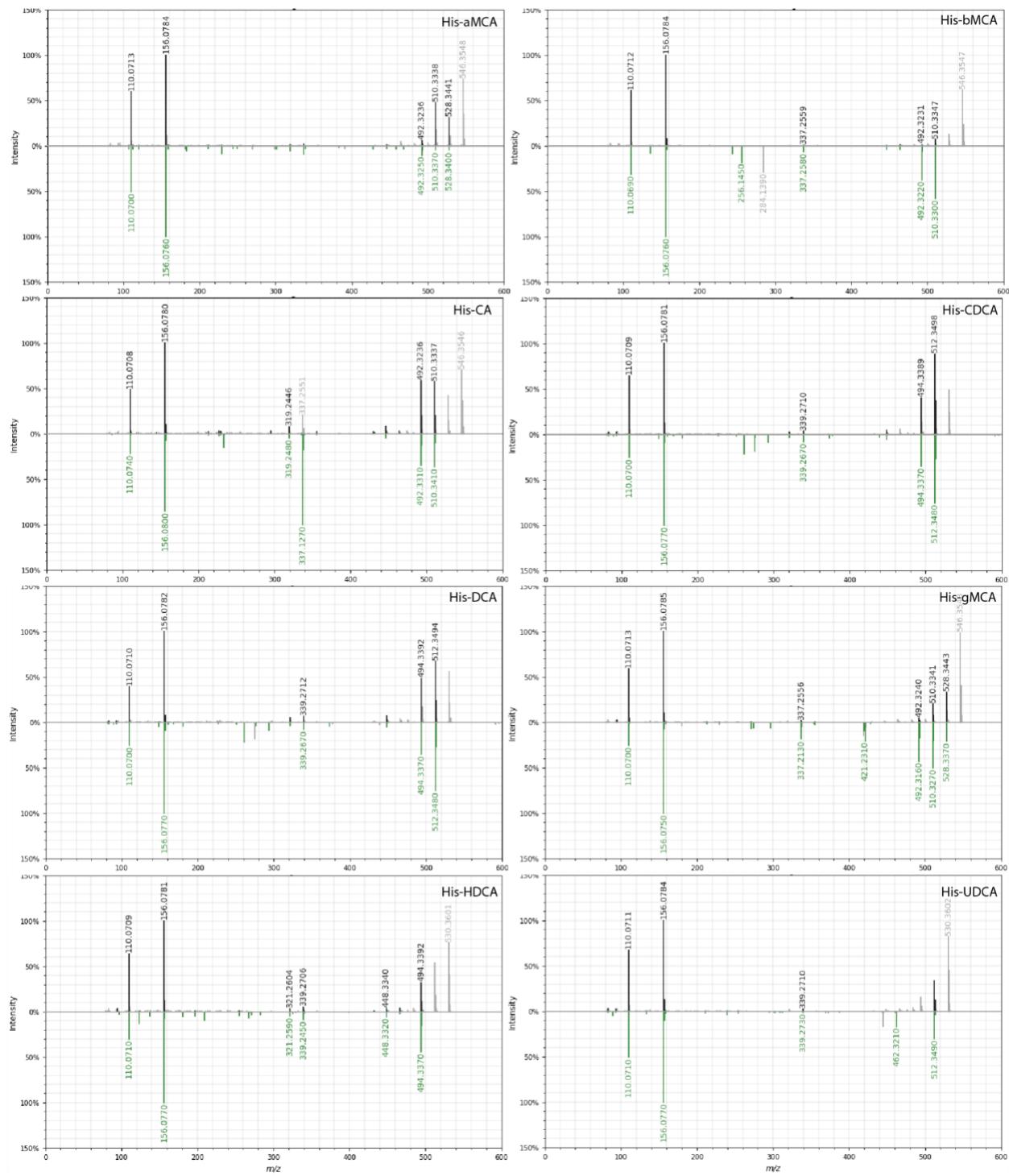
Supplementary Fig. 6: Mirror plots for MS/MS matches to Cit conjugated bile acids.



276
277
278

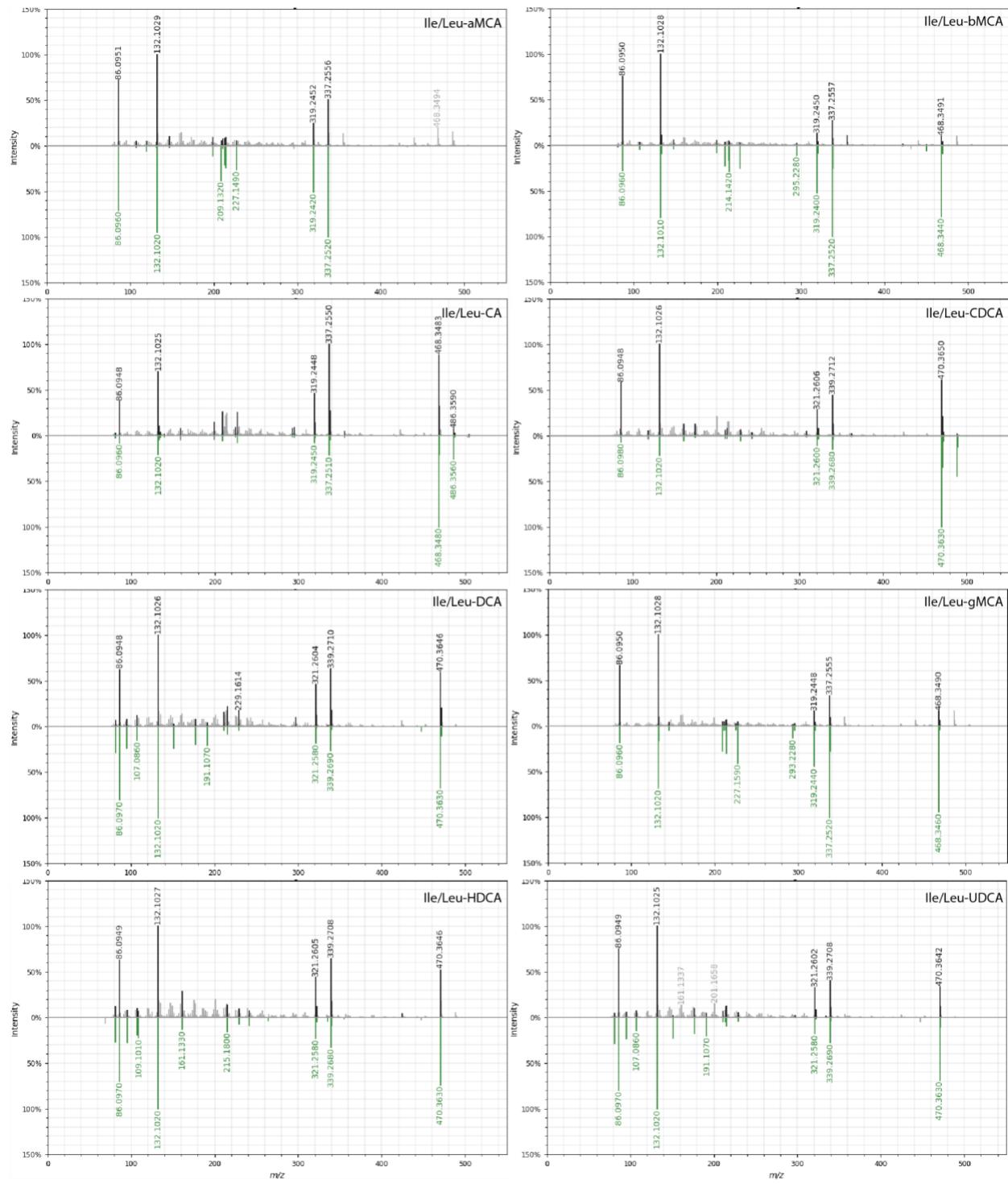
Supplementary Fig. 7: Mirror plots for MS/MS matches to Gln conjugated bile acids.





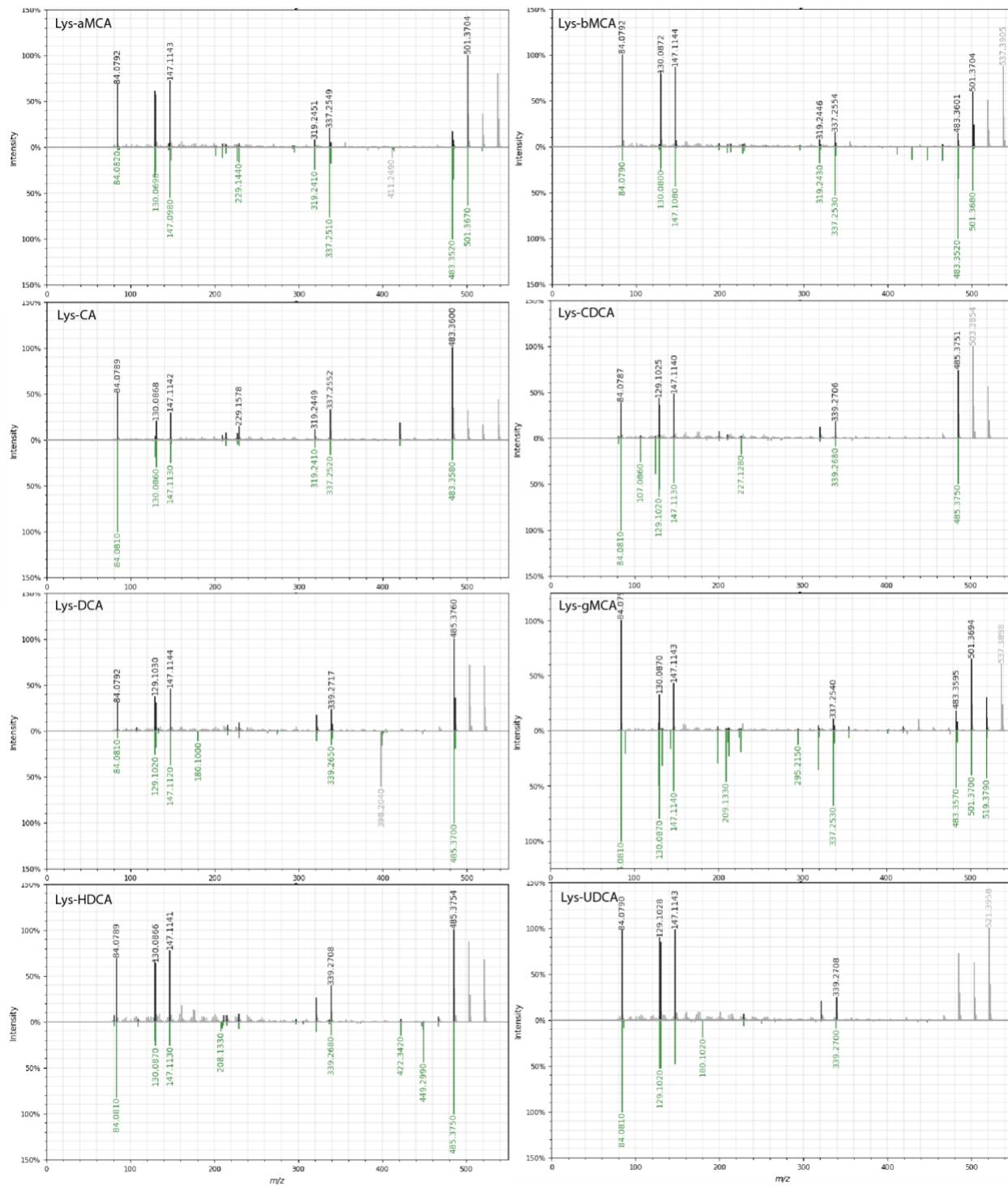
282
283
284

Supplementary Fig. 9: Mirror plots for MS/MS matches to His conjugated bile acids.



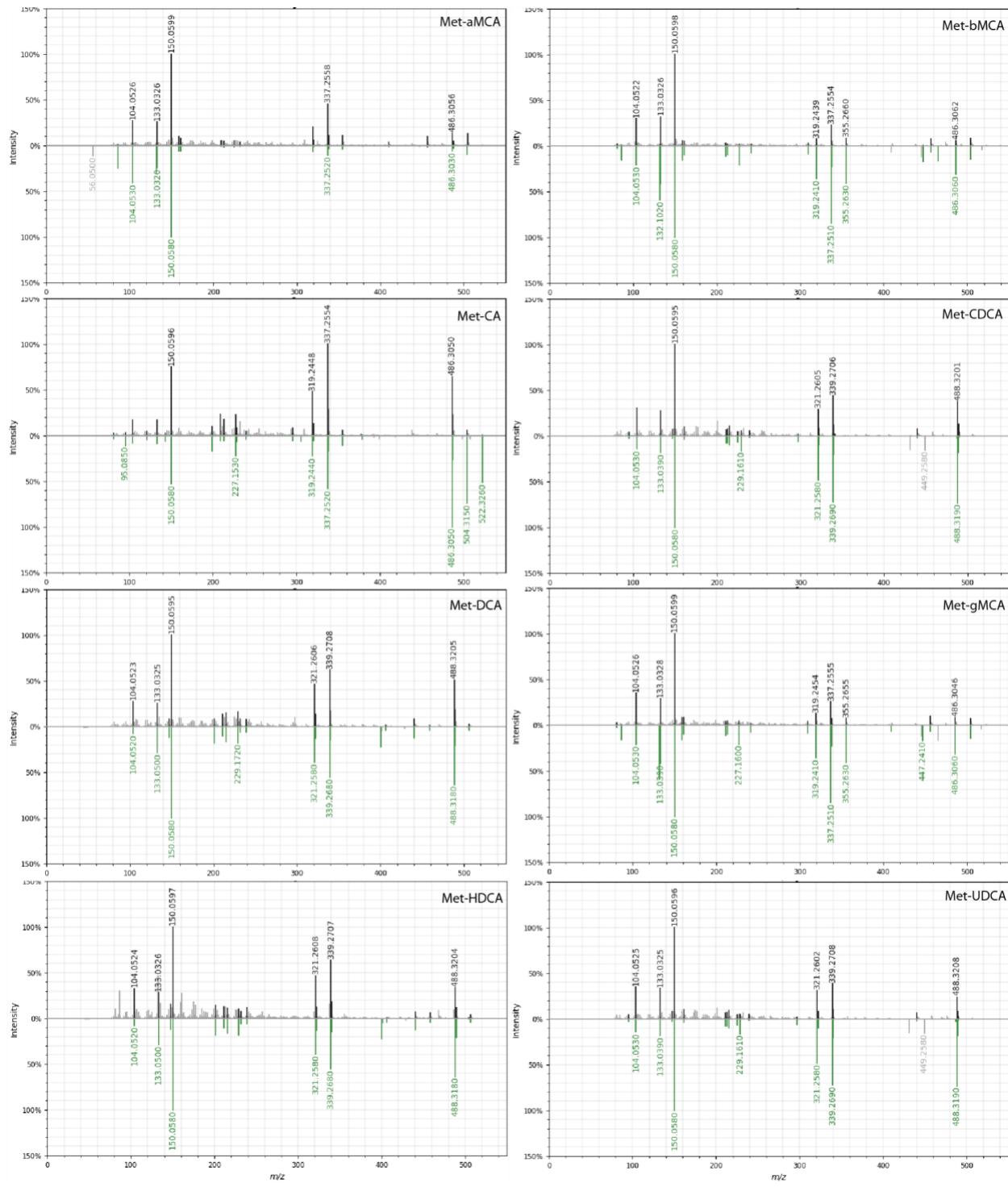
285
286
287

Supplementary Fig. 10: Mirror plots for MS/MS matches to Ile/Leu conjugated bile acids.



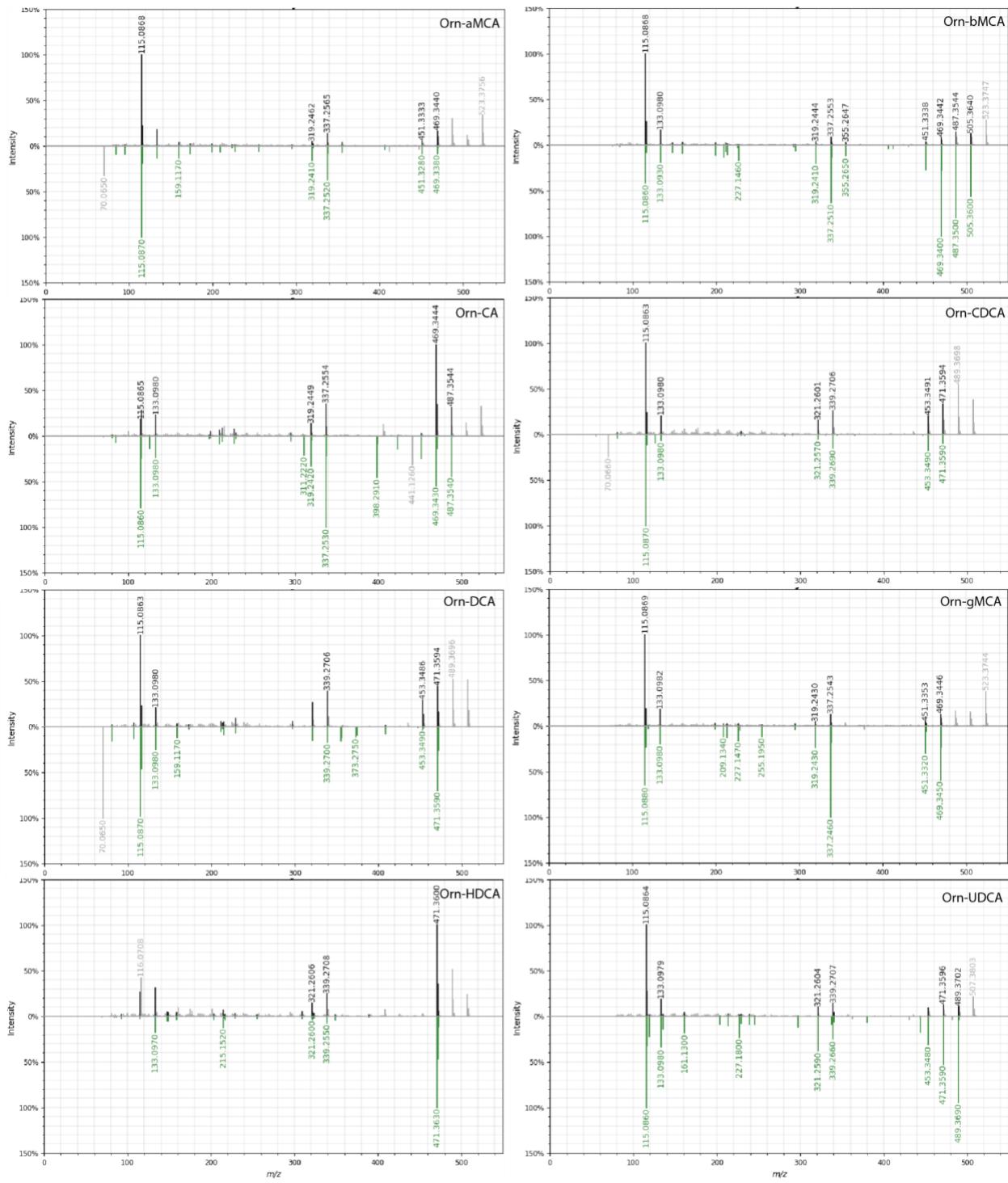
Supplementary Fig. 11: Mirror plots for MS/MS matches to Lys conjugated bile acids.

288
289
290



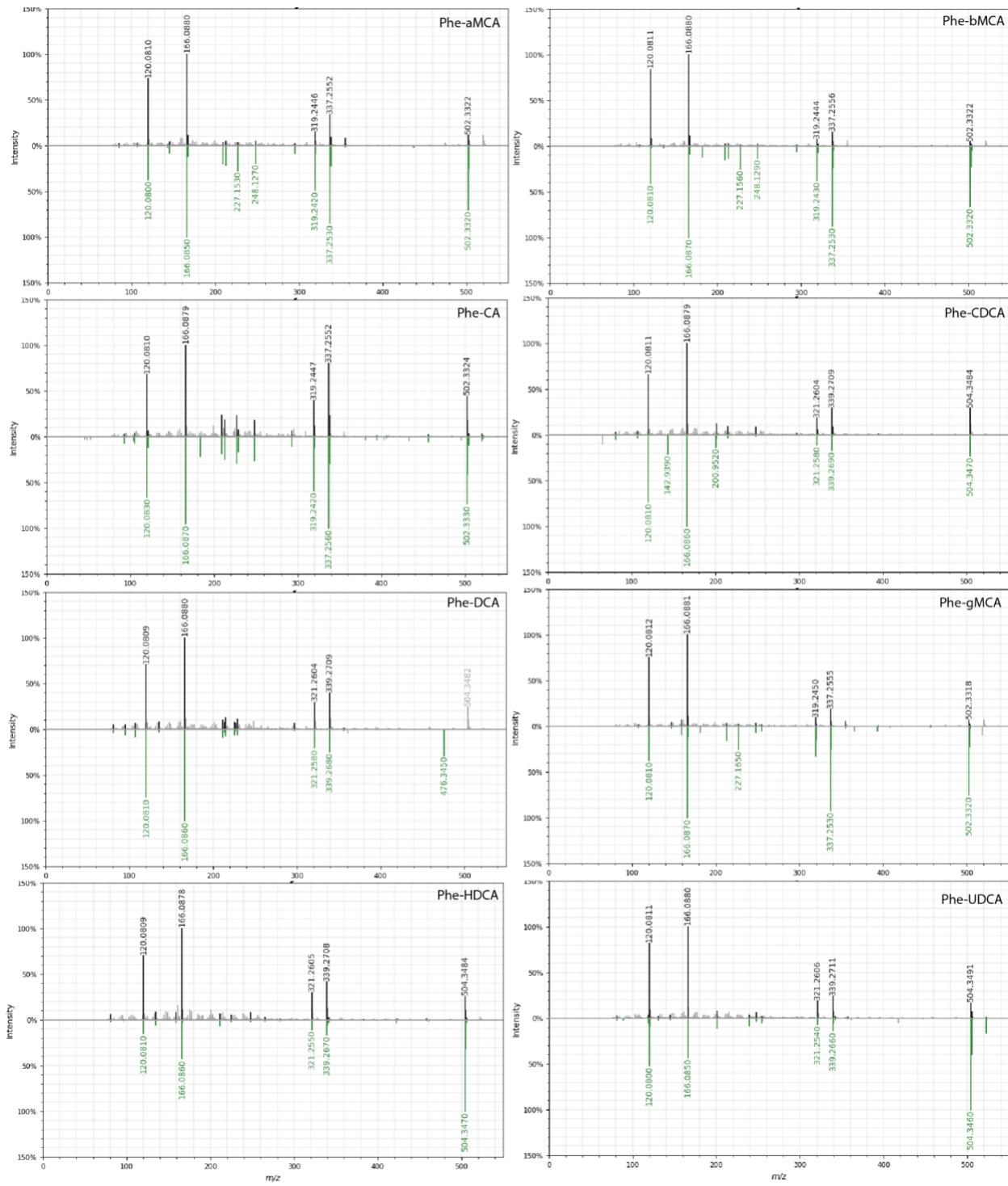
291
292
293

Supplementary Fig. 12: Mirror plots for MS/MS matches to Met conjugated bile acids.



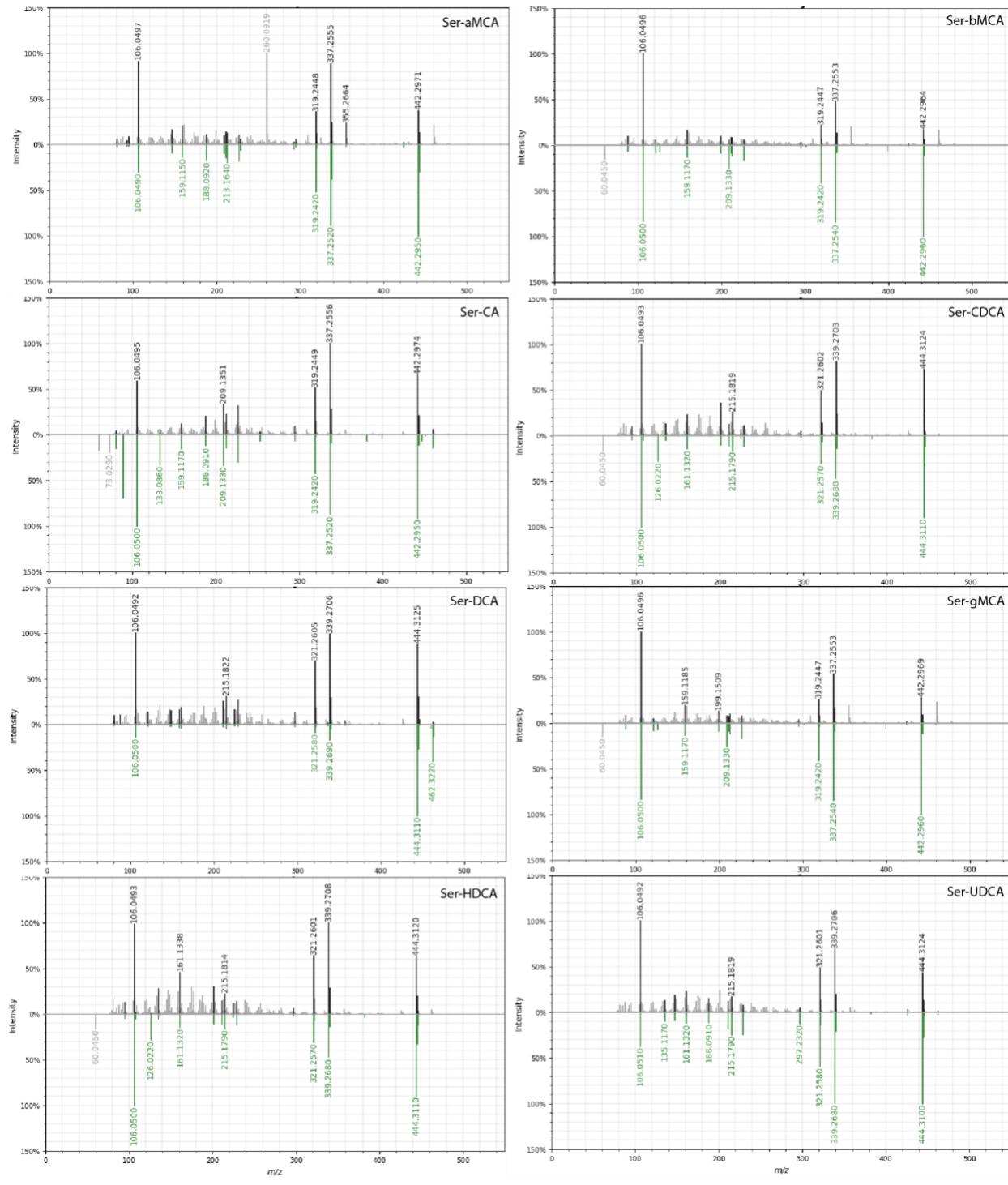
294
295
296

Supplementary Fig. 13: Mirror plots for MS/MS matches to Orn conjugated bile acids.



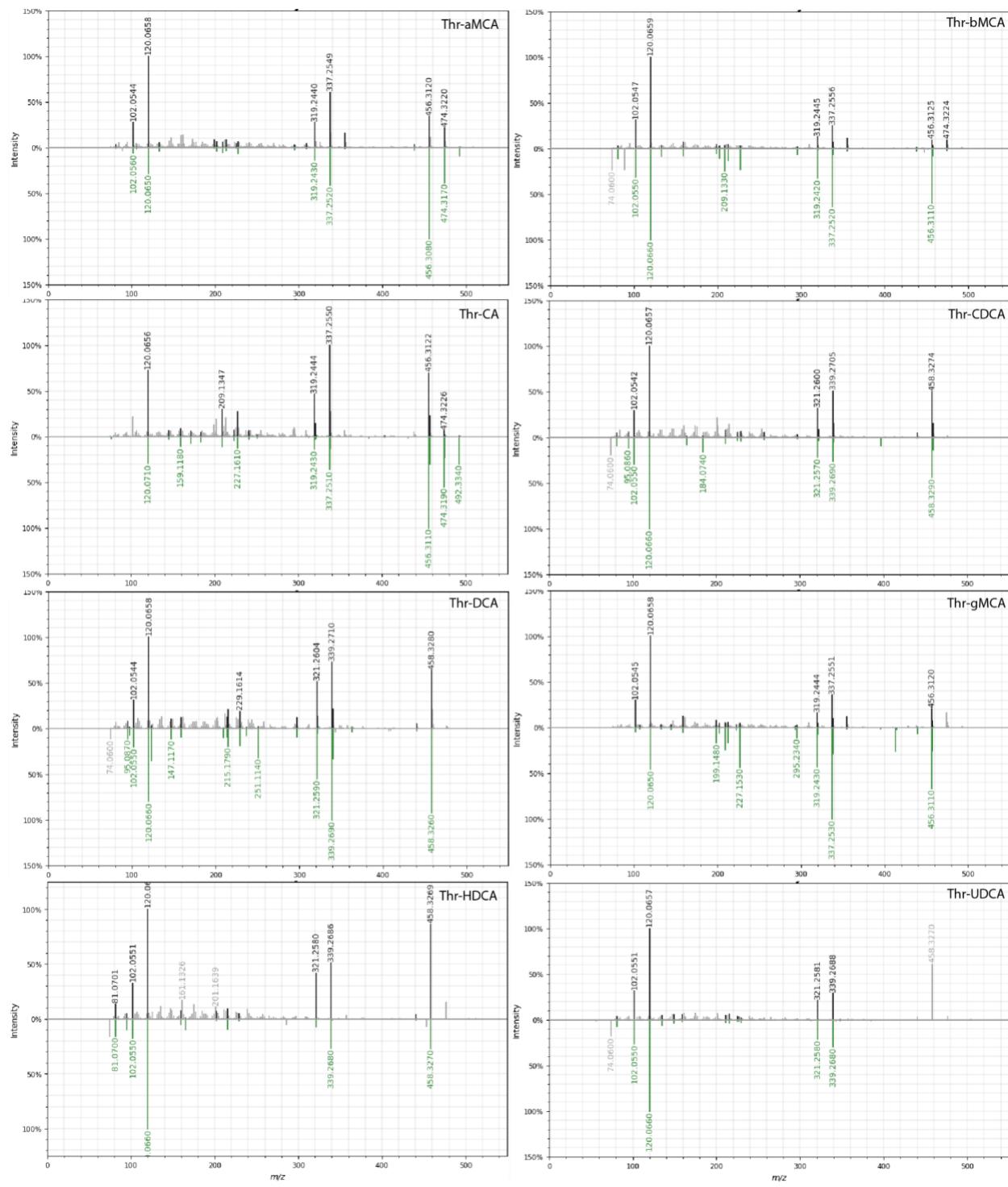
297
298
299

Supplementary Fig. 14: Mirror plots for MS/MS matches to Phe conjugated bile acids.



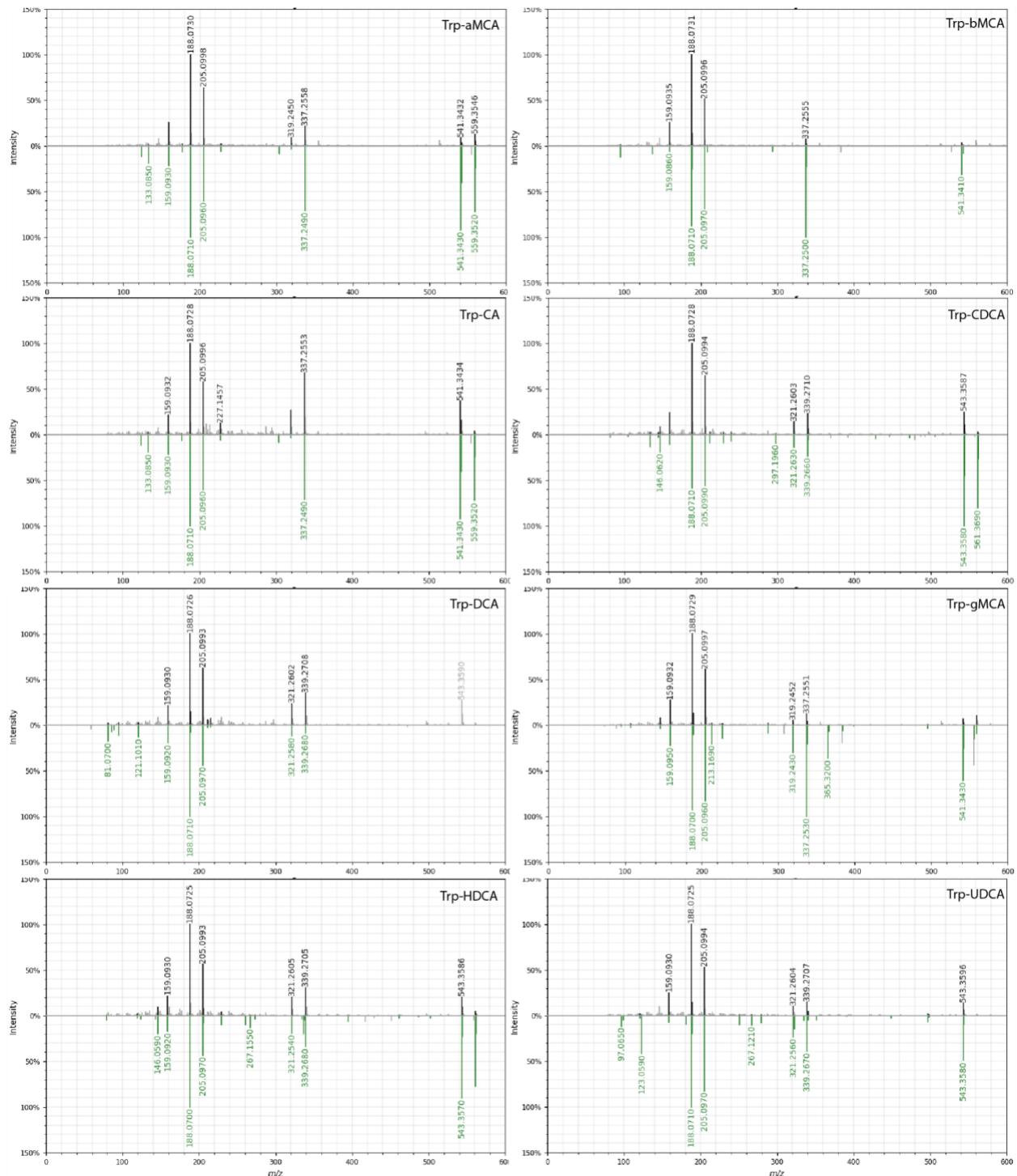
300
301
302

Supplementary Fig. 15: Mirror plots for MS/MS matches to Ser conjugated bile acids.



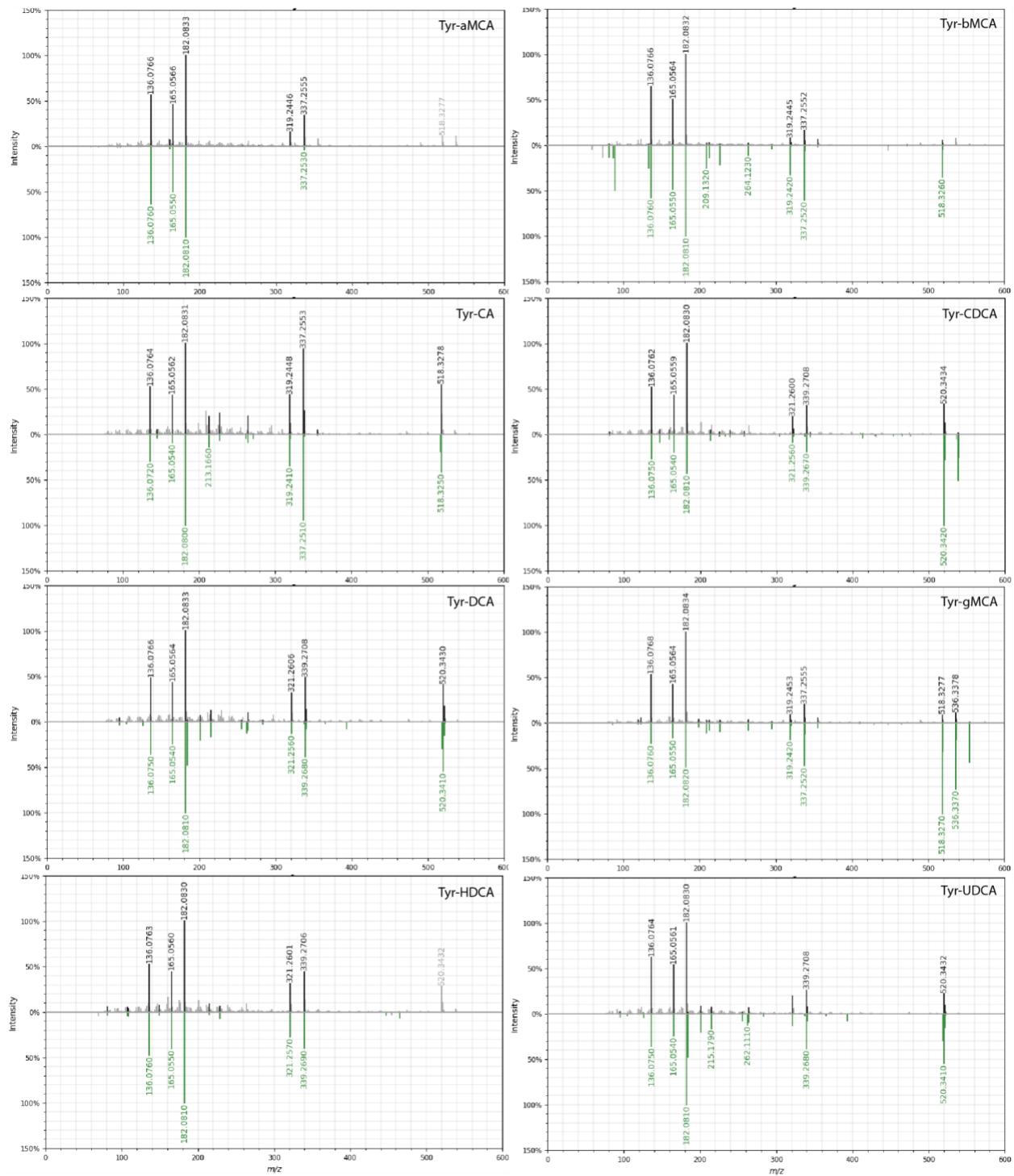
303
304
305

Supplementary Fig. 16: Mirror plots for MS/MS matches to Thr conjugated bile acids.



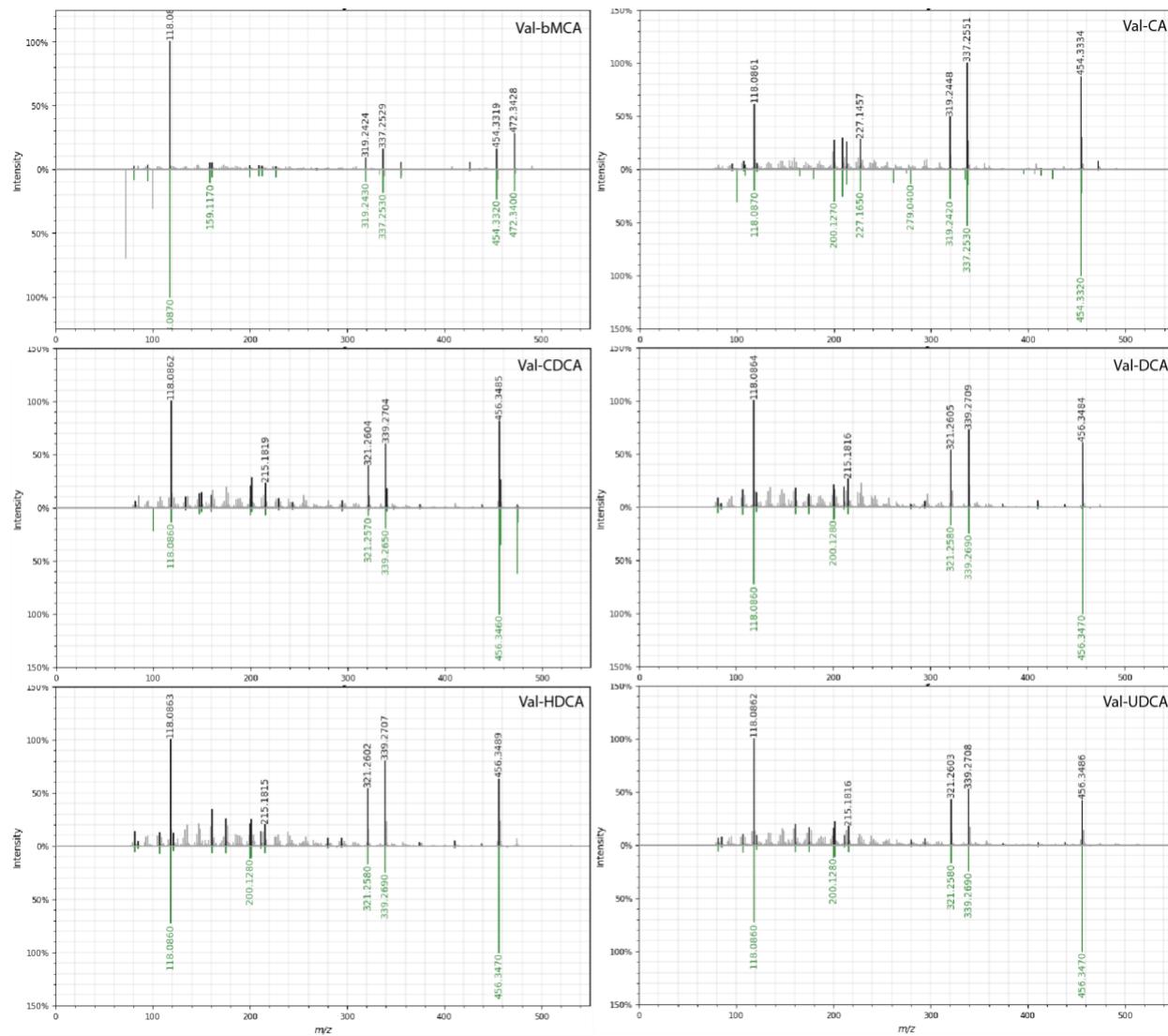
306
307
308

Supplementary Fig. 17: Mirror plots for MS/MS matches to Trp conjugated bile acids.



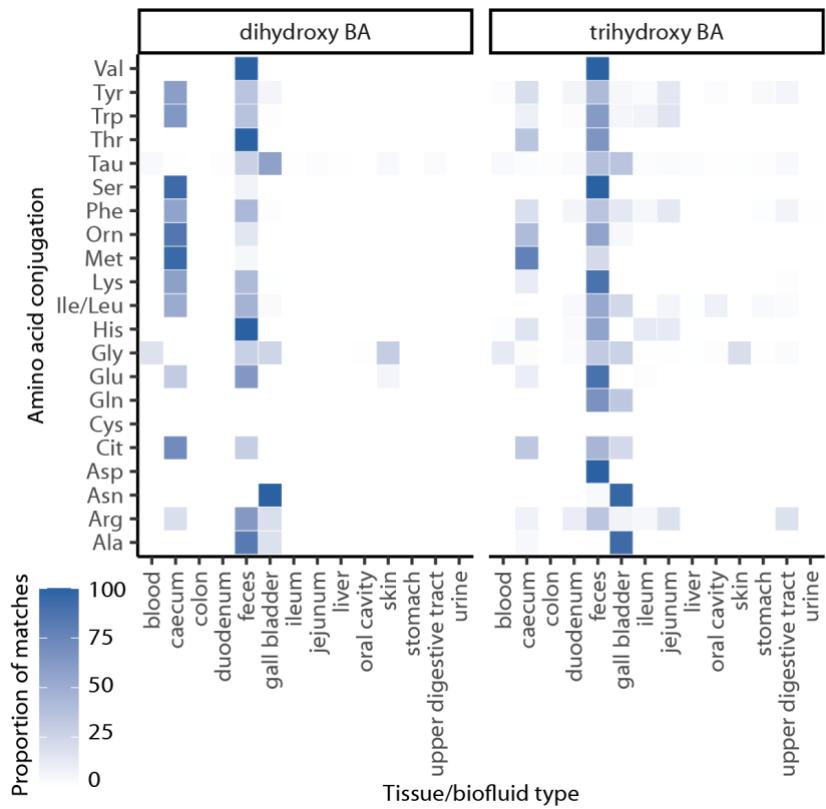
309
310
311

Supplementary Fig. 18: Mirror plots for MS/MS matches to Tyr conjugated bile acids.



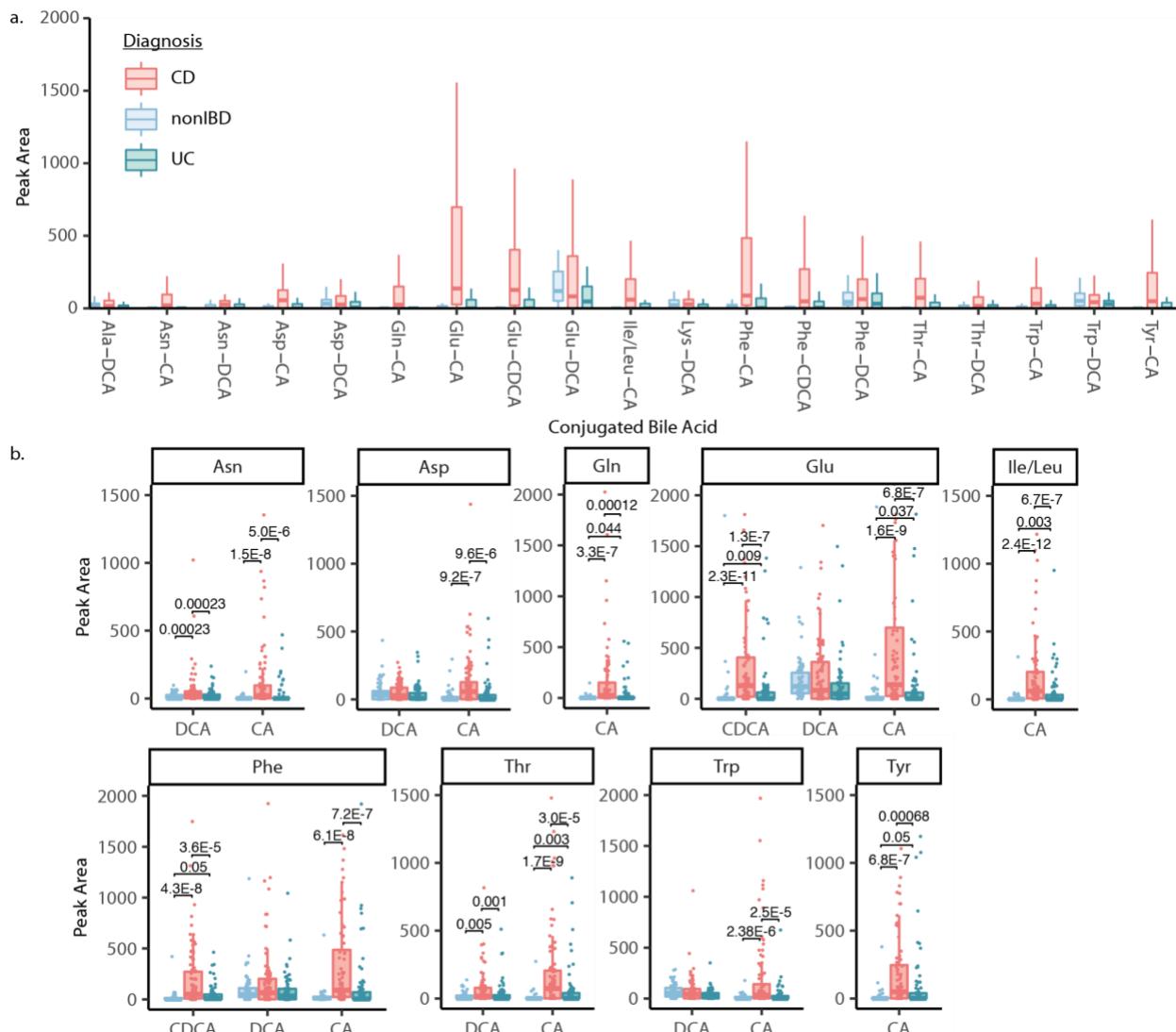
312
313
314
315

Supplementary Fig. 19: Mirror plots for MS/MS matches to Val conjugated bile acids.



316
317
318
319
320

Supplementary Fig. 20: Proportion of spectral matches per bile acid across tissue types and biofluids, faceted by number of hydroxyl groups. Each row or amino acid conjugation was binned and summed to one.

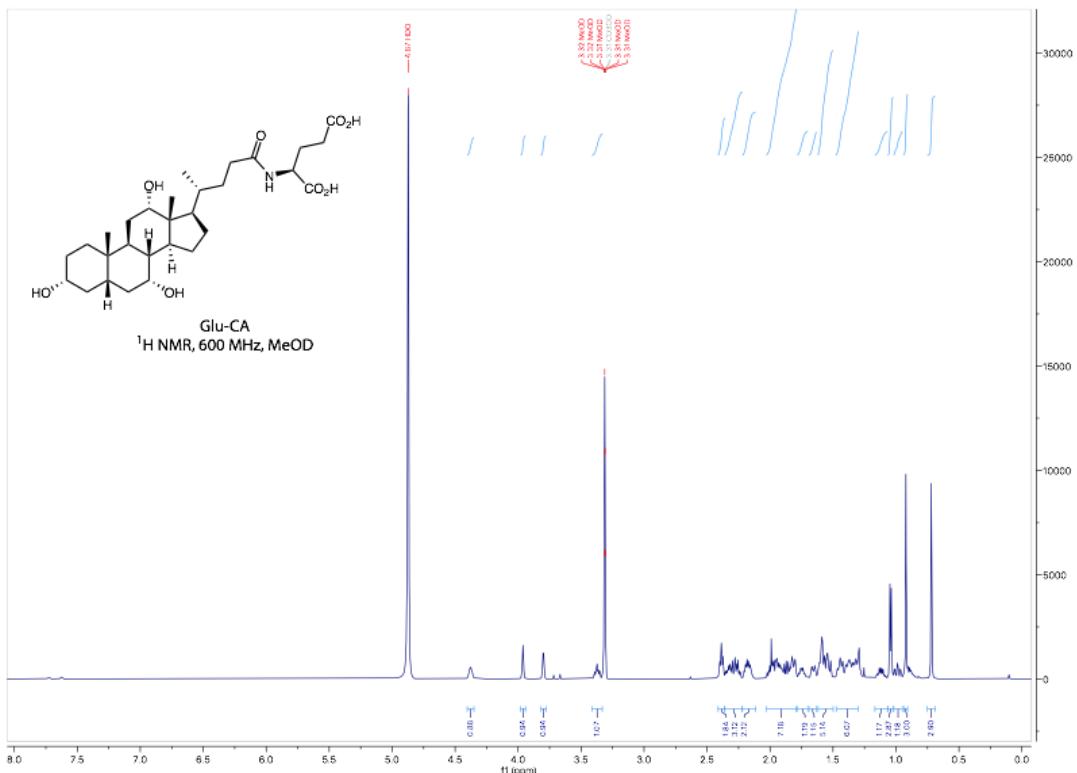


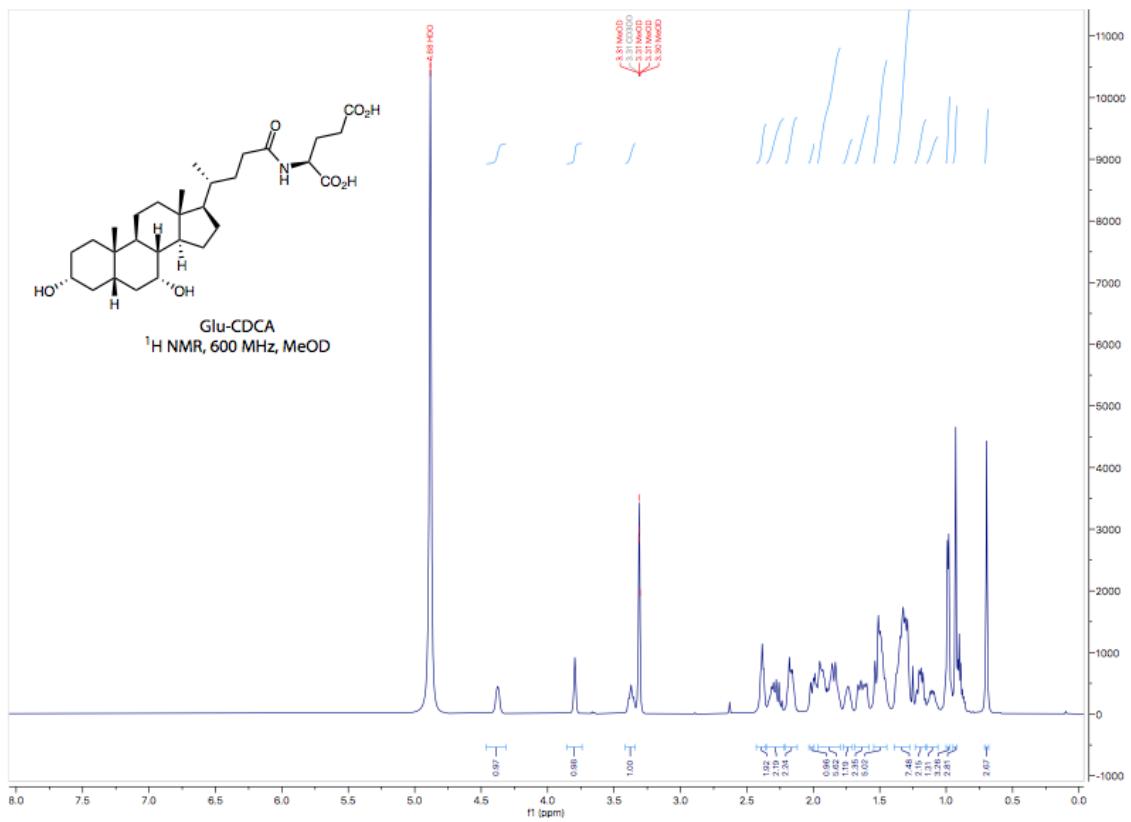
321
322 **Supplementary Fig. 21: Independent validation of new conjugated bile acids in PRISM**
323 **human IBD cohort.** a) Peak area abundances of conjugated bile acids detected in longitudinal
324 PRISM dataset.⁶ Boxes represent the interquartile range, center line is the median and whiskers
325 are 1.5 times the interquartile range. b) Peak area abundances of selected bile acids that were
326 higher in Crohn's and/or Ulcerative Colitis patients relative to non-IBD individuals, as determined
327 by pairwise two-sided Wilcoxon tests. Significance is shown using Benjamini-Hochberg corrected
328 p-values (n for CD = 68, n for non-IBD = 34 and n for UC = 53).

329
330
331
332
333
334
335
336
337

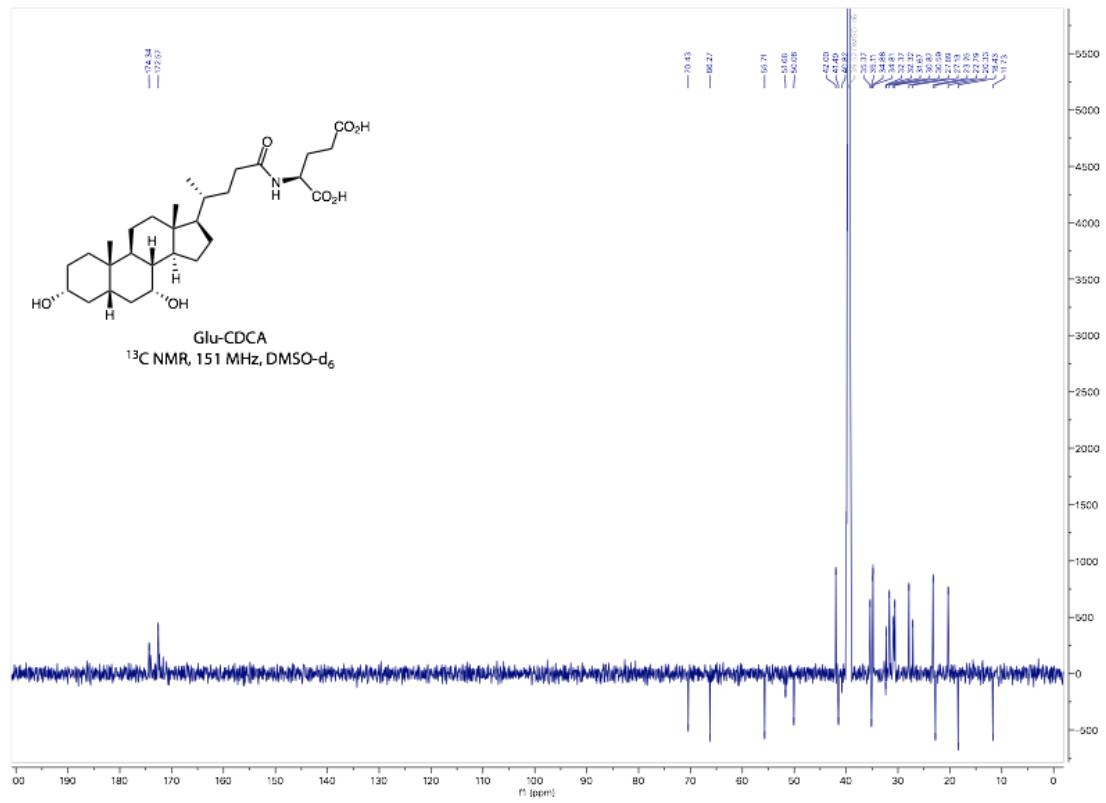
338 **Supplementary Data**

339 **^1H and ^{13}C NMR spectra of pure synthesized conjugated bile acids.**

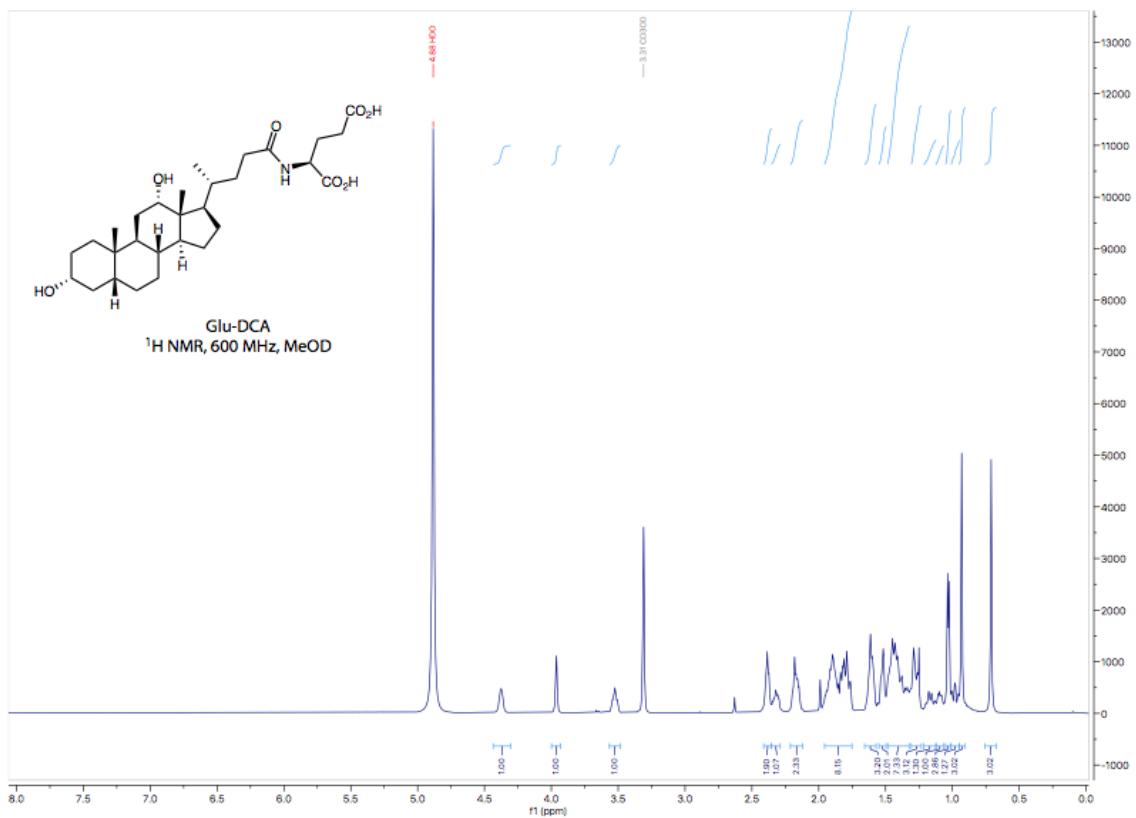




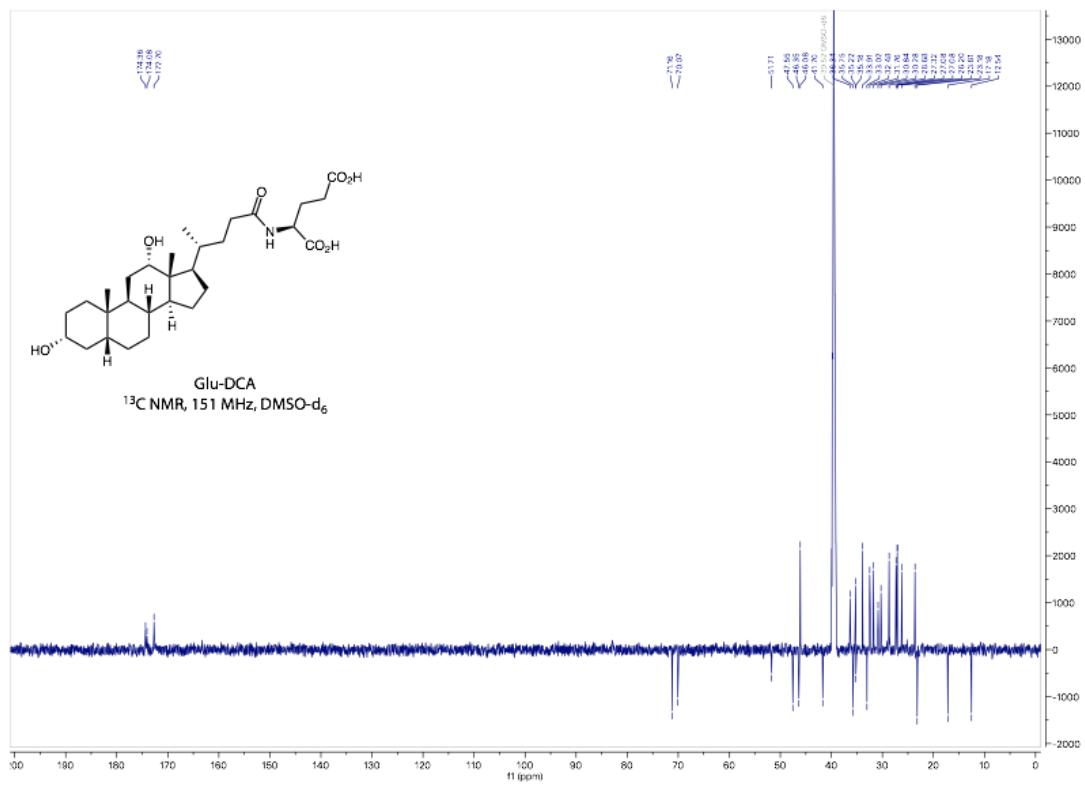
342



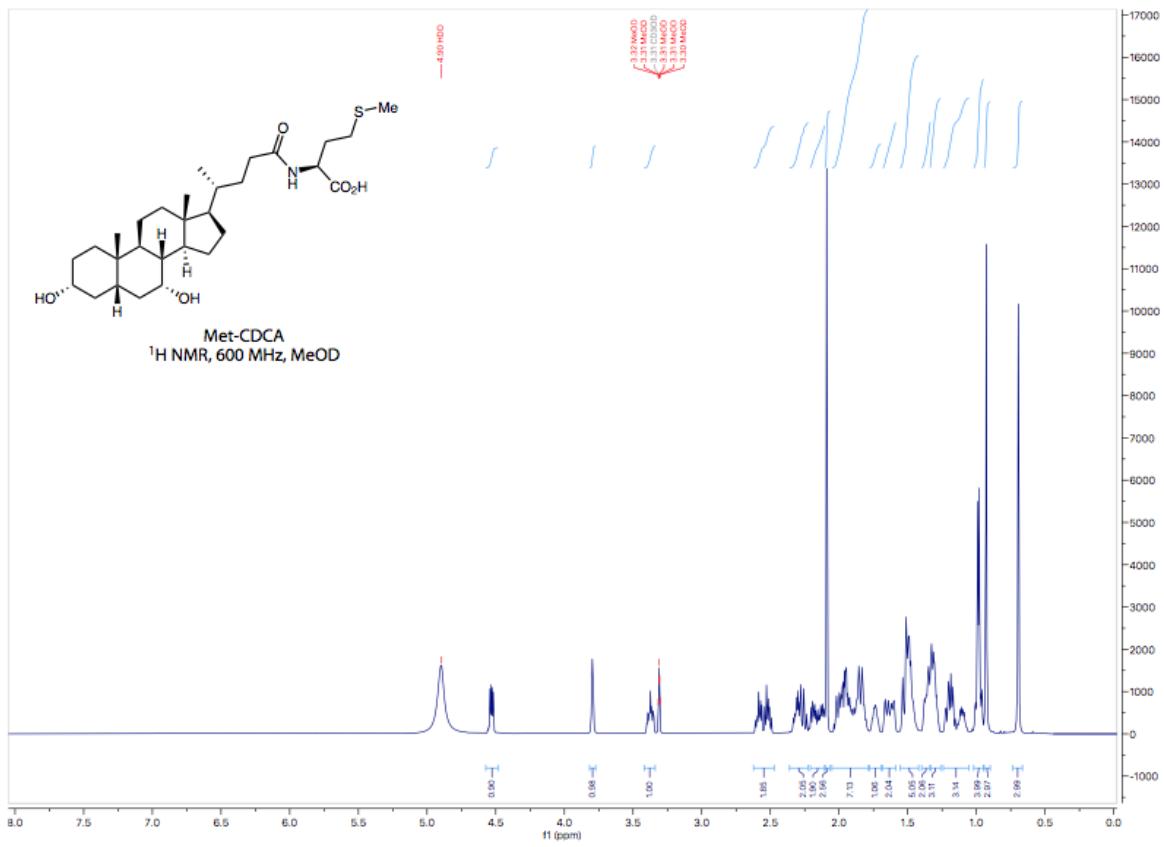
343



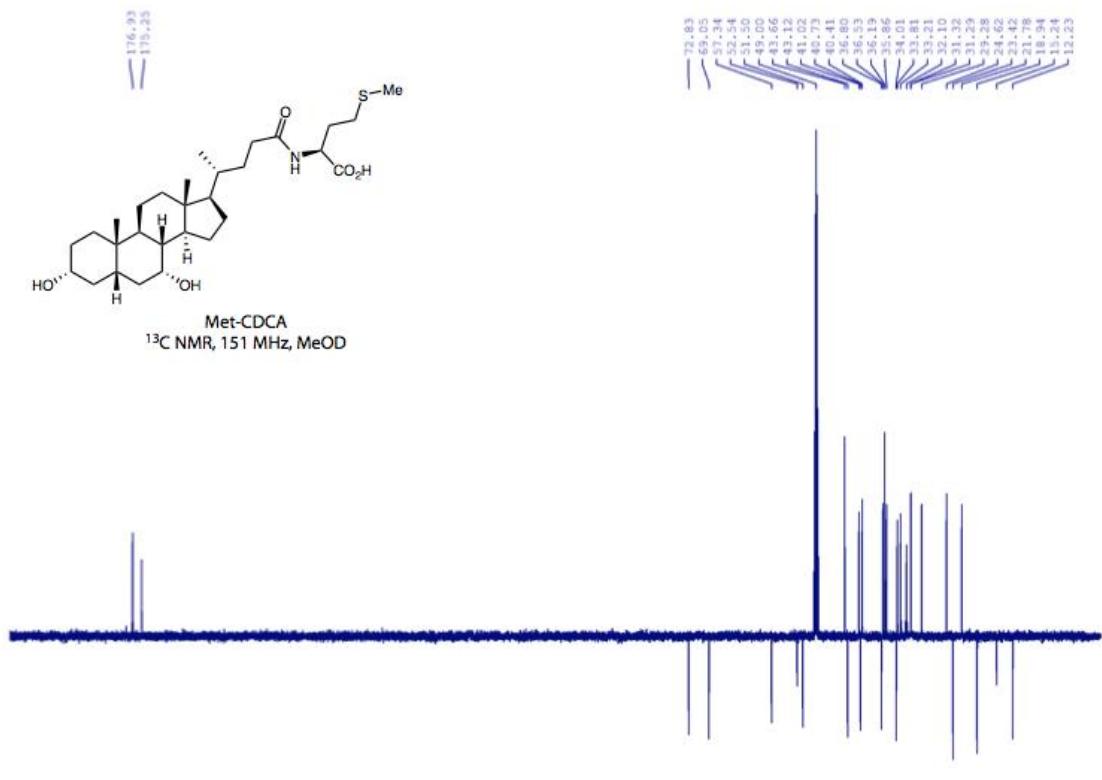
344



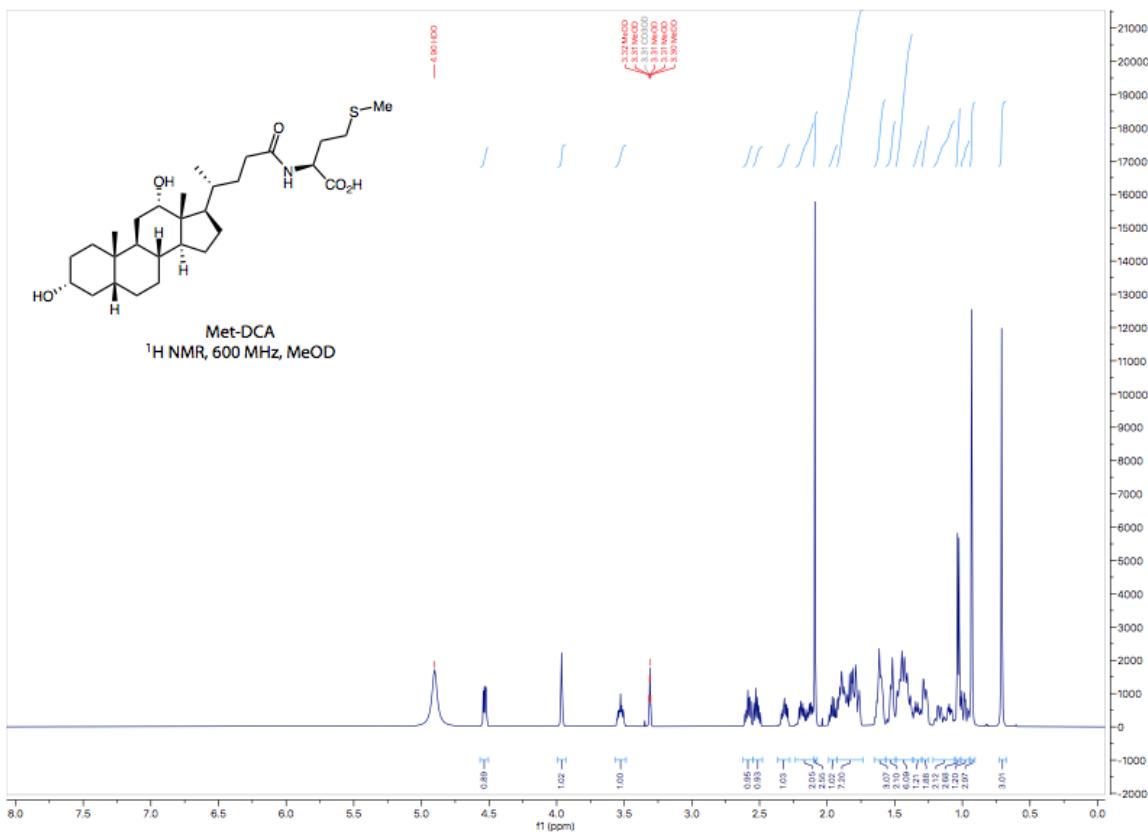
345



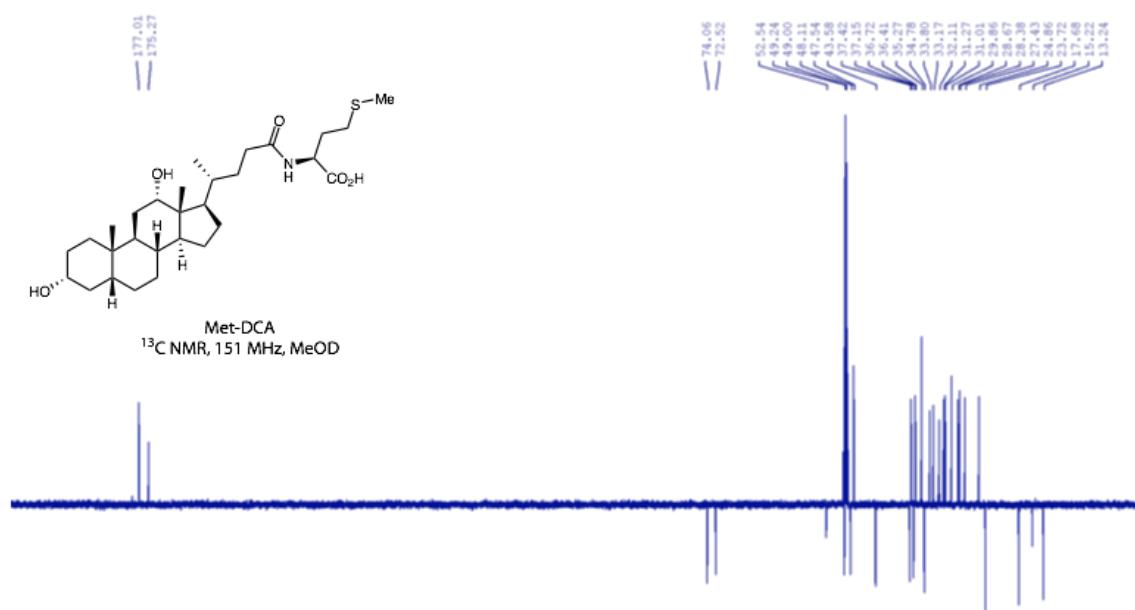
346



347

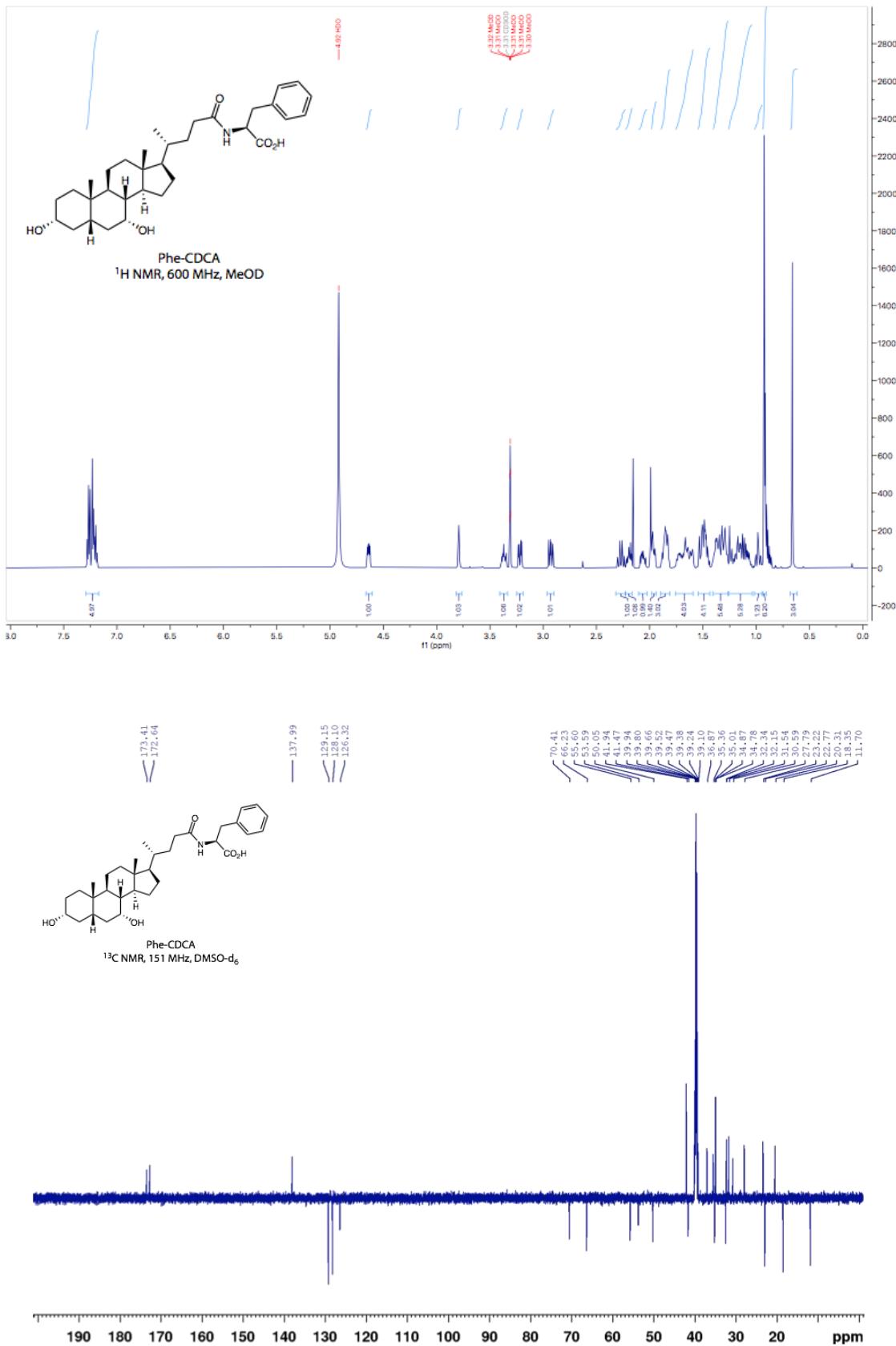


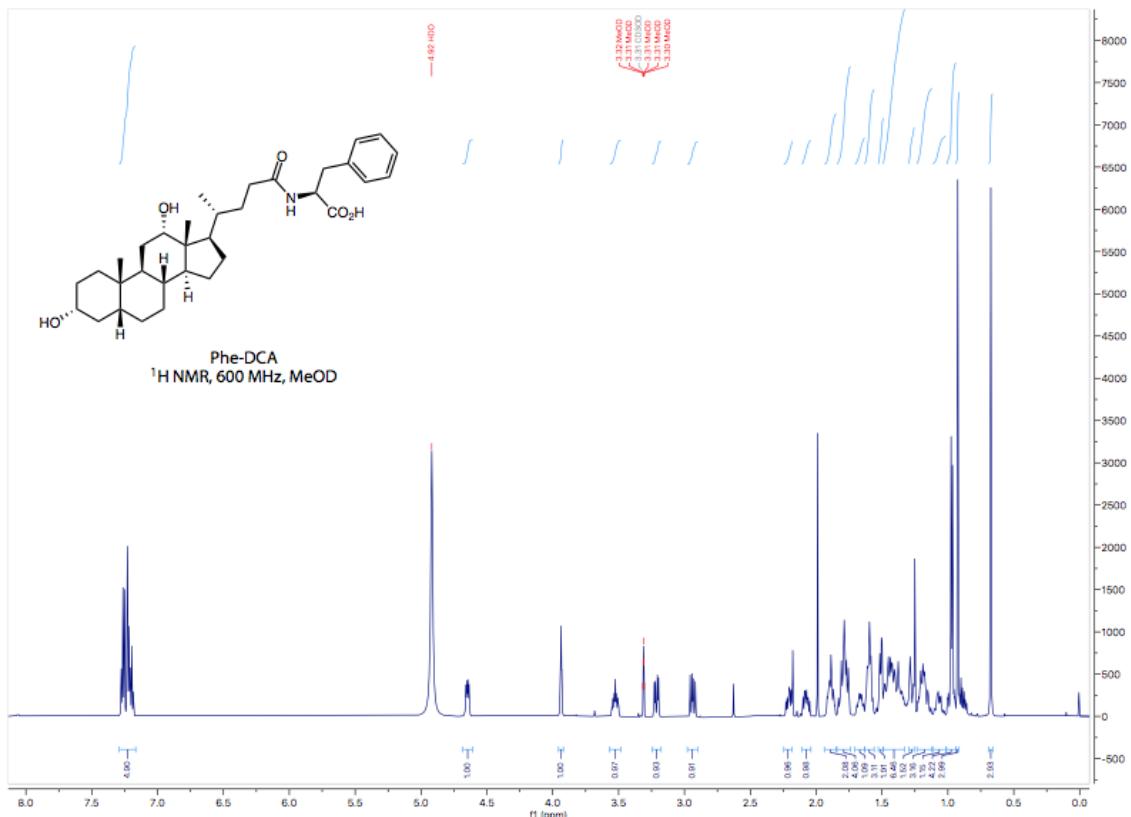
348



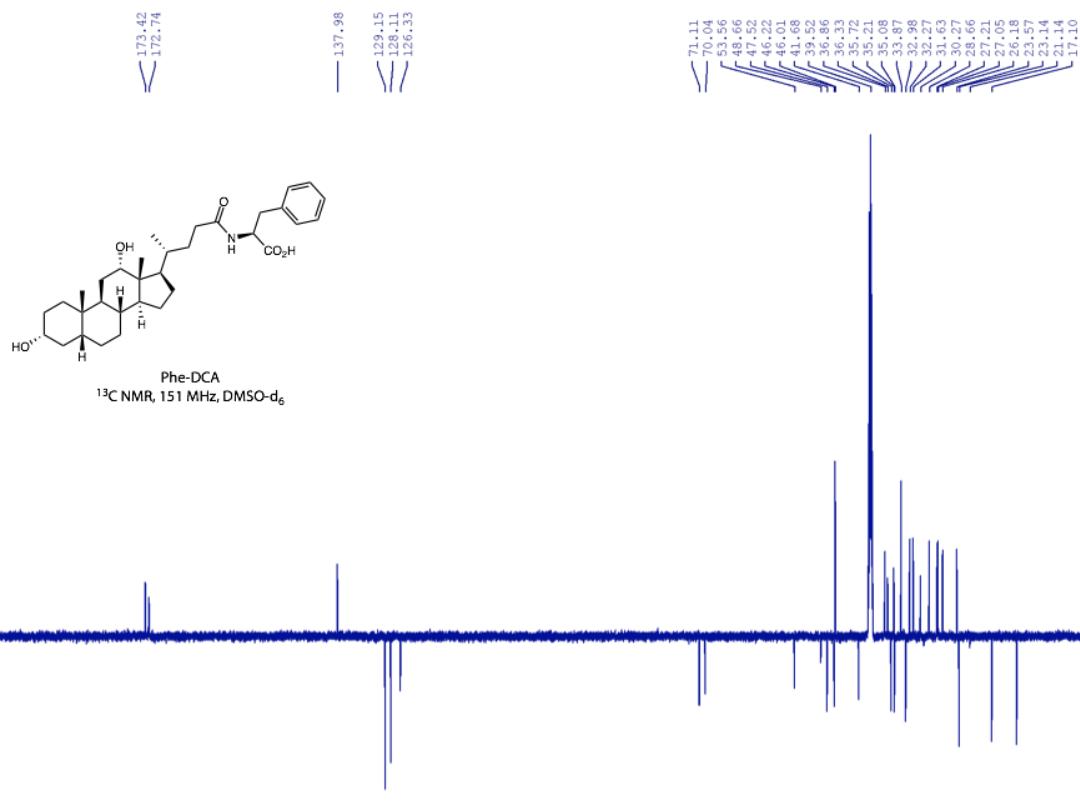
349



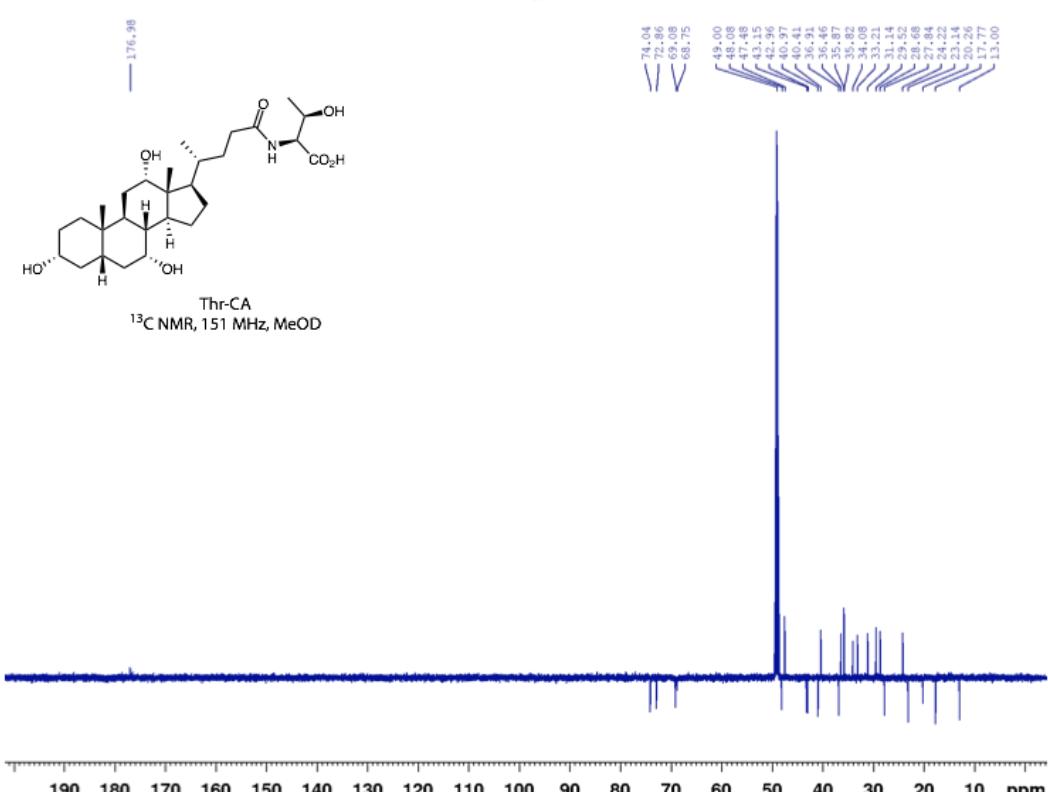
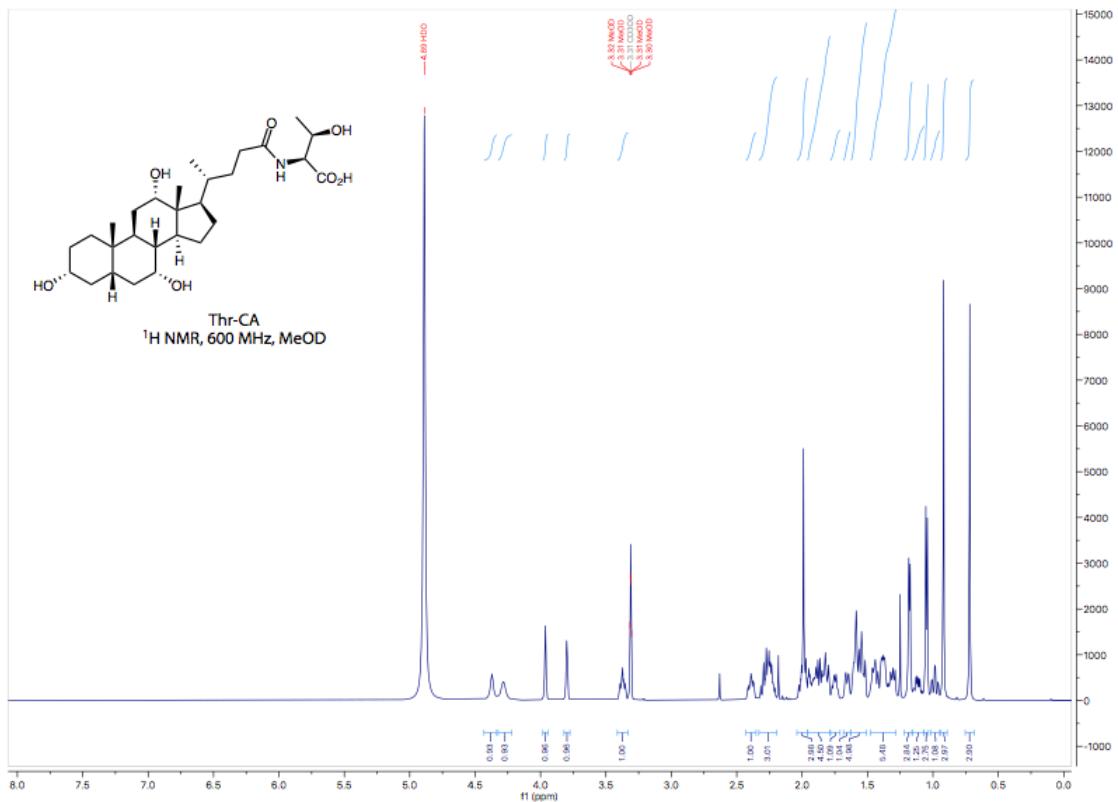


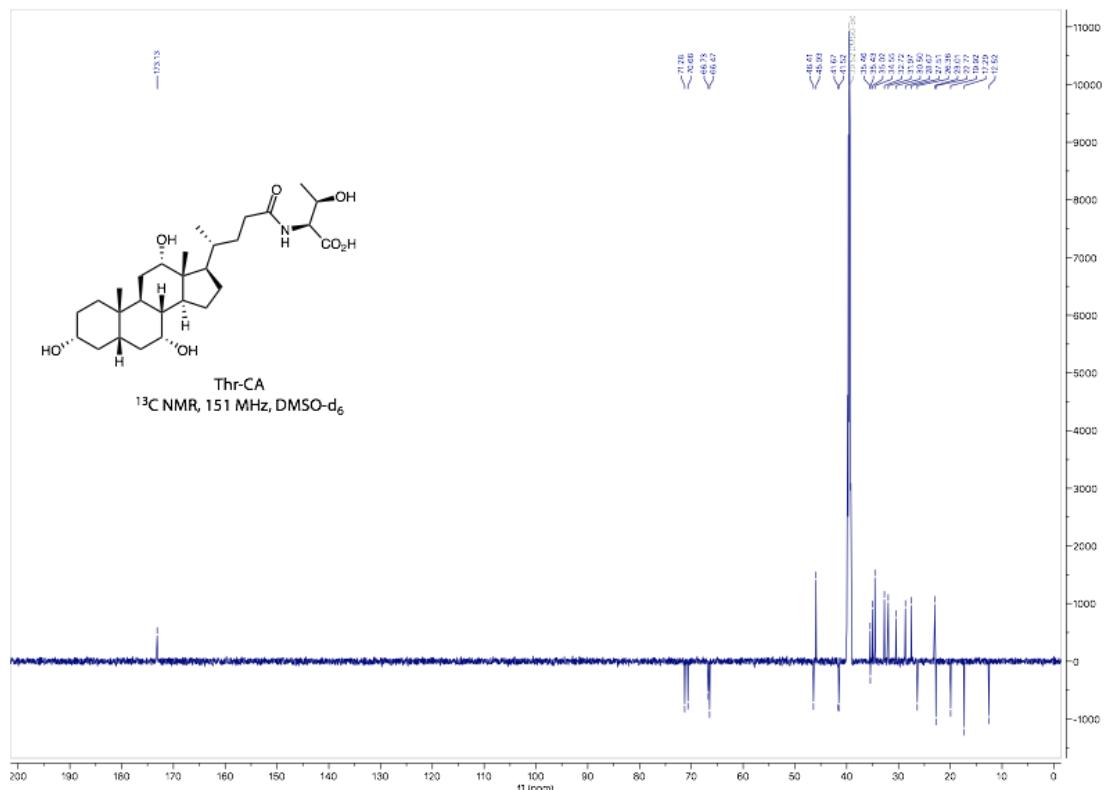


354

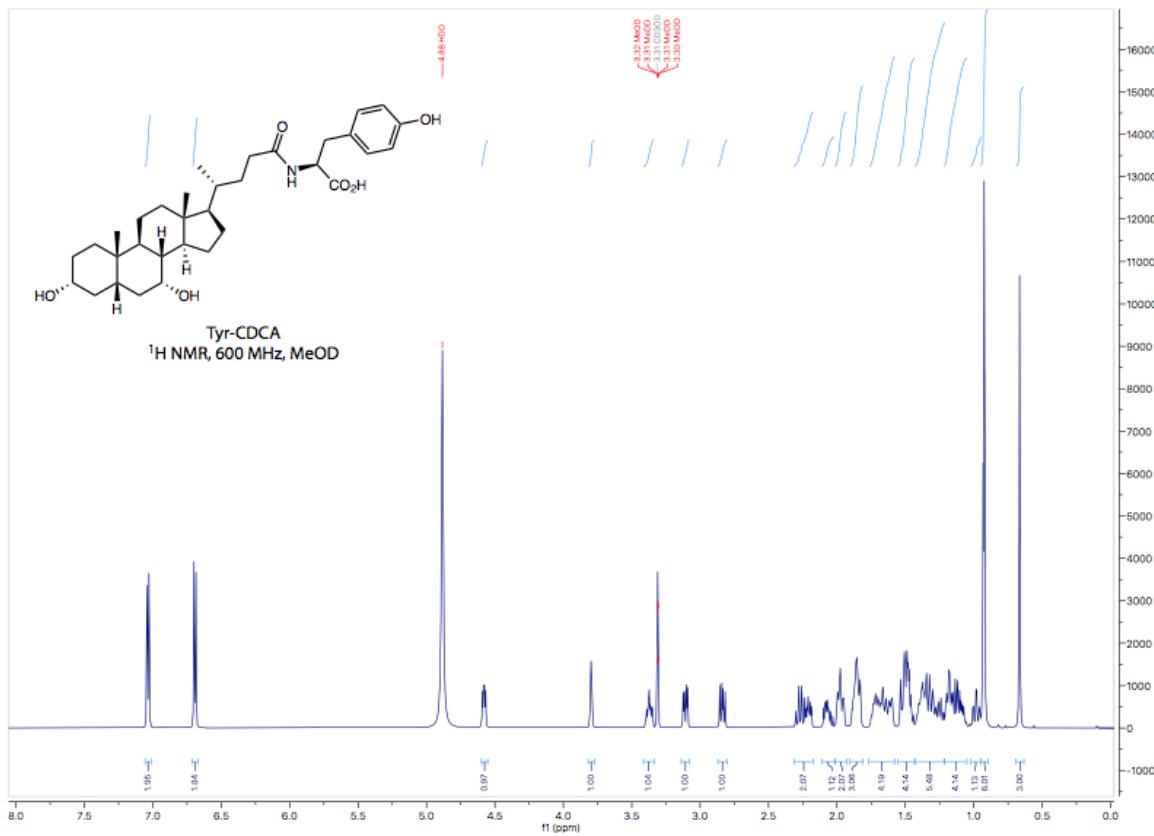


355

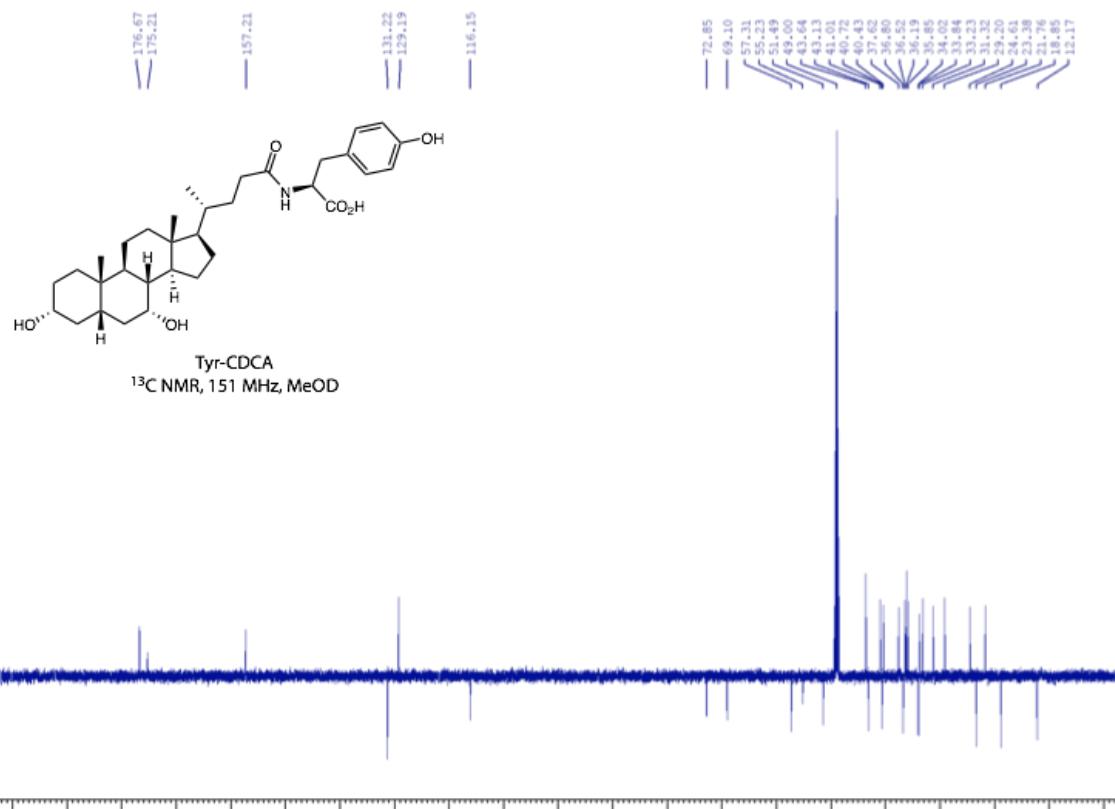




358



359



360

361 **Supplementary References**

362 1. McDonald, J. A. K. et al. Evaluation of microbial community reproducibility, stability and
363 composition in a human distal gut chemostat model. *J. Microbiol. Methods* 95, 167–174
364 (2013).

365 2. Katajamaa, M., Miettinen, J. & Oresic, M. MZmine: toolbox for processing and visualization of
366 mass spectrometry based molecular profile data. *Bioinforma. Oxf. Engl.* 22, 634–636 (2006).

367 3. Pluskal, T., Castillo, S., Villar-Briones, A. & Orešič, M. MZmine 2: Modular framework for
368 processing, visualizing, and analyzing mass spectrometry-based molecular profile data. *BMC
369 Bioinformatics* 11, 395 (2010).

370 4. Quinn, R. A. et al. Global chemical effects of the microbiome include new bile-acid
371 conjugations. *Nature* 579, 123–129 (2020).

372 5. Wang, M. et al. Interactive MS/MS Visualization with the Metabolomics Spectrum Resolver
373 Web Service. *bioRxiv* 2020.05.09.086066 (2020) doi:10.1101/2020.05.09.086066.

374 6. Franzosa, E. A. et al. Gut microbiome structure and metabolic activity in inflammatory bowel
375 disease. *Nat. Microbiol.* 4, 293–305 (2019).

376

377

378

379

380

381

382

383

384

385

386

387

388

389

390

391

392

393

394

395

396

397

398

399

400

401

402