Electronic Supplementary Material (ESI) for Molecular Omics.

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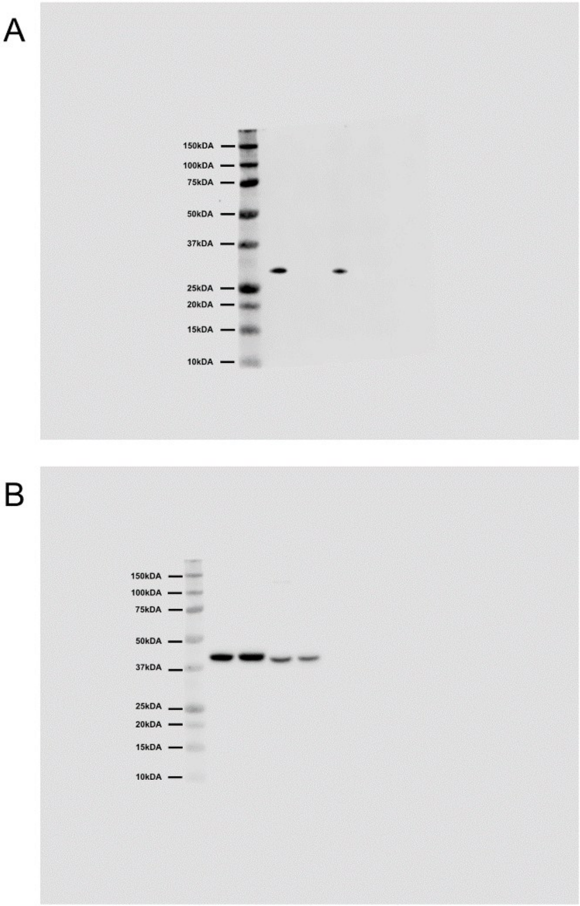
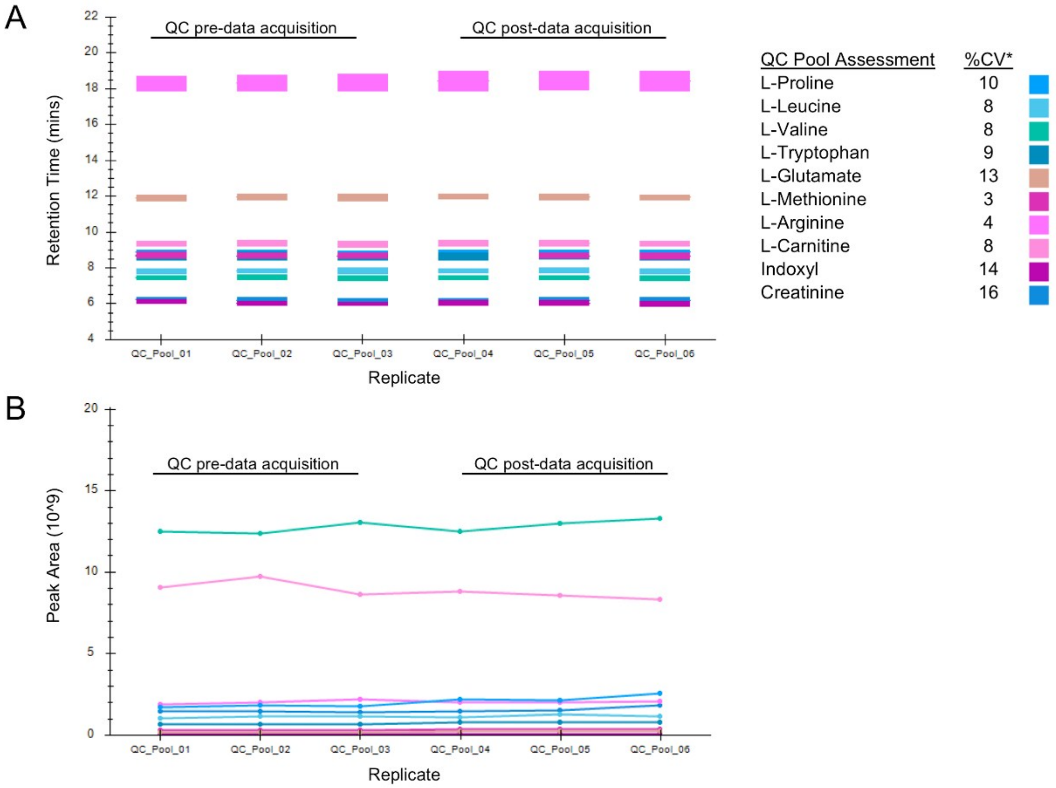
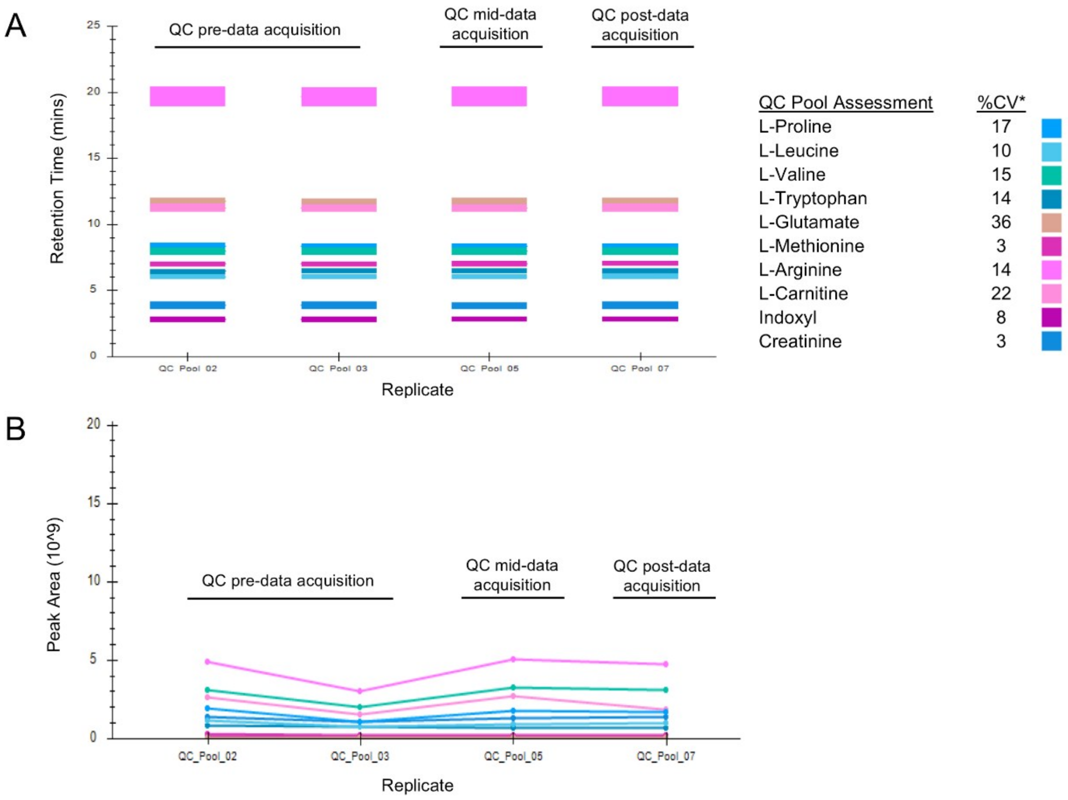


Fig. S1: Full immunoblots utilized for the generation of Fig. 1 to demonstrate loss of the specific Mblac1 immunoreactivity in KO mice. A. Full immunoblot for MBLAC1 1° antibody #4980. Left to right: cortex WT, cortex KO, liver WT, and liver KO. B. Full immunoblot for HRP-conjugated acting primary antibody. Left to right: cortex WT, cortex KO, liver WT, and liver KO.



* %CV was calculated within Progenesis QI by normalizing to all features.

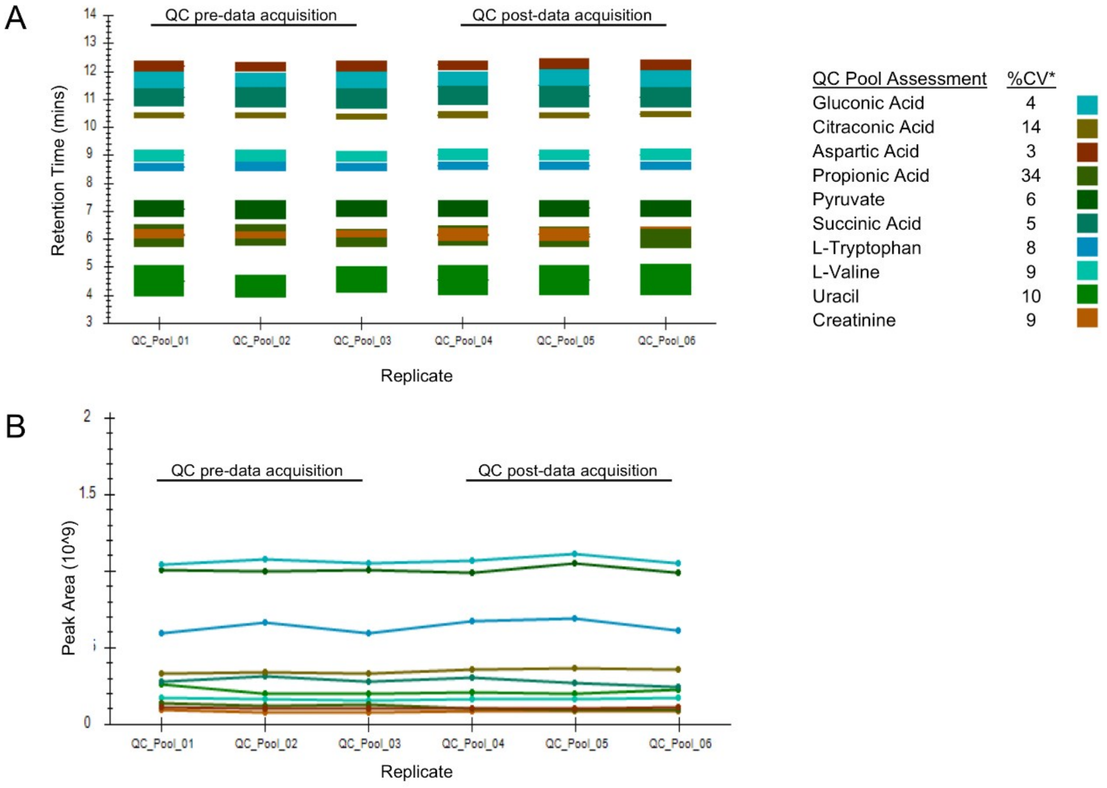
Fig. S2: Comparison of ten endogenous molecules in replicate injections of a pooled sample for QC assessment prior to and after the experimental sample data acquisition for *HILIC-POS collection, discovery sample set*. (A)The retention time and (B) peak area for the ten endogenous compounds are reliable and reproducible (compound legend indicates respective %CVs). Figures were generated in Skyline software.



QC Pool Assessment	%CV*	
L-Proline	17	🟦
L-Leucine	10	🟦
L-Valine	15	🟩
L-Tryptophan	14	🟦
L-Glutamate	36	🟫
L-Methionine	3	🟪
L-Arginine	14	🟪
L-Carnitine	22	🟪
Indoxyl	8	🟪
Creatinine	3	🟦

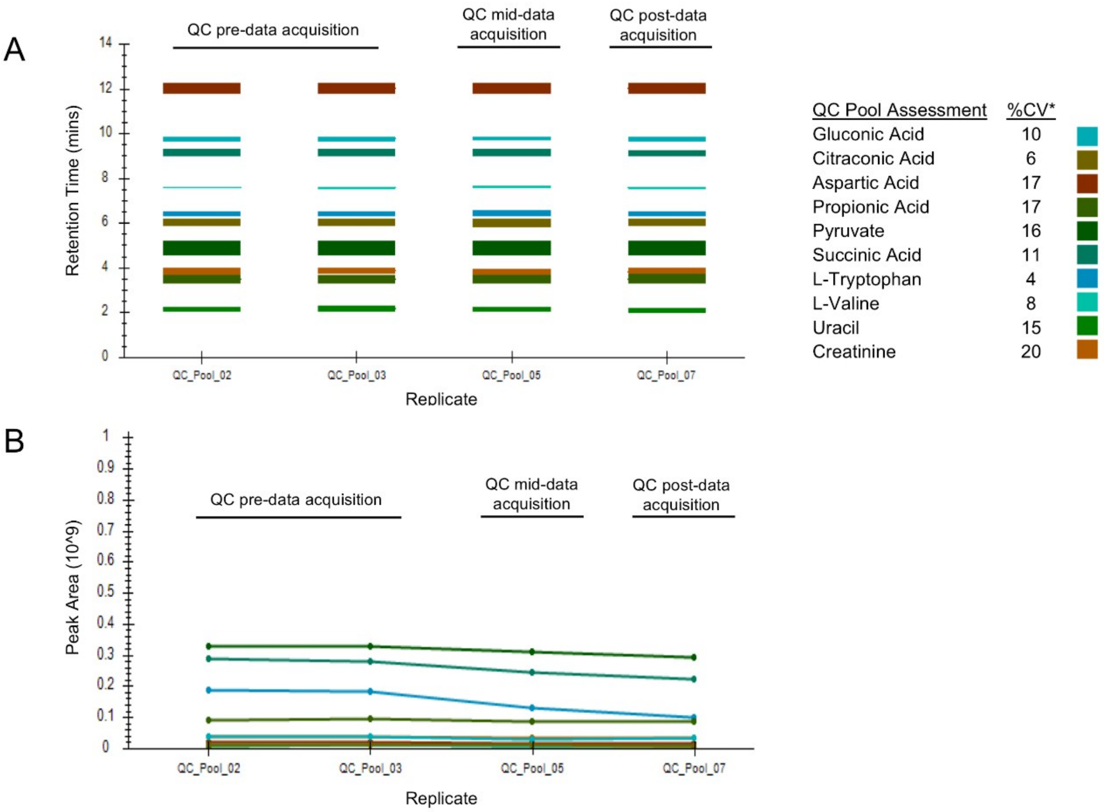
* %CV was calculated within Progenesis QI by normalizing to all features.

Fig. S3: Comparison of ten endogenous molecules in replicate injections of a pooled sample for QC assessment prior to, during, and after the experimental sample data acquisition for *HILIC-POS collection, validation sample set*. (A)The retention time and (B) peak area for the ten endogenous compounds are reliable and reproducible (compound legend indicates respective %CVs). Figures were generated in Skyline software.



* %CV was calculated within Progenesis QI by normalizing to all features.

Fig. S4: Comparison of ten endogenous molecules in replicate injections of a pooled sample for QC assessment prior to and after the experimental sample data acquisition for *HILIC-NEG collection, discovery sample set*. (A)The retention time and (B) peak area for the ten endogenous compounds are reliable and reproducible (compound legend indicates respective %CVs). Figures were generated in Skyline software.



* %CV was calculated within Progenesis QI by normalizing to all features.

Fig. S5: Comparison of ten endogenous molecules in replicate injections of a pooled sample for QC assessment prior to, during, and after the experimental sample data acquisition for *HILIC-NEG collection, validation sample set*. (A)The retention time and (B) peak area for the ten endogenous compounds are reliable and reproducible (compound legend indicates respective %CVs). Figures were generated in Skyline software.

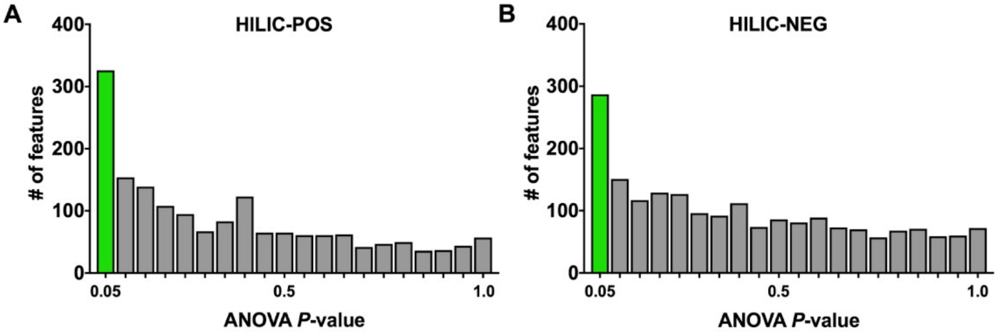


Fig. S6: Frequency histograms showing the distribution of nominal ANOVA *P*-values for the discovery datasets for A. HILIC-POS and B. HILIC-NEG. Green bar represents the total number of features declared to be significant with a nominal *P*-value ≤ 0.05, 326 and 287 features for HILIC-POS and HILIC-NEG respectively.

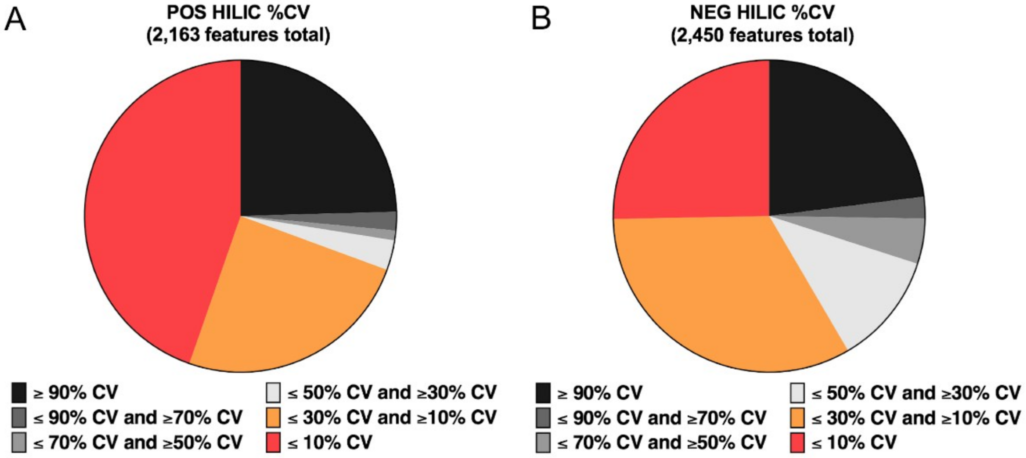


Fig. S7: Features detected by untargeted UPLC-MS/MS approach binned according to minimum percent coefficient of variance (min %CV), A. HILIC-POS and B. HILIC-NEG. For both ion modes, about 60% of the detected features have a min %CV ≤ 30%.

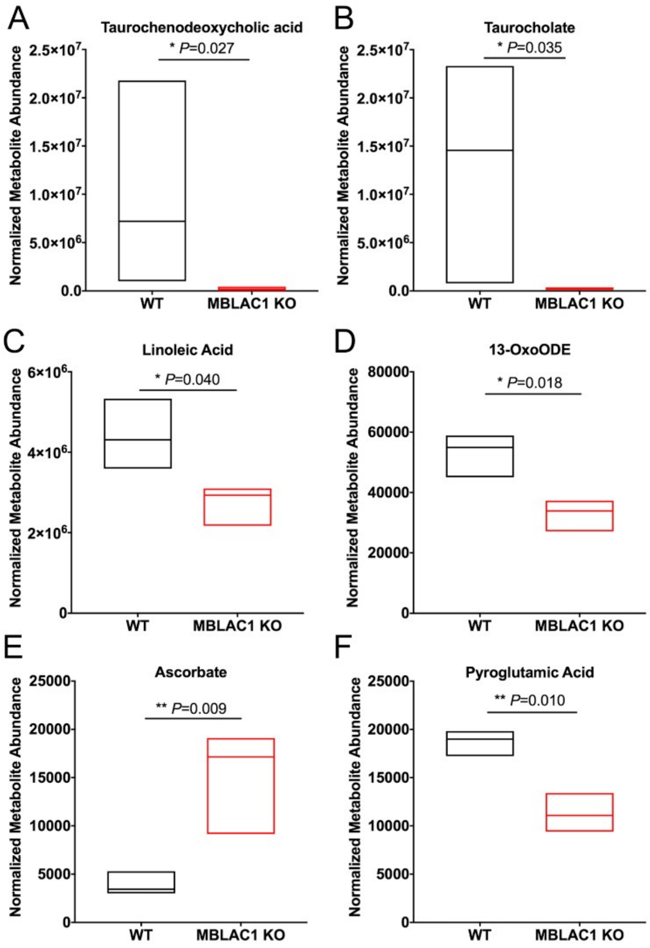
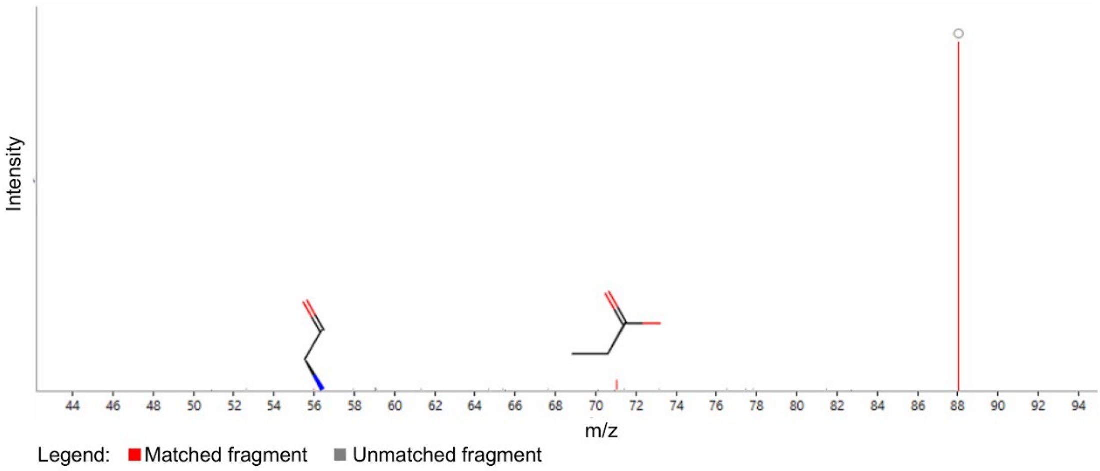


Fig. S8: Tentatively annotated features nominated in the discovery dataset as significantly impacted by loss of MBLAC1. A-B. Features within the taurine/primary bile acid pathway, A. taurochendeoxycholic acid (*P*-value=0.027) and B. taurocholate (*P*-value=0.035) are both significantly reduced in MBLAC1 KO serum. C-D. Features with in the linoleate metabolism pathway, C. linoleic acid (*P*-value=0.04) and D. 13-OxoODE (*P*-value=0.018). E-F. Features within the glutathione metabolism pathway, E. ascorbate (*P*-value=0.009) and F. pyroglutamic acid (*P*-value=0.01). Normalized metabolite abundancies depicted in box plots with full range of variation (box with line at median with minimum_maximum), nominal *P*-value determined by Progenesis QI ANOVA analysis of the initial, discovery serum dataset.

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.



* Instrument method scans low end of mass range at 70 Da, therefore we do not expect ions to be detected below 70 Da.

Fig. S9: Experimentally measured (shown above): Putative identification: **L-alanine**
Progenesis Fragmentation Score: 17.7*
Reference (not shown) matched fragments in red): HMDB: **L-alanine**: $C_3H_7NO_2$

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Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

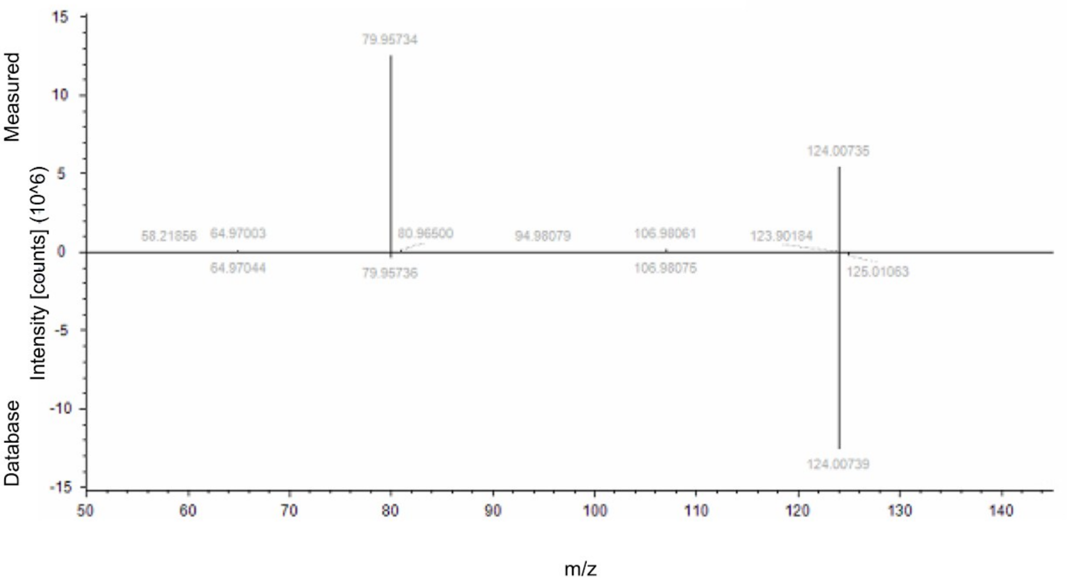


Fig. S10: Experimentally measured (Top): Putative identification**: Taurine**:
Compound Discoverer Fragmentation Score: 92.4
Reference (Bottom): mzCloud library: **Taurine**: C2H7NO3S

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

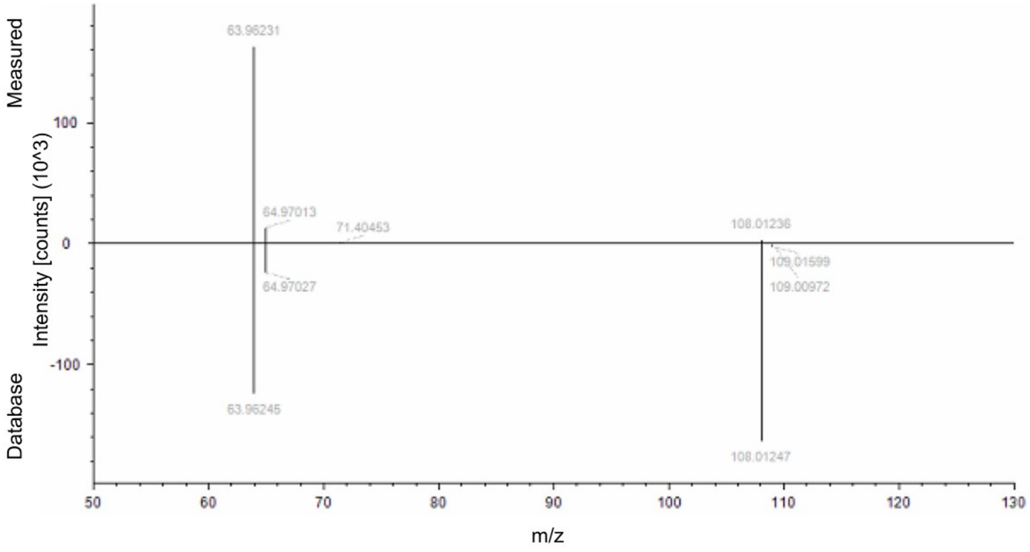


Fig. S11: Experimentally measured (Top): Putative identification: **Hypotaurine**:
Compound Discoverer Fragmentation Score: 82.4
Reference (Bottom): mzCloud library: **Hypotaurine**: C2H7NO2S

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

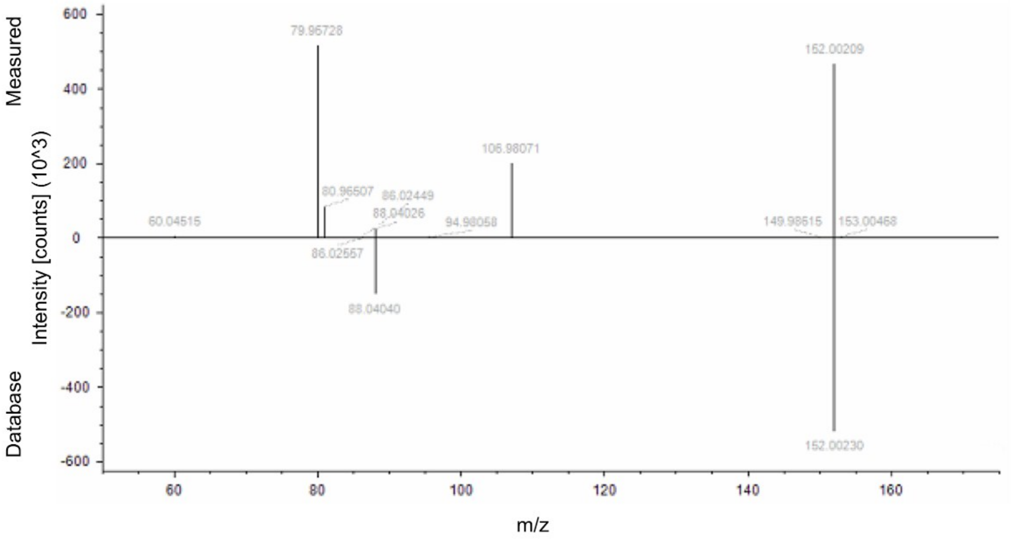


Fig. S12: Experimentally measured (Top): Putative identification: **3-Sulfinoalanine (syn: L-Cysteinesulfinic acid)**:
Compound Discoverer Fragmentation Score: 60.1
Reference (Bottom): mzCloud library: **L-Cysteinesulfinic acid**: C3H7NO4S

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

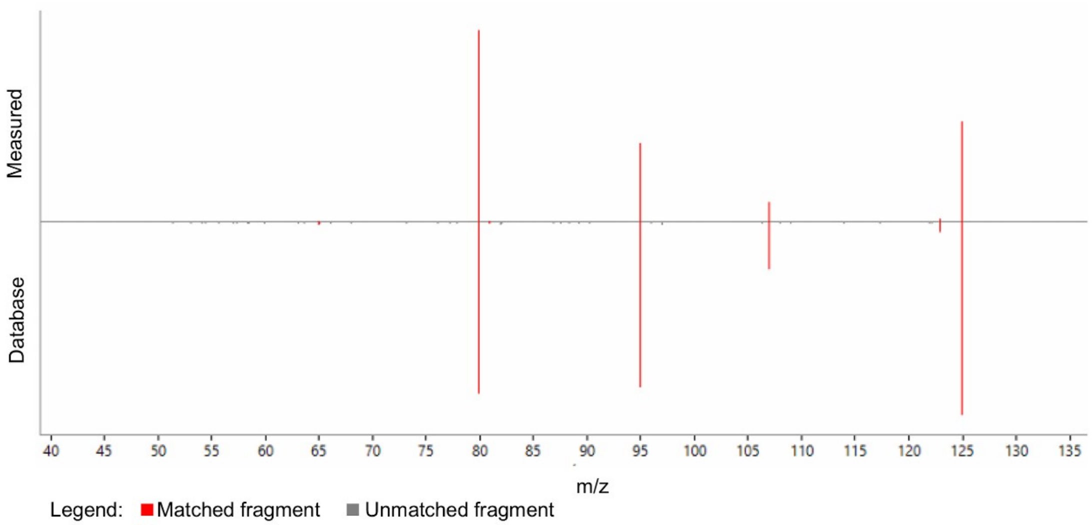
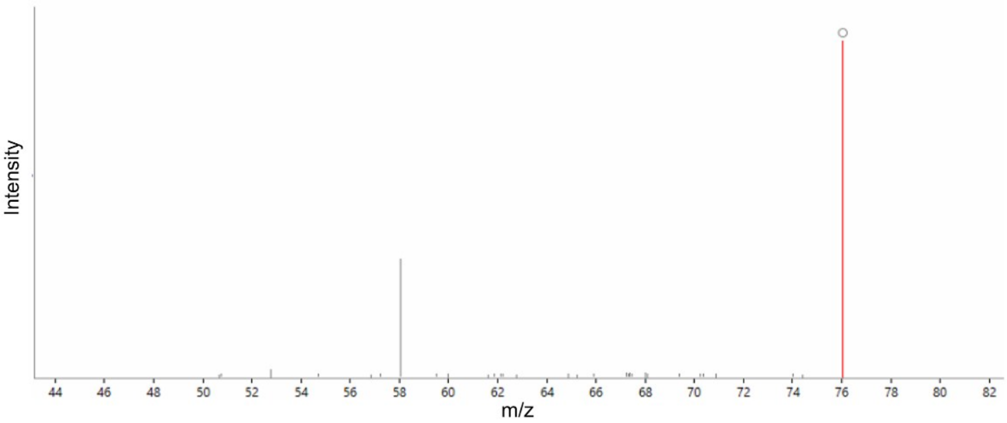


Fig. S13: Experimentally measured (Top): Putative identification: **2-Hydroxyethanesulfonate**: Progenesis Fragmentation Score: 92.6
Reference (Bottom): In-house library: **2-Hydroxyethanesulfonate**: $C_2H_6O_4S$

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.



Legend: 🟥 Matched fragment ■ Unmatched fragment

* Instrument method scans low end of mass range at 70 Da, therefore we do not expect ions to be detected below 70 Da.

Fig. S14: Experimentally measured (shown above): Putative identification: **Glycine**
Progenesis Fragmentation Score: 0.0*
Reference (not shown) matched fragments in red: HMDB: **Glycine**: $C_2H_5NO_2$

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

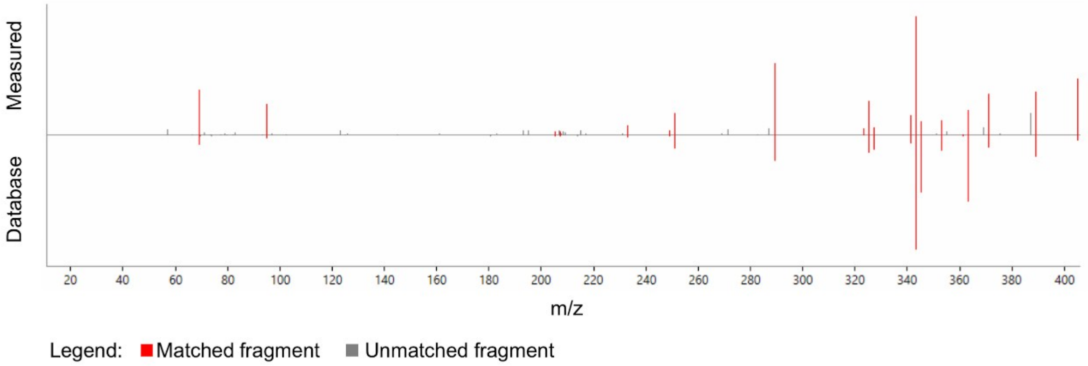


Fig. S15: Experimentally measured (Top): Putative identification: **Cholic Acid**:
Progenesis Fragmentation Score: 82
Reference (Bottom): In-house library: **Cholic Acid**: $C_{24}H_{40}O_5$

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

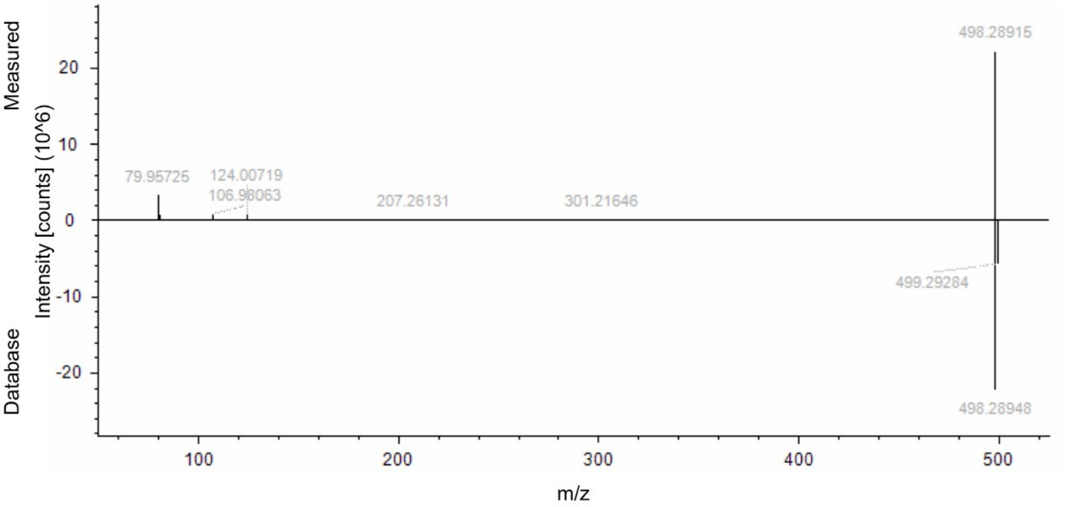


Fig. S16: Experimentally measured (Top): Putative identification: **Taurochenodeoxycholic acid**: Compound Discoverer Fragmentation Score: 81.3
Reference (Bottom): mzCloud library: **Taurochenodeoxycholic acid**: $C_{26}H_{45}NO_6S$

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

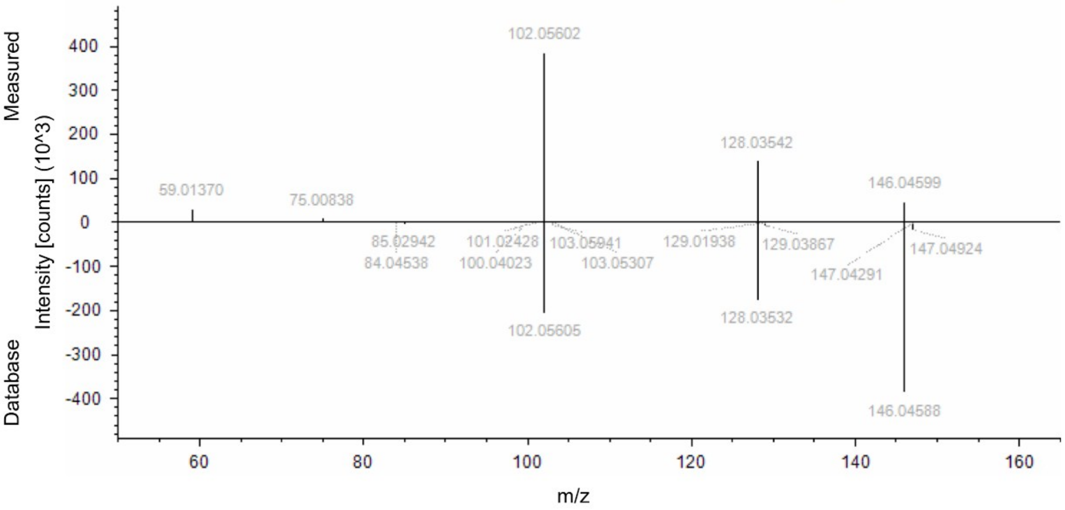


Fig. S17: Experimentally measured (Top): Putative identification: **L-Glutamate**:
Compound Discoverer Fragmentation Score: 89.4
Reference (Bottom): mzCloud library: **L-Glutamic acid**: C5H9NO4

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

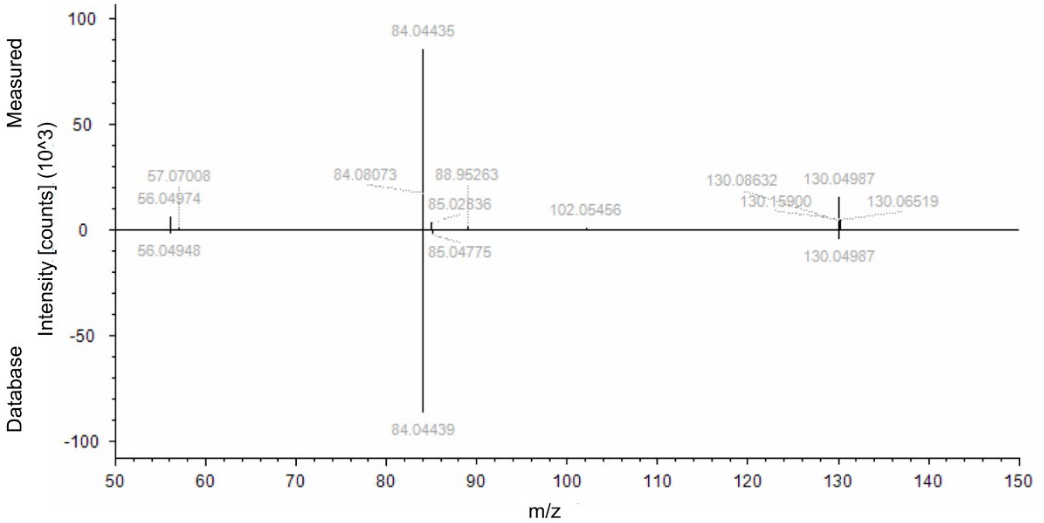


Fig. S18: Experimentally measured (Top): Putative identification: **Pyroglutamic acid**: Compound Discoverer Fragmentation Score: 83.0
Reference (Bottom): mzCloud library: **Pyroglutamic acid**: C5H7NO3

Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

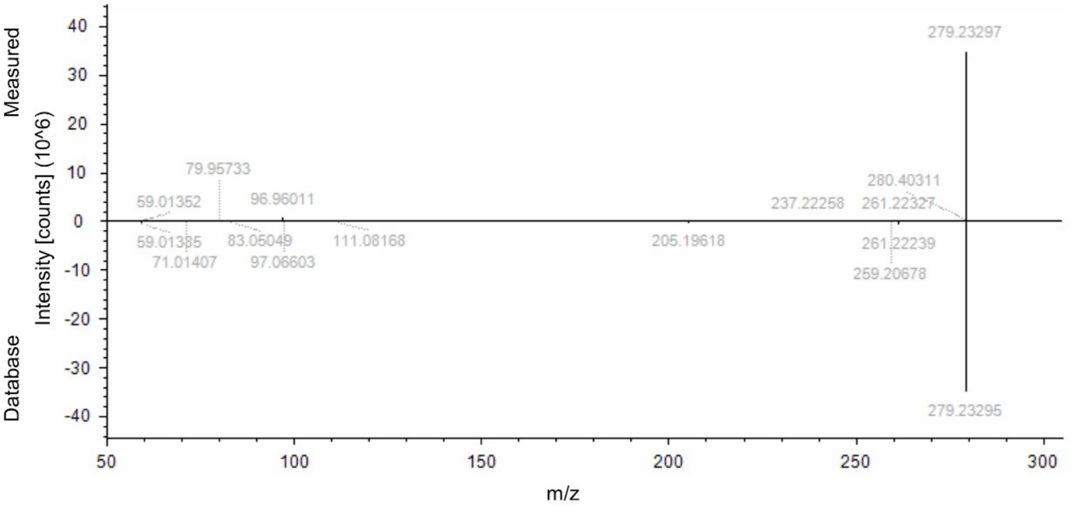


Fig. S19: Experimentally measured (Top): Putative identification: **Linoleic acid**:
Compound Discoverer Fragmentation Score: 87.1
Reference (Bottom): mzCloud library: **Linoleic acid**: $C_{18}H_{32}O_2$

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Experimental fragmentation data compared to spectral library match for level 2 (L2) putatively identified features in Table 1.

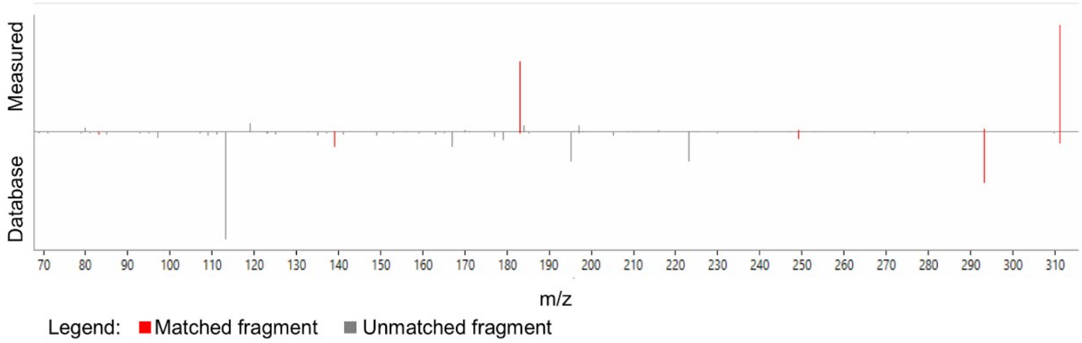

Fig. S20: Experimentally measured (Top): Putative identification: **13(S)-HpODE**:
Progenesis Fragmentation Score: 48.6
Reference (Bottom): Metlin: **13(S)-HpODE**: $C_{18}H_{32}O_4$