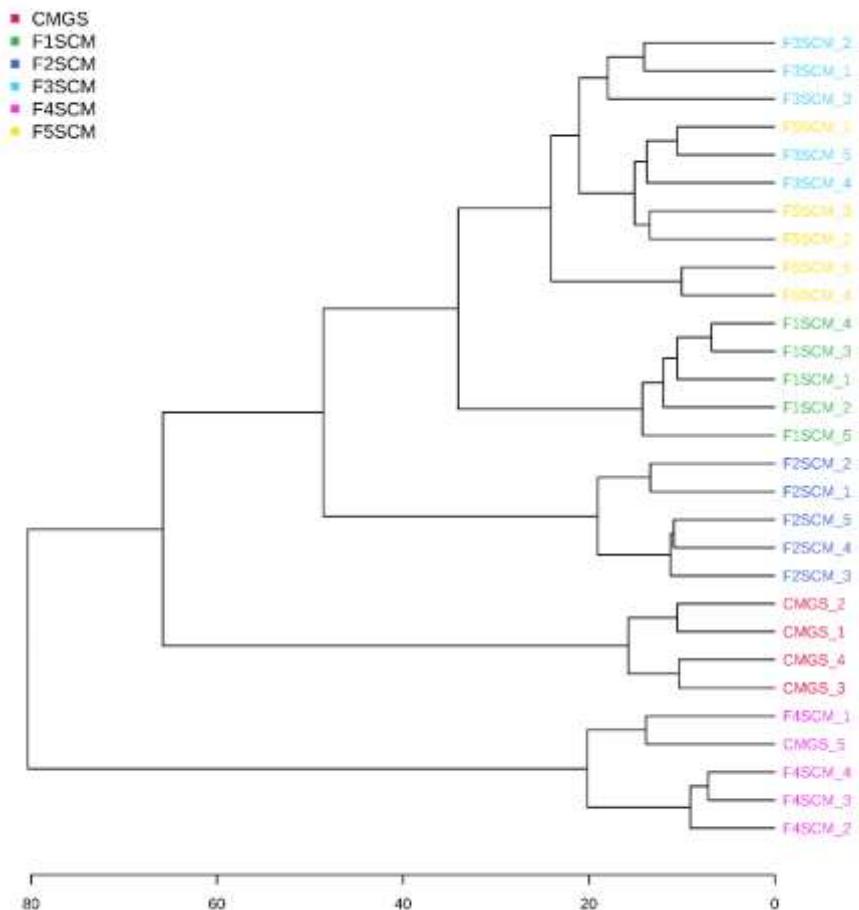
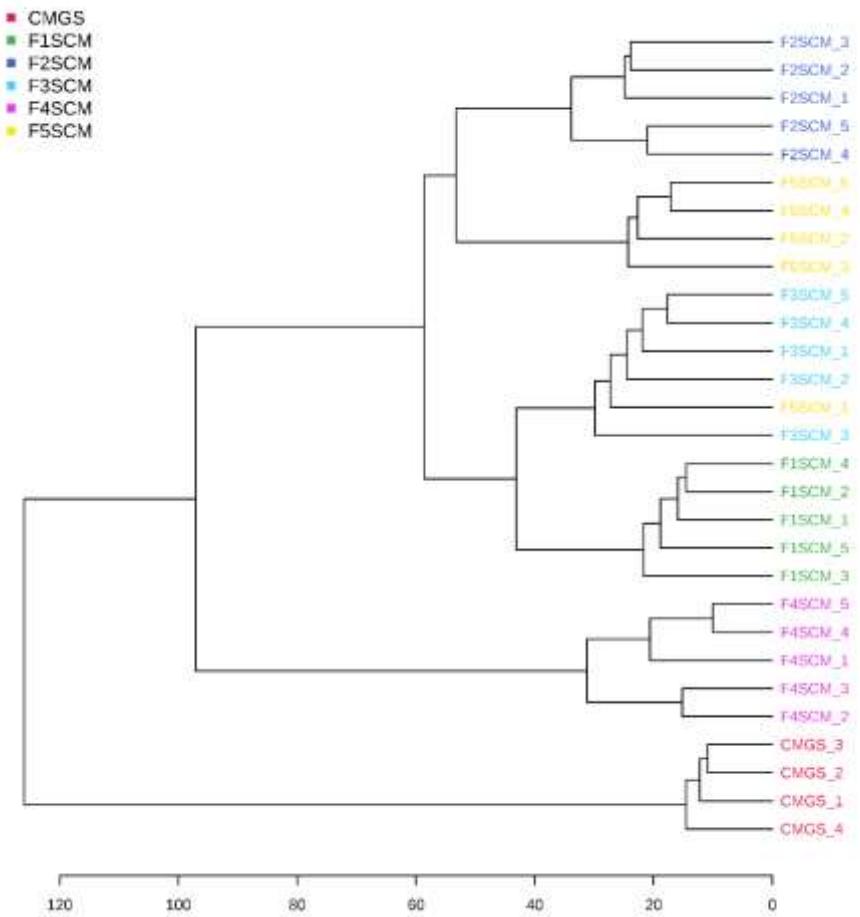


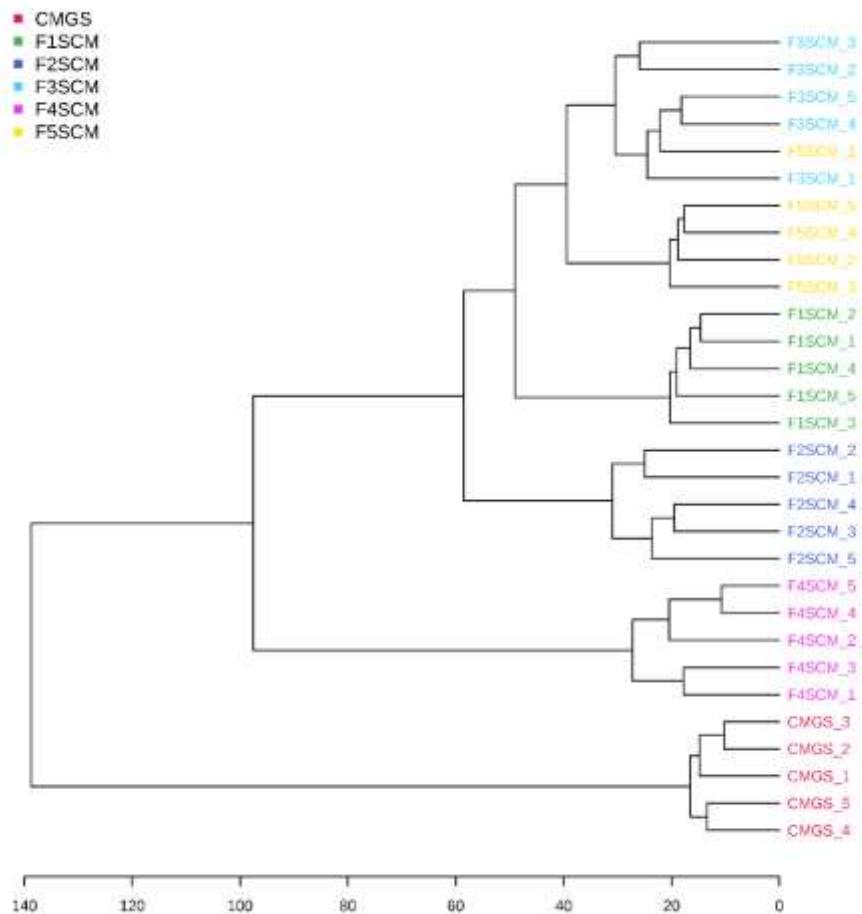
Supplementary Figure 1. Dendrogram showing the relationship between five soil CMs and CMGS medium based on their C18 negative ionization metabolite profiles. Dendrogram was constructed by ward clustering on the closest Euclidean distances between samples. Numbers represent sample ID.



Supplementary Figure 2. Dendrogram showing the relationship between five soil CMs and CMGS medium based on their C18 positive ionization metabolite profiles. Dendrogram was constructed by ward clustering on the closest Euclidean distances between samples. Numbers represent sample ID.

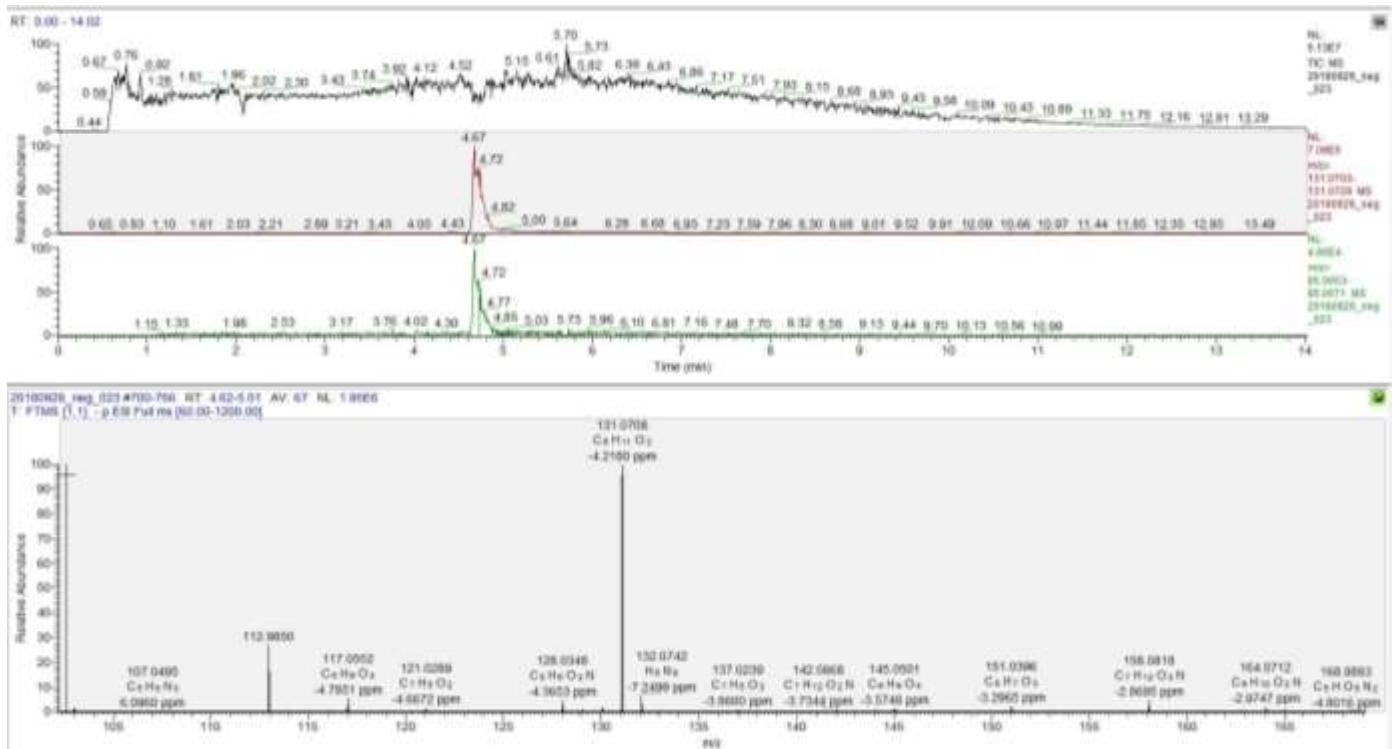


Supplementary Figure 3. Dendrogram showing the relationship between five soil CMs and CMGS medium based on their HILIC negative ionization metabolite profiles. Dendrogram was constructed by ward clustering on the closest Euclidean distances between samples. Numbers represent sample ID.



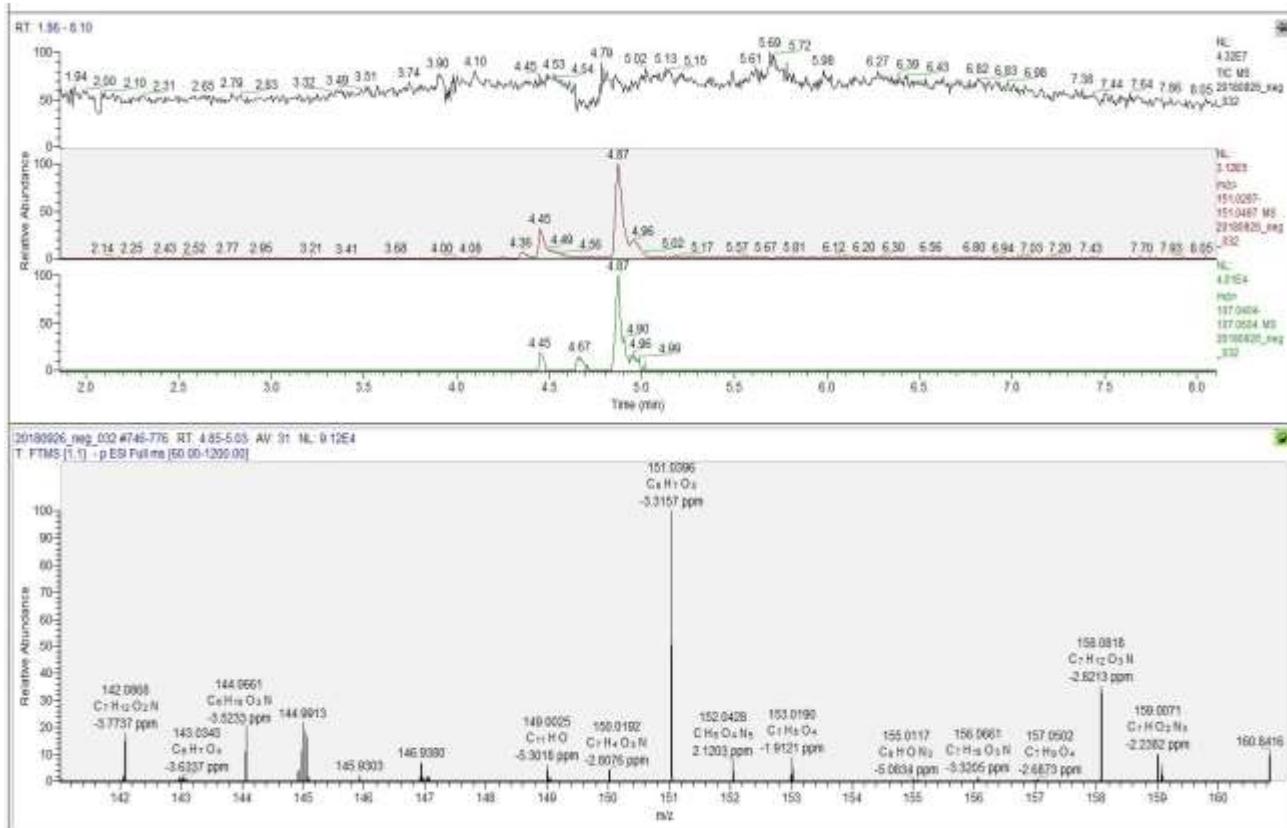
Supplementary Figure 4. Dendrogram showing the relationship between five soil CMs and CMGS medium based on their HILIC positive ionization metabolite profiles. Dendrogram was constructed by ward clustering on the closest Euclidean distances between samples. Numbers represent sample ID.

Compound name	m/z	RT (sec)	Molecular formula	Adduct	Fragmen ts (<i>m/z</i>)	Level of identification
2-hydroxyisocaproic acid	131.0708	284.2	C6H12O3	[M-H]-	85.0662	2



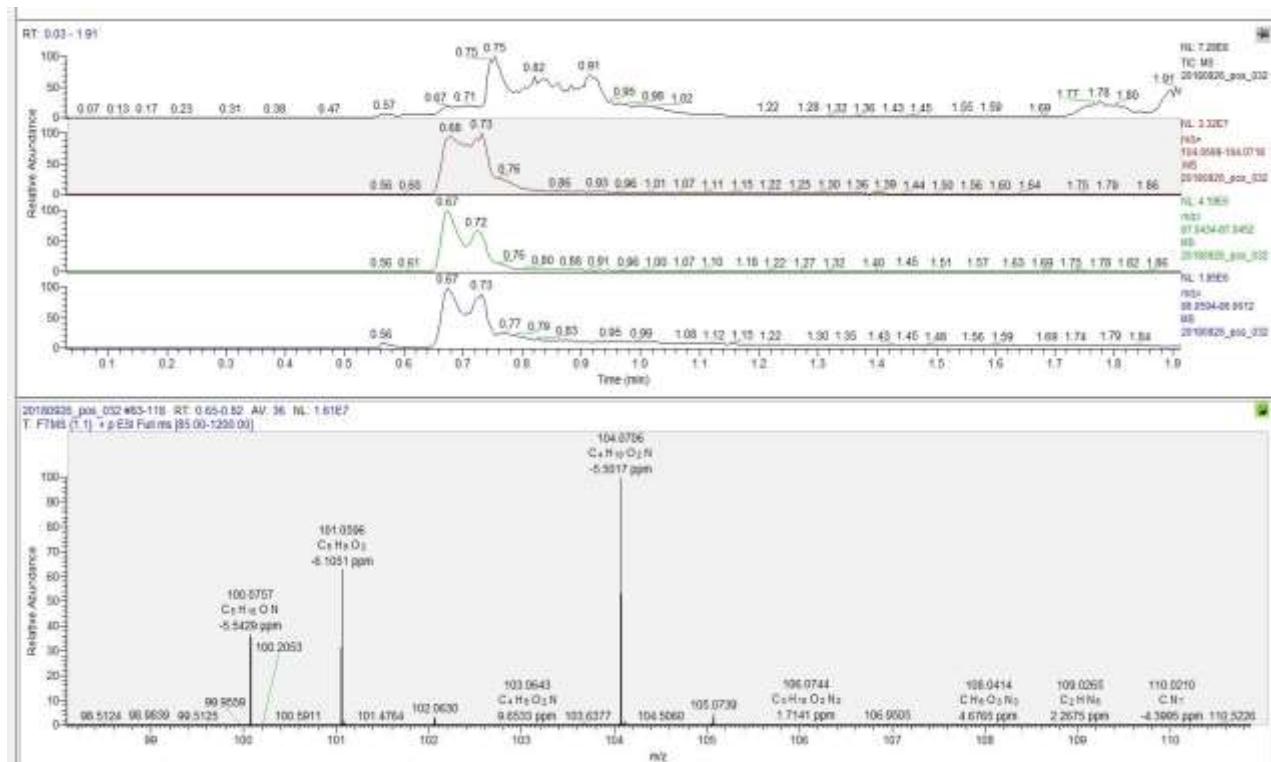
Supplementary Figure 5. Extracted ion chromatograms (C18 negative ionization) for parent masses and co-eluting diagnostic fragments of 2-hydroxyisocaproic acid in the public MS database.

Compound name	m/z	RT (sec)	Molecula r formula	Addu ct	Fragments (m/z)	Level of identification
3-Hydroxyphenylacetic acid	151.0395	295.3	C8H8O3	[M-H] ⁻	107.0504	2

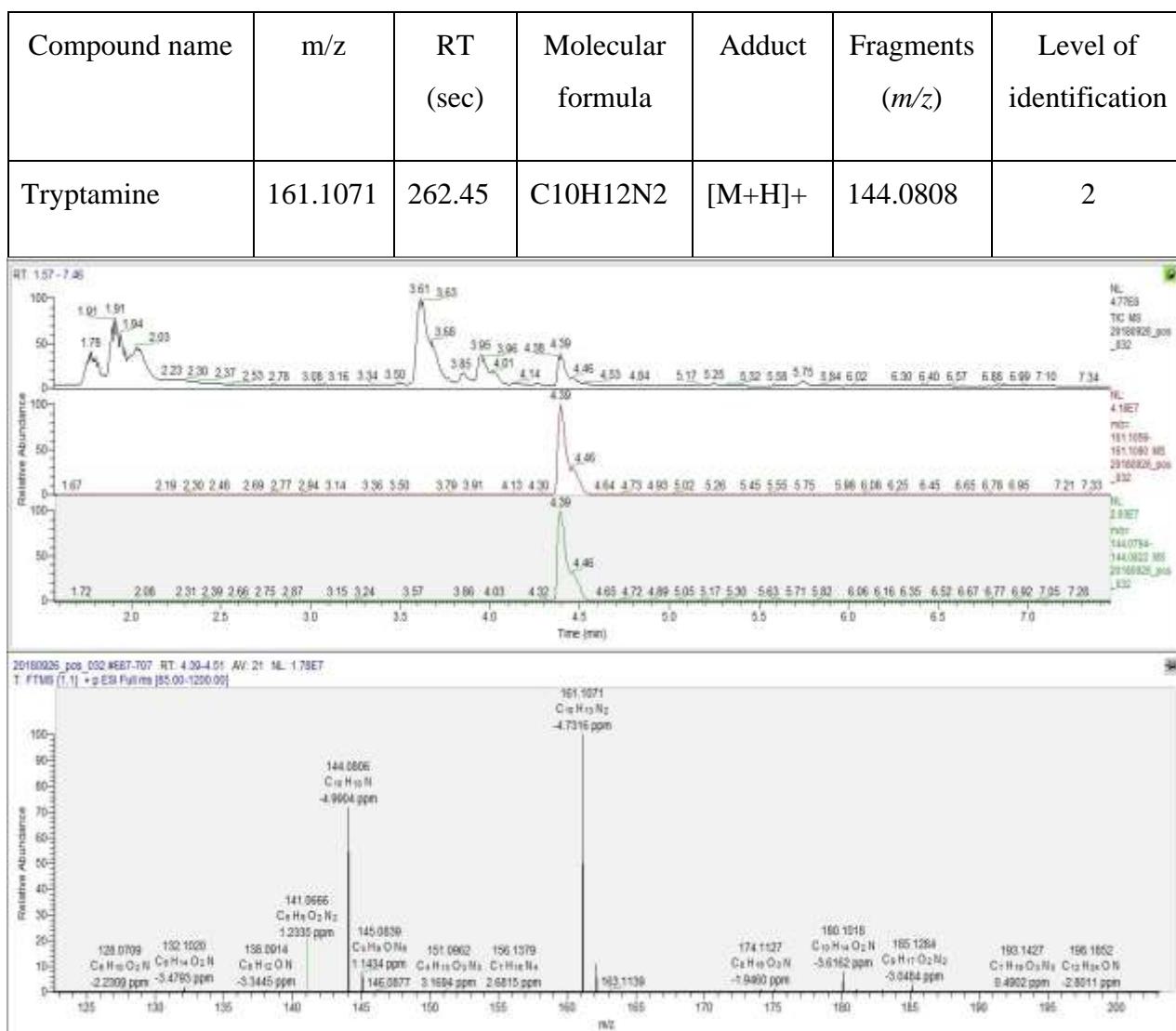


Supplementary Figure 6. Extracted ion chromatograms (C18 negative ionization) for parent masses and co-eluting diagnostic fragments of 3-hydroxyphenylacetic acid in the public MS database.

Compound name	m/z	RT (sec)	Molecular formula	Adduct	Fragments (<i>m/z</i>)	Level of identification
γ -Aminobutyric acid	104.0706	42.41	C4H9NO2	[M+H]+	87.0443, 86.0603	2

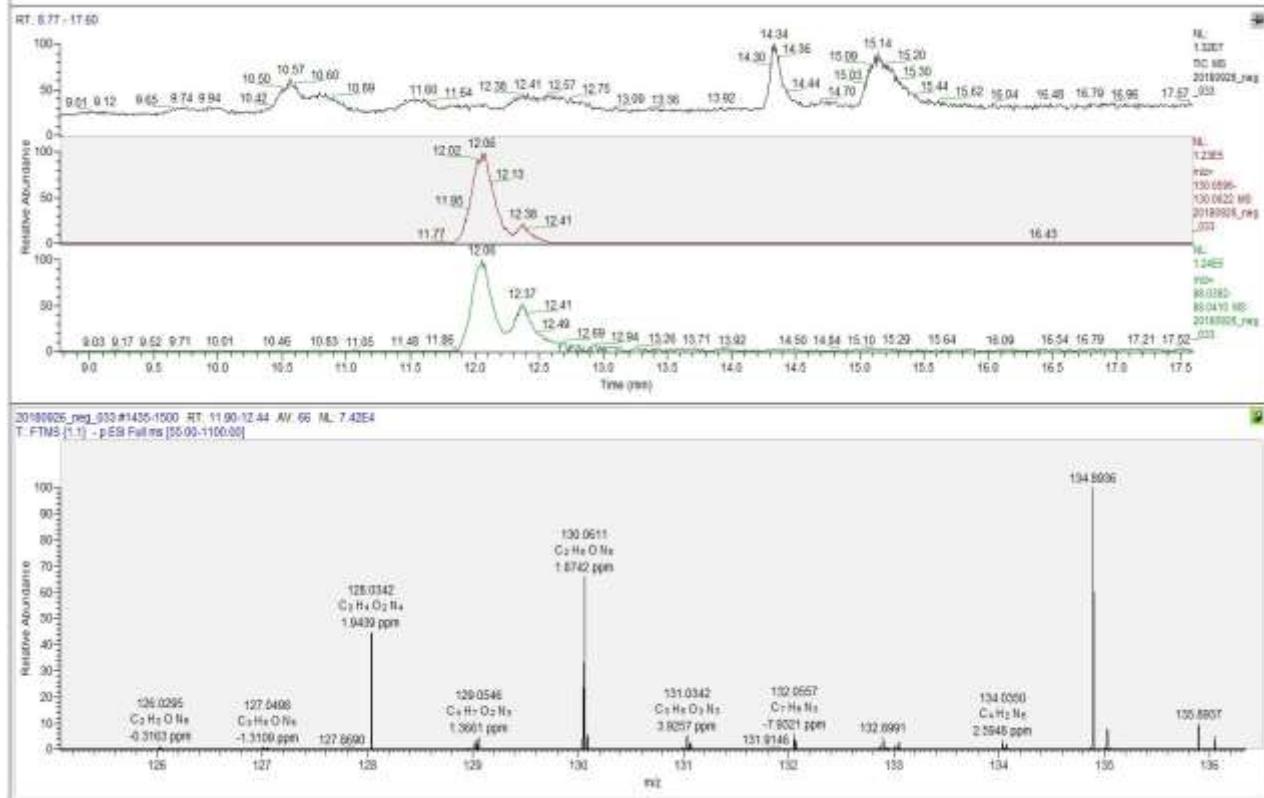


Supplementary Figure 7. Extracted ion chromatograms (C18 positive ionization) for parent masses and co-eluting diagnostic fragments of γ -aminobutyric acid in the public MS database.

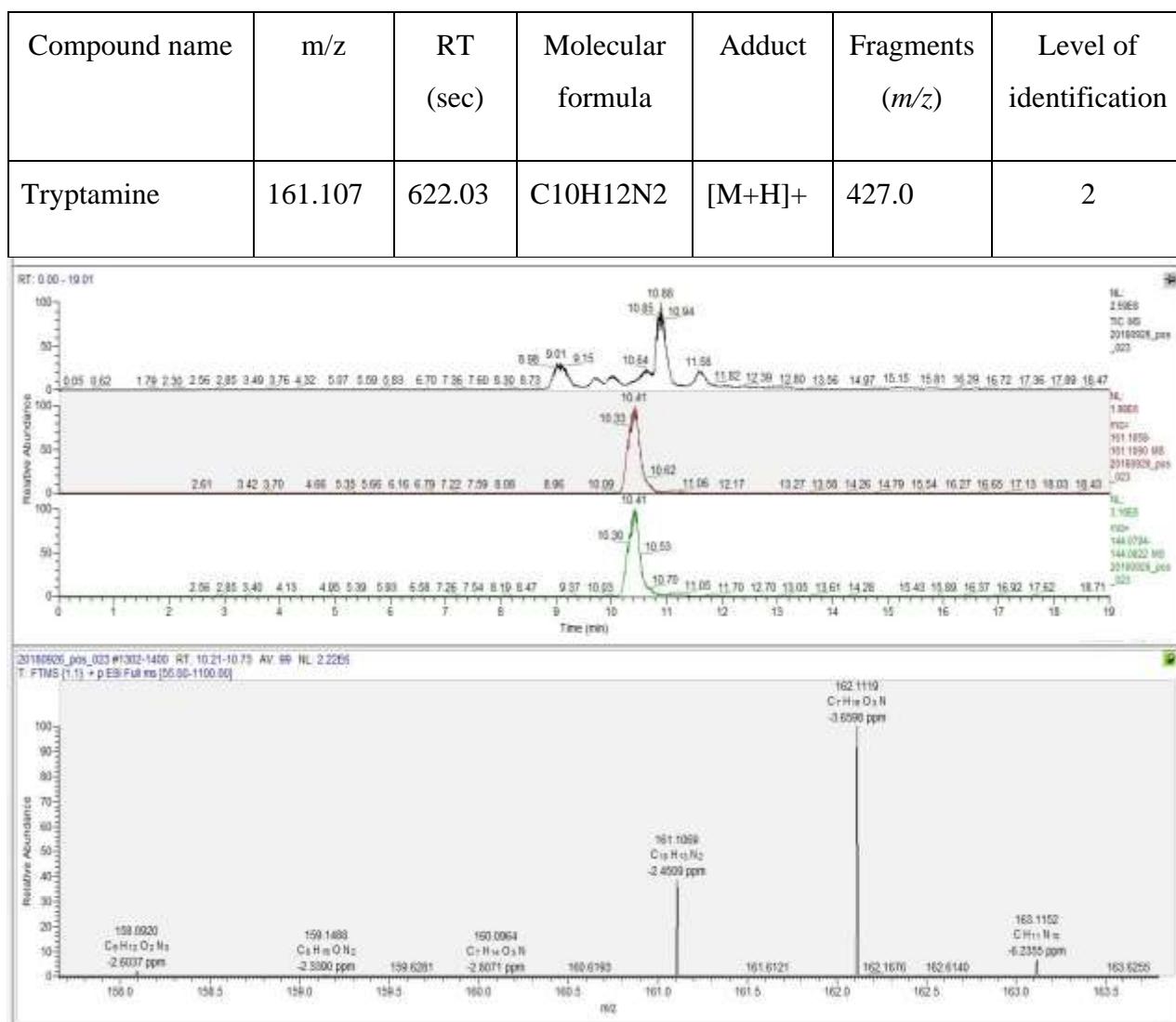


Supplementary Figure 8. Extracted ion chromatograms (C18 positive ionization) for parent masses and co-eluting diagnostic fragments of tryptamine in the public MS database.

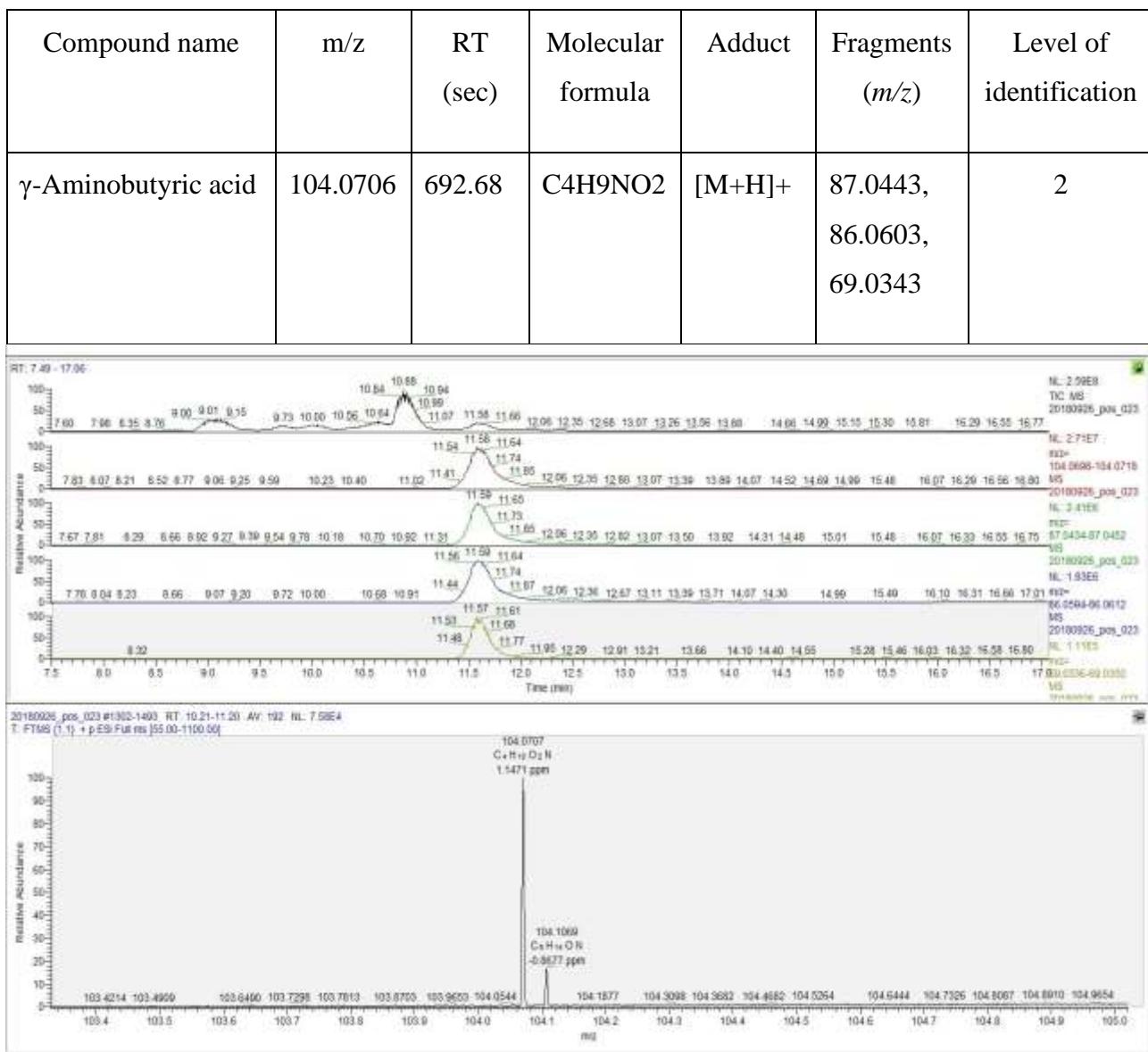
Compound name	m/z	RT (sec)	Molecular formula	Adduct	Fragments (m/z)	Level of identification
Creatine	161.1071	723.24	C4H9N3O2	[M-H]-	88.0401	2



Supplementary Figure 9. Extracted ion chromatograms (HILIC negative ionization) for parent masses and co-eluting diagnostic fragments of creatine in the public MS database.



Supplementary Figure 10. Extracted ion chromatograms (HILIC positive ionization) for parent masses and co-eluting diagnostic fragments of tryptamine in the public MS database.



Supplementary Figure 11. Extracted ion chromatograms (HILIC positive ionization) for parent masses and co-eluting diagnostic fragments of γ -aminobutyric acid in the public MS database.

	C18 negative ionization				C18 positive ionization				HILIC negative ionization				HILIC positive ionization			
	<i>m/z</i>	RT	<i>p</i> -value	FC	<i>m/z</i>	RT	<i>p</i> -value	FC	<i>m/z</i>	RT	<i>p</i> -value	FC	<i>m/z</i>	RT	<i>p</i> -value	FC
39	165.0551	326.7	1.25X10 ⁻⁶	44.7	360.1925	288.38	3.60X10 ⁻⁵	2.2	164.0014	648.7	2.70X10 ⁻⁵	2.4	69.0338	692.48	4.14X10 ⁻⁷	32.6
40	180.0741	345.69	1.25X10 ⁻⁶	777.4	220.1006	304.23	3.74X10 ⁻⁵	6.9	228.0983	652.23	2.83X10 ⁻⁵	4.5	105.066	437.15	4.33X10 ⁻⁷	6.5
41	382.1729	224.02	1.28X10 ⁻⁶	11.7	194.1181	285.91	3.76X10 ⁻⁵	23.4	207.0879	655.51	3.11X10 ⁻⁵	10.5	139.0942	637.23	4.76X10 ⁻⁷	112.1
42	336.12	254.66	1.42X10 ⁻⁶	6.9	177.102	216.42	3.81X10 ⁻⁵	11.7	227.1031	674.94	3.16X10 ⁻⁵	3.9	121.0648	636.81	4.94X10 ⁻⁷	188.5
43	262.1446	417.53	1.58X10 ⁻⁶	106.0	188.1284	308.67	4.48X10 ⁻⁵	109.4	130.0501	748.19	3.42X10 ⁻⁵	4.9	76.076	664.05	5.41X10 ⁻⁷	190.1
44	263.1481	417.51	1.61X10 ⁻⁶	951.3	192.598	222.94	4.94X10 ⁻⁵	9.1	147.0288	455.34	3.69X10 ⁻⁵	3.0	55.0545	649.88	6.01X10 ⁻⁷	6.7
45	149.0603	380.88	1.73X10 ⁻⁶	107.6	190.0864	376.55	5.10X10 ⁻⁵	142.0	171.0403	844.2	3.71X10 ⁻⁵	3.3	138.0909	637.15	7.04X10 ⁻⁷	181.6
46	344.1461	242.32	1.77X10 ⁻⁶	101.4	360.2131	298.49	5.15X10 ⁻⁵	8.4	279.1094	641.69	3.72X10 ⁻⁵	2.4	405.0904	515.91	7.13X10 ⁻⁷	3234.7
47	245.114	236.91	1.88X10 ⁻⁶	2.4	141.0655	78.9	6.44X10 ⁻⁵	12.7	403.0761	516.58	3.84X10 ⁻⁵	338.7	229.1541	511.18	8.04X10 ⁻⁷	13.3
48	288.1198	200.13	2.05X10 ⁻⁶	6.3	155.0792	36.58	7.34X10 ⁻⁵	3.0	127.039	650.04	4.34X10 ⁻⁵	3.7	212.1025	529.08	8.14X10 ⁻⁷	5.6
49	383.158	223.78	2.06X10 ⁻⁶	7.7	318.1668	243.86	1.13X10 ⁻⁴	2.0	215.0667	833.28	4.69X10 ⁻⁵	2.6	145.133	639.18	8.28X10 ⁻⁷	10.5
50	188.0347	253.01	2.19X10 ⁻⁶	7.3	216.1596	382.5	1.17X10 ⁻⁴	93.7	214.0827	689.38	4.81X10 ⁻⁵	3.0	123.0998	601.36	9.35X10 ⁻⁷	1553.7

m/z – mass to charge ratio

RT – retention time (seconds)

p-value - *t*-test between F4SCM and CMGS groups

FC – fold change value (F4SCM/CMGS)