Supplemental data S1. MS/MS data and notes concerning identifications of metabolites listed in Table 5 and Table 6. Readers should note that the analytical platform was optimized for reproducible ion detection under high-throughput conditions. There was no specific optimization for any of the ions detected to provide a realistic test of the utility of high-throughput analysis for quantification. The amino acid identifications and some of the other metabolites quantified here have been documented in previous publications and minimal repetition is provided for these. For the remainder, identification has been based upon multiple criteria. For most, coelution and MS/MS of ions in plasma consistent with retention time and MS/MS of authentic reference material provides evidence for correct identification; details are provided below. For some, additional verification is provided by agreement of abundance measurements with independent analyses of same samples Metabolon. For some, additional evidence is provided by correlation of ion intensities for multiple ions. For some, the accurate mass peak was readily apparent but the low ion intensity and presence of interfering ions within the isolation window prevented direct verification, but ionization in negative ESI provided MS/MS spectra, which were unambiguous.

Metabolite	ion	*m/z*	RT (s)
Metabolites of Table 5			
N8-Acetylspermidine	H^+	188.1751	38
Betaine	H^+	118.0857	47
Bilirubin	H^+	585.2675	181
Carnitine	H^+	162.1117	41
Choline	H^+	104.1064	44
Cortisol	H^+	363.2149	96
Cotinine	H^+	177.1014	234
Creatinine	H^+	114.0657	40
Glucose	Na^+	203.0518	45
Hypoxanthine	H^+	137.0458	46
3-Indolepropionic acid	H^+	190.0853	156
Kynurenine	H^+	209.0914	51
1-Methyl-histidine	H^+	170.0925	33
Oleic acid	H^+	283.2645	555
Oxoproline	H^+	130.0499	46
Uric acid	H^+	169.0349	47
Uridine	H^+	245.0759	47
Metabolites of Table 6			
Caffeine	H^+	195.0877	35
Chlorobenzoic acid	H^{+*}	157.0051	59
Chlorophenylacetic acid	H^{+*}	171.0206	64
Chlorsulfuron	H^+	358.0371	345
Dibutylphthalate	H^+	279.1580	391
Dipropylphthalate	H^+	251.1266	280
Hippuric acid	H^+	180.0657	140
Octylphenol	H^{+*}	207.1734	282

Pirimicarb	H^+	239.1483	552
Styrene	H^+	105.0693	298
Tetraethylene glycol	H^+	195.1211	38
Triethylphosphate	H^+	183.0773	329
Triphenylphosphate	H^+	327.0765	359
Tris(2-chlroropropyl) phosphate	H^+	327.0081	330
Xylylcarb	H^+	180.1018	264

*Note: These metabolites were confirmed in using negative mode ionization due to low abundance of parent ion in positive mode.

MS/MS Confirmation

The identity of the metabolites was verified by comparing spectra obtained using ion dissociation to authentic reference standards and/or spectra available in the MassBank database (http://www.massbank.jp/index.html). Spectra of parent ions selected for confirmation were obtained on a Thermo LTQ-FTICR or Thermo Fusion high resolution mass spectrometer. Data were collected using collision induced disassociation (CID) or high energy C-trap disassociation (HCD). The spectra obtained were first deprofiled using the *deprofile.scan* (Stravs et al. 2013) function in the R package RMassBank and spectra were compared to determine the similarity score by the *SpectrumSimilarity* (Dodder 2014) function in the R package OrgMassSpecR.

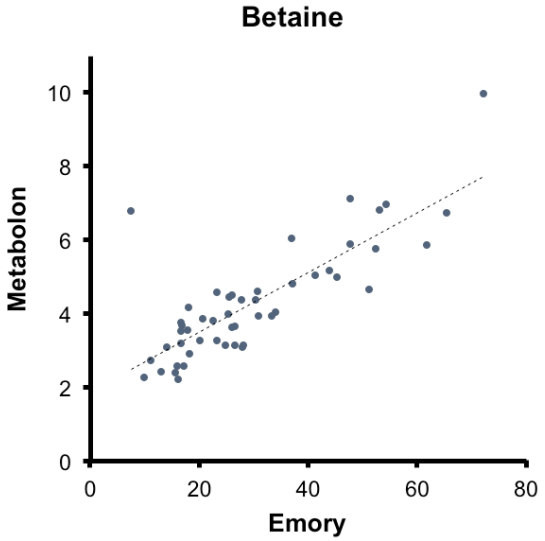
1. Stravs MA, Schymanski EL, Singer H, Hollender J. (2013) Automatic Recalibration and Processing of Tandem Mass Spectra using Formula Annotation, *Journal of Mass Spectrometry*, 48(1), 89-99.
2. Nathan G. Dodder and with code contributions from Katharine M. Mullen. (2014) OrgMassSpecR: Organic Mass Spectrometry. R package version 0.4-4. http://CRAN.R-project.org/package=OrgMassSpecR

N8-Acetylspermidine (H^+, *m/z* 188.1751, 38s)

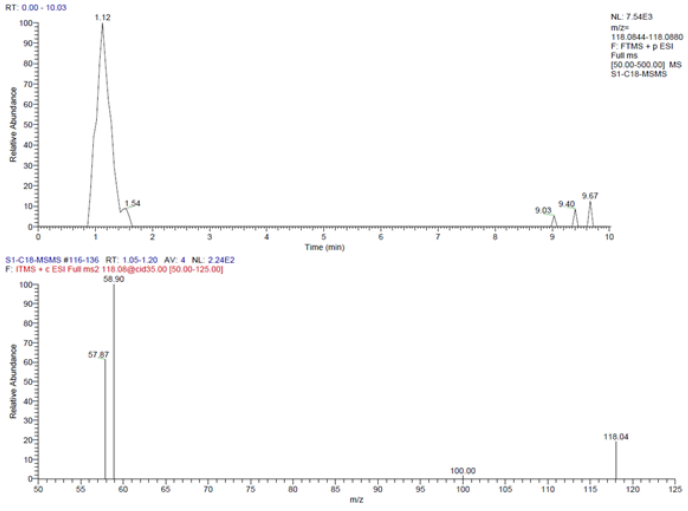
Acetylspermidine was confirmed by MS/MS and retention time relative to authentic standard as previously described (Roede JR, Uppal K, Park Y, Lee K, Tran V, Walker D, Strobel FH, Rhodes SL, Ritz B, Jones DP. (2013) Serum metabolomics of slow vs. rapid motor progression Parkinson's disease: a pilot study. *PLoS One*, 8: e77629.

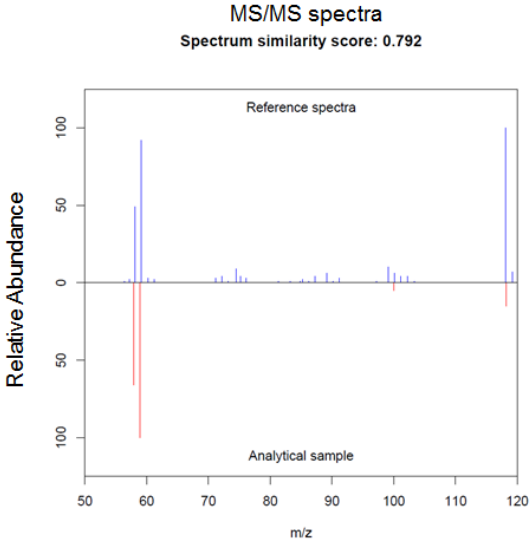
Betaine (H+, *m/z* 118.0857, 47s)

Betaine was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.80.



Betaine M+H, *m/z* = 118.0857



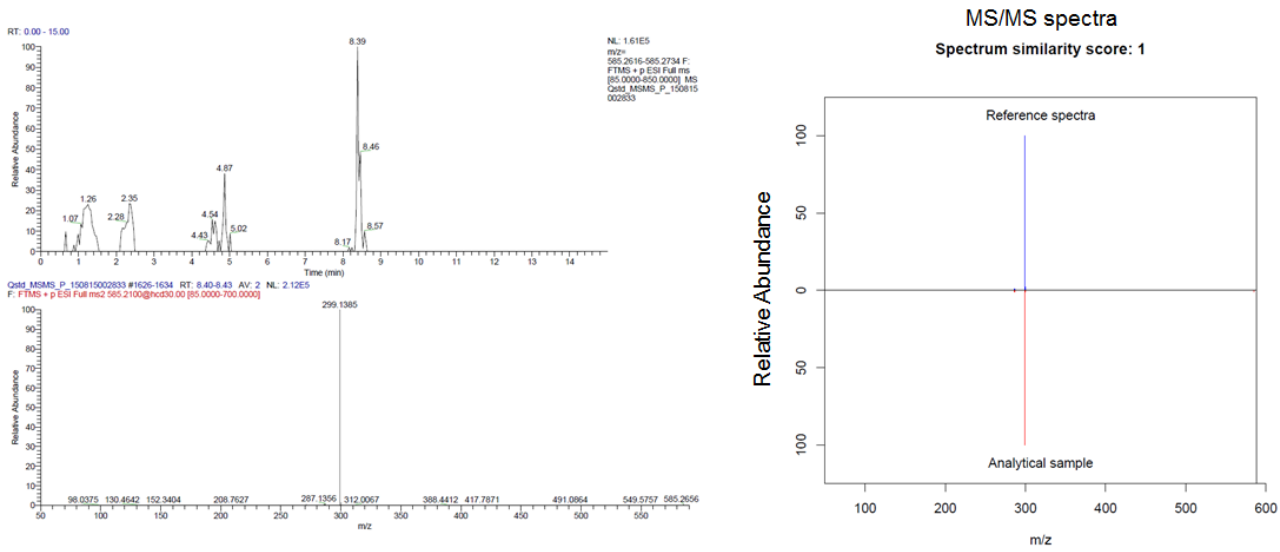


Reference spectra source: http://www.massbank.jp/jsp/Dispatcher.jsp?type=disp&id=MT000002&site=12

Bilirubin (H^+, *m/z* 585.2675, 181s)

Bilirubin was confirmed by retention time and MS/MS relative to standard (QStd); values reported for bilirubin by Metabolon correlated with the accurate mass ion for biliverdin.

Bilirubin M+H, *m/z* = 585.2675

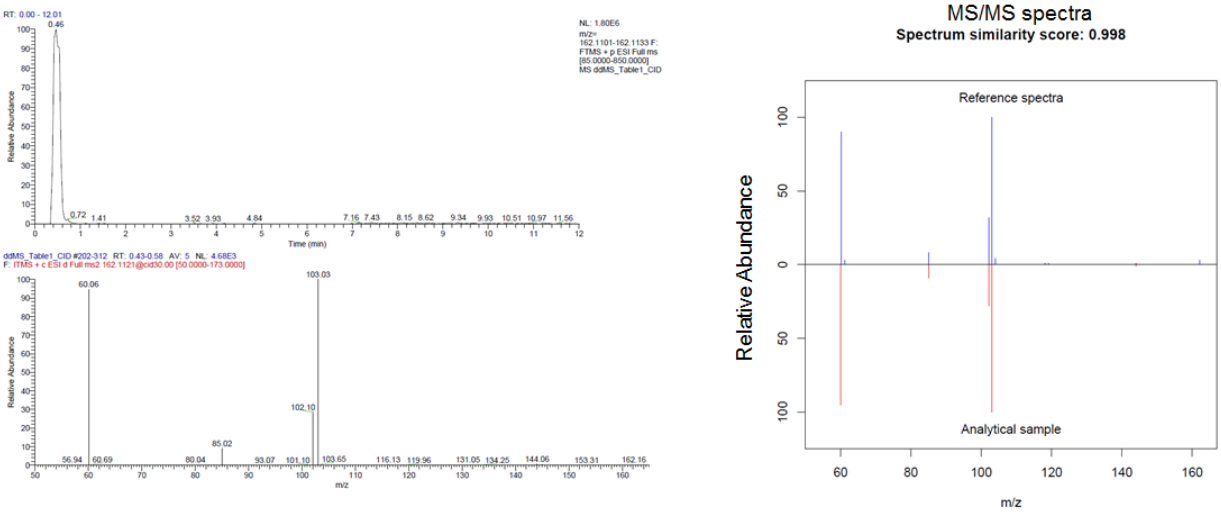


Reference spectra obtained on Thermo LTQ FTICR, Bilirubin (98%), Sigma Aldrich

Carnitine (H^+, *m/z* 162.1117, 41s)

Carnitine was confirmed by coelution and MS/MS matching standard. A coeluting ion with *m/z* 144.1013, consistent with the $-H_2O$ ($+H^+$) was also present and appeared suitable for quantification.

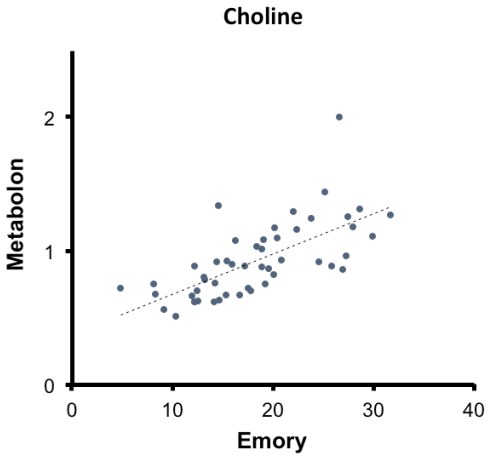
Carnitine M+H, *m/z* = 162.1117



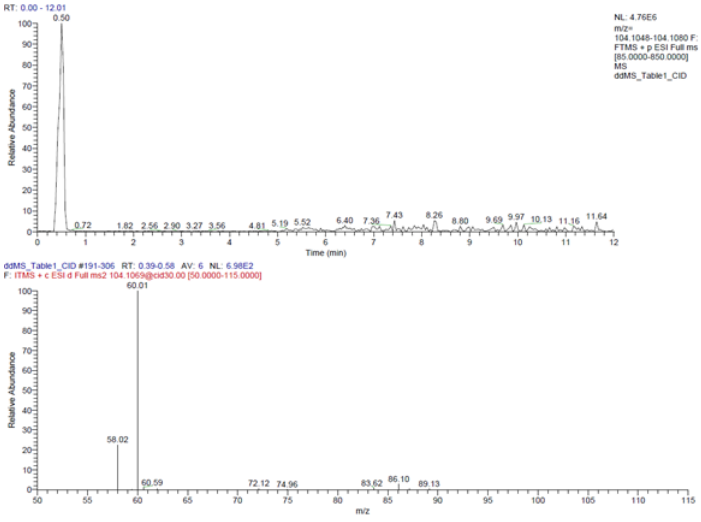
Reference spectra source: http://www.massbank.jp/jsp/Dispatcher.jsp?type=disp&id=MT000082&site=12

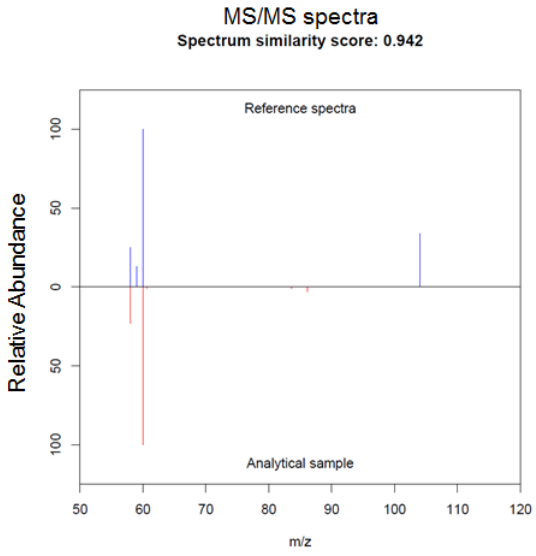
Choline (H^+, *m/z* 104.1064, 44s)

Choline was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.71. Additional studies of choline are available (Uppal K, Soltow QA, Promislow DEL, Wachtman L, Quyyumi AA, Jones DP. (2015) MetabNet: an R package for metabolic association analysis of high-resolution metabolomics data. *Frontiers in Bioengineering and Biotechnology*, 3: 87.



Choline M+H, *m/z* = 104.1064

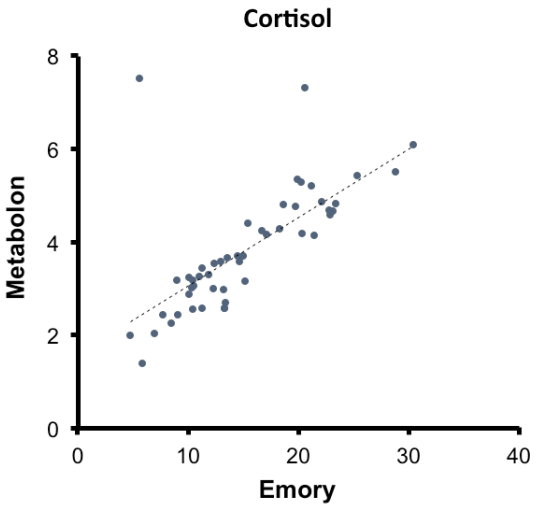




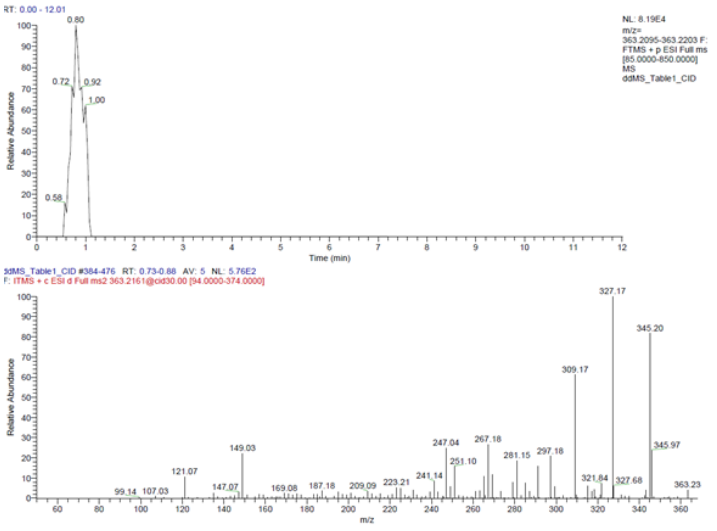
Reference spectra source: http://www.massbank.jp/jsp/Dispatcher.jsp?type=disp&id=PB001603&site=9

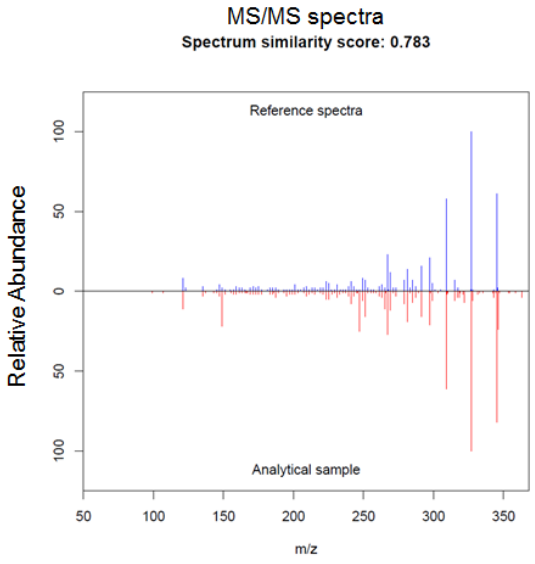
Cortisol (H^+, *m/z* 363.2149, 96s)

Cortisol was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.69.



Cortisol M+H, *m/z* = 363.2149



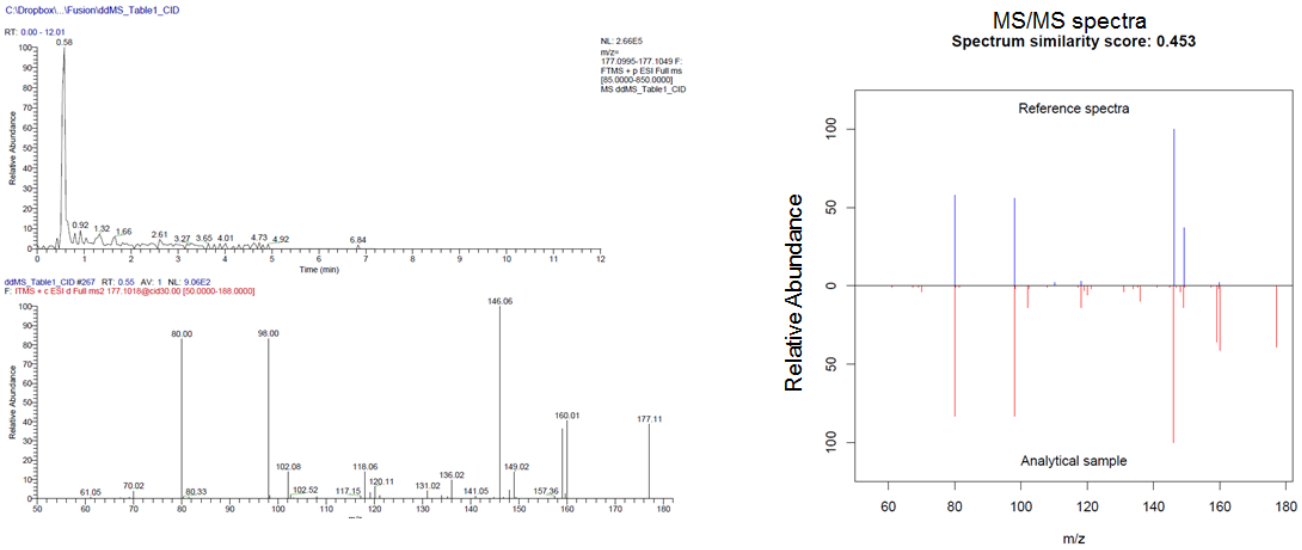


Reference spectra obtained on Thermo Fusion, Cortisol CRM, Sigma Aldrich

Cotinine (H^+, *m/z* 177.1014, 234s)

Cotinine was confirmed by coelution and MS/MS matching standard. This was a non-smoking population so cotinine concentrations were low; in other analyses of smokers plasma with the same platform, the signal for cotinine correlated (Pearson *r*=0.56) with hydroxycotinine (*m/z* 193.0966, 174 s).

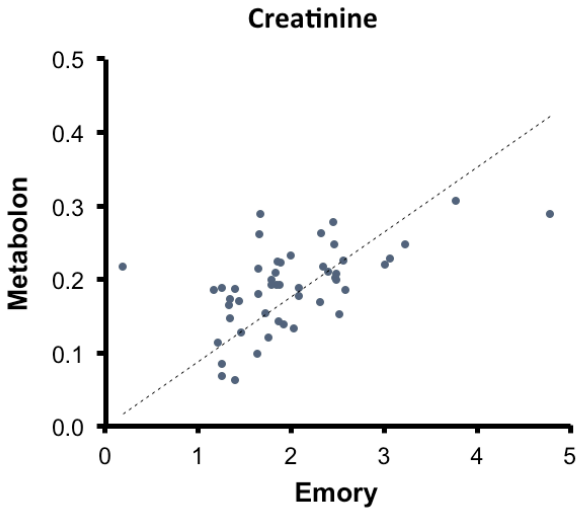
Cotinine M+H, *m/z* = 177.1022



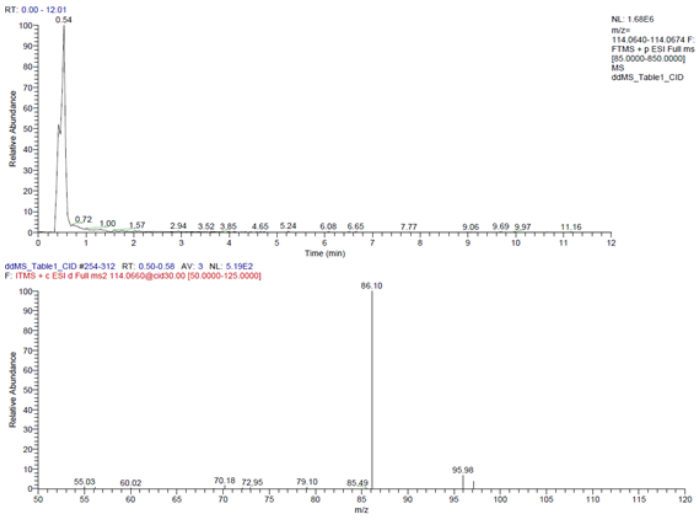
Reference spectra obtained on Thermo LTQ FTICR, Cotinine (98%), Sigma Aldrich

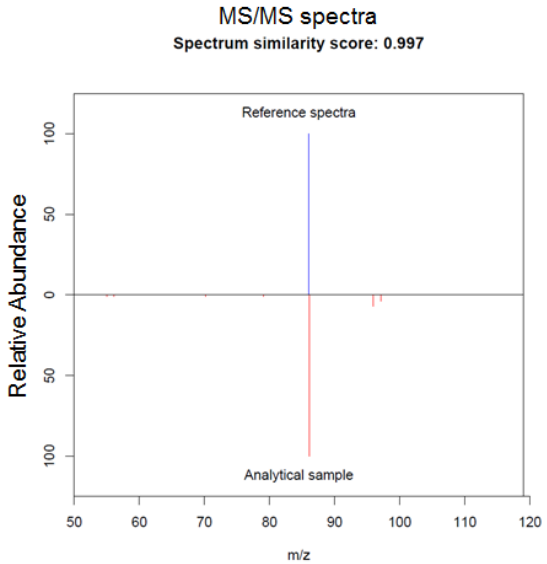
Creatinine (H^+, *m/z* 114.0657, 40s)

Creatinine was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.55.



Creatinine M+H, *m/z* = 114.0657

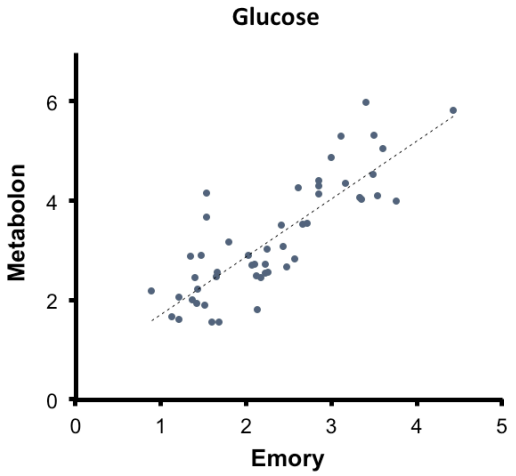




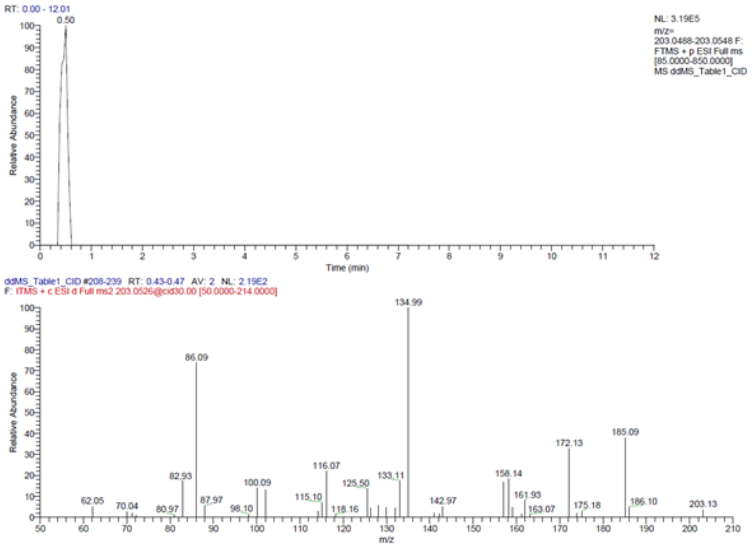
Reference spectra source: http://www.massbank.jp/jsp/Dispatcher.jsp?type=disp&id=UF412504&site=27

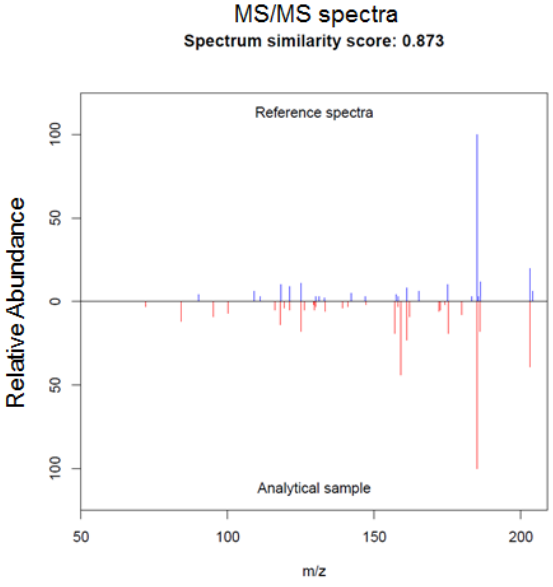
Glucose (Na^+, *m/z* 203.0518, 45s)

Glucose was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.86.



Glucose M+Na, *m/z* = 203.0518

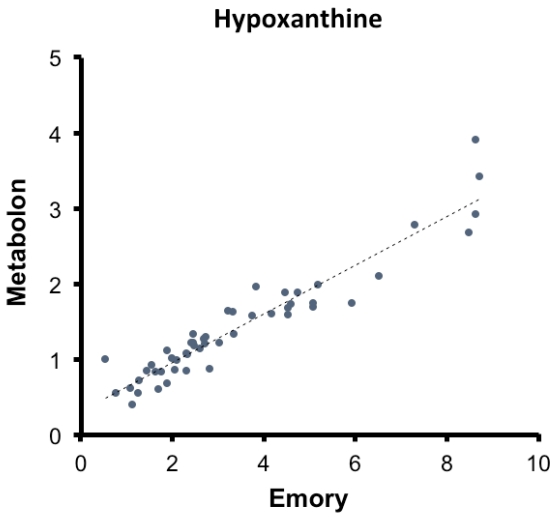




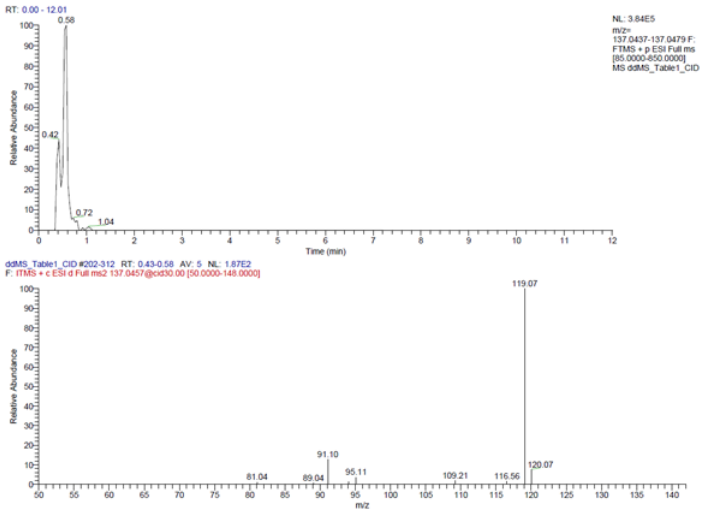
Reference spectra obtained on Thermo Fusion, Glucose (96%), Sigma Aldrich

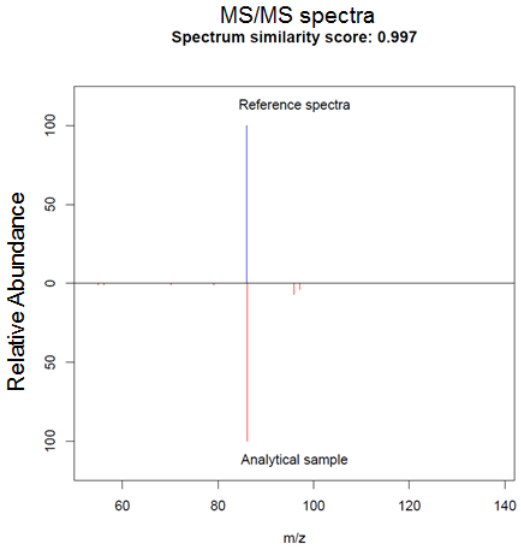
Hypoxanthine (H+, *m/z* 137.0458, 46s)

Hypoxanthine was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.95.



Hypoxanthine M+H, *m/z* = 137.0458

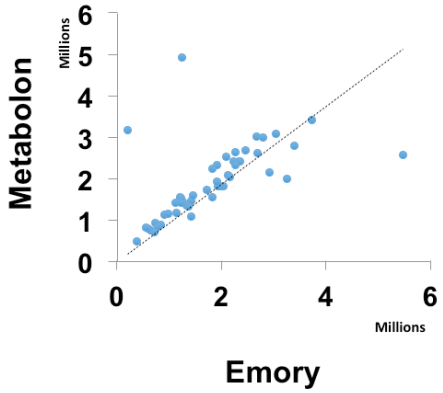


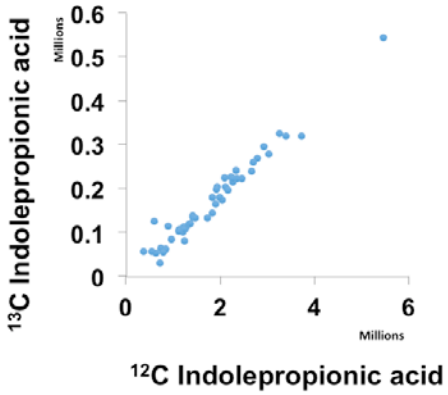


Reference spectra obtained on Thermo Fusion, Hypoxanthine (99%), Sigma Aldrich

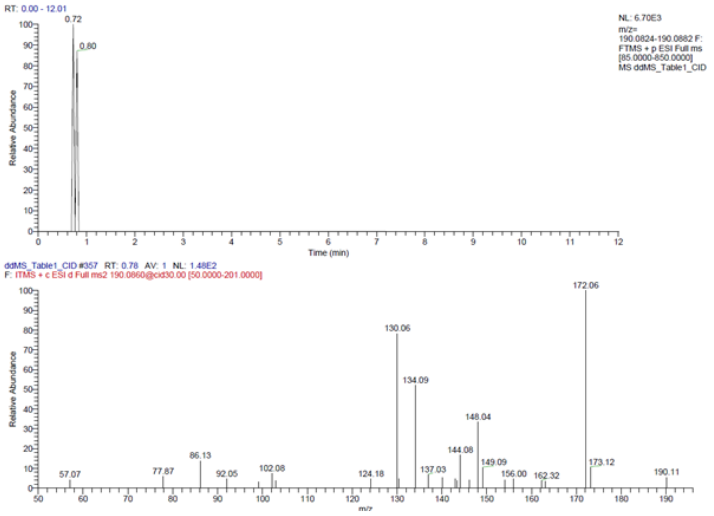
3-Indolepropionic acid (H^+, *m/z* 190.0853, 156s)

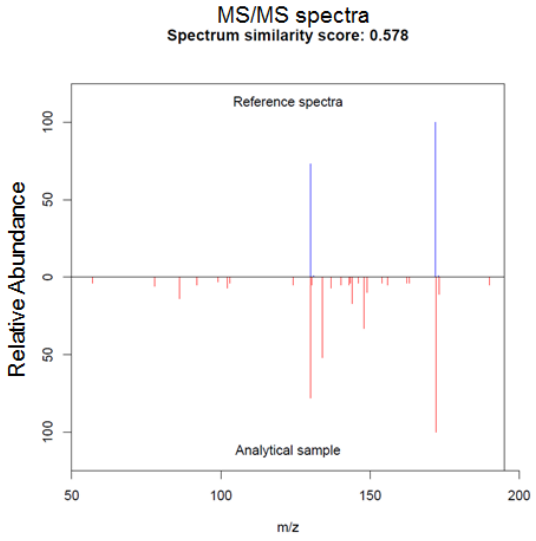
Indole was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.67.





3-Indolepropionic Acid M+H, *m/z* = 190.0853

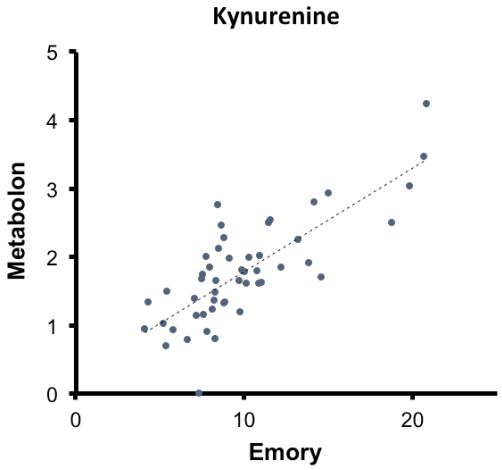




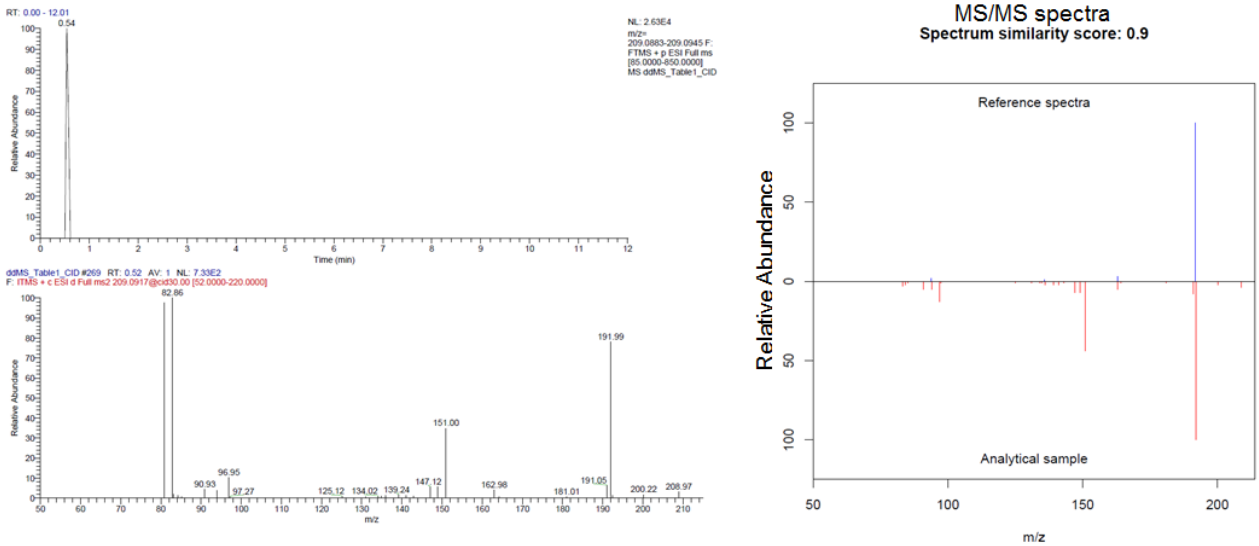
Reference spectra obtained on Thermo Fusion, Indole propionate (99%), Sigma Aldrich

Kynurenine (H^+, *m/z* 209.0914, 51s)

Kynurenine was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.80.



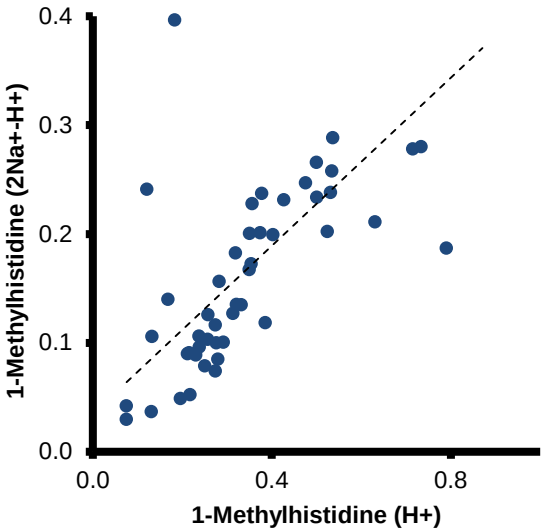
Kynerunine M+H, *m/z* = 209.0914



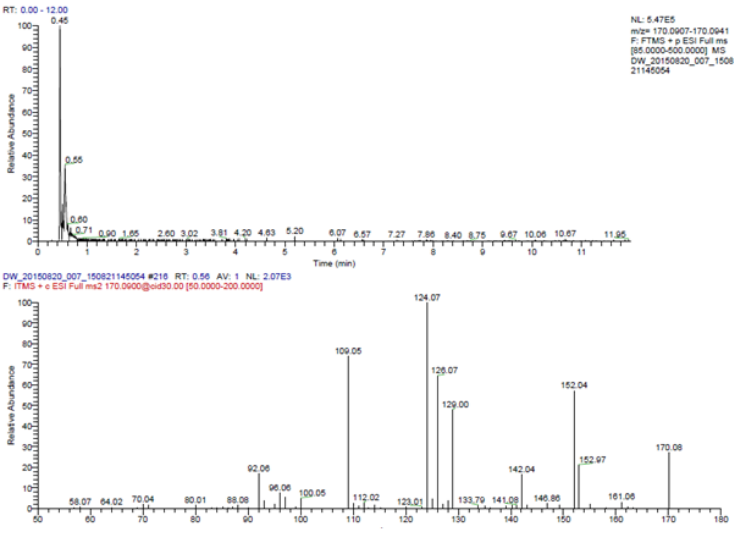
Reference spectra obtained on Thermo Fusion, Kynurenine (98%), Sigma Aldrich

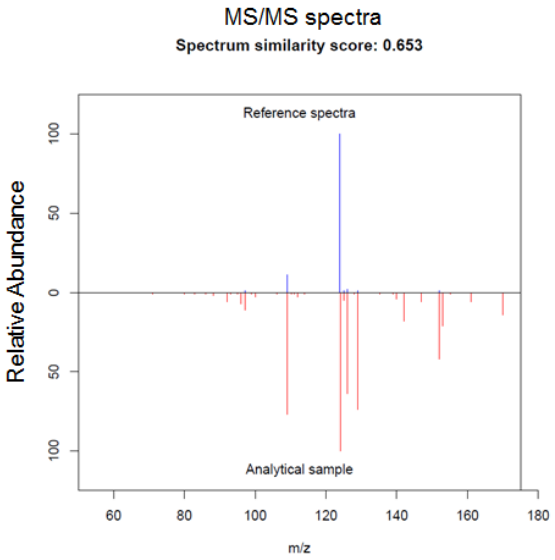
1-Methylhistidine (H^+, *m/z* 170.0925, 33s)

1-Methylhistidine was confirmed by coelution and MS/MS matching standard. In other studies using this protocol, a correlating signal consistent with the $2Na^+$-H^+ form (*m/z* 170.0913) is also present and also appears suitable for quantification. Note that another low-intensity signal is present consistent with 3-methylhistidine.



1-Methyl-histidine M+H, *m/z* = 170.0925



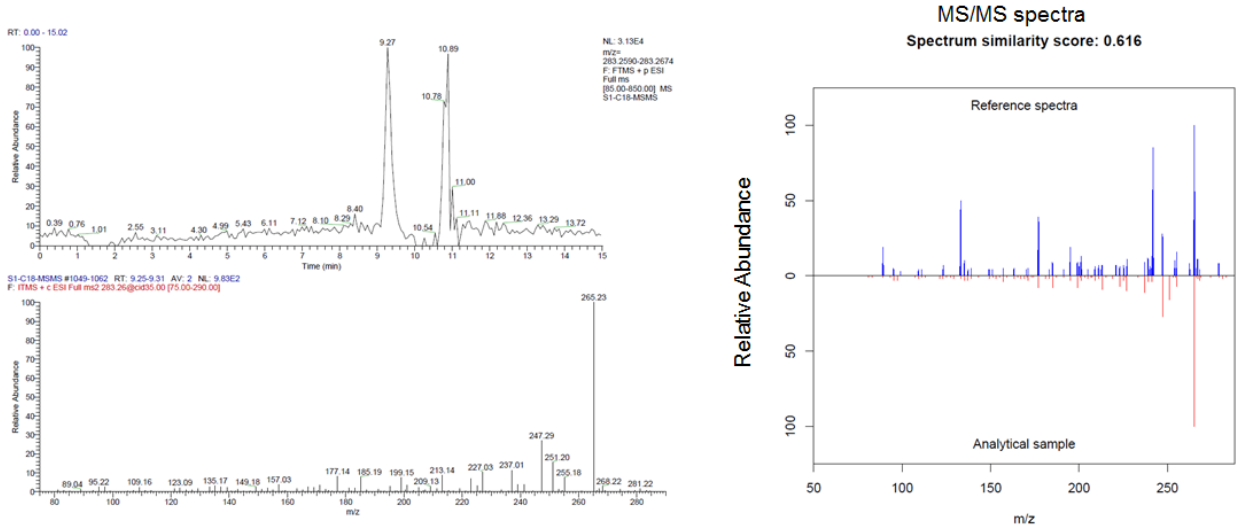


Reference spectra obtained on Thermo LTQ FTICR, 1-methyl-hisitidine (98%), Sigma Aldrich

Oleic acid (H^+, *m/z* 283.2645, 555s)

Oleic acid was confirmed by coelution and MS/MS matching standard.

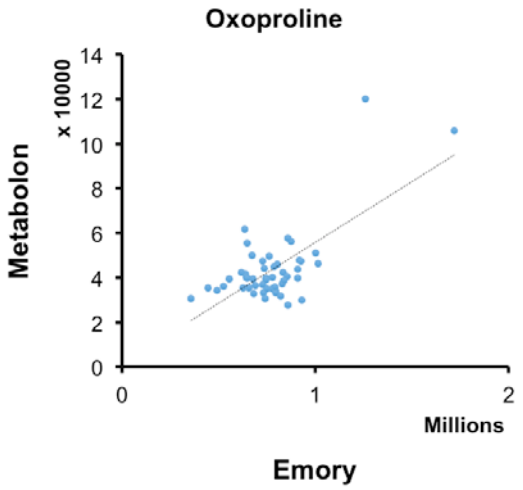
Oleic Acid M+H, *m/z* = 283.2645



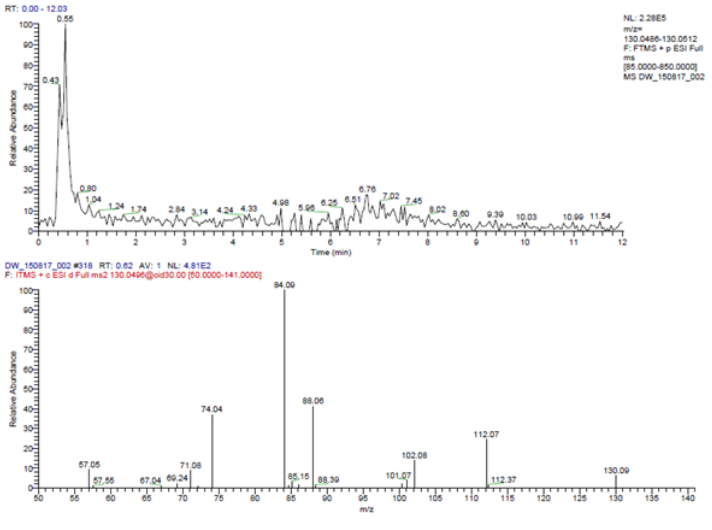
Reference spectra obtained on Thermo Fusion, Oleic acid (99%), Sigma Aldrich

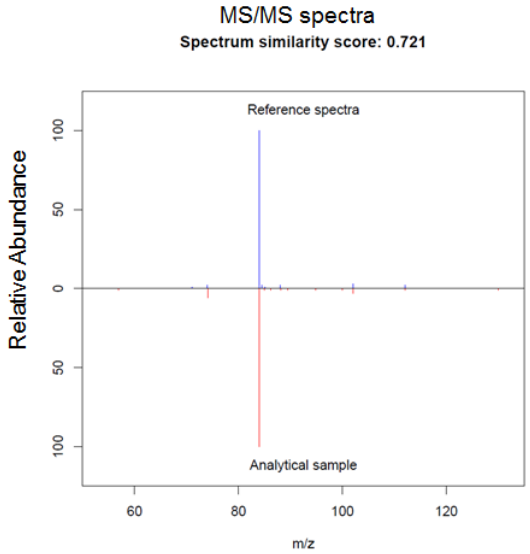
Oxoproline (H^+, *m/z* 130.0499, 46s)

Oxoproline was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.69.



Oxoproline M+H, *m/z* = 130.0499

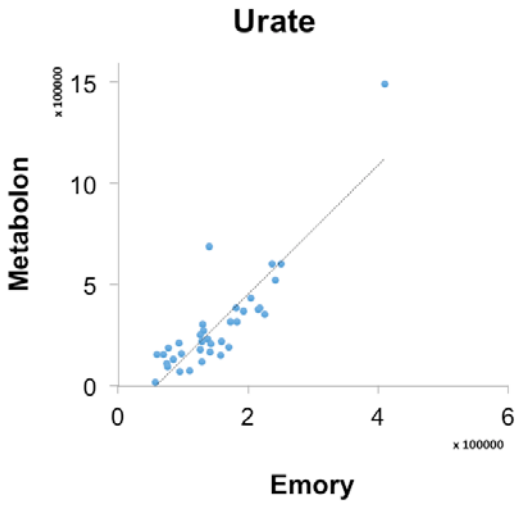




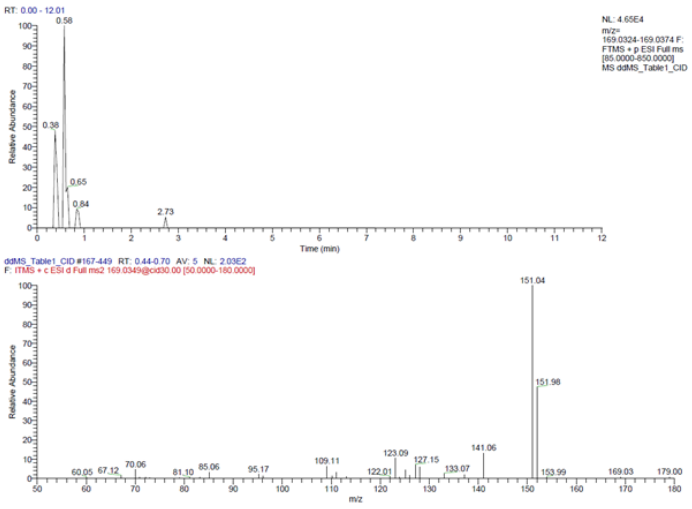
Reference spectra obtained on Thermo Fusion, Oxoproline (99%), Sigma Aldrich

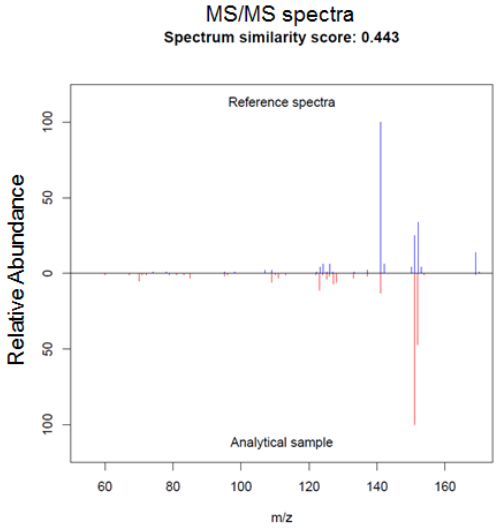
Uric acid (H^+, *m/z* 160.0349, 47s)

Uric acid was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.87.



Uric acid M+H, *m/z* = 169.0349

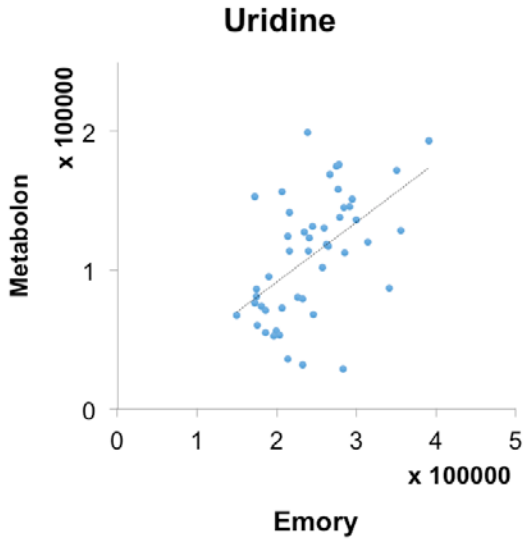




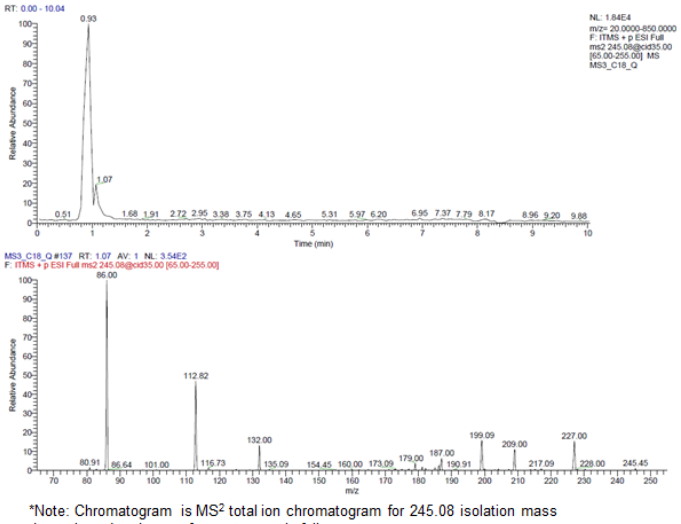
Reference spectra source: http://www.massbank.jp/jsp/Dispatcher.jsp?type=disp&id=MT000083&site=12

Uridine (H^+, *m/z* 245.0759, 47s)

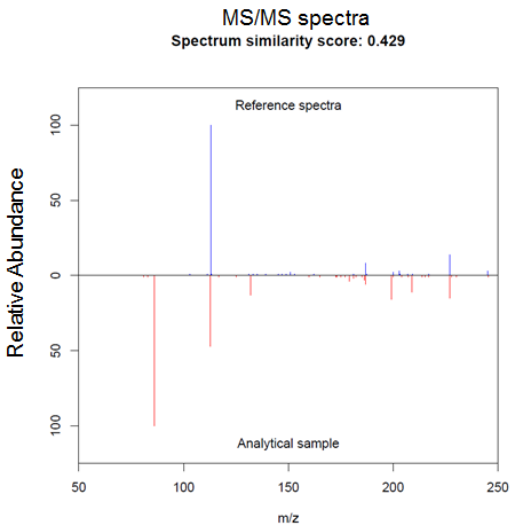
Uridine was confirmed by coelution and MS/MS matching standard. Metabolon measurement of uridine more strongly correlated with our measurement of uracil (r=0.59) than with our measurement of uridine (r=0.51). Our measurements of uracil and uridine had Pearson r=-0.62, supporting correct identification.



Uridine M+H, *m/z* = 245.0759



*Note: Chromatogram is MS^2 total ion chromatogram for 245.08 isolation mass due to low abundance of parent mass in full scant

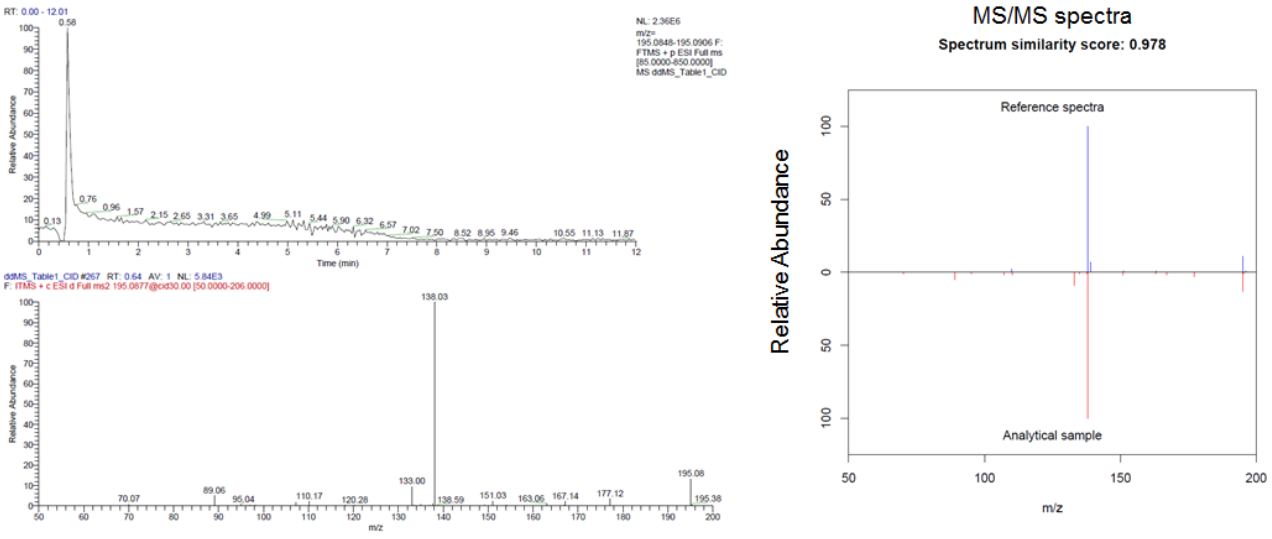


Reference spectra obtained on Thermo LTQ FTICR, Uridine (99%), Sigma Aldrich

Caffeine (H^+, *m/z* 195.0877, 35s)

Caffeine was confirmed by coelution and MS/MS matching standard.

Caffeine M+H, *m/z* = 195.0877

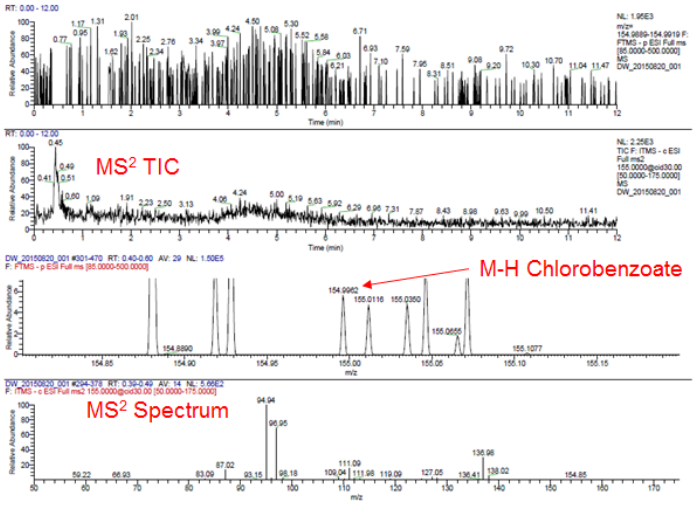


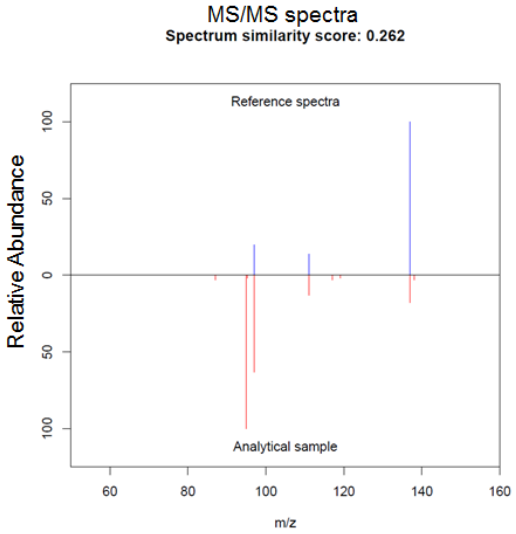
Reference spectra obtained on Thermo LTQ FTICR, Caffeine (99%), Sigma Aldrich

Chlorobenzoic acid (M-H, *m/z* 157.0051, 59s)

Chlorobenzoic acid was confirmed by coelution and MS/MS matching standard. Note that the peak was very low intensity so that fragmentation of other ions within the isolation window interfered with similarity scoring. Method of addition with authentic standard, along with MS/MS of added standard, was consistent with the interpretation as shown.

Chlorobenzoate M-H, *m/z* = 154.9904



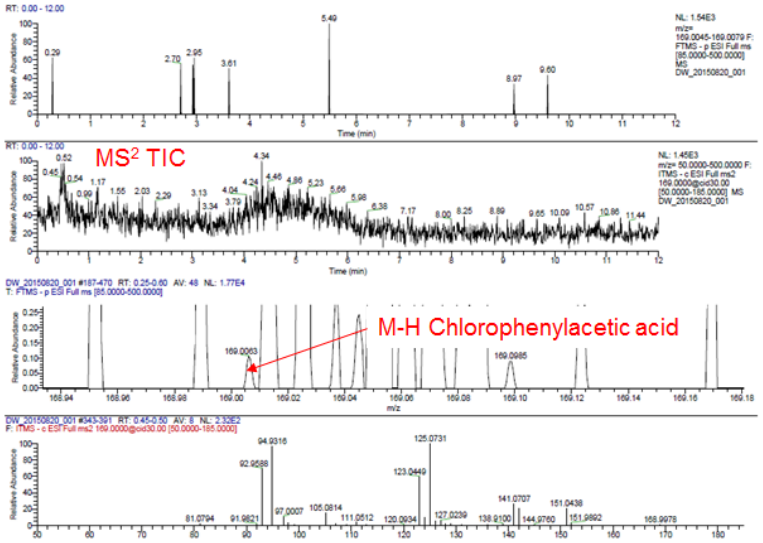


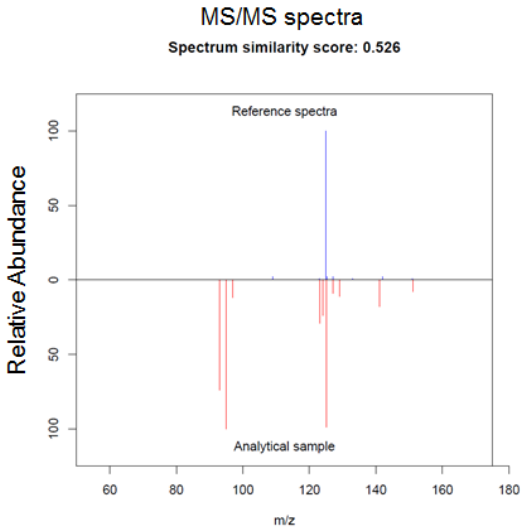
Reference spectra obtained on Thermo Fusion, Chlorobenzoate (99%), Sigma Aldrich

Chlorophenylacetic acid (M-H, *m/z* 171.0206, 64s)

Chlorophenylacetic acid was confirmed by coelution and MS/MS matching standard. Note that the peak was very low intensity so that fragmentation of other ions within the isolation window interfered with similarity scoring. Method of addition with authentic standard, along with MS/MS of added standard, was consistent with the interpretation as shown.

Chlorophenylacetic acid M-H, *m/z* = 169.0062





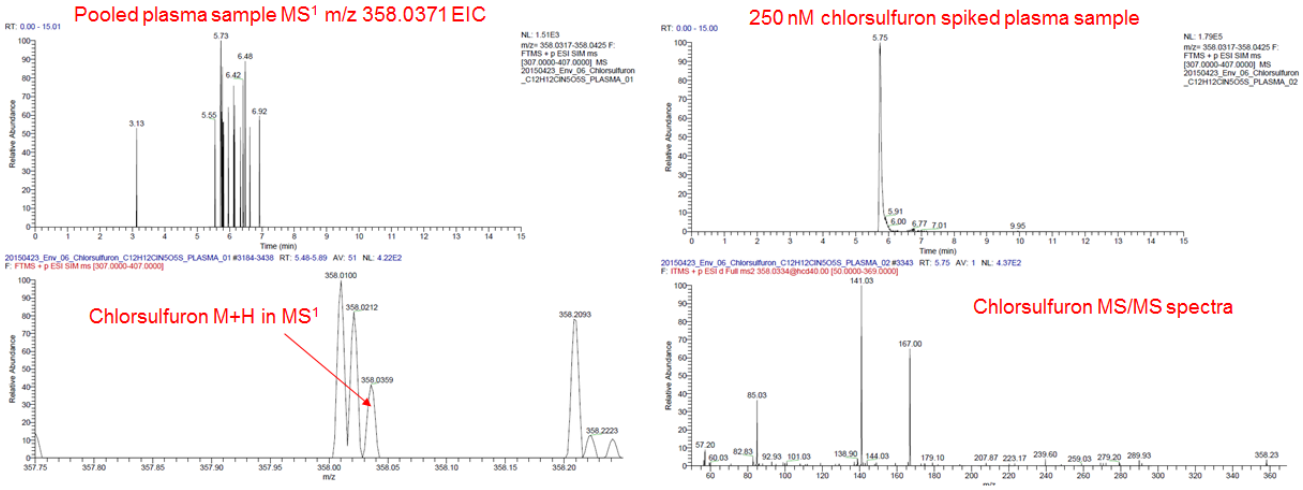
Due to low abundance of parent ion, MS^2 spectra was in negative mode and compared to retention time obtained in positive mode.

Reference spectra obtained on Thermo Fusion, Chlorophenylacetic acid (99%), Sigma Aldrich

Chlorsulfuron (H^+, *m/z* 358.0371, 345s)

Data are consistent with chlorsulfuron identification by coelution and MS/MS of added standard, but low intensity and fragmentation of other ions within the isolation window interfered absolute identification by MS/MS of samples without addition.

Chlorsulfuron M+H, *m/z* = 358.0371

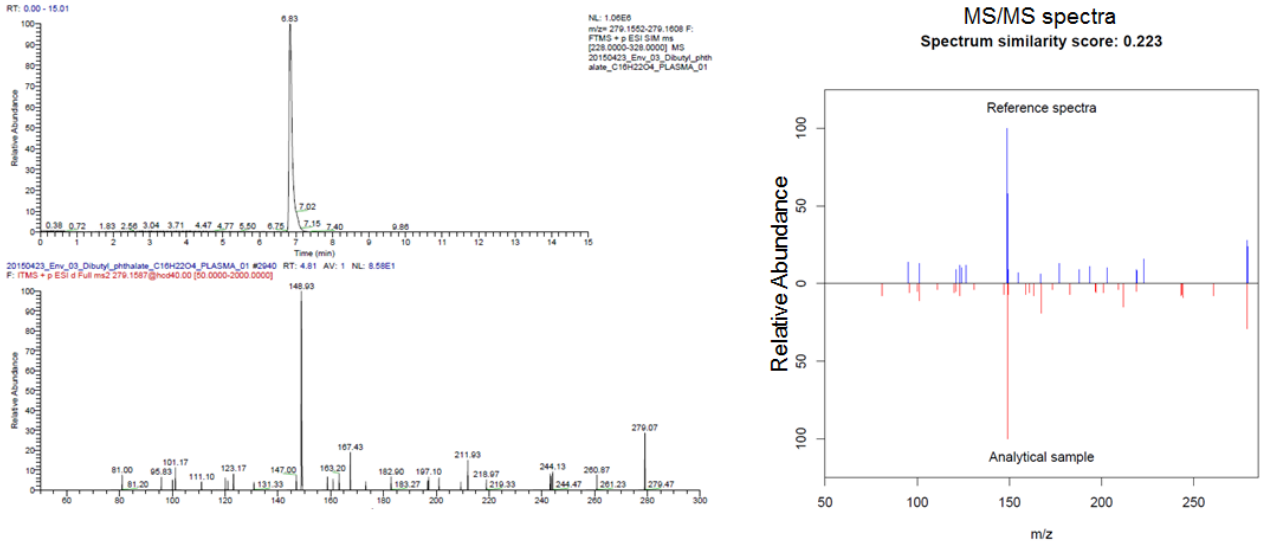


Reference spectra obtained on Thermo Fusion, Chlorsulfuron (99%), Sigma Aldrich

Dibutylphthalate (H^+, *m/z* 279.1580, 391s)

Dibutylphthalate was confirmed by coelution and MS/MS matching standard. Note that the peak coeluted with other chemicals in the isolation window so that fragmentation of other ions interfered with similarity scoring. Concern is frequently expressed that analysis of dibutylphthalate is invalid because of potential contamination due to contact of samples with plastics. The data reported in the present analysis represent the results of what was measured in the samples without any knowledge of how the phthalates were introduced into the plasma.

Dibutylphthalate M+H, *m/z* = 279.1580

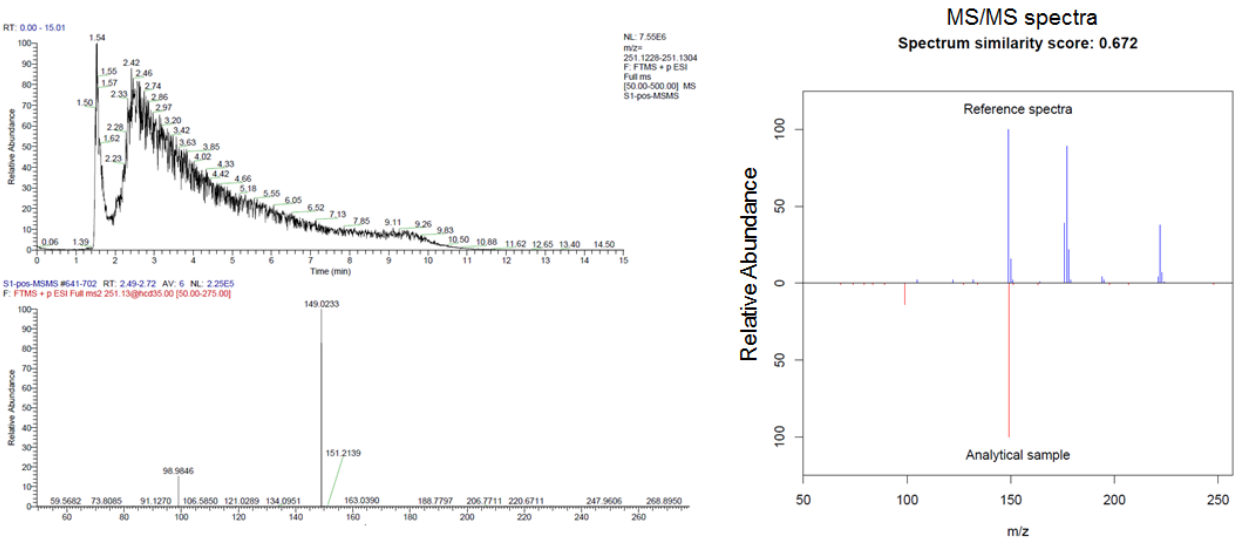


Reference spectra obtained on Thermo Fusion, Dibutyl Phthalate (99%), Sigma Aldrich

Dipropylphthalate (H^+, *m/z* 251.1266, 280s)

Dipropylphthalate was confirmed by coelution and MS/MS matching standard. Concern is frequently expressed that analysis of phthalates in plasma is invalid because of potential contamination due to contact of samples with plastics. The data reported in the present analysis represent the results of what was measured in the samples without any knowledge of how the phthalates were introduced into the plasma.

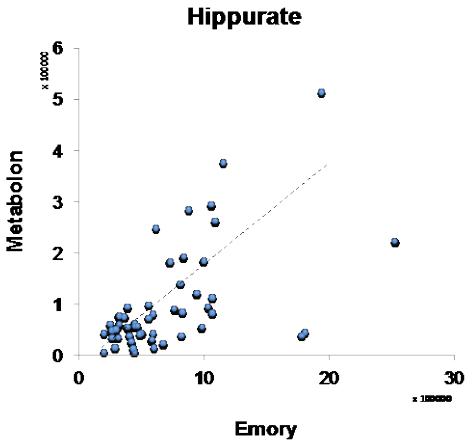
Dipropylphthalate M+H, *m/z* = 251.1266



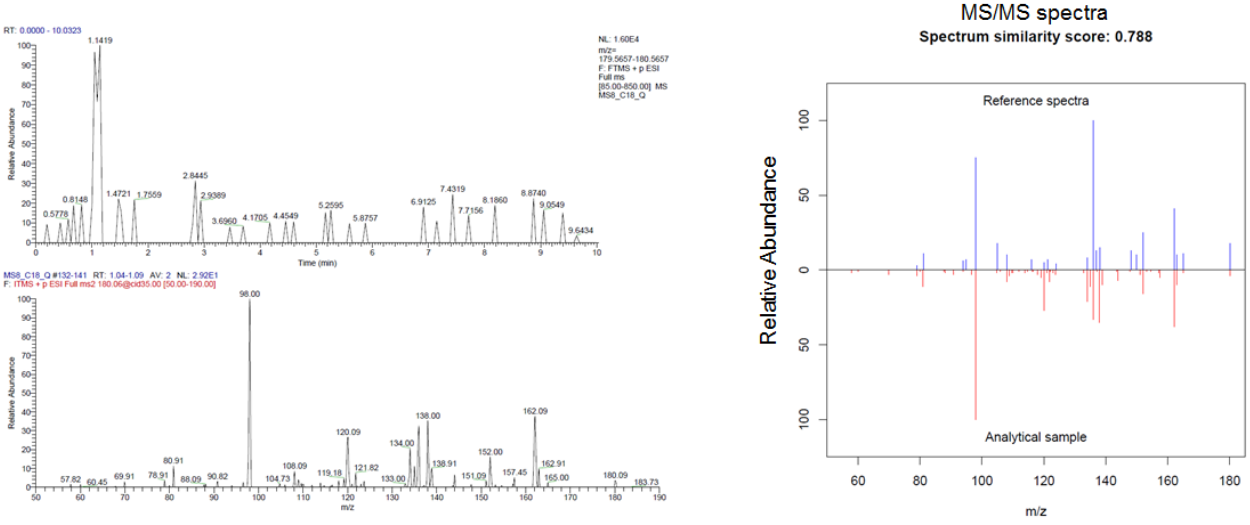
Reference spectra obtained on Thermo LTQ FTICR, Dipropylphthalate (98%), Sigma Aldrich

Hippuric acid (H^+, *m/z* 180.0657, 140s)

Hippuric acid was confirmed by coelution and MS/MS matching standard. Double-blind independent analysis (Emory platform vs Metabolon) on 50 marmoset samples showed a significant association with Pearson r= 0.56.



Hippuric acid M+H, *m/z* = 180.0657

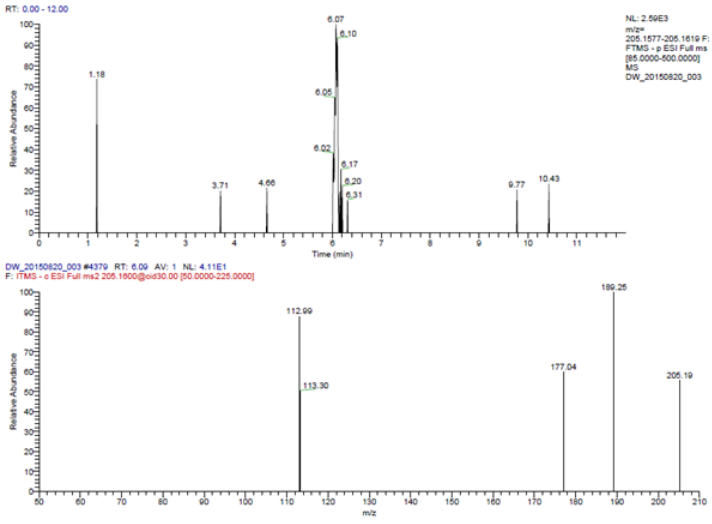


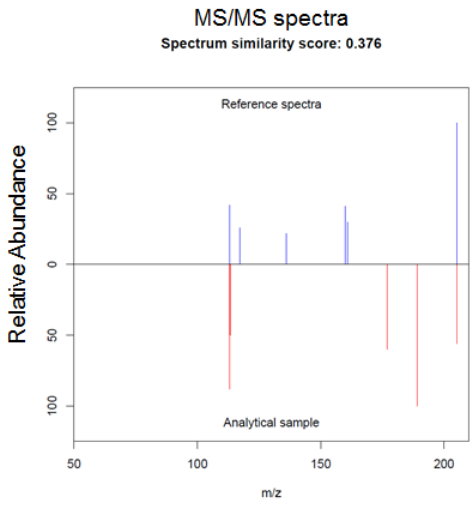
Reference spectra obtained on Thermo LTQ FTICR, Hippuric acid (98%), Sigma Aldrich

Octylphenol (M-H, *m/z* 207.1734, 282s)

Octylphenol ion intensity was too low in positive ESI to obtain useful MS/MS spectra. Corresponding analysis with negative ESI was used to confirm identity by coelution and MS/MS matching standard.

Octylphenol M-H, *m/z* = 205.1598





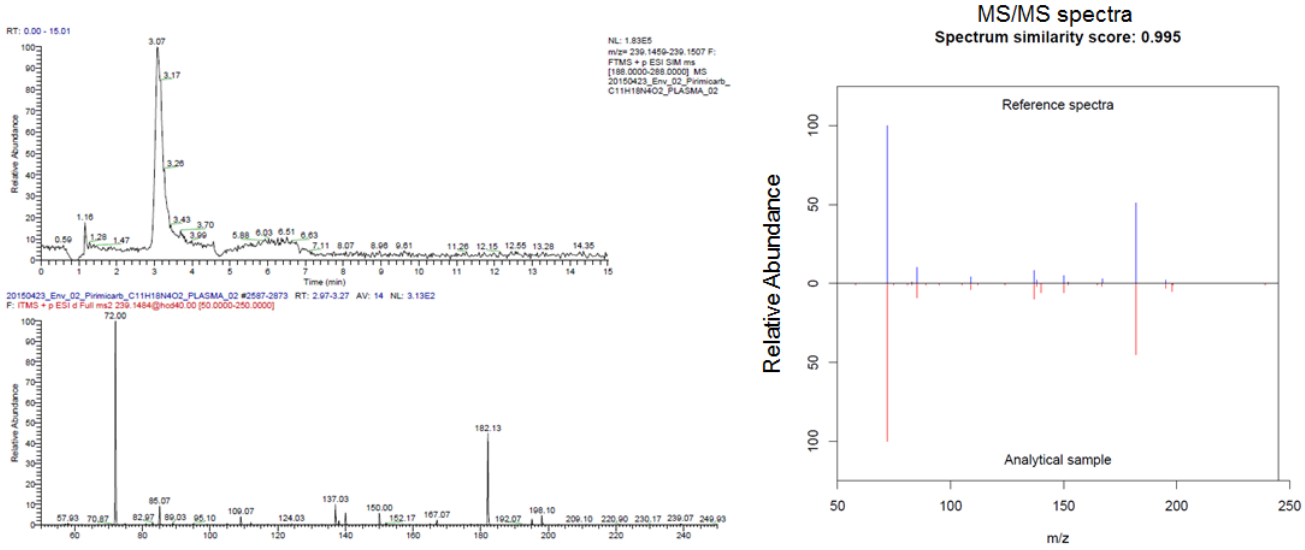
Due to low abundance of parent ion, MS/MS spectra was in negative mode and compared to retention time obtained in positive mode.

Reference spectra obtained on Thermo Fusion, Octylphenol(98%), Sigma Aldrich

Pirimicarb (H^+, *m/z* 239.1483, 552s)

Pirimicarb identity was established in earlier research (Park YH, Lee K, Soltow QA, et al. High-performance metabolic profiling of plasma from seven mammalian species for simultaneous environmental chemical surveillance and bioeffect monitoring. *Toxicology*. 2012;295(1-3):47-55. doi:10.1016/j.tox.2012.02.007.) and was confirmed by coelution and MS/MS comparison to authentic standard.

Pirimicarb M+H, *m/z* = 239.1483

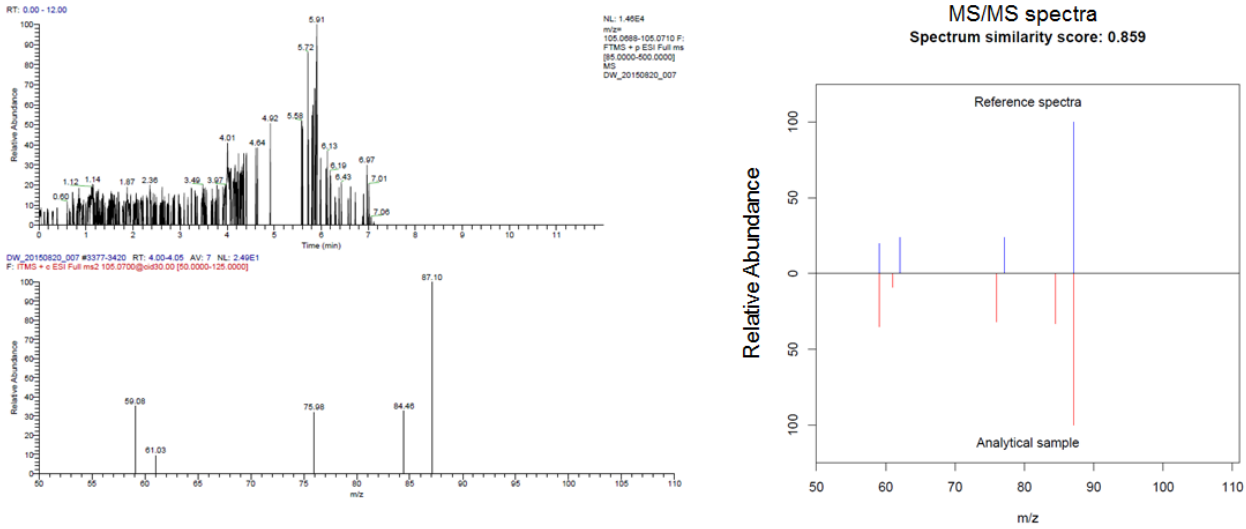


Reference spectra obtained on Thermo Fusion, Pirimicarb (99%), Sigma Aldrich

Styrene (H^+, *m/z* 105.0693, 298s)

Styrene was confirmed by coelution and MS/MS relative to authentic standard.

Styrene M+H, *m/z* = 105.0692

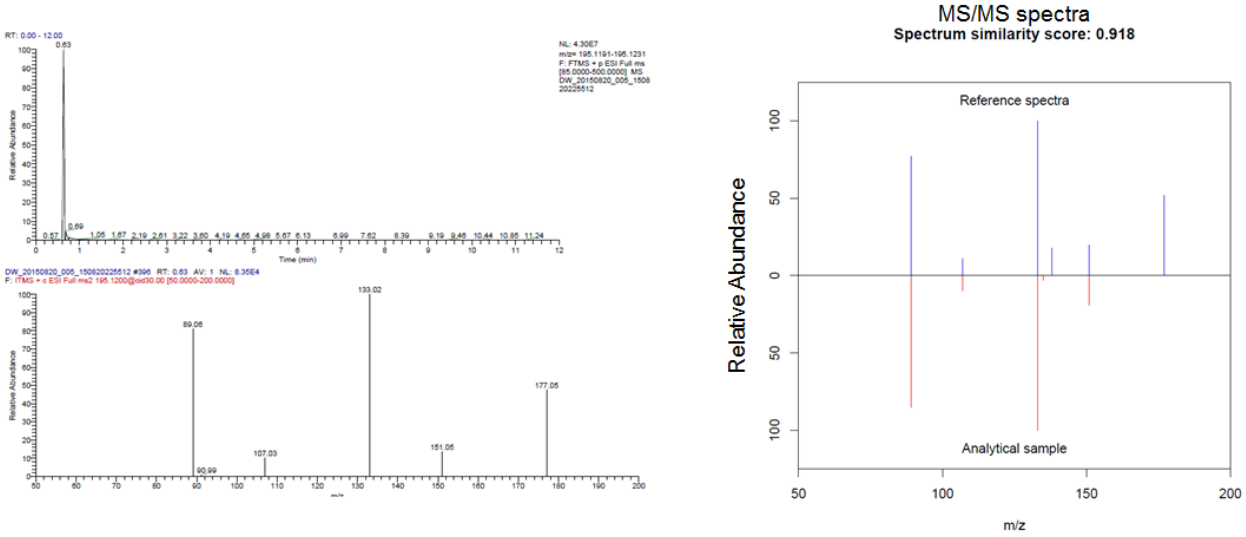


Reference spectra obtained on Thermo Fusion, Styrene (99%), Sigma Aldrich

Tetraethylene glycol (H^+, *m/z* 195.1211, 38s)

Tetraethylene glycol was confirmed by coelution and MS/MS matching standard.

Tetraethylene glycol M+H, *m/z* = 195.1211

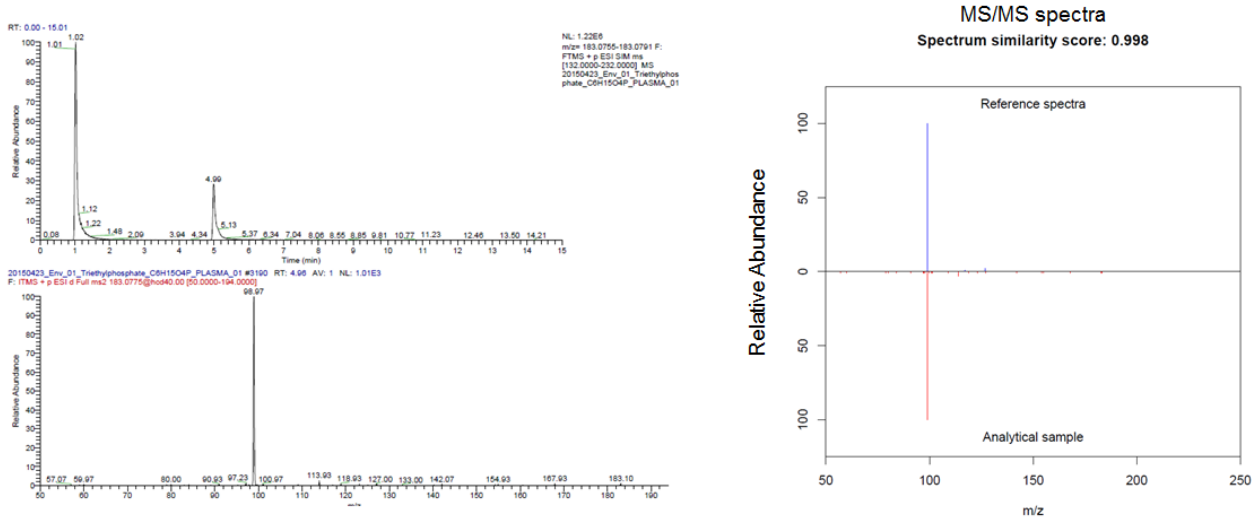


Reference spectra obtained on Thermo Fusion, Tetraethylene glycol (99%), Sigma Aldrich

Triethylphosphate (H^+, *m/z* 183.0773, 329s)

Triethylphosphate was confirmed by coelution and MS/MS matching standard.

Triethylphosphate M+H, *m/z* = 183.0773

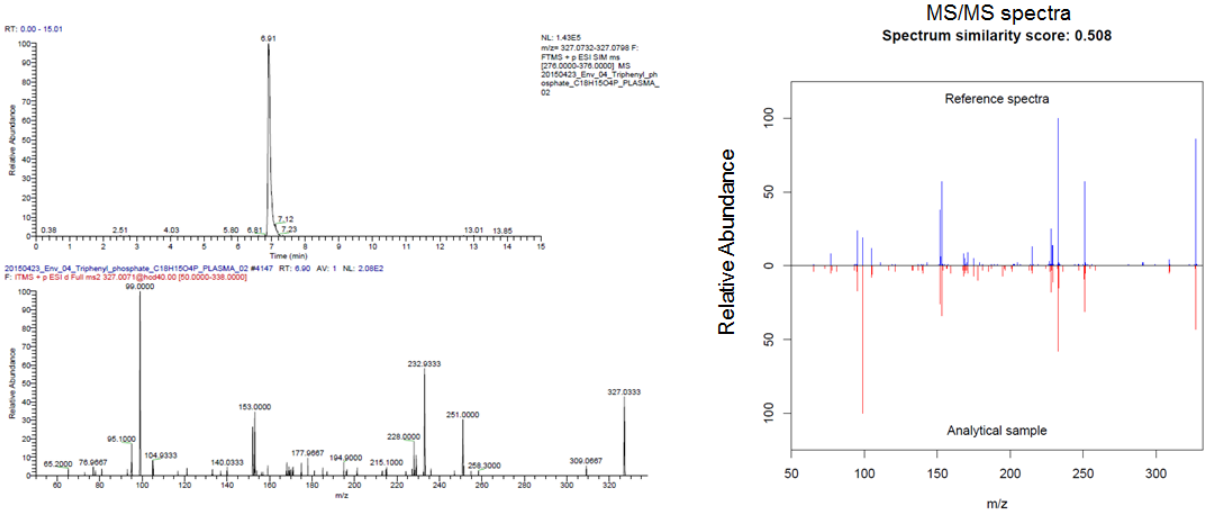


Reference spectra obtained on Thermo Fusion, Triethylphosphate (99.8%), Sigma Aldrich

Triphenylphosphate (H^+, *m/z* 327.0765, 359s)

Triphenylphosphate was confirmed by coelution and MS/MS matching standard.

Triphenylphosphate M+H, *m/z* = 327.0765

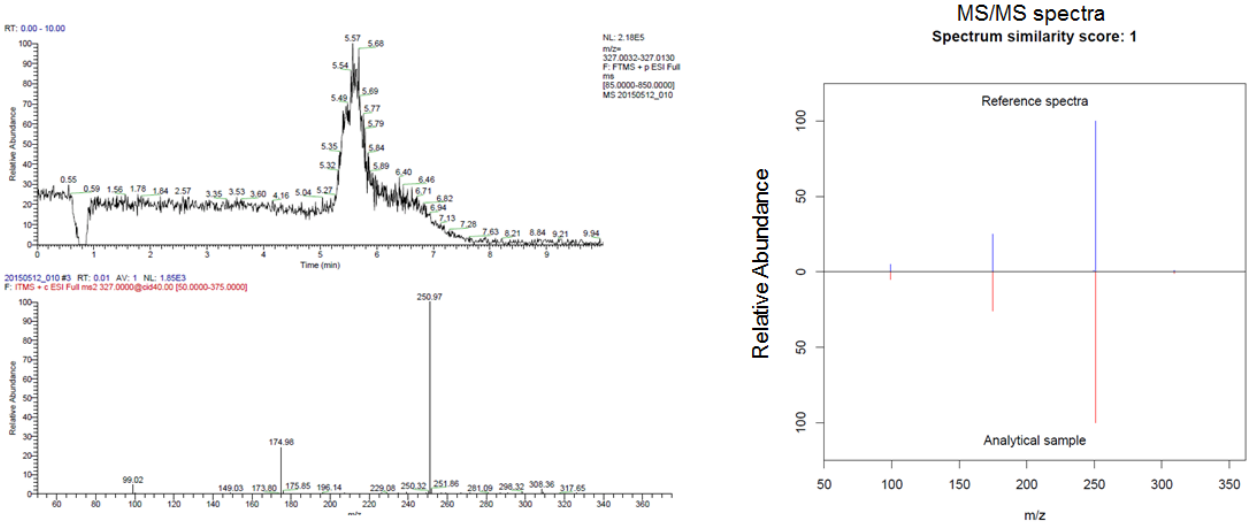


Reference spectra obtained on Thermo Fusion, Triphenylphosphate (99%), Sigma Aldrich

Tris(1-chloro-2-propyl) phosphate (H^+, *m/z* 327.0081, 330s)

Tris(1-chloro-2-propyl) phosphate was confirmed by coelution and MS/MS matching standard.

Tris(1-chloro-2-propyl) phosphate M+H, *m/z* = 327.0081

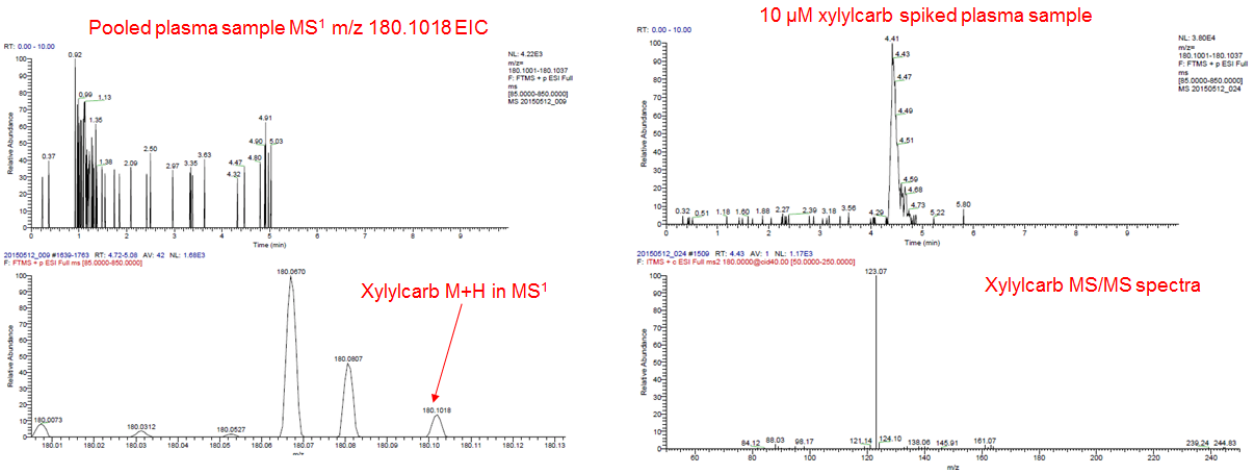


Reference spectra obtained on Thermo Fusion, Tris(3-chlorpropyl)phosphate (99%), Accustandard

Xylylcarb (H^+, *m/z* 180.1018, 264s)

Data are consistent with xylylcarb identification by coelution and MS/MS of added standard, but low intensity and fragmentation of other ions within the isolation window interfered absolute identification by MS/MS of samples without addition..

Xylylcarb M+H, *m/z* = 180.1018



Reference spectra obtained on Thermo Fusion, Xylylcarb (99%), HPC Standards