

1 **Global Tracking of Transformation Products of Environmental Contaminants**
2 **by ^2H -labeled Stable Isotope-Assisted Metabolomics**

3 Ke Chen^{1,*}, Yuhui Xiang¹, Xiaoyu Yan², Zhenghui Li³, Rui Qin⁴ and Jie Sun¹

4 ¹. College of Resources and Environmental Science, Key Laboratory of Resources
5 Conversion and Pollution Control of the State Ethnic Affairs Commission, South-
6 Central University for Nationalities, Wuhan, 430068, P.R. China;

7 ². Department of Chemistry, Renmin University of China, Beijing, 100872, P.R. China;

8 ³. School of Pharmaceutical Sciences, South-Central University for Nationalities,
9 Wuhan, Hubei 430074, P.R. China;

10 ⁴. College of Life Sciences, South-Central University for Nationalities, Wuhan, 430068,
11 P.R. China.

12

13 **Abbreviation List:**

14 TPs, transformation products;

15 GC, Gas Chromatography; LC, Liquid Chromatography;

16 UPLC, Ultra Performance Liquid Chromatography;

17 MS, Mass Spectrometry; HRMS, High Resolution Mass Spectrometry;

18 EI, Electron Ionization; ESI, Electrospray Ionization;

19 m/z, mass-to-charge ratio;

20 RT, retention time; EIC, Extracted Ion Chromatogram;

21 NMR, nuclear magnetic resonance spectrometer;

22 NTA, non-targeted analysis;

23 SIAM, Stable Isotope Assisted Metabolomics;

24 M, natural compounds; M', isotopically labeled M;

25

26

27 **Abstract**

28 Stable Isotope Assisted Metabolomics (SIAM) enables global tracking of isotopic
29 labels in non-targeted metabolomics in living organisms. However, its application in
30 tracking transformation products (TPs, as metabolites of contaminants) of
31 environmental contaminants is still a challenge due to limits in methodology,
32 unmatured algorithms, and the high cost of ^{13}C -labeled contaminants. Therefore, we
33 developed a ^2H -SIAM pipeline coupled with a highly flexible algorithm ^2H -SIAM(V1.0)
34 (<https://github.com/kechen1984/2H-SIAM>), facilitating tracking TPs of contaminants
35 in the environment matrix. A detailed discussion illustrates the theory, behavior, and
36 prospect of ^2H -SIAM. We demonstrate that the proposed ^2H -SIAM pipeline has unique
37 advantages over ^{13}C -SIAM, for example, cost-effective ^2H -labeled contaminants, easy
38 synthesis of ^2H -labeled emerging contaminants, and providing more structure
39 information. A pyrene soil degradation study further confirmed its high performance. It
40 efficiently discarded 99% noise signals and extracted 52 features from the non-targeted
41 High-Resolution Mass Spectrometry (HRMS) data. Among them, 13 features were
42 annotated as TPs of pyrene with identification confidence from Level 2a to Level 5,
43 and 5 TPs were reported for the first time. In conclusion, the proposed ^2H -SIAM
44 pipeline is powerful in tracking potential TPs of environmental contaminants with
45 unique advantages.

46 **Keywords:** Deuterium, Organic Contaminants, Transformation Products, Stable
47 Isotope, Non-targeted Analysis, High-Resolution Mass Spectrometry.

48 **Synopsis statement:** We provided a ^2H -labeled Stable Isotope-Assisted Metabolomics
49 pipeline as a powerful tool for tracking transformation products of environmental
50 contaminants.

51

52 **Introduction**

53 Anthropogenic organics in the earth generate countless transformation products
54 (TPs) by biological and non-biological factors. Their fates in the environment is of
55 increasing concern, as they may constitute higher toxicity than their parent
56 contaminants^{1,2}. Over the past decade, the growth, evolution, and accessibility of High
57 Resolution Mass Spectrometry (HRMS) has witnessed the progress of non-targeted
58 analysis (NTA), also referred to as "non-target screening", "untargeted metabolomics",
59 and "untargeted screening", among several other related terms³⁻⁵. Additionally, Stable
60 Isotope Assisted Metabolomics (SIAM) enables global tracking of isotopic labels from
61 parent compounds in non-targeted metabolomics in living organisms⁶⁻⁹. Numbers of
62 algorithms and software contribute to their raw data process, statistical analysis, and
63 annotation¹⁰⁻¹³.

64 However, the extremely high cost of ¹³C-labeled contaminants (e.g., ¹³C-labeled
65 persistent organic pollutants) limits the application of ¹³C-SIAM in the environmental
66 studies. As listed in Cambridge Isotope Laboratories (www.isotope.com), 0.12 mg of
67 pyrene-¹³C3 costs \$955, which is about 15000 times more expensive than pyrene-*d*10.
68 Then, it is only available to carry out ¹³C-SIAM in a very small microcosm, such as a
69 few grams of soil. The ¹³C-SIAM study, in a planted soil system or a 500-liter bioreactor,
70 is unacceptable due to the high cost of ¹³C-labeled contaminants.

71 An alternative solution is the use of ²H-labeled contaminants, that is ²H-SIAM,
72 costing much less than ¹³C-SIAM. Additionally, direct H/D exchange reactions enable
73 to add ²H-labels to emerging contaminants with mild reaction conditions¹⁴, broadening
74 the source of isotope-labeled contaminants. However, misunderstanding of ²H-labeled
75 contaminants, unmatured methodology and algorithms for SIAM limit the application
76 of ²H-SIAM in the environment studies.

77 Credentialing features and ALLocator are designed solely for ¹³C-labeled
78 isotopologue (Table S1)^{15, 16}. MetExtract II, HiTIME and ALLocator, collect data
79 directly from scans of the mass spectrum when isotopologue pairs are coeluted¹⁶⁻¹⁸.
80 ¹³C-labels always occur in the backbone of chemicals, and ²H-labels are located in the
81 surface layer of molecule architecture, which may result in an apparent difference of
82 retention time (RT) between ²H-labeled isotopologue pairs¹⁹. In this scenario, the scan-
83 based algorithm could not delicately deal with ²H-SIAM.

84 Additionally, some published algorithms for SIAM, for instance, X13CMS,
85 geoRge, ALLocator, and MzMatch-ISO, were designed with XCMS^{16, 20-22}, or with

86 embedded data processing algorithms ([Table S1](#))^{17, 18, 23}. The application of them needs
87 fundamental knowledge about those bioinformatics tools or limits the choice of data
88 processing algorithms to obtain a features list (features with m/z, RT, and intensities).
89 Other widely used data processing algorithms, for instance, MZmine2 and MS-DIAL,
90 were excluded. They are user-friendly, flexible, and easily extendable, covering the
91 entire LC-MS data analysis workflow, which could be a powerful tool in SIAM.

92 Then, we explored a ²H-SIAM pipeline to address the issue. A features-based
93 algorithm, namely ²H-SIAM(V1.0) (For Win10, by Visual Basic .NET), was developed
94 to extract ²H-labeled isotopologue pairs. The accuracy of the pipeline was evaluated by
95 non-targeted recovery of 7 isotopologue pairs mixed in soil extract. The possible
96 application of H/D exchange in ²H-SIAM was evaluated by the synthesis and structure
97 analysis of 6PPD-*d*9 (6PPD, N-(1,3-dimethylbutyl)-N'-phenyl-p-phenylenediamine).
98 The overall performance of the pipeline was finally evaluated by a soil pyrene
99 degradation study.

100 **Methods**

101 **Algorithm ²H-SIAM(1.0)**

102 When a features list (.csv format) is imported into ²H-SIAM(V1.0), it starts with
103 the calculation of means of replicates. Then, the features list is inspected within an
104 indicated duration of RT for pairs of two features as potential isotopologue pairs; the
105 potential natural compounds are denoted as M, and the potential isotope-labeled
106 compounds are denoted as M'. The mean intensities of the features M and M' from
107 samples Mix_{1:3} and Mix_{3:1} are denoted as M_{Mix1:3}, M_{Mix3:1}, M'_{Mix1:3} and M'_{Mix3:1}
108 respectively. They are used for the calculation of the following 3 actual ratios (f_n):

$$109 \quad f_1 = \frac{M_{Mix1:3}}{M'_{Mix1:3}}, \quad f_2 = \frac{M_{Mix3:1}}{M'_{Mix3:1}}, \quad f_3 = \frac{M'_{Mix1:3}}{M'_{Mix3:1}}$$

110 users defined parameters R_n and Tol._n are used to set triple filters (F₁, F₂ and F₃)
111 for TPs as following:

$$112 \quad \text{Filter } n, F_n: \quad R_n \times \text{Tol.}_n < f_n < R_n \times \text{Tol.}_n^{-1}$$

113 where, R_n is theoretic ratios for F_n, and Tol._n is tolerances for R_n, 0 < Tol._n < 1.

114 When f₁ follows the requirement of F₁, a pair of two features (isotopologue pair)
115 is tracked by the algorithm and further filters F₂ and F₃ will be sequentially evaluated.
116 The features passing triple filters contain features as potential TPs, deserving further
117 annotation and identification.

118 **Recovery of 7 Isotopologue Pairs from Soil Extract by ²H-SIAM**

119 Crude soil was air-dried and sieved (< 2 mm) to remove debris and ready for use
120 as blank soil as our previous report²⁴. Per gram of blank soil was extracted by 10 mL
121 of acetone (ACE) and hexane (HEX) (1:3, v/v) by microwave extraction (Anton Paar
122 GmbH, Multiwave PRO, Austria). After that, ACE and HEX were replaced by
123 acetonitrile (MeCN) by solvent exchange, and anhydrous Na₂SO₄ (baked at 450 °C for
124 4 h prior to use) was used to remove residual water. Extracts were concentrated to 2 mL
125 under nitrogen flow and divided into three aliquots, and one of them was used as blank.

126 10 ppm of 7 natural contaminants (dichlorvos, atrazine, sulfamethoxazole,
127 naphthalene, pyrene, fluorene, anthracene) and 30 ppm of their ²H-labeled
128 isotopologues (dichlorvos-*d*6, atrazine-*d*5, sulfamethoxazole-*d*4, naphthalene-*d*8,
129 pyrene-*d*10, fluorene-*d*10, anthracene-*d*10) were added into one aliquot to obtain Mix_{1:3}
130 sample. Meanwhile, 30 ppm of natural contaminants and 10 ppm of ²H-labeled
131 isotopologues were added to another aliquot to obtain a Mix_{3:1} sample. 20 ppm of 7
132 isotope pairs were prepared as standard. Fluorene-¹³C₆ was added to all the
133 extracts as an internal standard.

134 Standard, blanks and mixed samples were analyzed by UPLC-ESI-HRMS,
135 Ultimate 3000 (Dionex) coupled with a Q Exactive Orbitrap mass spectrometers
136 (Thermo) and heated electrospray ionization (ESI) source. More details were provided
137 in [Supporting Information 1](#).

138 **Synthesis and Structure of 6PPD-*d*9 and its Application in ²H-SIAM**

139 500 mg 6PPD, 100 mg 5% Pt/C, 50 mg 10% Pd/C and 15 mL D₂O were mixed in
140 a 100 mL glass reactor. Then, the air in the reactor was replaced by H₂ (99.999%), and
141 the reaction was stirred at 80 °C under an H₂ atmosphere for 24 h^{25,26}. Then the mixture
142 was extracted with ethoxyethane (ETH) and dried in a centrifuge evaporator (RVC 2-
143 25 CD Plus, Christ, Germany) to obtain brown color products (1st round products). The
144 reaction was repeated twice to obtain highly ²H-labeled 6PPD-*d*9 (3rd round products,
145 about 50 mg). 6PPD, 1st, and 3rd rounds of H/D exchange products were characterized
146 by GC-MS (Thermo, Trace 1300, TSQ9000EVO triple quadrupole). The 3rd round
147 product was further characterized by a 600 MHz nuclear magnetic resonance
148 spectrometer (NMR, Ascend 600, Bruker). ¹H NMR spectra were obtained by using
149 DMSO-*d*6 as solvent. The deuterium incorporation levels were determined by the ¹H
150 NMR spectrum, which showed hydrogen residue signals.

151 6PPD and synthesized 6PPD-*d*9 were added into soil extract to prepare Mix_{1:3} and
152 Mix_{3:1} samples independently as introduced above. Sulfadiazine-¹³C₆ was used as an

153 internal standard, and other details were provided in [Supporting Information 1](#).

154 **Non-targeted Analysis of TPs of Pyrene from Soil by ^2H -SIAM Pipeline**

155 To evaluate the performance of the ^2H -SIAM pipeline, a soil pyrene degradation
156 study was carried out. Pyrene and pyrene-*d*10 were dissolved in ACE and mixed with
157 one-quarter blank soil. After solvent evaporation, they were mixed respectively with
158 the rest bulk soils to obtain 100 ppm pyrene and 100 ppm pyrene-*d*10 contaminated
159 soils. Then, blank and contaminated soils were placed at room temperature for 60 days
160 and watered twice per month to keep soil moisture. One aliquot of contaminated soils
161 was stored in -80 °C to verify the stability of ^2H -labels.

162 After 60 days incubation, soils were air-dried at 60 °C until to constant weight. Per
163 gram of soils were extracted by 10 mL ACE and HEX (1:3, v/v) by microwave
164 extraction with the addition of ortho-terphenyl (OTP) as extraction surrogate, and
165 anhydrous Na₂SO₄ were used to remove residual water. The solvent was replaced by
166 acetonitrile (MeCN), and extracts were concentrated to 1 mL under nitrogen flow.

167 Extracts from pyrene and pyrene-*d*10 treatments were mixed with the ratio of 1:3
168 and 3:1 to obtain Mix_{1:3} and Mix_{3:1} samples. Anthracene-*d*10 was added into samples
169 as an internal standard. Then, samples were subjected to UPLC-ESI-HRMS analysis
170 and GC-EI-HRMS analysis, and details were provided in [Supporting Information 1](#).

171 Mass spectrum raw data were formatted to .mzXML and MZmine2 was used to
172 obtain features lists^{27,28}. Features of isotopologue pairs were tracked by ^2H -SIAM(1.0),
173 and it tracked 162 features from GC-EI-HRMS data (21955 features) and 52 features
174 from UPLC-ESI-HRMS data (4376 features).

175 The tracked features from HRMS were recorded as MS¹ precursors, and they were
176 annotated against KEGG and PubChem database (by MZmine2), or manually. Then,
177 the MS¹ precursors from UPLC-ESI-HRMS analysis were further fragmented in
178 quadrupole mode with a 0.4 m/z isolation window and nominal collision energy of 40,
179 and MS² fragmentations were scanned with orbitrap at a resolution of 140000. The MS²
180 fragments from UPLC-ESI-HRMS and fragments from GC-EI-HRMS were matched
181 against the mass spectrum predicted by CFM-ID 3.0 for further identification²⁹.
182 Detailed information was provided in [Supporting Information 1](#).

183 **Identification Confidence**

184 Compared to common NTA, the tracked features by ^2H -SIAM coeluted with their
185 isotopologues, confirming its origination from substrates and providing basic structure
186 information. Additionally, the number of ^2H -labels provides potential structure

187 information. Thus, we annotated TPs with identification confidence levels proposed by
188 Schymanski et al. but with little modification³⁰.

189 Level 1 was achieved by matching the RT and MS² with reference standards; Level
190 2a was achieved by matching the number of possible ²H-labels and at least two major
191 fragment ions with MS² libraries (from *in silico* or references spectrum), or achieved
192 by matching at least three major fragment ions with MS² libraries; Level 2b was
193 achieved by matching the number of possible ²H-labels and one major fragment ions
194 with MS² libraries, or achieved by matching at least two major fragment ions with MS²
195 libraries; Level 3 was achieved by matching the number of possible ²H-labels and
196 natural isotope pattern, or achieved by matching one major fragment ions with MS²
197 libraries; Level 4 was achieved by matching the number of possible ²H-labels, or natural
198 isotope pattern; Level 5 was achieved by matching the exact mass.

199 **Quality Control and Data Availability**

200 For qualitative analysis, quality control (QC) samples were prepared by a pool of
201 extracts, and it was used to stabilize the chromatographic system and to verify the
202 stability of the measurements. Indicated internal standard was added into samples to
203 calibrate the fluctuation of the instrument. Quantitative of pyrene and pyrene-*d*10 by
204 GC-MS were analyzed using one-way analysis of variance (ANOVA) followed by the
205 Duncan test, where different letters indicate significant differences at *p* < 0.05.

206 The code of ²H-SIAM (V1.0) was published in
207 <https://github.com/kechen1984/2H-SIAM>, which provide a link from Mendeley Data
208 with example data of the soil pyrene degradation study, software, and details for use of
209 ²H-SIAM(1.0).

210 **Results and Discussion**

211 **Methodology of ²H-SIAM**

212 The application of ²H-SIAM in the environmental studies still faces challenges.
213 People may worry about the stability of ²H-labeled contaminants due to the so-called
214 deuterium loss or H/D back exchange, resulting in the loss of ²H-labels during the study.
215 The stability of ²H-labels in contaminants depends on their location. H/D back
216 exchange generally occurs in the labile ²H atom, e.g., ²H in carboxyl and amino groups,
217 which may result in the loss of 20-30% ²H atoms, and it does not occur in the sites of
218 C-D, which is the most popular ²H-labeled site in contaminants^{31, 32}. Our study also
219 proved that 60 days incubation of pyrene and pyrene-*d*10 in soil under -80 °C or ambient
220 temperature (biotransformed by microorganisms) did not result in a significant

221 difference between signals from pyrene and pyrene-*d*10 ([Fig. S1](#)), confirming the
222 stability of ²H-labeled contaminants over the experiment.

223 Additionally, unmatured methodology and algorithms limit the use of ²H-SIAM in
224 the environment studies ([Table S1](#)). We developed a features-based algorithm ²H-
225 SIAM(V1.0) ([Fig S2](#)) to carry out SIAM, and the proposed pipeline is shown in [Fig. 1](#).
226 It is a fully GUI-based pipeline, lowering the skill barriers for its application. Parent
227 isotopologue pairs of contaminants are added into the environmental matrix
228 respectively and incubated for the indicated duration. They are extracted and mixed
229 with indicated ratios (e.g., 1:1 and 1:2, 1:3 and 3:1, 1:9 and 9:1). We propose a 1:3 and
230 3:1 ratio (Mix_{1:3} and Mix_{3:1} samples), keeping an appropriate equilibrium between
231 accuracy and sensitivity for tracking isotopologue pairs. That is because a high mix
232 ratio will dilute extracts, leading to the loss of positive signals.

233 Mixed samples are then determined by MS platforms (e.g., UPLC-ESI-HRMS,
234 GC-EI-HRMS). MS raw data from Mix_{1:3} and Mix_{3:1} samples are transformed
235 to .mzXML format and imported into MZmine2 to obtain a features list ([Fig. S3](#)). Any
236 other MS data processing algorithm, e.g., XCMS and MS-DIAL, are compatible when
237 they could output a features list. The key for efficiently tracking TPs is to acquire a
238 high-quality features list, and the optimized parameters for the selected algorithm are
239 critically important.

240 When the features list (.csv format) is imported into ²H-SIAM(V1.0), it starts with
241 qualitatively tracking of isotopologue pairs with the indicated isotope labels, m/z, and
242 RT tolerance ([Fig. S4](#)). Then, 3 quantitative filters F₁, F₂, and F₃ are used to track
243 features of TPs with isotopologues. After that, ²H-SIAM(V1.0) will output a new
244 features list, and only a small portion of features (1% - 2%) will be tracked by triple
245 filters and be marked with numbers of isotope labels ([Table 1, Supporting Information](#)
246 [2](#) and [3](#)). This step will exclude many noise features, and potential TPs could be
247 annotated among the tracked features, contributing to further identification. Although
248 the ²H-SIAM pipeline is designed for the tracking of ²H-labeled TPs by UPLC-ESI-
249 HRMS, data from any other types of LC-MS or GC-MS platform or any other types of
250 isotope-labeled atoms, e.g., ¹³C, ¹⁵N, and ¹⁸O, are compatible ([Table S2](#)).

251 Additionally, even though many MS²-based algorithms have been recently
252 developed for the discovery of unknown compounds ³³⁻³⁵, it is still critically important
253 to obtain TPs information by isotope labels and MS¹ features. That is because isotope
254 labels provide direct evidence for the origination of TPs. Meanwhile, the signals from

255 TPs of substrates are always weak, and their signals may be lost in data dependent or
256 independent acquisition of MS².

257 **Accuracy of the ²H-SIAM Pipeline**

258 To verify the accuracy of the proposed pipeline, 7 isotopologue pairs of typical
259 environmental contaminants were added into soil extract to examine whether the
260 designed pipeline could pick them up from soil extracts. Same amounts of contaminants
261 (10 ppm) were ionized by ESI with different efficiency, and signals varied from 3×10^5
262 to 7×10^7 (height, [Fig. 2a](#) and [Fig. S5](#)). Signals from polycyclic aromatic hydrocarbons
263 (PAHs, anthracene, pyrene, fluorene, and naphthalene) were lower than pesticides,
264 herbicides, and antibiotics due to relatively lower ionization efficiency.

265 The features-based algorithm ²H-SIAM(V1.0) compared features by their
266 maximum intensities (height/area) with indicated RT tolerance, avoiding the loss of
267 positive signals. All of the 7 isotopologue pairs were correctly tracked from thousands
268 of noises ([Table 1](#), [Supporting Information 2](#)), and two examples with triple filters were
269 shown in [Fig. 2b](#) and [2c](#). Filters F₁ and F₂ compare intensities of features from natural
270 and ²H-labeled compounds from Mix_{1:3} and Mix_{3:1} samples, and the ratios theoretically
271 should be 1/3 and 3, respectively. Filter F₃ compared intensities of ²H-labeled
272 compounds from Mix_{1:3} and Mix_{3:1}, and theoretically, it should be 3. Then combination
273 of the theoretic ratio and appropriate settled tolerance constitute triple filters embedded
274 in the algorithm. Additionally, since signals from the same amount of natural and ²H-
275 labeled contaminants are not always equivalent, F₁ and F₂ constitute relaxed filters with
276 a lower Tol. of 0.3, and F₃ constitute a stricter filter with a higher Tol. of 0.5.

277 The peak times of isotopologue pairs of PAHs were different, which may affect the
278 performance of SIAM analyzed by scan-based algorithms ([Table S1](#)). They compare
279 natural and isotope-labeled signals from the same scan, relying on the coelute of
280 isotopologue pairs. [Fig. 2d](#) and [Fig. 2e](#) depicted mass spectrums (MS scan #1691 and
281 MS scan #1726) from peaks of EIC (Extracted Ion Chromatogram) of pyrene and
282 pyrene-*d*10 of Mix_{1:3} sample at 14.75 and 15.05 minutes. As shown, when isotopologue
283 pairs elute at different times, there is an uncrossable gap between the theoretic (1:3,
284 equal to 0.333) and observed (0 and 53) ratio of height between isotopologue pairs.
285 That may result in the loss of positive signals for scan-based algorithms.

286 **H/D Exchange and its Application in ²H-SIAM**

287 Direct H/D exchange reaction enables unique or site-specific H/D-exchange,
288 providing valuable and cost-effective isotope-labeled contaminants ^{14, 36}. 6PPD-

289 quinone is the TPs of 6PPD, and the toxicity of 6PPD-quinone to *Oncorhynchus kisutch*
290 is confirmed by *Science* in 2021³⁷. Here we show how ²H-labels be selectively added
291 into this emerging contaminant when a ¹³C-labeled compound is unreachable. The H/D-
292 exchange reacted in a glass tube with catalysts, H₂, and D₂O as deuterium source at 80
293 °C for 24 hours (Fig. 3a) . After the 1st round reaction, we found 6PPD-*d*6, 6PPD-*d*7,
294 6PPD-*d*8, and 6PPD-*d*9 in the mass spectrum (Fig. 3d), and 6PPD-*d*9 signal accounts
295 for approximately 21% of all ²H-labeled 6PPD. After the 3rd round reaction, the 6PPD-
296 *d*9 (~50mg) accounts for approximately 51% of all ²H-labeled 6PPD, and 80% of ²H-
297 labels were added onto aromatic rings (Fig. 3be), which could be used to track 6PPD
298 by ²H-SIAM(1.0) (Fig. 3fg).

299 As 100 grams of D₂O (99.9%, Sigma-Aldrich) cost only ~\$300, and catalysts could
300 be reused, the possible H/D-exchange reaction offers various affordable ²H-labeled
301 contaminants. Thus, it enables us to carry out ²H-SIAM in a complex environmental
302 matrix, for instance, an ecotron with several cubic meters of reconstituted aquatic
303 ecosystem.

304 **Performances of ²H-SIAM in Tracking TPs of Pyrene in Soil**

305 The performance of ²H-SIAM in tracking possible TPs of contaminants is evaluated
306 by a soil PAHs degradation study. Pyrene was selected as the parent contaminant, as
307 TPs of pyrene have been widely studied and recorded in KEGG (<https://www.kegg.jp>),
308 enabling us to evaluate the accuracy of the ²H-SIAM pipeline. Additionally, the peak
309 times of its isotopologue pairs are different, and its ionization efficiency is relatively
310 low, providing a challenging situation for the proposed ²H-SIAM pipeline.

311 Overview of the performance of the ²H-SIAM pipeline carried out by UPLC-ESI-
312 HRMS and GC-EI-HRMS were provided in Table 1, and the pipeline efficiently
313 discarded ~99% features, and only ~1% features had been tracked by triple filters (162
314 and 52). It is, arbitrarily, more efficient than a Credentialing Features study, ¹³C-SIAM
315 of glucose, which discarded 93% features and ~1800 features left (~7%)¹⁵. It also
316 confirmed the importance of triple filters. If only one quantitative filter was used (F₁),
317 1122 and 318 features were left (Table 1), which is six times more than that from triple
318 filters (162 and 52 features). Thus, the algorithms with triple filters are better than
319 algorithms with only one filter (Table S1).

320 For data from UPLC-ESI-HRMS, the algorithm tracked 52 potential isotopologue
321 pairs, and 13 isotopologue pairs were annotated as potential TPs (Fig. 4, Table S3, Fig.
322 S6-S10), which accounts for highly to 25% of the total extracted features. Cheng

323 successfully annotated 7 isotopologue pairs as potential TPs of mono-*n*-butyl phthalate
324 using ²H-labeled contaminants and MetExtract II ³⁸. Tian annotated 6 isotopologue
325 pairs as potential TPs of pyrene by ¹³C-labeled pyrene and X13CMS ³⁹. By our
326 proposed pipeline, 13 TPs of pyrene were annotated proving its higher performance
327 with cost-effective properties.

328 4 isotopologue pairs detected from UPLC-ESI-HRMS data (e.g., M₂₂₁, [M+H]⁺)
329 were further tracked by GC-EI-HRMS (e.g., M₂₂₀, [M]⁺, [Table S4](#)). Their fragment
330 from natural and ²H-labeled contaminants fit well to the fragment predicted by CFM-
331 ID ([Fig. 4e](#), [Fig S11-S13](#)) ²⁹, contributing to improve the identification confidence
332 levels of TPs obtained by UPLC-ESI-HRMS data ([Table S3](#)).

333 Additionally, isotope labels are important for tracking possible TPs in the
334 environment because the environment matrix may contain TPs naturally. As shown in
335 [Fig. S14](#), we detected a feature annotated as phthalic acid, TPs of pyrene listed in KEGG.
336 However, we could not find its ²H-labeled isotopologue, indicating that the detected
337 phthalic acid is natural existed rather than TPs of pyrene in our experiment regime.

338 M₂₃₃ at 12.8 min and 13.6 min from UPLC-ESI-HRMS data were annotated as
339 pyrenequinone ([Fig. 4b](#), [Table S3](#)), and their isotopologue pairs M_{233-d8} were correctly
340 paired. According to the difference of LogK_{ow} of pyrenequinone estimated by EPISuite
341 (<https://www.epa.gov>) and RT of detected features, we could tentatively annotate M₂₃₃
342 at 12.8 min as 1,6- pyrenequinone and annotate M₂₃₃ at 13.6 min as 4,5-pyrenequinone
343 respectively. MS² of M₂₃₃ and M'_{233-d8} at 13.6 min were plotted in [Fig. 4d](#). The detected
344 MS² spectrum and isotope pattern of M₂₃₃ and M_{233-d8} matched the MS² spectrum and
345 isotope pattern predicted by algorithms within 5 ppm mass error, indicating
346 identification confidence at Level 2a.

347 Except for reported TPs of pyrene, we also detected 5 unreported potential TPs of
348 pyrene, M₂₃₅, M₂₂₅, M₂₄₄, M₂₄₇, and M₂₃₁. M₂₃₅, corresponding to [C₁₆H₁₀O₂+H]⁺ with
349 isotope patent score of 97% (MZmine2), was annotated by KEGG as dihydropyrene or
350 1-hydroxypyrene-6,7-oxide and 1-hydroxypyrene-7,8-oxide. However, the
351 isotopologue pair of M₂₃₅ is M'_{235-d10}, labeled with 10 of ²H atoms. The formation of
352 pyreneoxide is accomplished by cytochrome P450 superfamily, an unspecific
353 monooxygenase, which theoretically will not result in the loss of ²H-labels. Thus, M₂₃₅
354 was annotated as pyreno[4,5-b:9,10-b']bisoxirene, 3b,4a,7b,8a-tetrahydro- (PubChem
355 CID 616438) according to 10 discovered ²H atoms in M'_{235-d10}, which has not been
356 included in KEGG. This speculation exhibited the advantage of ²H-labels over ¹³C-

357 labels, as the numbers of ²H-labels contribute to deducing possible structure. Thus, as
358 introduced in the Methods, we slightly promote the identification confidence levels of
359 potential TPs with correct ²H-labels.

360 Speculation of the structure of M₂₃₁ and M₂₄₇ were ambiguous due to the
361 inconsistent numbers of ²H-labels. However, M₂₃₁, M₂₄₇, and M₂₄₄ point to the
362 possibility that carbon atom is directly added to aromatic rings, which has not been
363 reported before in the environmental studies. Due to the focus of the study, their
364 identification will be further confirmed in the future by separation, purification, and
365 NMR or MSⁿ structure analysis. Additionally, it should be noted that NTA by mass
366 spectrometry is blind to stereochemistry and often regiochemistry⁴⁰. Isomers of the TPs
367 cannot be excluded, and exact annotations should be done by comparing with references
368^{3, 41}.

369 Conclusion

370 In summary, our study confirms the performance of the ²H-SIAM pipeline in
371 tracking and discovering TPs of contaminants in the environment. The proposed fully
372 GUI-based pipeline is friendly to users. Additionally, it has shown unique advantages
373 over ¹³C-SIAM, for instance, affordable and highly customized ²H-labeled
374 contaminants, and providing more structure information. Thus, ²H-SIAM is
375 recommended as a powerful tool in understanding the fate of environmental
376 contaminants.

377 Acknowledgments

378 This work was financially supported by the National Natural Science Foundation
379 of China (41503067 and 31870513). This paper is dedicated to the memory of S.Y. Ke.

380 Author Contributions

381 K.C. designed the study; K.C., Y.H.X, X.Y.Y., and Z.H.L. collected and analyzed
382 the data; K.C. wrote the manuscript; R.Q. and J.S. financially supported the study; all
383 authors contributed substantially to the revision.

384 Competing interests declares:

385 The authors declare no competing financial interest.

386 Supporting Information:

387 [Supporting Information 1](#): supplemental methods, figures, and tables. [Supporting](#)
388 [Information 2](#): output files of ²H-SIAM(1.0) for the recovery study of 7 contaminants
389 (UPLC-ESI-HRMS). [Supporting Information 3](#): output files of ²H-SIAM(1.0) for the
390 soil pyrene degradation study (GC-EI-HRMS).

391 **References**

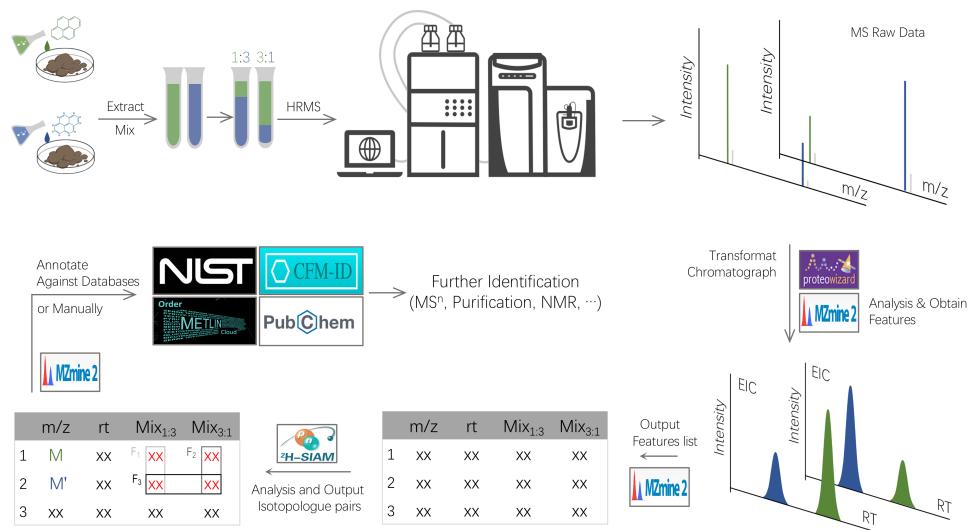
- 392 1. Brussaard, C. P. D.; Peperzak, L.; Beggah, S.; Wick, L. Y.; Wuerz, B.; Weber, J.; Arey, J. S.; van
393 der Burg, B.; Jonas, A.; Huisman, J.; van der Meer, J. R., Immediate ecotoxicological effects of
394 short-lived oil spills on marine biota. *Nature Communications* **2016**, *7*, 11206.
- 395 2. Gonzalez-Gaya, B.; Martinez-Varela, A.; Vila-Costa, M.; Casal, P.; Cerro-Galvez, E.; Berrojalbiz,
396 N.; Lundin, D.; Vidal, M.; Mompean, C.; Bode, A.; Jimenez, B.; Dachs, J., Biodegradation as an
397 important sink of aromatic hydrocarbons in the oceans. *Nat Geosci* **2019**, *12*, (2), 119–125.
- 398 3. Sindelar, M.; Patti, G. J., Chemical Discovery in the Era of Metabolomics. *J Am Chem Soc* **2020**,
399 *142*, (20), 9097-9105.
- 400 4. Perez de Souza, L.; Alseekh, S.; Scossa, F.; Fernie, A. R., Ultra-high-performance liquid
401 chromatography high-resolution mass spectrometry variants for metabolomics research. *Nat
402 Methods* **2021**.
- 403 5. Place, B. J.; Ulrich, E. M.; Challis, J. K.; Chao, A.; Du, B.; Favela, K.; Feng, Y.-L.; Fisher, C. M.;
404 Gardinali, P.; Hood, A.; Knolhoff, A. M.; McEachran, A. D.; Nason, S. L.; Newton, S. R.; Ng, B.;
405 Nuñez, J.; Peter, K. T.; Phillips, A. L.; Quinete, N.; Renslow, R.; Sobus, J. R.; Sussman, E. M.;
406 Warth, B.; Wickramasekara, S.; Williams, A. J., An Introduction to the Benchmarking and
407 Publications for Non-Targeted Analysis Working Group. *Anal Chem* **2021**, *93*, (49), 16289-16296.
- 408 6. Hootman, K. C.; Trezzi, J.-P.; Kraemer, L.; Burwell, L. S.; Dong, X.; Guertin, K. A.; Jaeger, C.;
409 Stover, P. J.; Hiller, K.; Cassano, P. A., Erythritol is a pentose-phosphate pathway metabolite and
410 associated with adiposity gain in young adults. *P Natl Acad Sci Usa* **2017**, *114*, (21), E4233-E4240.
- 411 7. Chen, Y. J.; Mahieu, N. G.; Huang, X. J.; Singh, M.; Crawford, P. A.; Johnson, S. L.; Gross, R. W.;
412 Schaefer, J.; Patti, G. J., Lactate metabolism is associated with mammalian mitochondria. *Nat Chem
413 Biol* **2016**, *12*, (11), 937-943.
- 414 8. Mueller, D.; Heinze, E., Stable isotope-assisted metabolomics to detect metabolic flux changes in
415 mammalian cell cultures. *Curr Opin Biotech* **2013**, *24*, (1), 54-59.
- 416 9. Creek, D. J.; Chokkathukalam, A.; Jankevics, A.; Burgess, K. E. V.; Breitling, R.; Barrett, M. P.,
417 Stable isotope-assisted metabolomics for network-wide metabolic pathway elucidation. *Anal Chem*
418 **2012**, *84*, (20), 8442-8447.
- 419 10. Llufrio, E. M.; Cho, K.; Patti, G. J., Systems-level analysis of isotopic labeling in untargeted
420 metabolomic data by X-13 CMS. *Nat Protoc* **2019**, *14*, (7), 1970-1990.
- 421 11. Forsberg, E. M.; Huan, T.; Rinehart, D.; Benton, H. P.; Warth, B.; Hilmers, B.; Siuzdak, G., Data
422 processing, multi-omic pathway mapping, and metabolite activity analysis using XCMS Online.
423 *Nat Protoc* **2018**, *13*, (4), 633-651.
- 424 12. Huan, T.; Forsberg, E. M.; Rinehart, D.; Johnson, C. H.; Ivanisevic, J.; Benton, H. P.; Fang, M. L.;
425 Aisporna, A.; Hilmers, B.; Poole, F. L.; Thorgeresen, M. P.; Adams, M. W. W.; Krantz, G.; Fields, M.
426 W.; Robbins, P. D.; Niedernhofer, L. J.; Ideker, T.; Majumder, E. L.; Wall, J. D.; Rattray, N. J. W.;
427 Goodacre, R.; Lairson, L. L.; Siuzdak, G., Systems biology guided by XCMS Online metabolomics.
428 *Nat Methods* **2017**, *14*, (5), 461-462.
- 429 13. Zhu, Z. J.; Schultz, A. W.; Wang, J. H.; Johnson, C. H.; Yannone, S. M.; Patti, G. J.; Siuzdak, G.,
430 Liquid chromatography quadrupole time-of-flight mass spectrometry characterization of

- 431 metabolites guided by the METLIN database. *Nat Protoc* **2013**, 8, (3), 451-460.
- 432 14. Atzrodt, J.; Derdau, V.; Kerr, W. J.; Reid, M., C-H functionalisation for hydrogen isotope exchange.
433 *Angew Chem Int Edit* **2018**, 57, (12), 3022-3047.
- 434 15. Mahieu, N. G.; Huang, X.; Chen, Y., Jr.; Patti, G. J., Credentialing Features: A Platform to
435 Benchmark and Optimize Untargeted Metabolomic Methods. *Anal Chem* **2014**, 86, (19), 9583-9589.
- 436 16. Kessler, N.; Walter, F.; Persicke, M.; Albaum, S. P.; Kalinowski, J.; Goesmann, A.; Niehaus, K.;
437 Nattkemper, T. W., ALLOCATOR: An Interactive Web Platform for the Analysis of Metabolomic LC-
438 ESI-MS Datasets, Enabling Semi-Automated, User-Revised Compound Annotation and Mass
439 Isotopomer Ratio Analysis. *Plos One* **2014**, 9, (11).
- 440 17. Bueschl, C.; Kluger, B.; Neumann, N. K. N.; Doppler, M.; Maschietto, V.; Thallinger, G. G.; Meng-
441 Reiterer, J.; Krska, R.; Schuhmacher, R., MetExtract II: A Software Suite for Stable Isotope-Assisted
442 Untargeted Metabolomics. *Anal Chem* **2017**, 89, (17), 9518-9526.
- 443 18. Leeming, M. G.; Isaac, A. P.; Pope, B. J.; Cranswick, N.; Wright, C. E.; Ziogas, J.; O'Hair, R. A. J.;
444 Donald, W. A., High-Resolution Twin-Ion Metabolite Extraction (HiTIME) Mass Spectrometry:
445 Nontargeted Detection of Unknown Drug Metabolites by Isotope Labeling, Liquid Chromatography
446 Mass Spectrometry, and Automated High-Performance Computing. *Anal Chem* **2015**, 87, (8), 4104-
447 4109.
- 448 19. Itoh, N.; Numata, M.; Aoyagi, Y.; Yarita, T., Comparison of the behavior of ¹³C- and deuterium-
449 labeled polycyclic aromatic hydrocarbons in analyses by isotope dilution mass spectrometry in
450 combination with pressurized liquid extraction. *Journal of chromatography. A* **2007**, 1138, (1-2),
451 26-31.
- 452 20. Chokkathukalam, A.; Jankevics, A.; Creek, D. J.; Achcar, F.; Barrett, M. P.; Breitling, R., mzMatch-
453 ISO: an R tool for the annotation and relative quantification of isotope-labelled mass spectrometry
454 data. *Bioinformatics* **2013**, 29, (2), 281-283.
- 455 21. Huang, X. J.; Chen, Y. J.; Cho, K.; Nikolskiy, I.; Crawford, P. A.; Patti, G. J., X13CMS: Global
456 Tracking of Isotopic Labels in Untargeted Metabolomics. *Anal Chem* **2014**, 86, (3), 1632-1639.
- 457 22. Capellades, J.; Navarro, M.; Samino, S.; Garcia-Ramirez, M.; Hernandez, C.; Simo, R.; Vinaixa,
458 M.; Yanes, O., geoRge: A Computational Tool To Detect the Presence of Stable Isotope Labeling in
459 LC/MS-Based Untargeted Metabolomics. *Anal Chem* **2016**, 88, (1), 621-628.
- 460 23. Hiller, K.; Wegner, A.; Weindl, D.; Cordes, T.; Metallo, C. M.; Kelleher, J. K.; Stephanopoulos, G.,
461 NTFD-a stand-alone application for the non-targeted detection of stable isotope-labeled compounds
462 in GC/MS data. *Bioinformatics* **2013**, 29, (9), 1226-1228.
- 463 24. Zhu, H.; Chen, L.; Xing, W.; Ran, S.; Wei, Z.; Amee, M.; Wassie, M.; Niu, H.; Tang, D.; Sun, J.;
464 Du, D.; Yao, J.; Hou, H.; Chen, K.; Sun, J., Phytohormones-induced senescence efficiently promotes
465 the transport of cadmium from roots into shoots of plants: A novel strategy for strengthening of
466 phytoremediation. *J Hazard Mater* **2020**, 388, 122080.
- 467 25. Ito, N.; Esaki, H.; Maesawa, T.; Imamiya, E.; Maegawa, T.; Sajiki, H., Efficient and selective Pt/C-
468 catalyzed H-D exchange reaction of aromatic rings. *B Chem Soc Jpn* **2008**, 81, (2), 278-286.
- 469 26. Sawama, Y.; Nakano, A.; Matsuda, T.; Kawajiri, T.; Yamada, T.; Sajiki, H., H-D Exchange
470 Deuteration of Arenes at Room Temperature. *Org Process Res Dev* **2019**, 23, (4), 648-653.

- 471 27. Pluskal, T.; Castillo, S.; Villar-Briones, A.; Oresic, M., MZmine 2: Modular framework for
472 processing, visualizing, and analyzing mass spectrometry-based molecular profile data. *Bmc*
473 *Bioinformatics* **2010**, *11*, 11.
- 474 28. Holman, J. D.; Tabb, D. L.; Mallick, P., Employing ProteoWizard to Convert Raw Mass
475 Spectrometry Data. *Curr Protoc Bioinformatics* **2014**, *46*, 13.24.1-9.
- 476 29. Djoumbou-Feunang, Y.; Pon, A.; Karu, N.; Zheng, J. M.; Li, C.; Arndt, D.; Gautam, M.; Allen, F.;
477 Wishart, D. S., CFM-ID 3.0: Significantly Improved ESI-MS/MS Prediction and Compound
478 Identification. *Metabolites* **2019**, *9*, (4), 23.
- 479 30. Schymanski, E. L.; Jeon, J.; Gulde, R.; Fenner, K.; Ruff, M.; Singer, H. P.; Hollender, J., Identifying
480 small molecules via high resolution mass spectrometry: communicating confidence. *Environ Sci*
481 *Technol* **2014**, *48*, (4), 2097-2098.
- 482 31. Yee, A. W.; Blakeley, M. P.; Moulin, M.; Haertlein, M.; Mitchell, E.; Forsyth, V. T., Back-exchange
483 of deuterium in neutron crystallography: characterization by IR spectroscopy. *J Appl Crystallogr*
484 **2017**, *50*, 660-664.
- 485 32. Walters, B. T.; Ricciuti, A.; Mayne, L.; Englander, S. W., Minimizing Back Exchange in the
486 Hydrogen Exchange-Mass Spectrometry Experiment. *J Am Soc Mass Spectr* **2012**, *23*, (12), 2132-
487 2139.
- 488 33. Hoffmann, M. A.; Nothias, L.-F.; Ludwig, M.; Fleischauer, M.; Gentry, E. C.; Witting, M.;
489 Dorrestein, P. C.; Dührkop, K.; Böcker, S., High-confidence structural annotation of metabolites
490 absent from spectral libraries. *Nat Biotechnol* **2021**.
- 491 34. Chen, L.; Lu, W.; Wang, L.; Xing, X.; Chen, Z.; Teng, X.; Zeng, X.; Muscarella, A. D.; Shen, Y.;
492 Cowan, A.; McReynolds, M. R.; Kennedy, B. J.; Lato, A. M.; Campagna, S. R.; Singh, M.;
493 Rabinowitz, J. D., Metabolite discovery through global annotation of untargeted metabolomics data.
494 *Nat Methods* **2021**, *18*, (11), 1377-1385.
- 495 35. Nothias, L. F.; Petras, D.; Schmid, R.; Duhrkop, K.; Rainer, J.; Sarvepalli, A.; Protsyuk, I.; Ernst,
496 M.; Tsugawa, H.; Fleischauer, M.; Aicheler, F.; Aksenov, A. A.; Alka, O.; Allard, P. M.; Barsch, A.;
497 Cachet, X.; Caraballo-Rodriguez, A. M.; Da Silva, R. R.; Dang, T.; Garg, N.; Gauglitz, J. M.;
498 Gurevich, A.; Isaac, G.; Jarmusch, A. K.; Kamenik, Z.; Kang, K. B.; Kessler, N.; Koester, I.; Korf,
499 A.; Le Gouellec, A.; Ludwig, M.; Martin, H. C.; McCall, L. I.; McSayles, J.; Meyer, S. W.;
500 Mohimani, H.; Morsy, M.; Moyne, O.; Neumann, S.; Neuweiger, H.; Nguyen, N. H.; Nothias-
501 Esposito, M.; Paolini, J.; Phelan, V. V.; Pluskal, T.; Quinn, R. A.; Rogers, S.; Shrestha, B.; Tripathi,
502 A.; van der Hooft, J. J. J.; Vargas, F.; Weldon, K. C.; Witting, M.; Yang, H. J.; Zhang, Z.; Zubeil, F.;
503 Kohlbacher, O.; Bocker, S.; Alexandrov, T.; Bandeira, N.; Wang, M. X.; Dorrestein, P. C., Feature-
504 based molecular networking in the GNPS analysis environment. *Nat Methods* **2020**, *17*, (9), 905-+.
- 505 36. Huang, L. W.; Liu, W.; Zhao, L. L.; Zhang, Z. Y.; Yan, X. Y., Base-Catalyzed H/D Exchange
506 Reaction of Difluoromethylarenes. *J Org Chem* **2021**, *86*, (5), 3981-3988.
- 507 37. Tian, Z. Y.; Zhao, H. Q.; Peter, K. T.; Gonzalez, M.; Wetzel, J.; Wu, C.; Hu, X. M.; Prat, J.; Mudrock,
508 E.; Hettinger, R.; Cortina, A. E.; Biswas, R. G.; Kock, F. V. C.; Soong, R.; Jenne, A.; Du, B. W.;
509 Hou, F.; He, H.; Lundein, R.; Gilbreath, A.; Sutton, R.; Scholz, N. L.; Davis, J. W.; Dodd, M. C.;
510 Simpson, A.; McIntyre, J. K.; Kolodziej, E. P., A ubiquitous tire rubber-derived chemical induces

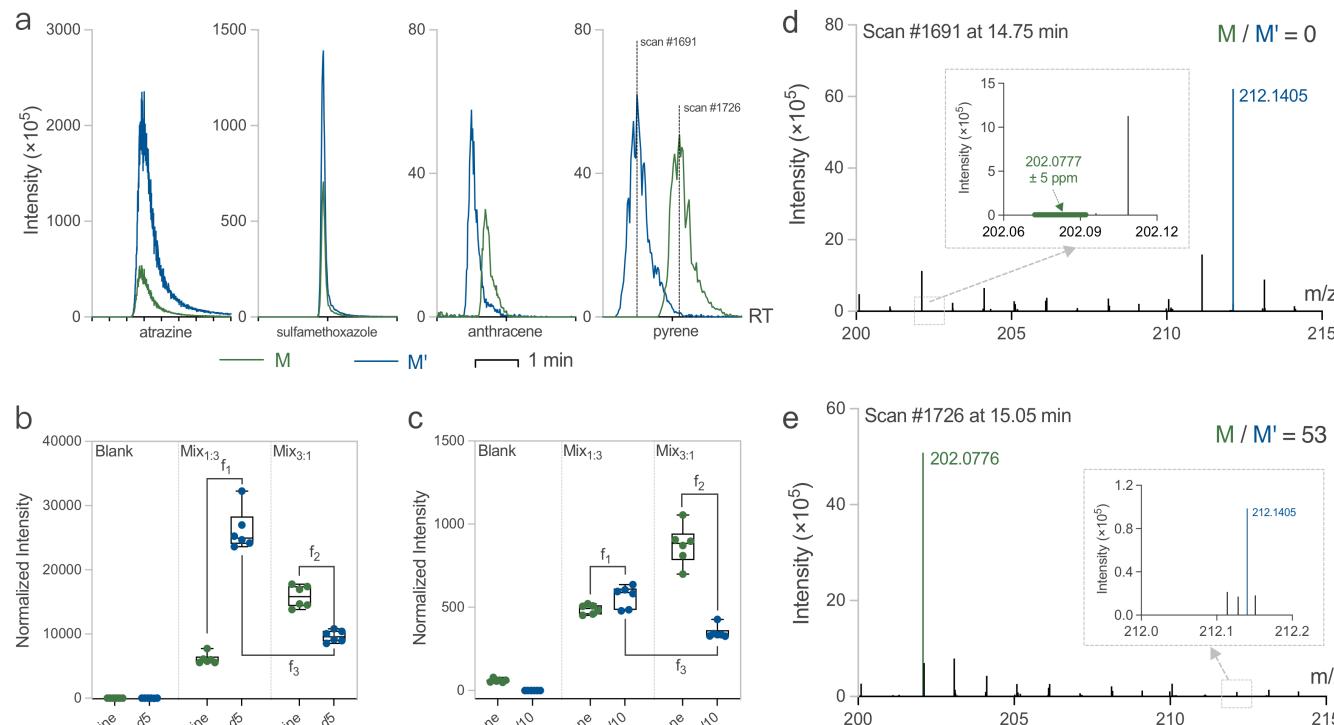
- 511 acute mortality in coho salmon. *Science* **2021**, *371*, (6525), 185-189.
- 512 38. Cheng, Z. P.; Sun, H. W.; Sidhu, H. S.; Sy, N. D.; Wang, X. R.; Gan, J., Conjugation of Di-n-butyl
513 Phthalate Metabolites in *Arabidopsis thaliana* and Potential Deconjugation in Human Microsomes.
514 *Environ Sci Technol* **2021**, *55*, (4), 2381-2391.
- 515 39. Tian, Z. Y.; Vila, J.; Yu, M. A.; Bodnar, W.; Aitken, M. D., Tracing the Biotransformation of
516 Polycyclic Aromatic Hydrocarbons in Contaminated Soil Using Stable Isotope-Assisted
517 Metabolomics. *Environmental Science & Technology Letters* **2018**, *5*, (2), 103-109.
- 518 40. Tripathi, A.; Vazquez-Baeza, Y.; Gauglitz, J. M.; Wang, M. X.; Duhrkop, K.; Nothias-Esposito, M.;
519 Acharya, D. D.; Ernst, M.; van der Hooft, J. J. J.; Zhu, Q. Y.; McDonald, D.; Brejnrod, A. D.;
520 Gonzalez, A.; Handelsman, J.; Fleischauer, M.; Ludwig, M.; Bocker, S.; Nothias, L. F.; Knight, R.;
521 Dorrestein, P. C., Chemically informed analyses of metabolomics mass spectrometry data with
522 Qemistree. *Nat Chem Biol* **2021**, *17*, (2), 146-+.
- 523 41. Konermann, L.; Ahadi, E.; Rodriguez, A. D.; Vahidi, S., Unraveling the Mechanism of Electrospray
524 Ionization. *Anal Chem* **2013**, *85*, (1), 2-9.
- 525

526



527

528 **Figure 1 Proposed pipeline for ^2H -labeled Stable Isotope Assisted Metabolomics**
529 (^2H -SIAM). Firstly, both natural and ^2H -labeled parent contaminants are individually
530 incubated in the environment matrix for the indicated duration; they are subsequently
531 extracted and mixed with the ratio of 1:3 and 3:1 ($\text{Mix}_{1:3}$ and $\text{Mix}_{3:1}$ samples); the
532 mixtures are determined by LC-MS or GC-MS and thereafter obtained raw data are
533 analyzed by MZmine2 to obtain feature list; then it is imported into the developed
534 algorithm ^2H -SIAM(V1.0) to obtain possible features with isotopologues as TPs of the
535 contaminants for further annotation and identification. Natural compounds are denoted
536 as M, and the isotope-labeled compounds are denoted as M'.



539 **Figure 2 Validation of ${}^2\text{H}$ -SIAM pipeline by addition of 7 isotopologue pairs into soil extract.** 7 typical environmental contaminants
 540 with their ${}^2\text{H}$ -labeled isotopologue were added into soil extract with the indicated concentration to obtain hypothetical Mix_{1:3} and Mix_{3:1}
 541 samples; then, they were analyzed by the UPLC-ESI-HRMS system, and obtained data were subjected to the proposed ${}^2\text{H}$ -SIAM pipeline.
 542 (a) EIC of 4 typical isotopologue pairs from the Mix_{1:3} sample which contain 10 ppm natural contaminants and 30 ppm ${}^2\text{H}$ -labeled
 543 contaminants; (b, c) selected normalized height of isotopologue pairs of atrazine and pyrene for triple filters; (d, e) extracted mass spectra
 544 #1691 and #1726 at peaks of EIC of pyrene and pyrene-d10; natural compounds are denoted as M (dark green), and the isotope-labeled
 545 compounds are denoted as M' (dark blue).

546

547

548

549

550

551

552

553

554

555

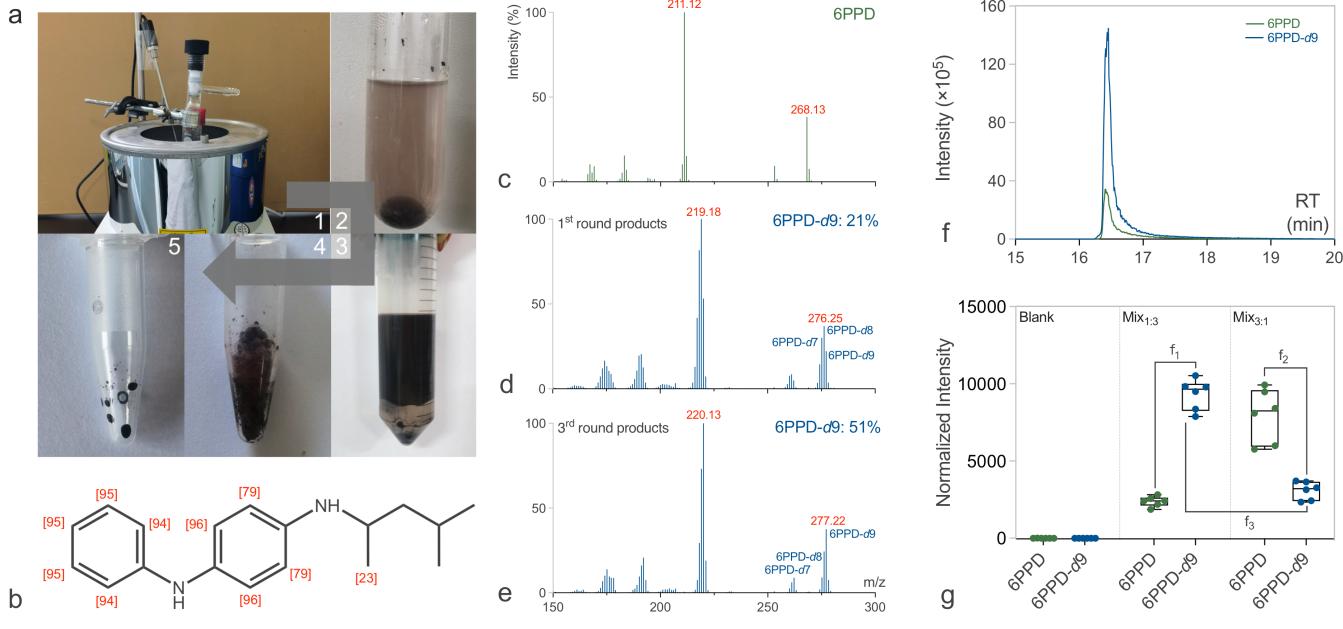


Figure 3 Synthesis of 6PPD-d9 by direct H/D exchange reactions and its performance in ${}^2\text{H}$ -SIAM. The reaction was carried out in a glass tube with D_2O as deuterium source, Pd/C and Pt/C as catalysts, and H_2 atmosphere at 80°C for 24 hours to obtain 1st round 6PPD-d9 products (a, 1-4); the reaction was then repeated for twice, and a grease-like brown product was obtained (a, 5); (b) 600M NMR determined the structure of the 3rd round 6PPD-d9 products; GC-MS spectrum of 6PPD (c), ${}^2\text{H}$ -labeled 6PPD from 1st round reaction (d), and ${}^2\text{H}$ -labeled 6PPD from the 3rd round reaction (e); (f) EIC of 6PPD and 6PPD-d9 from UPLC-ESI-HRMS data; (g) normalized height of 6PPD and 6PPD-d9 for ${}^2\text{H}$ -SIAM quantitative triple filters; natural compounds are marked as dark green, and the isotope-labeled compounds are marked as dark blue.

556
557
558
559
560
561
562
563
564
565

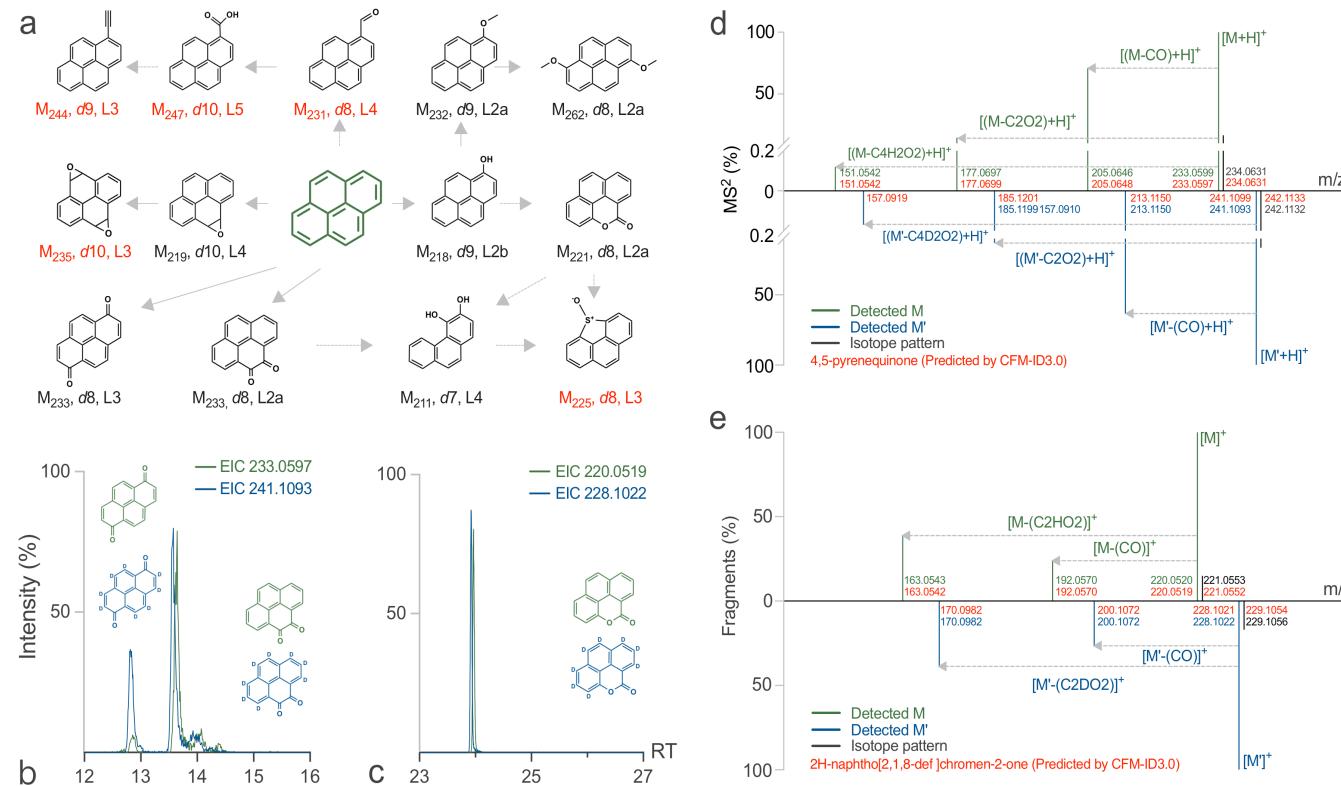


Figure 4 Performance of ²H-SIAM pipeline in a soil pyrene degradation study. Pyrene and pyrene-*d*10 were added into the soil and incubated for 2 months; they were subsequently subjected to the proposed ²H-SIAM pipeline study, which finally selected 52 features as isotopologue pairs, and 13 features were annotated as TPs of pyrene. (a) proposed TPs of pyrene in this study, *dn* indicates numbers of ²H-labels, Ln indicates identification confidence levels (see Methods); 5 of them (red) were annotated as the TPs of pyrene for the first time; (b) selected EIC of M₂₃₃ and M'_{233-d8} from UPLC-ESI-HRMS data; (c) selected EIC of M₂₂₀ and M'_{220-d8} from GC-EI-HRMS data; (d) comparison of MS² spectrum (NCE 40, UPLC-ESI-Q-HRMS) between M₂₃₃, M'_{233-d8} at 13.6 min and CFM-ID 3.0 predicted spectrum of 4,5-pyrenequinone; (e) comparison of fragments (70eV, GC-EI-HRMS) of M₂₂₀, M'_{220-d8} and CFM-ID 3.0 predicted spectrum of 2H-naphtho[2,1,8-def]chromen-2-one. Isotope pattern was extracted from MS¹. Natural compounds are denoted as M (dark green), and the isotope-labeled compounds are denoted as M' (dark blue).

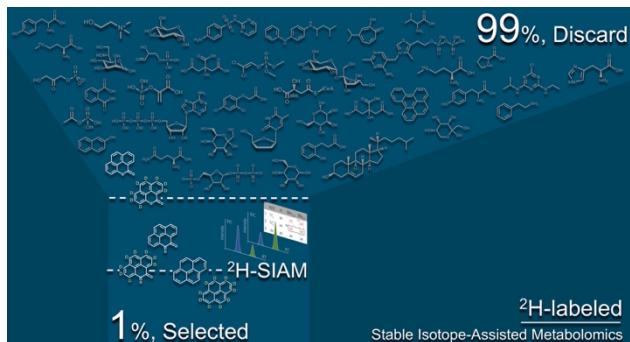
566 **Table 1 Performance of ²H-SIAM(1.0) in this study.**

Features	Experiments		
	7 Contaminants		Pyrene Degradation
	UPLC-ESI-HRMS	GC-EI-HRMS	UPLC-ESI-HRMS
Total	7704	21955	4376
Paired	1720	2548	658
Filter 1	891	1122	318
Filter 2	249	301	81
Filter 3	130	162	52
Annotated	7	5	14

567

568

569 For Table of Contents only



570