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3 1 **Quantitative *In Vitro*-to-*In Vivo* Extrapolation for Mixtures:**  
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6 2 **A Case Study of Superfund Priority List Pesticides**  
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**Abstract**

*In vitro* cell-based toxicity testing methods generate large amounts of data informative for risk-based evaluations. To allow extrapolation of the quantitative outputs from cell-based tests to the equivalent exposure levels in humans, reverse toxicokinetic (RTK) modeling is used to conduct *in vitro*-to-*in vivo* extrapolation (IVIVE) from *in vitro* effective concentrations to *in vivo* oral dose equivalents. IVIVE modeling approaches for individual chemicals are well-established; however, the potential implications of chemical-to-chemical interactions in mixture settings on IVIVE remains largely unexplored. We hypothesized that chemical co-exposures could modulate both protein binding efficiency and hepatocyte clearance of the chemicals in a mixture, which would in turn affect the quantitative IVIVE toxicokinetic parameters. To test this hypothesis, we used 20 pesticides from the Agency for Toxic Substances and Disease Registry (ATSDR) Substance Priority List, both individually and as equimolar mixtures, and investigated the concentration-dependent effects of chemical interactions on *in vitro* toxicokinetic parameters. Plasma protein binding efficiency was determined by using ultracentrifugation, and hepatocyte clearance was estimated in suspensions of cryopreserved primary human hepatocytes. We found that for single chemicals, the protein binding efficiencies were similar at different test concentrations. In a mixture, however, both protein binding efficiency and hepatocyte clearance were affected. When IVIVE was conducted using mixture-derived toxicokinetic data, more conservative estimates of Activity-to-Exposure Ratios (AERs) were produced as compared to using data from single chemical experiments. Because humans are exposed to mixtures of chemicals, this study is significant as it demonstrates the importance of incorporating mixture-derived parameters into IVIVE for *in vitro* bioactivity data in order to accurately prioritize risks and facilitate science-based decision-making.

## 42 Introduction

43 Traditional chemical safety evaluations rely on testing for potential adverse effects of  
44 chemical in laboratory animals; these studies identify target organs and dose levels where the effects  
45 may be undetectable, information that is used to extrapolate to humans and other exposure levels.  
46 Animal-based testing approaches are highly informative for both cancer (Krewski *et al.*, 2019) and  
47 non-cancer (Olson *et al.*, 2000) effects; however, these experiments are time- and resource-intensive  
48 and associated with a number of ethical and human relevance concerns, factors that make testing of  
49 a large number of environmental substances in animals impractical (Bell *et al.*, 2018). Therefore,  
50 new approach methodologies are being developed for environmental and industrial chemicals, using  
51 *in silico* and *in vitro* models of various biological complexity (Krewski *et al.*, 2020; Marx *et al.*,  
52 2020), followed by toxicokinetic modeling to extrapolate to *in vivo* human exposures through “*in*  
53 *vitro*-to-*in vivo* extrapolation” or IVIVE (Wambaugh *et al.*, 2015; Wetmore *et al.*, 2012). IVIVE  
54 calculations typically rely on the use of a steady state model that incorporates two key experimental  
55 parameters: plasma protein binding and hepatocyte clearance. These values are then used to  
56 calculate steady state plasma concentrations for a specific oral dose. While the new approach  
57 methodologies (NAMs)-derived data from *in vitro*-based tests are now available for thousands of  
58 chemicals, it is challenging to experimentally derive parameters that enable IVIVE on an equally  
59 massive scale (Wambaugh, *et al.*, 2015; Wetmore *et al.*, 2014; Wetmore *et al.*, 2013). Therefore,  
60 recent studies proposed computationally-derived parameter estimation (Bell *et al.*, 2020) to enable  
61 “high throughput toxicokinetic” (HTTK) modeling (Pearce *et al.*, 2017).

62 IVIVE is now widely recognized as a critical tool to facilitate chemical prioritization and  
63 decision making based on *in vitro* testing data (Bell, *et al.*, 2018; Yoon *et al.*, 2012). Both *in vitro*  
64 tests and IVIVE analyses are most often performed on individual chemicals; however, real-life  
65 exposures are not limited to a single chemical, but rather are a mixture of chemicals (Drakvik *et al.*,

2020). The application of new approach methodologies to studies of mixtures is a nascent field (Chen *et al.*, 2021; Escher *et al.*, 2020; Fang *et al.*, 2020; Hsieh *et al.*, 2021), which calls for re-evaluation of the suitability of current IVIVE approaches to mixture settings (Carpenter *et al.*, 2002). For example, plasma protein binding determined through the use of a traditional rapid equilibrium dialysis (RED) method (Bohnert and Gan, 2013) is not suitable for testing many highly lipophilic environmental chemicals (Ferguson *et al.*, 2019). In addition, biotransformation rate constants for polycyclic aromatic hydrocarbons (PAH) that were tested individually (Lee *et al.*, 2014) were much greater than those obtained when these PAH were tested as a mixture (OECD, 2018), suggesting that kinetics are different in a mixture setting compared to single chemical. Similarly, substance-specific differences in *in vitro* bioavailability were observed for the individual PAH tested as a mixture, or as components of complex petroleum substances (Luo *et al.*, 2020).

Most studies of mixtures still consider individual chemical effects and then mathematically reconstruct the mixture IVIVE using a number of modeling approaches (van der Voet *et al.*, 2020). While indirect mixture modeling is common, most often there are no *in vitro* or *in vivo* toxicokinetic data available for the mixture as a whole, hence limiting the options for direct modeling of mixtures (Chang *et al.*, 2021). Thus, there is a critical need to characterize *in vitro* toxicokinetic parameters of chemicals in a mixture setting. To address this need, we selected a subset of pesticides from the Superfund priority list (ATSDR, 2019) and tested these compounds for plasma protein binding and hepatocyte clearance in both single and mixture settings. Next, we derived steady-state plasma concentrations for each chemical under single or mixture testing conditions. Finally, we combined these steady-state concentrations with publicly available *in vitro* bioactivity data and exposure estimates to derive oral equivalent doses and activity to exposure levels for each chemical individually or in a mixture. The results of this study are informative for cumulative risk assessment of chemical mixture exposures and show that IVIVE for mixtures needs experimental priors.

90

**91 Materials and Methods**

92 **Chemicals.** Twenty pesticides and analytical internal standards (Table 1 and Supplemental Table 1)  
93 were purchased from Sigma Aldrich (St. Louis, MO) or Chem Service (West Chester, PA).  
94 Methanol (Cat No.: A456-500) and acetonitrile (Cat No.: A955-500) were purchased from Fischer  
95 Scientific (Hampton, NH). Pentane (Cat No.: 1.00882), diethyl ether (Cat No.: 309966), and distilled  
96 water with 0.1% formic acid (Cat No.: 1.59013) were acquired from Sigma Aldrich (St. Louis, MO).  
97 Cell culture media used in these experiments was from the iCell Cardiomyocytes Media Kit (Catalog  
98 No.: R1151) and was purchased from FujiFilmCDI (Madison, WI), and was used as a representative  
99 example of *in vitro* media.

100 **Selection of test compounds and preparation of a “designed” chemical mixture.** The Agency for  
101 Toxic Substances and Disease Registry (ATSDR) maintains a priority list of hazardous  
102 substances/chemicals that are commonly detected at the US National Priority List (NPL) sites, also  
103 known as “Superfund” sites; these chemicals are known to be hazardous to human health (ATSDR,  
104 2019). From the list of over 300 compounds, we selected 20 chemicals that are lipophilic and have  
105 IVIVE data in *httk* R package version 1.10.1 (Table 1). In addition, we created a molar-equivalent,  
106 “designed” mixture consisting of 20 chemicals (10  $\mu$ M each) to investigate the impacts of chemical  
107 co-exposure on quantitative IVIVE.

108 **Determination of protein binding efficiency.** Protein binding efficiency of 20 pesticides was  
109 determined using ultracentrifugation (Nakai *et al.*, 2004). To calculate the unbound fractions of test  
110 compounds, two sets of samples were prepared in this experiment. First, 995  $\mu$ L of the medium or  
111 human plasma was spiked with 5  $\mu$ L of 0.2 or 2 mM test chemical, which resulted in the final test  
112 concentrations of 1 or 10  $\mu$ M. Then, 300  $\mu$ L of the reaction mixture was immediately transferred  
113 and extracted in an Eppendorf tube (as described in sections 2.5 and 2.6), representing the initial

1  
2  
3 114 concentration of the test compound. For the second set of samples, the reaction mixture was prepared  
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5 115 using the identical procedures but further incubated at 37°C for 1 hour. Next, a portion of 300 µL  
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7 116 from the reaction mixture was transferred to a polycarbonate centrifuge tube (n=3). Samples  
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10 117 underwent ultracentrifugation with Optima MAX-XP Ultracentrifuge (Item No.: 393315; Beckman  
11  
12 118 Coulter, Brea, CA) at 90,000 rpm for 4.5 hours at 4°C. One hundred microliters of the middle layer  
13  
14 119 (clear portion) was transferred to a sample vial, representing the unbound concentration of the test  
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16  
17 120 compound. The collected samples were analyzed using liquid chromatography (LC) or gas  
18  
19 121 chromatography (GC) followed by tandem mass spectrometry (MS/MS), as detailed below.

20  
21 122 ***Determination of in vitro hepatocyte clearance.*** *In vitro* hepatocyte clearance was determined using  
22  
23 123 a suspension culture of cryopreserved human hepatocytes (Lot# HUE121, GIBCO, Frederick, MD)  
24  
25  
26 124 according to manufacturer's protocol. In brief, the cryopreserved human hepatocytes were  
27  
28 125 suspended in William's E medium and adjusted to the cell concentration to  $1 \times 10^6$  cells/mL. A  
29  
30 126 portion of the cell working stock was heated at 95°C for 5 mins to serve as negative control. Five  
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32  
33 127 hundred microliter of the chemical stock (20 µM) or designed mixture (20 chemicals, 20 µM each)  
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35 128 was spiked in 500 µL of the cell working stock or inactivated cell control to a final chemical  
36  
37  
38 129 concentration of 10 µM and cell number of  $5 \times 10^5$  cells/ml. One hundred microliters of the reaction  
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40 130 mixture were removed subsequently at 0, 15, 30, 60, 90, and 120 mins to individual 1.5 mL  
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42 131 Eppendorf tubes for further sample extraction detailed below.

43  
44 132 ***LC-MS/MS analyses.*** Each sample (100 µL) was spiked with 10 µL of 10 µM internal standards,  
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46  
47 133 mixed with 200 µL of ice-cold acetonitrile, and then centrifuged at 10,000 g for 5 mins. The  
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49 134 supernatant was dried under vacuum with a SpeedVac (Savant SPD1010, Thermo Scientific) and  
50  
51 135 reconstituted with 100 µL of mobile phase prior to analyses. LC-MS/MS analysis was performed  
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54 136 using 1290 Infinity II LC system and 6470 triple quadrupole mass spectrometer (both from Agilent  
55  
56 137 Technologies, Santa Clara, CA). Sample extract (10 µL) was chromatographed on a ZORBAX  
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3 138 SSHD Eclipse Plus C18 column (3.0×50 mm, 1.8 μm, Cat No.: 959757-302; Agilent Technologies)  
4  
5 139 with a guard column (2.1×5 mm, 1.8 μm, Cat No.: 821725-901; Agilent Technologies), and ionized  
6  
7 140 with an electrospray ionization source. Analytical signal was acquired in positive or negative ion  
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10 141 modes. For compounds analyzed in positive ion mode, chromatographic separation occurred  
11  
12 142 following an LC gradient [time (A%) ] at a flow rate of 400 μL/min: 0(98)-1(98)-3(20)-4(5)-5(98)-  
13  
14 143 8(98), where mobile phase A was 0.1% formic acid in water and mobile phase B was 0.1% formic  
15  
16 144 acid in methanol. The analysis of 2,4-dinitrophenol followed the same LC gradient, except that the  
17  
18 145 mobile phase A was water and mobile phase B was acetonitrile.

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20  
21 146 **GC-MS/MS analyses.** Sample extraction procedures for GC-MS/MS analysis were modified from  
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23 147 (Moreno Frias *et al.*, 2004). In brief, sample (100 μL) was spiked with 10 μL of 10 μM internal  
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25 148 standards, mixed with 50 μL of methanol and 200 μL of pentane: diethyl ether (1:1, v/v), vortexed,  
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27 149 and then centrifuged at 2,500 rpm for 5 mins. Supernatants were transferred to an amber vial for  
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29 150 analyses. Detection of analytes was achieved using 7890B GC and 7010 GC/MS triple quadruple  
30  
31 151 mass spectrometer (both from Agilent Technologies). Samples (1 μL) were injected in splitless  
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33 152 mode. Analytes were separated with a VF-5ms GC column (60 m×250 μm×0.25 μm, Agilent  
34  
35 153 Technologies) and ionized with an electron ionization source. The column head pressure was set at  
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37 154 21.5 psi with a constant flow rate at 1.2 mL/min using helium gas. Initial column temperature was  
38  
39 155 held at 70°C for 5 min, increased to 150°C at 50°C/min, ramped to 280°C at 4°C/min, and then held  
40  
41 156 for 15 min. The total run time was 42.1 min. The injector temperature was set at 250°C. The ion  
42  
43 157 source and transfer line temperatures were 300°C. Electron multiplier voltage was set at 1884V.  
44  
45 158 Nitrogen gas was used as the collision gas for all MS/MS experiments, and the pressure of collision  
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47 159 gas was set at 16.8 psi. Ion transitions of test chemicals were adapted from (Chamkasem *et al.*, 2013)  
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49 160 and are listed in Table 1. Response ratio of analyte and internal standard was used to derive unbound  
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3 161 fraction and *in vitro* hepatocyte clearance of test chemical. Fraction unbound ( $F_{ub}$ ), internal  
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5 162 clearance ( $Cl_{int}$ ), and steady-state blood concentration ( $C_{ss}$ ) were determined as stated below.

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7 163 **Determination of  $F_{ub}$ ,  $Cl_{in\ vitro}$  and steady-state blood concentration ( $C_{ss}$ ).** The unbound fraction of  
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9 164 chemical was calculated from the equation [1]:

$$10 \quad 165 \quad F_{ub} (\%free) = \frac{Response\ ratio_{free}}{Response\ ratio_{initial}} \quad [1]$$

$$11 \quad 166 \quad , \text{ where } Response\ ratio = \frac{Chemical\ response}{IS\ response}$$

12  
13  
14  
15 167 *In vitro* hepatocyte clearance ( $Cl_{in\ vitro}$ ) of test compound was estimated by substrate depletion  
16  
17 168 approach assuming a first-order kinetic for chemical elimination (Smith *et al.*, 2012):  $Cl_{in\ vitro} = kV/N$ ,  
18  
19 169 where  $k$ = first-order elimination rate constant,  $V$ =incubation volume (1 mL), and  $N$ =number of cells  
20  
21 170 in the incubation ( $5 \times 10^5$  cells).  $Cl_{in\ vitro}$  was further scaled up to the intrinsic hepatocyte clearance  
22  
23 171 ( $Cl_{int}$ ) according to the equation [2] (Wetmore, 2015):

$$24 \quad 172 \quad Cl_{int} = Cl_{in\ vitro} \times HPGL \times V_l \quad [2]$$

25  
26 173 , where HPGL = hepatocytes per gram liver ( $137 \times 10^6$  cells/g) and  $V_l$  = volume of the whole liver  
27  
28 174 (1820 g).

29  
30 175 The steady-state blood concentration ( $C_{ss}$ ) was derived from equation [3] (Wetmore, 2015;  
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32 176 Wilkinson and Shand, 1975):

$$33 \quad 177 \quad C_{ss} = \frac{k_0}{(GFR \times F_{ub}) + \left[ \frac{Ql \times F_{ub} \times Cl_{int}}{Ql + F_{ub} \times Cl_{int}} \right]} \quad [3]$$

34  
35 178 where  $k_0$ =a unit input dose (1 mg/kg-d = 0.042 mg/kg-h); GFR = glomerular filtration rate (6.7  
36  
37 179 L/h);  $F_{ub}$  = unbound fraction of tested compound at 10  $\mu$ M; and  $Ql$  = liver blood flow (90 L/h).

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39 180 **Quantitative *in vitro*-to-*in vivo* extrapolation.** The *in vitro* point of departure values (95<sup>th</sup> percentile  
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41 181 POD) were acquired from recent studies (Chen *et al.*, 2020; Paul Friedman *et al.*, 2020). The oral  
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43 182 equivalent doses (OEDs) of these PODs were further derived according to equation [4]:



$$OEDs = PODs (\mu M) \times \frac{1 \text{ mg/kg/day}}{C_{ss} (\mu M)} \quad [4]$$

184 **Calculation of the Activity-to-Exposure Ratios (AER).** The derived OEDs were compared to  
185 exposure estimates to obtain AER using equation [5]:

$$AER = \frac{OED (mg/kg/day)}{Exposure Estimate (mg/kg/day)} [5].$$

187 Exposure estimates were based on the estimated 95<sup>th</sup> percentile upper limit of aggregate exposure  
188 to U.S. population 20-65 years old acquired from EPA's Comptox Dashboard (Williams *et al.*, 2017).

## 190 Results

191 *In vitro* toxicokinetic parameters of protein binding and hepatocyte clearance were evaluated  
192 in a set of 20 lipophilic pesticide active ingredients. The chemicals were tested on an individual  
193 basis and within equimolar mixtures of all compounds. These data were taken together in  
194 combination with reverse dosimetry modeling to derive human oral equivalent doses which were  
195 further compared to regulatory exposure estimates.

### 196 Protein Binding Assay

197 For studies in human plasma, protein binding values that are reported in *httk* R package  
198 version 1.10.1 (Pearce, *et al.*, 2017) were compared to the experimental data in our study. Free  
199 fraction values in plasma for *httk*, single, and mixture experiments ranged from 0 to 21.4, 1.8 to  
200 14.4, and 1 to 9.8 %, respectively. Free fraction values in *httk* were obtained through the use of rapid  
201 equilibrium dialysis (RED) and these studies reported that all chemicals tested herein should be  
202 highly bound to proteins in human plasma; however, the data obtained using ultracentrifugation  
203 show that the free fraction is typically higher than that derived using RED assay (Figure 1A, left  
204 panel). Additionally, we found poor concordance (Figure 1B) in the values for single compounds  
205 between *httk* RED and our ultra-centrifugation data, similar to a previous observation comparing

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2  
3 206 RED and SPME for PAHs (Ferguson, *et al.*, 2019). Also, there was no significant correlation of free  
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5 207 fraction values from ultracentrifugation between single and mixture settings. Overall, free fraction  
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7 208 values for the mixture setting were lower than those in a single chemical test setting.

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10 209 Additionally, we investigated concentration-dependent effects on protein binding in cell  
11  
12 210 culture media (Figure 1A, center and right panels). For the most part, compounds tested in single  
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14 211 setting yielded free fraction values slightly higher than mixture setting in plasma when testing at 10  
15  
16 212  $\mu\text{M}$ . However, this trend was less apparent when testing at 1  $\mu\text{M}$ . Nonetheless, when tested at either  
17  
18 213 10 or 1  $\mu\text{M}$ , there were highly significant correlations between single and mixture experiments.  
19  
20 214 Moreover, free fraction values do not exhibit any concentration-dependent effect in media, and free  
21  
22 215 fraction values were highly correlated in both single and mixture settings ( $r > 0.94$ ,  $p < 0.0001$ ) when  
23  
24 216 the data at different concentrations were compared (data not shown).

### 27 28 217 ***Hepatocyte Clearance Assay***

29  
30 218 Next, we compared the data for hepatocyte clearance between those in *httk* (Pearce, *et al.*,  
31  
32 219 2017) and our experiments (Figure 2). Metabolic clearance values derived in this study for single  
33  
34 220 and mixture setting ranged from 0 to 43.2 and 0 to 5.5  $\mu\text{L}/\text{min}/10^6$  hepatocytes, respectively (Figure  
35  
36 221 2A). For a majority of chemicals in a mixture setting, we did not find any detectable hepatocyte  
37  
38 222 clearance. In general, clearance values reported by *httk* were higher than either single or mixture  
39  
40 223 setting values obtained in our study. Correlation analysis between *httk* and single setting testing did  
41  
42 224 not show significant concordance, with only two compounds showing slightly greater clearance in  
43  
44 225 our study as compared to *httk* data (Figure 2B). Additionally, correlation analysis between single  
45  
46 226 and mixture setting displayed even less concordance, with only two chemicals demonstrating greater  
47  
48 227 clearance in a mixture (Figure 2C).

### 53 54 228 ***Steady-State Blood Concentrations ( $C_{ss}$ )***

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2  
3 229 Data obtained through plasma protein binding and hepatocyte clearance assays were applied  
4  
5 230 to calculate  $C_{ss}$  as detailed in Methods.  $C_{ss}$  average values determined from *httk*, single, and  
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7 231 mixture setting ranged from 0.1 to 97.2  $\mu\text{M}$  (Figure 3A). For most compounds where a comparison  
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9  
10 232 between *httk* and this study could be made, toxicokinetic data obtained from *httk* yielded the lowest  
11  
12 233  $C_{ss}$  values while data from mixture setting produced the highest  $C_{ss}$  values. Correlation analyses  
13  
14 234 between *httk* and single setting (Figure 3B) and between mixture and single setting (Figure 3C)  
15  
16  
17 235 showed non-significant relationships. However, both analyses further highlight the trend of low  $C_{ss}$   
18  
19 236 values produced by *httk* and high  $C_{ss}$  values obtained through mixture setting.

### 21 237 ***Mixture to Single Setting Ratios***

22  
23  
24 238 In order to determine the impact of testing compounds in a mixture compared to individual  
25  
26 239 setting, values obtained for protein binding, hepatocyte clearance, and  $C_{ss}$  were compared as ratios.  
27  
28 240 The data from the mixture setting were divided by their corresponding values from the single setting.  
29  
30 241 The resulting ratios were plotted (Figure 4) to determine whether mixture setting overall yielded  
31  
32 242 higher, lower, or equal toxicokinetic parameters. Ratios for free fraction in plasma, media (10  $\mu\text{M}$ ),  
33  
34 243 and media (1  $\mu\text{M}$ ) ranged from 0.18 to 2.65, 0.26 to 2.24, and 0.28 to 3.30, respectively. On average,  
35  
36 244 unbound fractions were slightly lower in the mixture setting at 10  $\mu\text{M}$ , regardless of whether the  
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38 245 experiments were conducted in human plasma or cell culture media, and about the same at 1  $\mu\text{M}$ .  
39  
40 246 In all cases, the ratios were well within one order of magnitude.

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44 247 For hepatocyte clearance, the ratios ranged from 0.01 to 54.90. Overall, hepatocyte clearance  
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46 248 values in the mixture setting were much lower compared those in the single setting as evident by  
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48 249 the median ratio value of 0.03. When the results from plasma protein binding and hepatocyte  
49  
50 250 clearance are combined,  $C_{ss}$  ratios also ranged from 0.18 to 128.03, with the vast majority of the  
51  
52  
53 251  $C_{ss}$  ratios above 1. These results indicate that testing in a mixture setting yields may result in steady-

1  
2  
3 252 state blood concentrations that are up to 10 or 100-fold greater than those assumed from the data  
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5 253 obtained for single chemicals.  
6

### 7 254 ***Activity to Exposure Ratios (AERs)***

9  
10 255 Using results of two recent large-scale *in vitro* studies of bioactivity of the test chemicals  
11  
12 256 that have used these data to compare *in vitro* points of departure to estimates of human exposure,  
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14 257 AERs (Figure 5) were calculated for each chemical based on converting bioactivity to an oral  
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16 258 equivalent dose (OED) using *Css* values produced from *httk*, single, and mixture setting data as  
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18 259 described in Methods. As a reference, we used the estimated 95<sup>th</sup> percentile upper limit of aggregate  
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20 260 exposure to U.S. population 20-65 years old acquired from EPA's Comptox Dashboard (Williams,  
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22 261 *et al.*, 2017). Specifically, each AER was plotted based on *httk*, single, and mixture data and the  
23  
24 262 bioactivity results from either Paul Friedman *et al.* (2020) (data were available for 10 of the 20  
25  
26 263 chemicals tested here) or Chen *et al.* (2020) (data for 18-20 chemicals were available, depending on  
27  
28 264 the cell type used in the experiments). We found that AERs calculated using *httk*-derived IVIVE  
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30 265 data yielded the highest AER values, indicating the greatest margin of safety based on the *in vitro*  
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32 266 results and the estimates of human exposures. Toxicokinetic parameters obtained in this study for  
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34 267 the mixture setting produced the lowest AER values with both sets of bioactivity data. The median,  
35  
36 268 upper, and lower quartiles of the AERs for mixture data using Paul Friedman *et al.* (2020) points of  
37  
38 269 departure were 16154, 78026, and 5507, respectively. The median, upper, and lower quartiles of the  
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40 270 AER distribution for mixture data using Chen *et al.* (2020) points of departure were 3283, 17459,  
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42 271 and 1089, respectively. The minimum AER derived from Paul Friedman *et al.* (2020) data was 4551  
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44 272 for azinphos-methyl, whereas the minimum AER from Chen *et al.* (2020) data was 127 for  
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46 273 methoxychlor-o,p'.  
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## 276 Discussion

277 IVIVE is an essential tool for high-throughput screening of environmental compounds with  
278 limited toxicity data. By combining *in vitro* kinetic and bioactivity data, IVIVE facilitates the  
279 translation of *in vitro* testing concentrations to *in vivo* oral doses (Paul Friedman, *et al.*, 2020;  
280 Rotroff *et al.*, 2010; Wambaugh, *et al.*, 2015; Wetmore, *et al.*, 2012). The use of this well-established  
281 reverse toxicokinetic modeling approach enables regulators to prioritize chemicals through a risk-  
282 based interpretation of high-throughput screening (HTS) data that incorporates not only hazard  
283 identification but also takes into consideration actual exposure estimates (Krewski, *et al.*, 2020;  
284 Thomas *et al.*, 2013; Wambaugh *et al.*, 2019).

285 In this study, *in vitro* kinetic assays were performed on 20 lipophilic environmental  
286 chemicals chosen as a subset from the ATSDR's Substance Priority List (ATSDR, 2019). The *in*  
287 *vitro* kinetic assays were applied to derive two most informative parameters of IVIVE – plasma  
288 protein binding and hepatocyte clearance. All chemicals were tested on an individual basis, as well  
289 as in an equimolar mixture in order to investigate mixture effects on *in vitro* kinetics. The results  
290 from the *in vitro* assays were combined with IVIVE to estimate each chemical's concentration in  
291 blood at steady state for specific human exposure situations. Next, reverse dosimetry was  
292 incorporated to calculate oral doses that would produce a steady state blood concentration equivalent  
293 to the 95<sup>th</sup> percentile point of departure value of each chemical's *in vitro* bioactivity data. Lastly,  
294 OEDs were compared to exposure estimates to attain AERs under various testing conditions.

295 Currently, IVIVE has been applied to thousands of chemicals to yield large data sets that are  
296 highly informative for decision-making (Wambaugh, *et al.*, 2015; Wambaugh, *et al.*, 2019;  
297 Wetmore, 2015). Although a number of studies and analyses have used *in vitro* bioactivity to assess  
298 mixture effects from an exposure or cumulative risk point of view, they have all still used IVIVE  
299 kinetic data and models based on single chemicals, given the lack of IVIVE data for chemical

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3 300 mixtures (Chang, *et al.*, 2021; Lichtenstein *et al.*, 2020; van der Voet, *et al.*, 2020). Similarly,  
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5 301 available computational approaches to characterize *in vitro* bioavailability are currently limited to  
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7 302 individual chemicals (Armitage *et al.*, 2014; Fischer *et al.*, 2017; Stadnicka-Michalak *et al.*, 2021).  
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10 303 Therefore, our study is novel as it reported and compared IVIVE parameters for a large number of  
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12 304 environmental chemicals that were tested in single and mixture settings. Additionally, compared to  
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14 305 IVIVE data reported in *httk*, our study used ultracentrifugation to estimate plasma protein binding  
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16 306 instead of RED assay. As previously mentioned, RED has been shown to not be a suitable assay to  
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18 307 calculate plasma protein binding of lipophilic environmental compounds (Ferguson, *et al.*, 2019).  
19  
20 308 From our chemical set, almost half of all compounds were reported to have 0% unbound fraction in  
21  
22 309 human plasma according to *httk*; however, by using ultracentrifugation we were able to obtain  
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24 310 unbound fraction values greater than 0%, albeit still relatively low (<10%). Taken together, our  
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26 311 study demonstrates not only the impact of more accurate estimates of plasma protein binding, but  
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28 312 also the effects on kinetics by chemical mixtures compared to traditional single chemical analysis.  
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30 313 Knowing that most chemical exposures occur as mixtures rather than individual compounds  
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32 314 (Hernández and Tsatsakis, 2017) we believe this study is highly informative for cumulative risk  
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34 315 assessment of environmental chemical exposures.

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39 316 Our testing approach showed that a vast majority of the 20 pesticides screened in our study  
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41 317 did not show any clear impacts on plasma protein binding capabilities when tested as a mixture  
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43 318 compared to individual compound analysis. In both testing conditions, all compounds appeared to  
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45 319 be highly bound to proteins suggesting that the amount of albumin present in plasma is not a limiting  
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47 320 factor in binding efficiency. However, hepatocyte metabolic clearance data showed a pronounced  
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49 321 effect when tested as a mixture. In general, almost all chemicals had no detectable clearance under  
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51 322 mixture setting. This observation potentially indicates that hepatocytes were saturated with  
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53 323 chemicals under mixture setting and thus, could not metabolically clear them as efficiently  
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3 324 compared to exposure to a single chemical. The same effect has been noted in previous studies  
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5 325 conducted on hepatocyte clearance of environmental compounds (Lee, *et al.*, 2014). It is not  
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7 326 surprising that a major reduction in hepatocyte clearance under mixture setting yielded steady state  
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10 327 blood concentrations much higher compared to single chemical data. Compared to our study, *httk*  
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12 328 data had the lowest steady state blood concentrations that are likely due to very low unbound  
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14 329 fractions derived using RED and higher hepatocyte clearance values. Using our mixture data to  
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16  
17 330 estimate oral equivalent doses that would result in bioactive concentrations appeared to be the most  
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19 331 conservative approach compared to using our single chemical testing data or IVIVE data from *httk*.  
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21 332 When OEDs obtained from mixture data were compared to upper exposure estimates (95<sup>th</sup> percentile)  
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23 333 for the U.S. general population the data revealed that the margin for safety from chemical exposure  
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26 334 is not nearly as high compared to using data from single chemical screening. This conservative  
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28 335 approach takes into consideration simultaneous exposure to multiple chemicals which we believe to  
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31 336 be more relevant to actual human exposure scenarios.

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33 337 We note a few limitations in our study. First, our designed mixture of 20 compounds was  
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35 338 created as an equimolar mixture with each chemical present at a final concentration of 10  $\mu$ M.  
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37 339 Chemicals present in the environment occur at varying concentrations (Carpenter, *et al.*, 2002; Hsieh,  
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39 340 *et al.*, 2021; Martin *et al.*, 2013), and that 10  $\mu$ M across all 20 compounds may be rather high for  
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42 341 general population environmental exposure, or may be potentially cytotoxic. Still, we reason that in  
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44 342 the general population, this saturation effect may be less pronounced than we have observed. In  
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46 343 addition, we note that it is unlikely that the mixture as tested would have had an adverse effect on  
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48  
49 344 the hepatocytes in the study of clearance because exposure was limited to 4 hrs and most of these  
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51 345 substances were without effect on cytotoxicity in HepaRG cells or human hepatocytes as reported  
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53 346 in ToxCast (Supplemental Table 7). Also, in order to facilitate direct comparison between single  
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56 347 and mixture setting, we decided to use 10  $\mu$ M as the set concentration based on typical testing  
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3 348 concentrations for IVIVE studies (Rotroff, *et al.*, 2010; Wetmore, *et al.*, 2012). Alternative designs  
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5 349 can be used, such as 0.5  $\mu\text{M}$  of the 20 chemicals for a cumulative concentration of the mixture at 10  
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7  
8 350  $\mu\text{M}$ . Nonetheless, our results suggest the importance of considering reduced hepatocyte clearance  
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10 351 in real-life mixture settings, because AERs based on single-chemical data may not be conservative.  
11  
12 352 Even though such AERs may still be adequate for prioritization, there is less confidence in their use  
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14 353 in screening-level decision-making. Additionally, other existing limitations of IVIVE as it is  
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17 354 currently practiced (e.g., steady-state, hepatic-only metabolism, etc.) are well known; still, several  
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19 355 studies comparing IVIVE-based oral equivalents with *in vivo* data have suggested that errors are  
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21 356 about an order of magnitude (Honda *et al.*, 2019; Wambaugh *et al.*, 2018; Wambaugh, *et al.*, 2019).  
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23  
24 357 We also acknowledge that physicochemical properties such as water solubility play a key role in  
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26 358 determining the exact concentrations these lipophilic compounds may exist *in vitro* and in the  
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28 359 environment. For instance, available computational models for *in vitro* bioavailability have utilized  
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31 360 a range of chemical and system property information, including various partition coefficients,  
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33 361 temperature and dimensions of the test system, and presence of co-solvents (Armitage, *et al.*, 2014;  
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35 362 Fischer, *et al.*, 2017; Punt *et al.*, 2021).

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38 363 Second, protein precipitation with organic solvents may release some of the bound chemical,  
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40 364 which may cause overestimation for the unbound fraction. Nevertheless, the method we used to  
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42 365 determine free fraction in human plasma has been previously shown to yield free fraction values  
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44 366 similar to those measured *in vivo* (Nakai, *et al.*, 2004). Third, all the environmental compounds in  
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46  
47 367 our study were limited to only pesticides. Despite there being various classes of pesticides within  
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49 368 our study, we understand there are various other chemical classes in the environment such as  
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51 369 polyaromatic hydrocarbons (PAHs), polybrominated biphenyls (PCBs), etc. Follow up studies using  
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54 370 untargeted analyses would be highly beneficial to characterize which chemical compounds are  
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56 371 commonly found together in the environment.



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3 372 Overall, this case study used 20 chemicals commonly found in the environment to  
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5 373 demonstrate how chemical co-exposures affect *in vitro* pharmacokinetics of plasma protein binding  
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7 374 and hepatocyte metabolic clearance which directly impact IVIVE. The current paradigm shift of  
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10 375 toxicity testing from traditional animal models to more reliance on HTS assays (Krewski, *et al.*,  
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12 376 2020; Krewski *et al.*, 2014) requires an equal investment in the proper characterization of  
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14 377 pharmacokinetics of not only single chemicals, but mixtures as well. Data generated from mixture  
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16 378 analyses provide a more comprehensive guideline for cumulative risk assessment compared to  
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18 379 individual chemical testing. Thus, the impact of mixtures may require more attention as chemical  
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20 380 co-exposures are expected to impact both bioavailability *in vitro* as well as *in vitro* toxicokinetic  
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22 381 parameters used to conduct IVIVE.  
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387 **Table 1.** Chemicals used in this study. See Supplemental Table 1 for vendor and catalogue number  
 388 information.

Chemical	CASRN	Analytical Assay	Ionization mode	Mass transitions (m/z)	CE(eV)
<i>Test chemicals</i>					
Aldrin	309-00-2	GC-MS/MS	EI	263.0→191.0 293.0→186.0	40 40
DDD-p,p'	72-54-8	GC-MS/MS	EI	235.0→165.1 235.0→200.0	20 30
DDT-o,p'	789-02-6	GC-MS/MS	EI	235.0→165.0	30
DDT-p,p'	50-29-3	GC-MS/MS	EI	235.0→199.0	18
Dicofol	115-32-2	GC-MS/MS	EI	249.9→215.1	10
Dieldrin	60-57-1	GC-MS/MS	EI	277.0→241.0 263.0→193.0	10 40
Endosulfan I	115-29-7	GC-MS/MS	EI	240.9→205.9 240.9→203.9	15 20
Endrin	72-20-8	GC-MS/MS	EI	279.0→243.0 281.0→211.0	10 30
Heptachlor epoxide B	1024-57-3	GC-MS/MS	EI	352.9→281.9 352.9→262.8	20 15
Heptachlor	76-44-8	GC-MS/MS	EI	272.0→236.8 337.0→266.0	25 20
Lindane	58-89-9	GC-MS/MS	EI	218.8→145.0 218.8→183.0	20 5
Methoxychlor-o,p'	72-43-5	GC-MS/MS	EI	227.0→141.0 227.0→152.0	35 20
Parathion	56-38-2	GC-MS/MS	EI	291.1→ 81.0 291.1→109.0	40 10
Trifluralin	1582-09-8	GC-MS/MS	EI	306.0→264.0 306.0→160.0	7 25
2,4-dinitrophenol	51-28-5	LC-MS/MS	ESI(-)	183.0→137.0 183.0→123.0	5 5
Azinphos-methyl	86-50-0	LC-MS/MS	ESI(+)	318.0→160.1 318.0→132.0	13 21
Chlorpyrifos	2921-88-2	LC-MS/MS	ESI(+)	350.0→198.0 350.0→ 97.0	25 47
Diazinon	333-41-5	LC-MS/MS	ESI(+)	305.0→169.1 305.0→153.1	31 29
Disulfoton	298-04-4	LC-MS/MS	ESI(+)	275.0→ 89.2 275.0→ 61.2	11 33
Ethion	563-12-2	LC-MS/MS	ESI(+)	384.8→199.2 384.8→142.9	15 39
<i>Internal Standards</i>					
Atrazine	1912-24-9	GC-MS/MS	EI	200.1→103.9 200.1→ 94.1	20 20
Benzo[a]anthracene	56-55-3	GC-MS/MS	EI	228.0→226.2 228.0→202.1	30 30
Terbutryn	886-50-0	GC-MS/MS	EI	241.0→185.0 241.0→170.0	15 20
Mifepristone	84371-65-3	LC-MS/MS	ESI(+)	430.0→372.0	35
Troglitazone	97322-87-7	LC-MS/MS	ESI(-)	440.2→397.1 440.2→145.0	21 37

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## 541 **Figure Legends**

542 **Figure 1. Comparison of protein binding using rapid equilibrium dialysis (RED, open circles)**  
543 **or ultracentrifugation (UCF) in a single (orange triangles) and mixture (black squares) setting.**

544 **(A)** Plotted are free fractions (as % of tested, median±95%CI) of each chemical listed (the number  
545 in brackets indicates LogP of each compound). Data are shown for experiments with human plasma  
546 (left, chemicals tested at 10 µM) or cell culture media (middle and right, chemicals tested at 10 and  
547 1 µM, respectively). **(B)** Pair-wise correlation plots for % free values for each chemical tested under  
548 various conditions (as shown in a title of each plot). Pearson (*r*) correlations are listed in each graph  
549 together with a corresponding *p*-value. Correlations were considered statistically significant if *p*-  
550 value <0.05. Gray dotted line is a unit line. Values reported as 0% free were replaced with 0.1 for  
551 graphing purpose. See Supplemental Table 2 for individual data values.

552 **Figure 2. *In vitro* hepatocyte clearance of chemicals in *httk* (open circles), single (orange**  
553 **triangles) and mixture (black squares) setting. (A)** Plotted are *in vitro* hepatocyte clearances  
554 (median±95%CI) of each chemical listed. Data are shown for experiments using primary human  
555 hepatocytes. Each chemical was tested at 10 µM in single and mixture setting. Clearance values  
556 reported for each chemical in *httk* R package version 1.10.1 were tested at 10 µM **(B)** Pair-wise  
557 correlation plot for hepatocyte clearance values for each chemical tested in single setting and  
558 reported by *httk*. **(C)** Pair-wise correlation plot for hepatocyte clearance values for each chemical  
559 tested in single and mixture setting. Pearson (*r*) correlations are listed in both graphs with  
560 corresponding *p*-values. Correlations were considered statistically significant if *p*-value <0.05. Gray  
561 dotted line is a unit line. Values reported as 0 clearance were replaced with 0.1 for graphing purposes.  
562 See Supplemental Table 3 for individual data values.

563 **Figure 3. Variance of steady-state blood concentrations (C<sub>ss</sub>) between *httk* (open circles),**  
564 **single (orange triangles), and mixture (black squares) setting. (A)** Plotted are steady-state blood



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3 565 concentrations (median±95%CI) of each chemical listed. Data are shown for  $C_{ss}$  values derived  
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5 566 through single and mixture testing and reported in *httk* R package version 1.10.1. **(B)** Pair-wise  
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7 567 correlation plot for  $C_{ss}$  values for each chemical tested in single setting and reported in *httk*. **(C)**  
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9 568 Pair-wise correlation plot for  $C_{ss}$  values for each chemical tested in single and mixture setting.  
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11 569 Pearson ( $r$ ) correlations are listed in both graphs with corresponding  $p$ -values. Gray dotted line is a  
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13 570 unit line. Correlations were considered statistically significant if  $p$ -value <0.05. See Supplemental  
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15 571 Table 4 for individual data values.

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19 572 **Figure 4. Comparison of ratios (mixture over single) for fraction unbound, hepatocyte**  
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21 573 **clearance, and steady-state blood concentration ( $C_{ss}$ ).** Box plots are shown comparing ratio data  
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23 574 values for each compound (black circle) corresponding to the listed parameter. Within each box, the  
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25 575 black vertical lines inside the box denote median values; boxes extend from 25<sup>th</sup> to the 75<sup>th</sup> percentile  
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27 576 of each group's distribution of values; vertical extending lines denote minimum and maximum  
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29 577 values. The red dotted line at 1 represents an equal ratio between mixture and single data values.  
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31 578 See Supplemental Table 5 for individual data values.

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35 579 **Figure 5. Distribution of activity to exposure ratios (AERs) derived from *in vitro* point of**  
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37 580 **departures (PODs).** **(A)** Plotted are AERs for each chemical using PODs (95<sup>th</sup> percentile) reported  
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39 581 by (Paul Friedman, *et al.*, 2020) derived from steady-state blood concentrations reported in *httk* or  
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41 582 obtained in our study in single and mixture setting. Panel A has an  $n=10$  due to an overlap of 10  
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43 583 chemicals between our study and (Paul Friedman, *et al.*, 2020). **(B)** AERs for each chemical using  
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45 584 PODs (95<sup>th</sup> percentile) reported by (Chen, *et al.*, 2020) derived in the same manner as panel A. For  
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47 585 panel B, *httk* had an overlap of 18 chemicals with our study whereas single and mixture had  $n=20$ .  
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49 586 Red dotted line represents an AER of 1. See Supplemental Table 6 for individual data values.  
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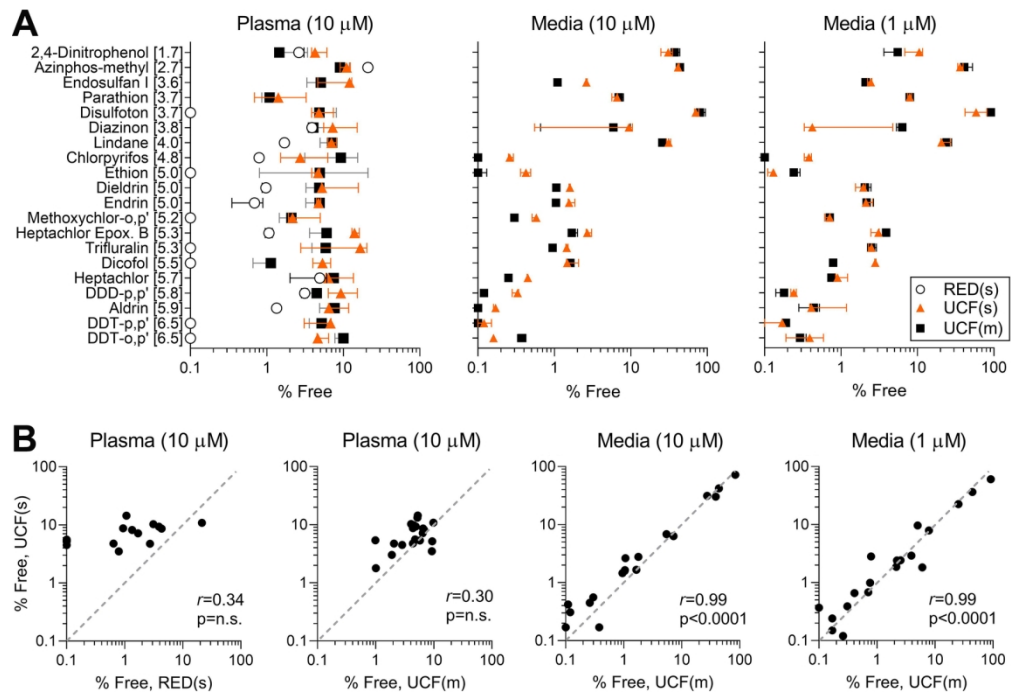


Figure 1. Comparison of protein binding using rapid equilibrium dialysis (RED, open circles) or ultracentrifugation (UCF) in a single (orange triangles) and mixture (black squares) setting. (A) Plotted are free fractions (as % of tested, median±95%CI) of each chemical listed (the number in brackets indicates LogP of each compound). Data are shown for experiments with human plasma (left, chemicals tested at 10 μM) or cell culture media (middle and right, chemicals tested at 10 and 1 μM, respectively). (B) Pair-wise correlation plots for % free values for each chemical tested under various conditions (as shown in a title of each plot). Pearson ( $r$ ) correlations are listed in each graph together with a corresponding  $p$ -value. Correlations were considered statistically significant if  $p$ -value < 0.05. Gray dotted line is a unit line. Values reported as 0% free were replaced with 0.1 for graphing purpose. See Supplemental Table 2 for individual data values.

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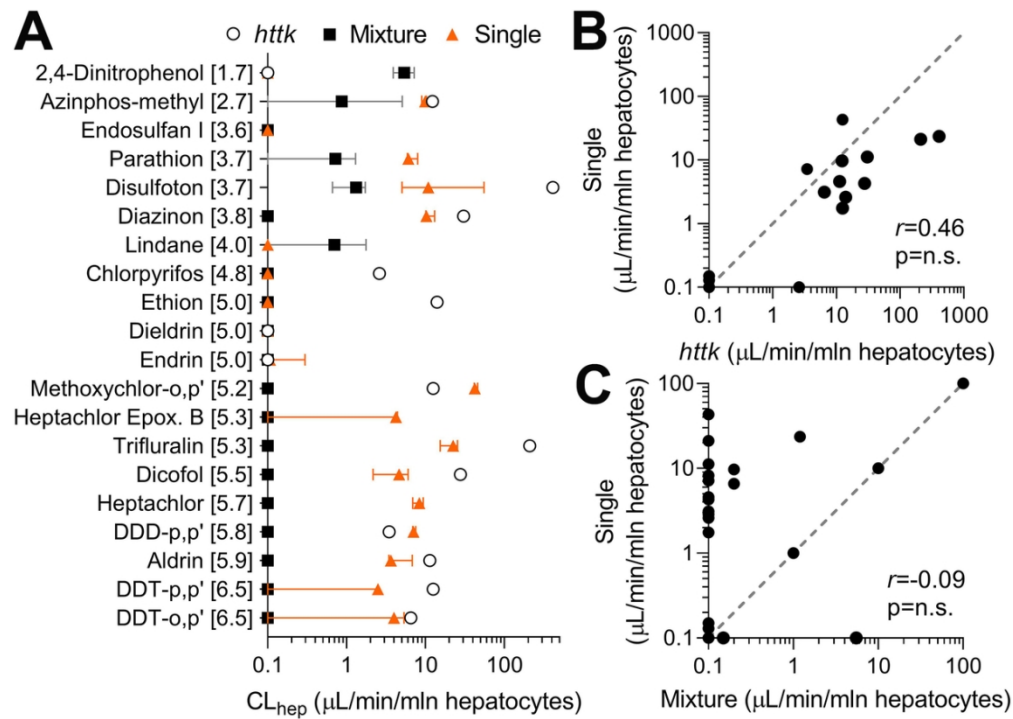


Figure 2. In vitro hepatocyte clearance of chemicals in htkk (open circles), single (orange triangles) and mixture (black squares) setting. (A) Plotted are in vitro hepatocyte clearances (median±95%CI) of each chemical listed. Data are shown for experiments using primary human hepatocytes. Each chemical was tested at 10 μM in single and mixture setting. Clearance values reported for each chemical in htkk R package version 1.10.1 were tested at 10 μM (B) Pair-wise correlation plot for hepatocyte clearance values for each chemical tested in single setting and reported by htkk. (C) Pair-wise correlation plot for hepatocyte clearance values for each chemical tested in single and mixture setting. Pearson ( $r$ ) correlations are listed in both graphs with corresponding  $p$ -values. Correlations were considered statistically significant if  $p$ -value < 0.05. Gray dotted line is a unit line. Values reported as 0 clearance were replaced with 0.1 for graphing purposes. See Supplemental Table 3 for individual data values.

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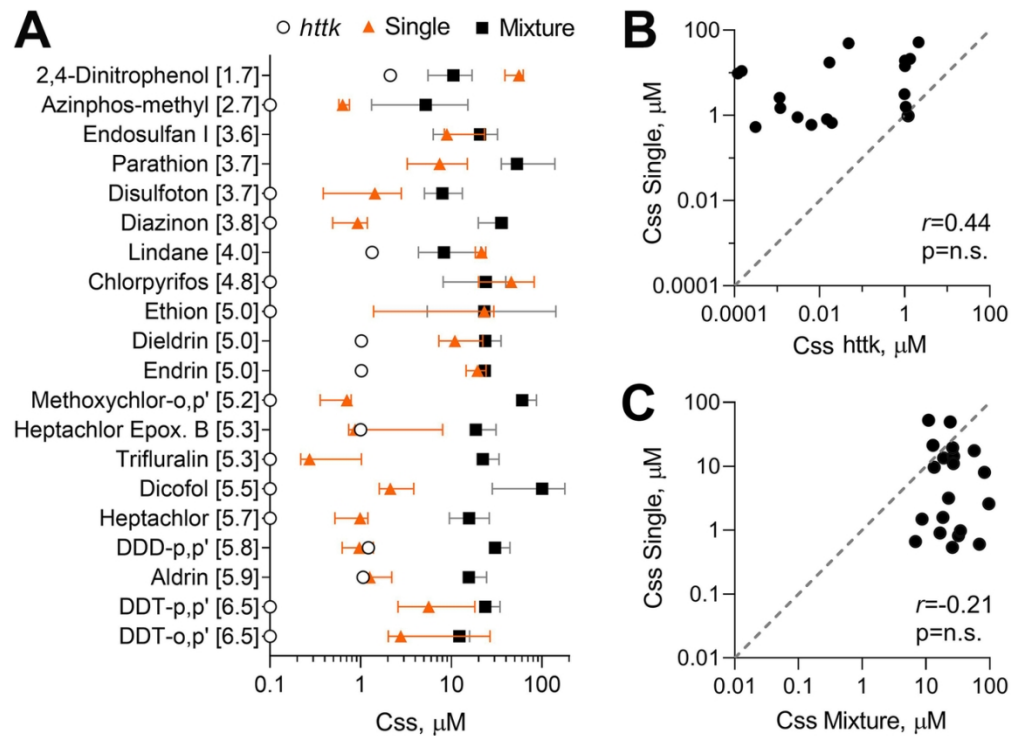


Figure 3. Variance of steady-state blood concentrations (Css) between *httk* (open circles), single (orange triangles), and mixture (black squares) setting. (A) Plotted are steady-state blood concentrations (median $\pm$ 95%CI) of each chemical listed. Data are shown for Css values derived through single and mixture testing and reported in *httk* R package version 1.10.1. (B) Pair-wise correlation plot for Css values for each chemical tested in single setting and reported in *httk*. (C) Pair-wise correlation plot for Css values for each chemical tested in single and mixture setting. Pearson ( $r$ ) correlations are listed in both graphs with corresponding  $p$ -values. Gray dotted line is a unit line. Correlations were considered statistically significant if  $p$ -value  $<0.05$ . See Supplemental Table 4 for individual data values.

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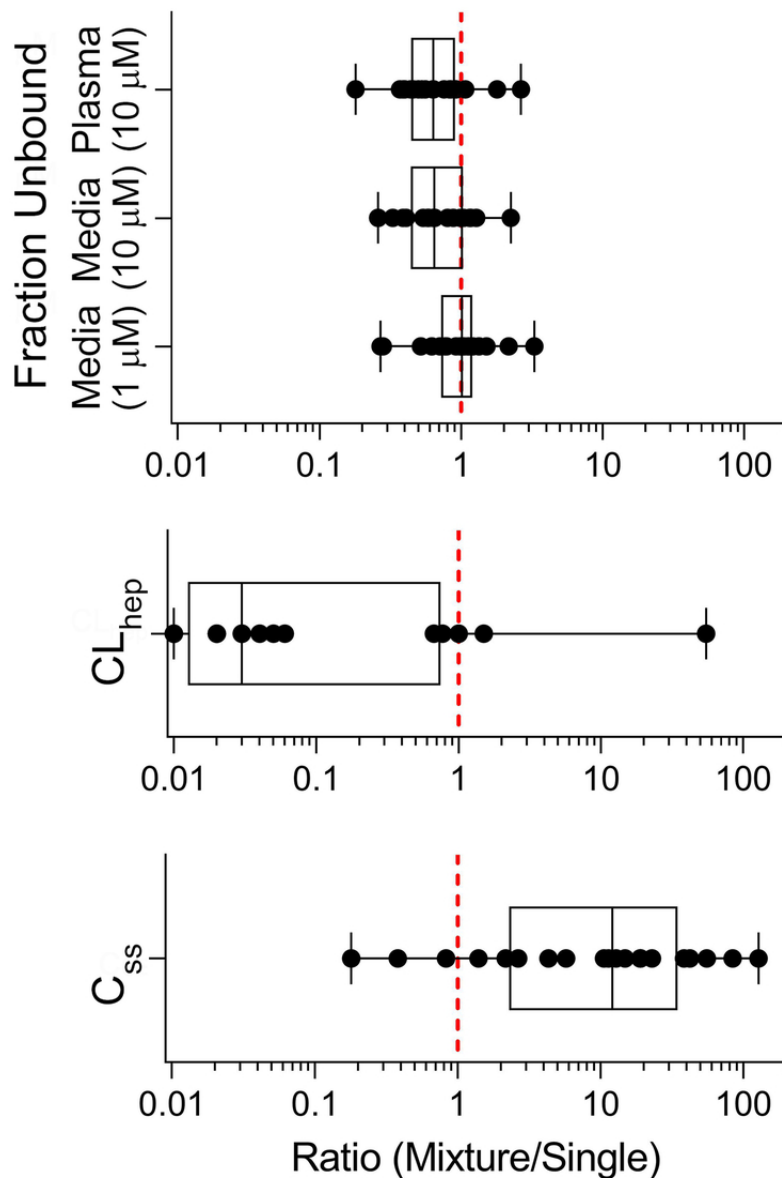


Figure 4. Comparison of ratios (mixture over single) for fraction unbound, hepatocyte clearance, and steady-state blood concentration ( $C_{ss}$ ). Box plots are shown comparing ratio data values for each compound (black circle) corresponding to the listed parameter. Within each box, the black vertical lines inside the box denote median values; boxes extend from 25th to the 75th percentile of each group's distribution of values; vertical extending lines denote minimum and maximum values. The red dotted line at 1 represents an equal ratio between mixture and single data values. See Supplemental Table 5 for individual data values.

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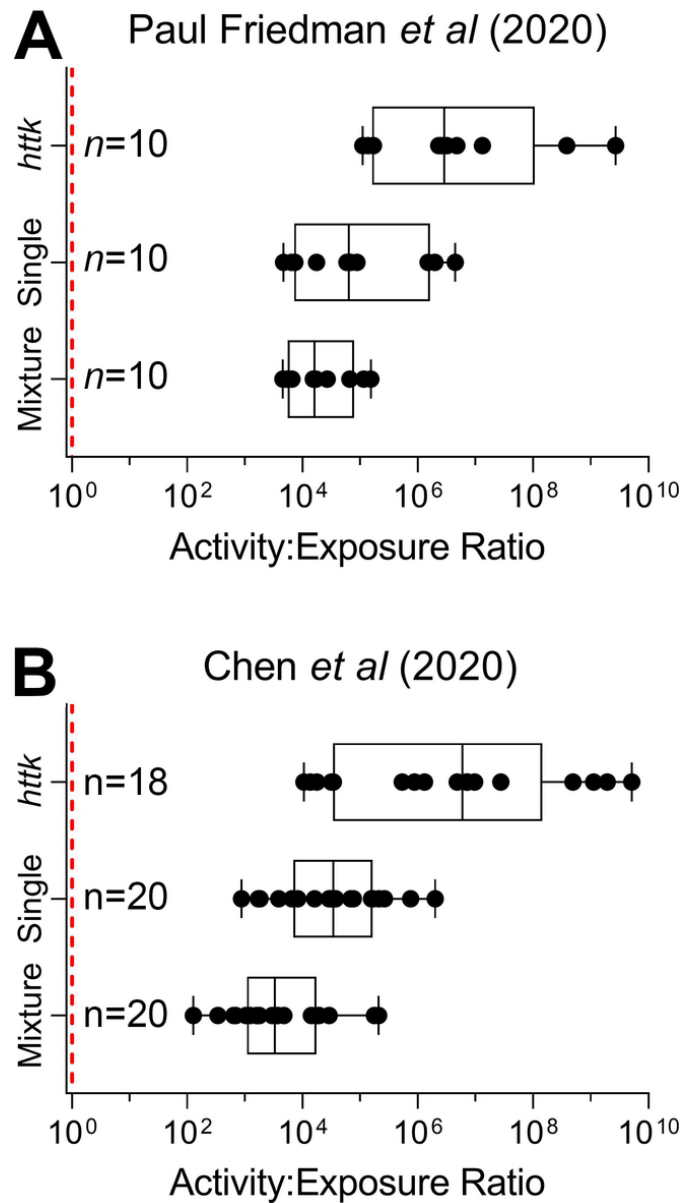


Figure 5. Distribution of activity to exposure ratios (AERs) derived from in vitro point of departures (PODs). (A) Plotted are AERs for each chemical using PODs (95th percentile) reported by Paul Friedman, et al., 2020 derived from steady-state blood concentrations reported in htkk or obtained in our study in single and mixture setting. Panel A has an  $n=10$  due to an overlap of 10 chemicals between our study and Paul Friedman, et al., 2020. (B) AERs for each chemical using PODs (95th percentile) reported by Chen, et al., 2020 derived in the same manner as panel A. For panel B, htkk had an overlap of 18 chemicals with our study whereas single and mixture had  $n=20$ . Red dotted line represents an AER of 1. See Supplemental Table 6 for individual data values.

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