

1 Comprehensive Subchronic Inhalation Toxicity
2 Assessment of an Indoor School Air Mixture of
3 PCBs

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18 **Table of Contents**

19 **Abbreviations**

20 **PCB Extraction and Quantification from Tissue and XAD**

21 **Morris Water Maze Test**

22 **Toxicity assessment**

23 **Tables:**

24 **Table S1.** Method Detection Limit (MDL) for each PCB congeners or co-eluted congeners.

25 **Table S2.** Recovery rate (%) of surrogate standards (PCB 14, d-PCB 65, and PCB 166) in tissues
26 and SAM vapor extraction.

27 **Table S3.1** Average PCB congeners concentration in liver of SAM-exposure group. Values are
28 expressed in ng/g wet tissue weight.

29 **Table S3.2** Average PCB congeners concentration in liver of SAM-exposure group. Values are
30 expressed in ng/g lipid weight.

31 **Table S3.3** Average PCB congeners concentration in lung of SAM-exposure group. Values are
32 expressed in ng/g wet tissue weight.

33 **Table S3.4** Average PCB congeners concentration in lung of SAM-exposure group. Values are
34 expressed in ng/g lipid weight.

35 **Table S3.5** Average PCB congeners concentration in brain of SAM-exposure group. Values are
36 expressed in ng/g wet tissue weight.

37 **Table S3.6** Average PCB congeners concentration in brain of SAM-exposure group. Values are
38 expressed in ng/g lipid weight.

39 **Table S3.7** Average PCB congeners concentration in adipose tissue of SAM-exposure group.
40 Values are expressed in ng/g wet tissue weight.

41 **Table S3.8** Average PCB congeners concentration in adipose tissue of SAM-exposure group.

42 Values are expressed in ng/g lipid weight.

43 **Table S3.9** Average PCB congeners concentration in serum of SAM-exposure group. Values are

44 expressed in ng/g wet weight.

45 **Table S3.10** Average PCB congeners concentration in serum of SAM-exposure group. Values

46 are expressed in ng/g lipid weight.

47 **Table S4.** Redox parameters and redox potentials (E_h) in plasma.

48 **Figures:**

49 **Figure S1.** Schematic of PCB generation and nose-only exposure system.

50 **Figure S2.** PCB congener profile (in mass percentage, %) in sequential three-day collections of

51 PCB vapor using XAD.

52 **Figure S3.** PCB homologue composition (in mass percentage, %) in sequential three-day

53 collections of PCB vapor using XAD.

54 **Figure S4.** PCB homolog composition (in mass percentage, %) in tissues of SAM-exposed rats

55 and in generated SAM vapor.

56 **Figure S5.** Body weight (g) and relative tissue weight (g/g body weight) of rats in SAM- and

57 sham-exposed groups.

58 **Figure S6.** Cytokines concentration (pg/ml) in plasma from rats in sham- and SAM-exposure

59 groups.

60 **Figure S7.** Thyroid hormones (total T4 and total T3) concentration (nmol/L) in serum after

61 exposed to SAM vapor.

62 **Figure S8.** Antioxidant enzyme activities in liver. A: GPx-1, B: GPx-4, and C: catalase activity.

63 **Figure S9.** Trace elements content (Cu, Mn, Se, and Zn) in dried liver from rats exposed to SAM
64 and sham.

65 **Figure S10.** Micronuclei (MN) number expressed as per 1000 reticulocytes (immature
66 erythrocytes) from acridine orange coated slides in SAM-exposed and sham-exposed group.

67 **Figure S11.** Ovarian follicle number in a single section from SAM- and sham-exposed rats.

68 **Abbreviations**

AMH	anti-mullerian hormone
ASE	accelerated solvent extractor
BP	bromopropane
CAT	catalase
CFC	colony-forming cell
CFU-G	colony forming unit-granulocytes
CFU-GM	colony forming unit-granulocytes, macrophage
CFU-M	colony forming unit-macrophages
CYPs	cytochrome P450
Cys	cysteine
CySS	cystine
CySSG	cysteine glutathione disulfide
DE	diatomaceous earth
EPA	Environmental Protection Agency
FSH	follicle stimulating hormone
GC	gas chromatography
GPx	glutathione peroxidase
GSH	glutathione
GSSG	glutathione disulfide
H&E	haematoxylin and eosin
HNE	hydroxynonenal
HPLC	high performance liquid chromatography
HSC	hematopoietic stem cells
IL	interleukin
LH	luteinizing hormone
MDA	malondialdehyde
MDL	method detection limit
MN	micronuclei
MS	mass spectrometry
MWM	Morris Water Maze
PCBs	polychlorinated biphenyls
PLSDA	partial least squares discriminant analysis
RNS	reactive nitrogen species
ROS	reactive oxygen species
SAM	school air mixture
TERT	telomerase reverse transcriptase
T3	triiodothyronine
T4	thyroxine
TNF	tumor necrosis factor
TRAP	telomeric repeat amplification protocol
TRF	telomeric repeat binding factors

70 **PCB Extraction and Quantification from Tissue and XAD.** About 1 g of tissue was
71 homogenized with diatomaceous earth (DE) and split into two equal fractions: fraction A (for
72 PCB extraction) and fraction B (for lipid content analysis). Fraction A or XAD were spiked with
73 a surrogate standard mixture (PCB 14, deuterium (²H)-labeled PCB 65, and PCB 166) before
74 accelerated solvent extraction (ASE 350, Dionex, Sunnyvale, CA) with acetone-hexane (1:1, v/v)
75 at 100°C and 10,340 kPa (1500 psi) with preheat for 6 min, 60% cell flush volume, and 1 static
76 cycle of 5 min. Collected extracts were concentrated to 1 ml using a TurboVap (Caliper Life
77 Science Inc., Hopkinton, MA) followed by mixing with 2 ml sulfuric acid for cleanup. The
78 organic phase (top) was eluted through another sulfuric acid-acidified silica gel column for
79 additional cleanup. Ultimately, concentrated extracts were transferred to vials and spiked with
80 internal standard (²H-labeled PCB 30 and PCB 204) for PCB quantification using gas
81 chromatography with tandem mass spectrometry (GC-MS/MS) modified from EPA method
82 1668A¹ as previously described.² Fraction B was extracted with chloroform-methanol (2:1, v/v)
83 using an ASE 200 as above. Lipid content in tissue was determined gravimetrically after
84 evaporating all solvents in a vacuum concentrator (SpeedVac, Fisher Scientific, Pittsburgh, PA).
85 Serum lipid content was calculated using the following formula:

86
$$\text{Serum total lipid} = (2.27 \times \text{total cholesterol}) + \text{total triglycerides} + 62.3 \text{ mg/dL.}^3$$

87 Total cholesterol and triglycerides were measured at the University of Iowa Diagnostic Lab.

88 **Morris Water Maze Test.** The method was adapted from Vorhees and Williams⁴. A black
89 circular tank (170 cm diameter, 60 cm high), surrounded with a black curtain, was filled with
90 water (23 to 25°C). Four different cues (circle, square, triangle, and plus sign) were affixed on
91 the tank wall above the water in four positions: north (N), east (E), south (S), and west (W). The

92 tank was divided into four equal-sized quadrants (NE, SE, SW and NW). A circular transparent
93 platform (11 cm diameter, 30 cm high), submerged 1 to 2 cm below the surface of water, was
94 placed in the center of SE quadrant and was unmoved during spatial acquisition test. In spatial
95 acquisition test, all rats performed four trials each day for five consecutive days. During the four
96 trials, rats were released into water facing the wall randomly from four positions (N, E, S and
97 W). For each trial, rats were allowed to swim until they found the platform and remained on the
98 platform for 20 s. If the rat didn't find the platform within 120 s, it was gently guided onto the
99 platform to stay for 20 s, then was removed from the tank and dried with towels. The swimming
100 paths were recorded by an overhead video tracking system. Several parameters reflecting the
101 spatial learning abilities were analyzed, including the time latency to reach the platform, the
102 length of the swimming path and the swimming speed. On the sixth day of probe trial, the hidden
103 platform was removed, and the rats were allowed to swim for 60 s. The number of crossing
104 platform and the time spent in the target quadrant where the previous platform was located were
105 compared among groups to evaluate the reference memory.

106 **Toxicity assessment**

107 **GPx1 activity assay.** Tissue samples were flash frozen in liquid nitrogen after harvesting and
108 stored at -80 °C until analyses. On the day of the assay, samples were homogenized in 1× RIPA
109 lysate buffer (containing protease and phosphatase inhibitors) and centrifuged at 10,000 g for 10
110 min, 4 °C. All activities were normalized to protein content, measured using the Lowry protein
111 assay (Bio-Rad, Hercules, CA).⁵ GPx1 activity was determined using UV-Vis spectroscopy, by
112 following the oxidation of NADPH as earlier described.^{6,7} First, a 55.6 mM (pH 7.4) potassium
113 phosphate buffer (PB) was made containing: 1.1 mM NaN₃ and 1.1 mM EDTA. Secondly, the
114 working buffer was made containing: 1.33 mM glutathione and 1.33 U/mL glutathione disulfide

115 reductase (GR) in stock buffer. A 2.5 mM H₂O₂ solution and a 4 mM NADPH solution were
116 prepared in PB and kept on ice to prevent oxidation. All components, except H₂O₂ were
117 combined, homogenized and incubated at 25 °C for 5 min. Then H₂O₂ solution was added to
118 start the reaction. The rate of NADPH oxidation was then monitored at 340 nm ($\epsilon = 6,220 \text{ M}^{-1}$
119 cm^{-1}).

120 **GPx4 activity assay.** The activity assay is based on a version described by Stolwijk, et al. ⁸. A
121 100 mM (pH 8.0) Tris/HCl buffer was made containing: 1.5 mM NaN₃ to inhibit catalase, and
122 2.0 mM EDTA (chelator). Additionally, Triton X-100, peroxide free (Sigma-Aldrich: X100PC),
123 was added as a surfactant to achieve a 0.1% volume percentage of Triton X-100. Glutathione
124 disulfide reductase, from baker's yeast (Sigma-Aldrich: G3664), solution of 15 U/mL was
125 made. A 60 mM glutathione (Sigma-Aldrich: G4251) was made in assay buffer, as well as, 4
126 mM NADPH in 0.1% NaHCO₃. The buffer, GR solution, GSH solution, NADPH solution, and
127 sample were combined in a cuvette and incubated at 37 °C for 5 min. To monitor the kinetics, the
128 oxidation of NADPH was monitored for 480 s (8 min). Background oxidation of NADPH was
129 monitored for 4 min, then, 15 μL of ~2 mM PCOOH solution was added into the cuvette to start
130 the reaction. The rate of NADPH oxidation was then monitored at 340 nm ($\epsilon = 6,220 \text{ M}^{-1} \text{ cm}^{-1}$).

131 **Catalase activity assay.** Catalase activity was determined using UV-Vis spectroscopy by
132 following the rate of removal (oxidation) of hydrogen peroxide due to catalase.^{9, 10} Hydrogen
133 peroxide has an absorbance at wavelength of 240 nm, $\epsilon_{240} = 39.4 \text{ M}^{-1} \text{ cm}^{-1}$ ¹¹ that was monitored.
134 The protein content (Lowry protein assay) in each assay was determined and used to normalize
135 the activity of catalase per mg protein (mk U/mg protein). The assay was conducted in a 55.6
136 mM (pH 7.0) potassium phosphate buffer. Then a 30 mM H₂O₂ solution was added and the

137 analysis was started. The absorbance of hydrogen peroxide was monitored over 120 s at 10 s
138 intervals.

139 **Micronuclei test**¹². Acridine orange (AO) was dissolved in distilled water (1 mg/ml) and spread
140 10 μ l using a glass rod onto pre-heated (70°C) clean glass slides and left to air dry. Five μ l of
141 whole blood was pipetted onto the center of the AO-coated slide and coverslipped. Scoring was
142 done with the combination of a blue excitation (e.g. 490 nm) and a yellow to orange barrier filter
143 (e.g. 525 nm) and coded slides were analyzed by counting micronuclei per 1000 reticulocytes
144 (immature erythrocytes).

145 **Bone marrow cells isolation.** Bone marrow nucleated cells were isolated from femurs of
146 Sprague-Dawley rats as described by Zhang, et al.¹³. The cells were washed with Dulbecco's
147 Modified Eagle Medium DMEM supplemented with 20% heat inactivated fetal bovine serum
148 (FBS) and 1% penicillin/streptomycin (complete DMEM) and passed through a 70 μ m nylon
149 strainer to remove cell clumps and debris. After initial centrifugation, red blood cells were lysed
150 and clearing of turbidity was achieved by incubating the cells with Flow Cytometry Mouse Lyse
151 Buffer (R&D Systems, Minneapolis, MN) for 10 min at room temperature. After washing with
152 Iscove's Modified Dulbecco's Medium IMDM/2% FBS, cell numbers were counted by an
153 Accuri flow cytometer and 3 different cell suspensions were made in IMDM/2% FBS.

154 **Colony forming cell (CFC) assay.** We performed a CFC assay to measure the absolute number
155 of viable and functional progenitor cells in the bone marrow. A total of 2×10^6 cells in 4 ml
156 IMDM were counted again and a new cell suspension of 6×10^5 cells in 2 ml IMDM/2% FBS was
157 made and 300 μ l of this was added into 3 ml rat Methycellulose Complete Media without Epo
158 (R&D Systems, Minneapolis, MN) to set the final cell number at 3×10^4 cells/ml. Then 1.1 ml of

159 the cell suspension was plated in duplicate in 35-mm untreated culture dishes. Dishes were
160 incubated in a humid incubator at 37°C, 5% CO₂ for 12 days prior to enumeration. Three
161 different colonies: colony forming unit-granulocytes (CFU-G), colony forming unit-
162 macrophages (CFU-M) and colony forming unit-granulocytes, macrophage (CFU-GM) were
163 counted via light microscopy and gridded scoring dish.

164 **Telomerase activity.** 3×10⁶ bone marrow cells were washed once with Phosphate buffered
165 saline (PBS) and were resuspended in cell lysis buffer and incubated on ice for 20 min. After
166 centrifugation at 16,000×g for 20 min at 4°C, the supernatant was transferred into new tubes and
167 stored at -80°C. The protein concentration of the supernatant was determined by Bradford
168 Protein Assay (Bio-Rad, Hercules, CA). The SYBR Green based quantitative PCR reaction was
169 performed by adding 100 ng of TS primer (5'-AATCCGTCGGAGCAGGTT-3'), 50 ng of CX
170 primer (5'-CCCTTACCCTTACCCTTACCCTAA-3')¹⁴, 2.5 µl cell lysate supernatant, 12.5 µl
171 Power SYBR Green PCR master mix from Applied Biosystems (Foster City, CA) and 9.7 µl of
172 DNase- and RNase-free water into the well of a 96-well microplate. Samples were incubated for
173 20 min at room temperature and PCR was performed by incubating the sample at 95°C for 10
174 min followed by 35 cycles of 95°C for 30 s and 60°C for 90 s using an Eppendorf RealPlex
175 Thermal Cycler (Eppendorf, Hamburg, Germany). The threshold cycle (Ct) value was
176 established from the semi-log amplification plots (log increase in fluorescence versus cycle
177 number) and compared with the standard curves generated from serial dilutions of cell extracts.
178 Each sample was analyzed in duplicate.

179 **Quantitative real-time PCR.** 4×10⁶ bone marrow cells were washed once with PBS and total
180 RNA was extracted from each sample using RNeasy Plus mini kit from Qiagen (Valencia, CA)
181 following the manufacturer's protocol and quantified using a NanoDrop2000 (Thermo Fisher

182 Scientific, Wilmington, DE). Total RNA was reverse transcribed using the High Capacity cDNA
183 Reverse Transcription Kit from Applied Biosystems (Foster City, CA). The cDNA was
184 subsequently used for quantitative real-time RT-PCR (qRT-PCR) using an Eppendorf RealPlex
185 thermal cycler. The PCR program used started with 95°C for 10 min followed by 35 cycles at
186 95°C for 30 s, 60°C for 30 s, and 72°C for 1 min. The primers for the quantification of selected
187 genes were purchased from Integrated DNA Technologies (IDT) (Coralville, IA) and were as
188 follows: *Tert*: Forward, 5'-AGCTGCTGAGGTCATTCTTC-3', and reverse, 5'-
189 GCTTGCTCCACACACTCTTA-3'; *Trf-1*: Forward, 5'-CAGCTCACTACAGGACAGTTAAA-
190 3', and reverse, 5'-CTCTCTCACACACACACAAA-3'; *Trf-2*: Forward, 5'-
191 GTGTTTCCCTTCAGTGGTTTG-3', and reverse, 5'-GAGAGCCTATGTGCTCCTAATG-3'
192 (all designed by PrimerQuest); *Gadph*: forward, 5'-TGGAGAAACCTGCCAAGTATG-3', and
193 reverse, 5'-GGGTGGTCCAGGGTTTCTTA-3'¹⁵. An amplification threshold in the linear range
194 of each sample was selected to calculate the C_T for each sample. The relative mRNA levels were
195 calculated with the relative standard curve method.

196 **Gut Microbiota analysis.** The colon fecal samples were sent to Argonne National Laboratory
197 (Argonne, IL) where DNA was extracted from all rat feces samples stored at -20°C. Following
198 the methods outlined by Denner, et al.¹⁶, primers specific for the V4 region of the created 16S
199 rRNA encoding gene was used for PCR amplification. These amplicons were then quantified
200 using the Illumina MiSeq (Illumina, San Diego, CA) at the Argonne National Laboratory. Once
201 quantified, amplicons were sequenced using customized sequencing primers to process for
202 operational taxonomic unity (OTU) picking.¹⁶ Subsequent analysis was then completed by using
203 QiiME2¹⁷ which was able to produce taxonomic profiles and metadata files. These files were
204 then analyzed through METAGENassist to produce relative abundance tables of genera,

205 heatmaps of total taxonomic ranks, and Partial Least Squares Discriminant Analysis (PLSDA)
206 plots.¹⁸

207 **Table S1.** Method Detection Limit (MDL) for each PCB congener or co-eluted congeners. MDL was
 208 determined from method blanks analyzed in parallel with samples and expressed as the upper limit of
 209 99% confidence interval of method blanks (average + t_{n-1} * standard deviation, t_{n-1} is Student's t-value of
 210 99% confidence level with n-1 degree of freedom). Values are expressed in ng.

PCB	MDL	PCB	MDL	PCB	MDL	PCB	MDL
1	0.024	51	0.007	106	0.002	161	0.002
2	0.031	52	0.177	107	0.004	162	0.017
3	0.051	54	0.002	108/124	0.003	164	0.002
4	0.062	55	0.007	110	0.129	165	0.002
5	0.008	56	0.032	111	0.002	167	0.018
6	0.024	57	0.003	112	0.001	169	0.003
7	0.010	58	0.001	114	0.068	170	0.008
8	0.047	59/62/75	0.022	115	0.106	171/173	0.008
9	0.007	60	0.021	117	0.269	172	0.012
10	0.014	61/70/74/76	0.241	118	0.089	174	0.008
11	0.109	63	0.006	120	0.002	175	0.008
12/13	0.061	64	0.045	121	0.001	176	0.002
15	0.044	66	0.116	122	0.003	177	0.007
16	0.044	67	0.004	123	0.002	178	0.005
17	0.033	68	0.086	126	0.002	179	0.005
18/30	0.057	72	0.008	127	0.002	180/193	0.012
19	0.018	73	0.023	129/138/163	0.062	181	0.028
20/28	0.081	77	0.006	130	0.003	182	0.058
21/33	0.041	78	0.006	131	0.003	183	0.006
22	0.024	79	0.001	132	0.016	184	0.069
23	0.011	80	0.001	133	0.004	185	0.007
24	0.008	81	0.002	134	0.004	186	0.003
25	0.017	82	0.017	135/151	0.021	187	0.018
26/29	0.043	83	0.007	136	0.015	188	0.034
27	0.030	84	0.052	137	0.003	189	0.009
31	0.057	85/116	0.081	139/140	0.002	190	0.018
32	0.026	86/97/109/119	0.051	141	0.008	191	0.007
34	0.017	87/125	0.060	142	0.003	192	0.007
35	0.004	88	0.004	143	0.003	194	0.010
36	0.004	89	0.002	144	0.002	195	0.006
37	0.020	90/101/113	0.137	145	0.002	196	0.004
38	0.007	91	0.015	146	0.004	197	0.028
39	0.003	92	0.032	147/149	0.060	198/199	0.007
40/71	0.053	93/100	0.003	148	0.003	200	0.017
41	0.006	94	0.002	150	0.002	201	0.003
42	0.022	95	0.123	152	0.002	202	0.028
43	0.004	96	0.002	153/168	0.047	203	0.002
44/47/65	0.290	98	0.002	154	0.002	205	0.004
45	0.005	99	0.058	155	0.002	206	0.078
46	0.056	102	0.003	156/157	0.008	207	0.013
48	0.016	103	0.002	158	0.002	208	0.008
49/69	0.077	104	0.002	159	0.013	209	0.086
50/53	0.063	105	0.035	160	0.002		

211 **Table S2.** Recovery rate (%) of surrogate standards (PCB 14, d-PCB 65, and PCB 166) in tissues and
 212 SAM vapor extraction. Values are expressed as mean \pm standard deviation.

	Liver (n = 15)	Lung (n = 20)	Brain (n = 14)	Adipose (n = 19)	Serum (n = 19)	SAM vapor (n = 13)
PCB 14	87 \pm 9	85 \pm 7	86 \pm 8	91 \pm 13	82 \pm 11	81 \pm 10
d-PCB 65	93 \pm 11	93 \pm 7	91 \pm 9	75 \pm 23	101 \pm 13	62 \pm 10
PCB 166	105 \pm 11	101 \pm 7	101 \pm 6	83 \pm 20	108 \pm 15	63 \pm 14

213

214 **Table S3.1** Average PCB congener concentrations in **liver** of SAM-exposure group. Values are expressed
 215 in ng/g wet tissue weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.03	51	0.01	107	0.25	162	0.02
2	0.04	52	1.86	108/124	0.01	164	0.02
3	0.06	54	0.00	110	1.86	165	0.00
4	0.07	55	0.11	111	0.00	167	0.02
5	0.01	56	0.06	112	0.05	169	0.01
6	0.03	57	0.00	114	0.22	170	0.02
7	0.01	58	0.00	115	0.76	171/173	0.02
8	0.06	59/62/75	0.12	117	0.62	172	0.02
9	0.01	60	2.40	118	4.84	174	0.03
10	0.02	61/70/74/76	9.10	120	0.00	175	0.02
11	0.13	63	0.14	121	0.00	176	0.00
12/13	0.07	64	0.21	122	0.01	177	0.02
14	0.00	66	12.1	123	0.14	178	0.01
15	0.06	67	0.01	126	0.00	179	0.01
16	0.15	68	0.10	127	0.00	180/193	0.06
17	0.04	72	0.01	128/166	0.00	181	0.03
18/30	0.22	73	0.04	129/138/163	1.26	182	0.07
19	0.15	77	0.03	130	0.08	183	0.05
20/28	0.68	78	0.01	131	0.00	184	0.08
21/33	0.22	79	0.01	132	0.08	185	0.01
22	0.15	80	0.02	133	0.01	186	0.00
23	0.03	81	0.01	134	0.00	187	0.08
24	0.11	82	0.10	135/151	0.05	188	0.04
25	0.05	83	0.02	136	0.02	189	0.01
26/29	0.10	84	0.06	137	0.12	190	0.03
27	0.04	85/116	3.81	139/140	0.14	191	0.02
31	0.23	86/97/109/119	1.09	141	0.05	192	0.02
32	0.26	87/125	1.08	142	0.00	194	0.02
34	0.09	88	0.02	143	0.00	195	0.01
35	0.04	89	0.00	144	0.01	196	0.01
36	0.01	90/101/113	6.51	145	0.00	197	0.04
37	0.02	91	0.12	146	0.16	198/199	0.02
38	0.06	92	0.85	147/149	0.40	200	0.02
39	0.01	93/100	0.04	148	0.00	201	0.00
40/71	0.06	94	0.00	150	0.00	202	0.03
41	0.01	95	0.51	152	0.00	203	0.01
42	0.07	96	0.00	153/168	1.08	204	0.00
43	0.01	98	0.00	154	0.04	205	0.01
44/47/65	1.94	99	15.0	155	0.00	206	0.09
45	0.01	102	0.01	156/157	0.01	207	0.02
46	0.07	103	0.00	158	0.15	208	0.01
48	0.05	104	0.00	159	0.02	209	0.10
49/69	2.08	105	1.81	160	0.00	SUM	78.6
50/53	0.08	106	0.01	161	0.00		

217 **Table S3.2** Average lipid-adjusted PCB congener concentrations in **liver** of SAM-exposure group.
 218 Values are expressed in ng/g lipid weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.47	51	0.14	107	4.15	162	0.33
2	0.61	52	30.6	108/124	0.10	164	0.26
3	1.01	54	0.05	110	30.2	165	0.03
4	1.22	55	1.78	111	0.04	167	0.35
5	0.15	56	1.02	112	0.80	169	0.16
6	0.48	57	0.05	114	3.57	170	0.35
7	0.20	58	0.03	115	12.5	171/173	0.36
8	0.94	59/62/75	1.89	117	10.1	172	0.38
9	0.14	60	39.4	118	79.2	174	0.44
10	0.28	61/70/74/76	149	120	0.06	175	0.36
11	2.15	63	2.24	121	0.03	176	0.05
12/13	1.20	64	3.49	122	0.19	177	0.37
14	0.00	66	198	123	2.26	178	0.10
15	0.92	67	0.09	126	0.05	179	0.13
16	2.49	68	1.71	127	0.05	180/193	1.05
17	0.65	72	0.15	128/166	0.00	181	0.56
18/30	3.74	73	0.72	129/138/163	20.5	182	1.14
19	2.33	77	0.51	130	1.23	183	0.83
20/28	11.4	78	0.17	131	0.06	184	1.36
21/33	3.45	79	0.19	132	1.40	185	0.21
22	2.53	80	0.33	133	0.14	186	0.06
23	0.47	81	0.20	134	0.07	187	1.30
24	1.93	82	1.70	135/151	0.88	188	0.67
25	0.77	83	0.29	136	0.34	189	0.20
26/29	1.67	84	1.02	137	1.97	190	0.48
27	0.69	85/116	62.2	139/140	2.33	191	0.25
31	3.73	86/97/109/119	17.8	141	0.86	192	0.28
32	4.25	87/125	17.7	142	0.06	194	0.29
34	1.43	88	0.34	143	0.05	195	0.14
35	0.60	89	0.05	144	0.17	196	0.12
36	0.20	90/101/113	107	145	0.03	197	0.68
37	0.39	91	1.99	146	2.64	198/199	0.30
38	1.05	92	14.0	147/149	6.63	200	0.37
39	0.13	93/100	0.63	148	0.05	201	0.07
40/71	1.06	94	0.05	150	0.03	202	0.55
41	0.13	95	8.37	152	0.03	203	0.18
42	1.09	96	0.05	153/168	17.6	204	0.00
43	0.17	98	0.04	154	0.60	205	0.16
44/47/65	31.8	99	245	155	0.03	206	1.55
45	0.12	102	0.10	156/157	0.17	207	0.26
46	1.10	103	0.05	158	2.45	208	0.17
48	0.84	104	0.03	159	0.26	209	1.69
49/69	34.1	105	29.7	160	0.06	SUM	1290
50/53	1.25	106	0.12	161	0.03		

219

220 **Table S3.3** Average PCB congener concentrations in **lung** of SAM-exposure group. Values are expressed
 221 in ng/g wet tissue weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.08	51	0.02	107	0.42	162	0.05
2	0.10	52	3.15	108/124	0.02	164	0.01
3	0.16	54	0.01	110	2.29	165	0.01
4	0.20	55	0.08	111	0.01	167	0.06
5	0.02	56	0.24	112	0.07	169	0.01
6	0.08	57	0.01	114	0.28	170	0.03
7	0.03	58	0.00	115	1.14	171/173	0.03
8	0.15	59/62/75	0.16	117	1.11	172	0.04
9	0.02	60	7.91	118	8.64	174	0.03
10	0.05	61/70/74/76	14.5	120	0.01	175	0.02
11	0.35	63	0.18	121	0.00	176	0.01
12/13	0.20	64	0.26	122	0.02	177	0.03
14	0.00	66	22.2	123	0.18	178	0.01
15	0.14	67	0.01	126	0.01	179	0.02
16	0.14	68	0.28	127	0.01	180/193	0.10
17	0.11	72	0.02	128/166	0.00	181	0.09
18/30	0.19	73	0.07	129/138/163	3.65	182	0.19
19	0.06	77	0.02	130	0.12	183	0.09
20/28	2.07	78	0.02	131	0.01	184	0.22
21/33	0.13	79	0.00	132	0.09	185	0.02
22	0.08	80	0.00	133	0.01	186	0.01
23	0.04	81	0.01	134	0.01	187	0.14
24	0.03	82	0.25	135/151	0.10	188	0.11
25	0.05	83	0.02	136	0.05	189	0.03
26/29	0.14	84	0.17	137	0.19	190	0.06
27	0.10	85/116	6.74	139/140	0.19	191	0.02
31	0.18	86/97/109/119	1.97	141	0.07	192	0.02
32	0.08	87/125	2.04	142	0.01	194	0.03
34	0.05	88	0.01	143	0.01	195	0.02
35	0.01	89	0.01	144	0.01	196	0.01
36	0.01	90/101/113	11.9	145	0.01	197	0.10
37	0.06	91	0.11	146	0.37	198/199	0.02
38	0.02	92	1.54	147/149	0.62	200	0.05
39	0.01	93/100	0.02	148	0.01	201	0.01
40/71	0.17	94	0.01	150	0.01	202	0.09
41	0.02	95	1.18	152	0.01	203	0.01
42	0.08	96	0.01	153/168	2.90	204	0.00
43	0.02	98	0.01	154	0.07	205	0.01
44/47/65	3.76	99	32.0	155	0.01	206	0.25
45	0.02	102	0.01	156/157	0.03	207	0.04
46	0.18	103	0.01	158	0.29	208	0.03
48	0.07	104	0.01	159	0.04	209	0.28
49/69	1.31	105	5.30	160	0.01	SUM	149
50/53	0.20	106	0.01	161	0.01		

223 **Table S3.4** Average lipid-adjusted PCB congener concentrations in **lung** of SAM-exposure group. Values
 224 are expressed in ng/g lipid weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	1.76	51	0.51	107	9.66	162	1.25
2	2.32	52	72.1	108/124	0.48	164	0.24
3	3.80	54	0.17	110	52.5	165	0.13
4	4.61	55	1.96	111	0.15	167	1.33
5	0.56	56	5.69	112	1.73	169	0.26
6	1.80	57	0.19	114	6.32	170	0.60
7	0.77	58	0.09	115	25.9	171/173	0.70
8	3.53	59/62/75	3.58	117	25.4	172	0.86
9	0.54	60	183	118	198	174	0.65
10	1.06	61/70/74/76	332	120	0.16	175	0.56
11	8.12	63	4.22	121	0.10	176	0.18
12/13	4.53	64	5.93	122	0.43	177	0.77
14	0.00	66	509	123	4.11	178	0.34
15	3.25	67	0.30	126	0.18	179	0.38
16	3.32	68	6.44	127	0.14	180/193	2.19
17	2.45	72	0.58	128/166	0.00	181	2.13
18/30	4.29	73	1.72	129/138/163	84.1	182	4.30
19	1.33	77	0.47	130	2.79	183	2.01
20/28	47.7	78	0.46	131	0.22	184	5.12
21/33	3.04	79	0.11	132	2.05	185	0.54
22	1.79	80	0.09	133	0.30	186	0.20
23	0.83	81	0.13	134	0.27	187	3.30
24	0.58	82	5.72	135/151	2.36	188	2.52
25	1.24	83	0.52	136	1.15	189	0.68
26/29	3.18	84	3.85	137	4.43	190	1.31
27	2.23	85/116	155	139/140	4.38	191	0.56
31	4.25	86/97/109/119	45.3	141	1.47	192	0.49
32	1.97	87/125	46.8	142	0.22	194	0.77
34	1.24	88	0.26	143	0.19	195	0.47
35	0.31	89	0.18	144	0.30	196	0.33
36	0.26	90/101/113	272	145	0.12	197	2.37
37	1.48	91	2.53	146	8.54	198/199	0.53
38	0.51	92	35.39	147/149	14.1	200	1.26
39	0.24	93/100	0.50	148	0.19	201	0.22
40/71	3.99	94	0.17	150	0.12	202	2.08
41	0.43	95	27.3	152	0.13	203	0.21
42	1.90	96	0.14	153/168	66.6	204	0.00
43	0.35	98	0.18	154	1.64	205	0.31
44/47/65	86.2	99	734	155	0.12	206	5.84
45	0.37	102	0.24	156/157	0.63	207	0.97
46	4.17	103	0.20	158	6.59	208	0.61
48	1.51	104	0.14	159	0.99	209	6.39
49/69	30.0	105	122	160	0.12	SUM	3420
50/53	4.72	106	0.15	161	0.13		

226 **Table S3.5** Average PCB congener concentrations in **brain** of SAM-exposure group. Values are
 227 expressed in ng/g wet tissue weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.03	51	0.01	107	0.25	162	0.03
2	0.04	52	1.37	108/124	0.04	164	0.02
3	0.07	54	0.00	110	1.59	165	0.00
4	0.13	55	0.08	111	0.00	167	0.03
5	0.01	56	0.05	112	0.12	169	0.01
6	0.04	57	0.00	114	0.25	170	0.02
7	0.02	58	0.00	115	0.55	171/173	0.02
8	0.06	59/62/75	0.12	117	0.62	172	0.03
9	0.01	60	2.05	118	4.28	174	0.01
10	0.06	61/70/74/76	9.00	120	0.00	175	0.12
11	0.19	63	0.13	121	0.00	176	0.00
12/13	0.08	64	0.19	122	0.01	177	0.01
14	0.00	66	10.5	123	0.13	178	0.02
15	0.06	67	0.01	126	0.00	179	0.01
16	0.14	68	0.12	127	0.00	180/193	0.06
17	0.04	72	0.02	128/166	0.00	181	0.04
18/30	0.21	73	0.04	129/138/163	1.05	182	0.13
19	0.75	77	0.01	130	0.08	183	0.06
20/28	0.87	78	0.01	131	0.01	184	0.09
21/33	0.11	79	0.00	132	0.07	185	0.02
22	0.03	80	0.00	133	0.02	186	0.00
23	0.02	81	0.00	134	0.01	187	0.11
24	0.71	82	0.09	135/151	0.06	188	0.05
25	0.02	83	0.08	136	0.02	189	0.08
26/29	0.06	84	0.08	137	0.11	190	0.04
27	0.16	85/116	3.09	139/140	0.09	191	0.01
31	1.16	86/97/109/119	1.03	141	0.05	192	0.01
32	0.04	87/125	0.84	142	0.00	194	0.01
34	0.20	88	0.00	143	0.00	195	0.01
35	0.04	89	0.00	144	0.01	196	0.01
36	0.00	90/101/113	5.20	145	0.00	197	0.04
37	0.03	91	0.10	146	0.17	198/199	0.02
38	0.01	92	0.76	147/149	0.30	200	0.03
39	0.00	93/100	0.03	148	0.00	201	0.01
40/71	0.10	94	0.00	150	0.00	202	0.04
41	0.01	95	0.44	152	0.00	203	0.01
42	0.06	96	0.00	153/168	0.97	204	0.00
43	0.01	98	0.00	154	0.03	205	0.01
44/47/65	1.68	99	12.0	155	0.00	206	0.11
45	0.01	102	0.00	156/157	0.01	207	0.02
46	0.08	103	0.00	158	0.12	208	0.01
48	0.05	104	0.00	159	0.02	209	0.12
49/69	0.59	105	1.60	160	0.00	SUM	69.7
50/53	0.09	106	0.01	161	0.00		

229 **Table S3.6** Average lipid-adjusted PCB congener concentrations in **brain** of SAM-exposure group.
 230 Values are expressed in ng/g lipid weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.35	51	0.10	107	2.69	162	0.29
2	0.46	52	15.0	108/124	0.50	164	0.18
3	0.76	54	0.03	110	17.4	165	0.03
4	1.47	55	0.94	111	0.03	167	0.30
5	0.15	56	0.53	112	1.28	169	0.07
6	0.47	57	0.04	114	2.70	170	0.25
7	0.18	58	0.02	115	5.93	171/173	0.19
8	0.71	59/62/75	1.27	117	6.70	172	0.37
9	0.14	60	22.3	118	46.7	174	0.16
10	0.65	61/70/74/76	98.3	120	0.03	175	1.25
11	2.07	63	1.43	121	0.02	176	0.04
12/13	0.91	64	2.09	122	0.16	177	0.15
14	0.00	66	115	123	1.37	178	0.19
15	0.65	67	0.06	126	0.04	179	0.08
16	1.54	68	1.29	127	0.04	180/193	0.70
17	0.49	72	0.20	128/166	0.00	181	0.42
18/30	2.25	73	0.38	129/138/163	11.5	182	1.43
19	8.15	77	0.09	130	0.86	183	0.60
20/28	9.53	78	0.09	131	0.06	184	1.02
21/33	1.15	79	0.02	132	0.80	185	0.17
22	0.36	80	0.04	133	0.19	186	0.04
23	0.17	81	0.03	134	0.09	187	1.22
24	7.35	82	1.02	135/151	0.70	188	0.50
25	0.25	83	0.92	136	0.23	189	0.92
26/29	0.64	84	0.86	137	1.25	190	0.42
27	1.81	85/116	33.7	139/140	1.02	191	0.16
31	12.0	86/97/109/119	11.2	141	0.59	192	0.14
32	0.39	87/125	9.11	142	0.05	194	0.15
34	2.27	88	0.05	143	0.04	195	0.14
35	0.38	89	0.04	144	0.15	196	0.09
36	0.05	90/101/113	56.7	145	0.03	197	0.47
37	0.30	91	1.05	146	1.84	198/199	0.24
38	0.12	92	8.31	147/149	3.30	200	0.31
39	0.05	93/100	0.37	148	0.04	201	0.10
40/71	1.09	94	0.03	150	0.02	202	0.42
41	0.09	95	4.85	152	0.03	203	0.07
42	0.65	96	0.03	153/168	10.6	204	0.00
43	0.10	98	0.03	154	0.34	205	0.06
44/47/65	18.3	99	130	155	0.02	206	1.17
45	0.09	102	0.04	156/157	0.13	207	0.23
46	0.83	103	0.03	158	1.35	208	0.15
48	0.54	104	0.02	159	0.20	209	1.28
49/69	6.42	105	17.5	160	0.04	SUM	760
50/53	0.94	106	0.08	161	0.03		

232 **Table S3.7** Average PCB congener concentrations in **adipose tissue** of SAM-exposure group. Values are
 233 expressed in ng/g wet tissue weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.06	51	0.05	107	12.5	162	0.04
2	0.07	52	147	108/124	0.77	164	0.76
3	0.12	54	0.00	110	130	165	0.01
4	0.15	55	0.02	111	0.01	167	0.64
5	0.02	56	4.18	112	0.00	169	0.01
6	0.13	57	0.01	114	7.79	170	0.78
7	0.06	58	0.00	115	24.9	171/173	0.66
8	0.46	59/62/75	6.13	117	6.67	172	0.21
9	0.05	60	129	118	226	174	0.40
10	0.03	61/70/74/76	585	120	0.01	175	0.06
11	0.26	63	9.46	121	0.00	176	0.03
12/13	0.14	64	16.1	122	0.01	177	0.99
14	0.00	66	738	123	6.02	178	0.27
15	0.10	67	0.08	126	0.01	179	0.04
16	0.11	68	0.21	127	0.01	180/193	1.76
17	0.16	72	0.16	128/166	0.00	181	0.13
18/30	1.14	73	0.05	129/138/163	93.3	182	0.09
19	0.04	77	0.01	130	4.72	183	1.38
20/28	56.2	78	0.01	131	0.37	184	0.09
21/33	0.10	79	0.01	132	6.78	185	0.02
22	0.06	80	0.00	133	1.23	186	0.01
23	0.03	81	0.00	134	0.52	187	1.60
24	0.02	82	9.14	135/151	5.76	188	0.08
25	0.13	83	0.02	136	0.55	189	0.02
26/29	0.24	84	3.34	137	6.77	190	0.14
27	0.07	85/116	187	139/140	7.35	191	0.05
31	4.76	86/97/109/119	61.3	141	3.95	192	0.02
32	0.35	87/125	52.5	142	0.01	194	0.19
34	0.04	88	0.01	143	0.02	195	0.09
35	0.01	89	0.09	144	1.38	196	0.09
36	0.01	90/101/113	355	145	0.01	197	0.08
37	0.62	91	6.59	146	11.0	198/199	0.29
38	0.02	92	57.9	147/149	28.5	200	0.04
39	0.01	93/100	1.88	148	0.07	201	0.05
40/71	3.58	94	0.04	150	0.01	202	0.22
41	0.12	95	28.3	152	0.01	203	0.15
42	3.96	96	0.02	153/168	65.4	204	0.00
43	0.24	98	0.03	154	2.62	205	0.01
44/47/65	126	99	633	155	0.01	206	0.19
45	0.23	102	0.33	156/157	1.87	207	0.04
46	0.13	103	0.20	158	10.5	208	0.07
48	2.50	104	0.00	159	0.03	209	0.25
49/69	49.6	105	86.8	160	0.09	SUM	4050
50/53	0.45	106	0.01	161	0.02		

235 **Table S3.8** Average lipid-adjusted PCB congener concentrations in **adipose tissue** of SAM-exposure
 236 group. Values are expressed in ng/g lipid weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.07	51	0.06	107	15.8	162	0.05
2	0.09	52	184	108/124	0.96	164	0.95
3	0.15	54	0.00	110	164	165	0.01
4	0.18	55	0.02	111	0.01	167	0.80
5	0.03	56	5.22	112	0.01	169	0.01
6	0.16	57	0.01	114	9.83	170	0.97
7	0.07	58	0.00	115	32.1	171/173	0.82
8	0.57	59/62/75	7.68	117	8.85	172	0.25
9	0.07	60	161	118	285	174	0.50
10	0.04	61/70/74/76	732	120	0.01	175	0.07
11	0.32	63	11.8	121	0.00	176	0.03
12/13	0.18	64	20.1	122	0.01	177	1.22
14	0.00	66	923	123	7.61	178	0.34
15	0.13	67	0.10	126	0.01	179	0.04
16	0.13	68	0.25	127	0.01	180/193	2.18
17	0.20	72	0.20	128/166	0.00	181	0.17
18/30	1.44	73	0.07	129/138/163	117	182	0.11
19	0.05	77	0.02	130	5.90	183	1.72
20/28	70.8	78	0.02	131	0.48	184	0.12
21/33	0.12	79	0.01	132	8.56	185	0.02
22	0.07	80	0.00	133	1.55	186	0.01
23	0.03	81	0.01	134	0.67	187	1.98
24	0.02	82	11.4	135/151	7.22	188	0.10
25	0.17	83	0.02	136	0.70	189	0.03
26/29	0.30	84	4.23	137	8.46	190	0.17
27	0.09	85/116	235	139/140	9.29	191	0.06
31	5.98	86/97/109/119	77.0	141	4.94	192	0.02
32	0.43	87/125	66.5	142	0.01	194	0.23
34	0.05	88	0.01	143	0.02	195	0.11
35	0.01	89	0.11	144	1.75	196	0.11
36	0.01	90/101/113	446	145	0.01	197	0.10
37	0.78	91	8.30	146	13.7	198/199	0.36
38	0.02	92	73.2	147/149	36.1	200	0.05
39	0.01	93/100	2.36	148	0.09	201	0.06
40/71	4.48	94	0.05	150	0.01	202	0.26
41	0.17	95	35.7	152	0.01	203	0.19
42	4.94	96	0.02	153/168	82.0	204	0.00
43	0.28	98	0.03	154	3.29	205	0.01
44/47/65	158	99	801	155	0.01	206	0.23
45	0.29	102	0.42	156/157	2.33	207	0.05
46	0.16	103	0.25	158	13.2	208	0.08
48	3.13	104	0.01	159	0.04	209	0.30
49/69	62.3	105	109	160	0.12	SUM	5090
50/53	0.57	106	0.01	161	0.02		

238 **Table S3.9** Average PCB congener concentrations in **serum** of SAM-exposure group. Values are
 239 expressed in ng/g wet weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	0.03	51	0.01	107	0.01	162	0.02
2	0.04	52	0.49	108/124	0.00	164	0.00
3	0.07	54	0.00	110	0.25	165	0.00
4	0.09	55	0.02	111	0.00	167	0.03
5	0.01	56	0.05	112	0.00	169	0.00
6	0.03	57	0.00	114	0.00	170	0.01
7	0.01	58	0.00	115	0.00	171/173	0.01
8	0.07	59/62/75	0.03	117	0.00	172	0.02
9	0.01	60	0.29	118	0.59	174	0.01
10	0.02	61/70/74/76	0.93	120	0.00	175	0.01
11	0.15	63	0.02	121	0.00	176	0.00
12/13	0.09	64	0.06	122	0.00	177	0.01
14	0.00	66	1.16	123	0.01	178	0.01
15	0.06	67	0.01	126	0.00	179	0.01
16	0.06	68	0.12	127	0.00	180/193	0.02
17	0.05	72	0.01	128/166	0.00	181	0.01
18/30	0.08	73	0.03	129/138/163	0.10	182	0.01
19	0.03	77	0.01	130	0.00	183	0.01
20/28	0.11	78	0.01	131	0.00	184	0.01
21/33	0.06	79	0.00	132	0.02	185	0.01
22	0.03	80	0.00	133	0.01	186	0.04
23	0.02	81	0.00	134	0.01	187	0.02
24	0.01	82	0.02	135/151	0.03	188	0.02
25	0.02	83	0.01	136	0.02	189	0.01
26/29	0.06	84	0.07	137	0.01	190	0.02
27	0.04	85/116	0.46	139/140	0.01	191	0.01
31	0.08	86/97/109/119	0.10	141	0.01	192	0.01
32	0.04	87/125	0.20	142	0.00	194	0.01
34	0.02	88	0.01	143	0.00	195	0.01
35	0.01	89	0.00	144	0.00	196	0.01
36	0.01	90/101/113	1.15	145	0.00	197	0.04
37	0.03	91	0.02	146	0.01	198/199	0.01
38	0.01	92	0.17	147/149	0.09	200	0.02
39	0.00	93/100	0.00	148	0.00	201	0.00
40/71	0.08	94	0.00	150	0.00	202	0.04
41	0.01	95	0.17	152	0.00	203	0.00
42	0.03	96	0.00	153/168	0.14	204	0.00
43	0.01	98	0.00	154	0.01	205	0.01
44/47/65	0.29	99	1.49	155	0.00	206	0.11
45	0.01	102	0.00	156/157	0.01	207	0.02
46	0.08	103	0.00	158	0.00	208	0.01
48	0.02	104	0.00	159	0.02	209	0.12
49/69	0.29	105	0.28	160	0.00	SUM	12.0
50/53	0.09	106	0.00	161	0.00		

241 **Table S3.10** Average lipid-adjusted PCB congener concentrations in **serum** of SAM-exposure group.
 242 Values are expressed in ng/g lipid weight.

PCB	Conc.	PCB	Conc.	PCB	Conc.	PCB	Conc.
1	9.38	51	2.73	107	2.77	162	6.66
2	12.4	52	137	108/124	1.06	164	0.69
3	20.2	54	0.61	110	71.3	165	0.69
4	24.5	55	5.81	111	0.79	167	7.10
5	2.99	56	12.9	112	0.58	169	1.37
6	9.56	57	1.03	114	0.35	170	3.20
7	4.10	58	0.50	115	0.74	171/173	3.18
8	18.8	59/62/75	8.77	117	0.67	172	4.60
9	2.89	60	81.1	118	165	174	3.29
10	5.66	61/70/74/76	260	120	0.87	175	3.01
11	43.2	63	4.46	121	0.56	176	0.96
12/13	24.1	64	17.7	122	1.34	177	2.65
14	0.00	66	322	123	1.80	178	1.80
15	17.3	67	1.60	126	0.00	179	2.05
16	17.7	68	34.31	127	0.74	180/193	4.72
17	13.1	72	3.07	128/166	0.00	181	2.50
18/30	22.8	73	9.13	129/138/163	29.3	182	2.60
19	7.08	77	2.50	130	1.22	183	2.54
20/28	32.2	78	2.45	131	1.15	184	2.58
21/33	16.2	79	0.58	132	6.41	185	2.86
22	9.53	80	0.50	133	1.59	186	9.72
23	4.43	81	1.05	134	1.43	187	7.02
24	3.11	82	6.65	135/151	8.36	188	4.54
25	6.58	83	3.23	136	6.10	189	3.60
26/29	17.0	84	20.5	137	3.72	190	6.96
27	11.9	85/116	127	139/140	3.80	191	2.68
31	22.7	86/97/109/119	28.4	141	3.28	192	2.59
32	10.5	87/125	56.7	142	1.17	194	4.08
34	6.62	88	1.41	143	0.99	195	2.52
35	1.63	89	0.96	144	0.97	196	1.77
36	1.41	90/101/113	322	145	0.65	197	10.9
37	7.88	91	6.04	146	2.70	198/199	2.83
38	2.73	92	47.8	147/149	23.9	200	6.69
39	1.27	93/100	1.31	148	1.21	201	1.19
40/71	21.2	94	0.93	150	0.94	202	11.1
41	2.27	95	48.9	152	0.67	203	0.99
42	8.85	96	0.76	153/168	39.4	204	0.00
43	1.47	98	0.88	154	1.62	205	1.68
44/47/65	81.9	99	416	155	0.64	206	31.1
45	1.95	102	1.17	156/157	3.37	207	5.18
46	22.2	103	0.78	158	1.11	208	3.25
48	6.23	104	0.64	159	5.27	209	34.0
49/69	82.2	105	78.2	160	0.63	SUM	3350
50/53	25.1	106	0.78	161	0.68		

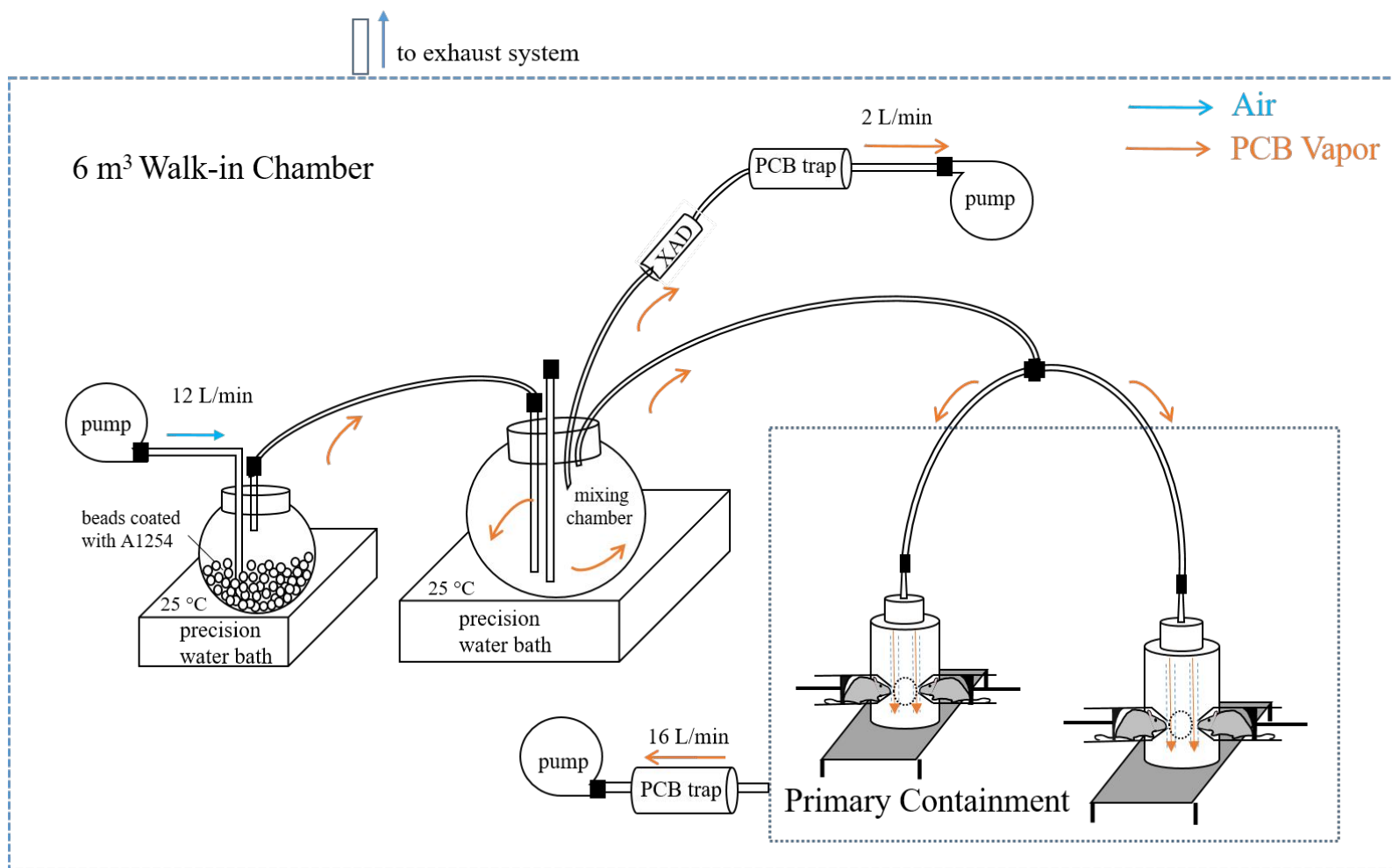
244 **Table S4.** Redox parameters and redox potentials (E_h) in plasma.

	CySS (μM)	Cys (μM)	CySSG (μM)	GSH (μM)	GSSG (μM)	E_h (GSSG/GSH) (mV)	E_h (CySS/Cys) (mV)	Total GSH (μM)	Total Cys (μM)
SAM	62.6 \pm 9.5	29.4 \pm 7.3	25.1 \pm 6.9	28.0 \pm 8.0	4.8 \pm 2.2	-152.1 \pm 13.5	-103.7 \pm 5.7	62.6 \pm 16.3	179.6 \pm 25.1
Sham	64.4 \pm 12.6	28.3 \pm 3.5	25.3 \pm 9.9	25.1 \pm 4.0	5.2 \pm 3.8	-148.1 \pm 6.4	-102.9 \pm 4.5	60.9 \pm 19.5	182.4 \pm 28.4

245 Values are expressed as mean \pm standard deviation (n = 8). CySS: cystine; Cys: cysteine; CySSG: cysteine-glutathione disulfide;

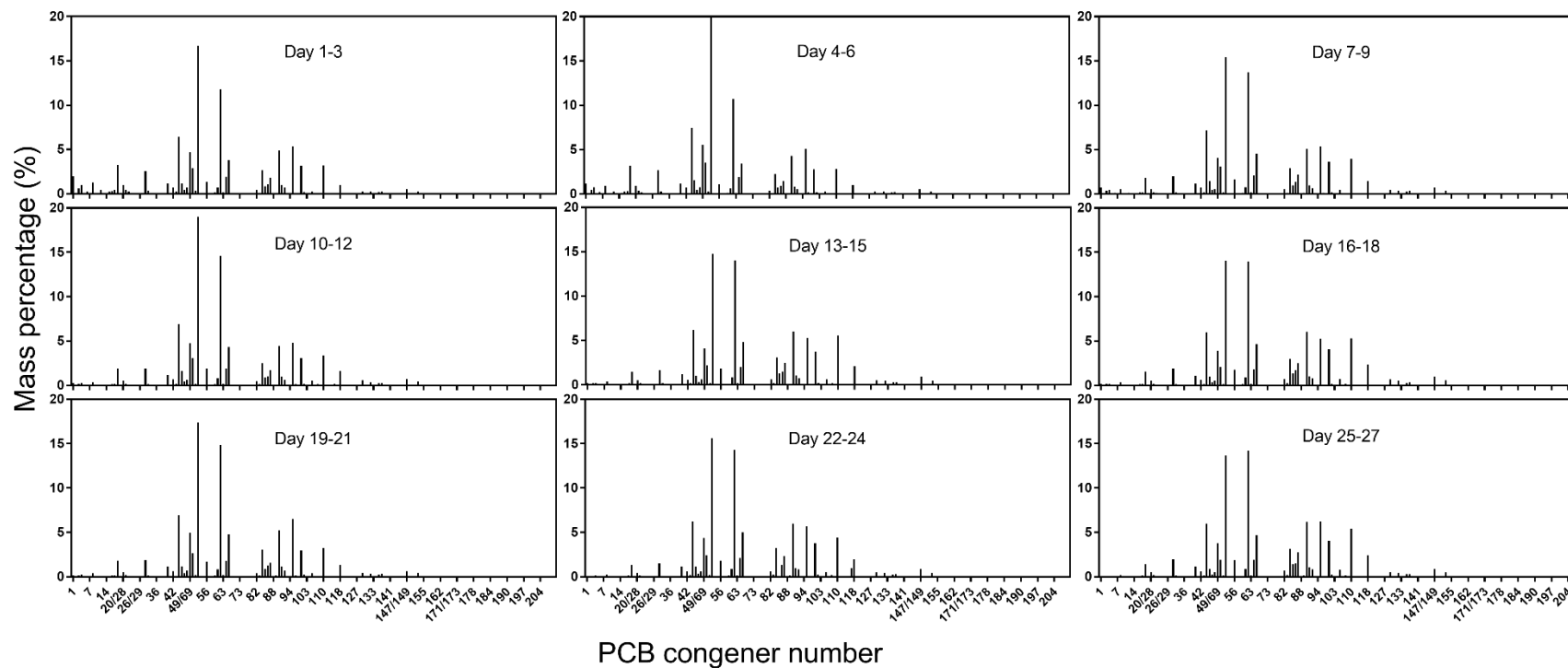
246 GSH: glutathione; GSSG: glutathione disulfide. E_h were calculated with the Nernst equation for pH 7.4: E_h (GSSG/GSH) = -264 + 30

247 * log (GSSG / GSH²); E_h (CySS / Cys) = -250 + 30 * log (CySS / Cys²).¹⁹



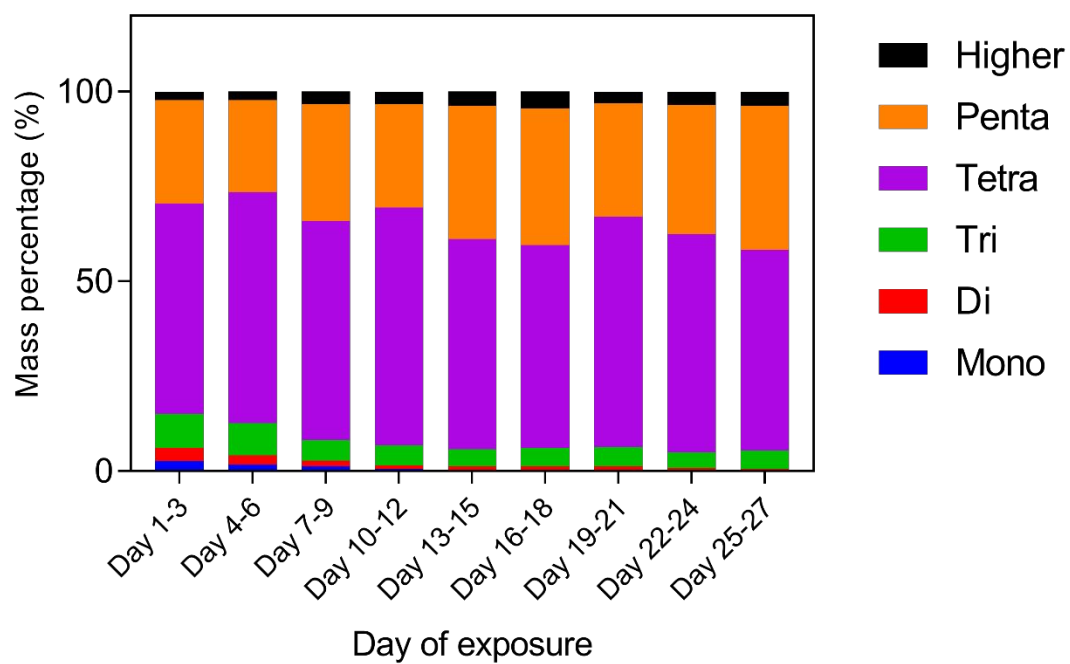
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249 **Figure S1.** Schematic of PCB generation and nose-only exposure system.



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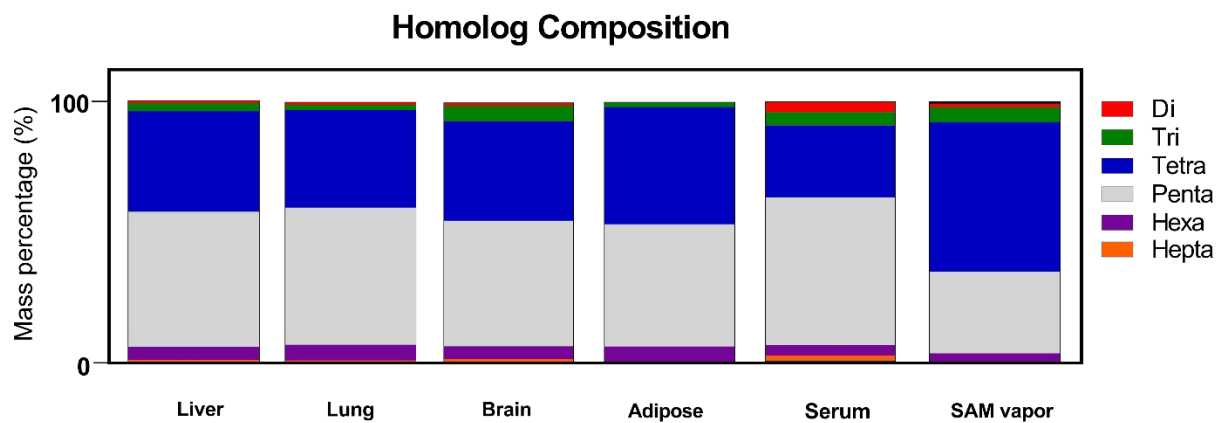
251 **Figure S2.** PCB congener profile (in mass percentage, %) in sequential three-day collections of PCB vapor using XAD.



252

253 **Figure S3.** PCB homologue composition (in mass percentage, %) in sequential three-day collections of

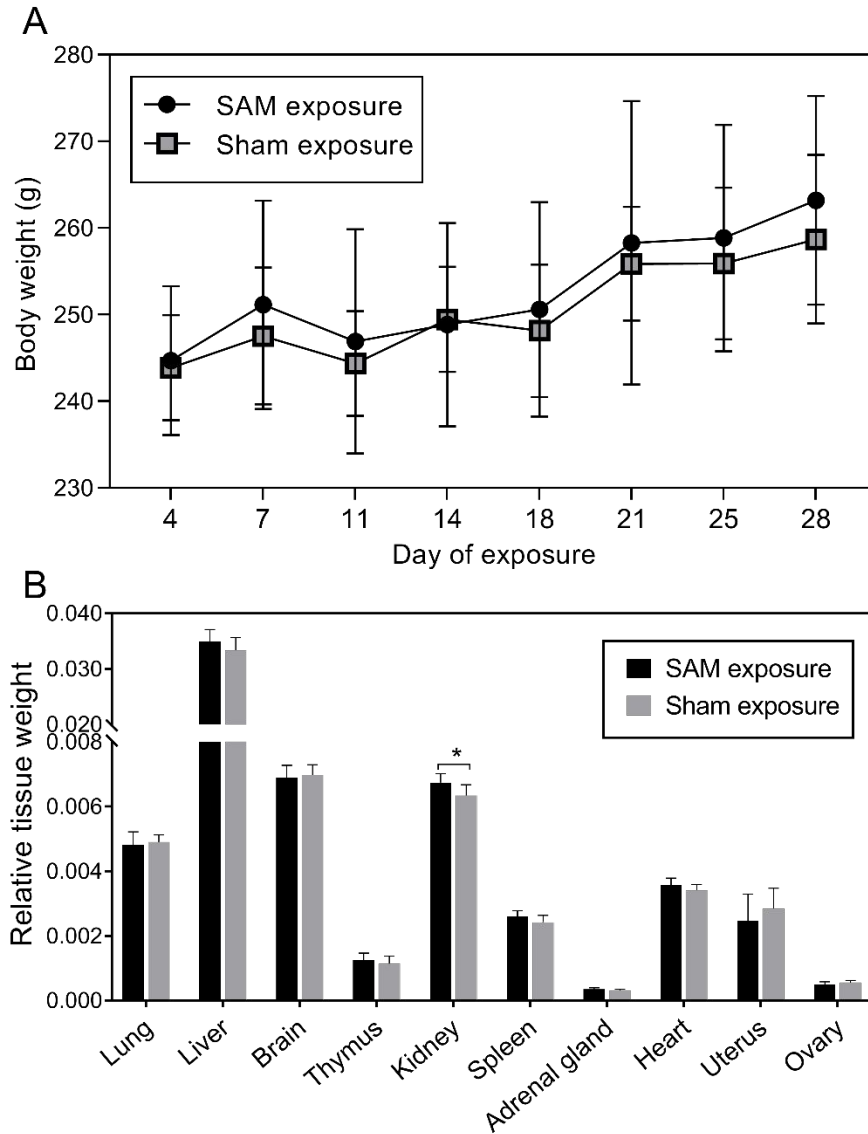
254 PCB vapor using XAD.



255

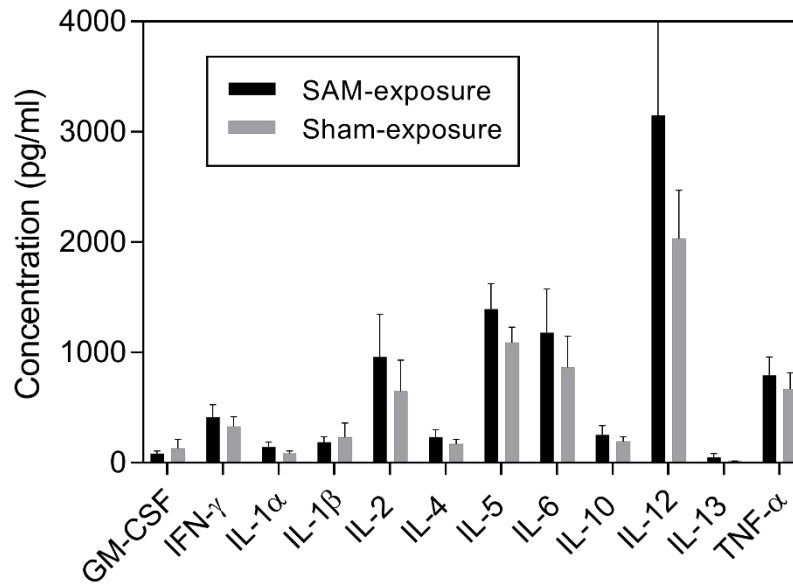
256 **Figure S4.** PCB homolog composition (in mass percentage, %) in tissues of SAM-exposed rats

257 and in generated SAM vapor.



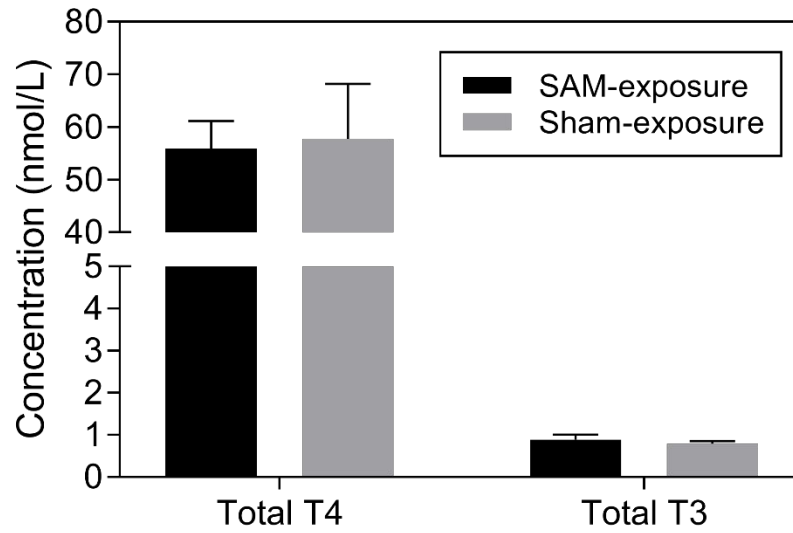
258

259 **Figure S5.** Body weight (S5A, g) and relative tissue weight (S5B, g/g body weight) of rats in
 260 SAM- and sham-exposed groups. No significant differences were found between the groups in
 261 body weight. Relative kidney weight in SAM was significantly higher than sham (* $p < 0.05$,
 262 Student's t-test). Values were expressed as mean \pm standard deviation (n = 8).



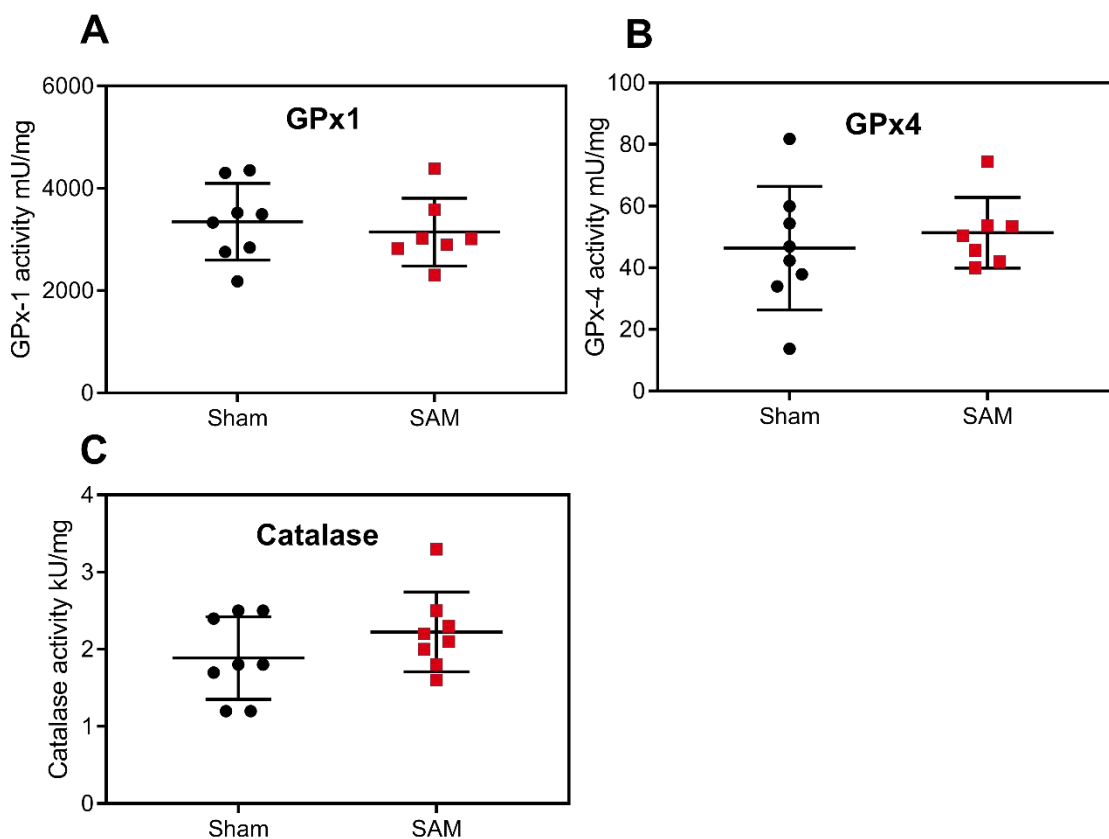
263

264 **Figure S6.** Cytokine concentrations (pg/ml) in plasma from rats in sham- and SAM-exposure
265 groups. Values are expressed as mean \pm standard error (n = 5). No significant differences were
266 found between sham and SAM rats.



267

268 **Figure S7.** Thyroid hormone (total T4 and total T3) concentrations (nmol/L) in serum after
269 exposed to SAM vapor. Values are graphed as mean \pm standard deviation (n = 8). There were no
270 significant differences between sham and SAM rats.



271

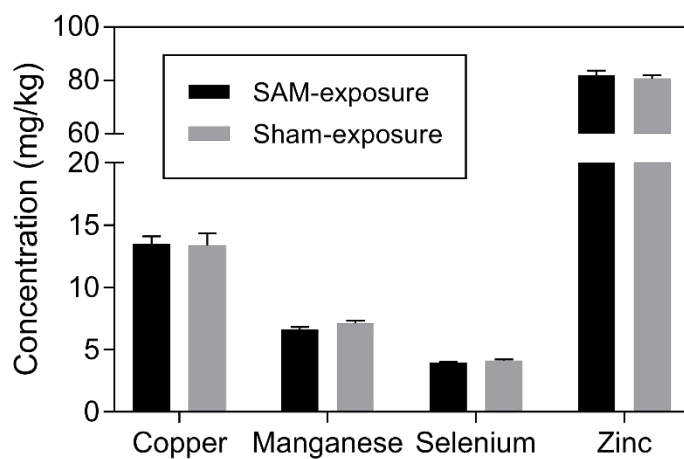
272 **Figure S8.** Antioxidant enzyme activities in liver. A: GPx1, B: GPx4, and C: catalase activity.

273 Activities were normalized by protein content. Each data point represents the mean of three

274 replicates of one sample of liver tissue. Values are expressed as mean \pm standard deviation ($n = 8$

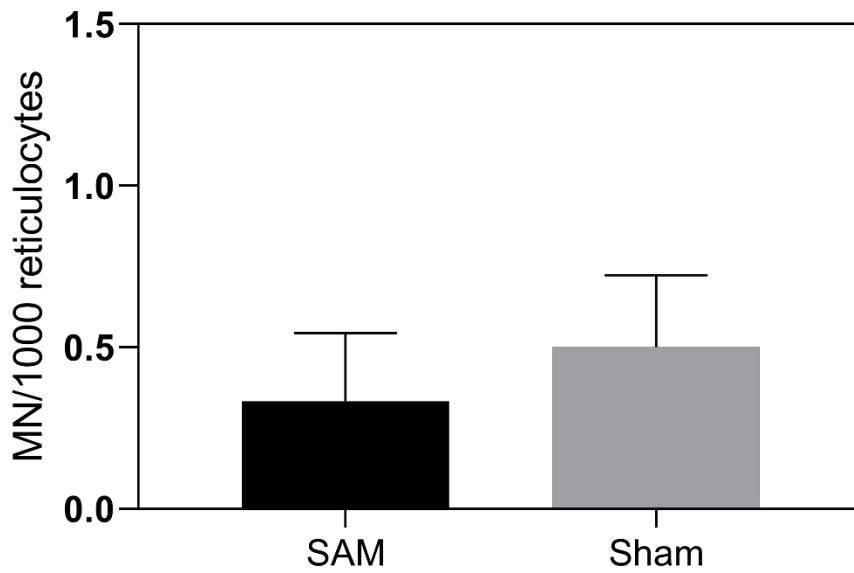
275 for sham, $n = 7$ for SAM). No significant differences were found between sham and SAM rats (p

276 >0.05).



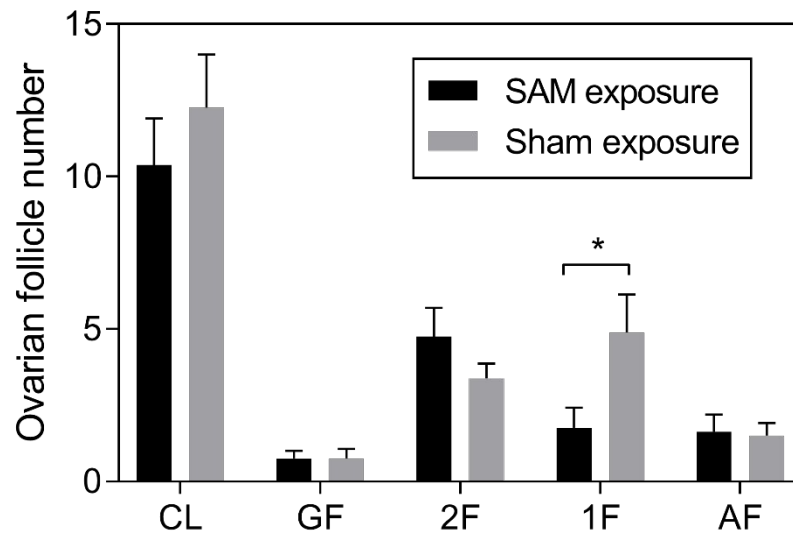
277

278 **Figure S9.** Trace elements content (Cu, Mn, Se, and Zn) in dried liver from rats exposed to SAM
279 and sham. Values are expressed as mean \pm standard error (n = 6). None of the trace elements
280 were significantly different between SAM and sham exposed rats.



281

282 **Figure S10.** Micronuclei (MN) number expressed as per 1000 reticulocytes (immature
283 erythrocytes) from acridine orange-coated slides in SAM-exposed and sham-exposed group.
284 Values are graphed as mean \pm standard error (n = 6). No significant differences were found
285 between sham and SAM rats.



286

287 **Figure S11.** Ovarian follicle number in a single section from SAM- and sham-exposed rats.

288 Values are expressed as mean \pm standard error (n = 7). * p < 0.05, compared to sham. CL: corpus

289 luteum; GF: graafian follicle; 2F: secondary follicle; 1F: primary follicle; AF: atretic follicle.

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