

1 **Supplemental File**

2 **Applied Microbiology and Biotechnology**

3 **TCDD administered on activated carbon eliminates bioavailability and subsequent shifts to a key**  
4 **murine gut commensal**

5 Robert D. Stedtfeld<sup>a</sup>, J. Brett Sallach<sup>e</sup>, Robert B. Crawford<sup>c,d</sup>, Tiffany M. Stedtfeld<sup>a</sup>, Maggie R. Williams<sup>a</sup>,  
6 Hassan Waseem<sup>a</sup>, Cliff T. Johnston<sup>f</sup>, Hui Li<sup>e</sup>, Brian J. Teppen<sup>e</sup>, Norbert E. Kaminski<sup>c,d</sup>, Stephen A.  
7 Boyd<sup>e</sup>, James M. Tiedje<sup>b</sup>, Syed A. Hashsham<sup>a,b\*</sup>

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11 <sup>a</sup>Department of Civil and Environmental Engineering, East Lansing, Michigan 48824

12 <sup>b</sup>Center for Microbial Ecology, Michigan State University, East Lansing, Michigan 48824

13 <sup>c</sup>Institute for Integrative Toxicology, Michigan State University, East Lansing, Michigan 48824

14 <sup>d</sup>Department of Pharmacology and Toxicology, Michigan State University, East Lansing, Michigan 48824

15 <sup>e</sup>Department of Plant, Soil, and Microbial Sciences, Michigan State University, East Lansing, Michigan, 48824

16 <sup>f</sup>Crop, Soil, and Environmental Science, Purdue University, West Lafayette, Indiana, 47907

17 \*Corresponding author:

18 Syed A. Hashsham, Ph. D.

19 Michigan State University

20 Center for Microbial Ecology

21 Department of Civil and Environmental Engineering

22 East Lansing, MI 48824-1319

23 Email: [hashsham@egr.msu.edu](mailto:hashsham@egr.msu.edu)

24 Phone: (517) 355 8241

25 Fax: (517) 355 0250

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30 **Additional Experimental Procedure**

31 For comparing the influence of corn-oil (CO) vehicle with sesame-oil vehicle, which has been used in  
 32 previous studies (Stedtfeld et al. 2017), the relative abundance of *Enterobacteriaceae* was measured in  
 33 fecal pellets (Fig S6). In all groups, fecal pellets were collected daily and were therefore less than 24  
 34 hours old at the time of collection and freezing. All pellets were stored at -20°C until analyzed. DNA was  
 35 extracted from fecal pellets (100 mg) using the PowerMax Soil DNA Isolation Kit (MOBIO  
 36 Laboratories). DNA samples were quantified on a Nanodrop ND-1000 UV-Vis spectrophotometer  
 37 (Nanodrop Products, Wilmington, DE). Extracted DNA was stored at -20°C. The 16S rRNA gene assay  
 38 targeting *Enterobacteriaceae* (Barman et al. 2008) and universal 16S rRNA gene were run on the  
 39 Chromo4 BioRad using reagents and cycling parameters recommended with the Power SYBR Green PCR  
 40 Master Mix. Relative abundance of ARGs in the total bacterial community was determined by qPCR  
 41 using 16S rRNA gene designed to be universal to bacteria.

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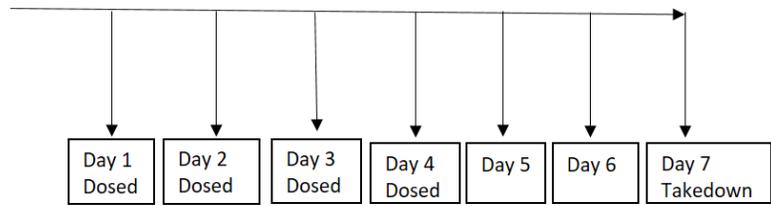
43 **Table S1** QPCR primers used to measure SFB specific 16S rRNA gene and putative functional genes.

Gene or putative function	Protein ID	Primer	Reference
Universal bacteria 16S rRNA gene		340F: ACTCCTACGGGAGGCAGCAGT 541F: ATTACCGCGGCTGCTGGC	(Barman et al. 2008)
SFB specific 16S rRNA gene		SFB_736F: GACGCTGAGGCATGAGAGCAT SFB_844R: GACGGCACGGATTGTTATTCA	(Bouskra et al. 2008)
actin-ADP-ribosylating toxin	BAK56539	TCTACCAATTAACATTTCTTGTTCAAATTC GGTTGAAATAAGAGCACCTAAAGGAA	This study
ADPRT Type-1	BAK55983.1	AAAAGATTATGATGTTGCCGTTTG AACTGATGCTGATAAATACGATGCTT	This study
Arginase	BAK56991.1	AGATGCTCATGGCGATTTGAA GCATGCGAGTGGCATTCC	This study
alpha-N-acetylglucosaminidase	BAK55848.1	TGTTAGATACAGTTTATAATCCGGTAACTG AT AATAGTTCCCCACTTAGACGCACTATT	This study
aluminum resistance protein	BAK56521.1	GATAGCTAATTGCCCATGCTCAA TCATGTGATGCTCCAATAAGAGAAC	This study
D-ala-D-ala dipeptidase	BAK55824.1	ACATCTACAGCACATGCCCTATTATG GGATGCTTATAGACCATTTTACATTCAAA	This study
fibronectin binding protein	BAK56752.1	TGGTAGCCATGTTATCCTTGCA	This study

flagellin domain-containing protein FliC2	BAK56419	TGAAGATGATGATGCCTTGCTATAAA TGCTCAAGGTAAGGCAATGGA AATTGCGAAACCTGCTGCAT	This study
flagellin domain-containing protein FliC3	BAK56361.1	GCATTGTCCGAGACTCAAGCA TCTGTATAAGTTCCGTTTGCAGATTG	This study
F-pilin acetylation protein TraX	BAK56001.1	ATTTAGGACGTATTGTTGCACCTACAT GCAGCAACAAACAATCTTATAGTAAATTC	This study
GMP synthase, large subunit	BAK56417.1	TCTTCCATTAGGTTTTATAGCAAATGC GGTGAAATTGAACCAGATGTATATTCTTAT C	This study
hemolysin A	BAK56433.1	GAGAGAGTTGTAGTGTGTTGAAAGGATGA CAATTGATGCAAAAATCCCCTTTAT	(Stedtfeld et al.)
histidine kinase	BAK56282.1	CTTGATAAGCAGATTGACATTATTAATTCG ATTCATAGGCCCTTTTATTATACGATCTAA	This study
metallo-beta-lactamase family protein	BAK56334.1	TCCATCGAAAAGTTGATGCTATTGTT TCCCATAAACCTTTCCTTTGTATCC	This study
myosin-cross-reactive antigen	BAK56130.1	ATGAGGCATTTGCAAGACCTATTAA AGATGCAAGTCCCGATCCAATAAGA	This study
phospholipase C zinc binding proteins	BAK56527.1	ACCCAGACATCCAGTTTGATTTGT TTTATGGTCCCTATTAAGGCAAGCT	This study
polysaccharide deacetylase family protein	BAK56650.1	TTTCGTCGTTGGAAGTTTGGTT TGTGTGAAGTCCCTATCGAATGGTTATT	This study
bleomycin resistance protein/dioxygenase	BAK56236.1	GTTGATTGTATATCATCGGTAAAGAATGTT CAAATAGAAGGAAAATATACTTGGACAGA AG	This study
RelA/SpoTdomain-containing protein	BAK57096.1	AGAGATGCTCAGAGATTATTTGATGTTAAA CGCTGTAAGTTGCATTTGATAATTTG	This study
rubrerythrin	BAK56170.1	GGAGAAGTTTTTTATAAGGCTCAAGATG CTGGAGCATATTTCCCATGTTT	(Stedtfeld et al.)
Type-3ADPRT	BAK56804.1	CAAAGTAACTTCCGAGTTGCA AAGGTACTAACCAATTAACCTTACACTTTTG AGA	This study

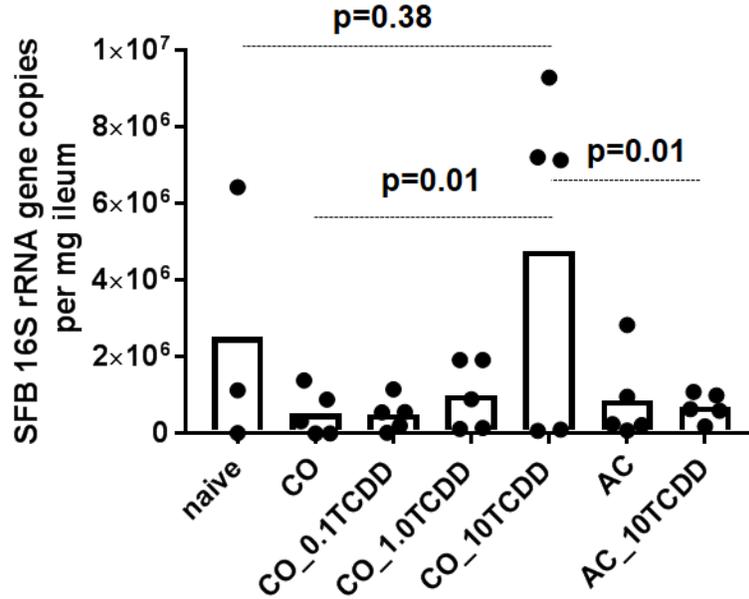
N=5 Naive  
N=5 vehicle corn oil (CO)  
N=5 CO & 0.1 µg/kg TCDD  
N=5 CO & 1.0 µg/kg TCDD  
N=5 CO & 10 µg/kg TCDD  
N=5 activated carbon (AC)  
N=5 AC & 0.1 µg/kg TCDD  
N=5 AC & 1.0 µg/kg TCDD  
N=5 AC & 10 µg/kg TCDD

Five mice in each group, nine different groups



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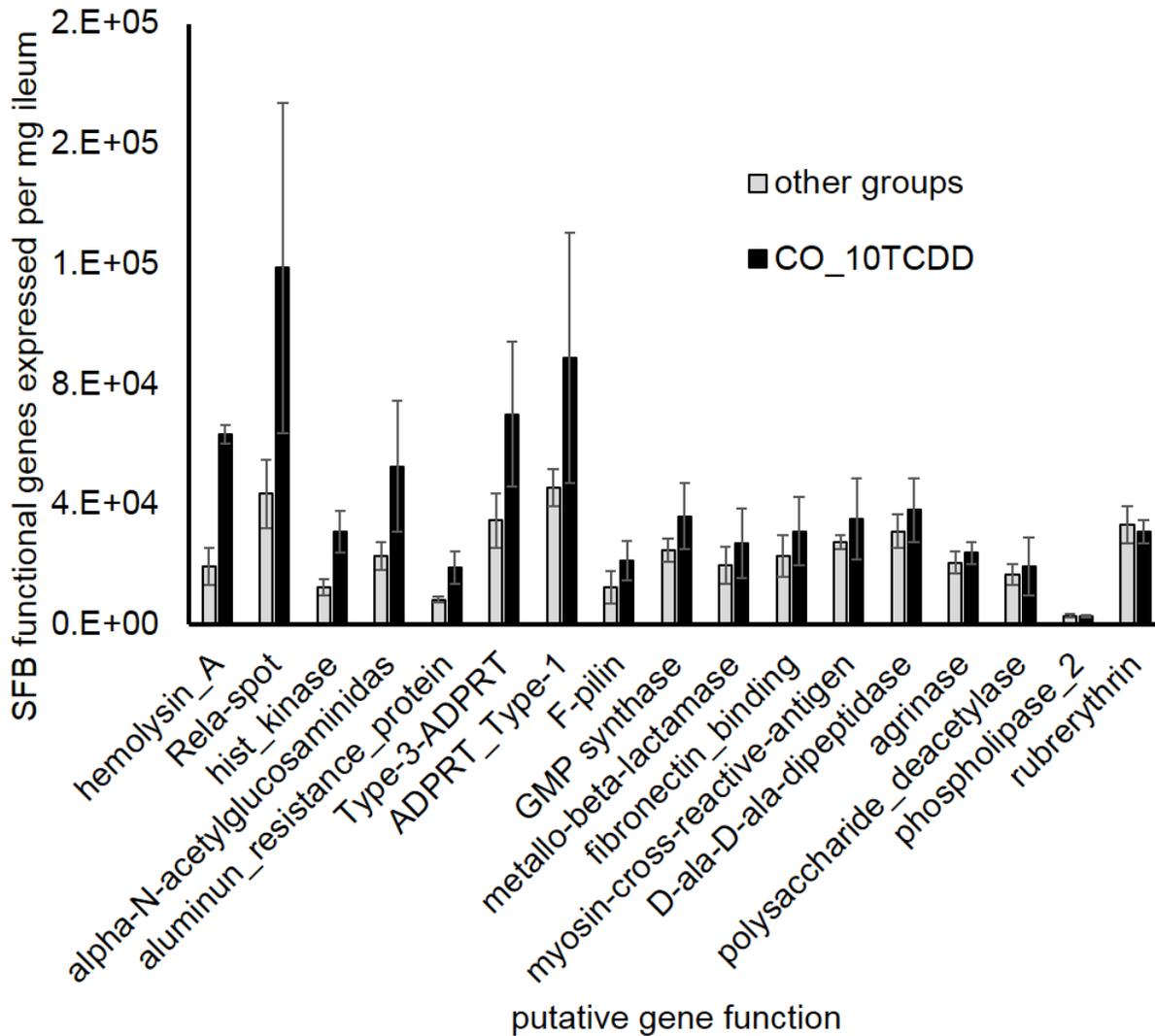
46 **Fig S1** Experimental design with nine groups, each with five mice. The vehicle of corn oil (CO) or  
47 activated carbon (AC) included 0, 0.1, 1.0 or 10 µg/kg TCDD. Dosing occurred on first four day of the  
48 experiment. No dosing was done on days 5, 6, and 7. The takedown and collection of ileal tissue was  
49 performed on day seven.



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52 **Fig S2.** Results of the replicate experiment; qPCR analysis of SFB 16S rRNA gene expression from ileal  
 53 tissue in response to 0, 0.1, 1.0 or 10  $\mu\text{g}/\text{kg}$  TCDD administered with corn oil vehicle (CO\_TCDD) or  
 54 activated carbon (AC\_TCDD). ANOVA analysis with a multiple mean comparison Sidak test comparing  
 55 naïve, CO with no TCDD (CO), and 10  $\mu\text{g}/\text{kg}$  TCDD administered on AC (AC\_10TCDD) versus 10  
 56  $\mu\text{g}/\text{kg}$  TCDD administered on CO (CO\_10TCDD) was used to calculate p-values. For the replicate  
 57 experiment, SFB expression was not measured in groups of mice dosed with 0.1 and 1.0  $\mu\text{g}/\text{kg}$  TCDD  
 58 administered on AC.

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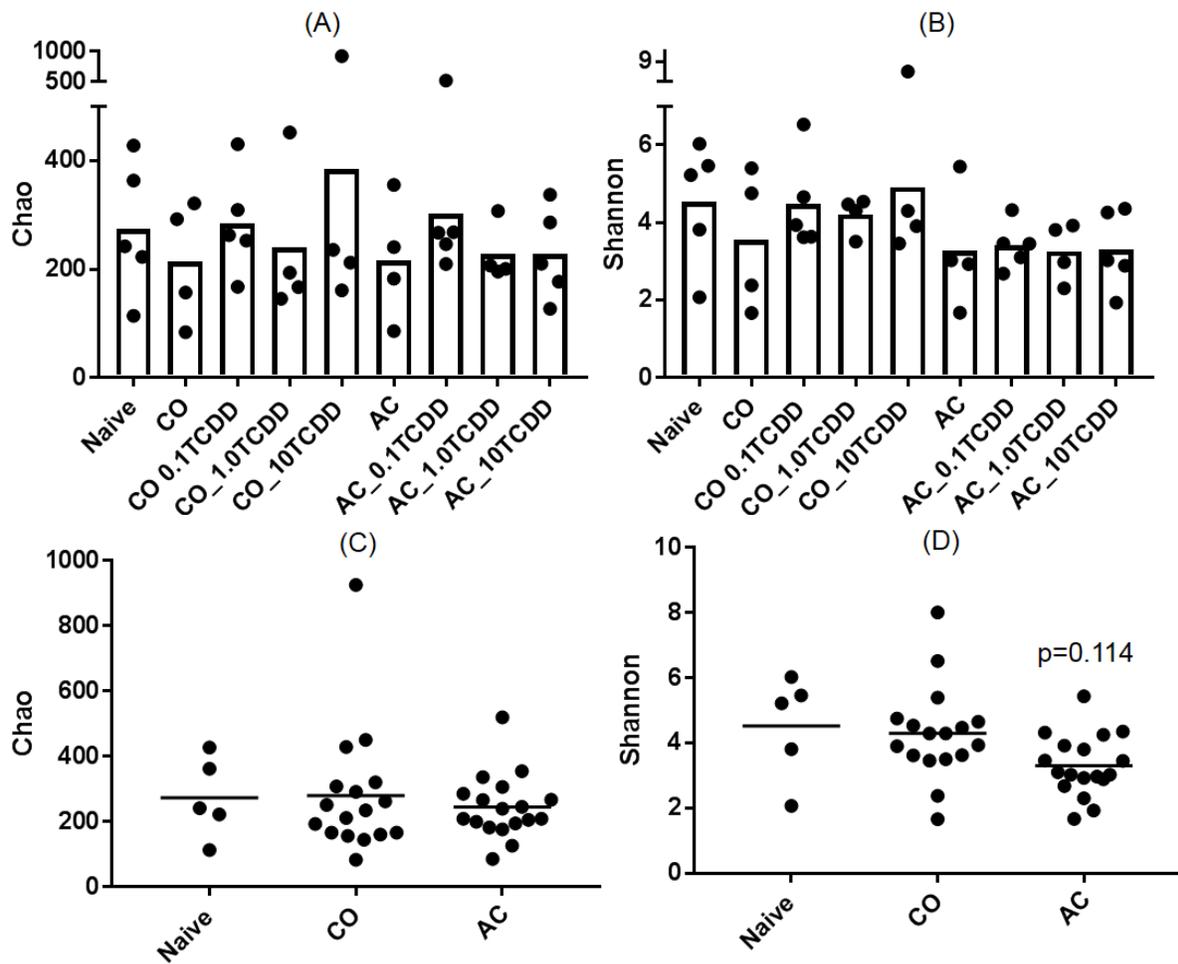


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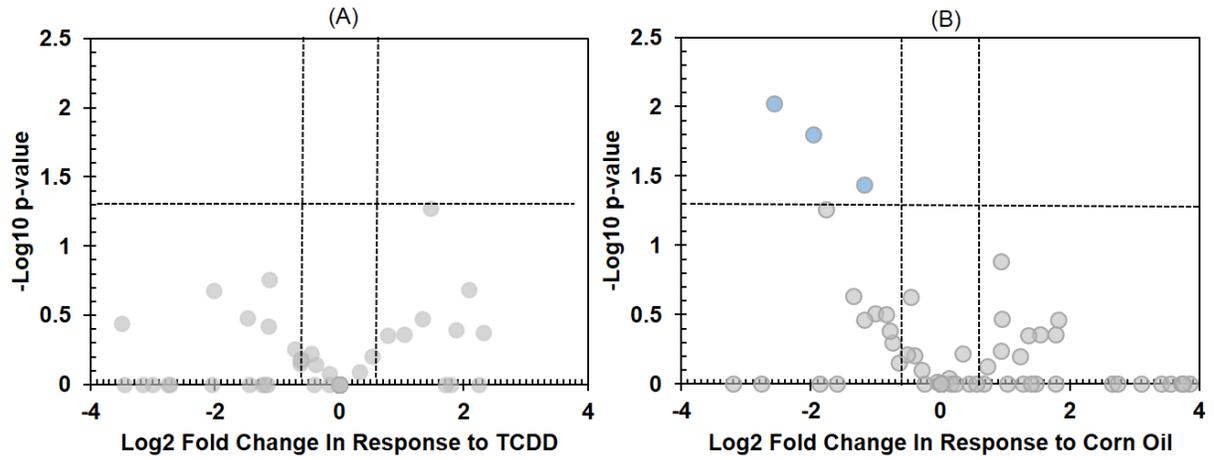
61 **Fig S3.** QPCR analysis of SFB gene expression from ileal tissue in response to 10 µg/kg TCDD  
 62 administered with corn oil vehicle (CO\_10TCDD) in black; and mean response of all other groups  
 63 including naïve, lower doses of TCDD administered on CO and all doses of TCDD administered with AC  
 64 in gray. Bars represent mean with standard error of expression per mg ileum. All other groups were  
 65 pooled because a significant response was only observed in the group dosed with 10 µg/kg TCDD  
 66 administered with corn oil vehicle.

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70 **Fig S4.** Analysis of bacterial community diversity in response to groups with various dosing, based on  
71 16S rRNA gene sequencing of DNA extracted from ileal tissue. (A) Chao and (B) Shannon diversity  
72 indices in separate groups, and, (C) Chao and (D) Shannon diversity indices after grouping all mice dosed  
73 with and without TCDD. A significant difference was not observed with either the Chao or Shannon  
74 indices.  
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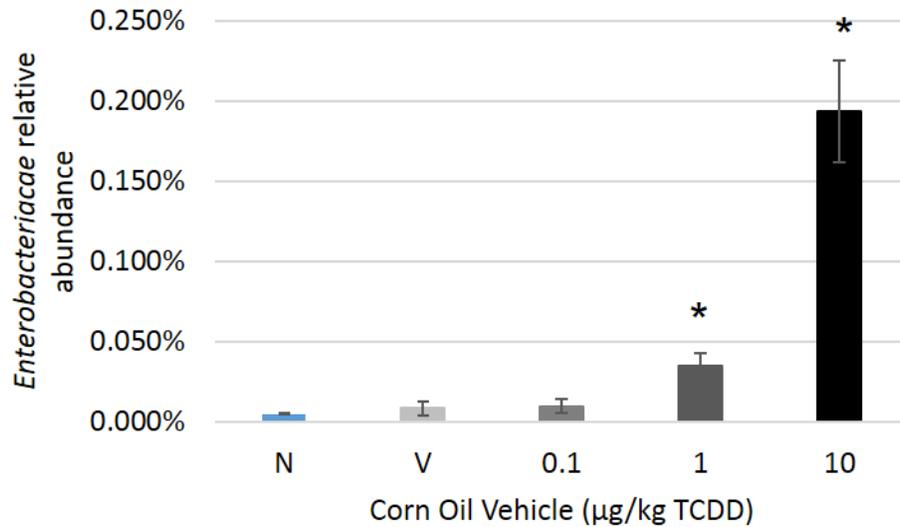
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77 **Fig S5.** Volcano plots of 16S rRNA gene community structure classified at family level using DNA

78 extracted from ileum with fold change as a response to TCDD (A) and, fold change in response to corn oil

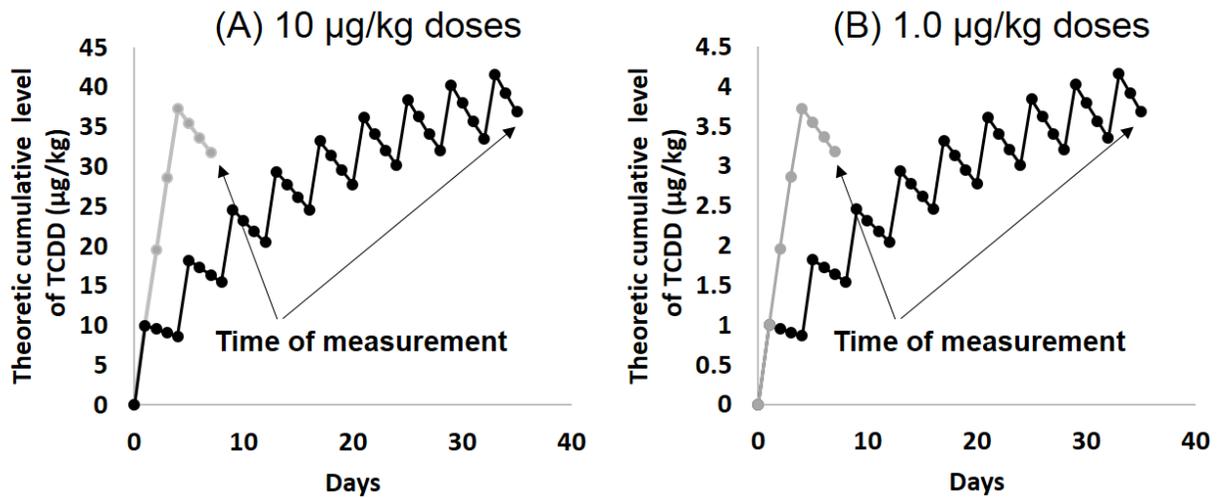
79 (B).

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82 **Fig S6.** QPCR analysis of DNA extracted from fecal pellets collected from cages on the fifth day of the  
 83 experiment shows the relative abundance of *Enterobacteriaceae* within the different groups. Stars  
 84 indicates a significant difference ( $p < 0.05$ ) between TCDD and vehicle (V) dosed mice and the naïve  
 85 control (N). Error bars represent standard deviation of three technical replicates. Fecal pellets were  
 86 collected daily, and thus all pellets were less than 24 hrs old at the time of collection. Stars indicate  
 87 significant difference ( $p < 0.05$ ) compared to vehicle and naïve control.



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89 **Fig S7.** Theoretical analysis of TCDD levels in mice assuming an 11 day half-life. The black arrows point  
 90 to the time of analysis, and the black lines shows theoretical amount of TCDD for a previous study  
 91 (Bhaduri 2015) with longer duration of exposure. Gray lines indicate the level of TCDD in the mice for  
 92 this current experiment.

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95 **Supplemental References**

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