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Supplemental Material

Metabolomic, Lipidomic, Transcriptomic, and Metagenomic Analyses in Mice Exposed to PFOS and Fed Soluble and Insoluble Dietary Fibers

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Table of Contents

- **Table S1.** Open Standard Diet supplemented with cellulose, inulin, or pectin dietary fibers.
- Figure S1. Metabolomic and lipidomic data analysis workflow.
- **Figure S2.** Body weight, food and water intake of male C57BL/6 mice exposed to PFOS and fed with cellulose, inulin or pectin supplemented diet for 7 weeks. A: water intake; B: food intake; C: body weight. Bars represent mean \pm SEM of 6-8 mice in each group. Detailed data are of body weight, food and water intake are listed in Excel Table S9-10.
- **Figure S3.** Heat map analysis of liver samples from mice exposed to PFOS and fed diets supplemented with one of the three fibers: cellulose (control), inulin, or pectin (n=6-8/group). Full metabolomic data are listed in Excel Table S5.
- **Figure S4.** Differences in the level of liver metabolites from mice exposed to PFOS and fed diets supplemented with one of the three fibers: cellulose (control), inulin, or pectin (n=6-8/group). MetaboAnalyst 5.0 analysis identified a total of 23 metabolites/compounds that had adjusted p<0.05 (adj-p) and fold change>2 after PFOS exposure in control, inulin and pectin fed groups. Log-transformed abundance values are shown as box and whisker plots (midline, median; box limits, upper and lower quartiles; whiskers, 10 th and 90 th percentiles). Data were compared using two-way ANOVA and Tukey test for multiple comparisons, * p <0.05; ** p < 0.01; **** p < 0.001; **** p < 0.0001. Full metabolomic data are listed in Excel Table S5.

Figure S5. Relative abundance of *Muribaculum* and *Duncaniella* in mouse cecal contents (Excel Table S7). Mice were exposed to PFOS and fed diets supplemented with one of the three fibers: cellulose (control), inulin, or pectin (n=5/group). Relative abundance values are shown as box and whisker plots (midline, median; box limits, upper and lower quartiles; whiskers, 10 th and 90 th percentiles). Data were analyzed using two-way ANOVA followed by the Tukey's post-hoc test. p < 0.05, **p < 0.01.

Additional File- Excel Document