

I. Supplemental table legends

Table S1. Human transporter gene names and categories according to the Hugo Gene Nomenclature Committee Reference Database (genenames.org) and GeneCards (genecards.org).

Table S2. RT-qPCR primer sequences of human CYP1A2, CYP2B6, CYP3A4, CYP4A11, and the housekeeping gene GAPDH used in the present study.

Table S3. KEGG pathways (BH-FDR < 0.05) for commonly differentially regulated genes by PFOA, PFNA, PFDA, and by PFNA and PFDA.

Table S4. Differentially expressed genes (BH-FDR < 0.05) and up-regulated gene ontology enrichment results (BH-FDR < 0.05) by CITCO and WY.

Table S5. Differentially expressed genes (BH-FDR < 0.05), predicted upstream regulators (BH-FDR < 0.1), and up- and down-regulated gene ontology enrichment results (BH-FDR < 0.05) by PFOA.

Table S6. Differentially expressed genes (BH-FDR < 0.05), predicted upstream regulators (BH-FDR < 0.1), and up- and down-regulated gene ontology enrichment results (BH-FDR < 0.05) by PFNA.

Table S7. Differentially expressed genes (BH-FDR < 0.05), predicted upstream regulators (BH-FDR < 0.1), and up- and down-regulated gene ontology enrichment results (BH-FDR < 0.05) by PFDA.

Table S8. Transporter-specific upstream regulator prediction (BH-FDR < 0.1) for PFOA, PFNA, and PFDA.