Supplemental material

Suppl. Table I. The number of DEGs in the liver.

	pval<			padj<		
	0.05	0.01	0.001	0.05	0.01	0.001
Control vs 10 ng/g/d	293	63	12	2	2	1
Control vs 300 ng/g/d	1109	379	103	20	4	3
Control vs 30000 ng/g/d	5179	3603	2364	3379	2370	1640

Mice received a Western-type diet without or with 10, 300 or 30000 ng/g/d PFOA, mRNA was isolated from liver tissue, and after further processing next generation sequencing analysis was performed. The table indicates the number of DEGs when compared to control. DEGs depicted in green were used for the pathway analysis in IPA (n = 8 mice per group). Padj < 0.05 indicates a higher level of stringency as compared to Pvalue < 0.01.

DEGs, differentially expressed genes; pval, p-value; padj, adjusted p-value; IPA, ingenuity pathway analysis.

Suppl. Table II. Hepatic pathways significantly regulated at 30000 ng/g/d PFOA dose.

Canonical pathway	Related to	P-value
FXR/RXR activation	lipid metabolism	1E-15
LPS/IL-1 mediated inhibition of RXR function	inflammation	1E-13
Stearate biosynthesis I (animals)	lipid metabolism	1E-11
Fatty acid β-oxidation I	lipid metabolism	1E-10
Coagulation system	coagulation	1E-10
LXR/RXR activation	lipid metabolism	1E-9
Acute Phase Response Signaling	inflammation	1E-8
Tryptophan degradation III (Eukaryotic)		1E-7
Superpathway of citrulline metabolism		1E-7
Complement system	inflammation	1E-7
Intrinsic prothrombin activation pathway	coagulation	1E-6
Estrogen biosynthesis		1E-6
Bile acid biosynthesis, neutral pathway	lipid metabolism	1E-6
Role of tissue factor in cancer	coagulation	1E-6
Isoleucine degradation I		1E-6
Glutathione-mediated detoxification		1E-6
Atherosclerosis signaling		1E-6
Glutaryl-CoA degradation		1E-5
Triacylglycerol biosynthesis	lipid metabolism	1E-5
Aryl hydrocarbon receptor signaling	xenobiotic metabolism	1E-5
Citrulline biosynthesis		1E-5
Nicotine degradation III		1E-5
Xenobiotic metabolism signaling	xenobiotic metabolism	1E-5
Superpathway of melatonin degradation		1E-5
PXR/RXR activation	xenobiotic metabolism	1E-5

Mice received a Western type diet without or with 30000 ng/g/d PFOA, mRNA was isolated from liver tissue and gene expression analysis was performed. Differentially expressed genes (DEGs) (see Supplemental Table I) were used as input for pathway analysis through ingenuity pathway analysis (IPA) suite. All DEGs with an adjusted P-

value <0.05 were used for the analysis. The top 25 most relevant canonical pathways are shown (n = 8 mice per group).

FXR, farnesoid X receptor; RXR, retinoid X receptor; LPS, lipopolysaccharides; LXR, liver X receptor; PXR, pregnane X receptor; DEGs, differentially expressed genes.

Suppl. Table III. Hepatic pathways significantly regulated at 300 ng/g/d PFOA dose.

Canonical pathway	P-value
Phagosome formation	1E-7
Leukocyte extravasation signaling	1E-6
Role of pattern recognition receptors in recognition	1E-6
Role of NFAT in regulation of the immune response	1E-6
Production of nitric oxide and reactive oxygen species	1E-6
FCγ receptor-mediated phagocytosis in macrophages	1E-5
Dendritic cell maturation	1E-5
Natural killer cell signaling	1E-5
Virus entry via endocytic pathways	1E-5
CD28 signaling in T helper cells	1E-5
IL-8 signaling	1E-5
TREM1 signaling	1E-4
CTLA4 signaling in cytotoxic T lymphocytes	1E-4
Macropinocytosis signaling	1E-4
T cell receptor signaling	1E-4
NF-κB activation by viruses	1E-4
Tec kinase signaling	1E-4
Reelin signaling in neurons	1E-4
Granulocyte adhesion and diapedesis	1E-4
fMLP signaling in neutrophils	1E-4
Epoxysqualene biosynthesis	1E-4
Endothelin-1 signaling	1E-4
CD40 signaling	1E-4
Inflammasome pathway	1E-3
PKCL signaling in T lymphocytes	1E-3

Mice received a Western type diet without or with 300 ng/g/d PFOA, mRNA was isolated from liver tissue and gene expression analysis was performed. Differentially expressed genes (DEGs) (see Supplemental Table I) were used as input for pathway

analysis through ingenuity pathway analysis (IPA) suite. All DEGs with a P-value <0.01 were used for the analysis. The top 25 most relevant canonical pathways are shown (n = 8 mice per group).

DEGs, differential expressed genes.