



**Supplementary Figure S1.** Correlation analysis of differential gene expression ( $\log_2$  fold-change) between custom cDNA vs. Agilent oligonucleotide microarrays. Custom cDNA (Boverhof *et al.*, 2005) and Agilent 4x44k whole-genome (Dere *et al.*, 2011b) microarray datasets were generated with the same RNA samples from mice treated with 30  $\mu\text{g}/\text{kg}$  TCDD for 2-168h. Differentially expressed genes were identified using the same microarray study design comprising 2-color labeling with dye swap and were analyzed using the same normalization procedure and selected based on  $P1(t) \geq 0.9999$ . Only genes matched by Entrez Gene ID and time point were included in the analysis, consisting of 291 genes. Pearson correlation analysis identified significant correlation between both platforms (PCC = 0.86,  $R^2 = 0.73$ ,  $p\text{-value} \leq 0.0001$ ).