Phenotypically anchored mRNA and miRNA expression profiling in zebrafish reveals flame retardant chemical toxicity networks

Subham Dasgupta[1], Cheryl L. Dunham[1], Lisa Truong[1], Michael T. Simonich[1], Robyn L. Tanguay[1]*

[1]Department of Environmental and Molecular Toxicology, Sinnhuber Aquatic Research Laboratory, Oregon State University, Corvallis, Oregon, USA

Supplemental Tables- 3

Supplemental Figures- 1

Supplemental table legends:

Table S1- Phenotypic, behavioral, mRNA and miR data for the selected FRCs. Phenotyping and behavioral data represented as lowest effect levels (LELs, Table S1.1). mRNA and miR data represented as $\log_2$ fold changes (Tables S1.2 and S1.3). Blank cells represent fold changes below statistical or fold change thresholds.
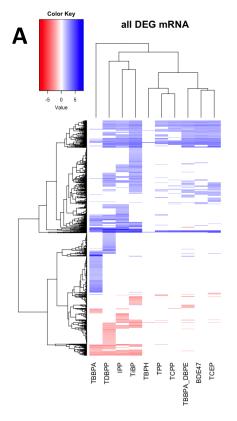
Table S2- TFmiR miR-TF-miR interaction data for all FRCs. Only experimentally validated data (Table S2.1), both experimentally validated and computationally predicted data (Table S2.2-2.9)

Table S3. Gene Ontology data for mRNA (Tables S3.1-3.10) and mRNA targets of miRs (Table S3.11)

Supplemental Figure legends

Figure S1. Heatmap representing $\log_2$ fold changes of (A) all differentially expressed mRNAs and (B) all differentially expressed miRs across FRCs.

Figure S1