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

Subham Dasgupta1, Cheryl L. Dunham1, Lisa Truong1, Michael T. Simonich1, Robyn L. Tanguay1\*

1Department 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 log2 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 log2 fold changes of (A) all differentially expressed mRNAs and (B) all differentially expressed miRs across FRCs.

**Figure S1**

****