Supplemental Table 2:MIAME Checklist

EXPERIMENT DESIGN

Type of experiment (for example, is it a comparison of normal vs. diseased tissue, a time course, or is it designed to study the effects of a gene knock-out?):
Expression profiling of testis from adult zebrafish (*Dario rerio)* exposed to low levels of TCDD

Experimental factors:
TCDD or Vehicle (DMSO)

The number of hybridizations performed in the experiment:
1 total hybridization

The type of reference used for the hybridizations, if any:
No references used

Hybridization design:
Comparison of TCDD-exposed and vehicle

Quality control steps taken:
Isolated total RNA was analyzed on an Agilent Bioanalyzer 2100. Processed ss cDNA was analyzed with Agilent Bioanalyzer. One of the control samples was excluded from the microarray and qPCR analysis because the array QC metrics flagged this sample as an outlier according to quality control All Probe Set RLE (Relative Log Expression) Mean metric and the RLE Signal graphs.

Number of replicates (Biological or Technical):
5 biological replicates for each condition tested

URL of any supplemental websites or database accession numbers:
Data will be hosted on GEO at: **http://www.ncbi.nlm.nih.gov/geo/** (GEO Accession number GSE77335).

SAMPLES USED, EXTRACT PREPARATION AND LABELING

Biological samples used:
Adult 12-month-old zebrafish (*Danio rerio*) testis

Manipulation of biological samples and protocols used: for example, growth conditions, treatments, separation techniques:
Zebrafish embryos kept at 27-30°C in lightly buffered RO water with a standard 14-h/10-h light/dark cycle

Protocol for preparing the hybridization extract:
Total RNA was isolated using the Qiagen RNeasy kit (Qiagen Inc.).

Labeling protocol(s):
Affymetrix GeneChip WT Terminal Labeling kit was used following the Genechip WT terminal Labeling and Hybridization User Manual.

External controls (spikes):
None

HYBRIDIZATION PROCEDURES AND PARAMETERS

Samples hybridized to Affymetrix Zebrafish Gene 1.0 ST array following the Genechip WT terminal Labeling and Hybridization User Manual

MEASUREMENT DATA AND SPECIFICATIONS

Quantitations based on the images:
Original Affymetrix .dat proprietory output files

Type of scanning hardware and software used:
Software – Affymetrix Command Console version 3.2.4.1515W
Scanning Hardware – GC3000 G7 Scanner

Type of image analysis software used:
Affymetrix Command Console version 3.2.4.1515W

A description of the measurements produced by the image-analysis software and a description of which measurements were used in the analysis:
Probe level measurements produced by Affymetrix Command Console. Analysis performed at level of raw signal.

The complete output of the image analysis *before* data selection and transformation (spot quantitation matrices):
Original Affymetrix output files

Data selection and transformation procedures:
The data was analyzed using Transcriptome Analysis Console (TAC; Affymetrix) and genes of interest were selected as having a p-value ≤0.05 and an absolute fold change ≥1.5.

ARRAY DESIGN

See Affymetrix.com (Zebrafish Gene 1.0 ST array)