Supplemental Table 3. MIQE checklist for authors, reviewers and editors. All essential information (E) must be submitted with the manuscript. Desirableinformation (D) should be submitted if available.

ITEM TO CHECK	IMPORTANCE	COMMENTS
EXPERIMENTAL DESIGN		
Definition of experimental and control groups	E	**TCDD-exposed and vehicle (DMSO)**
Number within each group	E	**5**
Assay carried out by core lab or investigator's lab?	D	Investigator's lab
Acknowledgement of authors' contributions	D	Yes
SAMPLE		
Description	E	**Testis from adult zebrafish exposed to sublethal levels of TCDD**
Volume/mass of sample processed	D	
Microdissection or macrodissection	E	**Microdissection**
Processing procedure	E	**Zebrafish tissues were collected and immediately frozen in liquid nitrogen**
If frozen - how and how quickly?	E	**Immediate**
If fixed - with what, how quickly?	E	**No**
Sample storage conditions and duration	E	**-80°C**
NUCLEIC ACID EXTRACTION		
Procedure and/or instrumentation	E	**Total RNA was extracted using the QIAGEN RNEasy mini kit following the manufacturer's protocol. Tissue was homogenized in Qiazol.**
Name of kit and details of any modifications	E	**QIAGEN RNEasy mini kit per manufacturer's protocol**
Source of additional reagents used	D	
Details of DNase or RNAse treatment	E	**N/A. RNeasy silicamembrane technology efficiently removes most of the DNA without DNase treatment. All plastic and reagents used are certified RNAse free.**
Contamination assessment (DNA or RNA)	E	**No reverse transcription reaction controls were run with qPCR probes**
Nucleic acid quantification	E	**RNA quantity was measured on Nanodrop-1000**
Instrument and method	E	**RNA quantity was measured on Nanodrop-1000 following manufacturer's protocol**
Purity (A260/A280)	D	See Supplemental Table 1
Yield	D	
RNA integrity method/instrument	E	**Agilent Bioanalyzer**
RIN/RQI or Cq of 3' and 5' transcripts	E	**See Supplemental Table 1**
Electrophoresis traces	D	
Inhibition testing (Cq dilutions, spike or other)	E	**Not performed. Amplification product for housekeeping gene assay sufficient to rule out the presence of inhibitors of PCR and reverse-transcriptase inhibitors.**
REVERSE TRANSCRIPTION		
Complete reaction conditions	E	**Reverse Transcription reaction carried out with the High Capacity cDNA Reverse Transcription Kit following manufacturer's protocol**
Amount of RNA and reaction volume	E	**Amount of RNA: 500 ng; Reaction volume: 20 µl**
Priming oligonucleotide (if using GSP) and concentration	E	**N/A**
Reverse transcriptase and concentration	E	**High Capacity cDNA Reverse Transcription Kit components**
Temperature and time	E	**Manufacturer's protocol**
Manufacturer of reagents and catalogue numbers	D	
Cqs with and without RT	D*	
Storage conditions of cDNA	D	
qPCR TARGET INFORMATION		
If multiplex, efficiency and LOD of each assay.	E	**N/A**
Sequence accession number	E	**See Supplemental Table 4**
Location of amplicon	D	
Amplicon length	E	**See Supplemental Table 4**
In silico specificity screen (BLAST, etc.)	E	**All Taqman assays have been designed through Thermo Fisher's validated bioinformatics pipeline**
Pseudogenes, retropseudogenes or other homologs?	D	
Sequence alignment	D	
Secondary structure analysis of amplicon	D	
Location of each primer by exon or intron (if applicable)	E	**See Supplemental Table 4**
What splice variants are targeted?	E	**None (See Supplemental Table 4)**
qPCR OLIGONUCLEOTIDES		
Primer sequences	E	**Not available due to intellectual property of Thermo Fisher**
RTPrimerDB Identification Number	D	
Probe sequences	D**	
Location and identity of any modifications	E	**See Supplemental Table 4**
Manufacturer of oligonucleotides	D	
Purification method	D	
qPCR PROTOCOL		
Complete reaction conditions	E	**See materials and methods**
Reaction volume and amount of cDNA/DNA	E	**Reaction volume: 20 µl; cDNA amount: 2 µl**
Primer, (probe), Mg++ and dNTP concentrations	E	**Primer concentration in 20x mix: 900nm; Probe concentration in 20x mix: 150 nm; Mg++ and dNTP (in Taqman universal master mix no Amperase UNG) concentration unavailable due to intellectual property of Thermo Fisher**
Polymerase identity and concentration	E	**Amplitaq Gold DNA polymerase. Concentration unavailable**
Buffer/kit identity and manufacturer	E	**Taqman universal master mix no Amperase UNG by Thermo Fisher**
Exact chemical constitution of the buffer	D	
Additives (SYBR Green I, DMSO, etc.)	E	**None**
Manufacturer of plates/tubes and catalog number	D	
Complete thermocycling parameters	E	**50°C for 2 minutes, 90°C for 10 minutes, 40 cycles of 95°C for 15 seconds and 60°C for 1 minute**
Reaction setup (manual/robotic)	D	**Robotic**
Manufacturer of qPCR instrument	E	**Applied Biosystems 7900**

qPCR VALIDATION		
Evidence of optimization (from gradients)	D	
Specificity (gel, sequence, melt, or digest)	E	
For SYBR Green I, Cq of the NTC	E	
Standard curves with slope and y-intercept	E	
PCR efficiency calculated from slope	E	
Confidence interval for PCR efficiency or standard error	D	
r2 of standard curve	E	
Linear dynamic range	E	
Cq variation at lower limit	E	
Confidence intervals throughout range	D	
Evidence for limit of detection	E	**All primers and probes were supplied by Thermo Fisher Scientific. Taqman probes have been prevalidated.[17]**
If multiplex, efficiency and LOD of each assay.	E	**Did not multiplex**
DATA ANALYSIS		
qPCR analysis program (source, version)	E	**Sequence Detection System 2.4**
Cq method determination	E	**Cycle Threshold**
Outlier identification and disposition	E	**Runs were performed in triplicate and variations were shown to be minimal**
Results of NTCs	E	**NTCs were shown to have undetermined Cts**
Justification of number and choice of reference genes	E	**Actb was chosen as the reference gene. Actb was unchanged on the microarray. As we have previously used actb as a housekeeping gene, it was chosen to maintain consistency.**
Description of normalization method	E	**Data normalization was carried out via the ΔΔ Ct method using actb as a housekeeping gene.**
Number and concordance of biological replicates	D	
Number and stage (RT or qPCR) of technical replicates	E	**qPCR reactions were done in triplicate**
Repeatability (intra-assay variation)	E	**Intra-experiment variation was assessed by triplicates**
Reproducibility (inter-assay variation, %CV)	D	
Power analysis	D	
Statistical methods for result significance	E	**Student's T-Test**
Software (source, version)	E	**Microsoft Excel 2013**
Cq or raw data submission using RDML	D	