Supporting Information

Acute Exposure to Tris(1,3-dichloro-2-propyl) Phosphate (TDCIPP) Causes Hepatic Inflammation and Leads to Hepatotoxicity in Zebrafish

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Table S1 Sequences of primers for selected genes

Gene Name	Sequence of the primers (5’-3’)	Amplicon size	Accession number
tlr18	Forward: ctagagtggcctcagcaacc Reverse: ctcttcatctgggccttcag	183 bp	NM_001089350.1
tlr8a	Forward: tgaggacgtgattgttctgc Reverse: gcctggttgtcgactcgtat	171 bp	AY389452.1
tlr8b	Forward: tgaagagggtgtggatgtga Reverse: caaacctaaccgcgtttctc	170 bp	AY389453.1
tlr20a	Forward: tttcgagaggctttgcgtat Reverse: tgtcgtgtcccaactgaaag	178 bp	AY389457.1
tlr9	Forward: atgcccaaacaaccagtctc Reverse: gtaaaaggtgccgttttgga	196 bp	NM_001130594.1
fos	Forward: gctccatctcagtcccagag Reverse: agagtgggctccagatcaga	160 bp	NM_205569.1
stat1b	Forward: ctccaggcactttccttctg Reverse: cattggagcagcaagtgtgt	185 bp	NM_200091.2
irf7	Forward: gcttcagtccagcaatcaca Reverse: cgtatttgctcccctctcag	167 bp	NM_200677.1
gclc	Forward: aaaatgtccggaactgatcg Reverse: aacgtttccattttcgttgc	157 bp	NM_199277.2
gsr	Forward: caaccttgaaaagggcaaaa Reverse: aaactggatcctggcacatc	171 bp	NM_001020554.1
nqo1	Forward: ctcaaggatttgccttcagc Reverse: cgcagcactccattctgtaa	169 bp	NM_001204272.1
chop	Forward: atatactgggctccgacacg Reverse: ttcgttcttcttgccttggt	198 bp	NM_001082825.1
grp78	Forward: caagaagaagacgggcaaag Reverse: ctcctcaaacttggctctgg	178 bp	NM_213058.1
il1b	Forward: cgctccacatctcgtactca Reverse: atacgcggtgctgataaacc	166 bp	NM_212844.2
il4	Forward: gtgaatgggatcctgaatgg Reverse: ttccagtcccggtatatgct	190 bp	NM_001170740.1
il6	Forward: tcctggtgaacgacatcaaa Reverse: tcatcacgctggagaagttg	177 bp	NM_001261449.1
il10	Forward: atttgtggagggctttcctt Reverse: agagctgttggcagaatggt	198 bp	NM_001020785.2
il22	Forward: cttggaatcagacgagcaca Reverse: ggccaaatccataattgcac	175 bp	NM_001020792.1

Table S1-*Continued*

Gene Name	Sequence of the primers (5’-3’)	Amplicon size	Accession number
il13	Forward: tcgggttttacgttgaaagg Reverse: atctcctcctcagcctgaca	197 bp	NM_001199905.1
il15	Forward: ccagaacagggactggaaga Reverse: ccctggtgagtcttctcctg	192 bp	NM_001039565.1
il12a	Forward: gaactcctacaagcccagca Reverse: cggatgtgaaacccttcagt	185 bp	NM_001007107.1
il26	Forward: aatgcagaactgtgcgactg Reverse: cctgaactgatccacagcaa	156 bp	NM_001020799.1
il34	Forward: gaacatccacacgcatgaac Reverse: aaaatgaaggagctggctga	160 bp	NM_001082955.1
gapdh	Forward: gatacacggagcaccaggtt Reverse: gccatcaggtcacatacacg	163 bp	NM_001115114.1

Table S2 Number of clean reads and mapped reads, and their percentage (clean reads/clean reads) in control and TDCPP treatment groups.

	Control-1	Control-2	TDCPP-1	TDCPP-2
Clean reads	52,451,294	52,208,818	55,223,302	54,749,504
Mapped reads	35,069,242	35,194,969	37,665,881	37,621,973
Percentage	66.86%	67.41%	62.21%	68.72%

Figure S1

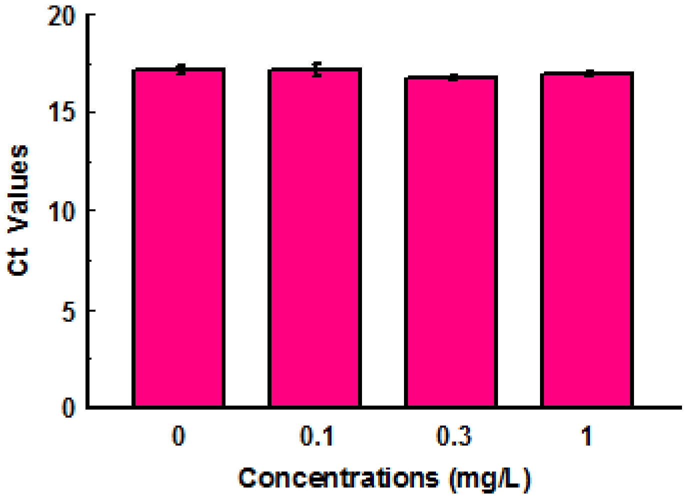


Figure S1: Actual cycle threshold (Ct) values for glyceraldehyde-3-phosphate dehydrogenase (*gapdh*) in response to different concentrations of TDCIPP. Values represent mean ± SEM. There were 3 replicated tanks for each concentration, and three fish from each tank were used and thus totally 9 fish were involved in each treatment.

Figure S2

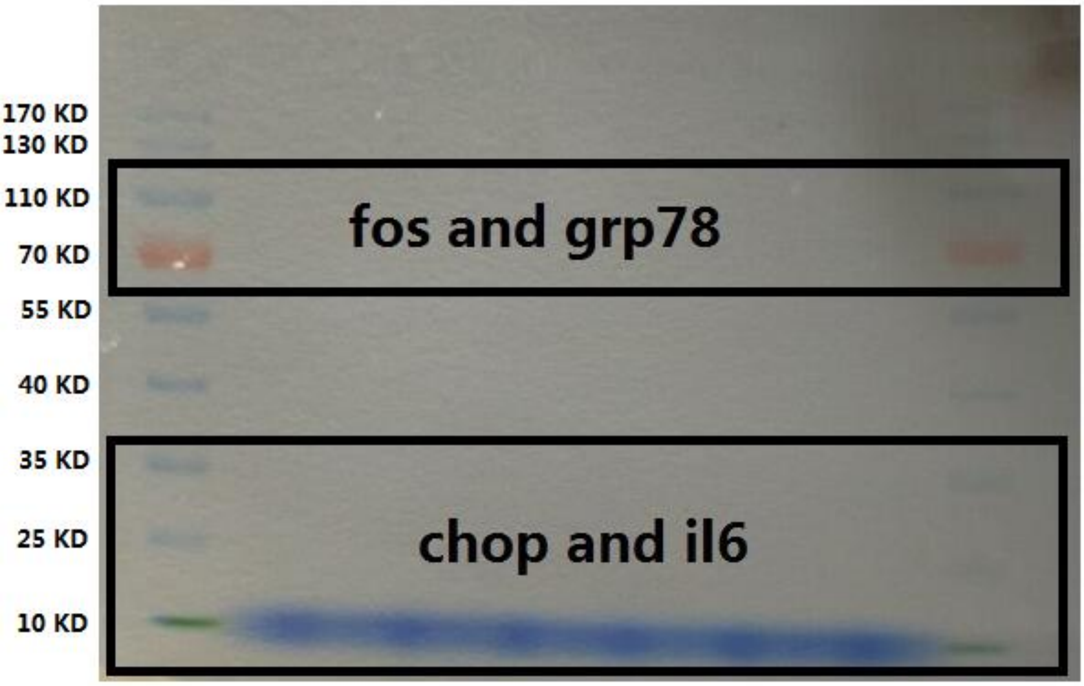


Figure S2: Positions where membrane strips were obtained according to molecular weights of marker.

Figure S3

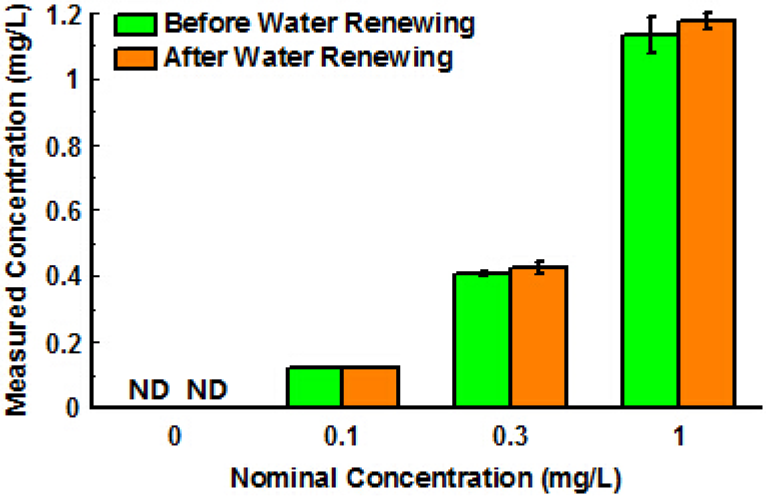
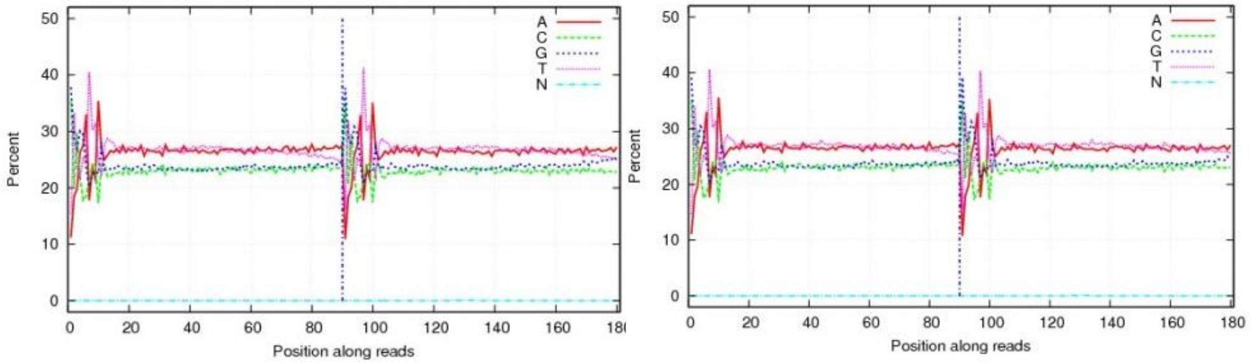


Figure S3: Measured concentrations of TDCIPP in exposure solutions at the last day of treatment. Value represent mean±SE (n=3).

Figure S4


(A) Control-1 **(B) Control-2**

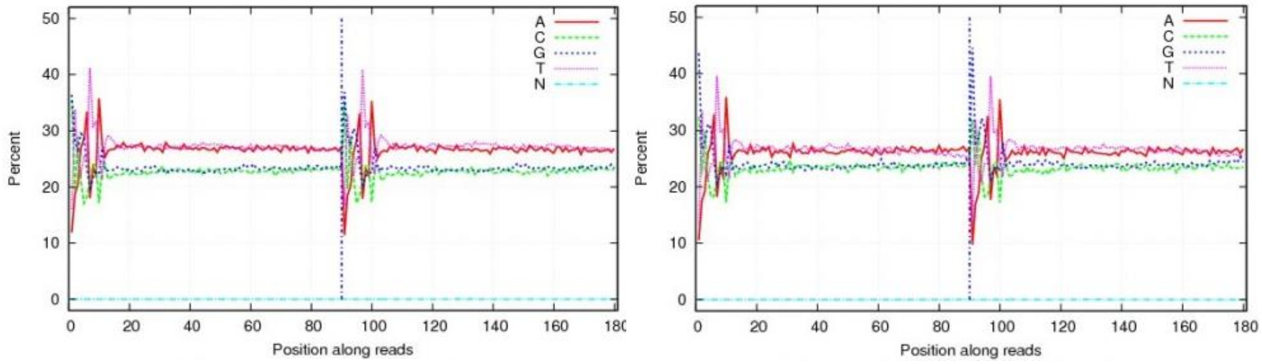
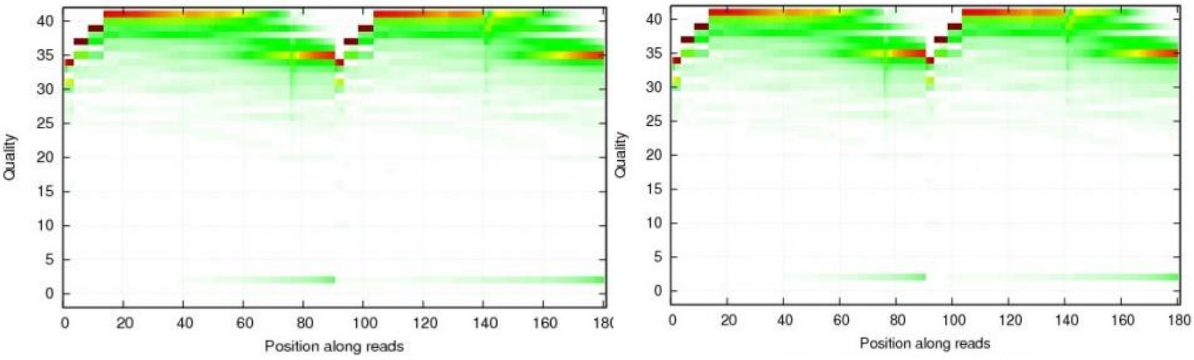

(C) TDCPP-1 **(D) TDCPP-2**

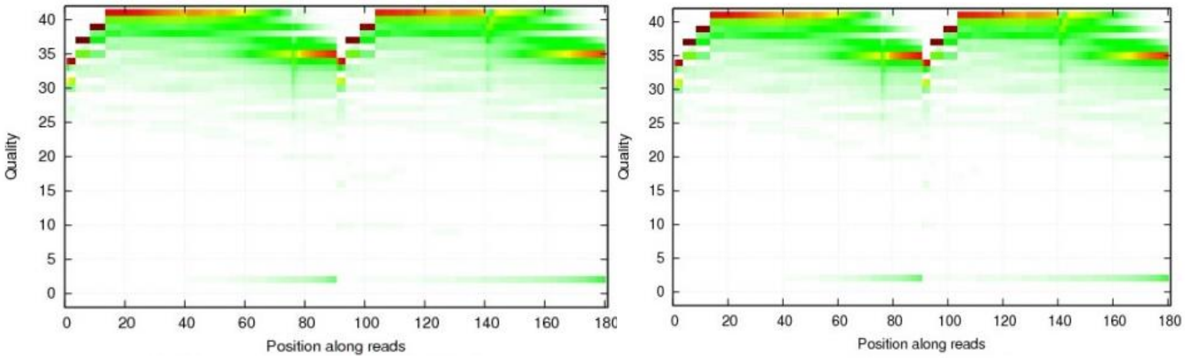
Figure S4: Representative images for the composition of bases. T and C curves were in accordance with A and G curves, respectively in all the samples tested, therefore, our results showed satisfactory base composition.

Figure S5



(A) Control-1

(B) Control-2



(C) TDCPP-1

(D) TDCPP-2

Figure S5: Representative images for quality distribution of bases. The percentage of the bases with low quality (<20) was very low in all the samples tested, therefore, the sequencing quality was good in the present study.

Figure S6

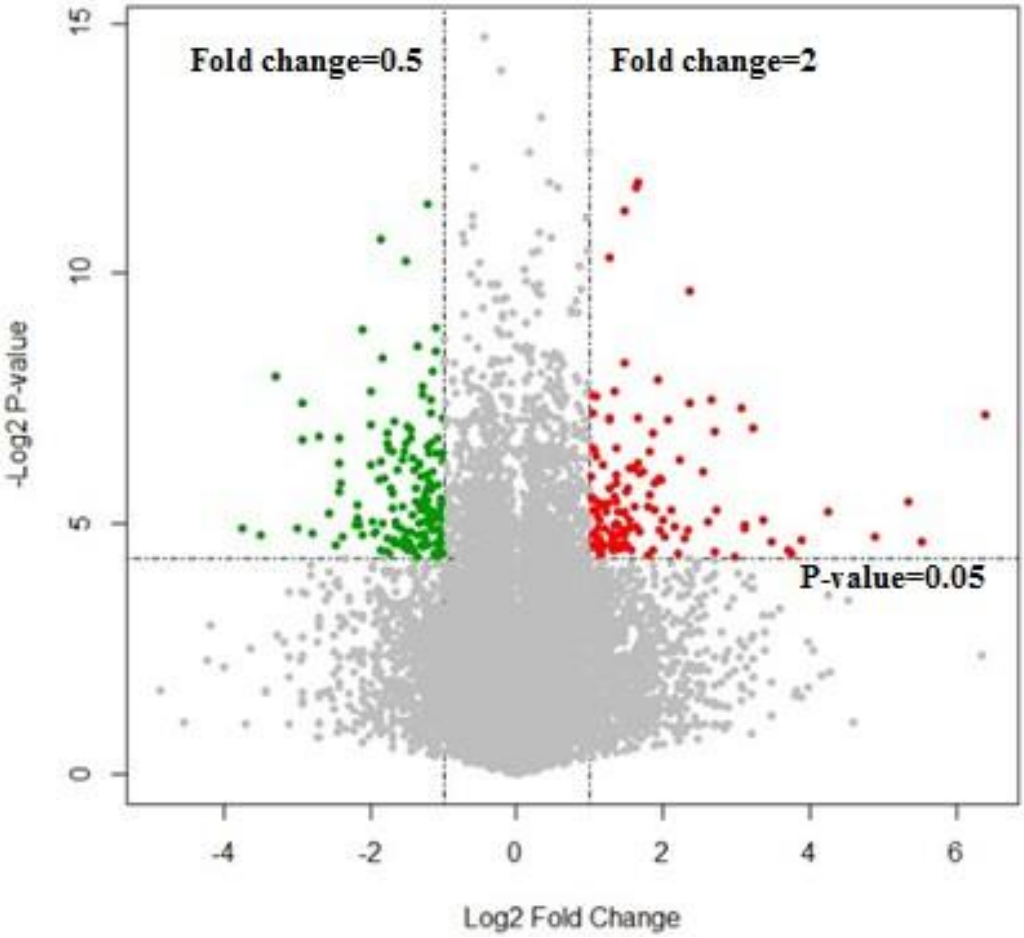


Figure S6: Volcano plot showing the distribution of transcripts over different fold change and *P*-value between control and treatment groups. Green plots indicate down-regulated genes, with fold change <0.5 and P-value <0.05; Red plots indicate up-regulated genes, with fold change >2 and P-value <0.05.

Figure S7

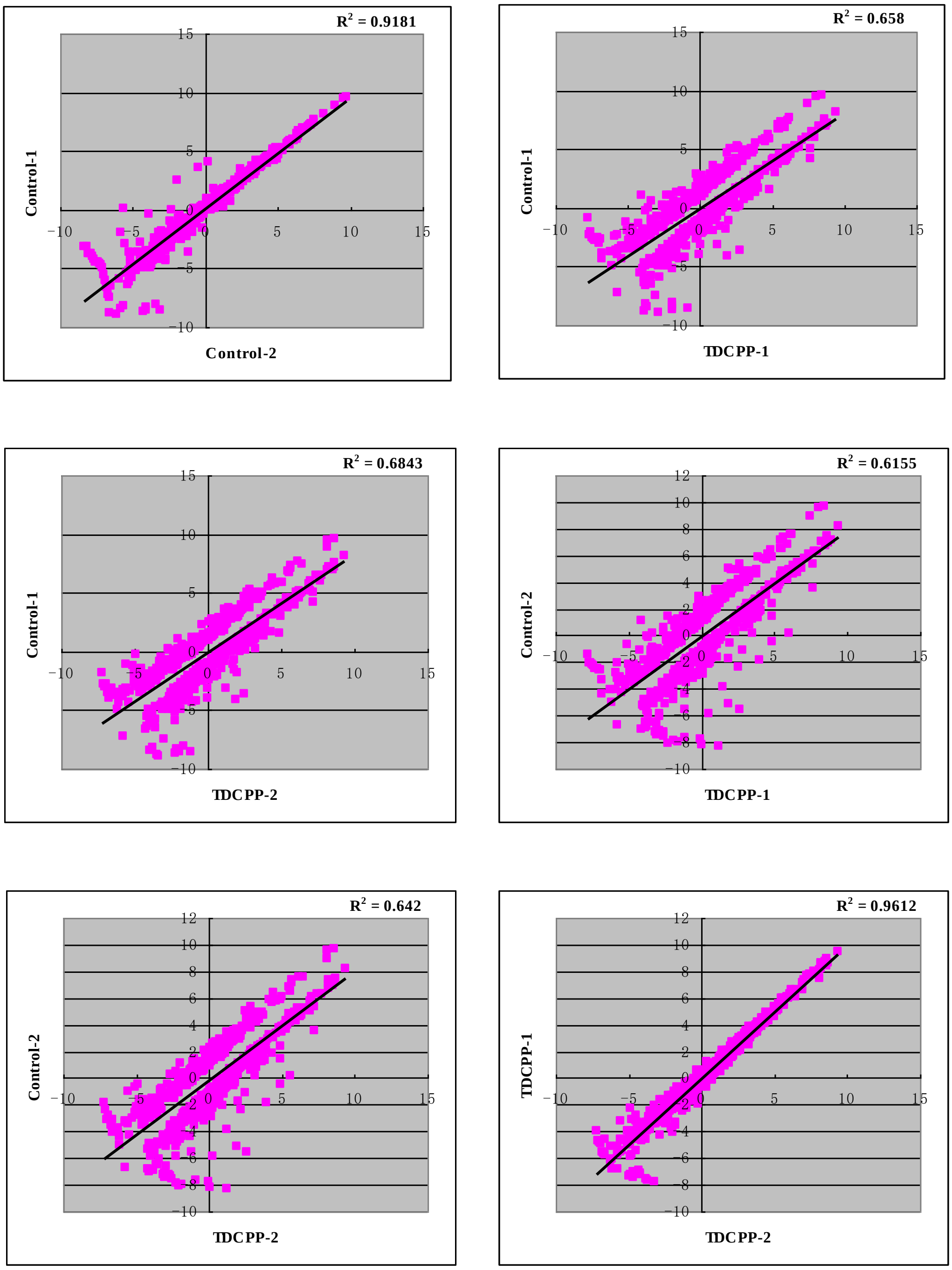


Figure S7: Regression analysis between two different RNA-Seq groups based on the relative (log2) RPKM value of identified 583 genes.