

Supplementary Figures

Effects of Short-Term Exposure to 2,3,7,8-Tetrachlorodibenzo-p-dioxin on MicroRNA Expression in Zebrafish Embryos

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Supplementary Figure 1. Heat map showing microRNA expression at both time points (36 and 60 hpf) and with DMSO or TCDD treatment, as measured using Exiqon LNA microarrays. The heat map shows the result of the two-way hierarchical clustering of microRNAs and samples. Each row represents a microRNA and each column represents a sample. The microRNA clustering tree is shown on the left. The color scale shown at the bottom illustrates the relative expression level of a microRNA across all samples: red color represents an expression level above mean, blue color represents expression lower than the mean.

Supplementary Figure 2. Heat map showing significant changes in microRNA expression between the two developmental time points (36 and 60 hpf) using custom Agilent microarrays. Average expression values of all the samples were used in clustering. Blue and Red colors represent lower and higher expression levels, respectively.

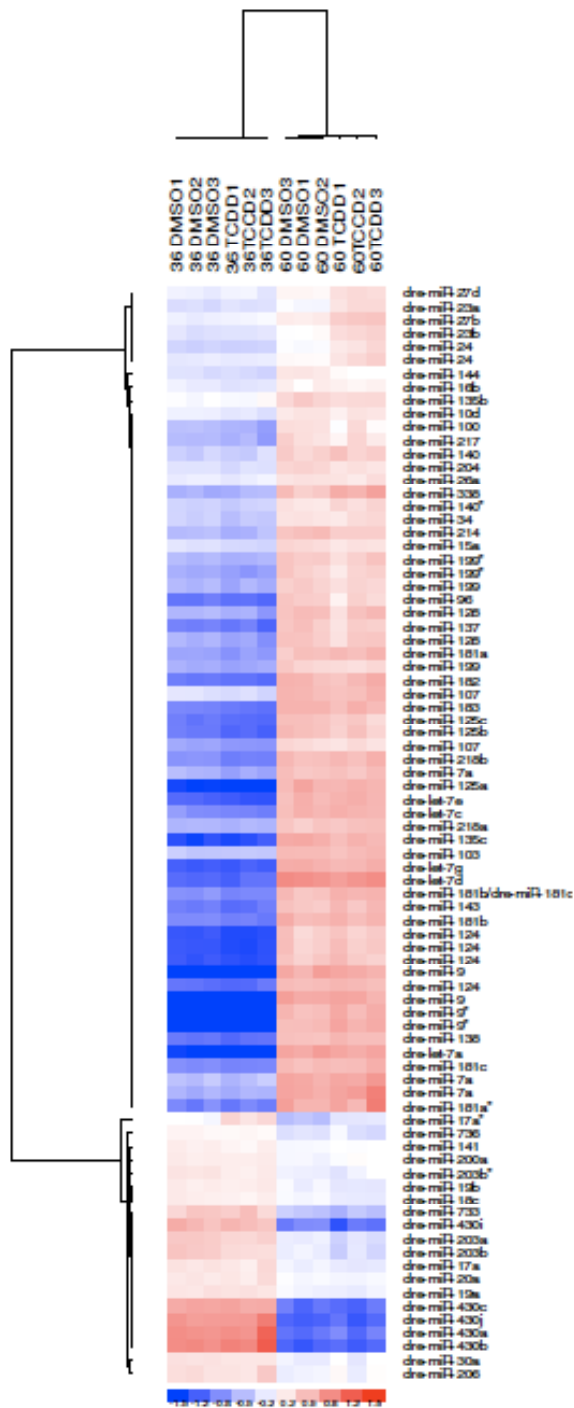
Supplementary Figure 3. Heat map showing significant changes in microRNA expression between the two developmental time points (36 and 60 hpf) based on the CLC Genomics analysis of the SOLiD microRNA sequencing results. Average expression values of all the samples were used in clustering. Blue and Red colors represent lower and higher expression levels respectively.

Supplementary Figure 4. Alignment demonstrating the homology between human, mouse and zebrafish members of the miR-27 family. The seed sequence is underlined.

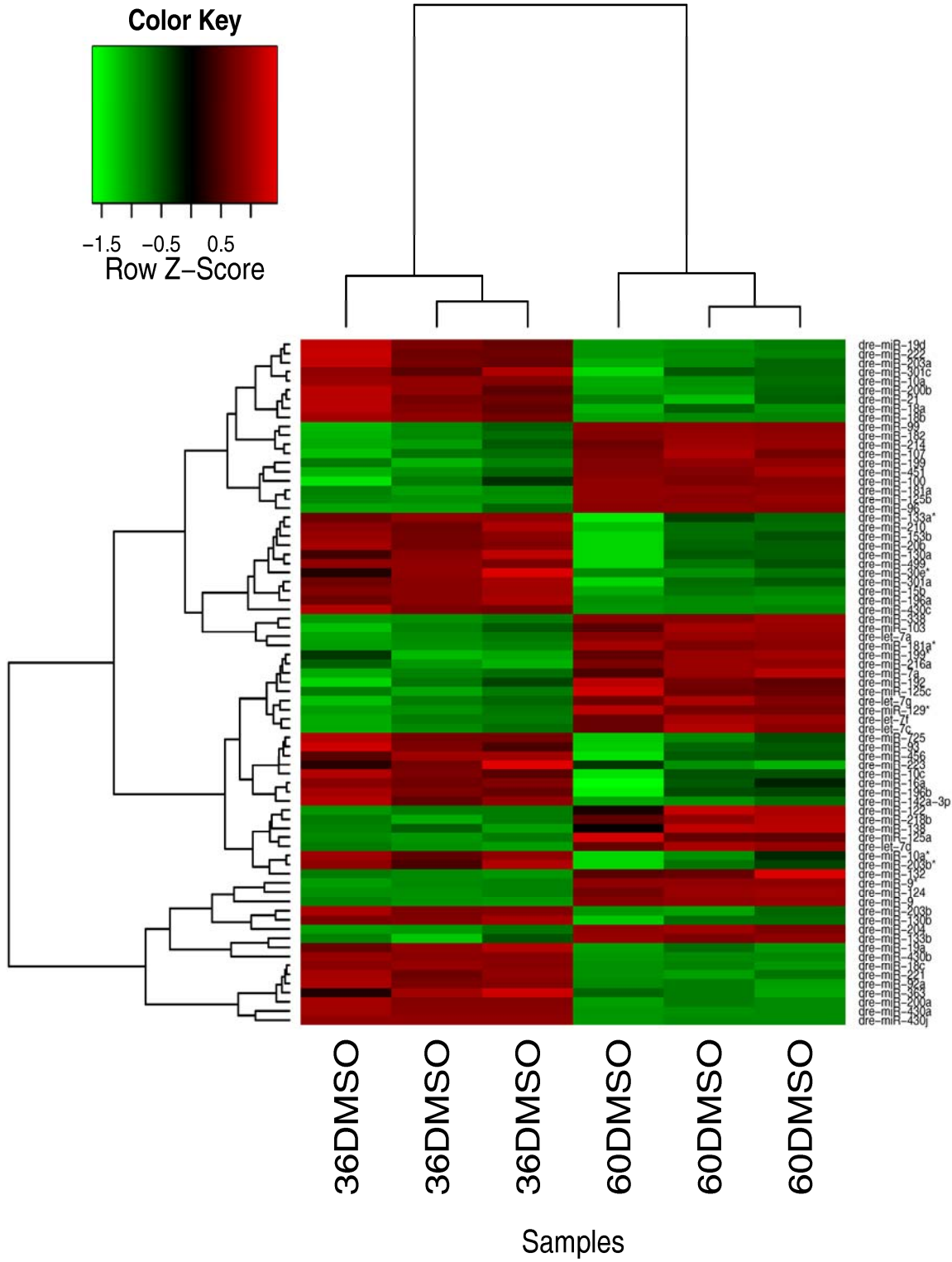
Supplementary Figure 5. Flow charts summarizing the three analysis pipelines used to analyze the small RNA sequencing data.

Supplementary Table 1. Read counts of mature miRNAs, star sequences and other non-coding RNAs identified using CLC Genomics Workbench 4.7.2. (Separate excel file)

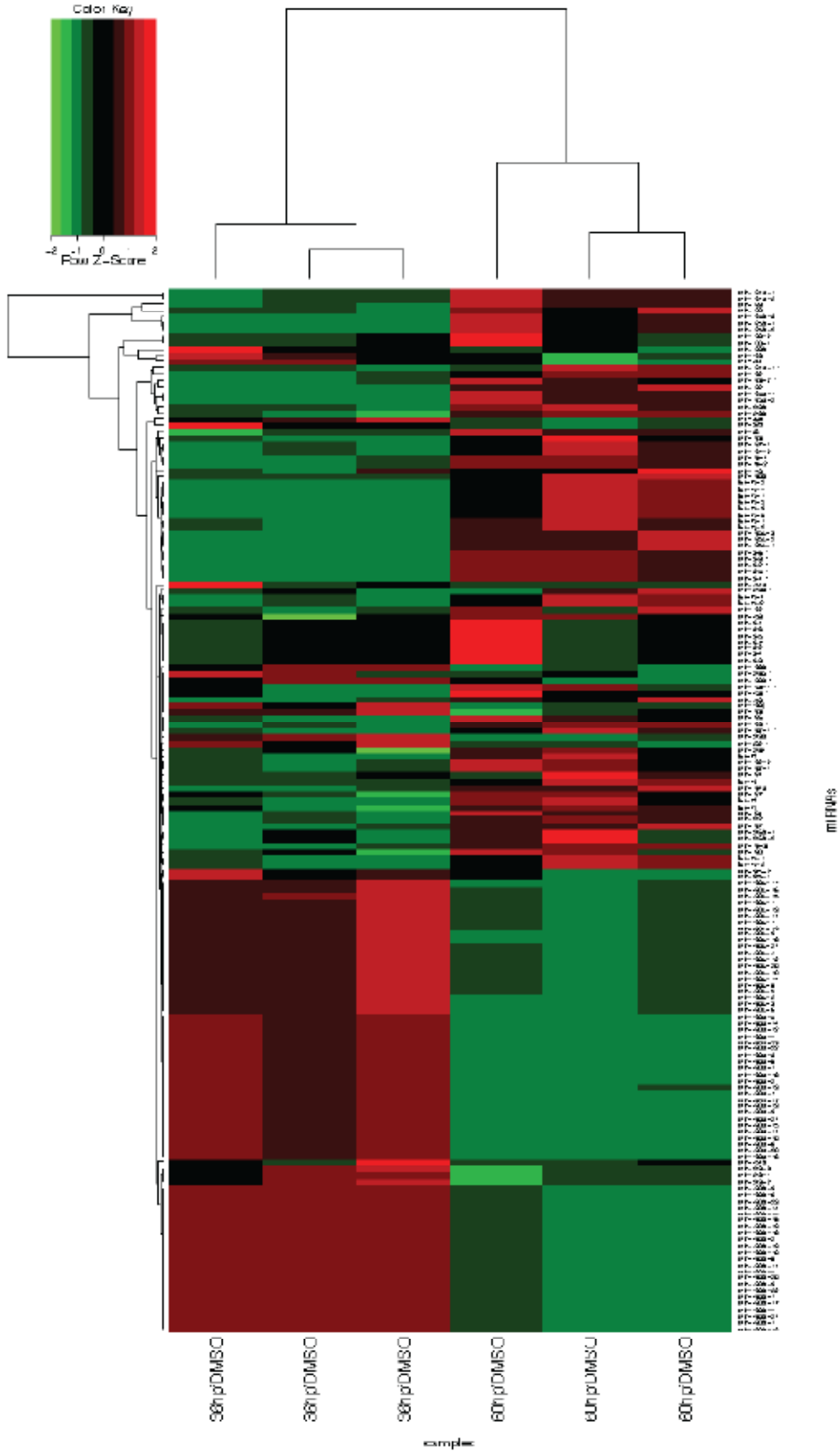
Supplementary Figure 1.



Supplementary Figure 2.



Supplementary Figure 3.

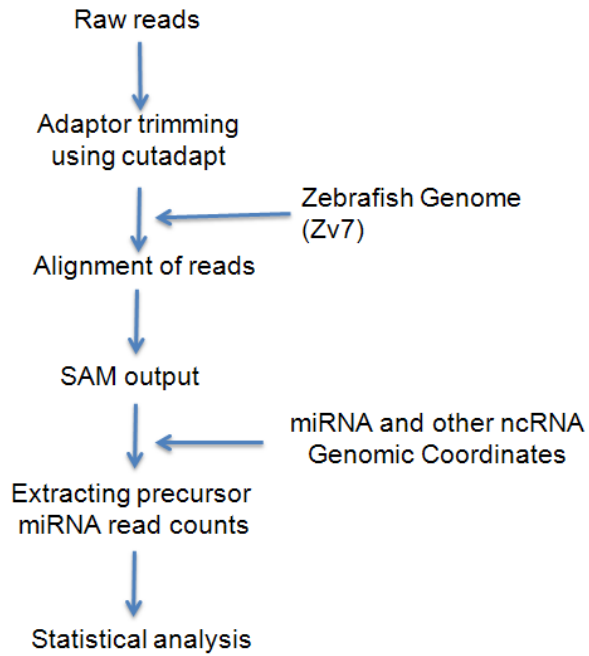


Supplementary Figure 4.

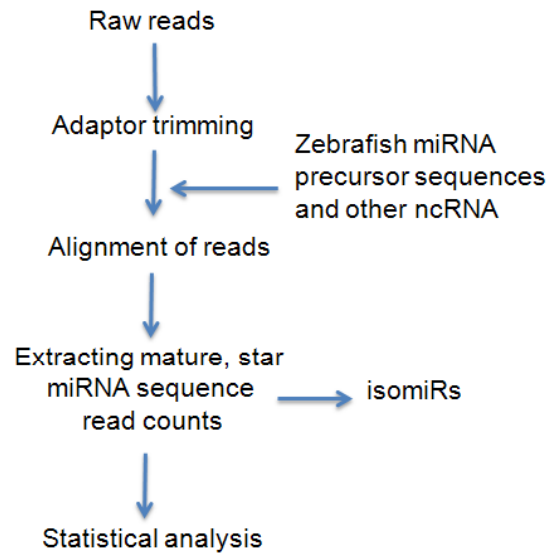
dre-miR-27a	UUCACAGUGGCUAAGUUC CGCU.....
dre-miR-27b	UUCACAGUGGCUAAGUUCUGCA.....
dre-miR-27c	UUCACAGUGGUUAAGUUCUGC.....
dre-miR-27d	UUCACAGUGGCUAAGUUCUUCA.....
dre-miR-27e	UUCACAGUGGCUAAGUUCAGUG.....
hsa-miR-27a	UUCACAGUGGCUAAGUUC CGC.....
hsa-miR-27b	UUCACAGUGGCUAAGUUCUGC.....
mmu-miR-27a	UUCACAGUGGCUAAGUUC CGC.....
mmu-miR-27b	<u>UUCACAGUGGCUAAGUUCUGC.....</u>

Supplementary Figure 5

Genome Mapping Method



CLC BioGenomics Workbench 4.7.



DNASTAR, ArrayStar/Qseq 3.0.

