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Transcriptome data on maternal RNA of 24 individual zebrafish eggs from five sibling mothers[☆]



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ABSTRACT

Maternal mRNA that is present in the mature oocyte plays an important role in the proper development of the early embryo. To elucidate the role of the maternal transcriptome we recently reported a microarray study on individual zebrafish eggs from five different clutches from sibling mothers and showed differences in maternal RNA abundance between and within clutches, "**Mother-specific signature in the maternal transcriptome composition of mature, unfertilized Eggs**" [1]. Here we provide in detail the applied preprocessing method as well as the R-code to identify expressed and non-expressed genes in the associated transcriptome dataset. Additionally, we provide a website that allows a researcher to search for the expression of their gene of interest in this experiment.

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[☆]Refers to: Rauwerda, H. *et al.* Mother-Specific Signature in the Maternal Transcriptome Composition of Mature, Unfertilized Zebrafish Eggs. *PLoS One* 11, e0147151 (2016).

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Specifications Table

Subject area	<i>Biology</i>
More specific subject area	<i>Developmental biology</i>
Type of data	<i>Figures, R-code</i>
How data was acquired	DNA microarray scanner G2565CA (Agilent Technologies) using Agilent Feature Extraction software version 10.7.3.1
Data format	<i>Raw, normalized</i>
Experimental factors	Mature non treated eggs from different mothers
Experimental features	Expression profiles from 24 individual zebrafish eggs from five different clutches (mothers that are siblings).
Data source location	<i>University of Amsterdam, The Netherlands</i>
Data accessibility	Data are within this article and <i>via accession number GEO: GSE72839 at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72839, and http://rnabiology.nl/Dr-Browser.html</i>

Value of the data

- This data contains the maternal transcriptomes of 24 individual zebrafish eggs, whereas up to date only a very limited amount of data is available on transcriptomes of individual eggs.
- In this dataset, maternal transcriptomes from several individual eggs from the same mother are available; an experimental design that makes this dataset unique.
- This data offers a valuable and searchable resource on maternal gene expression and can be used for zebrafish embryology studies.

1. Data

The data that are shared here include *the raw data of the experiment, via Geo submission GEO: GSE72839 (raw data: Agilent data extraction files, as well as the normalized data together with the experiment design).*

Data on the definition of expressed and non-expressed genes, together with the relevant R-code are also provided, as well as the plots of expression levels of expressed genes via a searchable web interface, which also allows to detect the set of genes that have a similar expression profile as the gene of interest.

See also <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72839> and <http://rnabiology.nl/Dr-Browser.html>

2. Experimental design, materials and methods

The basic material and methods, including “zebrafish eggs”, “RNA extraction & microarrays” are presented in the manuscript describing the original finding of the zebrafish oocyte study [1].

2.1. Data preprocessing and normalization

In order to distinguish expressed transcripts from non-expressed transcripts the procedure described in [Supplemental File SD1](#) has been applied to the raw data (the separate microarray data is combined in [Supplemental File SD2](#) and [Supplemental File SD3](#); the annotation file is in [Supplemental File SD4](#)). In short, for each microarray probe the log variance of the log intensity over the entire experiment of the Cy3 channel was determined. In the resulting bimodal distribution ([Supplemental](#)

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