***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/%22%20%5Ct%20%22_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info%3Adoi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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These informations are present in in the section “Materials and methods” and in figure legends.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

**Figure 3-source data 1:** Raw data for TLR4 immunofluorescence in the fetal membranes by confocal microscopy.

**Figure 4-source data 1:** Data on β-value forcg probes on the TLR4 gene for Figure 4A.

**Figure 4-source data 2:** Uncropped polyacrylamide gel for Figure 4B.

**Figure 4-source data 3:** qRT-PCR data and Western-blots data for TLR4 expression (Figure 4C).

**Figure 5-source data 1:** Data on β-value forcg probes on the MIR125B1 and LET7A2 genes for Figure 5B.

**Figure 5-source data 2:** qRT-PCR data for pri-miR-125b-1 and pri-let-7a-2 (Figure 5C).

**Figure 6-source data 1:** Data on luciferase activity in HEK293 cells transfected with pMIR-3’UTR TLR4-luc and pre-mir125b1 or let7A2 (Figure 6A)

**Figure 6-source data 2:** qRT-PCR data for TLR4 expression for Figure 6B.

**Figure 6-source data 3:** qRT-PCR data and Western-blots data for TLR4 expression in AV3 cells transfected with pre-miRNA (Figure 6C).

**Figure 6-source data 4:** qRT-PCR data and Western-blots data for TLR4 expression in Amniocytes transfected with pre-miRNA (Figure 6D).