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

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* 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.

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* 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 analysis methods should be described and justified
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* 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.)

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* 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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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).