***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/)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/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

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

**For sample size information can be found in:**

***Results section:***

Within first statements

***Supplementary Material:***

Supplementary table 20

**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
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* 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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***Experimental replicates including exclusion/inclusion criteria can be found in***

***Figures:***

Figure legend 4

Figure 5 and Figure 5 legend

Figure legend 6

***Methods section:***

Maternal immune activation

Gross anatomy, immunohistochemistry and image analyses

Immunoblotting

Transcriptomics

Differential expression analysis

Data analysis

***Supplementary Material:***

Supplementary figure 8.

**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.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

**Statistical reporting information can be found in:**

***Result section:***

Descriptive stats including results throughout within the text and figures.

Exact P-values are reported throughout the results and figures

***Methods section:***

Differential expression analysis.

SFARI gene set enrichment analysis

WGCNA

Gene Ontology enrichment analysis

Protein-protein interaction

Data Analysis

***Supplementary information***:

Throughout figures and figure legends

Supplementary tables 1 to 4

Supplementary tables 6 to 15

Supplementary tables 18 and 19

(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
* Indicate if masking was used during group allocation, data collection and/or data analysis

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**Group allocation related information can be found in:**

***Results section:***

WGCNA module allocation description.

***Methods section:***

Maternal immune activation

Gross anatomy, immunohistochemistry and image analysis (blinded to treatment)

SFARI gene set enrichment analysis

WGCNA

Gene Ontology Analysis

Data Analysis

**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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* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

**Supplementary information and data availability:**

Detailed results of DE analysis are reported in Supplemental Tables 1 – 15 and can be visualized using our interactive online browser *https://nordlab.shinyapps.io/mia\_browser/*