***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%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.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

**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:

The first section of our work is characterizing placental cells and does not involve statistical comparisons (Fig 2-3). A sample size calculation was not performed as this was the first part of our characterization and panel development. Single-cell analyses, such as the flow cytometry panel used in this work, collect hundreds of thousands of events and using larger sample sizes was beyond the scope of this work.

However, additional samples were assessed (n=27) using our smaller panel (created to FACS sort mesenchymal populations (on a BD FACS Aria II) in subsequent experiments) to compare the 2 gestational age groups (<10 weeks and >10 weeks). This includes all first trimester samples we were able to analyse and a power calculation was not calculated.

The second section investigates the *in vitro* culture influence on isolated mesenchymal cells and uses a sample size of 3 (Fig 4-5). Due to the difficulties of obtaining first trimester human tissue we were unable to assess a larger sample number of placentae. However, this sample size is often employed for tissue culture experiments using human primary tissues.

**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)

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**

* 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:

In figure 2, the proportion of a mesenchymal population (Subset two) was compared between two gestational age groups (<10 weeks and >10 weeks) and an unpaired t-test was used to compare these.

Bar graphs presented in Figure 4 depict SEM of mean and this information is provided in the figure legend.

(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

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:

This is not applicable to our manuscript

**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
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

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

The FCS files that relate to the flow cytometry data presented have been uploaded onto FlowRepository and have been made available to reviewers. They will be made publicly available with this manuscript when it is published.

FCS data files have been provided for flow cytometry presented in Figures 2-3 following the link:

http://flowrepository.org/id/RvFrkWsB6E0BWyozRxSDyKNas19ajMMwIZxhroMphFpJtRQvRTGbCJzhg4JNsswW.

Figure 4:

http://flowrepository.org/id/RvFr4iIRiLOF6MZYZnakhZBThS0frcxxJNHzLySjiu8oZ176MJVlfCk7BWaQaePD.

Figure 7:

https://flowrepository.org/id/RvFrpUTFiOvorOkiFWNTbwZSwYVHLIUkfpfv1ZK6d6bxkIKWpijBlfV5EH13lCoA.