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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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No explicit power analysis was used. The number of replicates chosen was based on our standard laboratory procedures and those adopted within the field. Furthermore, we did not perform experiments involving a heterogeneous population or pool of subjects, so the concept of sample size is not applicable to this manuscript.

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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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Each experiment was performed with at least two biological replicate, which we define as conducting the experiment on separate days and from new cultures. We additionally included technical replicates, which we define as chronologically and spatially parallel experiments, typically deriving from the same culture(s). The number of times experiments were performed is stated in the Methods, Figure legends and Figure supplement legends.

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* Statistical analysis methods should be described and justified
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Statistical methods, number of replicates, means, standard deviation and p-value definitions are provided in the figures and respective figure legends where appropriate. The statistical methods are described in the Methods section of 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
* Indicate if masking was used during group allocation, data collection and/or data analysis

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

Source data files are available for the following figures: Figure 1, Figure 2, and Figure 4. Source data files are available for the following figure supplements: Figure 2–figure supplement 2.

For Figure 1A, Figure 1–figure supplement 1, Figure 2C and Figure 2D, source sequencing data is available through the sequencing read archive.