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* 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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Samples size was not computed when the study was designed. We designed the study, including sample size, based on previous studies.

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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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Experiment performance and replication details are reported in the manuscript. A summary is provided at the end of the introduction, figure legends and full details are provided in the methods section. Outliers were not encountered. No data were excluded. Transcriptome data are available via the link provided in the data availability section of the manuscript.

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* 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)
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Statistical analysis methods are provided in the methods section. Raw data are provided where appropriate either in the main figures or as supplementary. Statistical tests, exact N values, etc. are provided in the results and methods sections. Exact p-values and data measures are also provided.

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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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Not application to this study.

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* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
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Please indicate the figures or tables for which source data files have been provided:

We have provided relevant additional data files in supplementary to support data summarized in figures. Code is provided. All 3D objects, raw datasets associated with figures, image analysis scripts, processed SBF-SEM stacks, and model files, are available for download from Figshare at: <https://tinyurl.com/yww6h9d9>. This information is also provided in the data availability section of the manuscript.