***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
* 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

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Replicates numbers were decided from the experience of the techniques performed and practical considerations.

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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
* 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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The time-lapse measurements, MIC test, deletion experiment in batch culture were repeated 2-4 times in each condition. All the raw data used for the analyses are available from a Github repository (https://github.com/YKogane/History-Dependent-Physiological-Adaptation-2021). Outliers of fluorescence data in time-lapse measurements due to high background noise were not used in the data analysis. Whole-genome sequence data have been deposited in the NCBI Sequence Read Archive (SRA) under BioProject accession in no. PRJNA774496. (https://www.ncbi.nlm.nih.gov/bioproject/774496).

**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.

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The definition of center and the errors of the reported values in the experimental data analysis were calculated by the raw data or estimated by resampling cell lineages as described in figure caption. The statistical analysis used were described in the text or figure caption. The differences were assumed significant when p-value is less than 0.01.

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

All the raw data obtained in this study and the Python codes for data analyses have been deposited to a Github repository (https://github.com/YKogane/History-Dependent-Physiological-Adaptation-2021).