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Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work we publish. This form is published with all life science papers and is intended to promote consistency and transparency in reporting. All life sciences submissions use this form; while some list items might not apply to an individual manuscript, all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined. | Sample sizes were chosen to provide statistical significance

2. Data exclusions

Describe any data exclusions. | n a

3. Replication

Describe whether the experimental findings were reliably reproduced. | Yes, as defined in the legends

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups. | n a

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis. | n a

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☒	☐	A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.
☐	☒	A statement indicating how many times each experiment was replicated
☐	☒	The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☒	☐	A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒	The test results (e.g. p values) given as exact values whenever possible and with confidence intervals noted
☐	☒	A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒	Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study. | defined in the methods section

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* guidance for providing algorithms and software for publication may be useful for any submission.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	n a

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	Defined in the methods and legends

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	Stated in the methods
b. Describe the method of cell line authentication used.	Authenticated by companies, as described in the methods
c. Report whether the cell lines were tested for mycoplasma contamination.	All lines are routinely tested and only used if negative
d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	n a

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	n a

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	n a

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☐ Initial submission ☐ Revised version ☒ Final submission

Flow Cytometry Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Data presentation

For all flow cytometry data, confirm that:

☒ 1. The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ 2. The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ 3. All plots are contour plots with outliers or pseudocolor plots.

☒ 4. A numerical value for number of cells or percentage (with statistics) is provided.

Methodological details

5. Describe the sample preparation.	For DNA repair reporter analysis, one million cells containing integrated reporter were nucleofected with 4µg of pDonor HR plasmid and 2.5µg of pCBASce plasmid. 48 hr after transfection, cells were trypsinized and resuspended in 25mM HEPES pH 7; 1% (v/v) FBS; 2mM EDTA; 1x PBS and directly subjected to flow cytometry analysis. For Cas9-LMNA reporter, 0.4 million cells were seeded in a 6-well plate and transfected 24 hours later using Lipofectamine 3000 with 4µg of mClover-LMNA HR donor plasmid and 2.5 µg of a plasmid expressing Cas9 D10A and a pair of gRNAs. Cells were analyzed by flow cytometry 72 hours after transfection. For cell cycle analysis, cultured cells were treated 10 min with 30 µM BrdU, fixed in PBS:Ethanol 1:3 (v/v) and labeled with Alexa488 anti BrdU and Propidium Iodide.
6. Identify the instrument used for data collection.	Mitenyi MACSQuant VYB
7. Describe the software used to collect and analyze the flow cytometry data.	Data were collected using MACSQuant analzer 10 and analyzed with FlowJo.
8. Describe the abundance of the relevant cell populations within post-sort fractions.	N/A
9. Describe the gating strategy used.	N/A as all cells were analyzed.

Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information. ☒