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☐ Initial submission ☐ Revised version ☒ Final submission

# Life Sciences Reporting Summary

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## q Experimental design

### 1. Sample size

Describe how sample size was determined.

No sample-size calculation was performed.

### 2. Data exclusions

Describe any data exclusions.

No data were excluded.

### 3. Replication

Describe whether the experimental findings were reliably reproduced.

All findings were reliably reproduced.

### 4. Randomization

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

Not applicable

### 5. Blinding

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

no blinding was done.

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 in the Methods section if additional space is needed).

n/a Confirmed

- ☒ ☒ The exact sample size ( ) 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. *h* values) given as exact values whenever possible and with confidence intervals noted
- ☐ ☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

## q Software

Policy information about [availability of computer code](#)

### 7. Software

Describe the software used to analyze the data in this study.

No custom algorithms, that are not in published literature, were used. All other details are described in the Online methods section.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). [V](#) [U](#) [guidance for providing algorithms and software for publication](#) provides further information on this topic.

## q 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.

all unique materials are available upon request

### 9. Antibodies

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

The major antibodies used (anti-H3K14pr and anti-H3K14bu) were validated by peptide dotblots, western blots (both from human and mouse cells), peptide competition assays and/or immunofluorescence. Other antibodies were validated by manufacturer or were kind gifts and in some cases were revalidated using siRNA knockdown in human (e.g anti-p300, anti-GCN5, anti-PCAF) or mouse cells (anti-Acads). Details of all antibodies used is in Supplementary table S2.

### 10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

IGBMC tissue culture facility

b. Describe the method of cell line authentication used.

None of the cell lines were authenticated

c. Report whether the cell lines were tested for mycoplasma contamination.

Cell lines were not tested for mycoplasma contamination except for HeLa and NIH3T3 cells which were mycoplasma tested by the IGBMC tissue culture facility.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

no commonly misidentified cell lines were used

## q 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.

Male mice from C57BL/6J strain aged 8-12 weeks were used for all experiments.

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.

Study did not involve human research participants.