

## Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

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### ▶ Experimental design

#### 1. Sample size

Describe how sample size was determined.

Human donor sample sizes were chosen to provide sufficient confidence to validate methodological conclusions of the applicability of Omni-ATAC. Mouse sample sizes were selected to minimize use as this study did not require multiple biological replicates to validate the methodology.

#### 2. Data exclusions

Describe any data exclusions.

No inclusion or exclusion criteria were used for human or animal studies.

#### 3. Replication

Describe whether the experimental findings were reliably reproduced.

All experiments were performed in technical duplicate. All conclusions were validated across multiple cell lines / cell systems.

#### 4. Randomization

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

No randomization was used.

#### 5. Blinding

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

No blinding was used.

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 ( $n$ ) 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 clear description of 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.

Where relevant, the software used for analysis is cited in the online methods. All custom software is available upon request.

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). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

## ► 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 materials other than donated biological material 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).

Anti-NEUN (ab177487) and anti-SOX10 (ab212843) antibodies were purchased from Abcam. These catalogs are associated with recommended manufacturer protocols and dilutions.

### 10. Eukaryotic cell lines

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

All cell lines used in this study were purchased from ATCC or DSMZ. Where possible, cell lines were validated by comparison to published sequencing data or by in-house genotyping with comparison to the Cancer Cell Line Encyclopedia

b. Describe the method of cell line authentication used.

All cell lines used in this study were purchased from ATCC or DSMZ. Where possible, cell lines were validated by comparison to published sequencing data or by in-house genotyping with comparison to the Cancer Cell Line Encyclopedia

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

Cell lines were tested for mycoplasma contamination upon receipt and periodically thereafter but not prior to each experiment.

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.

None of the cell lines used in this study are listed in the database of commonly misidentified cell lines.

## ► 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.

Mice used in this study were of the C57Bl/6j strain

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.

Information on human subject covariates is present in Supplementary Table 2