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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	CFX ConnectTM Real-Time System (Bio-Rad); ZEN 3.1 for Vert.A1 (ZEISS); SPARK CYTO 300 system (TECAN); CytoVision (Leica); ABI 3730xl DNA Analyzer (Applied Biosystems)
Data analysis	GraphPad Prism 8.0; bedtools 2.29.0; bigWigAverageOverBed 2; bowtie2 2.3.5; ChIPseeker 1.34.1; clusterProfiler 4.6.2; ComplexHeatmap 2.15.4; deeptools 3.3.1; DESeq2 1.38.3; FastQC 0.11.8; featureCounts 2.0.0; ggplot2 3.4.2; MACS2 2.2.5; picard 2.18.21; R 4.2.3; samtools 1.9; scater 1.14.0; STAR 2.7.3a; Trimmomatic 0.39; ArchR 1.0.2; Compass 6.3.0; GeneMapperID-X 1.6

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

We have included a data availability statement in the manuscript. All data are available in the main text or the supplementary materials. The raw sequencing data

have been deposited in GEO database. These data can be accessed using the GSE accession number GSE264658 and GSE264659. The human reference genome used was hg19 from UCSC (https://genome.ucsc.edu/). Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	As stated in the method, self-derived primary hADSCs and hASFs were obtained from participants of different ages and gender (Supplementary Table 3). Commercial primary cells' information was also shown in Supplementary Table 3.
Reporting on race, ethnicity, or other socially relevant groupings	All the samples were from Asian people.
Population characteristics	All the samples were obtained from donors of different genders and ages, ranging from 1 to 67 years old. Information about samples used in this study was shown in Supplementary Table 3.
Recruitment	With informed written consent, the human adipose tissues were obtained from donors without adipose related diseases and human skin fibroblasts from donors without skin related diseases. The recruitment of donors adhered to the principle of fairness and impartiality, regardless of gender, race and other differences, to ensure that every donor had an equal opportunity and was selected without bias.
Ethics oversight	Adult human adipose derived mesenchymal stromal cells (hADSCs) and human adult skin fibroblasts (hASFs) were isolated from donors with informed written consent and approval by the Institute of Ethics Committee Review Board in Peking University (IRB 00001052-19070).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	For hCiPSCs induction, we repeated the reprogramming protocols on all hADSCs and hASFs cell lines we had in our laboratory. And all cell lines were from donors of different genders and ages. From the results we showed in our study, the accelerated method enabled generation of hCiPSCs with a consistent 100% success rate across more than 15 different donors, increasing efficiency by over 20-fold. These results suggest our sample size is sufficient.
Data exclusions	No data were exclued from the analyses.
Replication	All experiments presented here been repeated several times with similar results, the number of repeated experiments is indicated in the figure legends.
Randomization	No randomization methods were used only for animals used for experiments that were randomly allocated.
Blinding	We performed experiments according to standard reprogramming protocols mentioned in our study and identification of hCiPSCs was through immunofluorescence. So we did not consider blinding in this study.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Antibody Company Cat.NO. Dilution
Rabbit monoclonal anti-Lin28A Abcam Cat# ab124765; RRID: AB_10975201; 1:500
Mouse monoclonal anti-OCT4 BD Biosciences Cat# 611203; RRID: AB_398737; 1:200
Rabbit monoclonal anti-OCT4 Invitrogen Cat# MA5-14845; RRID: AB_10979606; 1:200
Goat polyclonal anti-SOX2 R&D Cat# AF2018; RRID: AB_355110; 1:200
Nanog (D73G4) XP® Rabbit mAb Cell Signaling Technology Cat# 4903; RRID: AB_10559205; 1:200
Mouse monoclonal anti-TRA-1-60 Millipore Cat# MAB4360; RRID: AB_2119183; 1:200
Mouse monoclonal anti-TRA-1-81 Millipore Cat# MAB4381; RRID: AB_177638; 1:200
Anti-Histone H3 (tri methyl K27) Abcam Cat# ab6002; RRID: AB_305237; 1:50
Anti-Histone H3 (acetyl K27) Abcam Cat# ab4729; RRID: AB_2118291; 1:50
Anti-Histone H3 (mono methyl K4) Abcam Cat# ab8895; RRID: AB_306847; 1:50
Anti-Histone H3 (tri methyl K4) Abcam Cat# ab8580; RRID: AB_306649; 1:50
Alexa Fluor 488-AffiniPure Donkey Anti-Mouse IgG (H+L) Jackson Immuno Research Cat# 715-545-150; RRID:AB_2340846; 1:200
Alexa Fluor 488-AffiniPure Donkey Anti-Rabbit IgG (H+L) Jackson Immuno Research Cat# 711-545-152; RRID:AB_2313584; 1:200
Cy3-AffiniPure Donkey Anti-Rabbit IgG (H+L) Jackson Immuno Research Cat# 711-165-152; RRID:AB_2307443; 1:200
Cy3-AffiniPure Donkey Anti-Mouse IgG (H+L) Jackson Immuno Research Cat# 715-545-150; RRID:AB_2340846; 1:200
Alexa Fluor 647 Donkey Anti-Goat IgG (H+L) Jackson Immuno Research Cat# 705-605-147; RRID:AB_2340437; 1:200
Anti-beta Actin Rabbit mAb PTM Bio Cat# PTM-5028; RRID: AB_3662854; 1:50

Validation

All the antibodies used in this study are commercially available and validated for use in IF staining or western blot. Data are available on the manufacturer's websites.
Rabbit monoclonal anti-Lin28A, Cat# abl24765: https://www.abcam.com/lin28a-antibody-epr4640-abl24765.html
Mouse monoclonal anti-OCT4, Cat# 611203: https://www.bdbiosciences.com/en-eu/products/reagents/microscopy-imagingreagents/immunofluorescence-reagents/purified-mouse-anti-oct3-4.611203
Rabbit monoclonal anti-OCT4, Cat# MA5-14845: https://www.thermofisher.cn/cn/zh/antibody/product/OCT4-Antibody-cloneT-631-9-Monoclonal/MA5-14845
Goat polyclonal anti-SOX2, Cat# AF2018: https://www.rndsystems.com/cn/products/human-mouse-rat-sox2-antibody_af2018
Nanog (D73G4) XP® Rabbit mAb, Cat# 4903: https://www.cellsignal.com/products/primary-antibodies/nanog-d73g4-xp-rabbit-mab/4903
Mouse monoclonal anti-TRA-1-60, Cat# MAB4360: https://www.merckmillipore.com/CN/zh/product/Anti-TRA-l-60-Antibody-cloneTRA-l-60/MM_NF-MAB4360?ReferrerURL=https%3A%2F%2Fcn.bing.com%2F&bd=l
Mouse monoclonal anti-TRA-1-81, Cat# MAB4381: https://www.merckmiHipore.com/CN/zh/product/Anti-TRA-l-81-Antibody-cloneTRA-1-8LMM_NF-MAB4381
Anti-Histone H3 (tri methyl K27), Cat# ab6002: https://www.abcam.cn/products/primary-antibodies/histone-h3-tri-methyl-k27-antibody-mabcam-6002-chip-grade-ab6002.html
Anti-Histone H3 (acetyl K27), Cat# ab4729: https://www.abcam.cn/products/primary-antibodies/histone-h3-acetyl-k27-antibody-chip-grade-ab4729.html
Anti-Histone H3 (mono methyl K4), Cat# ab8895: https://www.abcam.cn/products/primary-antibodies/histone-h3-mono-methyl-k4-antibody-chip-grade-ab8895.html
Anti-Histone H3 (tri methyl K4), Cat# ab8580: https://www.abcam.cn/products/primary-antibodies/histone-h3-tri-methyl-k4-antibody-chip-grade-ab8580.html
Alexa Fluor 488-AffiniPure Donkey Anti-Mouse IgG (H+L), Cat# 715-545-150: https://www.jacksonimmuno.com/catalog/products/715-545-150
Alexa Fluor 488-AffiniPure Donkey Anti-Rabbit IgG (H+L), Cat# 711-545-152: https://www.jacksonimmuno.com/catalog/products/711-545-152
Cy3-AffiniPure Donkey Anti-Rabbit IgG (H+L), Cat# 711-165-152: https://www.jacksonimmuno.com/catalog/products/711-165-152
Cy3-AffiniPure Donkey Anti-Mouse IgG (H+L), Cat# 715-545-150: https://www.jacksonimmuno.com/catalog/products/715-545-150
Alexa Fluor 647 Donkey Anti-Goat IgG (H+L), Cat# 705-605-147: https://www.jacksonimmuno.com/catalog/products/705-605-147
Anti-beta Actin Rabbit mAb, Cat# PTM-5028: https://ptmbio.com/products/anti-beta-actin-rabbit-mab/PTM-5028.htm

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Human adipose-derived stromal cells were derived from tissues of different donors or obtained from ATCC or Lonza. Human dermal fibroblasts were obtained from Lonza. Human ES cell lines (H1 and H9) were obtained from WiCell. The HEK293T cell line was a gift from Rong Mu's lab . Details of different cell lines were supplied in Supplementary Table 3.
Authentication	Human adipose-derived stromal cells and human adult dermal fibroblasts were authenticated in house by q-PCR, RNA-seq and STR analysis. H1 and H9 were obtained directly from the WiCell and authenticated by q-PCR, RNA-seq and STR analysis.
Mycoplasma contamination	All cultured cells were tested negative for mycoplasma contamination by PCR.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in this study.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Mice was used in this study. The two-to-three-month-old male immunodeficient NPG mice that purchased from Beijing Vitalstar Biotechnology Company.The mice were housed with a 12-h light/12-h dark cycle between 06:00 and 18:00 in a temperature-controlled room (22±1°C) with 40–60% humidity. Water and food were accessible at all times.
Wild animals	This study did not involve wild animals.
Reporting on sex	In this study, the sex-based analysis is not nesscessary.
Field-collected samples	This study did not involve field-collected samples.
Ethics oversight	All of the mouse experiments performed were approved by the Institutional Animal Care and Use Committee of Peking University.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*