nature portfolio

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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.

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.
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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	Oosight Meta System.
Data analysis	BWA-MEM (v0.7.17); Picard tools (v2.18.2, v2.26.9); SAMtools (v1.10); FreeBayes (v1.3.1); R (v4.0.3); RStudio (v1.3.1093); IGV (2.11.3); Excel (v16.0.10392.20029); CellSens DIMENSION 4.3.

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

Data supporting the findings of this study are included in this manuscript. Since whole-genome and amplicon sequencing data can reveal the genetic identity of the study participants, OHSU IRB regulations, participant consent forms, and Oregon laws prohibit us from sharing these data publicly.

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	Male and female gamete, blood and skin fibroblast donors were recruited for this study. The sex of the embryos was not determined or taken into account as part of the study design.
Reporting on race, ethnicity, or other socially relevant groupings	This information was not considered.
Population characteristics	One adult sperm donor 53 years of age was enrolled in this study. Twelve healthy oocyte donors of 21-35 years of age that met inclusion criteria for egg donation were enrolled in this study: • age 21-35 years old; • Regular menstrual cycles every 21-35 days; • Not pregnant; • Be willing and able to sign informed consent and travel to one of the participating IVF clinics for trail related visits and procedures; • Willing to abstain from intercourse or use barrier method contraception during the stimulation cycle of their study participation. Exclusion: • Being diagnosed with polychystic ovarian syndrome (PCOS); • BMI (body mass index) over 28; • Any health conditions that might increase risk of participation, such as endocrine disorders, hypertension, diabetes, heart disease, autoimmune disorders, known allergy to anesthesia (lidocaine); • Current medical history of an active psychiatric disorder; • Significant bleeding disorder that might make a biopsy procedure unsafe; • Any clinical or laboratory findings by the PIs that leads them to believe that candidate is not suitable for egg donation (e.g. anti-mullerian levels too low. A family consisting of an adult female and both parents were recruited as skin fibroblast donors.
Recruitment	Recruitment was organized via print and web-based advertising. All research gamete donors met required inclusion criteria. There is potential bias for gamete donors without access to the Internet. Written informed consent was obtained from all subjects prior to enrollment in the study. Subjects were informed of risks to participation including risks associated with clinical procedures and loss of confidentiality. All consent forms included a lay language summary of somatic cell nuclear transfer and discussed the potential for incidental findings (genetic information potentially important to their future healthcare). Perspective participants were provided a copy of the consent form to review in advance of an in-person consent signing where the form is presented and discussed in further detail.
Ethics oversight	The study was approved by the OHSU Institutional Review Board (IRB) and included independent review by the OHSU Innovative Research Advisory Panel (IRAP) and OHSU Scientific Review Committee (SRC). The approved studies were subjected to bi-annual external regulatory monitoring and Data Safety Monitoring Committee (DSMC) reviews and annual IRB continuing review. Quantity of oocytes used in research studies were strictly regulated by DSMC/IRB and were justified; all studies were required to use the minimal number of oocytes necessary to answer research questions.

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	Minimal sample size was reviewed by OHSU Data Safety Monitoring Committee and approved by OHSU Institutional Review Board. A total of 270 mature oocytes were used for this study.
Data exclusions	No data were excluded from the analysis.
Replication	Results of random segregation have being confirmed in multiple oocytes/embryos (biological samples) derived from several different gamete donors (independent experiments).
Randomization	MII oocytes were randomly assigned into SCNT/Activation or SCNT/ICSI groups and into the Activated or ICSI control groups. Individual sperm for ICSI was randomly picked up and injected into the oocytes.

Blinding | During all analyses , the personnel involved was blinded from the sample origin.

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: Anti-centromere antybody. Antibodies Incorporated. Cat#15-234.
α-Tubulin (11H10) Rabbit mAb (Alexa Fluor® 488 Conjugate). Cell Signaling Technology. Cat# 5063.

Validation: Human Anti-Centromere Antibodies (derived from human CREST patient serum) are useful react with Species Reactivity: Hamster, Human, Mouse, Rat.
α-Tubulin (11H10) Rabbit mAb (Alexa Fluor® 488 Conjugate) detects endogenous levels of total α-tubulin protein and Species Reactivity: Human, Mouse, Rat, Monkey, D. melanogaster, Zebrafish, Bovine, Pig.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): Dermal fibroblast cell lines were generated from an adult female and two her parents for the SCNT experiments.

Authentication: We derived them from dermal biopsies and did whole genome sequencing.

Mycoplasma contamination: All cell lines were tested for Mycoplasma and appeared negative.

Commonly misidentified lines (See ICLAC register): No commonly misidentified cell lines were used.

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.*