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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.

   We used a minimum number of human oocytes/embryos required for statistical comparisons

2. Data exclusions

   Describe any data exclusions.

   no data were excluded

3. Replication

   Describe whether the experimental findings were reliably reproduced.

   Human embryo HDR and mosaicism findings were reproduced with multiple oocyte donations from different donors. All genotyping by Sanger were validated by deep sequencing (MiSeq) independently but two different teams.

4. Randomization

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

   Mutant and WT sperm from the heterozygous carrier was randomly picked up and injected into oocytes. CRISPR/Cas9 injection into zygotes or MII oocytes was randomized with controls

5. Blinding

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

   During all on-target and off-target sequencing, the personnel was blinded regarding the sample origin

   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.	We described all software used for sequence analyses in the method 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.	CRISPR/Cas9, ESCs and iPSCs from this study are available for distribution following MTA

9. Antibodies

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

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	All ESC and iPSC lines included in the study were generated in this study
b. Describe the method of cell line authentication used.	WGS, WES and Sanger sequencing, karyotyping
c. Report whether the cell lines were tested for mycoplasma contamination.	Yes, all cell lines were tested for mycoplasma contamination and were 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.	None

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.	Provided in detail in the material and method section