

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	No software was used.
Data analysis	Graphpad Prism 10, ImageJ, JMP 18

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](#)

De-identified data that is used to generate all the visuals in this study is provided as source data files in the Harvard Dataverse (<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7927/H72T-6Q9M>). Data is accessible to public with no login or approval requirements. Only the data for Figure 5 is not included in the source data files. The original data in Figure 5 was previously published by Huttler et al. (DOI: 10.1016/j.fertnstert.2025.07.029) and made available by the co-authors of that publication.

Clinical data has been de-identified at the time of testing per the national and local laws and HIPAA regulations. In addition, the oocyte retrieval and investigation dates are further de-identified in the available data to avoid any attempt to re-identify the participants in any way.

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	All discarded follicular fluid samples were collected from females voluntarily undergoing in vitro fertilization treatment cycle. No intervention was made to change their treatment. For the experiments outlined in Figure 3, discarded prescreened follicular fluid was recovered from females undergoing in vitro fertilization treatment as above. In Figure 3 males were also consented so as to provide sperm for the fertilization of the recovered oocytes from the prescreened follicular fluid. The sperm samples were provided during the routine collection for the initial in vitro fertilization cycle treatment. No extra samples were needed.
Reporting on race, ethnicity, or other socially relevant groupings	No discrimination was made on treatment groups. All couples undergoing voluntary routine in vitro fertilization treatment were available for recruitment.
Population characteristics	Patient characteristics were females of reproductive age between 18-43 voluntarily undergoing in vitro fertilization treatment. Male partners ranged between 25 to 65.
Recruitment	Patients that were aged 18 to 40 years of age undergoing a routine IVF cycle who elected the use of ICSI for fertilization were approached for consenting. IVF center's clinical coordinators and/or research staff approached eligible patients via email, when the patient's hormonal therapy cycle was initiated. If patients were interested to participate in the studies, a member of the study team contacted the patients via phone call and offer them the opportunity to participate. If a consented patient underwent an egg retrieval they were then eligible to have their prescreened follicular fluid processed by the FINDchip system.
Ethics oversight	WCG IRB, 1019 39th Avenue SE Suite 120, Puyallup, WA 98374-2115

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](https://www.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	The bovine cumulus oocyte complexes were shipped overnight in maturation medium from Simplot as stated in the Methods. Number of oocytes per experiment and number of repeats per day were based on the available number of oocytes received, and the number of experiments that could be conducted between receiving the oocytes and target time window (2-4h after shipment arrives) for optimal fertilization.
Data exclusions	No data were excluded from the analyses.
Replication	All the experiments were performed with at least 3 biological replicates with freshly received bovine oocytes and attempts at replication were successful (i.e. overall trends held across different groups tested.)
Randomization	Shipment lots of bovine cumulus oocyte complexes were randomly allocated to the 3 treatment groups.
Blinding	Blinding was not possible during the study as the bovine cumulus oocyte complexes were processed through the 3 different groups.

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

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, mosaicism, off-target gene editing) were examined.