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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	ZEN2009 Version 6.0.0.303
Data analysis	SortmeRNA Version 2.1, TopHat 2.1.0, SeqMonk Version 0.34.0, DESeq2 Version 1.20.0, edgeR Version 3.22.1, FIJI/ImageJ Version 1.51

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The statement for data availability was included in the Methods section under Data Availability" as shown below.

"The data that support the findings of this study including RNA-seq and proteomics analysis are available from the corresponding authors upon reasonable request."

We do not have data that is necessary for deposition in a public repository.

Field-specific reporting

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

☒ Life sciences ☐ Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences

Study design

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

Sample size	To compare PGC numbers between DMSO and drug conditions, sample size was estimated by G*Power program for t-test with means difference between two independent means, alpha (0.05) and power (0.9). For luciferase assays and RT-PCR, sample size was not calculated, because each biological replicate was made of at least more than 20 embryos.
Data exclusions	We did not exclude data that show even unusual high variance, because zebrafish embryos show a great variability in PGC numbers. However, we discarded or ignored embryos with severe deformity or delayed development, which may lead to confounding results.
Replication	Replications for experimental findings are reliably reproducible.
Randomization	Embryos from the same clutch were randomly divided into DMSO or drug conditions, prior to treatment. Embryos injected with mRNAs were randomly divided into two dishes or more prior to treatment. Adult fish were randomly chosen for mating. Mating time was randomly set from 9 am to 2 pm, since zebrafish mating efficiency and PGC numbers can be affected by mating time.
Blinding	Blinding was not done because it was impractical due to a large number of embryos and experimental complexities but we always randomized embryos for the control and drug treatment. In addition, we did not involve any clinical study or human samples that require a high demand of blinded experiment.

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☐	☒ Unique materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☐	☒ Research animals
☒	☐ Human research participants

Unique materials

Obtaining unique materials	primordazine A and B are available commercially from Chembridge. There are no restrictions on availability of the materials.

Antibodies

Antibodies used	anti-digoxigenin antibody conjugated with alkaline phosphatase (Roche, 11 093 274 910, Lot 12930025, 1:5,000 dilution) or -conjugated with peroxidase (Roche, 11 207 733 910, Lot 11650300, 1:5,000 dilution), rabbit anti-GFP antibody (Torrey Pines Biolabs, TP401, Lot 033019, 1;5,000 dilution), mixed anti-GFP antibodies for TRAP (clones 19C8 and 19F7, 100 µg per experiment), anti-Tubulin (EMD Millipore, 05-829, Lot DAM1764404, 1:10,000 dilution) anti-activated caspase-3 (BD Biosciences, No. 559565, Lot 7166718, 1:500 dilution)
Validation	anti-Digoxigenin-AP, http://custombiotech.roche.com/home/Product_Details/3_6_12_3_5_1.html; anti-Digoxigenin-POD, http://custombiotech.roche.com/home/Product_Details/3_6_12_3_2_1.html; rabbit anti-GFP antibody, http://www.chemokine.com/Houston/rat&other/GFP.PDF; mixed anti-GFP antibodies, Heiman, M. et al. Cell 135, 738–748 (2008); anti-Tubulin, http://www.emdmillipore.com/US/en/product/Anti-Tubulin-Antibody-clone-DM1A,MM_NF-05-829; anti-activated caspase-3, www.bdbiosciences.com/us/applications/research/intracellular-flow/intracellular-antibodies-and-isotype-controls/anti-human-antibodies/purified-rabbit-anti--active-caspase-3-c92-605/p/559565

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	F9 cells were acquired from ATCC (CRL-1720). DU145, MCF7, and H1573 cells were obtained from MGH cancer center.
Authentication	We didn't make addition effort for cell line authentication, since they were obtained either from ATCC or from MGH cancer center.

Mycoplasma contamination	The cell lines were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	We didn't use cell lines that are commonly misidentified.

Research animals

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Animals/animal-derived materials	Adult zebrafish (Danio rerio) of the wild type TuAB and the transgenic Tg(ddx4:EGFP) and Tg(xef1alpha:EGFP-rpl10a) transgenic lines were used in this study. The ratio of male to female for mating was 1:1-2. Mean ages: 7 months ± 3 months, Mean weights: 0.42 ± 0.06g and 0.71 ± 0.1g for male and female fish, respectively.

Method-specific reporting

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ Magnetic resonance imaging