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Reporting Summary

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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	Zeiss ZEN (blue and black versions) Camera (iPhone 6)
Data analysis	FlowJo ImageJ Microsoft Excel Microsoft Powerpoint GraphPad PRISM

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 data that support the findings of this study are available from the corresponding author upon reasonable request.

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	In our experience, approx. 60 embryos are needed per treatment group to achieve a reliable result in case of cmyb in situs. In case of low embryo availability the experiment was conducted with lower numbers and statistical significance was calculated in order to determine, whether an additional experiment to achieve the planned animal numbers is necessary. If statistical significance was reached, the conduction of an additional animal experiment was not conducted.
Data exclusions	No data were excluded
Replication	Due to animal welfare regulations in Germany, complete experiments involving zebrafish older than 5 dpf could only be performed once, since repeat experiments are not permissible once a statistical significant result has been obtained. Small-scale pre-experiments have been performed to estimate the effect strength in the assays performed, and the animal experiments were statistically planned and approved by the Regierungspräsidium Freiburg with sufficient numbers of animals to obtain statistically significant results. Confidence in the observed results and their reproducibility is strengthened by an experimental strategy, in which successive experiments not only investigate new biological questions, but are also based on and thus add supportive information to the preceding experiment (e.g. irradiation of different pigment mutants in Fig. 3c, anaesthesia experiment in Fig. 3e, or thrombocyte count in Extended Data Fig. 3e).
Randomization	Sample allocation to treatment groups was random. Each treatment group contained the same amount of embryos from the same clutch.
Blinding	Data collection and analysis was conducted in a blinded fashion. To confirm the robustness of the in situ read-out, a total of four researchers scored the initial in situs and achieved very results.

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

Antibodies

Antibodies used	Antibody recognizing Cyclobutane Pyrimidine Dimers (clone TDM2) from Cosmo Bio, Catalogue number: CAC-NM-DND-001
Validation	The TDM-2 antibody is a well established antibody. We followed the manufacturer's protocol and tested out the protocol on unirradiated and irradiated samples first. After this validation step, we proceeded with the experiments detailed in the paper.

Research animals

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

Animals/animal-derived materials	The following animals were used in the study. Zebrafish strains:

- Tg(Mmu.Runx1:NLS-mCherry) (called Tg(runx:mCherry) in the manuscript)
- Tg(cdh17:GFP)
- Tg(mitfa:GFP)
- Tg(CD41:GFP)
- TU (wildtype)
- nacre and sandy mutants

Most experiments were conducted up to an age of 8 dpf; sex could thus not be determined. In the experiment involving adults (age 2-6 months), sex was neglected for the analysis.

The following other species were examined in the study:
Ictalurus punctatus (adult)
Gasterosteus aculeatus (adult)
Lepomis macrochirus (juvenile)
Lepomis microlophus (juvenile)
Acipenser fulvescens (juvenile)
Atractosteus spatula (juvenile)
Petromyzon marinus (post metamorphic stage)
Protopterus annectans (adult)
Xenopus laevis (larva)
Epipedobates anthonyi (larva)
Phyllobates terribilis (adult)
Dendrobates tinctorius (larva to young adult)

Method-specific reporting

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

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Zebrafish kidney marrows were dissected from euthanized fish and placed in FACS buffer on ice. They were dissociated by repetitive pipetting and filtered into FACS tubes (BD Falcon). FACS buffer consisted of 0.9X Dulbecco's phosphate buffered saline, 2% heat inactivated fetal bovine serum, 1% penicillin/streptomycin, and 1 USP unit/µL heparin.
Instrument	BD LSR II (analysis), BD FACS Aria II (sorting, only Figure 2b)
Software	BD FACS Diva (collection), FlowJo (data analysis), Prism (statistical analysis)
Cell population abundance	Sorting was only performed in the experiment displayed in Figure 2b. Since cells were sorted directly onto slides, no post-sort control could be performed.
Gating strategy	Both for analysis and sorting: SSC-A vs. FSC-A to remove debris, FSC-H vs. FSC-A to isolate single cells, SSC-H vs. SSC-W to isolate single cells, Pacific Blue-A vs. FSC-A for live-dead staining (Sytox Blue-based), PE-A vs. mCherry-A for mCherry positive. For the abundance of cell populations (lymphocytes, progenitors, myelomonocytes), a plot of FSC vs. SSC was performed after the selection of live cells.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.