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Corresponding author(s): Xiaogang Li

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Reporting Summary

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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	None applicable
Data analysis	The data analysis were performed using Zeiss Zen software, ImageJ and Adobe Photoshop

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 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 authors declare that the data supporting the findings of this study are available within the paper and its supplementary information files.

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

Life sciences study design

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

Sample size	The sample sizes were 5-8 animals per group. ranged from 100 - 300 cells and/or cilia counted. These sample sizes were thought to be statistically sufficient based on literatures involving cilia.
Data exclusions	Not applicable
Replication	The experiments were replicated three times
Randomization	Not applicable
Blinding	Not applicable

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☐	☒ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	The antibodies used in this study included (a) anti-MIF (ab36136) antibody which was purchased from Abcam; (b) anti-PIP4K2a (sc-100406), anti-14-3-3ζ (sc-293415), anti-Cyclin B (sc-4135), anti-CDC20 (sc-14866), anti-CDH1 (sc-56312), anti-HYLS-1(sc-376721), anti-GFP (sc-9996) antibodies which were purchased from Santa Cruz Biotechnology Inc; (c) anti-T/S pan (# 9631), anti-Lamin A/C (# 2032) antibodies which were purchased from Cell Signaling Technology; (d) anti-KIF3a (13930-1-AP), anti-IFT20 (13615-1-AP), anti-IFT88 (13967-1-AP), anti-IFT140 (17460-1-AP) antibodies which were purchased from Proteintech; (e) anti-β-actin antibody (A5316) antibody which was purchased from Sigma-Aldrich. The secondary antibodies, including donkey anti-rabbit IgG–horseradish peroxidase (sc-2313) and goat anti-mouse IgG–horseradish peroxidase (sc-2005), were purchased from Santa Cruz Biotechnology, Inc. The antibodies used for Immunofluorescent staining included, (a) anti-MIF (ab36136), anti-MIF (sc-20121), anti-CEP135 (ab75005), anti-CEP290 (ab84870) antibodies which were purchased from Abcam, (b) anti-GFP (sc-9996), anti-CEP164 (sc-515403), anti-Ninein (sc-376420), anti-c-Nap1 (sc-390540), anti-HYLS-1(sc-376721), anti-PIP4K2a (sc-100406) antibodies which were purchased from Santa Cruz Biotechnology Inc; (c) anti-gamma-tubulin (T5326), anti-acetylated α-tubulin (T7451), anti-TTBK2 (HPA018113) antibodies which were purchased from Sigma-Aldrich; (d) anti-CP110 (127801-AP), anti-BBS4 (12766-1-AP), anti-KIF3a (13930-1-AP), anti-IFT20 (13615-1-AP), anti-IFT88 (13967-1-AP), anti-IFT140 (17460-1-AP) antibodies which were purchased from Proteintech; (e) anti-pericentrin (ABT59) antibody which was purchased from EMD Millipore.
Validation	The primary antibodies used were chosen based on already published data with the relevant citations included in the manuscript.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	RCTE cells were provided by Jinghua Hu (Mayo Clinic), all other cells used were purchased from ATCC.
Authentication	Not applicable

Mycoplasma contamination	The cells were not tested for Mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	Not applicable

Animals and other organisms

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

Laboratory animals	Both male and female MIF knockout or wild type mice (21 days old or 3 months old) were used in this study.
Wild animals	Not applicable
Field-collected samples	Not applicable
Ethics oversight	All experiments involving animals were conducted under the approval of Mayo Clinic IACUC.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

ChIP-seq

Data deposition

☒ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

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	70% ethanol-fixed cells were treated with 20µg/ml RNase A and 10µg/ml propidium iodide for 30min
Instrument	FACS Calibur flow cytometry (BD Biosciences)
Software	Flow Jo V10 or BD biosciences software

Cell population abundance	Acquire the DNA dye (PI) channel in linear, then acquire area width and height for the PI channel , ~30000 events per group.
Gating strategy	Using forward scatter (FSC) and side scatter (SSC) to find viable, single cell events. By drawing a gate that excludes those events with low FSC and high SSC to exclude debris and dead cells from the analysis. Then, using tools (PI dye) to reveal the data relevant to the experiment.

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

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