nature portfolio

Corresponding author(s): Dalei Wu

Last updated by author(s): Jan 1, 2025

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 (*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	Crystal data were collected on beamlines BL18U1, BL19U1 or BL02U1 at the Shanghai Synchrotron Radiation Facility (SSRF); Cryo-EM data were collected on a Titan Krios G3i (Thermo Fisher Scientific) operating at 300 kV equipped with a Gatan K3 (Gatan); RT-PCR was performed using a QuantStudio 3 (Applied Biosystems); Dual-luciferase XRE reporter assay was collected on a Spark microplate reader (Tecan); MST binding assay was performed using the Monolith NT.115 instrument (NanoTemper Technologies); Confocal microscopy data were collected on confocal microscope (Zeiss LSM900); MD simulations data were collected using Gromacs program package.
Data analysis	HKL3000 (v716.1); XDS (2023); Coot (v0.8.9); Phenix (v1.14-3260); PyMOL (v2.3); ESPript(3.x); ImageJ (1.53); MO. Affinity Analysis (v2.3); CryoSPARC (V4.5.1); Gromacs (2023.1); OpenMM (v7.7); ParmEd (4.1.0); gmx-MMPBSA (v1.6.1); AmberTools (23.3); CASTp (3.0).

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

The data that support the findings of this study are available within the paper and its Supplementary Information files. Coordinates and structure data that support the findings of this study have been deposited in the Protein Data Bank with the accession codes 8XS6 [http://doi.org/10.2210/pdb8XS6/pdb], 8XS7 [http://doi.org/10.2210/pdb8XS7/pdb], 8XS8 [http://doi.org/10.2210/pdb8XS8/pdb], 8XS9 [http://doi.org/10.2210/pdb8XS9/pdb], 8XSA [http://doi.org/10.2210/pdb8XSA/pdb] and 8XSB [http://doi.org/10.2210/pdb8XSB/pdb]. The accession codes for the previously released structures HIF-2α-ARNT-DNA, NPAS4-ARNT-DNA, mAHR-hARNT-DNA, hAHR-mARNT-DNA, AHR-HSP90-XAP2-Indirubin, AHR-HSP90-XAP2-BaP, AHR-HSP90-XAP2 in ligand-free, dAHR-ANF, and dAHR-dARNT in ligand-free are 4ZPK [http://doi.org/10.2210/pdb4ZPK/pdb], 7XI4 [http://doi.org/10.2210/pdb7XI4/pdb], 5V0L [http://doi.org/10.2210/pdb5V0L/pdb], 5NJ8 [http://doi.org/10.2210/pdb5NJ8/pdb], 7ZUB [http://doi.org/10.2210/pdb7ZUB/pdb], 8QMO [http://doi.org/10.2210/pdb8QMO/pdb], 8H77 [http://doi.org/10.2210/pdb8H77/pdb], 7VNH [http://doi.org/10.2210/pdb7VNH/pdb] and 7VNI [http://doi.org/10.2210/pdb7VNI/pdb], respectively. Source data are provided with this paper.

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	not applicable
Reporting on race, ethnicity, or other socially relevant groupings	not applicable
Population characteristics	not applicable
Recruitment	not applicable
Ethics oversight	not applicable

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

Life sciences study design

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

Sample size	Experiments were performed three times independently unless indicated. Choice of sample sizes guided by established precedents from leading works in the field.
Data exclusions	No data were excluded.
Replication	All experiments were repeated at least twice with similar results. The number of biological replicates is stated in the figure legends.
Randomization	The positions of samples on multi-well plates were different among individual experiments to minimize the systematic errors.
Blinding	Not applicable, as no animal or clinical experiments were involved and data were automatic readouts of the instruments.

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
[ ]	[x] Antibodies
[ ]	[x] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[x]	[ ] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[x]	[ ] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used

The primary antibodies anti-Flag polyclonal antibody (Proteintech, 20543-1-AP), anti-Myc polyclonal antibody (Sangon Biotech, D155014), anti-HA tag polyclonal antibody (Proteintech, 51064-2-AP) and Beta Actin Monoclonal Antibody (Proteintech, 66009-1-Ig) were used as 1:6000 dilution in the western blotting. The secondary antibodies HRP-conjugated Goat Anti-Rabbit IgG (Sangon Biotech, D110058) and HRP-conjugated Goat Anti-Mouse IgG (Sangon Biotech, D110087) were used as 1:6000 dilution in the western blotting.

Validation

Antibodies were validated for the indicated use by the manufacturer available on their websites:
1. Anti-Flag polyclonal antibody
https://www.ptgcn.com/products/Flag-Tag-Antibody-20543-1-AP.htm
2. Anti-Myc polyclonal antibody
https://store.sangon.com/productDetail?productInfo.code=D155014
3. anti-HA tag polyclonal antibody
https://www.ptgcn.com/products/HA-tag-Antibody-51064-2-AP.htm
4. Beta Actin Monoclonal Antibody
https://www.ptglab.com/products/Pan-Actin-Antibody-66009-1-Ig.htm
5. HRP-conjugated Goat Anti-Rabbit IgG
https://www.sangon.com/productDetail?productInfo.code=D110058
6. HRP-conjugated Goat Anti-Mouse IgG
https://www.sangon.com/productDetail?productInfo.code=D110087

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

HEK293 cells (Procell CL-0001) ; Hep3B (Beijing Dingguo CS0172) ; HaCaT (Procell, CL-0090) ; HT1080 and HT1080 AHR-KO (kindly gifted by Prof. Bo Chu of Shandong University)

Authentication

All commercially available cell lines were authenticated by the vendors.

Mycoplasma contamination

These cell lines were all tested negative for mycoplasma contamination.

Commonly misidentified lines
(See ICLAC register)

No commonly misidentified cell lines were used in this study.

Plants

Seed stocks

not applicable

Novel plant genotypes

not applicable

Authentication

not applicable