

Life Sciences Reporting Summary

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For further information on the points included in this form, see [Reporting Life Sciences Research](#). For further information on Nature Research policies, including our [data availability policy](#), see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

► Experimental design

1. Sample size

Describe how sample size was determined.

All statistical approaches are described and discussed in the methods section and figure legends. 3 biological replicates for proteomics experiments were chosen to ensure sufficient statistical power and false discovery rates have been controlled when appropriate.
For cellular and biochemical experiments at least three independent biological replicates were conducted.

2. Data exclusions

Describe any data exclusions.

N/A

3. Replication

Describe whether the experimental findings were reliably reproduced.

All experiments were found reproducible. Number of replicates are indicated.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

The results are quantitative (TR-FRET, FP assays, X-ray crystallography, mass spectrometry) or semi-quantitative (Western Blot) and would not significantly benefit from sample randomization.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Our study did not involve clinical trials, patient samples, or animal studies; therefore, blinding was not required.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

- | | |
|--------------------------|--|
| n/a | Confirmed |
| ☐ | ☒ The <u>exact sample size</u> (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.) |
| ☐ | ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☐ | ☒ A statement indicating how many times each experiment was replicated |
| ☐ | ☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section) |
| ☐ | ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons |
| ☐ | ☒ The test results (e.g. <i>P</i> values) given as exact values whenever possible and with confidence intervals noted |
| ☐ | ☒ A clear description of statistics including <u>central tendency</u> (e.g. median, mean) and <u>variation</u> (e.g. standard deviation, interquartile range) |
| ☐ | ☒ Clearly defined error bars |

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

Graphpad PRISM 7, R framework and limma package, proteome discoverer 2.1, FlowJo 10.3.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

no restrictions for academic users.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Vendor product numbers and LOT information for all antibodies are provided in the methods section.
Terbium-antiHis antibody used for TR-FRET assay is a common Thermo Fisher reagent widely used in HTS assays.
IRDye secondary antibodies were validated in Fischer et al., 2014.
Primary antibodies for BRD2, BRD3, and BRD4 were previously validated in Winter et al., 2015.
Primary antibodies for GAPDH were previously validated in An et al., 2017.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

HEK293 FlpIn cells were purchased from Thermo Fisher and routinely checked for mycoplasma contamination.
MM.1s cells were purchased from ATCC and routinely checked for mycoplasma contamination.
HEK293T were provided by Michael Eck (DFCI) and routinely checked for mycoplasma contamination.

b. Describe the method of cell line authentication used.

HEK293 FlpIn cells were freshly purchased. MM.1s and HEK293T were validated using STR profiling (atcc service).

c. Report whether the cell lines were tested for mycoplasma contamination.

Routinely tested for mycoplasma contamination using MycoAlert (Lonza)

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

No commonly misidentified cell lines were used.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

No animals were used in this study.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

This study did not involve human subject research.