Corresponding Author: Gang Li & Peter A. Nigrovic (co-corr)

Date: Jan 19, 2018

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work we publish. This form is published with all life science papers and is intended to promote consistency and transparency in reporting. All life sciences submissions use this form; while some list items might not apply to an individual manuscript, all fields must be completed for clarity.

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.

   For EMSA, DNA sequencing and Western blot, the data in each case represent three biological replicates with distinct samples.
   For qPCR, ChIP and luciferase reporter assays, the data represent a combination of three biological replicates with distinct samples except on the luciferase report assay in figure 7B that represent a combination of four biological replicates.

2. Data exclusions

   Describe any data exclusions.

   In our sequence analysis, we excluded the sequences that carry mutations to make sure that we eliminate random oligo synthesis, PCR and sequencing error

3. Replication

   Describe whether the experimental findings were reliably reproduced.

   For SNP-seq, we duplicated our sample reaction (two distinct samples) to verify the reproducibility of the experimental findings.
   For EMSA, DNA sequencing and Western blot, the data in each case represent three biological replicates with distinct samples.
   For qPCR, ChIP and luciferase reporter assays, the data represent a combination of three biological replicates with distinct samples except for the luciferase report assay in figure 7B that represents a combination of four biological replicates.

4. Randomization

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

   This study does not include animals and it is not a human subject study. Therefore, this is not an issue.

5. Blinding

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

   This study does not include animal and it is not a human subject study. Therefore, this is not an issue.

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 the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) 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. *p* values) given as exact values whenever possible and with confidence intervals noted
☐	☒	A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (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.	SAS was used for programing in our sequencing data extraction. R (https://cran.r-project.org, version 3.4.1) was used for statistical analysis of the extracted sequencing data e.g., correlation calculation and linear model fitting.

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* guidance for providing algorithms and software for publication may be useful for any submission.

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.	All the materials are available without any restriction.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	All the antibodies used are listed in Table S7.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	We bought THP-1, and Jurkat T cells from ATCC and BL2 cells from DSMZ.
b. Describe the method of cell line authentication used.	None of these cell lines used were otherwise authenticated.
c. Report whether the cell lines were tested for mycoplasma contamination.	We bought THP-1, BL2 and Jurkat T cells as mycoplasma free cell lines.
d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	These cell lines are not commonly misidentified cell lines.

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.	There is no animal use in this manuscript.

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.	There is no human subject use in this manuscript.