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Corresponding author(s):	Wei Liu
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## **Reporting Summary**

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Statistics		
For all statistical analys	es, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.	
n/a Confirmed		
☐ ☐ The exact sam	nple size $(n)$ for each experimental group/condition, given as a discrete number and unit of measurement	
A statement of	on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly	
The statistical Only common t	test(s) used AND whether they are one- or two-sided ests 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 descript  AND variation	ion of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) I (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)	
	thesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted a 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 e	effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated	
•	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.	
Software and o	code	
Policy information abo	ut availability of computer code	
Data collection	Zeiss LSM 800 confocal microscope; Bruker ASCEND 600MHz NMR magnet system; Odyssey infrared imaging system_v3.0; SpectraMax M5/M5e.	
Data analysis	Zen Lite 2012; Microsoft Excel 2007; NMRPipe_v2010; CCPN Analysis_v2.4.2; GraphPad Prism 8.0; Image J_v1.8.0; PyMOL_v2.3.2.	
	om algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.	
Data		
<ul><li>Accession codes, un</li><li>A list of figures that</li></ul>	ut <u>availability of data</u> include a <u>data availability statement</u> . This statement should provide the following information, where applicable: ique identifiers, or web links for publicly available datasets have associated raw data restrictions on data availability	
The data that support thi	s study are available from the corresponding authors upon reasonable request.	
Field-speci	fic reporting	
Please select the one b	elow 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

Validation

ll studies must disc	isclose on these points even when the disclosure is negative.		
Sample size	Sample sizes were determined depending on the experimental settings.		
Data exclusions	No data was excluded.		
Replication	Unless specified, experiments were confirmed with three biological replicates, and the representative results were shown.		
Randomization	No randomization was adopted in this study.		
Blinding	No blinding was adopted in this study.		
Ve require information	isted is relevant to your study. If you are not sure if a list item applies to	ems and methods  and methods used in many studies. Here, indicate whether each material, your research, read the appropriate section before selecting a response.	
	xperimental systems Methods		
	ces ChIP-seq ChIP-seq Flow cytometry ology MRI-based neuroimates esearch participants	ging	
Antibodies			
Antibodies used	Primary antibodies:		
	Rabbit anti-HA (0906-1; HuaBio), 1:1000 dilution for we Rabbit anti-p300 (SC-585, Santa Cruz); 1:200 dilution for Rabbit anti-GST (SC-33613, Santa Cruz); 1:500 dilution Mouse anti-Flag (SC-807, Santa Cruz); 1:500 dilution for Mouse anti-HA (SC-57592, Santa Cruz); 1:500 dilution for Mouse anti-acetylated-lysine (SC-32268, Santa Cruz); 1:000 dilution for Mouse anti-GCN5 (SC-365321; Santa Cruz); 1:200 dilution for Mouse anti-HDAC6 (SC-28386, Santa Cruz); 1:200 dilution for Mouse anti-ubiquitin (SC-8017; Santa Cruz); 1:500 dilution for Western Rabbit anti-GFP (598, MBL); 1:1000 dilution for western Rabbit anti-PCAF (C14G9, Cell Signaling Technology); 1:	ch), 1:1000 dilution for western blot; lution for western blot; lution for western blot; lution for western blot; estern blot, 1:100 for immunoprecipitation and immunofluorescence; stern blot, 1:100 for immunoprecipitation; r western blot; for western blot, 1:100 for immunoprecipitation; or western blot, 1:100 for immunoprecipitation; for western blot, 1:100 for immunoprecipitation; for dilution for western blot, 1:100 for immunoprecipitation; on for western blot; ion for western blot, 1:100 for immunofluorescence; i blot; lo000 dilution for western blot, ; lo1009y); 1:1000 dilution for western blot; ution for western blot, 1:100 for immunoprecipitation; lo100 dilution for western blot; ion for western blot, 1:100 for immunoprecipitation; lo100 dilution for western blot; lo100 dilution for western blot; lo20 dilution for immunoprecipitation; lo20 dilution for western blot.	
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All the antibodies have been verified by the manufacturers according to the introductions on their websites.

## Eukaryotic cell lines

Policy information about <u>cell lines</u>

Cell line source(s)

HEK293, HEK293T and HeLa cells were obtained from ATCC (http://www.atcc.org/). p62-KO HEK293 cells were generated by using CRISPR-Cas9 system.

Authentication

HEK293, HEK293T and HeLa cells used in this study were verified by ATCC (http://www.atcc.org/). p62-KO HEK293 cells were verified by western blot and immunofluorescence.

Mycoplasma contamination

The cell lines were not tested for mycoplasma contamination.

Commonly misidentified lines (See <u>ICLAC</u> register)

There are on misidentified cell lines in this study.