

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

Flow cytometry data were collected using CytExpert software (Beckman Coulter).
OD450 values were collected using Gen5 Software (Bio Tek).
qPCR data were collected using qPCRsoft (Analytik-Jena).

Data analysis

Flow cytometry data were analyzed using FlowJo (versions 10.8.1).
Statistical analysis was carried out using Prism (versions 10).
Image J (V1.53e) was used for RT-PCR gel gray scale analysis.
MaxQuant software (version 1.6.10.43) was used for MS/MS analysis.
Softwares used for RNA-seq analysis were listed as followed: Cutadapt (V1.9.1), FastQC (V0.10.1), HISAT2 (V2.0.1), HTSEQ (V0.6.1), DESeq2 (V1.6.3), R (V3.6.3), ClusterProfiler (V3.14.3)
rMATS turbo (v4.1.0) was used for analyzing differential AS events
IGV genome browser (V2.12.3) was used for exon junction visualization

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](#)

RNA-seq data for Hnrnpa1 and Hnrnpa2b1 expression across B cell subsets were obtained from the Immunological Genome Project (ImmGen; <https://www.immgen.org/>). Comparative RNA expression analyses between naïve and GC B cells were derived from GSE81999 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE81999>]. Expression data of Ezh2 in GC LZ and DZ MYC⁺ AP4⁺ versus MYC⁻ AP4⁻ subsets were retrieved from GSE80669 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE80669>]. Additional expression profiles for Hnrnpa1, Hnrnpa2b1, and Ezh2 in DZ B cells, plasmablasts, and three GC B cell fractions—Fraction1 (BCL6low, CD69high), Fraction2 (BCL6high, CD69high), and Fraction3 (BCL6high, CD69low)—were obtained from GSE109732 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE109732>]. RNA-seq data following EZH2 inhibitor (GSK343) treatment and integrated H3K27me3 target analyses in GC B cells were retrieved from GSE45982 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE45982>]. The RNA-seq datasets (raw and processed) of WT and hnRNP A1/A2B1 double knockout splenic B cells, including those stimulated with anti-CD40 and anti-IgM for 48 hours, have been deposited in the NCBI Gene Expression Omnibus under accession number GSE298944 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE298944>]. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE55 partner repository with the dataset identifier PXD077818 [<https://www.ebi.ac.uk/pride/archive/projects/PXD077818/public>]. All data are included in the Supplementary Information or available from the authors, as are unique reagents used in this Article. The raw numbers for charts and graphs are available in the Source Data file whenever possible.

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

Use the terms *sex* (biological attribute) and *gender* (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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](https://www.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

Data exclusions

Replication	All replicates were included in analyses.
Randomization	Allocation of experimental groups was not random.
Blinding	Blinding was not relevant to our experiments.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used

Rat Anti-Mouse CD45R eBioscience Cat#47-0452-82; RRID: AB_1518810;
 Rat anti-mouse CD93(AA4.1) Biotin eBioscience Cat#13-5892-85; RRID: AB_466768
 Rat anti-mouse CD21/CD35 Percp-Cy5.5 BD Pharmingen Cat#562797; RRID: AB_2737802
 Rat anti-mouse CD23 APC Biolegend Cat#101620; RRID: AB_2563439
 Rat anti-mouse CD43 FITC eBioscience Cat#11-0431-85; RRID: AB_465041
 Rat anti-mouse CD24 Percp-Cy5.5 BD Pharmingen Cat# 562360; RRID: AB_11151895
 Rat anti-mouse CD249 (BP1) PE BD Pharmingen Cat# 553735; RRID: AB_395018
 Rat anti-mouse IgD Biotin eBioscience Cat#13-5993-85; RRID: AB_466861
 Rat anti-mouse IgM PE-Cy7 eBioscience Cat#25-5790-82; RRID:AB_469655Rat
 Rat anti-mouse IgD FITC eBioscience Cat#11-5993-85; RRID: AB_465347
 BCL6 Monoclonal Antibody (BCL-DWN), PE, eBioscience™, Cat#12-5453-82
 Mouse Anti-Human CD38 Percp-Cy5.5 BD Pharmingen Cat#551400; RRID: AB_394184
 CD95 (APO-1/Fas) Monoclonal Antibody (15A7), APC eBioscience Cat#17-0951-82; RRID: AB_10717405
 CD95 (APO-1/Fas) Monoclonal Antibody (15A7), PE eBioscience Cat#12-0951-81; RRID: AB_465788
 GL7 Monoclonal Antibody (GL-7 (GL7)), eFluor™ 660 eBioscience Cat#50-5902-82; RRID: AB_2574252
 FITC Rat Anti-Mouse GL7 BD Pharmingen Cat#553666; RRID: AB_394981
 CD83 Monoclonal Antibody (Michel-17), FITC eBioscience Cat#11-0831-82; RRID: AB_465141
 PE/Cyanine7 anti-mouse CD83 Biolegend Cat#121518; RRID: AB_2566123
 Brilliant Violet 605™ anti-mouse CD184 (CXCR4) Biolegend Cat#146519; RRID: AB_2687359
 Ly-6G/Ly-6C Monoclonal Antibody (RB6-8C5), FITC eBioscience Cat#11-5931-82; RRID: AB_465314
 Biotin Rat Anti-Mouse CD138 BD Pharmingen Cat#553713; RRID: AB_394999
 CD267 (TACI) Monoclonal Antibody (ebio8F10-3), APC eBioscience Cat#17-5942-82; RRID: AB_842758
 Biotin anti-mouse CD3 Biolegend Cat#100244; RRID: AB_2563946
 Biotin Rat Anti-Mouse IgM BD Pharmingen Cat#553406; RRID: AB_394843
 Ly-6G/Ly-6C Monoclonal Antibody (RB6-8C5), Biotin eBioscience Cat#13-5931-85; RRID:AB_466801
 Rat anti-mouse CD38 APC eBioscience Cat#17-0381-82; RRID: AB_469382
 FITC Rat Anti-Mouse IgG1 BD Pharmingen Cat#553443; RRID: AB_394862
 Rat Anti-Mouse IgG1-BIOT SouthernBiotech Cat#1144-08; RRID: AB_2794640
 Rat Anti-Mouse IgM-BIOT SouthernBiotech Cat#1140-08; RRID: AB_2794630
 PE Hamster Anti-Mouse CD69 BD Pharmingen Cat#553237; RRID: AB_394726
 APC anti-mouse CD40 Antibody Biolegend Cat#124612; RRID: AB_1134072
 MHC Class II (I-A/I-E) Monoclonal Antibody (M5/114.15.2), FITC eBioscience Cat#11-5321-82; RRID: AB_465232
 PE Hamster Anti-Mouse CD80 BD Pharmingen Cat#553769; RRID: AB_395039
 FITC Rat Anti-Mouse CD86 BD Pharmingen Cat#553691; RRID: AB_394993
 HRP-conjugated anti-IgG1 SouthernBiotech Cat#1071-05
 HRP-conjugated anti-IgG2b SouthernBiotech Cat#1091-05
 HRP-conjugated anti-IgG3 SouthernBiotech Cat#1101-05
 HRP-conjugated anti-IgM SouthernBiotech Cat#1021-05
 HRP-conjugated anti-IgA SouthernBiotech Cat#1040-05
 beta Actin Rabbit PolyAb proteintech Cat#20536-1-AP

Mouse anti-hnRNP A1 Santa Cruz Biotechnology
 Cat#sc-32301 Mouse anti-hnRNP A2B1 Santa Cruz Biotechnology
 sc-53531
 Rabbit anti-EZH2/KMT6 pAb ABclonal Cat#A5743; RRID:AB_2769389
 Rabbit anti-EZH2/KMT6 mAb ABclonal Cat#A19577; RRID:AB_2862678
 Rabbit anti-H3K27me3 mAb ABclonal Cat#A22396;
 Rabbit anti-CDKN1A mAb Cell Signaling Technology Cat#2947;
 CHEMICALS, PEPTIDES, AND RECOMBINANT PROTEINS
 Streptavidin PE eBioscience Cat#12-4317-87
 Streptavidin Percp-Cy5.5 eBioscience Cat#45-4317-82
 Streptavidin APC Biolegend Cat#405207
 Streptavidin AP SouthernBiotech Cat#7100-04
 Streptavidin HRP SouthernBiotech Cat#7105—05

Validation

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	HEK293T cells were a gift from Yan Li's lab (Department of Biology of Southern University of Science and Technology). HEK293T cells were purchased from the Cell Bank affiliated to Shanghai Institute of Biochemistry and Cell Biology.
Authentication	Cell lines were authenticated roughly by observation of morphology.
Mycoplasma contamination	The cell lines were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	The study did not involved commonly misidentified lines.

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	All mice were on a C57BL/6 background and housed in a pathogen-free environment in Laboratory Animal Center of the Southern University of Science and Technology. Male and female mice, aged 6–12 weeks, served as breeders and experimental subjects. Animals were sacrificed according to approved protocols.
Wild animals	The study did not involved wild animals.
Reporting on sex	Both male and female mice were used in the experiments, and none of the experiments deliberately used single-sex mice. Sex was not considered in the study design or analysis. This decision was based on previous experience, generally accepted standards in the field, and prior published studies using similar experimental systems.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All experimental animal operations were approved by the Institutional Animal Care and Use Committee of the Southern University of Science and Technology.

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

Plants

Seed stocks	<i>Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.</i>
Novel plant genotypes	<i>Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.</i>
Authentication	<i>Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.</i>

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

Bone marrow cells were harvested from the tibiae and femora of mice, while splenocytes were obtained by mechanically dissociating the spleens. The resulting cell suspensions were filtered through a 70 µm cell strainer and resuspended in PBS containing 5% fetal bovine serum (FACS buffer). Single-cell suspensions were incubated with 1 mL of red blood cell lysis buffer (Biolegend) on ice for 4 minutes, followed by the addition of 4 mL FACS buffer and centrifugation.

Instrument

Beckman CytoFLEX.

Software

Data were collected using CytExpert software (Beckman Coulter) and analyzed using FlowJo (version 10.8.1)

Cell population abundance

Purity of MACS-sorted B cells was analysed by flow cytometry.
Purity was >95%.

Gating strategy

Supplementary Figure 2 shows exemplifying complete gating strategies of all analyzed B cells. Gates indicating boundaries between "positive" and "negative" are shown.

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