nature portfolio

Corresponding author(s): DAPR (NCOMMS-24-09119C-Z)

Last updated by author(s): Nov 3, 2024

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	No software was used.
Data analysis	No software was used.

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 raw sequence data reported in this paper have been deposited in the Genome Sequence Archive for Human(GSA-Human) in National Genomics Data Center, China National Center for Bioinformation/Beijing Institute of Genomics, Chinese Academy of Sciences(GSA-Human: HRA006849) that are publicly accessible at https://ngdc.cncb.ac.cn/gsa-human. 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	Sex and gender information has been collected and provided in the manuscript
Reporting on race, ethnicity, or other socially relevant groupings	All participants were Asian and Han Chinese.
Population characteristics	The ages of the HDs(47.3 years, range 30-59), patients who achieved CR(45 years, range 30-67) and patients with de novo AML(43.6 years, range 28-68) were not significantly different.
Recruitment	For in vitro study, BM specimens from patients with de novo AML(N=25), CR patients(N=25) and age-paired healthy donors (HDs, N=25) and CR with incomplete blood count recovery(CRi, N=12) collected for allo-HSCT were used as the healthy control group.
Ethics oversight	The study protocol was approved by the ethics committee review board of Peking University People's Hospital.

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	Based on the standard deviation and the experience of published articles of the research group, we determined different sample sizes for different experiments.
Data exclusions	No data were excluded from the analyses.
Replication	All attempts at replication were successful.
Randomization	Samples were allocated into experimental groups randomly.
Blinding	The investigators were blinded to group allocation during data collection and analysis.

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	Brilliant Violet 421™ anti-Bcl-2 Antibody,Biolegend,658709 Alexa Fluor® 488 anti-Bax Antibody,Biolegend,633603

APC Anti-p53 (phospho S15) Antibody,abcam,ab278570
Cleaved Caspase-3 (Asp175) Antibody,Cell Signaling Technology,9661T
Anti-P53,abcam,ab26
Anti-P53 （Phospho S15）,abcam,ab223868
Anti-Bcl-2,abcam,ab32124
Anti-Bax,abcam,ab32503
α-tubulin,Sigma-Aldrich,T5201
Anti-PUMA antibody,abcam,ab9645
V500 Mouse Anti-Human CD45,BD Bioscience,560777
PerCP/Cyanine5.5 anti-human CD34,BioLegend,343522
CD133/2 Antibody， anti-human,Miltenyi Biotec,130-113-184
PE Mouse Anti-Human CD309, BD Bioscience,560494
APC Annexin V,BioLegend,640920
7-Amino-Actinomycin D, BD Bioscience,559925
FITC anti-human CD34 Antibody,BioLegend,343504
BV421 Anti-Human CD144 ,BD,565670
BV510 Zombie Aqua™ Fixable Viability Kit,Biolegend,423102
FITC-conjugated AffiniPure Fab Fragment Donkey Anti-Rabbit IgG (H+L),Jackson ImmunoResearch,711-097-003
AffiniPure F(ab')$_2$ Fragment Goat Anti-Rabbit IgG (H+L),Jackson ImmunoResearch,111-126-144
FITC anti-human ZO1,abcam,ab150266
BV421 Anti-Human CD144 ,BD,565670
Anti-c-Kit antibody,abcam,ab231780
Anti-Endomucin antibody,abcam,ab106100
AF647 anti-mouse CD117 （c-Kit）,Biolegend,105818
AF647 anti-mouse TER-119/Erythroid Cells,Biolegend,116218
AF700 anti-mouse Lineage Cocktail with IsotyPe Ctrl,Biolegend,133313
APC/Cyanine7 anti-mouse CD45,Biolegend,103116
BV421 anti-mouse CD150 （SLAM）,Biolegend,115926
BV605 anti-mouse CD41,Biolegend,133921
BV711 anti-mouse CD31,Biolegend,102449
BV785 anti-mouse CD48,Biolegend,103449
PE anti-mouse CD48,Biolegend,103406
PE anti-mouse CD144,BD,562243
PE/Dazzle 594 anti-mouse Ly-6A/E （Sca-1）,Biolegend,108138

Validation

All antibodies are commercially mature antibodies in this study, and validation of each antibody can be found on the respective company website.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	GFP-expressing AML-ETO primary mouse AML cells were kindly provided by Professor Yue-Ying Wang of Rui-Jin Hospital, Shanghai Jiao Tong University School of Medicine. KG-1 cells or HL-60 cells were purchased from Cell Resource Center, Peking Union Medical College.
Authentication	All cell lines used were authenticated.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	There were no commonly misidentified cell lines used in the study.

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	BALB/c female mice(6-8 weeks old) were used in this study.
Wild animals	The study did not involve wild animals.
Reporting on sex	All BALB/c mice were female in this study.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All animal studies were approved by the Ethics Committee of Peking University People's Hospital.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJEguidelines for publication of clinical research and a completedCONSORT checklist must be included with all submissions.

Clinical trial registration	*Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*
Study protocol	*Note where the full trial protocol can be accessed OR if not available, explain why.*
Data collection	*Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*
Outcomes	*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

Plants

Seed stocks	*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.*
Novel plant genotypes	*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.*
Authentication	*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, mosiacism, off-target gene editing) were examined.*

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 mononuclear cells were isolated by density gradient centrifugation using lymphocyte separation medium.
Instrument	The flow cytometry data was analysed on a BD LSRFortessa(Becton Dickinson).
Software	The flow cytometry data was analysed on BD FACSDIVA v8.0 Software (BD Biosciences).
Cell population abundance	There was no post-sort fractions in this study.
Gating strategy	Gating strategies were shown in Figure. 1a and Figure. S2e.

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