nature portfolio

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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 used.
Data analysis	Single cell dataset analysis was performed using following software:Cell Ranger, Seurat 4.0.6, SingleR 1.4.1, monocle 2.18.0, CellChat 1.1.0; Bulk RNA seq dataset analysis was performed using the following software: HISAT2, Featurecount, CIBERSORTx.

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

Single cell gene expression matrix and bulk RNA gene expression eare available in OMIX(https://ngdc.cncb.ac.cn/omix/) with accession code OMIX005182 and OMIX005181.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	Cohort 1: This cohort was used to derive the immune cell landscape in AML patients receiving allo-HSCT between October 1, 2019, and January 31, 2021, at Peking University, Institute of Hematology (PUIH), based on scRNA-seq. The inclusion criteria were as followed: 1) age ≥ 16 years; 2) CR before allo-HSCT; 3) survived at least 1 month after allo-HSCT; and 4) without active graft-versus-host disease (GVHD), active infection, and hematologic relapse. Patients who were MRD positivity after allo-HSCT were enrolled in the MRD-positive group, and BM samples were collected within 1 week from the last positive results. MRD-negative patients were enrolled as the controlled group and were matched according to the age and length of follow up (±2 months) Cohort 2: This cohort was designed to identify the association between the change of specific immune cell clusters and MRD conversion before and after preemptive IFN- treatment based on scRNA-seq. The inclusion criteria were patients who met the definition of MRD positivity as mentioned below, and the key exclusion criteria included active acute GVHD, active infections, severe myelosuppression (white blood cell count < 1.0×109 cells/L, absolute neutrophil count < 0.5×109 cells/L, hemoglobin count < 65 g/L, or platelet count < 25×109 cells/L), and organ failure. Six MRD-positive patients were enrolled, and IFN--2b injections were administered subcutaneously. Cohort 3: This cohort was designed to derive the change of immune cells clusters after allo-HSCT based on the bulk RNA-seq profiles of BM mononuclear cells (BMNCs) with CIBERSORTx v.1.0.41 (https://cibersortx.stanford.edu),, which aimed to further verify the association between the change of specific immune cell clusters and MRD conversion. The inclusion criteria were as followed: 1) age ≥ 16 years; 2) CR before allo-HSCT; 3) urvived at least 1 month after allo-HSCT; and 4) without active GVHD, active infection, and hematologic relapse. BM samples collected at 1 to 7 months after allo-HSCT were obtained from the specimen repository of PUIH. More than one BM samples should have been collected for all enrolled patients. Seventy-eight AML patients receiving allo-HSCT from January 1, 2021, to July 31, 2021 were enrolled.
Ethics oversight	The study was approved by the Institutional Review Board of Peking University People's Hospital. The study was conducted in accordance with the Declaration of Helsinki.

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	NA
Data exclusions	No data were excluded.
Replication	All attempts at replication were successful.
Randomization	NA
Blinding	NA

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
[ ]	[x] Antibodies
[ ]	[x] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[x]	[ ] Animals and other organisms
[ ]	[x] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[ ]	[x] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used: Antibodies included PerCP-anti-CD3 (HIT3a, 317337), BV510-anti-CD8 (SK1, 344732), APC-Cy7-anti-CD56 (NCAM, 362512), BV421-anti-KLRG1 (SA231A2, 367706), PE-anti-KLRG1 (SA231A2, 367711), PE-CD107a (H4A3, 328607), Percp 5.5-CD107a (H4A3, 328616), PECy7- IFNγ (4S.B3, 502527), BV605-TNFα (Mab11, 502935), APC-IL2 (MQ1-17H12, 500309), BV421-IL2 (MQ1-17 H12, 500327), AF700-Ki67 (Ki67, 350529), PerCP 5.5- Ki67 (Ki67, 350519), BV421- Ki67 (Ki67, 350506) BV510-CD25 (BC96, 302639), APC-Cy7-CD69 (FN50, 310909), AF647-GZMB (QA16A02, 372219), BV421-GZMB (QA18A28, 396414), FITC-GZMK (GM26E7, 370507), PE-Cy7-Perforin (B-D48, 353304) from Biolegend. Antibodies were used at 1:200 dilution for staining cells.

Validation: Based on information provided by commercial vendors.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): U937and THP1 cell lines were originally from the American Type Culture Collection (Manassas, VA, USA).

Authentication: No specific procedure was taken to authenticate the cell line identity.

Mycoplasma contamination: The cell lines have been tested negative for mycoplasma contamination.

Commonly misidentified lines (See ICLAC register): No cell lines used are in the database of commonly misidentified cell lines.

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: NA

Study protocol: NA, this is not a clinical trial

Data collection: NA

Outcomes: NA

Plants

Seed stocks: NA

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 single-cell suspension was incubated in staining buffer (phosphate-buffered saline (PBS) supplemented with 1% fetal bovine serum (FBS) for 15 min before being stained with indicated monoclonal antibodies.
Instrument	FACSCanto II cytometer (BD Biosciences).
Software	Flowcytometry data were processed and analyzed using FlowJo V18.1.
Cell population abundance	At least 1000 events were acquired for cells in the defined gate.
Gating strategy	For all experiments FSC-A/ SSC-A gates of the starting cell population were used to identify viable cells. Singlet cells were identified using FSC-H/ FSC-A gating. Isotype control was used to distinguish between background and marker-positive events.

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