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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	PET/MR data were collected using a Bruker 9.4T small-animal PET/MR system (Bruker BioSpec 94/30, Germany). IVIS data were collected using an IVIS imaging system (PerkinElmer, USA).
Data analysis	Reconstructed PET data were analyzed using PMOD software (version 4.4, Switzerland), with radioactivity uptake quantified as the percentage of injected dose per gram of tissue (%ID/g) based on volumes of interest (VOIs) delineated on fused PET/MR images. Various data were analyzed and plotted using GraphPad Prism software (ver. 8.0 ; San Diego, CA). Histology data were visualized using cellSens Standard software (ver. 1.8.1; Olympus). Flow cytometry results were analyzed using the FlowJo software (ver. 10.8.1; Becton Dickinson). IVIS results were quantified using Living Image software (ver. 4.4; PerkinElmer). Absorbed doses data were analyzed using OLINDA/EXM software (version 2.1; Hermes Medical Solutions).

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 authors declare that the main data supporting the findings of this study are available within the publication and its Supplementary Information files. The corresponding author will make raw data and step-by-step protocols available upon request. However, the source data for all figures is available.

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 were not considered in the study design. Sex/gender analysis carried out are described in the protocol.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, or other socially relevant groupings were not considered in the study design.
Population characteristics	This study used peripheral blood samples obtained from healthy adult donors. No patient data or clinical populations were involved.
Recruitment	Fresh PBMCs from healthy donors were provided by the Affiliated Hospital of Xuzhou Medical University. The recruitments of healthy human blood donors were approved by the Clinical Research Ethics Committee of the Affiliated Hospital of Xuzhou Medical University. All donors provided written informed consent.
Ethics oversight	This study involving the collection of peripheral blood from healthy donors was approved by the Medical Ethics Committee of the Affiliated Hospital of Xuzhou Medical University (Approval No.: XYFY2020-KL062-01). Written informed consent was obtained from all healthy donors prior to participation. All procedures performed were 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	The sample size used depends on the particular experiment. No sample-size calculations were performed. For in vivo PET or PET/MR imaging studies, the sample size was limited by the number of animals that could be measured in the scanner in one day. In the cell pellet model imaging, the sample size for each experimental group was n = 3. In the therapeutic study of BC19 CAR-T cells using the Raji xenograft mouse model, the sample sizes for both the experimental and control groups were n = 5 each. In the therapeutic study of BC19 CAR-T cells using the U266 xenograft mouse model, the sample size for the experimental group was n = 6, while the sample sizes for the two control groups were n = 3 each. Sample size for in vitro assays was chosen based on literature and on established institutional protocols. In vitro assays were usually performed in triplicates and reproduced in biological and/or technical replications, as indicated in the figure legends. For flow cytometry, typically, a number of 10,000 events was analyzed per stained sample.
Data exclusions	Data from in vivo and vitro assays were not excluded.
Replication	In vitro experiments were mainly done in triplicates or quadruplicates (technical replication) to control for experimental variation, and experiments were repeated to show the reproducibility of the findings (biological replication). Figure panels either show results from different experiments (e.g., Fig. 3A-C) or from a representative experiment (e.g., Fig. 3D-F). Animal studies were conducted with a predefined number of animals as outlined in the approved animal experimentation license.
Randomization	Animals were randomly assigned to treatment and control groups.
Blinding	For the preclinical experiments, investigators were not blinded to the study groups. Outcome measures were primarily imaging data, which was recorded by the scanner in an unbiased fashion, survival , and ex vivo analysis (IHC, biodistribution analysis). The outcome parameter survival was unsuspicious to be unbiased as animals reached the predefined humane endpoint by body weight loss, which is an objective, unbiased parameter.Due to the kind of study and its outcome parameters, it is highly unlikely that a non-blinded researcher consciously or

unconsciously influenced the study's outcome.Quantitative data analysis and validation controls were used, minimizing the risk of introducing bias through the absence of blinding.

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

Used antibodies:
APC-conjugated anti-FMC63 antibody (ACROBiosystems, FM3-AY54A1, clone:Y45, lot# not available, dilutions: FACS: 1:50);
FITC-labeled human BCMA protein (ACROBiosystems, BCA-HF254, lot#: FL894-2256F1-171, dilutions: FACS: 3 μg/mL);
anti-human CD3 (Abcam, ab237707, clone CAL54, lot#: 1130270-4, dilutions: IHC:1:500);
anti-human CD19 (R&D Systems, MAB48671, clone: 1062947, lot#: COSVO12509A, dilutions: IHC: 5 μg/mL;);
anti-human BCMA (R&D Systems, MAB10762, clone: 1042028, lot#: CNWA012601A, dilutions: IHC: 5 μg/mL)

Validation

Vendors tested for Flow cytometry: APC-conjugated anti-FMC63 antibody (ACROBiosystems), FITC-labeled human BCMA protein (ACROBiosystems) ;
Vendors tested for Immunofluorescence: anti-human CD3 (Abcam), anti-human CD19 (R&D Systems), anti-human BCMA (R&D Systems)

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

Raji cells (human Burkitt's lymphoma) and U266 cells (human multiple myeloma) were obtained from the Cell Bank of the Chinese Academy of Sciences (Shanghai, China). Raji-Luc-GFP and U266-Luc-GFP reporter cell lines were generated by lentiviral transduction of parental Raji and U266 cells to stably express firefly luciferase and green fluorescent protein (GFP). Primary human T cells were isolated from peripheral blood mononuclear cells (PBMCs) of healthy donors under protocols approved by the Medical Ethics Committee of the Affiliated Hospital of Xuzhou Medical University (ethics approval no. XYFY2020-KL062-01). The sex of donors was not recorded.

Authentication

None of the cell lines used in this study were authenticated after receipt. The Raji and U266 cell lines were obtained directly from a reputable cell bank (Cell Bank of the Chinese Academy of Sciences). The reporter cell lines (Raji-Luc-GFP and U266-Luc-GFP) were generated in-house by lentiviral transduction. Primary human T cells were freshly isolated and used without authentication.

Mycoplasma contamination

All cell lines tested negative for mycoplasma contamination. Routine testing was performed using a commercially available mycoplasma detection kit. Primary human T cells were not tested for mycoplasma contamination as they were freshly isolated and used immediately.

Commonly misidentified lines
(See ICLAC register)

No commonly misidentified cell lines from the ICLAC Register were 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 mice were purchased from Cavens Experimental Animal Co., Ltd. (Jiangsu, China). NCG mice (NOD/ShiLtJGpt-Prkdcem26Cd52Il2rgem26Cd22/Gpt, strain code T001475) were purchased from GemPharmatech Co., Ltd. (Jiangsu, China). Mice were 6 to 8 weeks old with a body weight of 18 to 22 g at the start of the experiments. Animals were kept at 45-60% humidity and 20-24°C under specific pathogen-free conditions.

Wild animals

The study did not involve wild animals.

Reporting on sex	Female animals were used for most experiments to decrease biological variation
Field-collected samples	The study did not involve samples that were collected in the field.
Ethics oversight	All animal experiments were conducted in strict accordance with the National Institutes of Health (NIH) Guide for the Care and Use of Laboratory Animals and complied with national animal welfare regulations. The study protocols were approved by the Institutional Animal Care and Use Committee (IACUC) of the Jiangsu Institute of Nuclear Medicine (Approval Nos. JSINM-2025-097).

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

Plants

Seed stocks	Plant is not involved in this study.
Novel plant genotypes	Plant is not involved in this study.
Authentication	Plant is not involved in this study.

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	Primary peripheral blood mononuclear cells (PBMCs) were isolated from peripheral blood of the healthy donor and the patients with R/R MM. T lymphocytes were isolated using EasySep™ human T Cell Isolation Kit (STEMCELL) according to the manufacturer's instruction. 1×10^7 human T cells were infected by the lentivirus mentioned above. 1×10^6 CAR-T were used for Flow Cytometry.
Instrument	BD FACSCelesta cytometer (BD Biosciences, USA)
Software	FlowJo software (ver. 10.8; BD Biosciences)
Cell population abundance	These cells were not sorted
Gating strategy	The cells were identified by their FSC and SSC profiles. A polygon gate was drawn on a FSC-A vs SSC-A dot plot to include the cell population. Aggregates were identified and removed from the analyzed population by FSC-A vs FSC-H doublet discrimination gates. The boundaries between positive and negative gates were set based upon an unstained control.

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