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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	FACS Diva Software (BD BioScience)
Data analysis	FlowJo v10.2 (Tree Star Inc.), GraphPad Prism (GraphPad Software Inc.), Milliplex Analyte program

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The data that support the findings of this study will be available from the corresponding authors upon reasonable request

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	In this phase I clinical trial, 25 patients were enrolled based upon the inclusion and exclusion criteria.
Data exclusions	No data was excluded from the analysis
Replication	All attempts at replication of the pre-clinical experiments were successful
Randomization	This phase I trial is not randomized.
Blinding	Blinding is not possible for this phase I trial

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☐	☒ Human research participants

Methods

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

Antibodies

Antibodies used

Antibody name	Clone	Catalog No.	Vendor
Anti-EGFR	C225	Ab00279-10.0	Absolute antibody
FITC anti-human CD3	UCHT1	300406	BioLegend
PERCP anti-human CD4	RPA-T4	300528	BioLegend
PE/Cy7 anti-human CD8a	RPA-T8	301012	BioLegend
APC anti-human CD279(PD-1)	EH12.2H7	329908	BioLegend
APC Mouse IgG2a,K isotype Ctrl(Fc)	MOPC-21	400120	BioLegend
Brilliant Violet 421 anti-human CD45RA	HI100	304130	BioLegend
Brilliant Violet 510 anti-human CD45RO	UCHL1	304246	BioLegend
APC anti-human CD197(CCR7)	G043H7	353214	BioLegend
PE anti-human CD19	HIB19	302208	BioLegend
APC anti-human CD20	2H7	302310	BioLegend
PE/Cy7 anti-human CD27 antibody	M-T271	356411	BioLegend
Brilliant Violet 421 anti-human IgD antibody	IA6-2	348225	BioLegend
PE anti-human IgG Fc	HP6017	409304	BioLegend
Human Trustain	Fcx	422302	BioLegend

Validation: Certificates of analysis and validation statements are provided on manufacturer's websites

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s): 293T, Nalm6, Raji, and K562 cell lines from ATCC

Authentication	293T cell line was authenticated by using NIST published 9 species-specific STR markers. The Nalm6 cell line was authenticated by HLA typing and verified to express CD19. K562 and Raji cell lines were not authenticated.
Mycoplasma contamination	All cell lines have been tested negative for Mycoplasma spp.
Commonly misidentified lines (See ICLAC register)	None are among the ICLAC database of commonly misidentified cell lines.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	5-8 week-old female C.B.Igh-1b/GbmsTac-PrkdcscidLystbgN7 (SCID-beige) mice (Taconic)
Wild animals	*Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*
Field-collected samples	*For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*

Human research participants

Policy information about studies involving human research participants

Population characteristics	Population characteristics in this phase I trial provided in Table 1. The median age of the patients was 48 (range: 24-76). Twelve patients were female and 13 were male. Eighteen patients (72%) had refractory or relapsed diffuse large B-cell lymphoma (DLBCL), including 13 patients with nongerminal center B-cell-like (non-GCB) DLBCL, 3 patients with GCB DLBCL based on the Hans algorithm, one patient with double-hit lymphoma (BZ011), and one patient with DLBCL transformed from follicular lymphoma (FL) (BZ017). Seven patients (28%) had refractory FL including 4 patients with grade 2 FL and 3 patients with grade 3a FL. The patients had all received extensive prior treatment. The median number of prior treatments was 3 (range: 1-6). Six patients relapsed after autologous stem cell transplantation (ASCT), one patient experienced tandem ASCT. At enrollment, three patients had International Prognostic Index (IPI) scores of 4 and seven patients had IPI scores of 3.
Recruitment	25 patients were enrolled based upon the inclusion and exclusion criteria in this phase I clinical trial. There was no potential self-selection bias in recruiting patients.

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	Human blood processing in GMP-compliant facility or research lab.
Instrument	The BD FACSCalibur™ flow cytometer (BD Biosciences)
Software	FACS Diva Software version 8.0.1 (BD Biosciences), FlowJo v10.2 (Tree Star Inc.)
Cell population abundance	N/A
Gating strategy	FSC-A/FSC-H plots were used to determine singlet gates. FSC-A/SSC-A plots were used to determine cell population gates. Isotype controls were used to indicate the boundaries between positive and negative populations.

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