1 **Nanobody MET CAR T cells show efficacy in solid tumors**
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Abstract

Background: MET overexpression is associated with poor prognosis in many solid tumors due to its central role in tumor survival, invasion, metastasis, and chemoresistance. While targeting MET with antibody-drug conjugates has shown promising results, engineered cellular immunotherapeutic approaches have not been extensively explored. Compared to conventional single-chain variable fragments (scFv), naturally occurring single-domain antibodies consisting of variable heavy chains only (VHH or nanobodies) are smaller, retain high specificity, and exhibit remarkable biochemical stability. In this study, we tested the efficacy of MET-targeting VHH-CART (chimeric antigen receptor T cells).

Methods: We generated a panel of VHH-CARTs using mRNA electroporation. VHH-CART cells were evaluated in functional assays including cell binding avidity, cytokine production profiles, hydrogel microwell-based cellular kinetics, and in vitro cytotoxicity. We also assessed the therapeutic effectiveness of VHH-CART in an in vivo mouse model of metastatic triple negative breast cancer.

Results: Among the tested VHH, we identified those with intermediate avidity as most effective for in vitro tumor killing. Using the CD28 costimulatory domain with the VHH augmented cytotoxicity, yet the CARTs maintained selectivity as activation required a minimum antigen density threshold. Mechanistically, VHH-CARTs demonstrated low tonic signaling, high avidity, potent cytokine production, and rapid tumor killing kinetics. When administered in an mRNA format, VHH-CARTs exhibited potent and prolonged tumor growth control in an in vivo metastatic model of triple negative breast cancer.

Conclusion: Taken together, these results demonstrate that VHH-CARTs exhibit robust tumor selectivity and potent therapeutic efficacy both in vitro and in vivo. Given their demonstrated potency and specificity, VHH-CART represent a promising immunotherapeutic strategy for targeting MET-overexpressing solid tumors.

What is already known on this topic: MET signaling is an important contributor to the aggressiveness of many solid tumors, and targeting MET by antibody-drug conjugates has shown efficacy and safety. Targeting MET by CAR T cells has been under study, though with limited potency.

What this study adds: This study is the first to demonstrate effectiveness of anti-MET VHH-CART cells. Compared with other antigen binding domains, VHH-incorporated CAR T cells show low tonic signaling, a favorable cytokine profile, and potent tumor killing.

How this study might affect research, practice or policy: With the multiple advantages of VHHs including small size, stability, and low potential for tonic signaling, VHH-CART cells represent a promising approach for CAR T design against solid tumors.

INTRODUCTION

While chimeric antigen receptor (CAR) engineered T cells have shown impressive efficacy in hematologic malignancies, solid tumors pose many challenges. Target selection remains a challenge for solid tumors due to the lack of tumor-specific antigens[1]. Innovative CAR designs are also needed to promote tumor infiltration and persistence in the hostile tumor microenvironment, to overcome heterogeneous antigen expression, and to avoid on-target/off-tumor cytotoxicity.

The *MET* oncogene encodes the MET receptor tyrosine kinase, which is overexpressed in many solid tumors and is associated with poor prognosis due to its central role in mediating drug resistance and pro-survival signaling[2]. While tyrosine kinase inhibitors are available, their efficacy is limited to a select number of MET-addicted tumors with MET amplification or mutations[2]. In contrast, targeting MET expression with surface antibodies such as antibody-drug conjugates (ADCs) has shown safety and copy number/mutation-independent efficacy[3]. As CARs leverage the antigen recognition ability of antibodies with the additional benefits of adaptive T-cell responses, targeting MET overexpression using CAR T cells holds great potential.

The antigen recognition domain affects the target sensitivity, durability, and tonic signaling of CAR T cells[4,5]. Most CARs use a single-chain variable fragment (scFv) as the antigen binding domain, which commonly exhibits self-clustering and tonic signaling leading to T cell exhaustion[6,7].

A variable region of a heavy-chain-only antibody (VHH or nanobody) is emerging as an alternative to scFv[8–10]. VHH-based CARs have been successfully used in BCMA-CART cell therapy ciltacabtagene autoleucel (cilta-cel) against myeloma with approval from the U.S. Food and Drug Administration (FDA) [11]. Of particular importance for solid tumors, the stability of VHH helps avoid receptor clustering and tonic signaling; its uniquely long complementarity-determining region 3 (CDR3) enables targeting of cryptic epitopes and isoforms that may overcome tumor heterogeneity; its compact size allows flexible integration with other moieties (such as tandem VHH in cilta-cel) to facilitate innovative CAR designs

with enhanced functionality; finally, its high degree and ease of humanization reduce

immunogenicity and ensure safety in humans[8,11–15].

In this study, we constructed a panel of mRNA VHH-CART cells targeting MET, and

demonstrate that VHH-CART cells exhibit high avidity, potent cytokine production upon

stimulation, a potential therapeutic window for CAR activation, low tonic signaling, and

effective control of metastatic tumors in vivo – features that warrant further exploration as a

novel form of T cell immunotherapy for solid cancers.

MATERIALS AND METHODS

Cells cultures: MDA-MB-231 was purchased from ATCC (HTB-26) and its metastatic sub-

population LM2 was a kind gift from J. Massague. The A549 cell line was obtained from

Peter Glazer and the FaDu and CAL27 cell lines were obtained from Barbara Burtness.

These cells were cultured in DMEM+10% FBS+1% penicillin/streptomycin. 786-O was

obtained from Harriet Kluger and cultured in RPMI1640+10% FBS+1%

penicillin/streptomycin. Karpas-422 and OCI-LY3 were obtained from Markus Müschen and

cultured in RPMI1640+20% FBS+1% penicillin/streptomycin. Small cell lung cancer cell lines

NCI-H146 (ATCC HB173) and NCI-H1341(ATCC CRL-5864) were cultured in DMEM-F12

supplemented with 10% FBS, 1X Insulin-Transferrin-Selenium and 1%

penicillin/streptomycin.

Construction of CAR and *in vitro* transcription: The CAR construct consists of a T7

promoter, 5'UTR (human beta-globin), CAR, P2A self-cleavable sequence, GFP, and 3'UTR

(human beta-globin) (see **Supplemental Figure 1A**). Binding domains for the nanobodies

(VHH1-5), 1E4 (scFv1) and 5D5 (scFv2) sequences were adapted from patents

WO2012/042026[16], US10116622B2[17] and US20190085063A1[18], respectively. The

scFv3 and NK1-CAR sequences were adapted from previous publications [19–21]. The

CAR sequences were synthesized as gene blocks containing T7 promoter and 5' and 3'

UTR sequences. They were cloned into standard pUC57 plasmid using the InFusion cloning

kit (Takara).

For *in vitro* transcription, a PCR product encompassing the T7 promoter and 3' UTR,

where the reverse primer also added a 100 nucleotide poly-A tail[22], was used in the T7

ARCA HighScribe mRNA Kit with Tailing Reaction (NEB, Cat. #E6020S). Final mRNA was

purified using lithium chloride precipitation and concentrated to 1-2 μg/μL in water.

Isolation and activation of primary human T cells: Human peripheral blood mononuclear

cells were collected from healthy donors (either local draws under IRB protocol

HIC2000033275 or from the Gulf Coast Regional Blood Center). Bulk T cells were isolated

using the EasySep Human T Cell Enrichment Kit (STEMCELL Technologies, Cat. #17951),

activated with ImmunoCult Human CD3/CD2/CD28 T cell activator (STEMCELL, Cat.

#10990) at the recommended concentration, and cultured at 1 x 10^6 cells per mL in

RPMI1640 + 10% FBS in the presence of 100 IU/mL recombinant human IL-2 (Miltenyi

Biotec, Cat. #130-097743).

Production of mRNA CAR T cells: On days 7-10 post T-cell activation, T cells were

pelleted, washed, and resuspended in 20 μL MaxCyte buffer per 2 million cells.

Electroporation was performed using the MaxCyte ATX with the Expanded T-cell Protocol 1

at 1 μg mRNA/1 million T cells. Following electroporation, cells were rested in a 37^0C

incubator with 5% CO_2 for 10 minutes and resuspended in complete T-cell culture media at

2×10^6 cells/mL with 100 IU/mL IL-2. Cells were either frozen after 4 hours or used for

experiments after overnight incubation. Successful mRNA electroporation was confirmed by

GFP expression using either fluorescence microscopy or flow cytometry.

Flow cytometry: Immunophenotypes of all samples were analyzed using CytoFLEX S

(Beckman Coulter, CA, USA) flow cytometers. FlowJo software (Tree Star, OR, USA) was

used for data analysis. The following antibody-conjugated fluorophores were used: CD3

AlexaFlour 700 (1:100, clone OKT3, BioLegend 317340); CD8 BUV711 (1:100, clone RPA-

T8, BioLegend 301044); CD4 BUV605 (1:100, clone OKT4, BioLegend 317438); CD45RO

BV510 (1:100, clone UCHL1, BioLegend 304246); CCR7 BUV395 (1:100, clone 2-L1-A, BD

569108); CD69 PE/Cy5 (1:100, clone FN50, BioLegend 310908); TNF-α PE (1:50, clone

MAb11,BioLegend 502909); IFN-γ PerCP/Cy5.5 (1:100, clone XMG1.2, BioLegend 505822);

IL-2 BV785 (1:50, clone MQ1-17H12, BioLegend 500348); IL-4 PE/Dazzle 594 (1:100, clone

MP4-25D2, BioLegend 500832). MET expression was confirmed by flow cytometry with a

monoclonal anti-MET antibody (1:10, Roche, clone SP44) compared to an IgG isotype

control (BioLegend 400120).

CD69 activation assay for CAR-Jurkat: The protocol was similar to that previously

described [23]. Briefly, 30,000 target cells per well were plated in a 96-well plate. Jurkat cells

were electroporated with CAR mRNA and incubated at 37^0C for 4 hours before adding to

target cells at various E:T ratios (no target, 100:1, 10:1, 1:1). After overnight incubation,

Jurkat cell activation was measured by surface expression of CD69 using flow cytometry.

In vitro tumor killing assays: The flow-based killing assay was similar to that previously

described[24] with the following modification. Tumor cells labeled with 1 μM CellTrace Far

Red (Invitrogen C34572) were seeded in 24-well plates at a concentration of 1 x 10^5

cells/well. Mock or CAR T cells were added to the culture at different ratios (E:T of 0.5:1, 1:1,

2:1, 4:1) without adding exogenous cytokines. Cells were analyzed 16 hours later to

measure residual tumor cells by flow cytometry. Dead cells were identified by Live/Dead

Violet staining (Invitrogen L34955). Tumor killing was calculated using the formula: %

specific lysis = (1-# residual target cells in treated group/# target cells cultured alone without

T cells) x100%.

The luciferase-based killing assay was performed using cells expressing firefly luciferase

(MDA-MB-231, FaDu, and CAL27). Tumor cells were plated with CAR T cells at the desired

E:T ratio in 384-well plates in 30 μL media overnight. Luminescence was detected using the

ONE-Glo Luciferase Assay System (Promega E6120) and analyzed using a plate reader

(BioTek, SYNERGYMx). Cell lysis (%) = (1 - (experimental readout - spontaneous

readout)/spontaneous readout) x 100.

CellCyte tumor proliferation assay: A lentiviral plasmid encoding mKate2 with puromycin

selection was obtained from Dr. David Fox at the University of Michigan. A549 tumor cells

expressing mKate2 were co-cultured with T cells in 96-well optically clear flat-bottomed

plates at an E:T ratio of 3:1. Plates were imaged using the CellCyte system (ECHO) every

4 hours, and the number of mkate2-positive tumor cells was counted by the provided

software.

Mouse tumor xenograft: Six-week-old female NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice

were purchased from the Jackson Laboratory (Strain #005557). Tumor inoculation was

performed via tail vein injection of $2x10^5$ cells in 100 μL PBS when the mice reached 9-10

weeks of age. Once injected tumors reached a total flux between 10^7 to 10^8 photons/sec by

bioluminescence imaging (BLI) (~7-10 days), mice were randomized into respective groups

and given weekly injections of PBS or T cells as specified in the text. To avoid graft-versus-

host disease, the day before each subsequent T cell injection, 60 mg/kg cyclophosphamide

was injected intraperitoneally to deplete the previously injected T cells [25]. Tumor burden

was monitored by weekly BLI using the Xenogen *In Vivo* Imaging System (IVIS) (Caliper Life

Sciences) and analyzed with Living Image software.

Cell force binding assay (avidity): CAR-tumor binding force was measured using the z-

Movi device (LUMICKS, Amsterdam, The Netherlands). Target cells were seeded onto

microfluidic chips at a concentration of $5x10^7$ cells per mL to obtain a confluent monolayer.

CAR T cells were labeled with 1 μM CellTrace Far Red to enable T cell tracking. After co-

incubation of CART cells with the tumor monolayer for 2.5-5 minutes, a force ramp ranging

from 0 to 1000 pN was applied for 2.5 minutes. T cell detachment was detected by

fluorescence imaging. The binding force was analyzed using the Oceon software (V.1.0,

LUMICKS).

Cytokine release assay: For intracellular cytokine staining assays, T cells and target cells

were co-cultured at a 1:1 E:T ratio for 5-12 hours in the presence of 2 µM monensin (BD

GolgiPlug, cat # 51-2301KZ). For the bulk cytokine assay, the supernatants from overnight

co-culture were harvested and stored in -20^{0}C before shipping to Eve Technologies.

For the multiplexed secretome assay, after stimulation with target cells, approximately

30,000 magnetically enriched CD8+ CAR T cells were processed for membrane staining

(AF647-CD8, STAIN-1002-1). Subsequently, these cells were loaded onto the IsoCode chip

(IsoPlexis, ISOCODE-1001-4), comprising 12,000 chambers prepatterned with an array of

32 cytokine capture antibodies. The chip was then incubated in the IsoLight machine for

16 hours at 37°C with 5% CO_2 supplementation. A cocktail of detection antibodies was then

applied to detect the secreted cytokines, followed by fluorescence labeling. The resulting

fluorescence signals were analyzed using IsoSpeak v.2.8.1.0 (IsoPlexis) to determine the

number of specific cytokine-secreting cells and the intensity level of each cytokine.

Structural modeling: The structures of the VHH sequences, scFv1 (1E4) and scFv2 (5D5),

and their respective complexes with the human MET extracellular domain were predicted

using AlphaFold3[26]. Antibody-MET affinity was estimated using the HADDOCK PRODIGY

server [27,28]. Structural modeling and analysis were performed using PyMOL (Schrödinger,

LLC).

Microwell co-culture system: We used the TROVO system (Enrich Biosystems) for the

microwell assays. For the tumor killing and T cell proliferation assay, T cells (stained with

CD4/CD8-Alexa647) and MDA-MB-231 cells were plated at a 2:1 effector to target ratio in a

six-well culture plate, with each well containing 3,200 printed hydrogel microwells. Each

microwell was indexed by proprietary software and imaged every 12 hours over a four-day

period for downstream analysis. Tumor killing was defined as a ≥15% reduction in tumor

area compared to day 0. T cell proliferation was defined as a ≥2-fold increase in stained T

cell area compared to day 0. For the single cell killing assay, CAR T cells and tumor cells

were plated at a 1:10 E:T ratio, and only microwells containing a single T cell were selected

for further imaging analysis. The percentages of microwells with tumor killing/T cell

proliferation, and rate of killing were calculated by the proprietary software built into the

TROVO system.

In detail, percentage of microwells with tumor killing or T cell proliferation is calculated as

number of microwells meeting the killing/proliferation threshold stated above divided by total

number of microwells in this well. Bar graph is average +/- standard deviation of 3 technical

replicate wells.

Single-cell killing rate was estimated by fitting the paired T cell and tumor signals (area

or counts) at each time point to a mass action interaction model. For each CAR T clone

(and matched controls), we ran three independent 3,200 well microwell plates (9,600

wells/clone total). Dilute seeding targeted ~1 T cell and ~10 tumor cells per well. Plates were

imaged from 0–96 h; fluorescence at time zero was used to calibrate area to cell

conversions. Tumor only wells on the same plates were fit to an exponential model $C(t) =$

$C_0 e^{rC \cdot t}$ to estimate the plate level tumor growth rate rC. From the full set, we retained

~800–900 co culture wells per sample that met pre specified QC (confirmed single T at

time zero, adequate tumor baseline, stable focus/tracking, and finite parameter estimates).

An effective killing rate (k_eff) was then obtained per well using a simplified Lotka–Volterra–

type predator–prey coupling $dC/dt = rC \cdot C - k\_eff \cdot T \cdot C$ (classical LV prey equation) and the

same mass action kill term described in similar CAR T models[29], i.e., tumor loss

regressed against cumulative T cell exposure. Fits were performed by nonlinear least

squares with plate specific rC; Fitting results with goodness of fit $R^2 > 0.95$ are included.

For each clone, the distribution of k_eff was summarized per plate, and the clone‑level

average k_eff and standard deviation was calculated across the triplicated experiments.

Statistics: All statistical analyses were conducted using Prism v.10 (GraphPad). Unless

otherwise specified, data were presented as mean ± SD. Statistical significance was

determined by paired t-test, one-way analysis of variance (ANOVA), or two-way ANOVA as

indicated in the figure legends. The log-rank (Mantel-Cox) test was used to determine

statistical significance for overall survival in mouse experiments.

RESULTS

VHH-CART with intermediate avidity showed the most potent tumor killing

We curated five camelid-derived VHH nanobody sequences and incorporated them into a

second-generation mRNA CAR design with a CD8 hinge and transmembrane domain,

followed by 4-1BB and CD3ζ signaling domains (**Supplemental Figure 1 and Figure 1A**).

Since avidity represents the strength of the immune synapse and has been shown to

predict clinical response[30], we used the z-Movi system to measure the avidity of different

VHH-CART cells. To ensure that avidity measurement was not confounded by different CAR

expression levels, the amount of electroporated mRNA was adjusted so that all constructs

had >85% expression as determined by GFP; however, VHH5-CAR was consistently

expressed at ~75-80% regardless of amount of mRNA input (**Figure 1B**).

All VHH-CARTs showed varying percentages of bound T cells with increasing rupture

force (**Figure 1C**). VHH1, VHH2, and VHH3 showed relatively low avidity compared to

VHH4 and VHH5. Despite lower expression, VHH5 surprisingly showed the highest avidity.

The mean percentage of remaining T cells bound to targets at 1000 pN, from the lowest to

highest, was VHH3 (7%), VHH1 (12%), VHH2(19%), VHH4 (31%), and VHH5 (36%) (**Figure**

1D).

To gain structural insight into functional avidity, we modeled the binding of the different

VHHs to MET using AlphaFold3 (**Figure 1E**). VHH1, VHH2, and VHH5 are predicted to

overlap with the high affinity binding site for the HGF-α chain. VHH3 is predicted to bind to a

more membrane-distal epitope that overlaps with HGF-β chain. VHH4 appears to bind to a

distinct epitope separate from the other VHHs, slightly away from either HGF binding site.

These predictions are consistent with the reported antagonistic effect of these VHHs on the

HGF-MET interaction. The dissociation constant K_D was estimated by PRODIGY for the top-

ranked structures. The affinity for VHH3 ranged from ~10-50 nM; VHH1 and VHH2 showed

intermediate affinity, averaging 5-10 nM; VHH4 and VHH5 had the highest affinity, ranging

from 0.4-1.2 and 2-3 nM, respectively. The estimated affinities correlated with the observed

avidity, suggesting a direct relationship between affinity and immune synapse strength.

We then investigated whether different avidities correlate with the in vitro cytotoxic

functions of effector cells, expecting higher avidity to achieve better killing of MDA-MB-231

cells. Surprisingly, we found that low avidity CARs mediated stronger tumor killing, with

intermediate-avidity CARs (VHH1 and VHH2) achieving the highest level of cytotoxicity

(**Figure 1F**). VHH3 showed the lowest avidity, but nonetheless still achieved slightly better

killing than VHH4 and VHH5. The superior tumor killing by VHH1 and VHH2, and even

VHH3, was most notable at low E:T ratios. There was no significant difference in cytotoxicity

between VHH1 and VHH2. Using the CellCyte system and another cell line, A549, we

showed that both VHH1 and VHH2 demonstrated equivalent inhibition of tumor proliferation

over a 70-hr period (**Figure 1G**).

Although high-avidity CARs are generally favored and have been shown to correlate with

clinical response, our findings are consistent with emerging evidence documenting potential

advantages of lower-avidity CARs (see Discussion). Given that there was no significant

difference between VHH1 and VHH2 in terms of avidity and in vitro cytotoxicity, we used

VHH2 for further characterization.

CD28 costimulatory domain conferred stronger VHH-CART activation than 4-1BB

Using VHH2, we next investigated how different cytoplasmic costimulatory domains,

namely, CD28 versus 4-1BB, affect VHH-CART function.

Although not significantly different, VHH2-28z trends towards higher avidity than VHH2-

BBz (**Figures 2A and B**). VHH2-28z also achieved higher in vitro tumor killing and more

immune cytokine (IFN-γ, TNF-α, IL-2, and IL-4) and cytotoxic molecule Granzyme B

production, as well as higher polyfunctionality (**Figures 2C-E, and Supplemental Figure 2**).

In addition to these fixed-time point assays, we also used a microwell-based co-culture

platform to gain insights into the kinetics of CAR T cell killing. In microwells where we

seeded 1 effector T cell per 10 tumor cells, we found that VHH2-28z demonstrated a higher

single-cell killing rate than VHH2-BBz (**Figure 2F**). At an experimental setup of a 20:10 E:T

ratio, we observed more tumor killing and higher T cell proliferation associated with VHH2-

28z compared to VHH2-BBz over a four-day period (**Figures 2G-I**). Our data is consistent

with higher and more rapid cytotoxic function generally reported for CD28 compared to 4-

1BB[31,32].   Beyond four days, most likely due to diminishing mRNA, there was no

significant killing or proliferation observed with either construct (data not shown).

Although CD28 costimulatory domain confers immediate potency, it is reported to be

more prone to exhaustion than 4-1BB[31]. However, most likely due to the transient nature

of mRNA CAR expression, we did not observe significant increase in exhaustion markers

PD-1, LAG3, or PD-1+/TIM3+ for VHH2-28z (Supplemental Figure 3). Overall, because of its

better performance than VHH2-BBz (at least within the four days post mRNA

electroporation), we used VHH2-28z for the rest of the study (unless otherwise specified).

VHH2-CART eliminated MET+ tumor cells in vitro and in vivo

Since MET overexpression is associated with poor prognosis in many solid tumors, we

tested the efficacy of VHH2-CART against different subtypes of solid tumors with known

MET overexpression. VHH2-CART demonstrated cytotoxicity against tumor cell lines from

triple negative breast cancer (TNBC) (MDA-MB-231 and LM2), clear cell renal cell

carcinoma (786-O), and head and neck squamous cell carcinoma (CAL27 and FaDu)

(**Figures 3A and B**).

Recent clinical trials have shown that repeated CAR T cell injections exert better tumor

control than single CAR T administration in solid tumors[33,34]; presumably because fresh

supplies of T cells help overcome T-cell exhaustion in the tumor microenvironment [33]. We

tested the in vivo efficacy through weekly injections of fresh mRNA VHH2-CART cells

(**Figure 3C**). We focused on the aggressive lung metastatic TNBC model LM2. Luciferase-

expressing LM2 tumor cells were injected intravenously (IV) via the tail vein into NSG mice.

After 7-10 days, we confirmed tumor growth in bilateral lungs by bioluminescence imaging

(BLI). We then injected PBS, $20x10^6$ mRNA VHH2-CART cells or an equal number of mock

T cells via the tail vein, followed by three additional weekly injections of $5x10^5$ effector cells

or PBS.

Significant reduction in tumor growth was observed in the VHH2-CART group compared

to the mock T cell group (**Figure 3D**). Mice were euthanized on day 25 for necropsy.

Immunohistochemical (IHC) staining with anti-MET revealed heterogeneous MET

expression within the tumor bed in the mock T cell and PBS groups (**Figure 3E**). Although

some residual tumor cells were seen in the VHH2-CART group, they were mostly MET

negative by IHC (**Figure 3E**); the tumor growth curve also suggested slow growth of these

residual tumors (**Figure 3D**). In the VHH2-CART group, IHC for human CD3 showed clear

infiltration and aggregation of T-cells in the residual tumors, whereas the mock T cell group

showed only limited numbers of single scattered T cells (**Figure 3F**). Given the aggressive

nature of tumors generally associated with MET overexpression, these findings indicate that

VHH2-CART could efficiently control tumor growth by eliminating MET-positive tumor cells.

VHH2-CART activity is dependent on MET expression level

Given the necropsy findings that MET can be expressed at heterogenous levels in

different tumor cells, we next tested the antigen threshold for VHH2-CART activation. First,

in a panel of small cell lung cancer cell lines with varying levels of MET expression (**Figure**

4A), we observed that increased MET expression resulted in increased cytotoxicity by

VHH2-CART, indicating that targeted tumor lysis was dependent on MET expression level

(**Figure 4B-E**).

To further investigate antigen-dependent cytotoxicity, we compiled and analyzed a series

of cell lines with varying levels of MET expression and tested cytotoxicity at a high E:T ratio

of 5:1 (**Figure 4F-G**). As expected, co-culture of VHH2-CART with cell lines with high levels

of MET expression (786-O, NCI-H1341, LM2, and Karpas-422) led to significant tumor cell

death ranging from 80-100%. Although the intermediate MET-expressing cell line, NCI-H146,

still showed significant cell death, the killing by VHH2-CART dropped to approximately 45-50%

(against a background of ~10% mock T cell killing). For the low-MET cell line, OCI-LY3, and

MET-negative cell line, K562, VHH2-CART showed cytotoxicity not significantly different

from mock T cells.

Taken together, our findings suggest the existence of an antigen threshold level for

VHH2-CART activity. In normal tissues, MET is expressed at the highest level in

hepatocytes, whose MET expression level is predicted to fall between OCI-LY3 and K562

cell lines, for which we observed limited cytotoxicity and a potential therapeutic window for

VHH2-CART cells.

VHH-CART cells showed low tonic signaling

Since nanobodies generally show high stability[8,12], we tested how incorporation of

VHH influences CAR T cell function compared to MET-CART cells engineered with different

sources of antigen binding domains (ABDs).

To facilitate comparison, we adapted a previously reported CAR-Jurkat (CAR-J) assay

[23] (**Figure 5A**). We electroporated mRNA encoding CARs with various ABDs into Jurkat

cells, co-cultured them with tumor cell lines at various effector to target ratios for 16 hours,

and assessed CD69 expression by flow cytometry. The diffuse large B-cell lymphoma

(DLBCL) cell line, Karpas-422, served as a convenient target for this assay as it expresses

high levels of CD19 in addition to MET, thus allowing comparison with CD19-CAR (FMC63)

as a positive control (**Supplemental Figure 3**).

The selected ABD constructs included three different scFvs, one natural ligand, and

VHH1-4 (**Figure 5B**). ScFv1 and scFv3-CAR-J were constructed similarly to previously

described cell lines [19,20]; scFv2-CAR-J was derived from the monoclonal antibody

Onartuzumab (5D5)[35]. Finally, a natural ligand CAR previously shown to mediate

cytotoxicity against mesothelioma was derived from the NK1 domain of HGF[21].

As expected, CD19-CAR-J cells showed an antigen-dependent increase in CD69

expression, whereas mock Jurkat cells showed only basal levels of expression at all E:T

ratios (**Figure 5B**). The tested scFv-CAR-J cells, however, demonstrated a wide range of

antigen-dependent responses. Notably, scFv1-CARJ showed high basal levels of CD69

expression in the absence of Karpas-422, indicating tonic signaling. Indeed, increasing the

target cell ratio did not lead to a further increase in CD69 expression, suggesting T-cell

dysfunction. In contrast, scFv2-CAR-J showed low basal levels and an antigen-dependent

increase in CD69. scFv3-CAR-J showed low basal CD69 levels, but for an unknown reason

did not show an antigen-dependent response. The ligand-based NK1-CAR-J also failed to

show significant CD69 expression upon stimulation. In contrast to the varied behaviors of the

tested scFv- and ligand-CAR-J cells, all VHH-CAR-J cells demonstrated low basal levels

and an antigen-dependent increase in CD69 expression. The various tonic signaling profiles

seen in Jurkat cells could be replicated in co-cultures of primary human T cells and MDA-

MB-231 target cells (**Figure 5C**).

To further show that tonic signaling leads to T-cell dysfunction, we chose the tonic scFv1

and the low-tonic scFv2 and VHH2 for comparison. As expected, scFv1-CART cells showed

only limited tumor killing compared to scFv2- and VHH2-CART cells, both of which showed

equivalent tumor killing at various E:T ratios (**Figure 5D and 5E**).

The predisposition of different ABDs for tonic signaling is intriguing. Because previous

reports have correlated positive surface charges of ABDs with tonic signaling[36], we

modeled the electrostatic surfaces for scFv1, scFv2, and VHH2 (**Figure 5F**). However,

structural modeling showed no obvious differences in net surface charges, suggesting that

other mechanisms might contribute to tonic signaling (see Discussion).

Different binders endowed varying functional profiles to CAR

We further tested whether low tonic signaling of VHH affects avidity, cytokine secretion,

and tumor killing kinetics. Again, we compared VHH2 with scFv1 and scFv2. All three

appear to share similar predicted affinities (5-10 nM). However, structural modeling predicts

different binding epitopes on MET; while VHH2 and scFv1 occupy a more membrane-

proximal epitope, scFv2 binds to a more membrane-distal one (**Figure 6A**).

We first compared how the three ABDs influence avidity, expecting roughly equal avidity

given their equivalent affinities. Interestingly, despite similar expression levels of all

constructs (**Figure 6B**), VHH2 consistently showed stronger avidity than scFv2, which was

greater than scFv1 for two different tumor cell lines (**Figures 6C-D**). The low avidity of scFv1

could be related to factors that also contributed to its tonic signaling. The stronger avidity of

VHH2 over scFv2 was unclear, but one possible explanation could be related to VHH2's

binding to a more membrane-proximal epitope, as targeting membrane-proximal epitopes

has been shown to stabilize the immune synapse[37,38].

In terms of cytokine production, both scFv2 and VHH2 showed higher levels of IFN-γ,

TNF-α, and IL-2 after target stimulation than scFv1 (**Figure 6E** and **Supplemental Figure 4**).

Among the three constructs, scFv2 was noted to have the highest baseline cytokine

secretion in the absence of antigens (especially IFN-γ), suggesting some tonic signaling in

scFv2. Using IsoPlexis, VHH2 demonstrated the highest polyfunctional strength index (PSI)

in vitro (**Figure 6F**), including the highest effector, stimulatory, and chemoattractive and

lower regulatory cytokine levels. Although there were increased inflammatory cytokines

detected by IsoPlexis for VHH2, by ELISA VHH2 produced lower levels of proinflammatory

cytokines such as IL-6, IL-8, IL-10, IL-1β, and granzyme A (**Supplemental Figure 4**). The

reason for this difference is unclear but might be due to different assay conditions.

We also examined the kinetics of tumor cell killing using a microwell platform monitored over four days (as in Figure 2F-I). Although not statistically significant, VHH2-CART cells trended to have the highest single-cell killing rate (**Figure 6G**), the highest percentage of microwells with tumor killing (**Figure 6H**), as well as the highest T cell proliferation (**Figure 6I**). Taken together, these data suggest diverse behaviors of different MET-CART cells, and that VHH2-CART cells have high avidity, potent immune cytokine production including polyfunctionality, and rapid tumor killing kinetics.

VHH2-CART showed potent in vivo efficacy in comparison with scFv2-CART

Emerging evidence suggests that avidity correlates with in vivo and clinical efficacy more so than in vitro cytotoxicity[30]. We tested this hypothesis by comparing VHH2 and scFv2 in vivo given their overall similar in vitro cytotoxicity but differing avidities. Since multiple high doses of VHH2-CART cells appeared to provide potent tumor control (**Figure 3**), we performed a CAR T cell stress test by reducing the weekly dose to 2×10^6 CAR T cells per IV injection and monitored tumor growth over a longer time period (**Figure 7A**)

Both VHH2 and scFv2 showed significantly better survival than mock T cells and PBS, but VHH2 and scFv2 showed no statistically significant difference in overall survival (**Figure 7B**). There was a significant reduction in tumor luminescence in the VHH2 and scFv2 groups compared to saline or mock T cells (**Figure 7C**). Interestingly, after the last CAR T cell injection at day 21, many animals in the VHH2 group showed lower tumor burdens than the scFv2 group. Three animals in the VHH2 group showed continuous tumor control until approximately day 67. Overall, there were also fewer extrapulmonary metastases in the surviving mice in the VHH2 group compared to the scFv2 group (**Figure 7D**). Collectively, our in vivo model indicates that VHH2-CART cells are as effective as scFv2-CART cells with modestly enhanced tumor control, likely due to more complete elimination of MET-positive tumor cells by the stronger avidity VHH2.

Although there was no overall survival difference between VHH2- and scFv2-CART cells, some of the mice appeared to die due to factors other than tumor burden thus complicating

survival curve analysis. On-target/off-tumor cytotoxicity (OTOT) was unlikely as the VHH2

does not bind murine MET[39], and histology showed no obvious evidence of tissue damage.

Other etiologies including cytokine storm or development of early GVHD were also possible.

DISCUSSION

We used an array of functional assays to comprehensively characterize nanobody-based

CAR T against MET-positive solid tumors. Among a panel of VHH, we found that VHH1 and

VHH2 with intermediate avidity mediated the best killing especially at low E:T ratios. The

CD28 costimulatory domain enhanced VHH2-CART cell in vitro cytotoxicity and effectively

controlled tumor growth in vivo. Despite their potency, VHH2-CART cells displayed an

antigen threshold that could potentially discriminate between tumor and normal tissues.

Compared to the more variable behaviors of scFv-CART cells, VHH-CART cells showed low

tonic signaling, high avidity, a favorable cytokine profile, and rapid tumor killing kinetics -

features that likely contributed to prolonged tumor control in vivo despite the transient nature

of the injected mRNA CART cells.

This study highlights construct design as a crucial step in optimizing CARs. We examined

the fundamental aspects of changing the ABD with VHH as a comparison to scFv or ligand-

based approaches. Nanobodies are known for their small size and high stability [8–10]. We

demonstrated that all our tested VHHs have low tonic signaling, whereas the selected scFv

were more variable, with scFv1 being the most prominent example of a tonic signaling CAR.

Interestingly, structural modeling of scFv1 did not indicate excessive surface positive

charges that were previously reported to increase tonic signaling potential[36]. However,

other mechanisms, such as hydrophobic interactions and light-chain-heavy-chain mispairing

are also known to occur in scFv and might contribute to the tonic signaling of scFv1[5].

Although not without limitations (such as the need for humanization), VHHs might generally

offer an alternative solution for some tonic signaling CARs [4].

We found that the two intermediate avidity VHH1 and VHH2 were more efficacious at

eliminating tumors than either the higher avidity VHH4/VHH5 or the lower avidity VHH3.

There is a complicated relationship between avidity and cytotoxicity—some prior

publications suggest that increased avidity leads to better CAR T cell performance[40,41],

while others indicate that decreased avidity is preferable[37,42]. One potential explanation is

that CAR T cells with high avidity have low *Koff* and therefore prolonged engagement with

tumor cells, which can lead to activation-induced cell death and compromised tumor

killing[37,42]; on the other hand, excessively low avidity translates to an unstable immune

synapse. In another context, VHH2-28z showed a trend toward higher avidity and cytotoxic

function than VHH2-BBz, likely due to the predisposition of CD28 to dimerize and thus

promote multivalent interactions[31,43,44]. Finally, the higher avidity of VHH2 compared to

scFv2 could potentially be related to VHH2's binding to a more membrane-proximal epitope

and correlated with slightly better tumor killing kinetics and tumor control in vivo. These

findings reflect the multifactorial nature of avidity, which depends on CAR-target antigen

affinity, binding valency, and CAR-antigen orientation, among other factors. Future studies

will benefit from a better understanding of the factors that influence the avidity-CAR function

relationship.

Although the CD28 costimulatory domain led to higher and faster killing as shown here,

other studies have demonstrated earlier T-cell exhaustion than 4-1BB[31]. However, we did

not observe notable differences in PD-1 and LAG3 expression between VHH2-28z versus

VHH2-BBz, perhaps due to short duration of mRNA CAR expression. For targeting solid

tumors, it might be advantageous to couple CARs with the CD28 costimulatory domain in an

mRNA format to achieve immediate and maximal tumor killing without the development of T

cell exhaustion, as outlined in a recent review[33].

VHH2-CART cells appeared to have an antigen threshold for activation and thus a

possible therapeutic window. Encouragingly, a phase 1 trial of a MET CAR using the same

scFv2 (5D5) demonstrated safety with mostly clinically manageable grade 1-2 cytokine

release syndrome (CRS)[45]. Given that CAR T cells generally require a high number of

target antigens to be present to become activated, therapeutic windows are likely present

between normal tissues and MET-overexpressed tumors, as shown here and illustrated

elsewhere[46]. One future direction includes exploring logic-gated CAR design to further

minimize on-target/off-tumor toxicity.

Despite the short duration of our mRNA CARs, some VHH2-treated mice displayed

remarkably prolonged tumor control until day 67, even after cessation of CAR T cell

injections on day 21. This prolonged tumor control was likely due to the ability of the high

avidity and polyfunctional VHH2-CART cells to kill most of the MET-positive cells, which

were presumably more proliferative than the MET-negative cells within the same tumor. One

can imagine a future strategy against solid tumors that would deploy potent effector like

VHH2-CART cells to target a surface antigen related to tumor aggressiveness (e.g. MET) to

achieve prolonged tumor control before bridging to other therapies.

The use of mRNA in the current study offered many advantages but also some limitations.

The main advantages included uniform CAR expression and high T-cell viability, which

facilitated construct comparisons in multiple assays. However, in some experiments, such as

the microwell co-culture and xenograft mouse models, it would have been beneficial to use a

persistent CAR system so that one could monitor long-term tumor control and T cell

functions.

In summary, we have shown the efficacy of a novel class of VHH-CART cells against

MET with promising in vitro attributes as well as strong tumor control in vivo. The VHH-

CART cell system warrants further preclinical study and development, including VHH

humanization and further construct optimization.

Declarations:

Data availability statement: All data relevant to the study are included in the article or

uploaded as supplementary information.

Ethics statements: Patient consent for publication: Not applicable.

Ethics approval: This study did not include human subjects. All animal studies were

approved by the Yale Institutional Animal Care and Use Committee.

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contributed to data figures and experiments. R.R. and N.C. contributed to molecular biology

and cloning of different CAR constructs. M.N. and A.A. contributed cell lines and reviewed

the manuscript. Y.L. and Q.Y. helped design the *in vivo* experiment, and Y.L. assisted in the

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 FIGURE LEGENDS

 Figure 1 VHH-CART with intermediate avidity showed the most potent killing.

(A) Schematic diagram of VHH-CAR construct. (B) Expression level of VHH-CAR by GFP.

Red peak = mock electroporated T cells. (C) Avidity curve of VHH-CART against MDA-MB-

231, with the % T cells bound to target cells at 1000 pN shown in (D). N = 4 technical

replicates; P values comparing avidity at 1000 pN were calculated using one-way ANOVA).

(E) AlphaFold3 modeling of VHH binding sites on MET. MET = cyan; HGFα chain = light

gray; HGFβ chain = dark gray. (F) VHH-CART cytotoxicity against MDA-MB-231 (n=4

technical replicates; P values by two-way ANOVA). (G) VHH1 and VHH2-CART against

A549, with tumor proliferation monitored in CellCyte (n=6 technical replicates; P values by

two-way ANOVA). Data shown are mean±SD; *$P<0.05$; **$P<0.01$; ***$P<0.001$;

****$P<0.0001$.

Figure 2: CD28 costimulatory domain conferred stronger VHH2-CAR activation. (A)

Expression level of mRNA VHH2-BBz and VHH2-28z in primary human T cells. (B) Avidity

assay using Lumicks z-Movi, comparison between VHH2-BBz and VHH2-28z (n = 3

technical replicates; two-way ANOVA). (C) Comparison of MDA-MB-231 killing between

VHH2-BBz and VHH2-28z (n=8 technical replicates, two-way ANOVA). (D) Intracellular

cytokine production analyzed by flow cytometry; cells harvested 16 hours after co-culture

with MDA-MB-231 in the presence of 2μM of the Golgi inhibitor monensin (n = 4 technical

replicates, two-way ANOVA). (E) Polyfunctioinal strength index (PSI) using IsoPlexis,

comparison between CD8+ VHH2-BBz and CD8+ VHH2-28z 16 hours after co-culture with

Karpas-422. Effector cytokines (Granzyme B, IFN-γ, MIP-1a, perforin, TNF-α, TNF-β);

Stimulatory cytokines (GM-CSF, IL-12, IL-15, IL-2, IL-21, IL-5, IL-7, IL-8, IL-9);

Chemoattractive cytokines (CCL-11, IP-10, MIP-1b, RANTES); Regulatory cytokines (IL-10,

IL-13, IL-22, IL-4, sCD137, sCD40L, TGF-b1); Inflammatory cytokines (IL-17A, IL-17F, IL-1b,

IL-6, MCP-1, MCP-4). (F-I) Microwell assay using TROVO, comparing single cell killing rate

(F) (n=3 technical replicates; two-tailed Student's *t*-test), T cell proliferation (G) (n=2

donorsx3 replicates; two-tailed Student's *t*-test), and tumor killing (H) (n=2 donors x 3

replicates each, two-tailed Student's *t*-test). (I) Representative images used to calculate

data shown in (G) and (H). Each row represents one microwell monitored over 4 days. Each

microwell is set up with E:T =20:10. T cell = red. *P<0.05; **P<0.01; ***P:<0.001;

****P:<0.0001.*

Figure 3: In vitro and in vivo efficacy of VHH2-CAR. (A) MET expression in tumor cell

lines. Red = IgG isotype control. (B) Cytotoxicity of VHH2-CART cells at different E:T ratios

(n=3 technical replicates; two-way ANOVA). (C) Scheme of in vivo experiment using the

LM2 tumor model. (D) BLI of tumor growth in vivo. PBS = 3 animals; Mock T = 2 animals;

VHH2-CART = 3 animals. *P* values were calculated using two-way ANOVA. (E) MET IHC,

10x objective on the left and 20x objective on the right. The boxed regions were magnified

and shown on the right. (F) CD3 IHC, 20x objective. *P<0.05; **P<0.01; ***P<0.001;

****P<0.0001.*

Figure 4: Antigen threshold for VHH2-CAR. (A) mRNA and western blot of MET

expression levels in a series of small cell lung cancer cell lines. (B and C) MET expression

by flow cytometry and cytotoxicity in NCI-H1341. N= 3 technical replicates in the cytotoxicity

assay; *P* values from two-way ANOVA. (D-E) MET expression by flow cytometry and

cytotoxicity in NCI-H146. N= 3 technical replicates; *P* values calculated using two-way

ANOVA. (F) Histogram of MET expression levels in different cell lines. (G) Cytotoxicity of

VHH2-CARs against the same cell lines as in (E). N= 3 technical replicates; *P* values

calculated using two-way ANOVA. *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001.*

Figure 5: VHH-CARs showed low tonic signaling. (A) Experimental design of CAR-Jurkat

assay. (B) Comparison of CD69 expression in CAR-Jurkat cells with varying levels of

antigen stimulation. (C) Comparison of CD69 expression in primary human T cells

electroporated to express CARs. E:T ratio was 1:1, and co-culture was incubated for 16

hours before staining for flow cytometry. (D-E) Cytotoxicity comparison between VHH2,

scFv1, and scFv2 using two different cell lines with different MET expression levels. (F)

Electrostatic surface charge of MET binders. Modeling was performed using PyMol. Blue =

more basic/positive charge; red = more acidic/negative charge; white = neutral. In

experiments shown in B-E, n=3 technical replicates, and P values were calculated with two-

way ANOVA. *$P<0.05$; **$P<0.01$; ***$P<0.001$; ****$P<0.0001$.

Figure 6: Avidity and kinetics comparisons of CARs. (A) Different binding epitopes

predicted by AlphaFold3 for VHH2, scFv1, and scFv2. (B) Expression of compared CARs.

(C) Avidity measurement by Lumicks z-Movi using MDA-MB-231 as target cells. N = 3

technical replicates, with P values from two-tailed Student's t-test. (D) Avidity measurement

against the 786-O cell line. N = 4-5 technical replicates; P values from two-tailed Student's t-

test. (E) Intracellular cytokine production by flow cytometry. Cells were stained before and

16-hours after stimulation by Karpas-422. N=3 technical replicates; P values from two-way

ANOVA. (F) Polyfunctional strength index by IsoPlexis. Effector cytokines (Granzyme B,

IFN-γ, MIP-1a, perforin, TNF-α, TNF-β); Stimulatory cytokines (GM-CSF, IL-12, IL-15, IL-2,

IL-21, IL-5, IL-7, IL-8, IL-9); Chemoattractive cytokines (CCL-11, IP-10, MIP-1b, RANTES);

Regulatory cytokines (IL-10, IL-13, IL-22, IL-4, sCD137, sCD40L, TGF-b1); Inflammatory

cytokines (IL-17A, IL-17F, IL-1b, IL-6, MCP-1, MCP-4). (G-I) Hydrogel-based microwell co-

culture assay by TROVO, showing single cell killing rate (G, 1:10 E:T), killing (H, 20:10 E:T),

and T cell proliferation (I, 20:10 E:T). N=3 technical replicates; P values using two-tailed

Student's t-test. (J) Representative images of microwell co-culture at 20:10 E:T. Each row

represents one microwell monitored over time. *$P<0.05$; **$P<0.01$; ***$P<0.001$; ****$P<0.0001$.

Figure 7: In vivo comparison between scFv2 and VHH2-CAR. (A) Experimental design of

in vivo efficacy. (B) Survival curve. (C) Tumor growth curve by BLI imaging. Each group = 7

mice; each line = 1 mouse. (D) Representative images of BLI. *P<0.05; **P<0.01;

***P<0.001; ****P:<0.0001.

SUPPLEMENTAL FIGURES:

Supplemental figure 1: mRNA CAR manufacturing through electroporation. (A) mRNA

CAR design. (B) RNA gel showing examples of successful mRNA synthesis and poly(A) tail

incorporation. (C) CAR expression was dose-dependent as shown by GFP. (D) Time course

of GFP decay after mRNA electroporation in T cells.

Supplemental figure 2: Intracellular cytokine assessment. (A) Gating strategy. (B)

Example flow cytometry plot of cytokine production.

Supplemental figure 3: Lack of significant exhaustion marker expression in VHH2-28z.

(A) Representative flow cytometry plot of PD-1 versus TIM3 and PD-1 versus LAG3

expression. CAR T cells were co-cultured with Karpas-422 for 48 hours before harvesting for

flow cytometry. (B) Comparison of PD-1 and LAG3 expression, and PD-1/TIM3

coexpression between mock T, VHH2-28z, and VHH2-BBz T cells. N=3 technical replicates;

P values from two-way ANOVA. **P<0.05; **P<0.01; ***P<0.001; ****P:<0.0001.*

Supplemental Figure 4: Karpas-422 cell line with MET and CD19 expression. (A) Flow

cytometry demonstrating expression of both antigens. Red curve = IgG isotype control. (B)

Confirmation of cytotoxicity of different MET CART cells and CD19-CART cells against

Karpas-422. N = 3 technical replicates, with *P* values calculated from two-tailed Student's *t*-

test. **P<0.05; **P<0.01; ***P<0.001; ****P:<0.0001.*

Supplemental Figure 5: Bulk cytokine secretion by ELISA between various CAR

constructs against MDA-MB-231. Panel A shows selected effector cytokines, while panel

B shows selected cytokines known to mediate CAR T-cell related toxicity and inflammatory

responses.

A

Anti-MET VHH

CD8H/TM

4-1BB

CD3ζ

P2A GFP

B

VHH1 97%
VHH2 97%
VHH3 96%
VHH4 95%
VHH5 77%

GFP →

■ = Mock electroporated

C

MDA-MB-231

% T cells bound to target

Force (pN)

- Mock T
- VHH1
- VHH2
- VHH3
- VHH4
- VHH5

D

% T cells bound at 1000pN

Mock VHH1 VHH2 VHH3 VHH4 VHH5

E

HGFβ   HGFα

VHH1   VHH2   VHH3   VHH4   VHH5

MET

F

MDA-MB-231

% specific lysis

Effector:Tumor ratio

- Mock T
- VHH1
- VHH2
- VHH3
- VHH4
- VHH5

G

A549 cell count (/mm²)

Hours

- Mock T
- VHH1-CART
- VHH2-CART

Chen, et al., Figure 1

Chen, et al., Figure 2

Chen, et al., Figure 3

Chen, et al., Figure 4

Chen, et al., Figure 5

Chen, et al., Figure 6

Chen, et al., Figure 7

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Chen, et al., Supplemental Figure 2

A

B

Chen, et al., Supplemental Figure 3

A

MET   CD19

Karpas-422

IgG   IgG

MET →   CD19 →

B

% specific lysis

ns

****

**

E:T = 5:1

Mock T   scFv1-CAR   CD19-CAR   VHH2-CAR

A

B

Chen, et al., Supplemental Figure 5