Metabolic priming of GD2 *TRAC*-CAR T cells during manufacturing promotes memory phenotypes while enhancing persistence

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ABSTRACT. Manufacturing Chimeric Antigen Receptor (CAR) T cell therapies is complex, with limited understanding of how media composition impact T-cell phenotypes. CRISPR/Cas9 ribonucleoproteins can precisely insert a CAR sequence while disrupting the endogenous T cell receptor alpha constant (*TRAC*) gene resulting in *TRAC*-CAR T cells with an enriched stem cell memory T-cell population, a process that could be further optimized through modifications to the media composition. In this study we generated anti-GD2 *TRAC*-CAR T cells using "metabolic priming" (MP), where the cells were activated in glucose/glutamine low media and then expanded in glucose/glutamine high media. T cell products were evaluated using spectral flow cytometry, metabolic assays, cytokine production, cytotoxicity assays *in vitro* and potency against human GD2+ xenograft neuroblastoma models *in vivo*. Compared to standard *TRAC*-CAR T cells, MP *TRAC*-CAR T cells showed less glycolysis, higher CCR7/CD62L expression, more bound NAD(P)H activity and reduced IFN-γ, IL-2, IP-10, IL-1β, IL-17, and TGFβ production at the end of manufacturing *ex vivo*, with increased central memory CAR T cells and better persistence observed *in vivo*. Metabolic priming with media during CAR T cell biomanufacturing can minimize glycolysis and enrich memory phenotypes *ex vivo*, which could lead to better responses against solid tumors *in vivo*.

INTRODUCTION

Chimeric antigen receptor (CAR) T cells have emerged as an exciting alternative to traditional cancer treatments for hematologic malignancies with six FDA-approved therapies for multiple myeloma, non-Hodgkin B-cell lymphomas and B cell acute lymphoblastic leukemia available to date. [1] In contrast, CAR T therapies for solid tumors have had limited clinical responses, due to a lack of persistence, limited homing to the tumor, and exhausted T-cell phenotypes. [2,3] Clinically, neuroblastoma initially demonstrated the potential efficacy of CAR T cells in treating solid tumors. However, a subsequent analysis revealed a modest 15% response rate with durable responses only achieved in patients whose GD2 CAR T cells persisted longer than 6 weeks after infusion and formed central memory T cells. [4,5] Recently, promising results for advanced neuroblastoma with a third-generation anti-GD2 CAR T cell were reported, with a 63% partial or complete response rate; however, event-free survival remained low at 26%. [6] The critical quality attributes that contribute to CAR T cell persistence and central memory formation in solid tumors remain largely unknown.

Manufacturing CAR T-cells to reach therapeutic cell quantities (~0.1-10 billions cells per patient) involves inducing cell proliferation *ex vivo* through activation with cross-linked antibodies for CD3 and CD28, and cytokine-enriched media.[7,8,9] *Ex vivo* culture of CAR T-cells has been previously shown to accelerate differentiation. [10–12] Limiting differentiation of these cells into terminal effector or exhausted phenotypes pre-infusion is a goal for the field, since increased stem cell memory fractions in the pre-infusion product have correlated with better cytotoxicity post-infusion, transition to a central memory state, and better persistence *in vivo*. [13,14] Enhanced stem cell or central memory phenotypes in CAR T products could be achieved by manipulating media, cytokines, or T-cell metabolism during manufacturing. Tailored media and IL-7/IL-15-based expansion have been found to preserve a stem cell memory profile. [15] Metabolic interventions that maintain oxidative phosphorylation (OXPHOS) and suppress glycolysis through metabolic engineering, [16–18] small molecule inhibitors, or glucose/glutamine deprivation [19–23] have been shown to enhance the cell persistence, potency, and memory formation of CAR T products. These strategies

have yet to be explored with CAR T cell products that have been genome-edited using electroporation (EP) in a virus-free manner.

T cells have classically been transduced with γ-retroviral or lentiviral vectors yielding stable but uncontrolled genomic integration of the CAR transgene with a constitutively active promoter, [24,25] which has been implicated in excessive T-cell differentiation.[26] CRISPR/Cas9 is an alternative approach that makes a double-stranded DNA break at a precise genomic locus where the DNA repair pathways can stably integrate the desired CAR transgene.[27–29] This genome editing strategy has been used to insert a CAR transgene upstream of the endogenous T-cell receptor alpha constant (*TRAC*) gene using homology-directed repair (HDR).[30–32] For current *TRAC* integration strategies, the CAR T cell products lack an intact T cell receptor (TCR) because of the precise genetic knockout of the TCR alpha chain. Relative to conventional viral CAR T products, these *TRAC*-CAR products have more controlled transgene copy numbers in the genome (1 or 2) with CAR transcription driven by the *TRAC* promoter, limited off-target effects, and higher fractions of stem-cell memory phenotypes. [33,34] A benchtop-scale CAR T process for inserting an anti-GD2 construct into the *TRAC* locus using electroporation of CRISPR/Cas9 ribonucleoproteins with PCR-based donor templates showed promising results in a $GD2^+$ human neuroblastoma xenograft model. [35] Many studies have optimized culture conditions for CAR T cells manufactured using viral vectors[15,19,36] , but it is unknown whether these culture changes will affect *TRAC*-CAR T cells in a similar manner.

In this study, we evaluated various culture conditions to develop a flexible, process using GMP-compatible reagents for producing TRAC-CAR T cells at scales suitable for clinical use. We focused on metabolic priming (MP), where T-cells are activated in TexMACS media and then switched post-electroporation to Immunocult XF. TexMACS media is associated with attenuated cellular activation, possibly due to its lower glucose/glutamine content relative to Immunocult XF.[36] (Pham et al, manuscript in preparation) The result is that MP *TRAC*-CAR T cells are less reliant on glycolysis, exhibit more stem cell memory phenotypes, and consume less glucose than their non-primed counterparts. Furthermore, these MP *TRAC*-CAR T cells can adopt a central memory phenotype following exposure to solid tumors in neuroblastoma xenograft

models. This biomanufacturing approach thus holds promise for generating cells with enhanced potency and longevity *in vivo*.

RESULTS

TRAC-CAR T cell manufacturing at scale

CAR T cells ideally should proliferate *ex vivo* to achieve clinically relevant yields, while maintaining a naïve, stem cell memory/central memory state to achieve persistence *in vivo.* [10,14,37] We first explored whether a nanoplasmid template could provide a facile method to scale-up production of the donor template for HDR to generate *TRAC*-CAR T cells **(Fig. 1A)**. We electroporated this template along with a CRISPR-Cas9 ribonucleoprotein (RNP) specific for the *TRAC* locus and cultured the cells for 7 days. Robust gene editing at clinical or benchtop scale was observed by flow cytometry, as greater than 90% of T cells lacked expression of the endogenous TCR given the CRISPR-mediated knockout of the *TRAC* gene (**Fig. 1B**) when compared to untransfected T-cells (Clinical: 98.2% (0.7) or Benchtop: 90.7% (1.0) versus Untransfected: 8.6% (5.1), $p < 0.001$ respectively). *TRAC*-CAR T cells were produced equally well at both scales with over 17% CAR positivity using the Lonza or Xenon electroporation systems (Clinical: 17.1% (0.4) or Benchtop: 22.2% (7) versus Untransfected: 0.02% (0.01), $p = 0.024$ and $p = 0.049$ respectively) **(Fig. 1C)**.

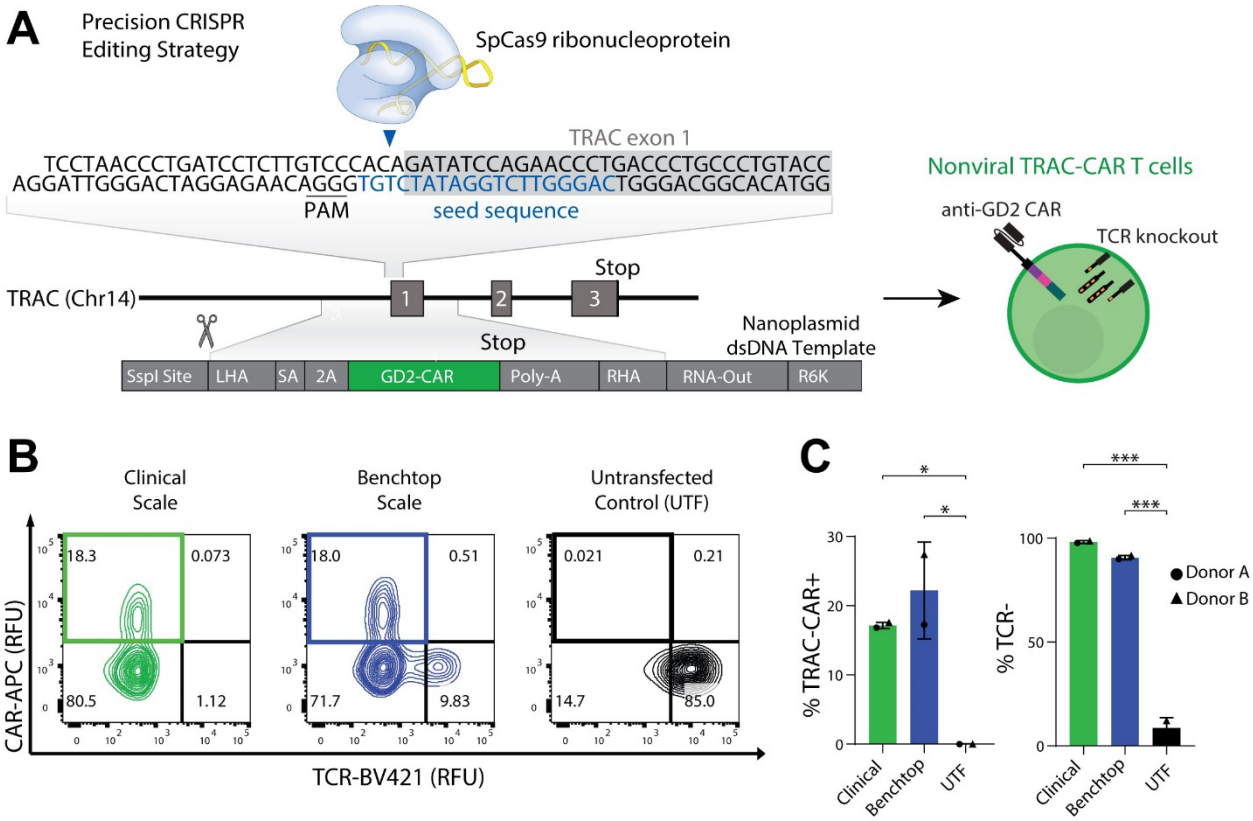

Figure 1. Manufacturing *TRAC*-CAR T cells at clinically relevant scales. (**A**) Schematic of non-viral CRISPR/Cas9 knock-in strategy with a nanoplasmid encoding the CAR. The CAR-containing nanoplasmid encodes for an anti-GD2 CAR under the control of the endogenous *TRAC* promoter. The CAR-containing nanoplasmid has an SSPI restriction site for linearization. (**B**) Representative flow cytometry plots of the relative GD2-CAR vs TCR expression of *TRAC*-CAR T Cells electroporated with SSPI-linearized nanoplasmid on the ThermoFisher Xenon or Lonza 4-D Nucleofector system and untransfected T-cells (Donor A shown). (**C**) Bar graphs comparing GD2 knock-in rates and TCR$^-$ percentages of *TRAC*-CAR T cells electroporated on the Xenon or Lonza systems and untransfected T-cells. 2 donors, $N_{Clinical}=N_{Benchtop}=N_{Untransfected} = 2$. SA, splice acceptor; 2A, cleavage peptide; LHA, left homology arm; RHA, right homology arm; Poly-A, rabbit β-globin polyA terminator; virus-free CRISPR; CAR, chimeric antigen receptor; *TRAC*, T-cell receptor alpha constant gene; RNP, ribonucleoprotein; PAM, protospacer adjacent motif; TCR, T-cell receptor. Error bars represent mean and standard deviation. Statistical significance was determined with a one-way ANOVA using Dunnett's T3 test for multiple comparisons (C); *$p<0.05$; ***$p<0.001$

Metabolic priming to enrich for stem cell memory

Generally, CAR T cell production uses a singular media source and cytokine cocktail throughout manufacturing to expand T cells into clinically relevant numbers *ex vivo*. Activation and expansion of *TRAC*-CAR T cells has previously been performed using Immunocult XF medium supplemented with IL-2,[35] generating stem cell memory T cells with high expression of CD45RA, CD62L, and CCR7 and CAR knock-in rates between 15-34%. [13,38] We sought to optimize culture conditions that could further increase the proportion of stem cell memory *TRAC*-CAR T-cells by manufacturing cells in two media conditions **(Fig. 2A)** using reagents produced via Good Manufacturing Practice (GMP) at a clinically relevant scale: (*1*) standard Immunocult XF Media [36] with IL-2 for 10 days ("Control cells"); or (*2*) a transient metabolic priming phase, where cells were activated in TexMACS with IL-7/IL-15 [15,39] before electroporation (EP) and then expanded in Immunocult XF with IL-7/IL-15 for 7 days post-EP ("MP cells").

Memory T cells primarily use oxidative phosphorylation and fatty acid oxidation for long-term survival, whereas effector T cells rely on glycolysis for rapid proliferation and immediate immune response. In cell cultures, a lower glucose consumption and lactate secretion may indicate a higher proportion of stem cell memory cells (**Fig. 2B**).[16–18] We measured the lactate and glucose concentrations of MP and Control *TRAC*-CAR T cells immediately after activation on day 3 and on day 10 of manufacturing to assess their stem cell memory properties. Post-activation MP *TRAC*-CAR T cells produced less lactate (MP: 4.2 mM (2.2) versus Control: 9.2 mM (0.3), $p = 0.002$) and consumed less glucose (MP: 3.63 mM (2.4) versus Control: 13.2 mM (0.5), $p < 0.001$) despite equal fold expansion during activation (MP: 1.1 (0.3) versus Control: 1.2 (0.02)) (**Fig. S1)**. On day 10 MP *TRAC*-CAR T cells produced 3.4-fold less lactate (MP: 3.9 mM (0.4) versus Control: 13.2 mM (0.6), $p < 0.001$) and consumed 1.9-fold less glucose (MP: 5.6 mM (0.2) versus Control: 10.6 mM (0.7), $p < 0.001$) than Control *TRAC*-CAR T cells during expansion in G-Rex6M plates despite having similar yields of cells by Day 10 (MP: 8.7 (1.6) versus Control: 10 (2.7)) (**Fig. 2C**), indicating that priming does not affect cell yield in this process. We also demonstrated the importance of priming in TexMACS for three days compared to manufacturing *TRAC*-CAR T cells with TexMACS only

(3-day versus 10-day MP) as three days of priming lowered glucose consumption and lactate production compared to the extended 10-day priming (**Fig. 2D**).

To specifically analyze the phenotypes of the CAR-positive cells in the cell product on day 10, we stained for surface markers of T-cell differentiation and memory phenotypes using a spectral flow cytometry panel and analyzed live CAR^+/TCR^- cells (**Fig. S2).** We classified T cell phenotypes by classic definitions: T_{SCM} (stem cell memory), T_{CM} (central memory), T_{EM} (effector memory) and T_{EFF} (effector). A stem cell memory state is often defined by the expression of surface markers such as CD45RA, CD62L, and CCR7 [13,40] an oxidative versus a glycolytic metabolism, commonly seen in activated effector T-cells, [41,42] and lower glucose consumption. [23,43,44] (**Fig. 2B**). We defined T_{SCM} *TRAC*-CAR T cells as $CCR7^+/CD62L^+$ which indicates increased capacity for lymphoid homing.[45,46] *TRAC*-CAR T cells grown in Immunocult XF are often CD45RA/CD45RO double positive, likely reflecting a transitional state that cannot be assigned to canonical memory subsets.[33,35] This transitional phenotype is present in both MP and Control *TRAC*-CAR T cells **(Fig. S3)**. We found that MP *TRAC*-CAR T cells produced 2.3-fold more $CD62L^+/CCR7^+$ CAR^+ T-cells than Control *TRAC*-CAR T cells (MP: 46.9% (12.3) versus Control: 23.9% (7.0), $p = 0.028$) **(Fig. 2E, F)**. We also observed no significant impacts of priming on CD8 or CD4 expression **(Fig. S3).**

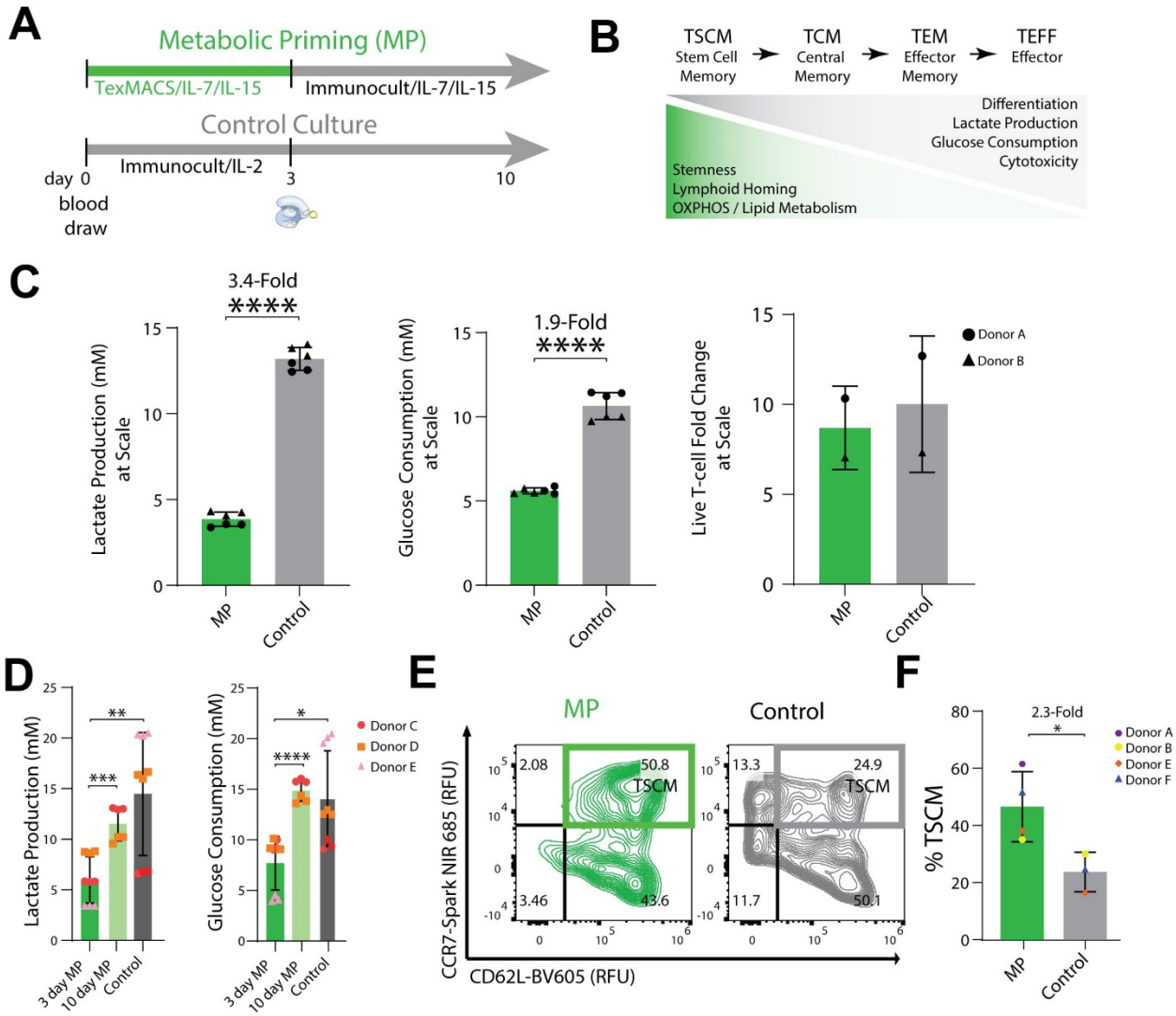

Figure 2. Metabolically primed *TRAC*-CAR T cells produce stem cell memory phenotypes. (**A**) Manufacturing timeline for *TRAC*-CAR T cells: metabolically primed (MP) *TRAC*-CAR T cells are cultured in TexMACS medium for three days during activation and, then Immunocult XF medium supplemented with IL-7/IL-15 for seven days during expansion. Control *TRAC*-CAR T cells are cultured in only Immunocult XF medium supplemented with IL-2 during activation and expansion. **(B)** Schematic of the definition of CAR T cell phenotypes: T_{SCM} (stem cell memory), T_{CM} (central memory), T_{EM} (effector memory), T_{EFF} (effector) as defined by their inherent properties. **(C)** Bar graphs of the lactate production, glucose consumption and live T-cell fold-change of MP or Control *TRAC*-CAR T cells during expansion in G-Rex6M plates. 2 donors, (lactate/glucose) $N_{MP}=N_{Control} = 6$; (proliferation) $N_{MP}=N_{Control} = 2$ **(D)** Bar graphs of lactate production and glucose consumption of *TRAC*-CAR T cells undergoing 3- or 10-day metabolic priming and Control culture during day 8-10 of expansion. (3 Day MP: 6.0 mM (2.3) versus 10 Day MP: 11.5 mM (1.7) or Control: 14.5 (6.0), $p = 0.008$ and $p < 0.001$ respectively) and glucose consumption (3 Day MP: 7.7 mM (2.5) versus 10 Day MP: 14.9 mM (1.0) or Control: 14.1 mM (4.5), $p = 0.011$ and $p < 0.001$ respectively). 3 donors, $N_{3dayMP} = 6$, $N_{10dayMP} = 9$, $N_{Control} = 9$. **(E)** Representative contour plots of CD62L/CCR7 co-expression for CAR^+/TCR^- MP and Control *TRAC*-CAR T cells for same conditions. CD62L/CCR7 double positive cells represent a stem cell memory population (T_{Scm}) (Donor F shown). (**F**) Bar graph depicting the CD62L/CCR7 double positive population in CAR^+ T-cells for all conditions. 4 donors, $N_{MP} = 4$, $N_{Control} = 3$. Error bars represent standard deviation. Statistical significance was determined with a paired t-test (C), Brown-Forsythe and Welch ANOVA using Dunnett's T3 test for multiple comparisons (D), and Welch's t-test (F); *p<0.05; **p<0.01; ***p<0.001; ****p<0.0001.

Priming lowers glycolysis and effector phenotypes

To further characterize metabolism, we harvested cells at the on Day 10 of manufacturing for use in a Seahorse assay to analyze oxygen consumption and extracellular acidification rates and for mitochondrial staining for flow cytometry. MP *TRAC*-CAR T cells had lower rates of ECAR (extracellular acidification) and OCR (oxygen consumption) than Control *TRAC*-CAR T cells, indicating lower rates of both glycolysis and overall oxygen consumption **(Fig. 3A)**. Lower basal respiration (MP: 32 pmol/min (15) versus Control: 180 pmol/min (140), $p = 0.02$), maximal respiration (MP: 72 pmol/min (41) versus Control: 298 pmol/min (74), $p = 0.002$), and spare respiratory capacity (MP: 40 pmol/min (27) versus Control: 118 pmol/min (66), $p = 0.03$) were seen in MP compared to Control *TRAC*-CAR T cells **(Fig. 3A)**. Additionally, MP *TRAC*-CAR T cells had 6% higher normalized mitochondrial mass (MP: 2.3 (0.4) versus Control: 2.2 (0.4) , $p < 0.001$, d = 0.33) and 11% higher membrane potential (MP: 1.9 (0.2) versus Control: 1.7 (0.3) , $p < 0.001$, d = 0.64) than Control *TRAC*-CAR T cells, further supporting an oxidative phenotype (**Fig. 3B)**. A 27% reduction in granularity (MP: 246 (76) versus Control: 336 (98), $p < 0.001$, d = 1.02) and 14% lower cell size (MP: 310 (52) versus Control: 360 (78), $p < 0.001$, d = 0.74) indicates that MP *TRAC*-CAR T cells may be in a less cytotoxic state[47] after manufacturing than Control *TRAC*-CAR T cells (**Fig. 3B**).

To resolve metabolism at single-cell resolution and assess heterogeneity, we also performed fluorescence lifetime imaging of *TRAC*-CAR T cells after manufacturing. We specifically measured autofluorescence lifetimes of NAD(P)H and FAD and report the NAD(P)H mean fluorescence lifetime (NAD(P)H τ_m) and free NAD(P)H fraction (NAD(P)H α_1) of CAR^+ *TRAC*-CAR T cells, which reflect NAD(P)H binding activity. MP *TRAC*-CAR T cells had higher NAD(P)H τ_m (MP: 1000 ps (93) versus Control: 942 ps (110), $p = 0.003$) and lower NAD(P)H α_1 (MP: 72 % (4) versus Control: 75% (4), $p < 0.001$) than Control-*TRAC*-CAR T cells indicating a higher proportion of bound NAD(P)H (**Fig. 3C**) in MP *TRAC*-CAR T cells. These label-free, single cell analyses confirm the presence of more primed cells with increased NAD(P)H binding activity within the MP *TRAC*-CAR T cell products and are consistent with lifetime imaging of similar *TRAC*-CAR products (Pham et al, manuscript in preparation).

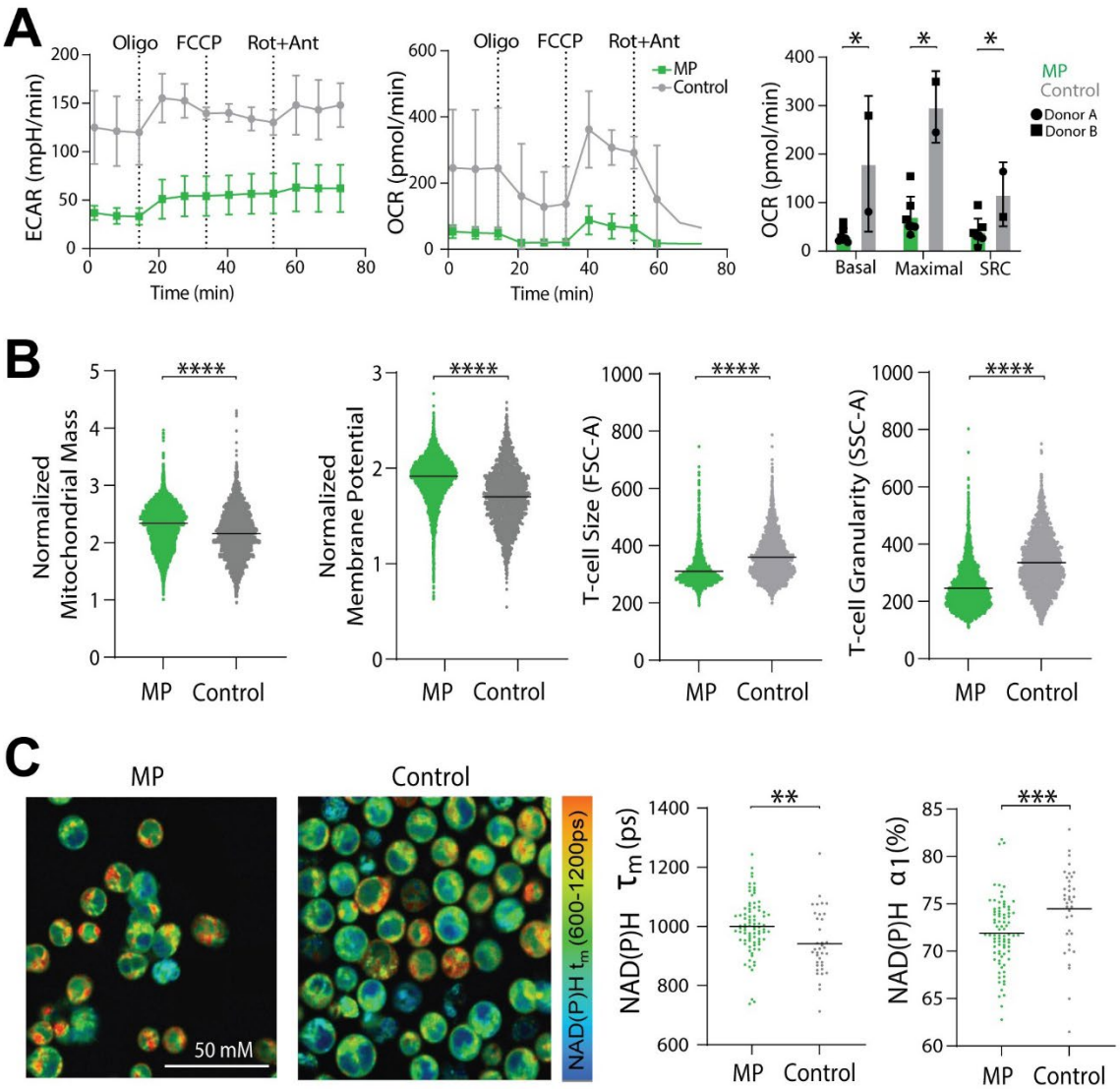

Figure 3. MP *TRAC*-CAR T cells are less glycolytic and have increased mitochondrial mass. (A) ECAR, OCR, basal/maximal respiration rates and spare respiratory capacity for MP and Control *TRAC*-CAR T cells measured by Seahorse. Oligomycin (2.5 μM), FCCP (1 μM), rotenone/antimycin A (0.5 μM). 2 donors, N_{MP} = 7, $N_{Control}$ = 2. **(B)** Dot plots for normalized mitochondrial mass (MitoTracker Green intensity divided by FSC-A) normalized mitochondrial membrane potential (TMRE dye intensity divided by FSC-A), cell size (FSC-A), and granularity (SSC-A) for CAR^+ MP and Control *TRAC*-CAR T cells. 2 donors, N_{MP} = 4264, $N_{Control}$ = 2439. **(C)** Images and bar graphs of NAD(P)H mean lifetime (NAD(P)H τ_m) and free NAD(P)H fraction (NAD(P)H α_1) of CAR^+ MP and Control *TRAC*-CAR T cells as measured by fluorescence lifetime imaging. 2 donors, N_{MP} = 84, $N_{Control}$ = 37 OCR, oxygen consumption rate; ECAR, extracellular acidification rate; SSC-A, side scatter area; FSC-A, forward scatter area; TMRE, tetramethylrhodamine ethyl ester perchlorate. Error bars represent standard deviation. Statistical significance was determined with unpaired t-tests; *p<0.05; **p<0.01; ***p<0.001; ****p<0.0001.

High potency of MP *TRAC*-CAR T cell products

To assess the potency of the MP *TRAC*-CAR T cells, we measured cytotoxicity and cytokine production after co-culture with the $GD2^+$ neuroblastoma cell line, CHLA20. These target cells were seeded at various effector:target (E:T) ratios into 24 or 96-well plates and grown for 24 hours, after which *TRAC*-CAR T cell products were added. The supernatant was taken at 24 hours, and the co-culture was imaged continuously for 48 hours on the Incucyte platform **(Fig. 4A).** MP and Control *TRAC*-CAR T cells achieved similar extents of cytotoxicity for 5:1 and 2.5:1 E:T ratios **(Fig. 4B)**. After 24 hours of co-culture, MP *TRAC*-CAR T cells lysed fewer cancer cells than Control *TRAC*-CAR T cells at 2.5:1 (MP: -26% (38.1) versus -70.2% (12.1), $p = 0.041$) and 1:1 (MP: 86.5% (38.8) versus Control: -2.5% (29.3), $p = 0.011$) ratios **(Fig. 4C**), but had similar levels of cytotoxicity at the 5:1 ratio. In terms of cytokine production, soluble IFN-γ (MP: 3151 pg/mL (4119) versus Control: 38453 pg/mL (16037), p = 0.0045), IL-2 (MP: 88 pg/mL (121) versus Control: 496 pg/mL (229), $p = 0.0195$), IP-10 (MP: 254 pg/mL (257) versus Control: 17853 pg/mL (8494), p = 0.004), IL-1β (MP: 185 pg/mL (358) versus Control: 16882 pg/mL (14578), $p = 0.0372$), IL-17 (MP: 81 pg/mL (93) versus Control: 664 pg/mL (460), p = 0.0323), and TGFβ (MP: 6.4 pg/mL (13.7) versus Control: 51.9 pg/mL (32.2), $p = 0.0338$) levels produced by MP *TRAC*-CAR T cells in the media were significantly lower than Control *TRAC*-CAR T cells while all other measured cytokines had no differences **(Fig. 4D-F)**. Compared to Control *TRAC*-CAR T cells, MP *TRAC*-CAR T cells have comparable but slower cytotoxic activity with overall lower cytokine production immediately following antigen stimulation *in vitro.* These characteristics have been observed in less differentiated cells, notably T_{SCM} cells. [13,44]

To assess the impact of these critical quality attributes on potency *in vivo*, *TRAC*-CAR T cells of both groups were infused into a xenograft NSG mouse model of neuroblastoma. There was similar tumor regression across the two groups **(Fig. S4)**, indicating comparable *in vivo* potency of cells from both culture conditions. Despite lower levels of initial cytotoxicity and cytokine release *in vitro*, MP *TRAC*-CAR T cells demonstrate high potency against solid tumors *in vivo.* Because they were less active in culture, it was

unclear if these attributes would make them less prone to exhaustion and exhibit better persistence and central memory formation *in vivo.*

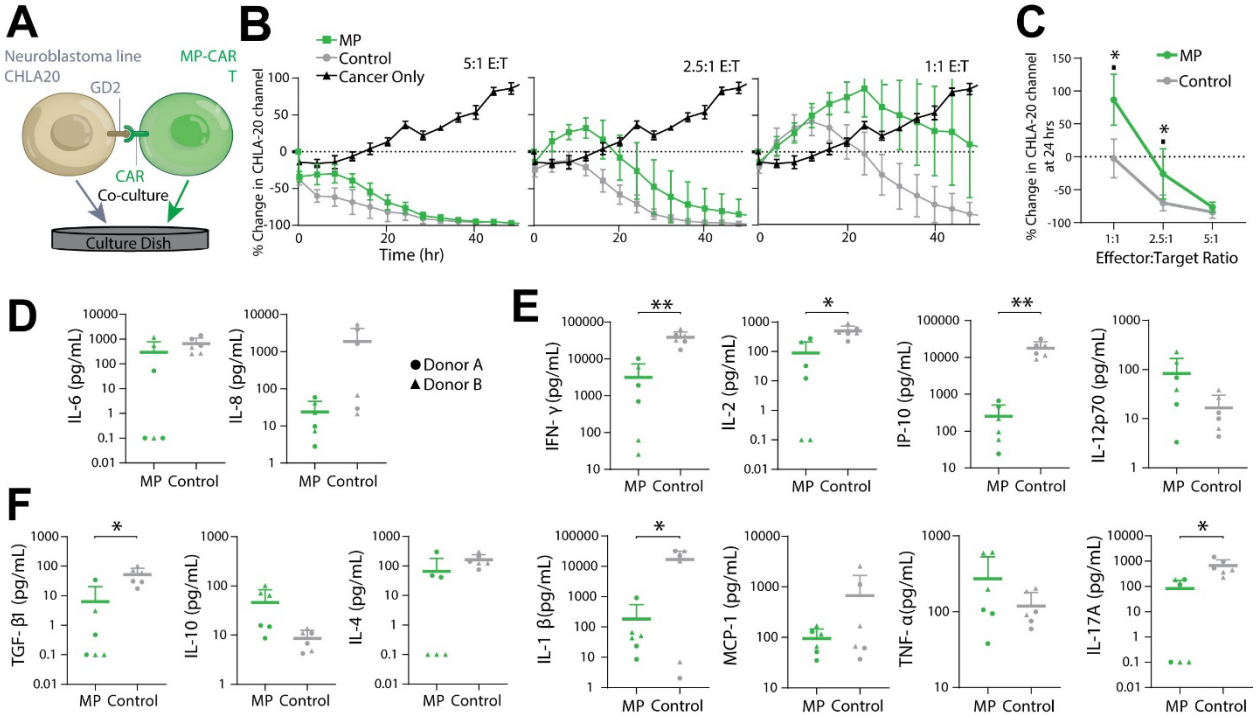

Figure 4. MP *TRAC*-CAR T cells have reduced cytokine production but are equipotent *in vitro* against GD2$^+$ neuroblastoma. (A) GD2$^+$ neuroblastoma CHLA-20 cells were plated in 24 or 96 well plates 24 hrs before *TRAC*-CAR T cell addition. The supernatant was analyzed for cytokine secretion after 24 hours, and potency was measured continuously for up to 48 hours. **(B)** Percentage change in GFP fluorescence from GD2$^+$ CHLA-20 neuroblastoma cells versus time in cancer/MP or Control *TRAC*-CAR T cell co-cultures for E:T ratios of 5:1, 2.5:1, or 1:1. **(C)** The percentage change in GFP signal at 24 hours versus E:T ratio is shown for MP or Control *TRAC*-CAR T cells. Co-culture supernatant was analyzed using the LegendPlex Human Essential Immune Response (BioLegend) assay. **(D)** pleiotropic, **(E)** Pro-inflammatory, and **(F)** anti-inflammatory cytokines. The histograms depict the relative levels of secreted cytokines normalized to live T-cell count after co-culture on log scale (pg/mL per 1e6 T-cells). GFP, green fluorescent protein. 2 donors, $N_{MP} = 6$, $N_{Control} = 6$. Error bars represent standard deviation. Statistical significance was determined with paired t-tests; *$p<0.05$; **$p<0.01$.

Enhanced central memory and persistence *in vivo*

To assess memory phenotypes and persistence of MP *TRAC*-CAR T cells *in vivo*, we injected T cell products into a xenograft NSG mouse model for neuroblastoma **(Fig 5A).** Groups included MP *TRAC*-CAR or Control *TRAC*-CAR cells and No CAR Control cells, which are *TRAC*-T cells expressing an mCherry reporter gene instead of CAR and cultured in the standard "Control" conditions. On day 19 post-injection, we isolated splenocytes, and stained samples for spectral flow cytometry of memory, activation, and exhaustion markers (**Fig. S5**). We found significantly higher amounts of human CD5/CD45$^+$ (MP: 2025 cells (3433), Control: 244 cells (487), No CAR Ctrl: 2055 (2841), p (MP vs Control) = 0.0423) amounts of lymphocytes in spleens from mice injected with MP *TRAC*-CAR T cells than Control *TRAC*-CAR T cells **(Fig 5B),** indicating improved T cell persistence *in vivo* for MP products. Among transgene$^+$/TCR$^-$ cells we found no significant differences in CD8 or CD4 expression with nearly 90% of cells being cytotoxic T lymphocytes across conditions (**Fig. S5**).

We assessed splenic lymphocytes according to T cell differentiation and exhaustion using six markers: CD45RA, CD45RO, CD62L, CCR7, LAG3, and TIGIT. MP or Control *TRAC*-CAR T cells separated from each other in a reduced two-dimensional Uniform Manifold Approximation and Projection (UMAP) space (**Fig. 5C**) while no CAR Control cells spanned the entire space more uniformly. The vertical UMAP2 axis separated lymphocytes by differentiation status, with central memory (T_{CM}) (CD45RO$^+$/CD45RA$^-$) and effector (T_{EFF}) (CD45RA$^+$/CD45RO$^-$) T-cells on opposing ends of the axis (**Fig. 5C-D**). This differentiation *in vivo* is expected as T_{SCM} will differentiate after antigen exposure [48,49]. T_{CM} cells showed less LAG3 but more TIGIT expression than T_{EFF} **(Fig. S6)**. Higher percentages of T_{CM} were found in the spleens of mice treated with MP *TRAC*-CAR T cells than with Control *TRAC*-CAR T cells (MP: 28% (16), Control: 5% (4), No CAR Ctrl: 18% (21), p (MP vs Control) = 0.0025) (**Fig. 5D, E**), indicating improved central memory MP *TRAC*-CAR T cell persistence *in vivo*. In contrast, there were more T_{EFF} cells in spleens from mice treated with Control *TRAC*-CAR T cells (MP: 35% (18), Control: 83% (7), No CAR Ctrl: 54% (23), p (MP

vs Control) < 0.001) **(Fig. 5D, E)**. Overall, these data indicate that MP *TRAC*-CAR T cells show better persistence *in vivo*, with enrichment of T_{CM} cells noted in the spleen.

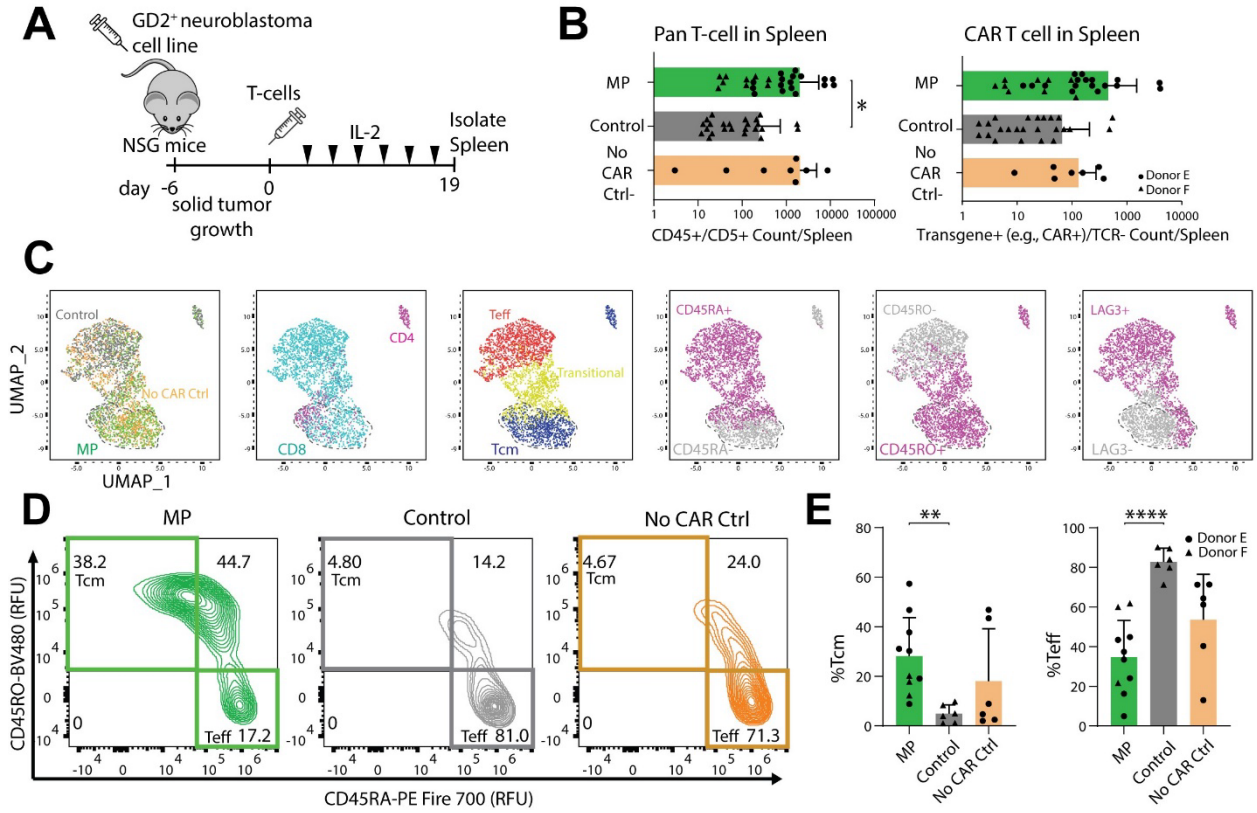

Figure 5. MP *TRAC*-CAR T cells display a central memory phenotype and better persistence *in vivo* after treatment of GD2+ neuroblastoma. (A) NSG™ mice were injected with CHLA-20 cells 1 week before *TRAC*-CAR T injection upon which mice were treated with 3 million CAR$^+$ cells by tail vein injection. IVIS imaging was performed every 3-4 days with IL-2 supplementation by tail vein. Mouse spleens were isolated on Day 19 post-injection and stained to immunophenotype human T lymphocyte via flow cytometry. **(B)** Bar graphs depicting the number of CD5/CD45$^+$ events from isolated mouse spleens (left) and CAR$^+$ or mCherry$^+$/TCR$^-$ lymphocytes within that population for mice treated with MP *TRAC*-CAR T, Control *TRAC*-CAR T, or no CAR Control (mCherry) cells (right) on log scale. 2 donors, N_{MP} = 26, $N_{Control}$ = 24, $N_{NoCARCtrl}$ = 8. **(C)** Marker expression UMAPs of MP, Control *TRAC*-CAR T cells, or No CAR Control T-cells. These maps were generated using flow cytometry to track CD45RA, CD45RO, CD62L, CCR7, LAG3, and TIGIT levels. Dot plots separate cells by condition, CD4/CD8 levels, memory or effector status (CD45RA$^-$/CD45RO$^+$ (Central memory (T_{cm})), CD45RA$^+$/CD45RO$^-$ (Effector (T_{eff})), or CD45RA$^+$/CD45RO$^+$(transitional T-cells)), CD45RO, CD45RA, or LAG3 levels. **(D)** Representative contour plots of the levels of CD45RA versus CD45RO separate MP *TRAC*-CAR T (Donor E), Control *TRAC*-CAR T (Donor F), and no CAR Control cells (Donor E) by central memory or effector status. **(E)** Bar graphs show the relative expression of cell populations for mice with greater than 20 transgene$^+$/TCR$^-$ events in the spleen: T_{cm} or T_{eff}. 2 donors, N_{MP} = 10, $N_{Control}$ = 6, $N_{NoCARCtrl}$ = 6. Error bars represent standard deviation. Statistical significance was determined with Brown-Forsythe and Welch ANOVA tests using Dunnett's T3 test for multiple comparisons; *p<0.05; **p<0.01; ****p<0.0001.

DISCUSSION

We improved upon the manufacturing process of an anti-GD2 *TRAC*-CAR T cell [35] by adapting it for higher scales and enriching for desirable stem cell/central memory and metabolic phenotypes. Via priming T-cells in media with lower concentration of glucose, glutamine and potentially other key nutrients, we subsequently reprogrammed T cell metabolism pre- and post-EP during *ex vivo* expansion. Our process used GMP-compatible reagents and can accommodate the electroporation of 100 million T-cells in a 'single-shot' cartridge and up to 25 billion in a 'multi-shot' cartridge. [50] We used CRISPR/Cas9 to insert a linearized nanoplasmid construct at the *TRAC* locus via HDR, a process that is more scalable than PCR-generated HDR templates due to the facile nanoplasmid amplification within recombinant bacteria. [51,52] Priming T-cells with TexMACS supplemented with IL-7/IL-15 pre-EP to briefly slow glycolysis and proliferation followed by expansion in Immunocult XF with IL-7/IL-15 post-EP produced a final MP *TRAC*-CAR T product enriched for stem cell memory T cells with a unique metabolic profile that showed comparable potency to *TRAC*-CAR T generated under a single media source, but better persistence and higher enrichment of central memory T cells *in vivo*, an ongoing goal of the field of CAR T therapy for solid tumors.

Compared to Control cells, MP *TRAC*-CAR T cells had higher populations of $CD62L^+/CCR7^+$ cells, lower lactate production, glucose consumption, and ECAR post-manufacturing, making them distinctly more T_{SCM}-like[13,16,44] (**Fig. 2C, 2F, 3A**). Additionally, MP *TRAC*-CAR T cells had higher mitochondrial membrane potential and mass when normalized to cell size **(Fig. 3B)** which is often seen in memory cells as they switch to OXPHOS and fatty acid oxidation metabolism. [41] Surprisingly, these cells also had lower rates of oxygen consumption (**Fig 3A**): this finding is consistent with another study on the effects of intermittent fasting *in vivo* in murine bone-marrow T-cells where a similarly low ECAR and OCR were observed along with reduced mTOR activity. [53,54] The reduced OCR and ECAR in MP *TRAC*-CAR T cells could be due to reduced mTOR signaling, considering that mTOR is upregulated in effector T-cells [55] and

MP *TRAC*-CAR T cells were less cytotoxic than Control *TRAC*-CAR T s *in vitro* **(Fig. 4),** but further studies of the role of mTOR within MP *TRAC*-CAR T cells are needed.

The lower OCR, ECAR, and glucose consumption in MP *TRAC*-CAR T cells may have also reduced granzyme production, mediators of cytotoxic activity, especially given the lower granularity (side scatter by flow cytometry) in MP *TRAC*-CAR T cells. However, this reduced granularity *ex vivo* is overcome *in vivo* as both culture conditions produced *TRAC*-CAR T cells that can successfully suppress tumor growth in a xenograft mouse model **(Fig. S4)**. An advantage of MP *TRAC*-CAR T cells was the generation of more central memory cells compared to Control *TRAC*-CAR T cells *in vivo* **(Fig. 5),** with better persistence in the periphery (spleen). Given this known limitation for retrovirally-transduced anti-GD2 CAR T cells generated with standard biomanufacturing techniques to treat neuroblastoma [5], clinical trials with virus-free GD2 *TRAC*-CAR T cells with a MP biomanufacturing process will be needed to determine if enhanced persistence and central memory can be achieved in patients.

Our novel metabolic priming process demonstrates how modulating media composition and cytokines of *TRAC*-CAR T cells pre- and post-EP influences CAR T-cell phenotype, metabolism and persistence post-infusion. Additional strategies will need to be explored to determine if these effects can be enhanced even further. For example, treating T-cells during activation with N-acetylcysteine, a well-known antioxidant, can promote expression of stem cell memory markers and lower glycolysis. [23] T cell metabolism could be manipulated using genetic engineering [32], as *PRODH2* overexpression can shift cells to an OXPHOS-based metabolism with more active mitochondria and an increased percentage of $CD45RA^{+}/CD62L^{-}$ T-cells post-tumor challenge.[32] Transient glucose restriction and treatment of T-cells with the glutamine inhibitor DON have also both been shown to increase T_{SCM} surface marker expression and lower glycolysis. Also, priming *TRAC*-CAR T cells with different cytokines could produce similar stem cell memory phenotypes with enhanced *in vivo* performance (Pham et al, manuscript in preparation). Advances to *TRAC*-CAR T cell biomanufacturing has the capacity to produce cell therapies with favorable biologic characteristics that could potentially improve CAR T cell responses against solid tumors.

MATERIALS AND METHODS

Cell Lines: $GD2^+$ human neuroblastoma CHLA-20 cells were gifted by Dr. Mario Otto (University of Wisconsin-Madison). These cells were cultured in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% fetal bovine serum (FBS) (Gibco) and 1% penicillin-streptomycin (P/S) (Gibco). AkaLucGFP CHLA-20 cells were created through viral transduction by Dr. James Thomson (Morgridge Institute for Research). In short, Phoenix cells (ATCC) were grown in DMEM with 10% FBS and 1% P/S and selected with 1 ug/mL of diphtheria toxin (Cayman Biologics) and 300 ug/mL hygromycin (ThermoFisher Scientific). Selection for transgene-positive cells was confirmed by flow cytometry for mouse Lyt2 expression as a reporter gene (Biolegend). 3T3 cells were grown in DMEM with 10% FBS and 1% P/S. Cell authentication was performed using short tandem repeat analysis (Idexx BioAnalytics, Westbrook, Maine, USA) and per ATCC guidelines using cell morphology, growth curves, and *Mycoplasma* testing within 6 months using the MycoStrip Mycoplasma Detection Kit (Invitrogen, Waltham, MA). Cell lines were maintained in culture at 37°C in 5% CO_2.

Plasmid Constructs: A GD2-CAR plasmid construct encoding a 2A.14G2A-CD28-OX40-CD3ζ CAR gifted by Malcolm Brenner (Baylor College of Medicine) was synthesized and the sequence verified (GenScript). A separate no CAR Control (mCherry) construct was contained in an H2B-mCherry sequence in place of the GD2-CAR and designed, synthesized, and sequenced the same as the GD2-CAR plasmid (Genscript). Both transgenes were flanked by 500 bp homology arms and cloned into a pUC57 backbone, grown in 5-alpha competent *Escherichia coli* (NEB) and purified using the PureYield MidiPrep System (Promega).

Sanger Sequencing: The GD2-CAR and no CAR Control had their sequences verified via Sanger Sequencing at the UW-Biotechnology Center. Briefly, each construct was separated into 20 uL aliquots with appropriate primers for sequencing found in Supplementary Table 1. PCR was performed, the amplicons separated by gel electrophoresis, and peaks analyzed for sequence identity.

Nanoplasmid Production: Linear dsDNA templates were made via PCR amplification was done using the GD2-CAR or no CAR Control plasmid as a template using Q5 Hot Start Polymerase in 50 uL reaction volumes. The cycling parameters were 98°C for 10 s, 65°C for 20 s, and 72°C for 90s, for a total of 35 cycles. These reactions were then pooled into 600 uL reactions for Solid Phase Reversible Immobilization (SPRI) cleanup (1x) using AMPure XP beads according to the manufacturer's instructions and eluted at 2 mg/mL in DNAase free water. The linear products were shipped to Aldevron (Fargo, ND) where they were blunt cloned into a nanoplasmid backbone consisting of two components: R6K origin of replication and an anti-levansucrase RNA sequence that enables antibiotic free selection. The RNA-OUT platform prevents the expression of SacB which prevents toxicity from Levansucrase as well as transgene silencing after genomic insertion. [56] Nanoplasmid DNA was manufactured on-site at Aldevron and resuspended in DNAase free water a 2 mg/mL. Nanoplasmid sequences can be found in Supplementary Table 2. Primer sequences are shown in Supplementary Table 3.

Nanoplasmid Linearization by Restriction Digest: To linearize nanoplasmid for use as a dsDNA HDR template, a restriction digest of the nanoplasmid constructs using SSPI-HF (New England Biolabs) was performed. Four restriction digest batch reactions in 1.5 mL Eppendorf tubes (50 uL nanoplasmid, 125 uL CutSmart buffer, 25 uL SSPI-HF enzyme, and 1050 uL DNAase-free water for 1250 uL total) were aliquoted (50 uL into PCR tubes for a total of 96 reactions). These were incubated in a thermocycler at 37°C for 15-60 min and heat inactivated at 65°C for 20 min according to the manufacturer's instructions. Gel electrophoresis was then performed on the finished product to assess if proper cutting took place, followed by SPRI cleanups to purify and concentrate the material to 2 mg/mL. PCR reactions were pooled into eight 1.5 mL Eppendorf tubes (600 uL) with an equal volume of SPRI beads that incubated for 5 minutes at room temperature. The product was washed twice with 70% ethanol and eluted in 75 uL of DNase-free water and pooled into one tube (600 uL). This product was subject to a second round of cleanups and was eluted in 30 uL of water. DNA was quantified using the NanoDrop2000 Qubit double-strand DNA (dsDNA) Broad Range (BR) Assay (ThermoFisher Scientific) and diluted to 2 mg/mL according to Qubit measurements.

Isolation of T-cells from Peripheral Blood: Peripheral blood was drawn from healthy donors using an IRB-approved protocol (2018-0103). Blood was collected into Lithium Heparin-coated vacutainer tubes and transferred to 50 mL conical tubes. $CD3^+$ primary human T-cells were isolated by negative selection as per manufacturer's instructions (RosetteSep Human T-cell Enrichment Cocktail, STEMCELL Technologies). T-cell pellets were resuspended in dilution medium and counted using a hemocytometer with 0.4% Trypan blue viability stain (ThermoFisher Scientific). Cells were then resuspended at 1 million/mL in either Immunocult-XF T-cell Expansion Medium (STEMCELL Technologies) or TEXMACs Cell Culture Medium (Miltenyi Biotec). T-cell cultures were supplemented with 200 U/mL IL-2 (Peprotech) or 10 ng/mL of IL-7 (BioTechne) and 10 ng/mL of IL-15 (BioTechne) and stimulated with Immunocult Human CD3/CD28/CD2 T-cell Activator (25 uL for each mL of culture, STEMCELL) for 48 hours or T-cell TransAct (10 uL for each mL of culture) for 72 hours respectively.

Isolation of T-cell from LRS Cone: LRS cones (Versiti Blood Bank, Milwaukee, WI) were purchased as an alternative to drawing from healthy donors. Briefly, RBC-depleted peripheral blood was flushed out of the cone with a blunt gauge needle and dilution medium. The solution was diluted 1:1 with dilution medium and 30 mL was carefully layered on top of 15 mL of Lymphoprep solution. Tubes were centrifuged for 1200 g x 20 min with the brake off. The white monolayer containing leukocytes was then gently disturbed and pipetted into a 15 mL conical tube which was spun at 300 g x 5 min and washed twice. T-cells were then positively selected using an EasySep T-cell kit (STEMCELL Technologies) and an EasySep Magnet (STEMCELL Technologies) as per the manufacturer's protocol. T-cell supernatant was collected from the magnet and the cells were then counted, resuspended in culture medium, and activated as above.

T-cell Electroporation on Lonza 4D Nucleofector: Following T-cell activation, RNP's and DNA were electroporated (EP) into T-cells in 16 well electroporation cuvettes on a 4-D Nucleofector X unit (Lonza) using pulse code EH-115. One million cells were electroporated per well in the cuvette. Per reaction, a single guide RNA specific for the TRAC locus (2 uL of 100 uM, IDT) was incubated with SpCas9 (0.8 uL of 10 mg/mL, Aldevron) and Poly-L-Glutamic acid (PGA, 1.6 uL of 10 mg/mL solution in DNase free

water) for 15 minutes at 37°C to form the RNP complex. During incubation, T-cells were centrifuged for 300 g x 5 min and counted on the Countess II FL Automated Cell Counter with 0.4% Trypan Blue viability stain. One million cells per reaction were then aliquoted and spun for 90 g x 10 min. Following RNP incubation, linearized dsDNA HDR templates were added to the mixtures (2 uL) in PCR tubes and incubated for at least 5 minutes. Cells were then resuspended in 17.6 uL of P3 buffer (Lonza) and transferred to PCR tubes containing the RNP:DNA mixtures. Contents were then transferred to cuvettes (total volume 24 uL) and electroporated. Immediately following electroporation, 80 uL of Immunocult XF or TexMACS medium with *no cytokines* was added to each reaction which were then rested for 30 minutes at 37°C. Cells were then moved to a flat-bottom 96 well plate containing 160 uL of medium supplemented with 500 U/mL IL-2 (Peprotech) or 10 ng/mL of IL-7 (BioTechne) and 10 ng/mL of IL-15 (BioTechne). Cells were cultured for 24 hours and then transferred to 12 well plates with 1 mL of media and incubated at 37 C for 48 hours. The TRAC guide sequence can be found in Supplementary Table 3.

T-cell Culture: Metabolically-primed (MP) or Control *TRAC*-CAR T cells were cultured in TexMACS or Immunocult XF media supplemented with IL-7/IL-15 (10 ng/mL) or IL-2 (200 U/mL) at 1 million cells/mL respectively for the first three days. After electroporation both MP and Control *TRAC*-CAR T cells were cultured in Immunocult XF for 7 days with IL-7/IL-15 (10 ng/mL) or IL-2 (500 U/mL). Every 2 days cells were centrifuged for 300 g x 5 min and counted on the Countess II FL Automated Cell Counter with 0.4% Trypan Blue viability stain. Cells were then resuspended in culture medium at 1 million cells/mL and the process repeated on days 5 and 7 post-EP.

Scaled-Up GMP-compatible T-cell Manufacturing: For GMP-compatible experiments, T-cells were isolated and activated and cultured with either TransAct in TexMACS supplemented with IL-7 (10 ng/mL) or IL-15 (10 ng/mL) or with Immunocult XF activator and medium supplemented with 200 U/mL IL-2. Following activation, 20-50 million cells were electroporated on the CTS Xenon Electroporation System (ThermoFisher). TRAC sgRNA (1 uL/1E6 cells) and SpCas9 (0.8 uL/1E6 cells) were mixed and incubated for 15 min at 37 C. Following incubation, linearized nanoplasmid template 1 uL/1E6 cells) was then added

to the RNP mixtures. Cells were spun, counted, spun again for 5 minutes at 300 g, and resuspended in enough Genome Editing Buffer (ThermoFisher) for a final volume of 1 mL when combined with the RNP:DNA mixture. Cells, DNA and RNPs were then added together, loaded into a Single-Shot cuvette (ThermoFisher), and electroporated on the Xenon unit at 1720 volts with a pulse width of 20 ms. Cells were then transferred to a T-25 flask with 4 mL of Immunocult XF medium containing no additives. After 30 minutes of rest at 37 C, Immunocult XF medium containing either IL-7 (10 ng/mL) with IL-15 (10 ng/mL) or 500 U/mL IL-2 was added to the T-75's to bring the final concentration to 4 million cells/mL. After 24 hours, cells were transferred to a G-Rex 6M plate (10e6 per well) and the final volume brought to 100 mL per well. Cells were then cultured at 37 C for 6 days after which 75 mL of media were aspirated, cells were collected, spun for 300 g x 5 min, and counted for use in endpoint assays.

Flow Cytometry Analysis: CAR was detected using a 1A7 anti-14G2A antibody (National Cancer Institute, Biological Resources Branch) conjugated to APC using a Lightning Link APC Antibody Labeling kit (Novus Biologicals). TCR was detected using an anti-human TCR α/β antibody conjugate to BV421 (Biolegend). Flow cytometry to assess CAR and TCR positivity was performed on Day 8 of manufacturing on an Attune NxT flow cytometer (ThermoFisher). Immunophenotyping of cells was performed on Day 10 of manufacturing using a spectral immunophenotyping panel on an Aurora spectral cytometer (Cytek). Briefly, cells were plated in a 96-round bottom well plate (100k for CAR/TCR and 250k for spectral immunophenotyping), washed with 200 uL of PBS and spun at 1200 g x 1 min, twice. Cells were then stained for viability with either GhostRed 780 (Tonbo Biosciences) or Live-Dead Blue (ThermoFisher). For CAR/TCR staining, 1 uL of Ghostred 780 was added to 10 mL of PBS to make a stock solution, 100 uL of stock solution was added to each sample and incubated for 30 minutes in the dark. For spectral flow staining, Live-Dead Blue stain was resuspended in 50 uL of DMSO, 1 uL added per 1 mL PBS to make a stock solution, and 200 uL of stock solution was added to each sample and incubated for 30 minutes in the dark. After viability stained, samples were washed twice and blocked for 30 minutes with 50 uL FACS buffer (0.5% BSA in PBS) with TruStain FcX solution (0.5 uL/sample). Antibodies were then added to 100

uL of BD Brilliant Stain Buffer (BD) at the optimized amounts found in Supplementary Table 4 and incubated for 1 hour. Cells were then washed, resuspended in 200 or 75 uL of FACs buffer, and analyzed on the Attune or Aurora respectively. For spectral immunophenotyping, we used CD4, CD8, TCR, and CAR positivity to define populations and for all markers cells were gated by relative size, shape, singlets, viability, TCR negativity and CAR transgene positivity to find an analyzable population of viable CAR T cells. All antibodies are listed in Supplementary Table 4.

In Vitro Cytotoxicity Assay on Incucyte: 5,000 AkaLUC-GFP CHLA-20 cells were seeded in triplicate on 96-well plates and incubated for 24 hours at 37 C. 24 hours later 50,000, 25,000, or 10,000 CAR^+ T-cells from Day 10 of manufacturing were added to each well for effector:target ratios of 5:1, 2.5:1, or 1:1. The plate was centrifuged for 5 minutes at 100g and then placed in the IncuCyte S3 Live-Cell Analysis System (Sartorius) and stored at 37°C, 5% CO_2. Images were taken every 3 hours for 48 hours. Green object count was used to calculate the number of cancer cells in each well and fluorescent images were analyzed with IncuCyte Base Analysis Software.

In vivo Infusion into Mice with Human Xenografts: All animal experiments were approved by the University of Wisconsin-Madison Animal Care and Use Committee (ACUC protocol M005915). Male and female NOD-SCID-$\gamma c^{-/-}$ (NSG^{TM}) mice (9-25 weeks old; Jackson Laboratory) were subcutaneously injected with 10 million AkaLUC-GFP CHLA-20 $GD2^+$ human neuroblastoma cells in the flank to establish tumors. After six days, tumor size was verified using bioluminescence measurements on the PerkinElmer *In Vivo* Imaging System (IVIS), and 3 million CAR^+ T cells from Day 10 of manufacturing were injected into the tail vein of each mouse. Mice were imaged on the IVIS every 3-4 days after being sedated with Isoflurane and intraperitoneal injections of ~120 mg/kg D-luciferin (GoldBio). Mice were injected with 100,000 IU of human IL-2 (National Cancer Institute, Biological Resources Branch) subcutaneously on day 0 and following imaging. To quantify the total flux in images, a region of interest was drawn around established tumors on day 0 and calculated by Living Image Software (PerkinElmer; Total flux = radiance (photons/sec)

in each pixel integrated over ROI area (cm^2) x 4π). The minimum flux value was subtracted from each image to normalize for background signal.

Flow cytometry of splenocytes: Spleens were removed, mechanically dissociated, and filtered using a Corning 70 uM cell strainer. Suspensions were centrifuged for 10 minutes at 300g and digested with ACK lysing buffer (Lonza). The cells were then washed with PBS, centrifuged for 10 minutes at 300g, and resuspended in 1 mL of PBS. Cells were counted using Trypan Blue exclusion on the Countess II FL Automated Cell Counter. $1x10^6$ total cells were then added to 96-round well plates and stained for a spectral immunophenotyping panel for analysis on an Aurora spectral cytometer (Cytek). Briefly, samples were washed with PBS, stained with Live-Dead Blue for 30 minutes, blocked with FACS buffer and Trustain FcX, and incubated with the spectral immunophenotyping panel overnight. For spectral immunophenotyping, we used CD4, CD8, TCR, and CAR positivity to define populations and for all markers cells were gated by relative size, shape, singlets, viability, CD5 positivity, CD45 positivity, TCR negativity and CAR transgene positivity to find an analyzable population of viable CAR T cells. All antibodies and amounts are listed in Supplementary Table 4.

Cytokine Analysis: The supernatant of CAR T and cancer co-culture systems was measured for their expression of cytokines using the LegendPlex Human Essential Immune Response Panel (BioLegend) (IL-4, IL-2, CXCL10 (IP-10), IL-1β, TNF-α, CCL2 (MCP-1), IL-17A, IL-6, IL-10, IFN-γ, IL-12p70, CXCL8 (IL-8), TGF-β1 (Free Active Form). In brief, 50,000 AkaLUC-GFP CHLA-20 neuroblastoma cells were plated in 24 well plates with the addition of 250,000 CAR T cells 24 hours later. Suspension cells were harvested 24 hours later, spun for 5 minutes at 300g, cells counted, the supernatant flash frozen in liquid nitrogen, and stored at -20 C. Media samples were thawed and the manufacturer's protocol for bead staining and analysis on an Attune NxT Cytometer (ThermoFisher) was followed. Briefly, standards for cytokines were prepared using 1:4 serial dilutions and co-culture supernatant added directly to a 96-well V-bottom plate. Mixed beads wereadded to each well and incubated on a plate mixer for 2 hours. The plate was then washed twice, detection antibody added to each well, incubated for 1 hour, and SA-PE was added to each

well. The plate was incubated for 30 minutes, washed twice, and analyzed on the Attune Cytometer. Data was exported to LEGENDplex™ Data Analysis Software Suite where cytokine concentration was calculated. The data was exported to Excel, and cytokine concentration was normalized to the total number of T-cells in co-culture.

Mitochondrial Staining: The mitochondrial mass and membrane potential of T-cells was measured by performing flow cytometry on cells stained with MitoTracker Green (ThermoFisher) and tetramethylrhodamine methyl ester perchlorate (TMRE) (ThermoFisher) dyes. Briefly, a stock solution of PBS containing 0.08 uL/mL of Mitotracker Green and 0.1 uL/mL of a 10 uM TMRE dye stock was created (200 uL per sample of 250,000 T-cells). Cells were stained for 20 minutes at 37°C, washed, and resuspended in 75 uL of FACS buffer (0.5% BSA in PBS).

Metabolite Analysis: Media samples were taken from CAR T cell cultures on Day 10 of manufacturing and frozen at -20 C for future analysis. The Glucose-Glo and Lactate-Glo kits were used to measure the apparent glucose and lactate concentrations in media samples according to the manufacturer's protocol. Raw luminescence data were converted to concentration using the metabolite standards.

Extracellular Flux Assay (Seahorse Assay): The oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) were measured following the manufacturer's instructions for the Seahorse XF Cell Mito Stress Test Kit (Agilent). Briefly, $5x10^5$ T-cells were resuspended in RPMI XF medium supplemented with 10mM glucose and 2mM glutamine and plated in a poly-L-lysine-coated XF96 plate. The T cell culture plate was centrifuged at 200g for 1 minute (no brake) and checked under the microscope to ensure even adhesion of T cells. T cells were then kept in a non-CO2 incubator for at least 1 hour before running the assay. The OCR and ECAR under basal conditions and in response to oligomycin (2.5 μM), fluorocarbonylcyanide-phenylhydrazone (FCCP) (1 μM), and rotenone/antimycin A (R/A) (0.5 μM) were measured using an XF96 Extracellular Flux Analyzer (Seahorse Bioscience). Data was exported into Excel (V2311) using Agilent's software and converted into graphs.

Spectral Flow Cytometry Data Analysis: Analysis of spectral flow cytometry data was performed using Cytek's SpectroFlo program., Single positive controls for each color were collected and analyzed in SpectroFlo for positive and negative populations. SpectroFlo's unmixing algorithm was then used to compensate for spillover and autofluorescence of cells. Data was then exported to FlowJo (V10.9.0) where samples were gated for non-debris, singlets, and live cells. TCR, and CAR positivity were used to gate cell populations for *in vitro* samples and CD45, CD5, TCR, and CAR positivity for *in vivo* T-cell samples. Median fluorescent intensity (MFI)'s for each sample were calculated and input into Excel. Representative plots were generated in FlowJo using fluorescence minus one controls to set positive gates.

Optical Metabolic Imaging: As previously described [57,58], 200,000 CAR T cells in 75μL fresh media were plated on Poly-D-Lysine coated 35mm glass bottom imaging dish (MatTek). Autofluorescence signals from NAD(P)H and FAD were imaged on a two-photon microscope (Ti-E, Nikon) at 750nm excitation (440/80nm emission) and 890nm excitation (550/50 emission), respectively. Fluorescence decay was collected with time-correlated single-photon counting electronics (SPC 150, Becker & Hickl GmbH) and fitted to a two-component exponential decay in SPCImage (v8.0, Becker and Hickl GmbH) to extract mean fluorescence lifetime (τ_m) and fractional contribution of short- and long-lifetime components (α_1 and α_2). Single-cell nucleus and cytoplasm were manually segmented in CellProfiler and applied to the corresponding OMI images to quantify mean values of OMI parameters for each cell cytoplasm.

Data Analysis and Software: All data analyses were performed in GraphPad Prism (V.10.0.2) and Microsoft Excel. Statistical tests were done in GraphPad Prism and indicated in the figure legends. Nanoplasmid sequences were designed in Benchling. FlowJo was used to analyze.fcs files exported from SpectroFlo and Attune NxT software. Representative flow plots were exported from FlowJo. UMAPs were created using the DownSample and UMAP_R plugins from to FlowJo to select for and cluster pooled data in a concatenated .fcs file. Figures were created and organized using Adobe Illustrator (V28.0). A p value less than 0.05 was defined as significant. Cohen's effect size was calculated by dividing the difference between treated and control groups means and dividing by the pooled standard deviation of them.

DATA AVAILBILITY STATEMENT

Data are available upon request.

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AUTHOR CONTRIBUTIONS

These authors contributed equally: DC, DP, MHF. DC and MB developed the restriction digest and two-step purification procedure for HDR templates. DC, MB and AT optimized electroporation protocols. DC, MB, and AT isolated and cultured T cells and performed virus-free transfections. DP, BH, and LM assisted

with cell culture. DC, MB, AT, BH, and LM performed flow cytometry. DC, DP and MHF performed cytokine experiments. MHF conducted in vivo experiments with support from QS. DC, DP, and MHF isolated mouse spleens/tumors and performed flow cytometry. DC, MB, and AT performed in vitro co-cultures. JV and TL performed analysis of metabolites in media. DC wrote the manuscript with input from all authors. DC, DP, MHF, MB, AT, JV, TL, BH, LM, and QS performed experiments and analyzed the data. DP provided integral initial insights that determined the direction of the study. KS, QS, MCS, and CMC supervised the research.

DECLARATION OF INTERESTS

KS receives honoraria for advisory board membership for Andson Biotech and Notch Therapeutics. CMC receives honoraria for advisory board membership for Bayer, Elephas, Nektar Therapeutics, Novartis and WiCell Research Institute. No other conflicts of interest are reported.

KEYWORDS

Gene editing, CAR T cells, cancer, metabolism, stem cell memory, CRISPR, GMP-compatible, pre-clinical, scale-up

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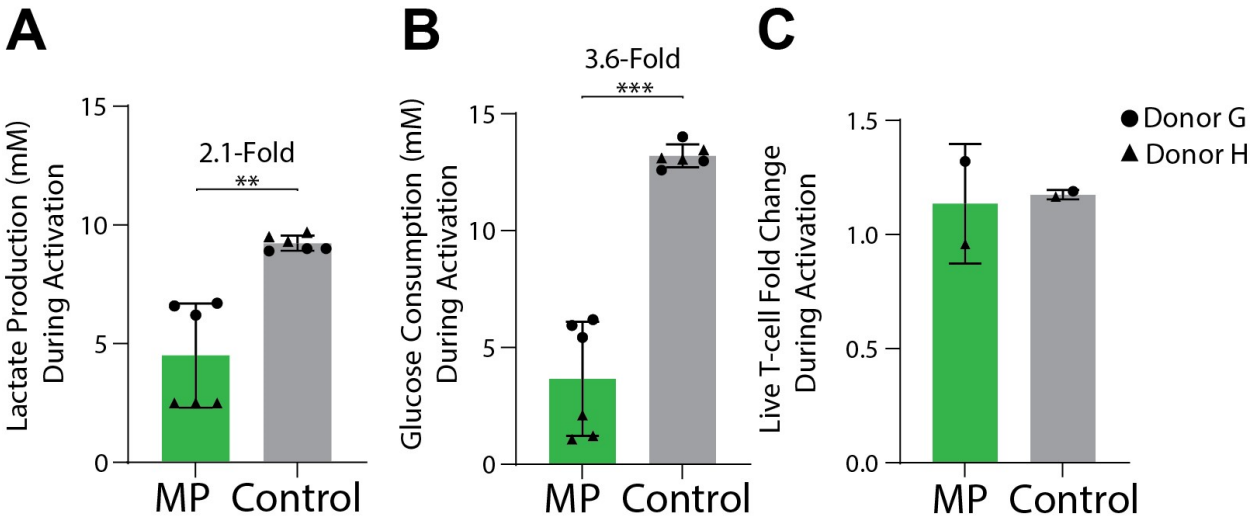

Figure S1. Effect of Activation Conditions on Lactate Production and Glucose Consumption. (A) Lactate production, (B) glucose consumption and (C) proliferation of MP or Control T cells during activation (MP – 72 hours; Control – 48 hours). 2 donors, (lactate/glucose) $N_{MP} = N_{Control} = 6$, (proliferation) $N_{MP} = N_{Control} = 2$. Statistical significance was determined with a paired-test; **$p<0.01$; ***$p<0.001$.

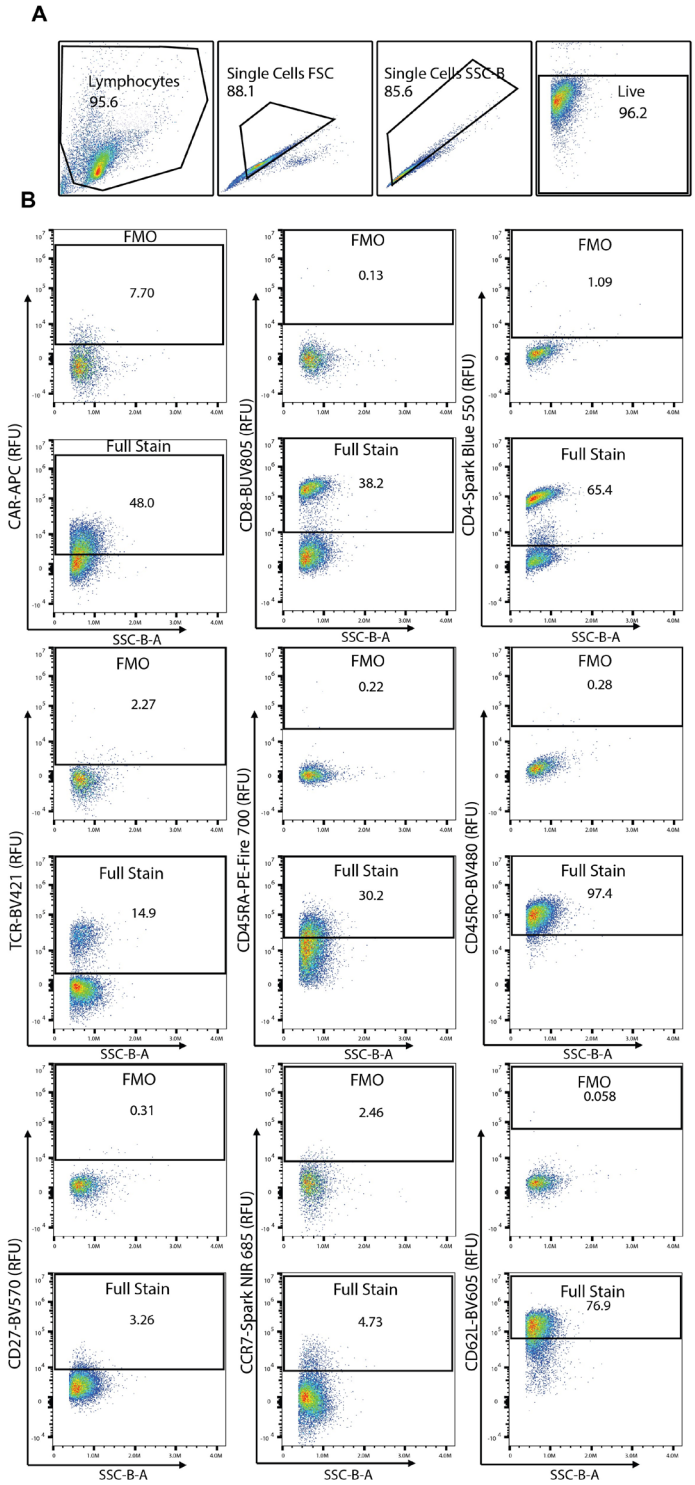

Figure S2. Post-Manufacturing CAR T Cell Gating Strategy. (A) Gating strategy for analysis of spectral immunophenotyping flow cytometry data of CAR T cells post-manufacturing. **(B)** FMO's and representative positive populations depicting positive and negative gates.

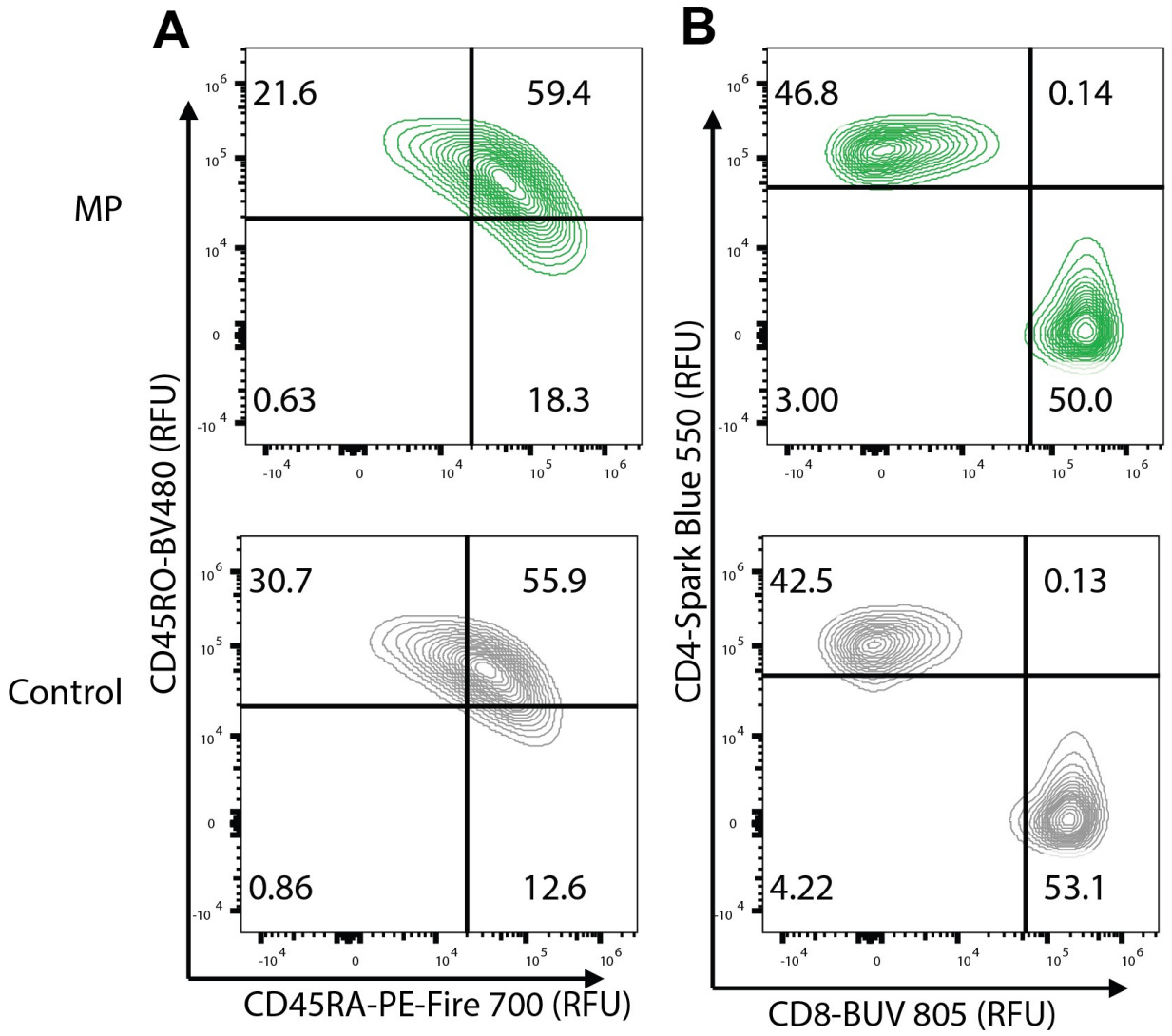

Figure S3. Expression of CD45RA/CD45RO and CD4/CD8 in MP *TRAC*-CAR T Cells at Scale. Representative contour plots for expression of (A) CD45RA/CD45RO and (B) CD4/CD8 MP or Control *TRAC*-CAR T cells (Donor F shown).

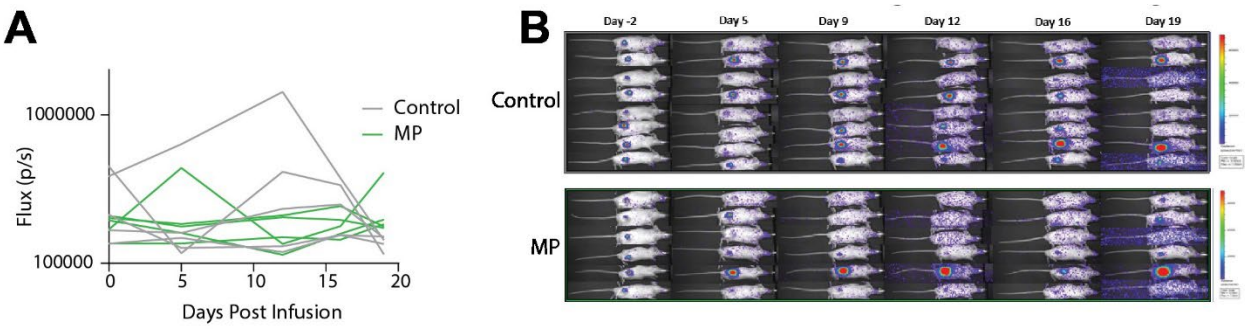

Figure S4. In Vivo Potency of MP and Control TRAC-CAR T cells. (A) The flux over time (luminescence from IVIS images) is shown for mice treated with MP or Control *TRAC*-CAR T cells. **(B)** IVIS images depict tumor growth over time for the same conditions. (2 donors, $N_{MP} = 6$, $N_{Control} = 8$).

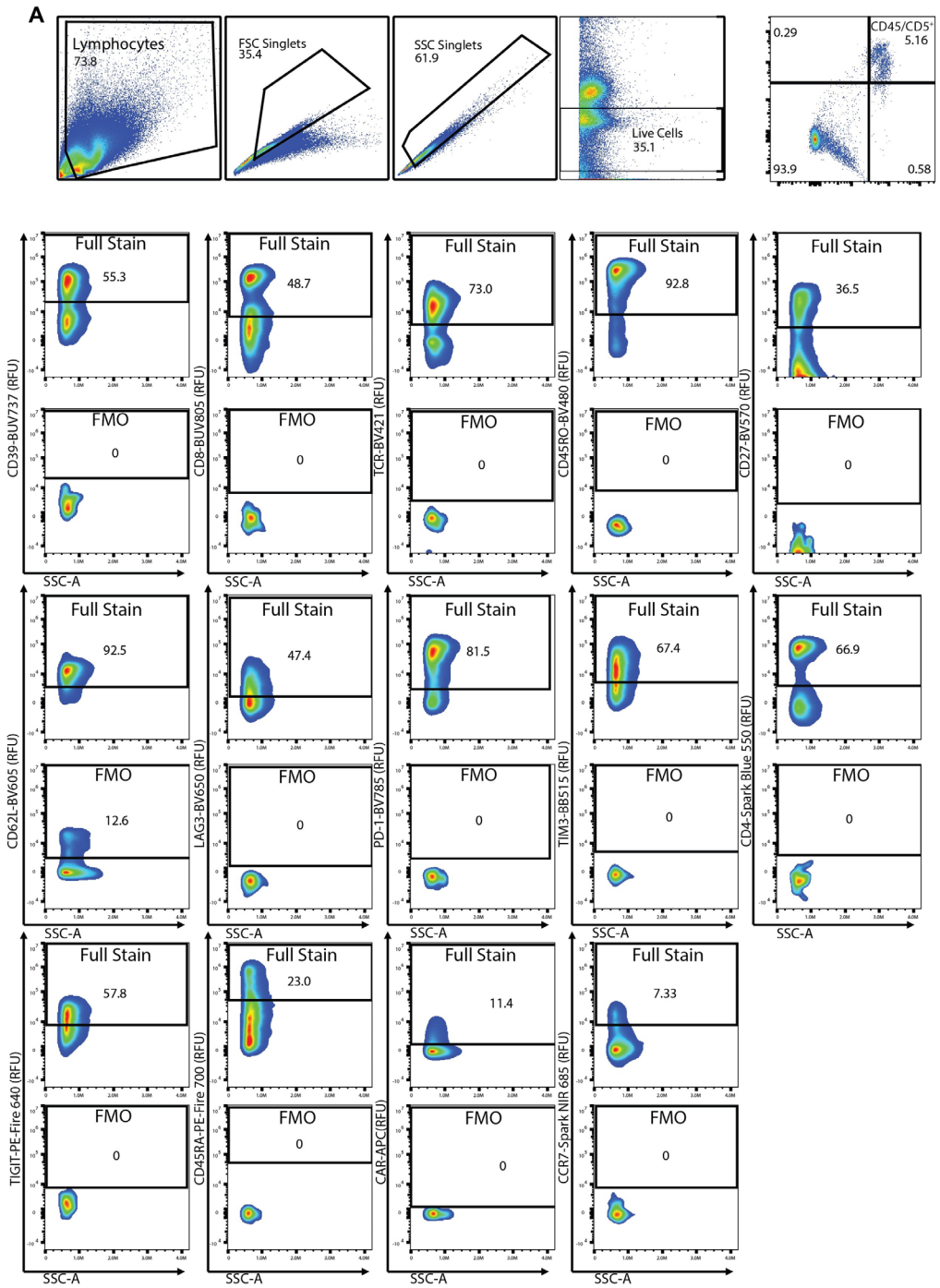

Figure S5 Gating Scheme for Analysis of Lymphocytes in Mouse Spleens. Gating strategy for analysis of live, CD5/CD45^{+} lymphocytes in isolated mouse spleens. **(B)** FMO's and representative positive populations depicting positive and negative gates.

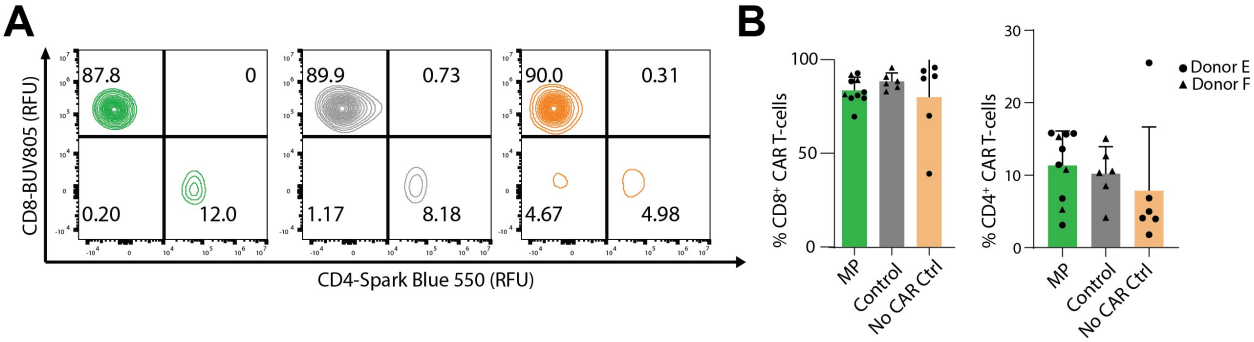

Figure S6. Expression of CD4 and CD8 Post In Vivo Tumor Challenge. (A) Representative contour plots for CD4/CD8 expression in CD5+/CD45+/TCR-/transgene+ lymphocytes isolated from mouse spleens (Green = MP, Donor E; Gray = Control, Donor F; Orange = No CAR Ctrl, Donor E). **(B)** Bar graphs for relative expression of CD4 and CD8 for MP or Control -CAR T cells and no CAR control T-cells. Samples with less than 20 CD5+/CD45+/TCR-/transgene+ events were excluded from analysis. 2 donors, $N_{MP} = 10$, $N_{Control} = 6$, $N_{NoCARCtrl} = 6$..

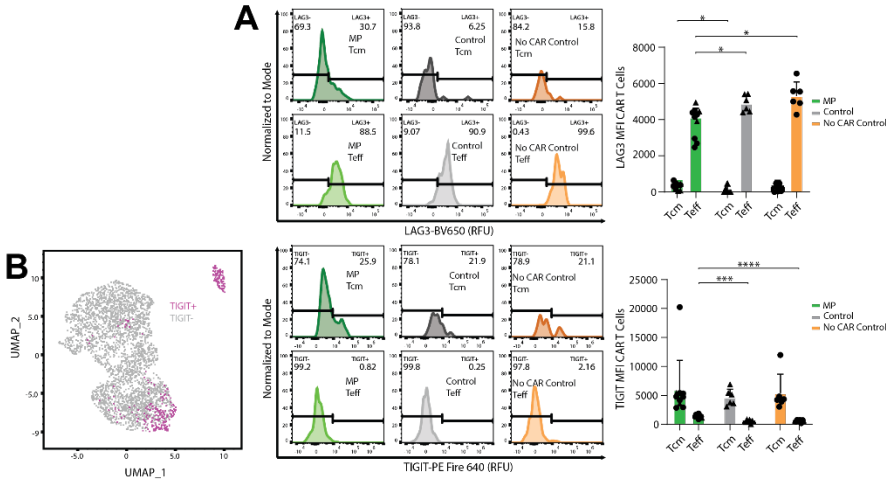

Figure S7. Expression of Exhaustion Markers in Splenic Lymphocytes. The expression of **(A)** LAG3 (Tcm: MP: 730 (342), Control: 115 (200), No CAR Control: 325 (325), p (MP vs Control) = 0.0014) (Teff: MP: 4117 (508), Control: 4895 (467), No CAR Control: 5311 (774), p (MP vs Control and MP vs No CAR Control) = 0.0278 and 0.0274)and **(B)** TIGIT (Tcm: MP: 5931 (5118), Control: 4654 (1422), No CAR Control: 5381(3282))(Teff: MP: 1407 (288), Control: 521 (287), No CAR Control: 571 (220), p (MP vs Control and MP vs No CAR Control) < 0.001 for both) in CD5+/CD45+/TCR-/transgene+ splenic lymphocytes are depicted on UMAP plots, representative histograms and bar graphs for Tcm and Teff. 2 donors, $N_{MP} = 10$, $N_{Control} = 6$, $N_{NoCARCtrl} = 6$. Statistical significance was determined with a Brown-Forsythe and Welsch ANOVA test using Dunnett's T3 test for multiple comparisons; *p<0.05; ***p<0.001; ****p<0.0001.