Poster nr. 273

Chimeric PGC1\alpha expression in CAR-T cells improves metabolic function and anti-tumor efficacy in solid tumors



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Abstract

Background: The solid tumor microenvironment (TME) suppresses CAR T cell function through various mechanisms including competition for nutrients and chronic stimulation resulting in limited T cell effector functions or T cell exhaustion. Therefore, CAR T cells with enhanced metabolic fitness or more durable early memory phenotype could improve the clinical outcome against solid tumors. PPAR gamma coactivator 1α (PGC1 α) is a transcriptional coactivator that influences many aspects of cellular metabolism. Previous studies have indicated that exogenous expression of PGC1 α can enhance T cell anti-tumor activity, however the large size of PGC1 α renders it difficult to co-express with a CAR. An N-terminal truncated PGC1 α (NT-PGC1 α) has previously been shown to improve co-expression with a CAR, however, despite imparting mitochondrial benefits, NT-PGC1 α failed to increase anti-tumor activity.

Methods: We developed a novel chimeric PGC1 α consisting of an N-terminal truncation with the addition of an exogenous DNA binding domain derived from PPARg The chimeric PGC1 α was co-expressed with a ROR1-targeted CAR in human T cells and was compared to CAR alone in in vitro and in vivo studies.

Results: We observed a decrease in the number of dysfunctional mitochondria and a subsequent increase in glucose uptake in CAR T cells expressing the chimeric PGC1 α compared to CAR alone. These cells also demonstrated enhanced resistance to chronic antigen stimulation and a less differentiated and less exhausted phenotype compared to CAR alone. Moreover, when tested in vivo, CAR T cells expressing the chimeric PGC1 α had superior anti-tumor activity compared to CAR T alone in a solid tumor model of clear cell renal cell carcinoma.

Conclusions: These data suggest that incorporation of this novel chimeric PGC1 α in CAR T cells may be a promising approach to enhance CAR T cell efficacy in patients with solid tumors.

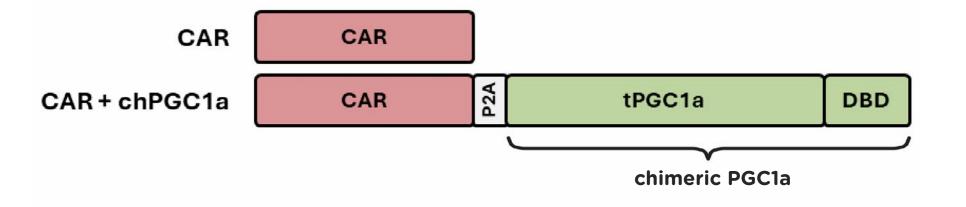
PERIPHERY Effector T cell PGC1a Metabolic exhaustion Metabolic ally-reprogrammed effector T cell PGC1a PGC1a

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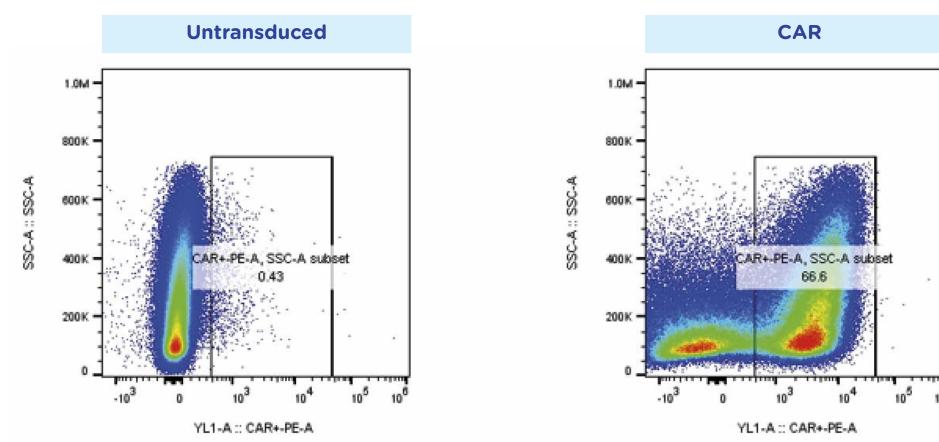
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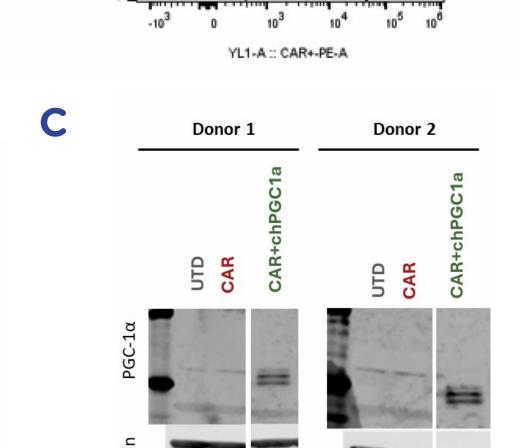
Introduction

- PGC1a is master transcriptional regulator of mitochondrial genes
- Overexpression has been shown to increase mitochondrial biogenesis and function
- Advantageous for T cells in immuno-suppressive environments
- Very large protein >700 residues
- Engineering effort to reduce size to a smaller functional entity ~300 residues



Co-Expression of CAR + chPGC1a





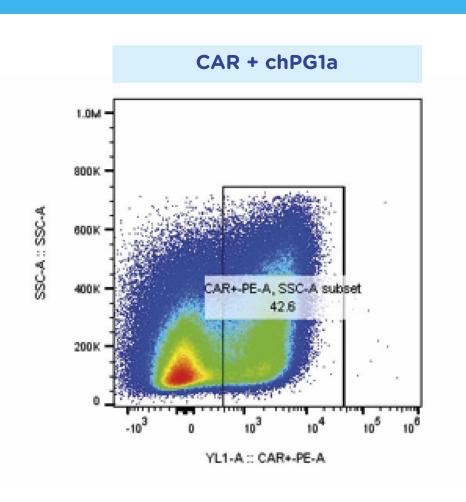


Figure 1. Expression of chPGC1a in CAR T cells. Human healthy donor PBMC were transduced with CAR or CAR + chPGC1a and assessed for CAR expression by flow cytometry.

(A) Scatter plots shown for representative donor, (B) % CAR expression shown for N= 2 donors.

(C) PGC1a and chPGC1a were detected by western blot, N = 2 donors.

chPGC1a Improves CAR T Metabolic Function

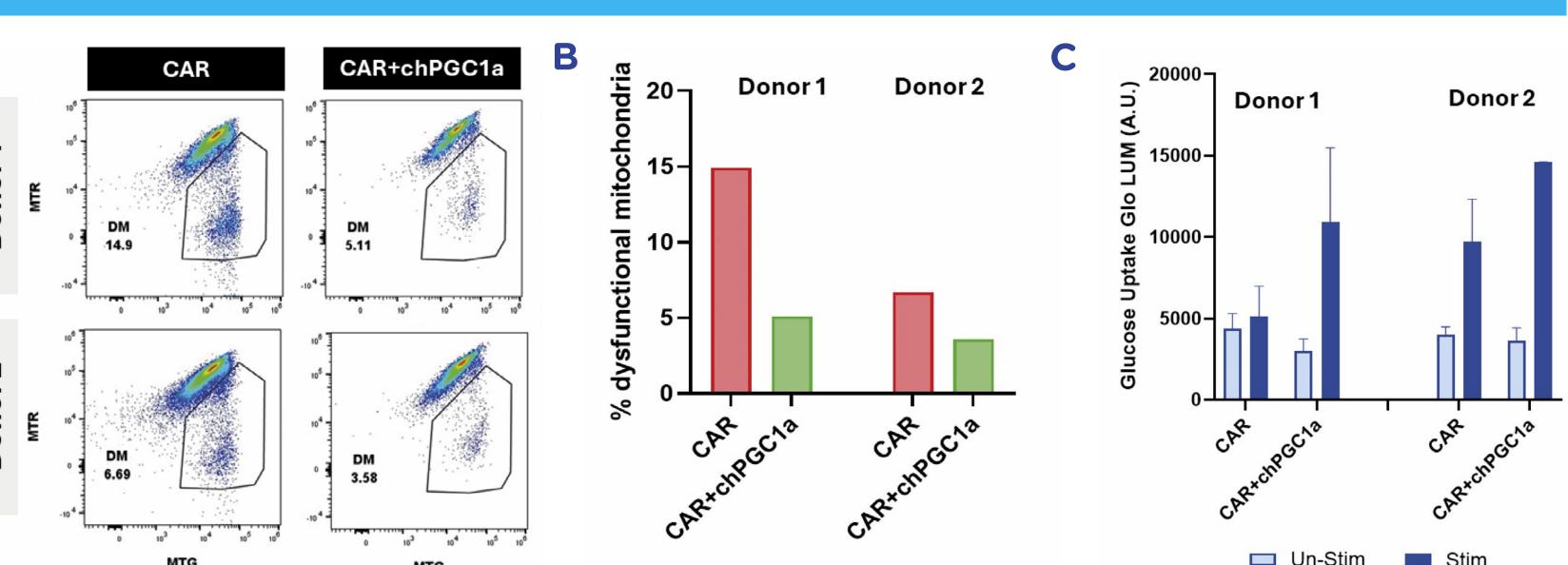


Figure 2. chPGC1a reduces the number of dysfunctional mitochondria and improves glucose uptake.

(A and B) Dysfunctional mitochondria present in CAR or CAR+chPGC1a T cells were quantified using flow cytometry and defined as MitoTracker Red low/negative and MitoTracker Green positive.

(C) Respective transduced cells were stimulated with ROR1 antigen for 72 h and glucose and uptake was measured in a luminescence-based assay and reported as background-subtracted arbitrary luminescence units (A.U.).

TN+SCM Cell Subset Enriched in chPGC1a CAR T Cells

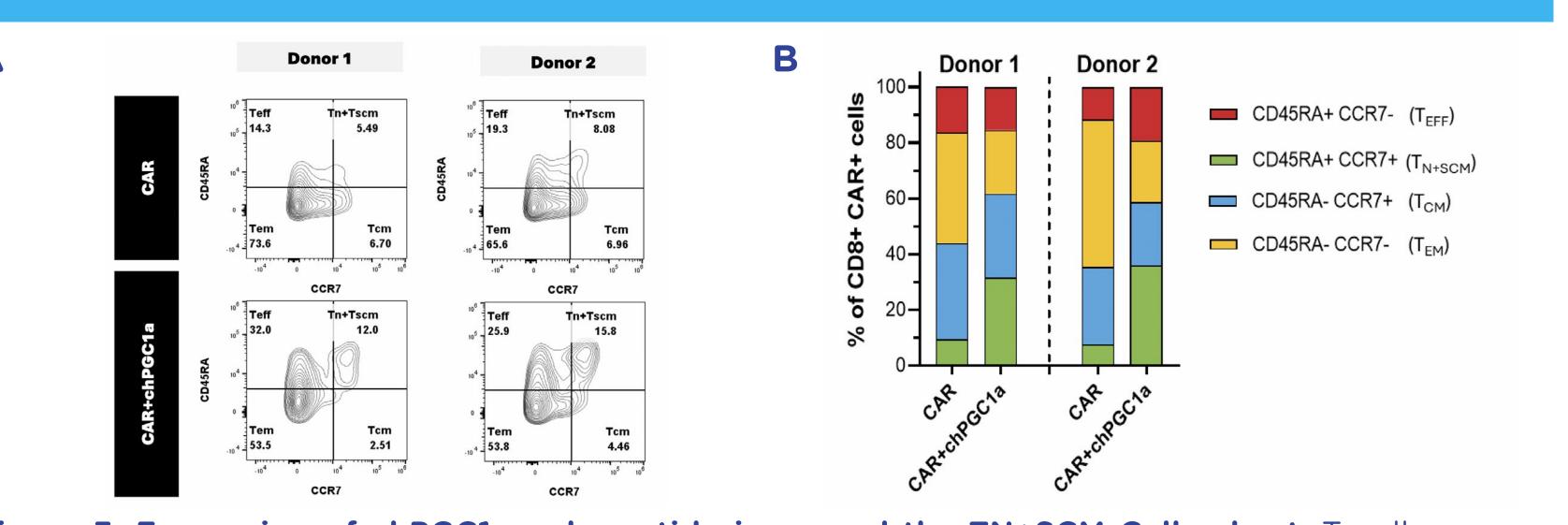


Figure 3. Expression of chPGC1a polypeptide increased the TN+SCM Cell subset. T cell memory subsets were analyzed in CAR T or CAR+chPGC1a Tcells by flow cytometry. (A). Representative flow cytogram indicates the gating strategy used in analyzing the T cell memory subsets. (B) Tabulated flow cytometric data gated on CD8+ CAR+ T cells. Results shown here are from two independent donors. Gating strategy – Effector T cell (Teff): CD3+ CD8+ CAR+ CD45RA+ CCR7-; Naïve and Stem Cell Memory (Tn+scm): CD3+ CD8+ CAR+ CD45RA+ CCR7+; Central Memory T cell (Tcm): CD3+ CD8+ CAR+ CD45RA- CCR7+; Effector Memory T cell (Tem): CD3+ CD8+ CAR+ CD45RA- CCR7-.

TN+SCM Cell Subset is Further Enriched Following Antigen Stimulation

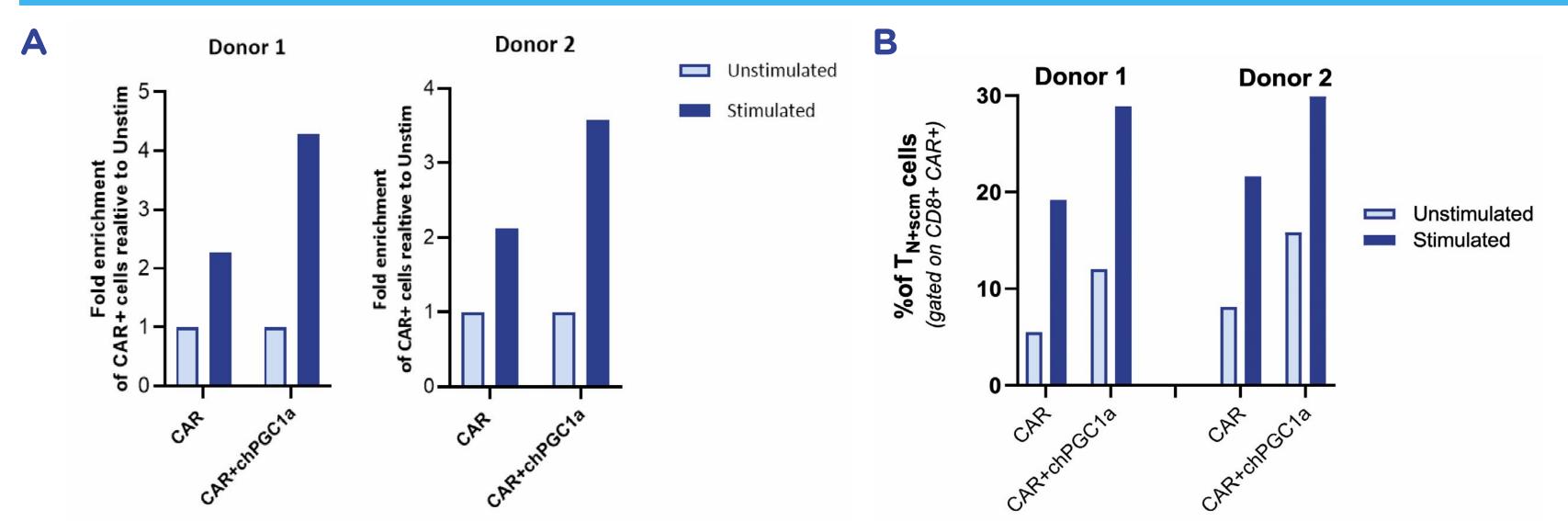
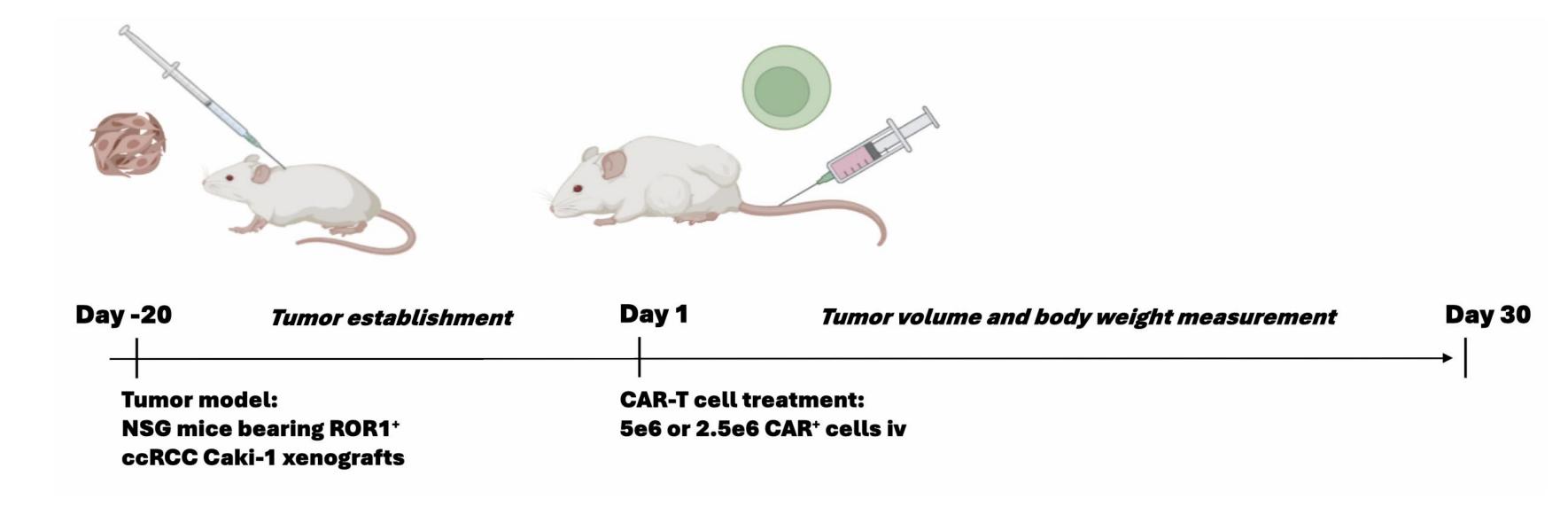


Figure 4. Impact of antigen stimulation on CAR expression and TN+SCM cell subset dependent on chimeric PGC1a polypeptide expression. CAR or CAR+chPGC1a T cells were stimulated for 72h with plate-bound ROR1 antigen. CAR expression and T cell memory subsets were analyzed by flow cytometry. (A) Fold-change of CAR expression of unstimulated or antigen-stimulated CAR+ T cells relative to unstimulated CAR+ T cells. (B) % of TN+SCM cell subset of unstimulated or antigen-stimulated CAR+ T cells relative to unstimulated CAR+ T cells gated on CD3+CD8+CAR+ T cells. Gating strategy: Naïve and Stem Cell Memory (TN+SCM) = CD45RA+CCR7+. The scFv of the CAR is directed to ROR1. Results shown here are from two independent donors.

Co-expression with chPGC1a Improves Anti-Tumor Efficacy



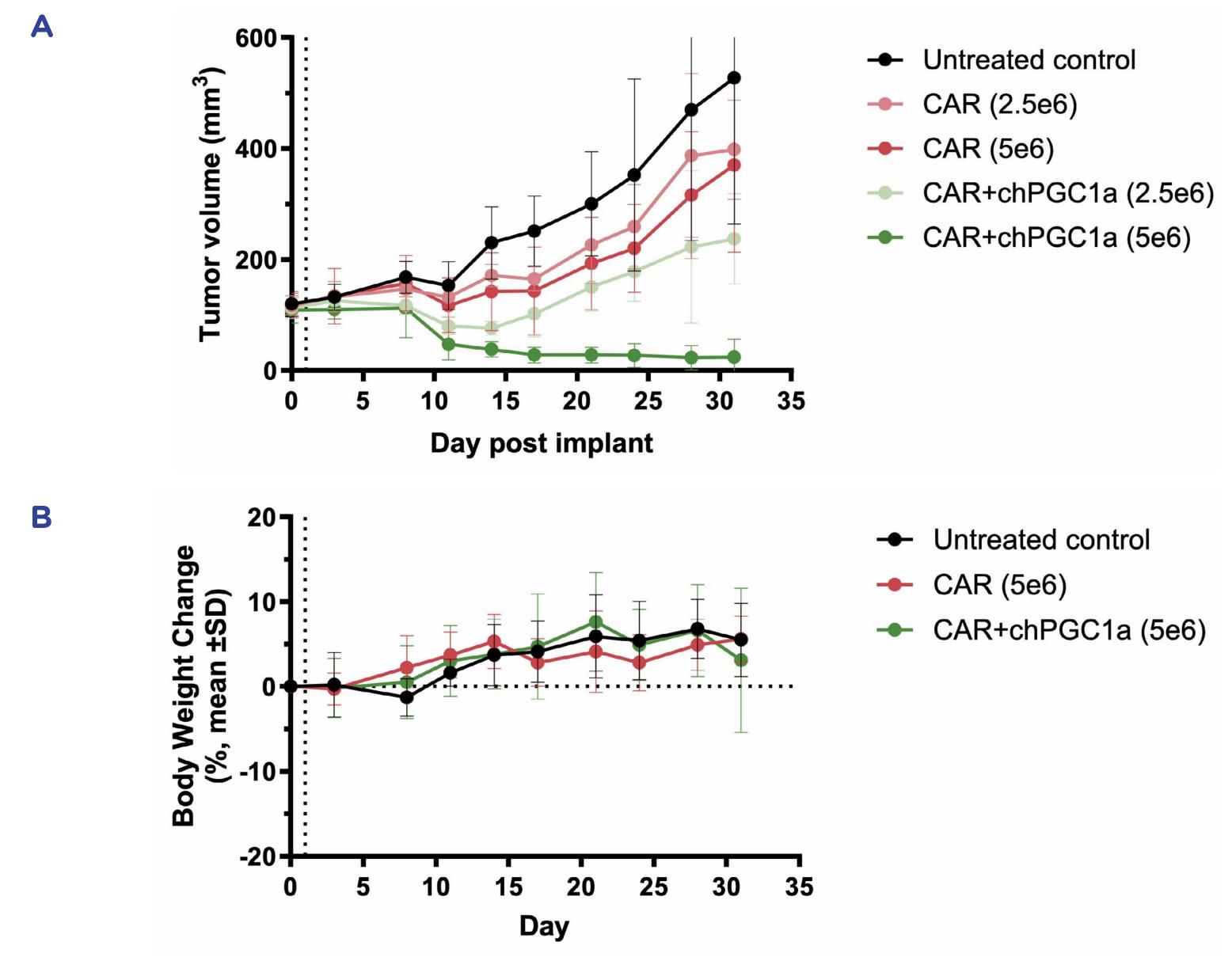


Figure 5. In vivo anti-tumor efficacy in CAKI-1 (Human Renal Cell Carcinoma) xenograft mouse model. NOD-SCID-IL2Rγ null (NSG) mice having established CAKI-1 (human clear cell renal cell carcinoma) tumors were randomized into treatment groups based on tumor volume (117 ±25 mm³ on day 20 post implantation). Animals received a single intravenous administration of ROR1-targeted CAR-Ts on Day 21 post tumor implantation (study day 1) at 5x 106 or 2.5x106 CAR+ T cells. Control animals were left untreated. Tumor volume and body weights were monitored twice weekly until Day 30. Mice were euthanized when tumor volumes reached 1000 mm³, or in the event of tumor ulceration. (A) Plot shows mean tumor volume of tumor-bearing mice (B) Plot shows in graph body weight change in % in untreated and treated groups receiving 5x 106 CAR+ T cells (No change in bodyweights for 2.5x106 dose, data not shown). (N=5 mice per group)

Summary:

- Expression of a chimeric PGC1a transgene in CAR T cells have fewer dysfunctional mitochondria and improved glucose uptake compared to CAR T cell controls
- CAR+chPGC1a T cells have more TN+SCM, and this less-differentiated phenotype is enriched following antigen stimulation.
- chPGC1a enhances CAR T anti-tumor efficacy with no overt signs of toxicity.
- These data suggest that co-expression CAR + chPGC1a is a promising approach to enhancing CAR T cell efficacy in solid tumors.



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