

## Supplementary Materials for

### **Combined tumor-directed recruitment and protection from immune suppression enable CAR T cell efficacy in solid tumors**

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#### **The PDF file includes:**

Figs. S1 to S4  
Legend for movie S1  
Methods for Supplementary Figures  
References

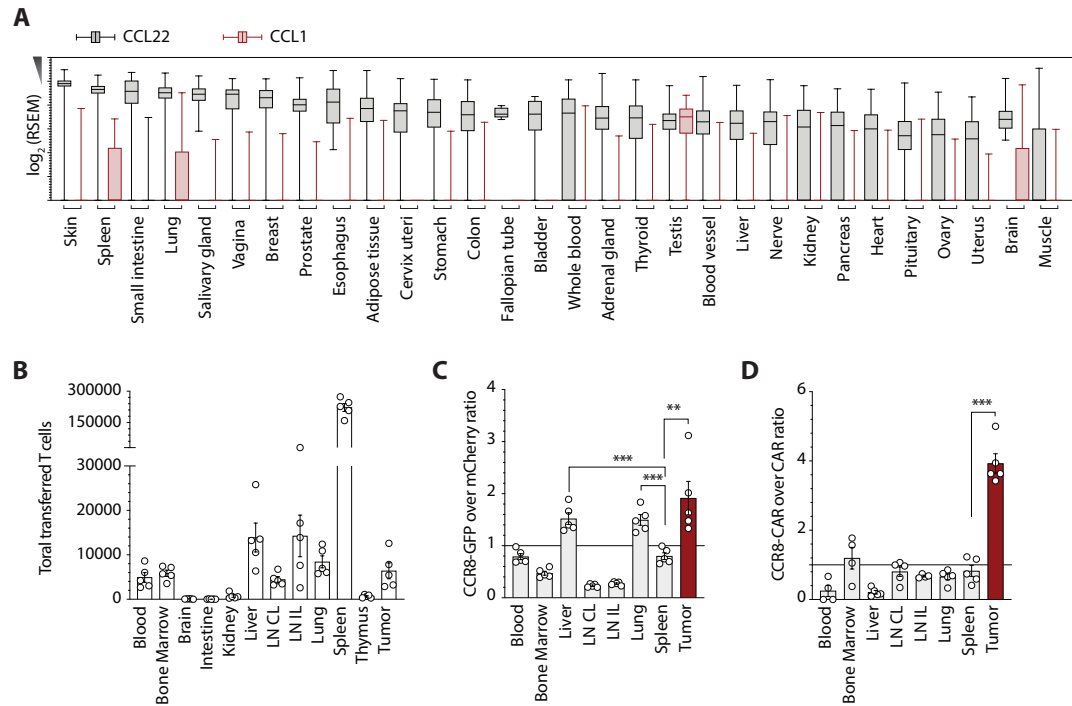
#### **Other Supplementary Material for this manuscript includes the following:**

(available at [advances.sciencemag.org/cgi/content/full/7/24/eabi5781/DC1](https://advances.sciencemag.org/cgi/content/full/7/24/eabi5781/DC1))

Movie S1

## I Supplementary Figures

Supplementary figure S1: CCL22 and CCL1 expression in several healthy human tissues and CCR8-transduced T cell homing pattern in several murine tissues.



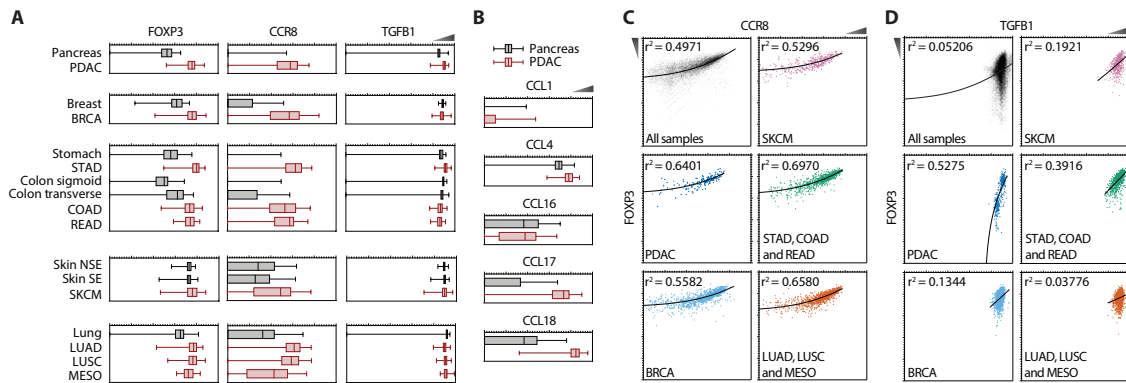
### Supplementary figure S1: CCL22 and CCL1 expression in several healthy tissues and CCR8-transduced T cell homing pattern in several murine tissues.

(A) Boxplots comparing CCL22 and CCL1 gene expression levels in several healthy tissues.

Samples analyzed for skin  $n = 557$ , spleen  $n = 101$ , small intestine  $n = 93$ , lung  $n = 289$ , salivary gland  $n = 56$ , vagina  $n = 86$ , breast  $n = 180$ , prostate  $n = 101$ , esophagus  $n = 557$ , adipose tissue  $n = 516$ , cervix uteri  $n = 11$ , stomach  $n = 175$ , colon  $n = 309$ , fallopian tube  $n = 6$ , bladder  $n = 10$ , whole blood  $n = 338$ , adrenal gland  $n = 129$ , thyroid  $n = 280$ , testis  $n = 166$ , blood vessel  $n = 557$ , liver  $n = 111$ , nerve  $n = 279$ , kidney  $n = 29$ , pancreas  $n = 168$ , heart  $n = 378$ , pituitary  $n = 108$ , ovary  $n = 89$ , uterus  $n = 79$ , brain  $n = 557$  and muscle  $n = 397$ . Scales are depicted in a  $\log_2$  scale (minimum 0.5 and maximum 16, major tick interval

of 1 power of 2) and mRNA normalization was estimated by the TCGA using the RSEM (RNA-seq by expectation maximization) method. **(B to D)** Flow cytometry ACT tracking experiments with a similar layout to the one described in Figure 2I. n = 5 mice. **(B and C)** Panc02-tumor bearing mice treated with a mixed ratio of CCR8-GFP or mCherry-transduced T cells. n = 5 mice. **(D)** Panc02-EpCAM-tumor bearing mice treated with a mixed ratio of CCR8-CAR- or CAR -ransduced T cells. n = 5 mice.

Supplementary figure S2: FOXP3, CCR8 and TGFB1 genes are upregulated in pancreatic adenocarcinomas and other cancer types.

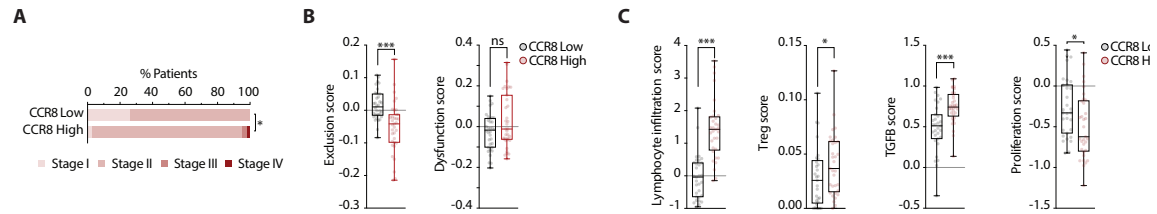


**Supplementary figure S2: FOXP3, CCR8 and TGFB1 genes are upregulated in pancreatic adenocarcinomas and other cancer types.**

(A and B) Boxplots comparing FOXP3, CCR8 (and its ligands) and TGFB1 gene expression levels in various cancers to corresponding healthy tissue in various cancers. (C and D) Correlation of CCR8 and FOXP3 and correlation of TGFB1 and FOXP3, respectively, in different tissues.  $r^2$  was used to evaluate the fit estimated by the Pearson's squared method. PDAC pancreatic adenocarcinoma, BRCA breast invasive carcinoma, STAC stomach adenocarcinoma, COAD colon adenocarcinoma, READ rectum adenocarcinoma, NSE not-sun exposed, SE sun exposed, SKCM skin cutaneous melanoma, LUAD lung adenocarcinoma, LUSC lung squamous cell carcinoma, MESO mesothelioma. Samples analyzed for pancreas tissue n = 167, PDAC n = 183, breast mammary tissue n = 179, BRCA n = 1212, stomach n = 175, STAC n = 450, colon sigmoid n = 141, colon transverse n = 167, COAD n = 331, READ n = 103, skin NSE n = 233, skin SE n = 324, SKCM n = 470, lung n = 288, LUAD n = 574, LUSC n = 548 and MESO n = 87. All scales are depicted in a log<sub>2</sub> scale (minimum 0.5 and maximum 16, major tick interval of 1 power of 2) and mRNA normalization was estimated by the TCGA using the RSEM (RNA-seq by expectation maximization) method.



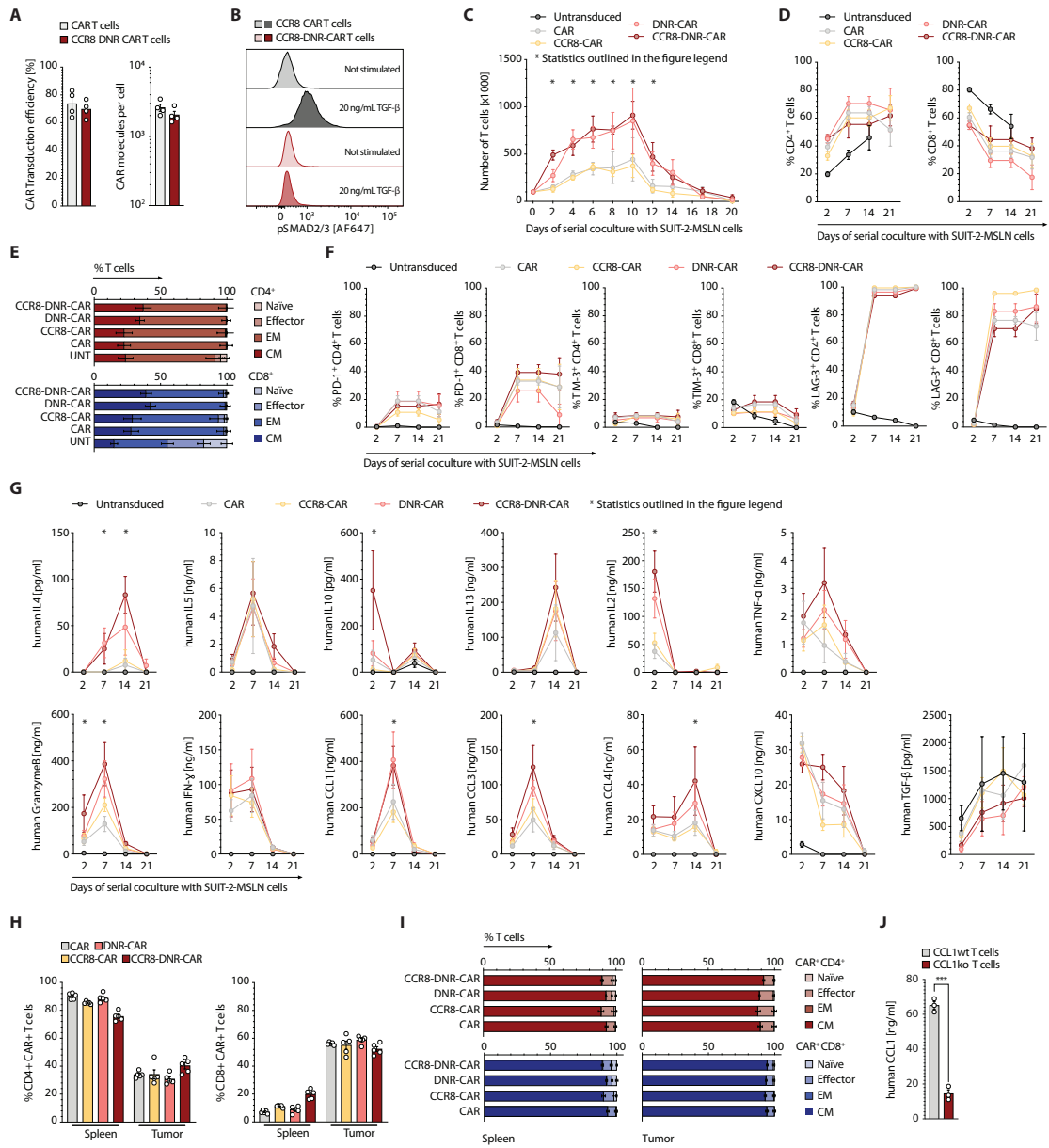
Supplementary figure S3: T cell exclusion and dysfunction signatures in PDAC patients according to CCR8 expression.



**Supplementary figure S3: T cell exclusion and dysfunction signatures in PDAC patients according to CCR8 expression.**

(A) PDAC staging correlation with CCR8-expression. (B) TIDE analysis of CCR8 expression in T cell exclusion and dysfunction signatures in PDAC patients. (C) Lymphocyte infiltration, T<sub>reg</sub>, TGFB and Proliferation scores according to CCR8-expression in PDAC patients. PDAC patients from the TCGA database were included according to their CCR8 expression in a CCR8 High group (top 20<sup>th</sup> percentile) (n = 26) or in a CCR8 Low group (bottom 20<sup>th</sup> percentile) (n = 26). Statistical analysis for (A) was performed using a Chi-squared test, and two-tailed Mann-Whitney test for (B and C).

Supplementary figure S4: Extended *in vitro* and *ex vivo* characterization of human T cells.



**Supplementary figure S4: Extended *in vitro* and *ex vivo* characterization of human T cells.**

(A) Transduction efficiency and surface expression of CAR in CAR- and CCR8-DNR-CAR-transduced T cells, as determined by flow cytometry and QIFIKIT (Agilent Technologies), respectively. (B) Phospho-specific flow cytometry of SMAD2/3. (C to G) Long-term coculture assay was carried out as described:  $10^5$  CAR-, CCR8-CAR-, DNR-CAR- or CCR8-

DNR-CAR-transduced T cells were cocultured with  $2 \times 10^4$  SUIT-MSLN tumor cells. T cells were serially transferred to new tumor cells every 2 days. **(C)** An equal volume of T cells was collected at each T cell transfer to monitor T cell proliferation. Day 2 CCR8-DNR-CAR vs CCR8-CAR  $p = 0.028$ , CCR8-DNR-CAR vs CAR  $p = 0.045$ . Day 4 CCR8-DNR-CAR vs CCR8-CAR  $p = 0.047$ , DNR-CAR vs CCR8-CAR  $p = 0.045$ . Day 6 CCR8-DNR-CAR vs CCR8-CAR  $p = 0.011$ , CCR8-DNR-CAR vs CAR  $p = 0.007$ . Day 8 CCR8-DNR-CAR vs CCR8-CAR  $p = 0.004$ , DNR-CAR vs CCR8-CAR  $p = 0.024$ , CCR8-DNR-CAR vs CAR  $p = 0.012$ , DNR-CAR vs CAR  $p = 0.045$ . Day 10 CCR8-DNR-CAR vs CCR8-CAR  $p < 0.001$ , DNR-CAR vs CCR8-CAR  $p = 0.010$ , CCR8-DNR-CAR vs CAR  $p = 0.002$ , DNR-CAR vs CAR  $p = 0.042$ . Day 12 CCR8-DNR-CAR vs CCR8-CAR  $p = 0.036$ .  $n = 6$  healthy donors.

**(D)** Changes in the frequency of  $CD4^+$  and  $CD8^+$  T cells assessed by flow cytometry after 2, 7, 14 and 21 days of coculture. **(E)** Phenotypic characterization of T cell products using CD45RO and CCR7 expression, allowing for the differentiation of effector memory (EM), central memory (CM), effector or naïve T cells in after 2 days of coculture. **(F)** Frequency of expression of PD-1, TIM-3 and LAG-3 in  $CD4^+$  and  $CD8^+$  T cell populations after 2, 7, 14 and 21 days of coculture. **(G)** Secreted IL-4, IL-5, IL-10, IL-13, IL-2, TNF- $\alpha$ , granzyme B, IFN- $\gamma$ , CCL1, CCL3, CCL4, CXCL10 and TGF- $\beta$  cytokine concentrations determined by ELISA across different coculture conditions after 2, 7, 14 and 21 days of coculture. CCL1 on day 7 for CCR8-DNR-CAR vs CCR8-CAR  $p = 0.013$ , CCR8-DNR-CAR vs CAR  $p = 0.043$ , DNR-CAR vs CCR8-CAR  $p < 0.001$ , DNR-CAR vs CAR  $p = 0.007$ . CCL3 on day 7 for CCR8-DNR-CAR vs CCR8-CAR  $p < 0.001$ , CCR8-DNR-CAR vs CAR  $p < 0.001$ , DNR-CAR vs CAR  $p = 0.035$ . CCL4 on day 14 for CCR8-DNR-CAR vs CCR8-CAR  $p = 0.009$ , CCR8-DNR-CAR vs CAR  $p = 0.029$ . Granzyme B on day 7 CCR8-DNR-CAR vs CCR8-CAR  $p = 0.005$ , CCR8-DNR-CAR vs CAR  $p < 0.001$ , DNR-CAR vs CAR  $p = 0.006$ . IL-2 on day 2 CCR8-DNR-CAR vs DNR-CAR  $p = 0.028$ , CCR8-DNR-CAR vs CCR8-CAR  $p <$

0.001, CCR8-DNR-CAR vs CAR  $p < 0.001$ , DNR-CAR vs CCR8-CAR  $p < 0.001$ , DNR-CAR vs CAR  $p < 0.001$ . IL-4 on day 14 CCR8-DNR-CAR vs CCR8-CAR  $p < 0.001$ , CCR8-DNR-CAR vs CAR  $p < 0.001$ , DNR-CAR vs CCR8-CAR  $p = 0.026$ , DNR-CAR vs CAR  $p = 0.009$ . IL-10 on day 2 CCR8-DNR-CAR vs DNR-CAR  $p < 0.001$ , CCR8-DNR-CAR vs CCR8-CAR  $p < 0.001$ , CCR8-DNR-CAR vs CAR  $p < 0.001$ . TGF- $\beta$  concentrations was significantly increased over time for all conditions,  $p = 0.001$ . **(H and I)** Data for tumor and spleen infiltrating T cells after 19 days *in vivo*, from the experiment in Figure 5M.  $n = 5$  mice per group. **(H)** Frequency of expression of CD45<sup>+</sup>CD3<sup>+</sup> SUIT-2-Mesothelin-CCL1 infiltrating CD4<sup>+</sup> and CD8<sup>+</sup> T cells. **(I)** Phenotypic characterization using CD45RO and CCR7 expression, allowing for the differentiation of effector memory (EM), central memory (CM), effector or naïve T cells. **(J)** Technical validation of CCL1 knock-out from primary human T cells through CCL1 ELISA on supernatant of T cells activated for 24 hours with anti-CD3 and anti-CD28 antibodies.  $n = 3$  healthy donors.

### **Supplementary movie 1: Multiphoton intra-vital microscopy tracking of tumor infiltrating CCR8-GFP T cells versus mCherry T cells.**

ACT tracking experiment in a mouse implanted with a tumor within a dorsal skin-fold chamber to enable multi-photon intra-vital imaging.

## **II Methods for supplementary Figures**

### *Data mining*

We utilized the bioinformatics tool UCSC Xena to retrieve data from TCGA (The Cancer Genome Atlas). TCGA RNA sequencing datasets were analysed in comparison to GTex (Genotype-tissue Expression) healthy tissue reference datasets concerning the expression of multiple genes. Correlations were assessed through  $r^2$ , goodness of fit estimated by the Pearson's squared. mRNA normalization was estimated by the TCGA using the RSEM

(RNA-seq by expectation maximization) method. For Tumor Immune Dysfunction and Exclusion (TIDE) analysis on PDAC patients we used the TIDE tool with CCR8 as the query gene (<http://tide.dfci.harvard.edu/query/>) (54). PDAC datasets were stratified by bulk tumor expression levels of CCR8 in groups that included the 20% higher and 20% lower expression levels of CCR8. These high and low groups were then evaluated for evidence of T cell dysfunction and exclusion. Immune tumor microenvironment was analyzed using the iAtlas deconvolution tool (<https://www.cri-iatlas.org/>) (55) and datasets stratified as for TIDE analysis.

#### *Long-term coculture assay*

T cell and tumor cell cocultures were set-up at indicated effector to target ratios. T cells expressing either CAR, CCR8-CAR, DNR-CAR or CCR8-DNR-CAR were coincubated with SUIT-MSLN tumor cells, and serially transferred to newly plated SUIT-MSLN cells every two to three days. To assess the impact of regular antigen restimulation on transduced T cells, collected supernatant to assess the cytokine profile of the cells after 2, 7, 14 and 21 days of coculture. DuoSet ELISA kits were purchased from R&D to assess the cytokine concentrations of human TNF- $\alpha$  (DY210), CCL3 (DY270), CCL4 (DY271), CXCL10 (DY266), IL-2 (DY202), IL-4 (DY204), IL-5 (DY205), IL-10 (DY217B), IL-13(DY213), granzyme B (DY2906-05), and TGF- $\beta$  (DY240). At the same time points, we used flow cytometry to assess T cell proliferation and phenotype. An equal volume of cells was stained using antibodies from Biolegend against human CD3 (HIT3a), CD4 (A161A1), CD8 (SK1), PD-1 (EH12.2H7), LAG-3 (11C3C65), TIM-3(F38-2E2), as well as the Miltenyi antibody against c-myc (SH1-26E7.1.3) to assess CAR expression. CountBright counting beads were used to assess and normalize T cell proliferation across conditions and over time.

#### *Phospho-Flow of SMAD2/3*

The antibody from BD against pSMAD2/3 (O72-670) was used to assess downstream signaling of TGF- $\beta$  according to the manufacturers protocol.

*Cell surface molecule quantification through quantitative analysis kit*

Surface antigen density of constructs was evaluated through flow cytometry with QIFIKIT (Agilent) using a Biolegend antibody against c-Myc (9E10).

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