(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
04 August 2022 (04.08.2022)

WIPO | PCT

(10) International Publication Number
WO 2022/165440 A3

(51) International Patent Classification:
A61K 39/395 (2006.01) *A61P 35/04* (2006.01)

(21) International Application Number:
PCT/US2022/014792

(22) International Filing Date:
01 February 2022 (01.02.2022)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
63/144,337 01 February 2021 (01.02.2021) US

(71) Applicant: **THE REGENTS OF THE UNIVERSITY OF CALIFORNIA** [US/US]; 1111 Franklin Street, Twelfth Floor, Oakland, CA 94607 (US).

(72) Inventors: **PRUSSAK, Charles, E.**; c/o 9500 Gilman Drive, La Jolla, CA 92093 (US). **OH, Christopher**; c/o The Regents of the University of California, 1111 Franklin Street, Twelfth Floor, Oakland, CA 94607 (US).

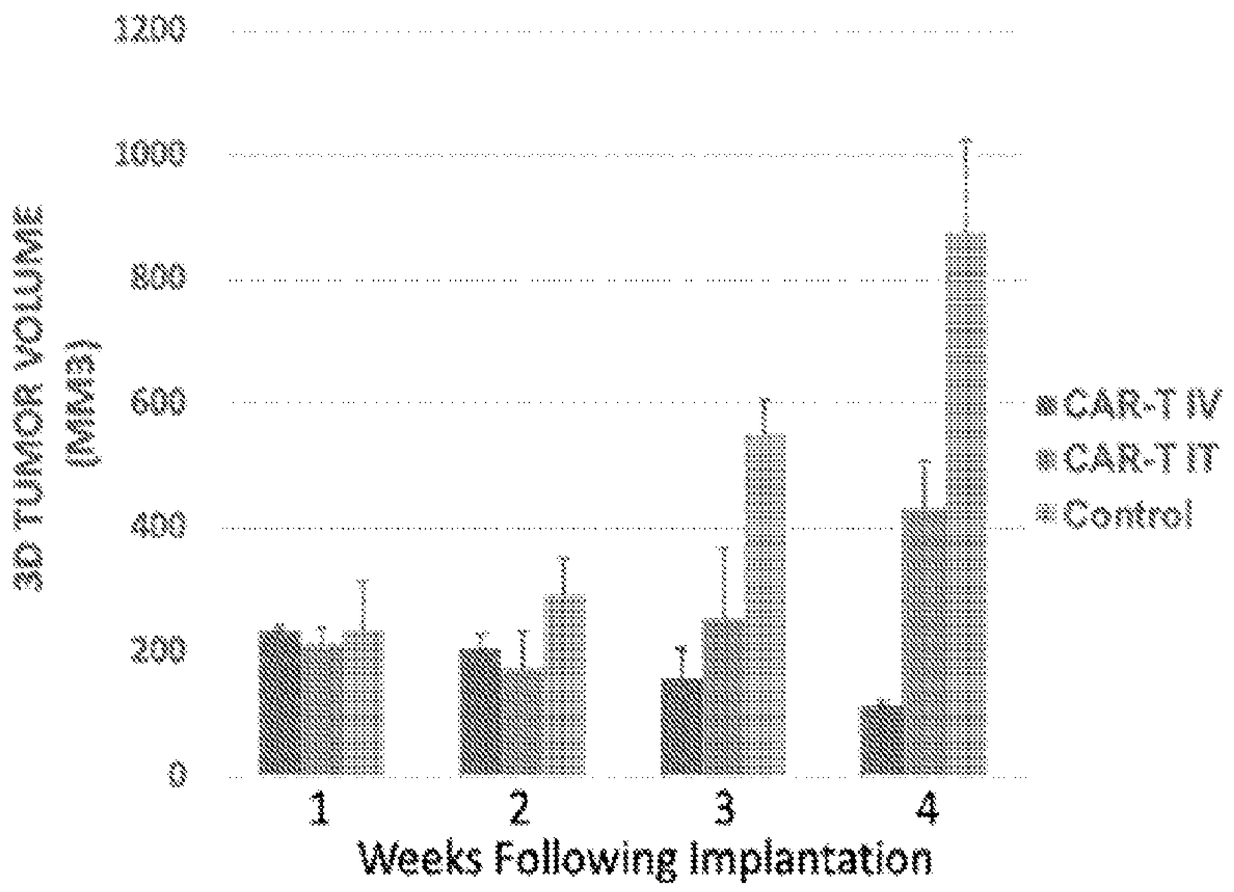
(74) Agent: **DI NOLA-BARON, Liliana** et al.; Mintz Levin Cohn Ferris Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

(54) **Title:** TREATMENT OF NEUROENDOCRINE CANCERS

FIGURE 12



(57) **Abstract:** Provided herein are complositions and methods for treating neuroendocrine cancer and preventing or treating metastasis originating from a neuroendocrine cancer.

[Continued on next page]

WO 2022/165440 A3

WO 2022/165440 A3

Published:
— *with international search report (Art. 21(3))*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
— *with sequence listing part of description (Rule 5.2(a))*

(88) Date of publication of the international search report:
01 September 2022 (01.09.2022)

TREATMENT OF NEUROENDOCRINE CANCERS

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 63/144,337, filed February 1, 2021, which is hereby incorporated by reference in its entirety and for all purposes.

SEQUENCE LISTING

[0002] The Sequence Listing written in file 048537-640001WO SEQUENCE LISTING ST25.TXT, created onMarch 23, 2020, 69,632 bytes, machine format IBM-PC, MS-Windows operating system, is hereby incorporated by reference.

BACKGROUND OF THE INVENTION

[0003] Neuroendocrine tumors (NET) are rare types of tumor that arise from neuroendocrine cells. These cells have traits of both nerve cells and hormone-producing cells, and release hormones into the blood in response to signals from the nervous system. Because neuroendocrine tumors arise from cells that produce hormones, the tumors can also produce hormones. Most neuroendocrine tumors occur in the digestive tract, pancreas, rectum, lungs, appendix, and prostate gland. Neuroendocrine tumors include, but are not limited to, carcinoid tumors, islet cell tumors, medullary thyroid cancer, pheochromocytomas, neuroendocrine carcinoma of the skin (Merkel cell cancer), small cell lung cancer, large cell neuroendocrine carcinoma, and neuroendocrine prostate cancer (NEPC).

[0004] NEPC is an aggressive histologic subtype of prostate cancer that most commonly arises in later stages of prostate cancer as treatment-resistant cancer. The poor prognosis of NEPC is attributed in part to late diagnosis and a lack of effective therapeutic agents. Prostate cancer is a disease regulated by androgen, and androgen deprivation therapy (ADT) in combination with drugs that target androgen receptor (AR) signaling is standard therapy for metastatic prostate cancer. Inevitably, however, the cancer becomes resistant to ADT, developing into lethal castration resistant prostate cancer (CRPC). CRPC is a lethal disease and the second leading cause of cancer death of men in the United States. One in six men will eventually be diagnosed with prostate cancer (PCa), making it a major health problem in the U.S. One quarter of the men diagnosed with this cancer, develop advanced PCa, which has a poor medical prognosis and greatly reduced relative five-year survival expectancies. Moreover, PCa often metastasizes to bone where it typically becomes resistant to therapy and is not curative at this stage of development. A particularly malignant form of CRPC called neuroendocrine prostate cancer

(NEPC) is emerging with increasing frequency in patients treated with ADT. Despite the recent development of several novel therapies that have improved patient survival, nearly all patients with CRPC develop resistance to therapy and disease progression. Recent genome-wide next generation sequencing studies have identified recurrent molecular alterations in prostate cancer, elucidating mechanisms of treatment resistance and potential therapeutic vulnerabilities.

[0005] Prostate cancers may be targeted by CAR-T cells or other forms of immune therapy. Because there is early evidence of clinical activity of the CAR-T cells, many large multi-center clinical trials targeting either the prostate-specific membrane antigen (PMSA) (NCT04249947, NCT04227275) or the plasma membrane calcium ATPase (PSCA) (NCT04227275) are ongoing. However, there are aggressive CRPCs and NEPC that do not express PSMA or PSCA, and thus, there is an urgent unmet need to identify new prostate cancer antigens, which can be targeted by CAR T cells.

[0006] Tyrosine-protein kinase transmembrane receptor ROR1, also known as neurotrophic tyrosine kinase, receptor-related 1, is an enzyme that in humans is encoded by the ROR1 gene. ROR1 is a member of the receptor tyrosine kinase-like orphan receptor family. ROR1 is expressed on CRPC and NEPC, but not on normal post-natal and adult tissues. In addition, ROR1 appears to play a functional role in oncogenesis of PCa including the expansion of cancer specific stem-cells. Because it is expressed on the parental tumor and tumor and metastasis promoting stem-cells, ROR1 is an attractive therapeutic target.

[0007] WNT signaling is known to regulate many key cellular processes, and aberrant Wnt signaling and mutations in the pathway have been associated with tumorigenesis, progression, and metastasis in many cancers including prostate cancer (5, 6). Likewise, the deregulated expression of the WNT co-receptors ROR1 and ROR2 has been associated with several cellular features that promote malignancy, namely cell proliferation, survival, migration/invasion, and stemness. Wnt signaling was originally discovered as a group of signal transduction pathways critical for normal development and physiology (5, 6). Aberrant Wnt signaling, which is comprised of the canonical (β-catenin dependent) and noncanonical pathways, is frequently altered in prostate cancer. Comprehensive sequencing studies in patients with castration-resistant prostate cancer (CRPC) have identified recurrent molecular alterations in Wnt signaling pathway components in about 20% of advanced prostate cancer patients (4). Analysis of

circulating tumor cells (CTCs) from CRPC patients demonstrate expression of Wnt5A, the prototypical noncanonical Wnt ligand, in >60% of patients with refractory disease (7, 8).

[0008] The Wnt signaling pathway is complex and context-dependent activities of Wnt signaling are mediated via crosstalk between the canonical and noncanonical Wnt signaling. The Wnt pathway interacts with androgen receptor (AR) signaling, a key pathway in prostate cancer pathogenesis (9). Noncanonical Wnt signaling is mediated in part through ROR1 tyrosine-kinase-like orphan receptor activation by Wnt5A ligand (FIG 1). ROR1 is a conserved oncoembryonic surface protein expressed in prostate cancer cells (10). The expression of ROR1 can enhance epithelial-mesenchymal transition, cancer cell proliferation, migration and metastasis (11-13). Noncanonical Wnt signaling, mediated through ROR1, promotes bone metastases via induction of osteoblast activity (14). Moreover, ROR1 is overexpressed in chemoresistant tumors (15, 16). ROR1 expression is associated with adverse outcomes in patients, including poor therapy response and tumor recurrence (17-21). ROR1 regulates stability and transcription of the drug efflux pump ABCB1 which is overexpressed in chemoresistant tumors (22). ROR1 inhibition sensitizes cancer cells to chemotherapeutic agents and is directly correlated with decreased efflux of chemotherapeutic drugs from tumor cells (22). Furthermore, the interaction between ROR1 and cortactin plays an important role in cancer cell migration and metastasis (23, 24).

[0009] In preclinical models, Wnt5A stimulates and accelerates prostate cancer tumor growth, which is reduced by Wnt5A knockdown or haploinsufficiency (12). In addition to playing a role in tumorigenesis, noncanonical Wnt ligands have been shown to induce drug resistance to enzalutamide *in vitro* (25). Several clinical studies in advanced prostate cancer patients have shown that the noncanonical Wnt pathway is activated in advanced prostate cancer and correlates with poor prognosis in CRPC (8, 26-31). Whole transcriptome RNA-seq of single CTCs demonstrate significant enrichment for noncanonical Wnt signaling in patients with resistance to enzalutamide (7). Furthermore, Wnt5A expression in CTCs using multiplex qPCR found that Wnt5A was independently predictive of worse overall survival (8, 26).

[0010] To target this proto-oncogene, cirmtuzumab, a first-in-class ROR1 binding monoclonal antibody (mAb) was developed at the University of California San Diego (UCSD) (32). This human mAb has a high affinity for human ROR1 and no apparent off-target activities in *in vitro* or *in vivo* test systems. In a clinical study, the anti-ROR1 mAb was well tolerated with no

antibody associated serious adverse events noted, a for a prolonged half-life suggesting limited or no off-tumor binding and early evidence of anti-tumor activity (NCT02222688)(33). Because of its favorable therapeutic index, cirmtuzumab has subsequently been employed in a number of clinical studies targeting lymphoid and solid tumor cancers in combination with standard chemotherapies (NCT02776917, 02860676 and 03088878), as the targeting moiety for an antibody drug conjugate (ADC) (NCT03833180) and clinical studies with this mAb are being planned for patients with CRPC.

[0011] Elevated expression of ROR1 have been demonstrated in highly malignant, taxane resistant, breast cancer cells. Because this mAb blocks ROR1 signaling by blocking Wnt5A mediated activation, cirmtuzumab has demonstrated substantial therapeutic activity against these chemotherapy resistant tumors in preclinical models. Based on these studies, a phase Ib clinical trial combining cirmtuzumab with paclitaxel is being tested in patients with advanced breast cancer (NCT02776917) (34). Like breast cancer, a taxane (docetaxel) based chemotherapy regimen is a mainstay for the treatment of patients with advanced CRPC (35). However, when combined with abiraterone and enzalutamide, this docetaxel containing chemotherapy cocktail has minimal activity in treating CPRC, generating a 3- month median time to progression and limited impact on reducing PSA levels (<30% of patients)(36). Additionally, noncanonical Wnt signaling has been hypothesized to be a mechanism of resistance to enzalutamide (7) and taxane chemotherapy (16). Available data suggest that Wnt blockade with chemotherapy may be the most effective way to implement Wnt pathway modulation (6).

[0012] A successful potent and specific therapy that targets treatment of progressive, malignant and lethal neuroendocrine tumors is urgently needed. The methods provided herein address these and other needs in the art.

BRIEF SUMMARY OF THE INVENTION

[0013] Described herein, *inter alia*, are compositions and methods for treating a neuroendocrine cancer and methods of preventing or treating metastasis originating from a neuroendocrine cancer, that comprise the administration of cells that express chimeric antigen receptors that target human ROR-1. The chimeric antigen receptors described herein may be expressed by T lymphocytes or natural killer cells isolated from an individual afflicted with neuroendocrine cancer and re-administered to the individual. Administration of T cells expressing the CARs described herein may serve as an effective therapeutic treatment for

neuroendocrine cancers that express ROR-1. The function and efficacy of anti- ROR-1 CAR-T cells may be improved by optimized intracellular signaling domains and membrane spacers, as described herein.

[0014] In aspects, the chimeric antigen receptors comprise i) an antigen binding region, wherein the antigen binding region specifically binds ROR-1 and wherein the antigen binding region comprises a light chain variable domain and a heavy chain variable domain, ii) a spacer domain, iii) a transmembrane domain, and iv) an intracellular domain. The light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45, and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48. Alternatively, the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51, and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54.

[0015] In embodiments, the light chain variable domain is covalently linked to the heavy chain variable domain through a polypeptide linker. In embodiments, the polypeptide linker comprises an amino acid sequence of SEQ ID NO: 24.

[0016] In embodiments, the spacer domain comprises an antibody domain. In embodiments, the antibody domain comprises an immunoglobulin hinge domain, an immunoglobulin constant heavy chain 3 (CH3) domain, an immunoglobulin constant heavy chain 2 (CH2) domain, or a combination thereof.

[0017] In embodiments, the spacer domain comprises an amino acid sequence represented by SEQ ID NO: 29, SEQ ID NO: 41 or SEQ ID NO: 42.

[0018] In embodiments, the light chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 21.

[0019] In embodiments, the heavy chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 27.

[0020] In embodiments, the transmembrane domain comprises a CD8α transmembrane domain, a CD28 transmembrane domain, a CD4 transmembrane domain, a CD3ζ transmembrane

domain, or any combination thereof. In embodiments, the transmembrane domain is a CD28 transmembrane domain.

[0021] In embodiments, the intracellular domain comprises an intracellular co-stimulatory signaling domain, an intracellular T-cell signaling domain, or a combination thereof. The intracellular co-stimulatory signaling domain is a 4-1BB intracellular co-stimulatory signaling domain, a CD28 intracellular co-stimulatory signaling domain, a ICOS intracellular co-stimulatory signaling domain, an OX-40 intracellular co-stimulatory signaling domain, or any combination thereof. In embodiments, the intracellular costimulatory signaling domain comprises a 41-BB intracellular co-stimulatory signaling domain. In embodiments, the intracellular costimulatory signaling domain comprises a CD28 intracellular co-stimulatory signaling domain and a 41-BB intracellular co-stimulatory signaling domain.

[0022] In embodiments, the intracellular costimulatory signaling domain further comprises an intracellular T-cell signaling domain. In embodiments, the intracellular T-cell signaling domain is a CD3ζ intracellular T-cell signaling domain.

[0023] In embodiments, the chimeric antigen receptor binds to a cell expressing ROR-1. In embodiments, the cell expressing ROR-1 is a neuroendocrine cancerous cell.

[0024] In embodiments, the cell is a T lymphocyte. In embodiments, the T lymphocyte is a CD4+ T lymphocyte or a CD8 + T lymphocyte.

[0025] In embodiments, the cell is a natural killer cell. In embodiments, the natural killer cell is autologous to the subject. In embodiments, the natural killer cell is heterologous to the subject. In embodiments, the natural killer cell is allogeneic to the subject.

[0026] Aspects disclosed herein provide a nucleic acid encoding the chimeric antigen receptor described herein. In embodiments, the nucleic acid is a viral vector. In embodiments, the viral vector is a lentiviral vector.

[0027] Aspects disclosed herein provide a cell comprising the nucleic acid described herein. Aspects disclosed herein also provide a cell expressing the chimeric antigen receptor described herein. In embodiments, the cell is a T lymphocyte. In embodiments, the T lymphocyte is a CD4+ T lymphocyte or a CD8 + T lymphocyte. In embodiments, the cell is a natural killer cell, a genetically engineered natural killer cell or a CD56+ cell. In embodiments, the cell is a natural killer cell. In embodiments, the natural killer cell is autologous to the subject. In embodiments,

the natural killer cell is heterologous to the subject. In embodiments, the natural killer cell is allogeneic to the subject.

[0028] Aspects disclosed herein provide a pharmaceutical composition comprising a therapeutically effective amount of the cells described herein and a pharmaceutically acceptable diluent, carrier, or excipient. In embodiments, the composition is formulated for intravenous injection.

[0029] Aspects disclosed herein provide methods of treating a neuroendocrine cancer in an subject in need thereof, and methods of preventing or treating a metastasis in a subject with a neuroendocrine cancer, which comprise administering to the subjects the cells as described herein, and pharmaceutical compositions comprising the cells provided herein and excipients, additives and the like. In embodiments, the neuroendocrine cancer is a carcinoid tumor, an islet cell tumor, a medullary thyroid cancer, a pheochromocytoma, a neuroendocrine carcinoma of the skin, small cell lung cancer, large cell neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), or metastatic castration-resistant prostate cancer (CRPC). In embodiments, the neuroendocrine cancer is metastatic castration-resistant prostate cancer (CRPC).

[0030] In embodiments, the neuroendocrine cancerous cells express ROR-1. In embodiments, the subject has failed to respond to androgen deprivation therapy. In embodiments, the neuroendocrine cancer has metastasized to bone.

[0031] In embodiments, the methods provided herein further comprise administering cirmtuzumab to the subject. In embodiments, the cirmtuzumab and the cells expressing the disclosed chimeric antigen receptors are administered separately. In embodiments, the cirmtuzumab and the cells are administered together.

[0032] In embodiments, the methods provided herein further comprise administering to the subject platinum-based chemotherapy. In embodiments, the platinum-based chemotherapy comprises carboplatin, cisplatin, etoposide, a taxane, or any combination thereof. In embodiments, the platinum-based chemotherapy comprises administering to the subject an antibody-drug conjugate.

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] Figure 1 is a schematic representation showing signaling through the non-canonical Wnt pathway is mediated by Wnt5A binding to its receptor ROR1 and ROR2. Cirmtuzumab is a monoclonal antibody which targets ROR1.

[0034] Figure 2 is a schematic representation showing a Cirmtuzumab-based Chimeric Antigen Receptor (CAR) T cell targeting ROR-1.

[0035] Figure 3 present graphs showing *in vitro* cell killing activity of ROR1 CAR T-cells in a 4h chromium release assay (left panel) and 120h ACEA impedance assay (right panel) from T cells of two healthy donors, that were tranduced with ROR1 at the indicated effect to target (E:T) ratios against leukemic Mec1 ROR1pos cells in the left panel and an ACEA impedance assay against MB 231 ROR1pos breast cancer cells in the right panel. The anti-ROR1 CAR T-cells demonstrated high and specific cytotoxicity without significant killing of ROR1-negative target cells.

[0036] Figure 4 shows bioluminescence imaging of mice inoculated with MEC1-ROR1 cells and with ROR1 CAR T-Cells. Animals treated with CAR-T cells had reduced disease burden compared to controls. The highest dose ($3x10^6$ CAR-T cells) cohort showed reduction of the leukemic burden to background levels by day 30, and had only minimal amounts of disease for the duration of the study. Animals in the control groups (untreated, mock transduced) had to be sacrificed on day 20. The right panel shows the total bioluminescent product collected from the mice. Blue square and circle are controls and green triangles ROR1-CAR T treated mice.

[0037] Figure 5 shows ROR-1 CAR T cell expression in mouse tissues at various times. Following ROR-1 CAR-T administration, animals were sacrificed on days 11 (top panels) and day 25 (bottom panels). Blood and organs were collected and subjected to flow analysis for CAR expression and confirmatory ROR1 binding activity. The ROR-1 CAR-T cell number was substantially greater in mice bearing MEC-1 ROR1 cells (CAR + MEC1-ROR-1) vs control (CAR only), demonstrating elevated expansion of ROR-1 CAR-T cells in animals with tumor burden. Bars represent the mean values from the five mice in each group and error bars represent the S.E of the mean.

[0038] Figure 6 shows the results obtained from the analysis of tumor RNA sequences obtained from 66 prostate cancer samples, expressed as association of single-sample Gene Set Enrichment Analysis profiles of non-canonical WNT and stem cell gene sets with the expression of ROR1 (mRNA). The analysis shows a significant enrichment of WNT non-canonical and stem cell gene sets against ROR1 mRNA expression.

[0039] Figures 7A-7C present xenograft models obtained from prostate cancer patients. Figure 7A shows hierarchical cluster of RNA-seq analysis on PCSD1 and PCSD13. Figure 7B shows

flow cytometry (FACS) of ROR-1 protein on the cell surface of PCSD13 cells. Figure 7C shows that ROR1 is expressed on the cell surface of prostate cancer cell lines. Antibody Isotype controls are in gray. Negative control cell line: Breast cancer line, MCF7, and ROR-1 over-expressing line, MCF7_ROR1. Prostate Cancer lines: PC3 and DU145.

[0040] Figure 8 shows PCSD1 PDX tumors cells from three-dimensional organoids that replicate histomorphology of the xenografts growing in the femur bone. Three-dimensional organoid cell cultures from subjects with prostate cancer were established. The 3D cultures consisted of two main cell masses: spheroids and epithelial cysts similar to gland-like structures seen in sections from xenografts growing within the femur bone displacing bone marrow and in the patient. Spheroids were resistant to androgen deprivation-induced death. Spheroid masses contained cyst-like structures surrounded by tumor cells that were similar to gland-like structures. Black Arrows point to the cyst structures. Organoids are GFP+. PDXs were obtained from prostate cancer bone metastases. PCSD1 expressing GFP-Luciferase formed different morphologies under 3D-culture conditions. Enzalutamide treatment of PCSD1 reduced lumen size and number of epithelial cysts. Transcriptome analysis showed that AR-responsive genes such as PSA (KLK3) and TMPRSS2 were downregulated under ADT while stem-cell transcription factors, steroidogenic and neurogenic pathway genes were upregulated. Thus, anti-androgens could still suppress canonical AR-responsive genes, but the tumor and organoid growth were resistant to ADT including the anti-androgen, enzalutamide.

[0041] Figure 9 presents graphs showing that ROR1 CAR-T cells kill ROR1 expressing prostate cancer cell lines. ROR1 CAR-T cells showed significant cytotoxic killing of PCa cell lines, PC3 or DU145 cells, in culture. Increasing effect (E=T cell) to Target (T=PCa cell) ratio showed increased killing compared to Control T cells in Incucyte assay. CAR-Ts cytotoxic T cell killing is Effect: Target (E:T) dose-dependent.

[0042] Figure10A-10B presents graphs showing that anti-ROR1 CAR-T cells specifically killed PDX pCSD13 cells in Effector:Target (E:T) dose-dependent manner in culture in Incucyte Cytotoxicity assay. Left panel (A): control T cells plus PCSD13 (Target) cells freshly isolated from xenograft and cultured for 48 hours. Right panel (B): anti-ROR1 CAR-T (Effectors). The highest dose of anti-ROR1 CAR-T cells completely killed the PCSD13 cells (Blue line, E:T 3) compared to no CAR-Ts (black line E:T 0).

[0043] Figure 11 shows bioluminescence imaging of mice implanted subcutaneously with PC3 PCa cells and treated with ROR1 CAR-T cells. Animals were implanted withGFP luciferase expressing PC3 cells on day 1 and were treated with a one-time injection of 3e7 CAR-T cells IV (CAR IV) or activated mock transduced cell (Control) or 1e7 cells administered intra-tumorly (CAR IT) As shown, the CAR-T treated mice that received a single intravenous or intra-tumoral injection had reduced disease burden when compared to control animals, which had to be sacrificed by week 5. The CAR-T IV treated cohort had only minimal amounts of disease at the end of the study.

[0044] Figure 12 is a graph showing tumor Volume Measurement of Implanted PC3 cells by Caliper Measurement. Tumor volumes were measured by weekly caliper measurement for mice treated as described in Figure 11. Results are consistent with the bioluminescent measurements and better demonstrate the activity of the intravenously administered CAR product. Tumor Volume was determined with the formula (mm^3) = (L x w^2) / 2 The value w (width) is the smaller of two perpendicular tumor axes and the value L (length) is the larger of two perpendicular axes. Error bars represent the SO of the mean for the 3 measurements.

[0045] Figure 13 shows optimized IHC staining analysis of ROR1 protein expression patterns in formalin-fixed paraffin-embedded (FFPE) breast adenocarcinoma tissue as compared to a negative control.

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

[0046] While various embodiments and aspects of the present invention are shown and described herein, it will be understood to those skilled in the art that such embodiments and aspects are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention.

[0047] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in the application including, without limitation, patents, patent applications, articles, books, manuals, and treatises are hereby expressly incorporated by reference in their entirety for any purpose.

[0048] The abbreviations used herein have their conventional meaning within the chemical and biological arts. The chemical structures and formulae set forth herein are constructed according to the standard rules of chemical valency known in the chemical arts.

[0049] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by a person of ordinary skill in the art. See, e.g., Singleton et al., Dictionary Of Microbiology And Molecular Biology 2nd ed., J. Wiley & Sons (New York, NY 1994); Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Springs Harbor Press (Cold Springs Harbor, NY 1989). Any methods, devices and materials similar or equivalent to those described herein can be used in the practice of this invention. The following definitions are provided to facilitate understanding of certain terms used frequently herein and are not meant to limit the scope of the present disclosure.

[0050] As used herein, the term "about" means a range of values including the specified value, which a person of ordinary skill in the art would consider reasonably similar to the specified value. In embodiments, the term "about" means within a standard deviation using measurements generally acceptable in the art. In embodiments, about means a range extending to +/- 10% of the specified value. In embodiments, about means the specified value.

[0051] "Nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, and complements thereof. The term "polynucleotide" refers to a linear sequence of nucleotides. The term "nucleotide" typically refers to a single unit of a polynucleotide, i.e., a monomer. Nucleotides can be ribonucleotides, deoxyribonucleotides, or modified versions thereof. Examples of polynucleotides contemplated herein include single and double stranded DNA, single and double stranded RNA (including siRNA), and hybrid molecules having mixtures of single and double stranded DNA and RNA. Nucleic acid as used herein also refers to nucleic acids that have the same basic chemical structure as a naturally occurring nucleic acid. Such analogues have modified sugars and/or modified ring substituents, but retain the same basic chemical structure as the naturally occurring nucleic acid. A nucleic acid mimetic refers to chemical compounds that have a structure that is different from the general chemical structure of a nucleic acid, but that functions in a manner similar to a naturally occurring nucleic acid. Examples of such analogues include, without limitation, phosphorothiolates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, and peptide-nucleic acids (PNAs).

[0052] The term "gene" means the segment of DNA involved in producing a protein; it includes regions preceding and following the coding region (leader and trailer) as well as intervening sequences (introns) between individual coding segments (exons). The leader, the trailer, as well as the introns, include regulatory elements that are necessary during the transcription and the translation of a gene. Further, a "protein gene product" is a protein expressed from a particular gene.

[0053] The word "expression" or "expressed" as used herein in reference to a gene means the transcriptional and/or translational product of that gene. The level of expression of a DNA molecule in a cell may be determined on the basis of either the amount of corresponding mRNA that is present within the cell or the amount of protein encoded by that DNA produced by the cell. The level of expression of non-coding nucleic acid molecules may be detected by standard PCR or Northern blot methods well known in the art. See, Sambrook et al., 1989 Molecular Cloning: A Laboratory Manual, 18.1-18.88.

[0054] Expression of a transfected gene can occur transiently or stably in a cell. During "transient expression" the transfected gene is not transferred to the daughter cell during cell division. Since its expression is restricted to the transfected cell, expression of the gene is lost over time. In contrast, stable expression of a transfected gene can occur when the gene is co-transfected with another gene that confers a selection advantage to the transfected cell. Such a selection advantage may be a resistance towards a certain toxin that is presented to the cell.

[0055] The terms "transfection", "transduction", "transfecting" or "transducing" are used interchangeably throughout and are defined as a process of introducing a nucleic acid molecule or a protein to a cell. Nucleic acids are introduced to a cell using non-viral or viral-based methods. The nucleic acid molecules may be gene sequences encoding complete proteins or functional portions thereof. Non-viral methods of transfection include any appropriate transfection method that does not use viral DNA or viral particles as a delivery system to introduce the nucleic acid molecule into the cell. Exemplary non-viral transfection methods include calcium phosphate transfection, liposomal transfection, nucleofection, sonoporation, transfection through heat shock, magnetifection, and electroporation. In some embodiments, the nucleic acid molecules are introduced into a cell using electroporation following standard procedures well known in the art. For viral-based methods of transfection any useful viral vector may be used in the methods described herein. Examples for viral vectors include, but are not

limited to retroviral, adenoviral, lentiviral and adeno-associated viral vectors. In some embodiments, the nucleic acid molecules are introduced into a cell using a retroviral vector following standard procedures well known in the art. The terms "transfection" or "transduction" also refer to introducing proteins into a cell from the external environment. Typically, transduction or transfection of a protein relies on attachment of a peptide or protein capable of crossing the cell membrane to the protein of interest. See, e.g., Ford et al. (2001) Gene Therapy 8:1-4 and Prochiantz (2007) Nat. Methods 4:119-20.

[0056] The term "plasmid" or "expression vector" refers to a nucleic acid molecule that encodes for genes and/or regulatory elements necessary for the expression of genes. Expression of a gene from a plasmid can occur in cis or in trans. If a gene is expressed in cis, gene and regulatory elements are encoded by the same plasmid. Expression in trans refers to the instance where the gene and the regulatory elements are encoded by separate plasmids.

[0057] The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function in a manner similar to a naturally occurring amino acid.

[0058] Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

[0059] The terms "numbered with reference to" or "corresponding to," when used in the context of the numbering of a given amino acid or polynucleotide sequence, refer to the numbering of the residues of a specified reference sequence when the given amino acid or

polynucleotide sequence is compared to the reference sequence. An amino acid residue in a protein "corresponds" to a given residue when it occupies the same essential structural position within the protein as the given residue. One skilled in the art will immediately recognize the identity and location of residues corresponding to a specific position in a protein (e.g., ROR-1) in other proteins with different numbering systems. For example, by performing a simple sequence alignment with a protein (e.g., ROR-1) the identity and location of residues corresponding to specific positions of the protein are identified in other protein sequences aligning to the protein. For example, a selected residue in a selected protein corresponds to glutamic acid at position 138 when the selected residue occupies the same essential spatial or other structural relationship as a glutamic acid at position 138. In some embodiments, where a selected protein is aligned for maximum homology with a protein, the position in the aligned selected protein aligning with glutamic acid 138 is the to correspond to glutamic acid 138. Instead of a primary sequence alignment, a three dimensional structural alignment can also be used, e.g., where the structure of the selected protein is aligned for maximum correspondence with the glutamic acid at position 138, and the overall structures compared. In this case, an amino acid that occupies the same essential position as glutamic acid 138 in the structural model is the glutamic acid 138 residue.

[0060] The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues, wherein the polymer may optionally be conjugated to a moiety that does not consist of amino acids. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymers. A "fusion protein" refers to a chimeric protein encoding two or more separate protein sequences that are recombinantly expressed as a single moiety.

[0061] The term "recombinant" when used with reference, for example, to a cell, a nucleic acid, a protein, or a vector, indicates that the cell, nucleic acid, protein or vector has been modified by or is the result of laboratory methods. Thus, for example, recombinant proteins include proteins produced by laboratory methods. Recombinant proteins can include amino acid residues not found within the native (non-recombinant) form of the protein or can be include amino acid residues that have been modified (e.g., labeled).

[0062] The term "isolated", when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is essentially free of other cellular components with which it is associated in the

natural state. It can be, for example, in a homogeneous state and may be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein that is the predominant species present in a preparation is substantially purified.

[0063] The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., 60% identity, optionally 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity over a specified region, e.g., of the entire polypeptide sequences of the invention or individual domains of the polypeptides of the invention), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Such sequences are then "substantially identical." This definition also refers to the complement of a test sequence. Optionally, the identity exists over a region that is at least about 50 nucleotides in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides in length.

[0064] "Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

[0065] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison

algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

[0066] A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of, e.g., a full length sequence or from 20 to 600, about 50 to about 200, or about 100 to about 150 amino acids or nucleotides in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Any methods of alignment of sequences for comparison well known in the art are contemplated. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1970) Adv. Appl. Math. 2:482c, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel et al., Current Protocols in Molecular Biology (1995 supplement)).

[0067] Example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) Nuc. Acids Res. 25:3389-3402, and Altschul et al. (1990) J. Mol. Biol. 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are

halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci.* USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

[0068] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

[0069] An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross-reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically or substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequence.

[0070] Antibodies are large, complex molecules (molecular weight of ~150,000 or about 1320 amino acids) with intricate internal structure. A natural antibody molecule contains two identical pairs of polypeptide chains, each pair having one light chain and one heavy chain. Each light chain and heavy chain in turn consists of two regions: a variable ("V") region involved in

binding the target antigen, and a constant ("C") region that interacts with other components of the immune system. The light and heavy chain variable regions come together in 3-dimensional space to form a variable region that binds the antigen (for example, a receptor on the surface of a cell). Within each light or heavy chain variable region, there are three short segments (averaging 10 amino acids in length) called the complementarity determining regions ("CDRs"). The six CDRs in an antibody variable domain (three from the light chain and three from the heavy chain) fold up together in 3-dimensional space to form the actual antibody binding site which docks onto the target antigen. The position and length of the CDRs have been precisely defined by Kabat, E. et al., Sequences of Proteins of Immunological Interest, U.S. Department of Health and Human Services, 1983, 1987. The part of a variable region not contained in the CDRs is called the framework ("FR"), which forms the environment for the CDRs.

[0071] An "antibody variant" as provided herein refers to a polypeptide capable of binding to an antigen and including one or more structural domains (e.g., light chain variable domain, heavy chain variable domain) of an antibody or fragment thereof. Non-limiting examples of antibody variants include single-domain antibodies or nanobodies, monospecific Fab2, bispecific Fab2, trispecific Fab3, monovalent IgGs, scFv, bispecific antibodies, bispecific diabodies, trispecific triabodies, scFv-Fc, minibodies, IgNAR, V-NAR, hcIgG, VhH, or peptibodies. A "peptibody" as provided herein refers to a peptide moiety attached (through a covalent or non-covalent linker) to the Fc domain of an antibody. Further non-limiting examples of antibody variants known in the art include antibodies produced by cartilaginous fish or camelids. A general description of antibodies from camelids and the variable regions thereof and methods for their production, isolation, and use may be found in references WO97/49805 and WO 97/49805 which are incorporated by reference herein in their entirety and for all purposes. Likewise, antibodies from cartilaginous fish and the variable regions thereof and methods for their production, isolation, and use may be found in WO2005/118629, which is incorporated by reference herein in its entirety and for all purposes.

[0072] The terms "CDR L1", "CDR L2" and "CDR L3" as provided herein refer to the complementarity determining regions (CDR) 1, 2, and 3 of the variable light (L) chain of an antibody. In embodiments, the variable light chain provided herein includes in N-terminal to C-terminal direction a CDR L1, a CDR L2 and a CDR L3. Likewise, the terms "CDR H1", "CDR H2" and "CDR H3" as provided herein refer to the complementarity determining regions (CDR)

1, 2, and 3 of the variable heavy (H) chain of an antibody. In embodiments, the variable light chain provided herein includes in N-terminal to C-terminal direction a CDR L1, a CDR L2 and a CDR L3.

[0073] The term "antibody" is used according to its commonly known meaning in the art. Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to VH-CH1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Fundamental Immunology (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty et al., *Nature 348*:552-554 (1990)).

[0074] The term "antigen" as provided herein refers to molecules capable of binding to the antibody binding domain provided herein. An "antigen binding domain" as provided herein is a region of an antibody that binds to an antigen (epitope). As described above, the antigen binding domain is generally composed of one constant and one variable domain of each of the heavy and the light chain (VL, VH, CL and CH1, respectively). The paratope or antigen-binding site is formed on the N-terminus of the antigen binding domain. The two variable domains of an antigen binding domain typically bind the epitope on an antigen.

[0075] Antibodies exist, for example, as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to VH-CH1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially the antigen binding portion with part of the hinge region (see Fundamental Immunology (Paul ed.,

3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g.,e.g., single chain Fv) or those identified using phage display libraries (see, e.g.,e.g., McCafferty et al., Nature 348:552-554 (1990)).

[0076] A single-chain variable fragment (scFv) is typically a fusion protein of the variable regions of the heavy (VH) and light chains (VL) of immunoglobulins, connected with a short linker peptide of 10 to about 25 amino acids. The linker may usually be rich in glycine for flexibility, as well as serine or threonine for solubility. The linker can either connect the N-terminus of the VH with the C-terminus of the VL, or vice versa.

[0077] The term "polypepetide linker" alternatively referred to as "polypeptide sequence" refers to a polypeptide segment that covalently links two adjacent domains within a protein. "Polypeptide linker" or "polypeptide sequence" as used herein covalently couple the light chain variable domain to the heavy chain variable domain. The linker can either connect the N-terminus of the V_H with the C-terminus of the V_L, or vice versa.

[0078] Polypeptide linkers may range from about 20 to about 60 amino acids in length. Short linker peptides may comprise from about 10 to about 25 amino acids. In embodiments, the polypeptide linker comprises between 10 and 50 amino acids. In embodiments, the polypeptide linker comprises between 10 and 40 amino acids. In embodiments, the polypeptide linker comprises between 10 and 30 amino acids. In embodiments, the polypeptide linker comprises between 10 and 20 amino acids. In embodiments, the polypeptide linker comprises between 10 and 15 amino acids.The linker may usually be rich in glycine for flexibility, as well as serine or threonine for solubility.

[0079] The epitope of an antibody is the region of its antigen to which the antibody binds. Two antibodies bind to the same or overlapping epitope if each competitively inhibits (blocks) binding of the other to the antigen. That is, a 1x, 5x, 10x, 20x or 100x excess of one antibody inhibits binding of the other by at least 30% but preferably 50%, 75%, 90% or even 99% as measured in a competitive binding assay (see, e.g., Junghans et al., Cancer Res. 50:1495, 1990). Alternatively, two antibodies have the same epitope if essentially all amino acid mutations in the

antigen that reduce or eliminate binding of one antibody reduce or eliminate binding of the other. Two antibodies have overlapping epitopes if some amino acid mutations that reduce or eliminate binding of one antibody reduce or eliminate binding of the other.

[0080] The term "ROR-1" or "ROR1" as used herein refers to any of the recombinant or naturally-occurring forms of tyrosine kinase-like orphan receptor 1 (ROR-1) or variants or homologs thereof that maintain ROR-1 activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to ROR-1). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g., a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring ROR-1 protein. In embodiments, the ROR-1 protein is substantially identical to the protein identified by Accession No. NP_005003.1 or a variant or homolog having substantial identity thereto. In embodiments, the ROR-1 protein includes the amino acid sequence of SEQ ID NO:55. In embodiments, the ROR-1 protein is the amino acid sequence of SEQ ID NO: 55. In embodiments, the ROR-1 protein includes the amino acid sequence of SEQ ID NO:56. In embodiments, the ROR-1 protein includes the amino acid sequence of SEQ ID NO:57.

[0081] The terms "cirmtuzumab", "UC-961", and "99961.1" refer to a humanized monoclonal antibody capable of binding the extracellular domain of the human receptor tyrosine kinase-like orphan receptor 1 (ROR-1). In embodiments, cirmtuzumab is any one of the antibodies or fragments thereof disclosed in US Patent Application No. 14/422,519, which is incorporated by reference herein in its entirety and for all purposes.

[0082] The term "CD28 transmembrane domain" as provided herein includes any of the recombinant or naturally-occurring forms of the transmembrane domain of CD28, or variants or homologs thereof that maintain CD28 transmembrane activity (e.g. within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the CD28 transmembrane domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring CD28 transmembrane domain polypeptide. In embodiments, the CD28 transmembrane domain is a human CD28 transmembrane domain protein. In embodiments, a variant or mutant of the CD28 transmembrane domain protein includes no more than 5, 4, 3, 2,

or 1 deletions compared to the naturally occurring CD28 transmembrane domain protein. In embodiments, a variant or mutant of the CD28 transmembrane domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring CD28 transmembrane domain protein. In embodiments, a variant or mutant of the CD28 transmembrane domain protein does not include deletions compared to the naturally occurring CD28 transmembrane domain protein. In embodiments, a variant or mutant of the CD28 transmembrane domain protein does not include insertions compared to the naturally occurring CD28 transmembrane domain protein. In embodiments, a variant or mutant of the CD28 transmembrane domain protein includes substitutions that are conservative substitutions compared to the naturally occurring CD28 transmembrane domain protein. In embodiments, the CD28 transmembrane domain includes all or a portion of the protein as identified by NCBI sequence reference NP_001230006.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD28 transmembrane domain includes all or a portions of the protein as identified by the NCBI sequence reference NP_ 001230007.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD28 transmembrane domain includes all or a portion of the protein as identified by the NCBI sequence reference NP_006130.1, or an isoform or naturally occurring mutant or variant thereof.

[0083] The term "CD4 transmembrane domain" as provided herein includes any of the recombinant or naturally-occurring forms of the transmembrane domain of CD4, or variants or homologs thereof that maintain CD4 transmembrane domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the CD4 transmembrane domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring CD4 transmembrane domain polypeptide. In embodiments, the CD4 transmembrane domain is a human CD4 transmembrane domain protein. In embodiments, a variant or mutant of the CD4 transmembrane domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring CD4 transmembrane domain protein. In embodiments, a variant or mutant of the CD4 transmembrane domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring CD4 transmembrane domain protein. In embodiments, a variant or mutant of the CD4 transmembrane domain protein does not include

deletions compared to the naturally occurring CD4 transmembrane domain protein. In embodiments, a variant or mutant of the CD4 transmembrane domain protein does not include insertions compared to the naturally occurring CD4 transmembrane domain protein. In embodiments, a variant or mutant of the CD4 transmembrane domain protein includes substitutions that are conservative substitutions compared to the naturally occurring CD4 transmembrane domain protein. In embodiments, the CD4 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_000607.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD4 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001181943.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD4 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001181944.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD4 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001181945.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD4 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001181946.1, or an isoform or naturally occurring mutant or variant thereof.

[0084] The term "CD8 transmembrane domain" as provided herein includes any of the recombinant or naturally-occurring forms of the transmembrane domain of CD8, or variants or homologs thereof that maintain CD8 transmembrane domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the CD8 transmembrane domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring CD8 transmembrane domain polypeptide. In embodiments, the CD8 transmembrane domain is CD8A transmembrane domain. In embodiments, the CD8 transmembrane domain is a CD8B transmembrane domain. In embodiments, the CD8 transmembrane domain is a human CD8 transmembrane domain protein. In embodiments, a variant or mutant of the CD8 transmembrane domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring CD8 transmembrane domain protein. In embodiments, a variant or mutant of the CD8 transmembrane domain protein includes no more than 5, 4, 3, 2, or 1 insertions

compared to the naturally occurring CD8 transmembrane domain protein. In embodiments, a variant or mutant of the CD8 transmembrane domain protein does not include deletions compared to the naturally occurring CD8 transmembrane domain protein. In embodiments, a variant or mutant of the CD8 transmembrane domain protein does not include insertions compared to the naturally occurring CD8 transmembrane domain protein. In embodiments, a variant or mutant of the CD8 transmembrane domain protein includes substitutions that are conservative substitutions compared to the naturally occurring CD8 transmembrane domain protein. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001139345.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001181943.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001181944.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001181945.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_741969.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001759.3, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference XP_011531466.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001171571.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_757362.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_742100.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence

reference NP_742099.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD8 transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_004922.1, or an isoform or naturally occurring mutant or variant thereof.

[0085] The term "CD3-zeta transmembrane domain" as provided herein includes any of the recombinant or naturally-occurring forms of the transmembrane domain of CD3-zeta, or variants or homologs thereof that maintain CD3-zeta transmembrane domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the CD3-zeta transmembrane domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring CD3-zeta transmembrane domain polypeptide. In embodiments, the CD3-zeta transmembrane domain is a human CD3- zeta transmembrane domain protein. In embodiments, a variant or mutant of the CD3-zeta transmembrane domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring CD3-zeta transmembrane domain protein. In embodiments, a variant or mutant of the CD3-zeta transmembrane domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring CD3-zeta transmembrane domain protein. In embodiments, a variant or mutant of the CD3-zeta transmembrane domain protein does not include deletions compared to the naturally occurring CD3-zeta transmembrane domain protein. In embodiments, a variant or mutant of the CD3-zeta transmembrane domain protein does not include insertions compared to the naturally occurring CD3-zeta transmembrane domain protein. In embodiments, a variant or mutant of the CD3-zeta transmembrane domain protein includes substitutions that are conservative substitutions compared to the naturally occurring CD3-zeta transmembrane domain protein. In embodiments, the CD3-zeta transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_000725.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD3-zeta transmembrane domain includes all or a portion of the protein identified by the NCBI sequence reference NP_932170.1, or an isoform or naturally occurring mutant or variant thereof.

[0086] The term "CD28 co-stimulatory domain" as provided herein includes any of the recombinant or naturally-occurring forms of the co-stimulatory domain of CD28, or variants or

homologs thereof that maintain CD28 co-stimulatory domain activity (e.g. within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the CD28 co-stimulatory domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring CD28 co-stimulatory domain polypeptide. In embodiments, the CD28 co-stimulatory domain is a human CD28 co-stimulatory domain protein. In embodiments, a variant or mutant of the CD28 co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring CD28 co-stimulatory domain protein. In embodiments, a variant or mutant of the CD28 co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring CD28 co-stimulatory domain protein. In embodiments, a variant or mutant of the CD28 co-stimulatory domain protein does not include deletions compared to the naturally occurring CD28 co-stimulatory domain protein. In embodiments, a variant or mutant of the CD28 co-stimulatory domain protein does not include insertions compared to the naturally occurring CD28 co-stimulatory domain protein. In embodiments, a variant or mutant of the CD28 co-stimulatory domain protein includes substitutions that are conservative substitutions compared to the naturally occurring CD28 co-stimulatory domain protein. In embodiments, the CD28 co-stimulatory domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001230006.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD28 co-stimulatory domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001230007.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD28 co-stimulatory domain includes all or a portion of the protein identified by the NCBI sequence reference NP_006130.1, or an isoform or naturally occurring mutant or variant thereof.

[0087] The term "4-1BB co-stimulatory domain" as provided herein includes any of the recombinant or naturally-occurring forms of the co-stimulatory domain of 4-1BB, or variants or homologs thereof that maintain 4-1BB co-stimulatory domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the 4-1BB co-stimulatory domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the

sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring 4-1BB co-stimulatory domain polypeptide. In embodiments, the 4-1BB co-stimulatory domain is a human 4-1BB co-stimulatory domain protein. In embodiments, a variant or mutant of the 4-1BB co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring 4-1BB co-stimulatory domain protein. In embodiments, a variant or mutant of the 4-1BB co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring 4-1BB co-stimulatory domain protein. In embodiments, a variant or mutant of the 4-1BB co-stimulatory domain protein does not include deletions compared to the naturally occurring 4-1BB co-stimulatory domain protein. In embodiments, a variant or mutant of the 4-1BB co-stimulatory domain protein does not include insertions compared to the naturally occurring 4-1BB co-stimulatory domain protein. In embodiments, a variant or mutant of the 4-1BB co-stimulatory domain protein includes substitutions that are conservative substitutions compared to the naturally occurring 4-1BB co-stimulatory domain protein. In embodiments, the 4-1BB co-stimulatory domain protein amino acid sequence has at least or about 50%, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identify to SEQ ID NO:14. In embodiments, the 4-1BB co-stimulatory domain includes all or a portion of the protein identified by the NCBI sequence reference NP_001552.2 or an isoform or naturally occurring mutant or variant thereof.

[0088] The term "ICOS co-stimulatory domain" as provided herein includes any of the recombinant or naturally-occurring forms of the co-stimulatory domain of ICOS, or variants or homologs thereof that maintain ICOS co-stimulatory domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the ICOS co-stimulatory domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring ICOS co-stimulatory domain polypeptide. In embodiments, the ICOS co-stimulatory domain is a human ICOS co-stimulatory domain protein. In embodiments, a variant or mutant of the ICOS co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring ICOS co-stimulatory domain protein. In embodiments, a variant or mutant of the ICOS co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring ICOS co-stimulatory domain protein. In

embodiments, a variant or mutant of the ICOS co-stimulatory domain protein does not include deletions compared to the naturally occurring ICOS co-stimulatory domain protein. In embodiments, a variant or mutant of the ICOS co-stimulatory domain protein does not include insertions compared to the naturally occurring ICOS co-stimulatory domain protein. In embodiments, a variant or mutant of the ICOS co-stimulatory domain protein includes substitutions that are conservative substitutions compared to the naturally occurring ICOS co-stimulatory domain protein. In embodiments, the ICOS co-stimulatory domain includes all or a portion of the protein identified by the NCBI sequence reference NP_036224.1, or an isoform or naturally occurring mutant or variant thereof.

[0089] The term "OX-40 co-stimulatory domain" as provided herein includes any of the recombinant or naturally-occurring forms of the co-stimulatory domain of OX-40, or variants or homologs thereof that maintain OX-40 co-stimulatory domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the OX-40 co-stimulatory domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring OX-40 co-stimulatory domain polypeptide. In embodiments, the OX-40 co-stimulatory domain is a human OX-40 co-stimulatory domain protein. In embodiments, a variant or mutant of the OX-40 co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring OX-40 co-stimulatory domain protein. In embodiments, a variant or mutant of the OX-40 co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring OX-40 co-stimulatory domain protein. In embodiments, a variant or mutant of the OX-40 co-stimulatory domain protein does not include deletions compared to the naturally occurring OX-40 co-stimulatory domain protein. In embodiments, a variant or mutant of the OX-40 co-stimulatory domain protein does not include insertions compared to the naturally occurring OX-40 co-stimulatory domain protein. In embodiments, a variant or mutant of the OX-40 co-stimulatory domain protein includes substitutions that are conservative substitutions compared to the naturally occurring OX-40 co-stimulatory domain protein. In embodiments, the OX-40 co-stimulatory domain includes all or a portion of the protein identified by the NCBI sequence reference NP_003318.1, or an isoform or naturally occurring mutant or variant thereof.

[0090] The term "CTLA-4 co-stimulatory domain" as provided herein includes any of the recombinant or naturally-occurring forms of the co-stimulatory domain of CTLA-4, or variants or homologs thereof that maintain CTLA-4 co-stimulatory domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the CTLA-4 co-stimulatory domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g. a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring CTLA-4 co-stimulatory domain polypeptide. In embodiments, CTLA-4 co-stimulatory domain protein is a human CTLA-4 co-stimulatory domain protein. In embodiments, the CTLA-4 co-stimulatory domain includes no more than 5, 4, 3, 2, or 1 deletions. In embodiments, the CTLA-4 co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 insertions. In embodiments, the CTLA-4 co-stimulatory domain protein does not include deletions. In embodiments, CTLA-4 co-stimulatory domain protein does not include insertions. In embodiments, the CTLA-4 co-stimulatory domain protein includes substitutions that are conservative substitutions. In embodiments, the CTLA-4 co-stimulatory domain is a human CTLA-4 co-stimulatory domain protein. In embodiments, a variant or mutant of the CTLA-4 co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring CTLA-4 co-stimulatory domain protein. In embodiments, a variant or mutant of the CTLA-4 co-stimulatory domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring CTLA-4 co-stimulatory domain protein. In embodiments, a variant or mutant of the CTLA-4 co-stimulatory domain protein does not include deletions compared to the naturally occurring CTLA-4 co-stimulatory domain protein. In embodiments, a variant or mutant of the CTLA-4 co-stimulatory domain protein does not include insertions compared to the naturally occurring CTLA-4 co-stimulatory domain protein. In embodiments, a variant or mutant of the CTLA-4 co-stimulatory domain protein includes substitutions that are conservative substitutions compared to the naturally occurring CTLA-4 co-stimulatory domain protein.

[0091] The term " CD3ζ intracellular T-cell signaling domain " as provided herein includes any of the recombinant or naturally-occurring forms of the CD3ζ intracellular T-cell signaling domain, or variants or homologs thereof that maintain CD3ζ intracellular T-cell signaling domain activity (e.g. within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100%

activity compared to the CD3ζ intracellular T-cell signaling domain). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g., a 50, 100, 150 or 200 continuous amino acid portion) compared to a naturally occurring CD3ζ intracellular T-cell signaling domain polypeptide. In embodiments, the CD3ζ intracellular T-cell signaling domain is a human CD3ζ intracellular T-cell signaling domain protein. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain protein includes no more than 5, 4, 3, 2, or 1 deletions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain protein. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain protein includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain protein. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain protein does not include deletions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain protein. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain protein does not include insertions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain protein. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain protein includes substitutions that are conservative substitutions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain protein. In embodiments, the CD3ζ intracellular T-cell signaling domain includes all or a portion of the protein identified by the NCBI sequence reference NP_000725.1, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD3ζ intracellular T-cell signaling domain includes all or a portion of the protein identified by the NCBI sequence reference NP_932170.1, or an isoform or naturally occurring mutant or variant thereof. Non-limiting examples of human CD3-zeta amino acid sequences available under NCBI sequence references are identified supra.

[0092] In embodiments, the CD3ζ intracellular T-cell signaling domain is encoded by all or a portion of the nucleic acid sequence identified by the NCBI sequence reference NM_000734.3, or an isoform or naturally occurring mutant or variant thereof. In embodiments, the CD3ζ intracellular T-cell signaling domain is encoded by all or a portion of the nucleic acid sequence identified by the NCBI sequence reference NM_198053.2, or an isoform or naturally occurring mutant or variant thereof. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain nucleic acid sequence includes no more than 5, 4, 3, 2, or 1 deletions compared

to the naturally occurring CD3ζ intracellular T-cell signaling domain nucleic acid sequence. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain nucleic acid sequence includes no more than 5, 4, 3, 2, or 1 insertions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain nucleic acid sequence. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain nucleic acid sequence does not include deletions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain nucleic acid sequence. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain nucleic acid sequence does not include insertions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain nucleic acid sequence. In embodiments, a variant or mutant of the CD3ζ intracellular T-cell signaling domain nucleic acid sequence includes substitutions that are conservative substitutions compared to the naturally occurring CD3ζ intracellular T-cell signaling domain nucleic acid sequence.

[0093] "T cells" or "T lymphocytes" as used herein are a type of lymphocyte (a subtype of white blood cell) that plays a central role in cell-mediated immunity. They can be distinguished from other lymphocytes, such as B cells and natural killer cells, by the presence of a T-cell receptor on the cell surface. T cells include, for example, natural killer T (NKT) cells, cytotoxic T lymphocytes (CTLs), regulatory T (Treg) cells, and T helper cells. Different types of T cells can be distinguished by use of T cell detection agents.

[0094] A "control" sample or value refers to a sample that serves as a reference, usually a known reference, for comparison to a test sample. For example, a test sample can be taken from a test condition, e.g., in the presence of a test compound, and compared to samples from known conditions, e.g., in the absence of the test compound (negative control), or in the presence of a known compound (positive control). A control can also represent an average value gathered from a number of tests or results. One of skill in the art will recognize that controls can be designed for assessment of any number of parameters. For example, a control can be devised to compare therapeutic benefit based on pharmacological data (e.g., half-life) or therapeutic measures (e.g., comparison of side effects). Controls are also valuable for determining the significance of data. For example, if values for a given parameter are widely variant in controls, variation in test samples will not be considered as significant.

[0095] As used herein, the term "cancer" or "tumor" refers to all types of cancer, neoplasm or malignant tumors found in mammals (e.g., humans), including leukemias, lymphomas,

carcinomas and sarcomas. Exemplary cancers that may be treated with a compound or method provided herein include brain cancer, glioma, glioblastoma, neuroblastoma, prostate cancer, colorectal cancer, pancreatic cancer, Medulloblastoma, melanoma, cervical cancer, gastric cancer, ovarian cancer, lung cancer, cancer of the head, Hodgkin's Disease, and Non-Hodgkin's Lymphomas. Exemplary cancers that may be treated with a compound or method provided herein include cancer of the thyroid, endocrine system, brain, breast, cervix, colon, head & neck, liver, kidney, lung, ovary, pancreas, rectum, stomach, and uterus. Additional examples include, thyroid carcinoma, cholangiocarcinoma, pancreatic adenocarcinoma, skin cutaneous melanoma, colon adenocarcinoma, rectum adenocarcinoma, stomach adenocarcinoma, esophageal carcinoma, head and neck squamous cell carcinoma, breast invasive carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, non-small cell lung carcinoma, mesothelioma, multiple myeloma, neuroblastoma, glioma, glioblastoma multiforme, ovarian cancer, rhabdomyosarcoma, primary thrombocytosis, primary macroglobulinemia, primary brain tumors, malignant pancreatic insulanoma, malignant carcinoid, urinary bladder cancer, premalignant skin lesions, testicular cancer, thyroid cancer, neuroblastoma, esophageal cancer, genitourinary tract cancer, malignant hypercalcemia, endometrial cancer, adrenal cortical cancer, neoplasms of the endocrine or exocrine pancreas, medullary thyroid cancer, medullary thyroid carcinoma, melanoma, colorectal cancer, papillary thyroid cancer, hepatocellular carcinoma, or prostate cancer.

[0096] As used herein, the terms "neuroendocrine cancer" or "neuroendocrine tumor" refer to cancers or tumors that form from cells that release hormones into the blood in response to a signal from the nervous system. Neuroendocrine tumors may make higher-than-normal amounts of hormones, which can cause many different symptoms. Neuroendocrine tumors may be benign (not cancer) or malignant (cancer). Neuroendocrine cancers and tumors include, but are not limited to, carcinoid tumors, islet cell tumors, medullary thyroid cancer, pheochromocytomas, neuroendocrine carcinoma of the skin (Merkel cell cancer), small cell lung cancer, large cell neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), and metastatic castration-resistant prostate cancer (CRPC).

[0097] As used herein, the terms "metastasis," "metastatic," and "metastatic cancer" can be used interchangeably and refer to the spread of a proliferative disease or disorder, e.g., cancer, from one organ or another non-adjacent organ or body part. "Metastatic cancer" is also called

"Stage IV cancer." Cancer occurs at an originating site, e.g., breast, which site is referred to as a primary tumor, e.g., primary breast cancer. Some cancer cells in the primary tumor or originating site acquire the ability to penetrate and infiltrate surrounding normal tissue in the local area and/or the ability to penetrate the walls of the lymphatic system or vascular system circulating through the system to other sites and tissues in the body. A second clinically detectable tumor formed from cancer cells of a primary tumor is referred to as a metastatic or secondary tumor. When cancer cells metastasize, the metastatic tumor and its cells are presumed to be similar to those of the original tumor. Thus, if lung cancer metastasizes to the breast, the secondary tumor at the site of the breast consists of abnormal lung cells and not abnormal breast cells. The secondary tumor in the breast is referred to a metastatic lung cancer. Thus, the phrase metastatic cancer refers to a disease in which a subject has or had a primary tumor and has one or more secondary tumors. The phrases non-metastatic cancer or subjects with cancer that is not metastatic refers to diseases in which subjects have a primary tumor but not one or more secondary tumors. For example, metastatic lung cancer refers to a disease in a subject with or with a history of a primary lung tumor and with one or more secondary tumors at a second location or multiple locations, e.g., in the breast.

[0098] "Treating" or treatment" as used herein (and as well-understood in the art) also broadly includes any approach for obtaining beneficial or desired results in a subject's condition, including clinical results. Beneficial or desired clinical results can include, but are not limited to, alleviation or amelioration of one or more symptoms or conditions, diminishment of the extent of a disease, stabilizing (i.e., not worsening) the state of disease, prevention of a disease's transmission or spread, delay or slowing of disease progression, amelioration or palliation of the disease state, diminishment of the reoccurrence of disease, and remission, whether partial or total and whether detectable or undetectable. In other words, "treatment" as used herein includes any cure, amelioration, or prevention of a disease. Treatment may prevent the disease from occurring; inhibit the disease's spread; relieve the disease's symptoms; fully or partially remove the disease's underlying cause; shorten a disease's duration; or do a combination of these things.

[0099] "Treating" and "treatment" as used herein also include prophylactic treatment. Treatment methods include administering to a subject a therapeutically effective amount of an active agent. The administering step may consist of a single administration or may include a series of administrations. The length of the treatment period depends on a variety of factors,

such as the severity of the condition, the age of the patient, the concentration of active agent, the activity of the compositions used in the treatment, or a combination thereof. It will also be appreciated that the effective dosage of an agent used for the treatment or prophylaxis may increase or decrease over the course of a particular treatment or prophylaxis regime. Changes in dosage may result and become apparent by standard diagnostic assays known in the art. In some instances, chronic administration may be required. For example, the compositions are administered to the subject in an amount and for a duration sufficient to treat the patient. In embodiments, the treating or treatment is no prophylactic treatment.

[0100] "Patient" or "subject in need thereof" refers to a living organism suffering from or prone to a disease or condition that can be treated by administration of a pharmaceutical composition as provided herein. Non-limiting examples include humans, other mammals, bovines, rats, mice, dogs, monkeys, goat, sheep, cows, deer, and other non-mammalian animals. In some embodiments, a patient is human.

[0101] An "effective amount" is an amount sufficient for a compound to accomplish a stated purpose relative to the absence of the compound (e.g., achieve the effect for which it is administered, treat a disease, reduce enzyme activity, increase enzyme activity, reduce a signaling pathway, or reduce one or more symptoms of a disease or condition). An example of an "effective amount" is an amount sufficient to contribute to the treatment, prevention, or reduction of a symptom or symptoms of a disease, which could also be referred to as a "therapeutically effective amount." A "reduction" of a symptom or symptoms (and grammatical equivalents of this phrase) means decreasing of the severity or frequency of the symptom(s), or elimination of the symptom(s). A "prophylactically effective amount" of a drug is an amount of a drug that, when administered to a subject, will have the intended prophylactic effect, e.g., preventing or delaying the onset (or reoccurrence) of an injury, disease, pathology or condition, or reducing the likelihood of the onset (or reoccurrence) of an injury, disease, pathology, or condition, or their symptoms. The full prophylactic effect does not necessarily occur by administration of one dose, and may occur only after administration of a series of doses. Thus, a prophylactically effective amount may be administered in one or more administrations. An "activity decreasing amount," as used herein, refers to an amount of antagonist required to decrease the activity of an enzyme relative to the absence of the antagonist. A "function disrupting amount," as used herein, refers to the amount of antagonist required to disrupt the

function of an enzyme or protein relative to the absence of the antagonist. The exact amounts will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (see, e.g., Lieberman, Pharmaceutical Dosage Forms (vols. 1-3, 1992); Lloyd, The Art, Science and Technology of Pharmaceutical Compounding (1999); Pickar, Dosage Calculations (1999); and Remington: The Science and Practice of Pharmacy, 20th Edition, 2003, Gennaro, Ed., Lippincott, Williams & Wilkins).

[0102] For any compound described herein, the therapeutically effective amount can be initially determined from cell culture assays. Target concentrations will be those concentrations of active compound(s) that are capable of achieving the methods described herein, as measured using the methods described herein or known in the art.

[0103] As is well known in the art, therapeutically effective amounts for use in humans can also be determined from animal models. For example, a dose for humans can be formulated to achieve a concentration that has been found to be effective in animals. The dosage in humans can be adjusted by monitoring compounds effectiveness and adjusting the dosage upwards or downwards, as described above. Adjusting the dose to achieve maximal efficacy in humans based on the methods described above and other methods is well within the capabilities of the ordinarily skilled artisan.

[0104] The term "therapeutically effective amount," as used herein, refers to that amount of the therapeutic agent sufficient to ameliorate the disorder, as described above. For example, for the given parameter, a therapeutically effective amount will show an increase or decrease of at least 5%, 10%, 15%, 20%, 25%, 40%, 50%, 60%, 75%, 80%, 90%, or at least 100%. Therapeutic efficacy can also be expressed as "-fold" increase or decrease. For example, a therapeutically effective amount can have at least a 1.2-fold, 1.5-fold, 2-fold, 5-fold, or more effect over a control.

[0105] Dosages may be varied depending upon the requirements of the patient and the compound being employed. The dose administered to a patient, in the context of the present disclosure, should be sufficient to effect a beneficial therapeutic response in the patient over time. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects. Determination of the proper dosage for a particular situation is within the skill of the practitioner. Generally, treatment is initiated with smaller dosages which are less than the optimum dose of the compound. Thereafter, the dosage is increased by small

increments until the optimum effect under circumstances is reached. Dosage amounts and intervals can be adjusted individually to provide levels of the administered compound effective for the particular clinical indication being treated. This will provide a therapeutic regimen that is commensurate with the severity of the individual's disease state.

[0106] As used herein, the term "administering" means oral administration, administration as a suppository, topical contact, intravenous, parenteral, intraperitoneal, intramuscular, intralesional, intrathecal, intranasal or subcutaneous administration, or the implantation of a slow-release device, e.g., a mini-osmotic pump, to a subject. Administration is by any route, including parenteral and transmucosal (e.g., buccal, sublingual, palatal, gingival, nasal, vaginal, rectal, or transdermal). Parenteral administration includes, e.g., intravenous, intramuscular, intra-arteriole, intradermal, subcutaneous, intraperitoneal, intraventricular, and intracranial. Other modes of delivery include, but are not limited to, the use of liposomal formulations, intravenous infusion, transdermal patches, etc. In embodiments, the administering does not include administration of any active agent other than the recited active agent.

[0107] By "Co-administer" it is meant that a composition described herein is administered at the same time, just prior to, or just after the administration of one or more additional therapies. The compounds provided herein can be administered alone or can be coadministered to the patient. Coadministration is meant to include simultaneous or sequential administration of the compounds individually or in combination (more than one compound). Thus, the preparations can also be combined, when desired, with other active substances (e.g. to reduce metabolic degradation). The compositions of the present disclosure can be delivered transdermally, by a topical route, or formulated as applicator sticks, solutions, suspensions, emulsions, gels, creams, ointments, pastes, jellies, paints, powders, and aerosols.

[0108] An "anticancer agent" as used herein refers to a molecule (e.g. compound, peptide, protein, nucleic acid, 0103) used to treat cancer through destruction or inhibition of cancer cells or tissues. Anticancer agents may be selective for certain cancers or certain tissues. In embodiments, anticancer agents herein may include epigenetic inhibitors and multi-kinase inhibit "Anti-cancer agent" and "anticancer agent" are used in accordance with their plain ordinary meaning and refers to a composition (e.g. compound, drug, antagonist, inhibitor, modulator) having antineoplastic properties or the ability to inhibit the growth or proliferation of cells. In some embodiments, an anti-cancer agent is a chemotherapeutic. In some embodiments, an anti-

cancer agent is an agent identified herein having utility in methods of treating cancer. In some embodiments, an anti-cancer agent is an agent approved by the FDA or similar regulatory agency of a country other than the USA, for treating cancer. Examples of anti-cancer agents include, but are not limited to, MEK (e.g. MEK1, MEK2, or MEK1 and MEK2) inhibitors (e.g. XL518, CI-1040, PD035901, selumetinib/ AZD6244, GSK1120212/ trametinib, GDC-0973, ARRY-162, ARRY-300, AZD8330, PD0325901, U0126, PD98059, TAK-733, PD318088, AS703026, BAY 869766), alkylating agents (e.g., cyclophosphamide, ifosfamide, chlorambucil, busulfan, melphalan, mechlorethamine, uramustine, thiotepa, nitrosoureas, nitrogen mustards (e.g., mechloroethamine, cyclophosphamide, chlorambucil, meiphalan), ethylenimine and methylmelamines (e.g., hexamethlymelamine, thiotepa), alkyl sulfonates (e.g., busulfan), nitrosoureas (e.g., carmustine, lomusitne, semustine, streptozocin), triazenes (decarbazine)), anti-metabolites (e.g., 5- azathioprine, leucovorin, capecitabine, fludarabine, gemcitabine, pemetrexed, raltitrexed, folic acid analog (e.g., methotrexate), or pyrimidine analogs (e.g., fluorouracil, floxouridine, Cytarabine), purine analogs (e.g., mercaptopurine, thioguanine, pentostatin), etc.), plant alkaloids (e.g., vincristine, vinblastine, vinorelbine, vindesine, podophyllotoxin, paclitaxel, docetaxel, etc.), topoisomerase inhibitors (e.g., irinotecan, topotecan, amsacrine, etoposide (VP16), etoposide phosphate, teniposide, etc.), antitumor antibiotics (e.g., doxorubicin, adriamycin, daunorubicin, epirubicin, actinomycin, bleomycin, mitomycin, mitoxantrone, plicamycin, etc.), platinum-based compounds (e.g. cisplatin, oxaloplatin, carboplatin), anthracenedione (e.g., mitoxantrone), substituted urea (e.g., hydroxyurea), methyl hydrazine derivative (e.g., procarbazine), adrenocortical suppressant (e.g., mitotane, aminoglutethimide), epipodophyllotoxins (e.g., etoposide), antibiotics (e.g., daunorubicin, doxorubicin, bleomycin), enzymes (e.g., L-asparaginase), inhibitors of mitogen-activated protein kinase signaling (e.g. U0126, PD98059, PD184352, PD0325901, ARRY-142886, SB239063, SP600125, BAY 43-9006, wortmannin, or LY294002, Syk inhibitors, mTOR inhibitors, antibodies (e.g., rituxan), gossyphol, genasense, polyphenol E, Chlorofusin, all trans-retinoic acid (ATRA), bryostatin, tumor necrosis factor-related apoptosis-inducing ligand (TRAIL), 5-aza-2'-deoxycytidine, all trans retinoic acid, doxorubicin, vincristine, etoposide, gemcitabine, imatinib (Gleevec.RTM.), geldanamycin, 17-N-Allylamino-17-Demethoxygeldanamycin (17-AAG), flavopiridol, LY294002, bortezomib, trastuzumab, BAY 11-7082, PKC412, PD184352, 20-epi-1, 25 dihydroxyvitamin D3; 5-ethynyluracil; abiraterone;

aclarubicin; acylfulvene; adecypenol; adozelesin; aldesleukin; ALL-TK antagonists; altretamine; ambamustine; amidox; amifostine; aminolevulinic acid; amrubicin; amsacrine; anagrelide; anastrozole; andrographolide; angiogenesis inhibitors; antagonist D; antagonist G; antarelix; anti-dorsalizing morphogenetic protein-1; antiandrogen, prostatic carcinoma; antiestrogen; antineoplaston; antisense oligonucleotides; aphidicolin glycinate; apoptosis gene modulators; apoptosis regulators; apurinic acid; ara-CDP-DL-PTBA; arginine deaminase; asulacrine; atamestane; atrimustine; axinastatin 1; axinastatin 2; axinastatin 3; azasetron; azatoxin; azatyrosine; baccatin III derivatives; balanol; batimastat; BCR/ABL antagonists; benzochlorins; benzoylstaurosporine; beta lactam derivatives; beta-alethine; betaclamycin B; betulinic acid; bFGF inhibitor; bicalutamide; bisantrene; bisaziridinylspermine; bisnafide; bistratene A; bizelesin; breflate; bropirimine; budotitane; buthionine sulfoximine; calcipotriol; calphostin C; camptothecin derivatives; canarypox IL-2; capecitabine; carboxamide-amino-triazole; carboxyamidotriazole; CaRest M3; CARN 700; cartilage derived inhibitor; carzelesin; casein kinase inhibitors (ICOS); castanospermine; cecropin B; cetrorelix; chlorins; chloroquinoxaline sulfonamide; cicaprost; cis-porphyrin; cladribine; clomifene analogues; clotrimazole; collismycin A; collismycin B; combretastatin A4; combretastatin analogue; conagenin; crambescidin 816; crisnatol; cryptophycin 8; cryptophycin A derivatives; curacin A; cyclopentanthraquinones; cycloplatam; cypemycin; cytarabine ocfosfate; cytolytic factor; cytostatin; dacliximab; decitabine; dehydrodidemnin B; deslorelin; dexamethasone; dexifosfamide; dexrazoxane; dexverapamil; diaziquone; didemnin B; didox; diethylnorspermine; dihydro-5-azacytidine; 9-dioxamycin; diphenyl spiromustine; docosanol; dolasetron; doxifluridine; droloxifene; dronabinol; duocarmycin SA; ebselen; ecomustine; edelfosine; edrecolomab; eflornithine; elemene; emitefur; epirubicin; epristeride; estramustine analogue; estrogen agonists; estrogen antagonists; etanidazole; etoposide phosphate; exemestane; fadrozole; fazarabine; fenretinide; filgrastim; finasteride; flavopiridol; flezelastine; fluasterone; fludarabine; fluorodaunorunicin hydrochloride; forfenimex; formestane; fostriecin; fotemustine; gadolinium texaphyrin; gallium nitrate; galocitabine; ganirelix; gelatinase inhibitors; gemcitabine; glutathione inhibitors; hepsulfam; heregulin; hexamethylene bisacetamide; hypericin; ibandronic acid; idarubicin; idoxifene; idramantone; ilmofosine; ilomastat; imidazoacridones; imiquimod; immunostimulant peptides; insulin-like growth factor-1 receptor inhibitor; interferon agonists; interferons; interleukins; iobenguane; iododoxorubicin; ipomeanol,

4-; iroplact; irsogladine; isobengazole; isohomohalicondrin B; itasetron; jasplakinolide; kahalalide F; lamellarin-N triacetate; lanreotide; leinamycin; lenograstim; lentinan sulfate; leptolstatin; letrozole; leukemia inhibiting factor; leukocyte alpha interferon; leuprolide+estrogen+progesterone; leuprorelin; levamisole; liarozole; linear polyamine analogue; lipophilic disaccharide peptide; lipophilic platinum compounds; lissoclinamide 7; lobaplatin; lombricine; lometrexol; lonidamine; losoxantrone; lovastatin; loxoribine; lurtotecan; lutetium texaphyrin; lysofylline; lytic peptides; maitansine; mannostatin A; marimastat; masoprocol; maspin; matrilysin inhibitors; matrix metalloproteinase inhibitors; menogaril; merbarone; meterelin; methioninase; metoclopramide; MIF inhibitor; mifepristone; miltefosine; mirimostim; mismatched double stranded RNA; mitoguazone; mitolactol; mitomycin analogues; mitonafide; mitotoxin fibroblast growth factor-saporin; mitoxantrone; mofarotene; molgramostim; monoclonal antibody, human chorionic gonadotrophin; monophosphoryl lipid A+myobacterium cell wall sk; mopidamol; multiple drug resistance gene inhibitor; multiple tumor suppressor 1-based therapy; mustard anticancer agent; mycaperoxide B; mycobacterial cell wall extract; myriaporone; N-acetyldinaline; N-substituted benzamides; nafarelin; nagrestip; naloxone+pentazocine; napavin; naphterpin; nartograstim; nedaplatin; nemorubicin; neridronic acid; neutral endopeptidase; nilutamide; nisamycin; nitric oxide modulators; nitroxide antioxidant; nitrullyn; O6-benzylguanine; octreotide; okicenone; oligonucleotides; onapristone; ondansetron; ondansetron; oracin; oral cytokine inducer; ormaplatin; osaterone; oxaliplatin; oxaunomycin; palauamine; palmitoylrhizoxin; pamidronic acid; panaxytriol; panomifene; parabactin; pazelliptine; pegaspargase; peldesine; pentosan polysulfate sodium; pentostatin; pentrozole; perflubron; perfosfamide; perillyl alcohol; phenazinomycin; phenylacetate; phosphatase inhibitors; picibanil; pilocarpine hydrochloride; pirarubicin; piritrexim; placetin A; placetin B; plasminogen activator inhibitor; platinum complex; platinum compounds; platinum-triamine complex; porfimer sodium; porfiromycin; prednisone; propyl bis-acridone; prostaglandin J2; proteasome inhibitors; protein A-based immune modulator; protein kinase C inhibitor; protein kinase C inhibitors, microalgal; protein tyrosine phosphatase inhibitors; purine nucleoside phosphorylase inhibitors; purpurins; pyrazoloacridine; pyridoxylated hemoglobin polyoxyethylerie conjugate; raf antagonists; raltitrexed; ramosetron; ras farnesyl protein transferase inhibitors; ras inhibitors; ras-GAP inhibitor; retelliptine demethylated; rhenium Re 186 etidronate; rhizoxin; ribozymes; RII retinamide; rogletimide; rohitukine; romurtide;

roquinimex; rubiginone B1; ruboxyl; safingol; saintopin; SarCNU; sarcophytol A; sargramostim; Sdi 1 mimetics; semustine; senescence derived inhibitor 1; sense oligonucleotides; signal transduction inhibitors; signal transduction modulators; single chain antigen-binding protein; sizofuran; sobuzoxane; sodium borocaptate; sodium phenylacetate; solverol; somatomedin binding protein; sonermin; sparfosic acid; spicamycin D; spiromustine; splenopentin; spongistatin 1; squalamine; stem cell inhibitor; stem-cell division inhibitors; stipiamide; stromelysin inhibitors; sulfinosine; superactive vasoactive intestinal peptide antagonist; suradista; suramin; swainsonine; synthetic glycosaminoglycans; tallimustine; tamoxifen methiodide; tauromustine; tazarotene; tecogalan sodium; tegafur; tellurapyrylium; telomerase inhibitors; temoporfin; temozolomide; teniposide; tetrachlorodecaoxide; tetrazomine; thaliblastine; thiocoraline; thrombopoietin; thrombopoietin mimetic; thymalfasin; thymopoietin receptor agonist; thymotrinan; thyroid stimulating hormone; tin ethyl etiopurpurin; tirapazamine; titanocene bichloride; topsentin; toremifene; totipotent stem cell factor; translation inhibitors; tretinoin; triacetyluridine; triciribine; trimetrexate; triptorelin; tropisetron; turosteride; tyrosine kinase inhibitors; tyrphostins; UBC inhibitors; ubenimex; urogenital sinus-derived growth inhibitory factor; urokinase receptor antagonists; vapreotide; variolin B; vector system, erythrocyte gene therapy; velaresol; veramine; verdins; verteporfin; vinorelbine; vinxaltine; vitaxin; vorozole; zanoterone; zeniplatin; zilascorb; zinostatin stimalamer, Adriamycin, Dactinomycin, Bleomycin, Vinblastine, Cisplatin, acivicin; aclarubicin; acodazole hydrochloride; acronine; adozelesin; aldesleukin; altretamine; ambomycin; ametantrone acetate; aminoglutethimide; amsacrine; anastrozole; anthramycin; asparaginase; asperlin; azacitidine; azetepa; azotomycin; batimastat; benzodepa; bicalutamide; bisantrene hydrochloride; bisnafide dimesylate; bizelesin; bleomycin sulfate; brequinar sodium; bropirimine; busulfan; cactinomycin; calusterone; caracemide; carbetimer; carboplatin; carmustine; carubicin hydrochloride; carzelesin; cedefingol; chlorambucil; cirolemycin; cladribine; crisnatol mesylate; cyclophosphamide; cytarabine; dacarbazine; daunorubicin hydrochloride; decitabine; dexormaplatin; dezaguanine; dezaguanine mesylate; diaziquone; doxorubicin; doxorubicin hydrochloride; droloxifene; droloxifene citrate; dromostanolone propionate; duazomycin; edatrexate; eflornithine hydrochloride; elsamitrucin; enloplatin; enpromate; epipropidine; epirubicin hydrochloride; erbulozole; esorubicin hydrochloride; estramustine; estramustine phosphate sodium; etanidazole; etoposide; etoposide phosphate; etoprine; fadrozole

hydrochloride; fazarabine; fenretinide; floxuridine; fludarabine phosphate; fluorouracil; fluorocitabine; fosquidone; fostriecin sodium; gemcitabine; gemcitabine hydrochloride; hydroxyurea; idarubicin hydrochloride; ifosfamide; iimofosine; interleukin I1 (including recombinant interleukin II, or rlL.sub.2), interferon alfa-2a; interferon alfa-2b; interferon alfa-n1; interferon alfa-n3; interferon beta-1a; interferon gamma-1b; iproplatin; irinotecan hydrochloride; lanreotide acetate; letrozole; leuprolide acetate; liarozole hydrochloride; lometrexol sodium; lomustine; losoxantrone hydrochloride; masoprocol; maytansine; mechlorethamine hydrochloride; megestrol acetate; melengestrol acetate; melphalan; menogaril; mercaptopurine; methotrexate; methotrexate sodium; metoprine; meturedepa; mitindomide; mitocarcin; mitocromin; mitogillin; mitomalcin; mitomycin; mitosper; mitotane; mitoxantrone hydrochloride; mycophenolic acid; nocodazoie; nogalamycin; ormaplatin; oxisuran; pegaspargase; peliomycin; pentamustine; peplomycin sulfate; perfosfamide; pipobroman; piposulfan; piroxantrone hydrochloride; plicamycin; plomestane; porfimer sodium; porfiromycin; prednimustine; procarbazine hydrochloride; puromycin; puromycin hydrochloride; pyrazofurin; riboprine; rogletimide; safingol; safingol hydrochloride; semustine; simtrazene; sparfosate sodium; sparsomycin; spirogermanium hydrochloride; spiromustine; spiroplatin; streptonigrin; streptozocin; sulofenur; talisomycin; tecogalan sodium; tegafur; teloxantrone hydrochloride; temoporfin; teniposide; teroxirone; testolactone; thiamiprine; thioguanine; thiotepa; tiazofurin; tirapazamine; toremifene citrate; trestolone acetate; triciribine phosphate; trimetrexate; trimetrexate glucuronate; triptorelin; tubulozole hydrochloride; uracil mustard; uredepa; vapreotide; verteporfin; vinblastine sulfate; vincristine sulfate; vindesine; vindesine sulfate; vinepidine sulfate; vinglycinate sulfate; vinleurosine sulfate; vinorelbine tartrate; vinrosidine sulfate; vinzolidine sulfate; vorozole; zeniplatin; zinostatin; zorubicin hydrochloride, agents that arrest cells in the G2-M phases and/or modulate the formation or stability of microtubules, (e.g. Taxol.TM (i.e. paclitaxel), Taxotere.TM, compounds comprising the taxane skeleton, Erbulozole (i.e. R-55104), Dolastatin 10 (i.e. DLS-10 and NSC-376128), Mivobulin isethionate (i.e. as CI-980), Vincristine, NSC-639829, Discodermolide (i.e. as NVP-XX-A-296), ABT-751 (Abbott, i.e. E-7010), Altorhyrtins (e.g. Altorhyrtin A and Altorhyrtin C), Spongistatins (e.g. Spongistatin 1, Spongistatin 2, Spongistatin 3, Spongistatin 4, Spongistatin 5, Spongistatin 6, Spongistatin 7, Spongistatin 8, and Spongistatin 9), Cemadotin hydrochloride (i.e. LU-103793 and NSC-D-669356), Epothilones (e.g. Epothilone A, Epothilone B,

Epothilone C (i.e. desoxyepothilone A or dEpoA), Epothilone D (i.e. KOS-862, dEpoB, and desoxyepothilone B), Epothilone E, Epothilone F, Epothilone B N-oxide, Epothilone A N-oxide, 16-aza-epothilone B, 21-aminoepothilone B (i.e. BMS-310705), 21-hydroxyepothilone D (i.e. Desoxyepothilone F and dEpoF), 26-fluoroepothilone, Auristatin PE (i.e. NSC-654663), Soblidotin (i.e. TZT-1027), LS-4559-P (Pharmacia, i.e. LS-4577), LS-4578 (Pharmacia, i.e. LS-477-P), LS-4477 (Pharmacia), LS-4559 (Pharmacia), RPR-112378 (Aventis), Vincristine sulfate, DZ-3358 (Daiichi), FR-182877 (Fujisawa, i.e. WS-9885B), GS-164 (Takeda), GS-198 (Takeda), KAR-2 (Hungarian Academy of Sciences), BSF-223651 (BASF, i.e. ILX-651 and LU-223651), SAH-49960 (Lilly/Novartis), SDZ-268970 (Lilly/Novartis), AM-97 (Armad/Kyowa Hakko), AM-132 (Armad), AM-138 (Armad/Kyowa Hakko), IDN-5005 (Indena), Cryptophycin 52 (i.e. LY-355703), AC-7739 (Ajinomoto, i.e. AVE-8063A and CS-39.HCl), AC-7700 (Ajinomoto, i.e. AVE-8062, AVE-8062A, CS-39-L-Ser.HCl, and RPR-258062A), Vitilevuamide, Tubulysin A, Canadensol, Centaureidin (i.e. NSC-106969), T-138067 (Tularik, i.e. T-67, TL-138067 and TI-138067), COBRA-1 (Parker Hughes Institute, i.e. DDE-261 and WHI-261), H10 (Kansas State University), H16 (Kansas State University), Oncocidin A1 (i.e. BTO-956 and DIME), DDE-313 (Parker Hughes Institute), Fijianolide B, Laulimalide, SPA-2 (Parker Hughes Institute), SPA-1 (Parker Hughes Institute, i.e. SPIKET-P), 3-IAABU (Cytoskeleton/Mt. Sinai School of Medicine, i.e. MF-569), Narcosine (also known as NSC-5366), Nascapine, D-24851 (Asta Medica), A-105972 (Abbott), Hemiasterlin, 3-BAABU (Cytoskeleton/Mt. Sinai School of Medicine, i.e. MF-191), TMPN (Arizona State University), Vanadocene acetylacetonate, T-138026 (Tularik), Monsatrol, lnanocine (i.e. NSC-698666), 3-IAABE (Cytoskeleton/Mt. Sinai School of Medicine), A-204197 (Abbott), T-607 (Tuiarik, i.e. T-900607), RPR-115781 (Aventis), Eleutherobins (such as Desmethyleleutherobin, Desaetyleleutherobin, lsoeleutherobin A, and Z-Eleutherobin), Caribaeoside, Caribaeolin, Halichondrin B, D-64131 (Asta Medica), D-68144 (Asta Medica), Diazonamide A, A-293620 (Abbott), NPI-2350 (Nereus), Taccalonolide A, TUB-245 (Aventis), A-259754 (Abbott), Diozostatin, (-)-Phenylahistin (i.e. NSCL-96F037), D-68838 (Asta Medica), D-68836 (Asta Medica), Myoseverin B, D-43411 (Zentaris, i.e. D-81862), A-289099 (Abbott), A-318315 (Abbott), HTI-286 (i.e. SPA-110, trifluoroacetate salt) (Wyeth), D-82317 (Zentaris), D-82318 (Zentaris), SC-12983 (NCI), Resverastatin phosphate sodium, BPR-OY-007 (National Health Research Institutes), and SSR-250411 (Sanofi)), steroids (e.g., dexamethasone), finasteride,

aromatase inhibitors, gonadotropin-releasing hormone agonists (GnRH) such as goserelin or leuprolide, adrenocorticosteroids (e.g., prednisone), progestins (e.g., hydroxyprogesterone caproate, megestrol acetate, medroxyprogesterone acetate), estrogens (e.g., diethlystilbestrol, ethinyl estradiol), antiestrogen (e.g., tamoxifen), androgens (e.g., testosterone propionate, fluoxymesterone), antiandrogen (e.g., flutamide), immunostimulants (e.g., Bacillus Calmette-Guérin (BCG), levamisole, interleukin-2, alpha-interferon, etc.), monoclonal antibodies (e.g., anti-CD20, anti-HER2, anti-CD52, anti-HLA-DR, and anti-VEGF monoclonal antibodies), immunotoxins (e.g., anti-CD33 monoclonal antibody-calicheamicin conjugate, anti-CD22 monoclonal antibody-pseudomonas exotoxin conjugate, etc.), radioimmunotherapy (e.g., anti-CD20 monoclonal antibody conjugated to 111In, 90Y, or 131I, etc.), triptolide, homoharringtonine, dactinomycin, doxorubicin, epirubicin, topotecan, itraconazole, vindesine, cerivastatin, vincristine, deoxyadenosine, sertraline, pitavastatin, irinotecan, clofazimine, 5-nonyloxytryptamine, vemurafenib, dabrafenib, erlotinib, gefitinib, EGFR inhibitors, epidermal growth factor receptor (EGFR)-targeted therapy or therapeutic (e.g. gefitinib (Iressa ™), erlotinib (Tarceva ™), cetuximab (Erbitux™), lapatinib (Tykerb™), panitumumab (Vectibix™), vandetanib (Caprelsa™), afatinib/BIBW2992, CI-1033/canertinib, neratinib/HKI-272, CP-724714, TAK-285, AST-1306, ARRY334543, ARRY-380, AG-1478, dacomitinib/PF299804, OSI-420/desmethyl erlotinib, AZD8931, AEE788, pelitinib/EKB-569, CUDC-101, WZ8040, WZ4002, WZ3146, AG-490, XL647, PD153035, BMS-599626), sorafenib, imatinib, sunitinib, dasatinib, or the like.

[0109] "Selective" or "selectivity" or the like of a compound refers to the compound's ability to discriminate between molecular targets (e.g. a compound having selectivity toward ROR1).

[0110] "Specific", "specifically", "specificity", or the like of a compound refers to the compound's ability to cause a particular action, such as inhibition, to a particular molecular target with minimal or no action to other proteins in the cell.

[0111] An "ROR1 inhibitor" refers to a compound (e.g. compounds described herein) that reduces the activity of ROR1 when compared to a control, such as absence of the compound or a compound with known inactivity.

[0112] "Contacting" is used in accordance with its plain ordinary meaning and refers to the process of allowing at least two distinct species (e.g., chemical compounds including biomolecules or cells) to become sufficiently proximal to react, interact or physically touch. It

should be appreciated; however, the resulting reaction product can be produced directly from a reaction between the added reagents or from an intermediate from one or more of the added reagents that can be produced in the reaction mixture.

[0113] As defined herein, the term "inhibition", "inhibit", "inhibiting" and the like in reference to a protein-inhibitor interaction means negatively affecting (e.g., decreasing) the activity or function of the protein relative to the activity or function of the protein in the absence of the inhibitor. In embodiments inhibition means negatively affecting (e.g., decreasing) the concentration or levels of the protein relative to the concentration or level of the protein in the absence of the inhibitor. In embodiments inhibition refers to reduction of a disease or symptoms of disease. In embodiments, inhibition refers to a reduction in the activity of a particular protein target. Thus, inhibition includes, at least in part, partially or totally blocking stimulation, decreasing, preventing, or delaying activation, or inactivating, desensitizing, or down-regulating signal transduction or enzymatic activity or the amount of a protein. In embodiments, inhibition refers to a reduction of activity of a target protein resulting from a direct interaction (e.g., an inhibitor binds to the target protein). In embodiments, inhibition refers to a reduction of activity of a target protein from an indirect interaction (e.g., an inhibitor binds to a protein that activates the target protein, thereby preventing target protein activation). A "ROR1 inhibitor" is a compound that negatively affects (e.g., decreases) the activity or function of ROR1 relative to the activity or function of ROR1 in the absence of the inhibitor.

[0114] The term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion. Expression can be detected using conventional techniques for detecting protein (e.g., ELISA, Western blotting, flow cytometry, immunofluorescence, immunohistochemistry, etc.).

[0115] The term "associated" or "associated with" in the context of a substance or substance activity or function associated with a disease (e.g. a protein associated disease, a cancer associated with ROR1 activity, ROR1 associated cancer, ROR1 associated disease (e.g., cancer, inflammatory disease, autoimmune disease, or infectious disease)) means that the disease (e.g., cancer, inflammatory disease, autoimmune disease, or infectious disease) is caused by (in whole or in part), or a symptom of the disease is caused by (in whole or in part) the substance or substance activity or function. As used herein, what is described as being associated with a

disease, if a causative agent, could be a target for treatment of the disease. For example, a cancer associated with ROR1 activity or function or a ROR1 associated disease (e.g., cancer, inflammatory disease, autoimmune disease, or infectious disease), may be treated with a ROR1 modulator or ROR1 inhibitor, in the instance where increased ROR1 activity or function (e.g., signaling pathway activity) causes the disease (e.g., cancer, inflammatory disease, autoimmune disease, or infectious disease). For example, an inflammatory disease associated with ROR1 activity or function or an ROR1 associated inflammatory disease, may be treated with an ROR1 modulator or ROR1 inhibitor, in the instance where increased ROR1 activity or function (e.g. signaling pathway activity) causes the disease.

[0116] The term "signaling pathway" as used herein refers to a series of interactions between cellular and optionally extra-cellular components (e.g. proteins, nucleic acids, small molecules, ions, lipids) that conveys a change in one component to one or more other components, which in turn may convey a change to additional components, which is optionally propagated to other signaling pathway components.

[0117] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

CHIMERIC ANTIGEN RECEPTORS

[0118] Provided herein are recombinant protein/chimeric antigen receptor (these terms are used interchangeably throughout), nucleic acids encoding the recombinant proteins, cells expressing the chimeric antigen receptors disclosed herein, compositions thereof, and methods of using the same that are, *inter alia*, useful for treating a neuroendocrine cancer and for treating or preventing a metastasis originating from a neuroendocrine cancer. Applicants have discovered that chimeric antigen receptors (CARs) directed to ROR-1 provide for highly active and efficient immunotherapeutic compositions to treat a neuroendocrine cancer and treat or prevent metastasis in a subject with a neuroendocrine cancer. Without being bound to any particular theory, antibodies known to inhibit the receptor they bind and downregulate its surface expression are generally not considered good clinical candidates for CARs. Therefore, it was very surprising

that CARs including CDRs of ROR-1 antibodies described herein including embodiments thereof exhibit effective neuroendocrine cancer-specific cytotoxicity when expressed by T cells.

[0119] In one aspect, the chimeric antigen receptor includes: an antibody binding region, wherein the antibody binding region specifically binds ROR-1, a transmembrane domain, a spacer domain that couples the antigen binding region and the transmembrane domain, and an intracellular domain. The terms "antibody region," "antigen binding region," or "antigen binding domain" as provided herein are used interchangeably throughout and refer to a monovalent or multivalent protein moiety that forms part of the protein (i.e. recombinant protein, chimeric antigen receptor) provided herein including embodiments thereof. A person of ordinary skill in the art would therefore immediately recognize that the antibody region or antigen binding region is a protein moiety capable of binding an antigen (epitope). The antibody region provided herein may include a domain of an antibody or fragment (e.g., Fab) thereof. Thus, the antibody region may include a light chain variable domain (VL) and/or a heavy chain variable domain (VH).

[0120] In embodiments, the ROR-1 binding domain includes an antibody region including a light chain variable region (VL) and a heavy chain variable region (VH). In embodiments, the light chain variable domain includes a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45, and the heavy chain variable domain including a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48. It is noted that those CDRs are of or are derived from cirmtuzumab (also known as UC-961 or 99961.1). The development and structure of cirmtuzumab is disclosed in US Patent No.9,758,591, which is incorporated by reference herein in its entirety and for all purposes. In embodiments, the ROR-1 binding domain includes an antibody region including CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51, and the heavy chain variable domain includes a CDR H1 as set forth in SEQ ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54.

[0121] In one aspect, the chimeric antigen receptor includes: i. an antibody binding region, wherein the antibody binding region specifically binds ROR-1, and wherein the antibody binding region includes a light chain variable domain and a heavy chain variable domain; (a) wherein the light chain variable domain includes a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set

forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45; and the heavy chain variable domain includes a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48; or (b) wherein the light chain variable domain includes a CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51; and the heavy chain variable domain includes a CDR H1 as set forth in SEQ ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54; ii. a spacer domain, between 14 and 120 amino acids in length; iii. a transmembrane domain; and iv. an intracellular domain.

[0122] In one aspect, the chimeric antigen receptor includes: i. an antibody binding region, wherein the antibody binding region specifically binds ROR-1, and wherein the antibody binding region includes a light chain variable domain and a heavy chain variable domain; (a) wherein the light chain variable domain includes a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45; and the heavy chain variable domain includes a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48; or (b) wherein the light chain variable domain includes a CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51; and the heavy chain variable domain includes a CDR H1 as set forth in SEQ ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54; ii. a spacer domain; iii. a transmembrane domain, wherein the transmembrane domain comprises a CD8α transmembrane domain, a CD28 transmembrane domain, a CD4 transmembrane domain, a CD3ζ transmembrane domain, or any combination thereof.; and iv. an intracellular domain.

[0123] In one aspect, the chimeric antibody receptor includes: i. an antibody binding region, wherein the antibody binding region specifically binds ROR-1 and wherein the antibody binding region includes a light chain variable domain and a heavy chain variable domain; (a) wherein the light chain variable domain includes a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45; and the heavy chain variable domain includes a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48; or (b) wherein said light chain variable domain includes a CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51; and the heavy chain variable domain

including a CDR H1 as set forth in SEQ ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54; ii. a linker domain; iii. a transmembrane domain; and iv. an intracellular domain, wherein the intracellular domain includes an intracellular T cell signaling domain and an intracellular co-stimulatory domain selected from, 4-1BB, ICOS, OX-40, and combinations thereof.

[0124] A light chain variable (VL) domain as provided includes CDR sequences and framework region (FR) sequences of the light chain of an antibody, an antibody variant or fragment thereof. In embodiments, the antibody region or antigen binding region includes a variable light chain domain and a variable heavy chain domain. A "variable light chain domain" as provided herein refers to a polypeptide included in (forming part of) a light chain variable (VL) region. In embodiments, the variable light chain region is a light chain variable (VL) domain. A "variable heavy chain domain" as provided herein refers to a polypeptide included in (forming part of) a heavy chain variable (VH) region. In embodiments, the variable heavy chain region is a heavy chain variable (VH) domain. In embodiments, the light chain variable (VL) domain includes CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45). In embodiments, the heavy chain variable (VH) domain includes CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48).

[0125] In embodiments, the light chain variable domain includes the amino acid sequence of SEQ ID NO:21, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21. In embodiments, the light chain variable domain has the amino acid sequence of SEQ ID NO:21, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21. In embodiments, the heavy chain variable domain includes the amino acid sequence of SEQ ID NO:27, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27. In embodiments, the heavy chain variable domain has the amino acid sequence of SEQ ID NO:27, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27.

[0126] In embodiments, the light chain variable domain includes the amino acid sequence of SEQ ID NO:19, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19. In embodiments, the light chain variable domain has the amino acid sequence of SEQ ID NO:19, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19. In embodiments, the light chain variable domain includes the amino acid sequence of

SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20. In embodiments, the light chain variable domain has the amino acid sequence of SEQ ID NO:20, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20. In embodiments, the heavy chain variable domain includes the amino acid sequence of SEQ ID NO:25, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:25. In embodiments, the heavy chain variable domain has the amino acid sequence of SEQ ID NO:25, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:25. In embodiments, the heavy chain variable domain includes the amino acid sequence of SEQ ID NO:26, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:26. In embodiments, the heavy chain variable domain has the amino acid sequence of SEQ ID NO:26, or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:26.

[0127] In embodiments, the C-terminus of the light chain variable domain is bound to the N-terminus of the heavy chain variable domain. In embodiments, the N-terminus of the light chain variable domain is bound to the C-terminus of the heavy chain variable domain. In embodiments, the light chain variable domain is covalently bound to the heavy chain variable domain through a chemical linker. A "chemical linker," as provided herein, is a covalent linker, a non-covalent linker, a peptide linker (a linker including a peptide moiety), a cleavable peptide linker, a substituted or unsubstituted alkylene, substituted or unsubstituted heteroalkylene, substituted or unsubstituted cycloalkylene, substituted or unsubstituted heterocycloalkylene, substituted or unsubstituted arylene or substituted or unsubstituted heteroarylene or any combination thereof. Thus, a chemical linker as provided herein may include a plurality of chemical moieties, wherein each of the plurality of chemical moieties is chemically different. Alternatively, the chemical linker may be a non-covalent linker. Examples of non-covalent linkers include without limitation, ionic bonds, hydrogen bonds, halogen bonds, van der Waals interactions (e.g. dipole-dipole, dipole-induced dipole, London dispersion), ring stacking (pi effects), and hydrophobic interactions. In embodiments, a chemical linker is formed using conjugate chemistry including, but not limited to nucleophilic substitutions (e.g., reactions of amines and alcohols with acyl halides, active esters), electrophilic substitutions (e.g., enamine reactions) and additions to carbon-carbon and carbon-heteroatom multiple bonds (e.g., Michael reaction, Diels-Alder addition). In embodiments, the chemical linker is a peptide linker, which comprises 5-100, 5-80, 5-70, 5-60, 5-50, 10-50, 10-40, or 10-30 amino acids in length. Any

sequence that provides sufficient flexibility between the light chain variable domain and the heavy chain variable domain is contemplated for the recombinant proteins provided herein including embodiments thereof. In embodiments, the peptide linker includes or has the amino acid sequence of SEQ ID NO:24. In embodiments, the peptide linker has an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:24.

[0128] The term "transmembrane domain" refers to a membrane-spanning protein domain capable of anchoring a protein to the membrane. Any transmembrane domain capable of anchoring the proteins provided herein including embodiments thereof are contemplated. While any suitable transmembrane domains are contemplated herein, exemplary, but non-limiting examples of transmembrane domains include the transmembrane domains of CD28, CD8, CD4, CD3ζ, or CD8α. In some embodiments, the transmembrane domain is a CD28 transmembrane domain. The term "CD28 transmembrane domain" as provided herein includes any of the recombinant or naturally-occurring forms of the transmembrane domain of CD28, or variants or homologs thereof that maintain CD28 transmembrane domain activity (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the CD28 transmembrane domain). In some aspects, the variants or homologs have at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity across the whole sequence or a portion of the a naturally occurring CD28 transmembrane domain polypeptide. In embodiments, the CD28 transmembrane domain includes an amino acid sequence of SEQ ID NO:32. In embodiments, the CD28 transmembrane domain is an amino acid sequence of SEQ ID NO:32. In embodiments, the CD28 transmembrane domain in the ROR-1 CAR described herein has a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:32.

[0129] In embodiments, the C-terminus of the heavy chain variable domain is coupled to the N-terminus of the transmembrane domain. In embodiments, the C-terminus of the light chain variable domain is coupled to the N-terminus of the transmembrane domain. In embodiments, the heavy chain variable domain or light chain variable domain is covalently bound to the transmembrane domain through a spacer domain. In embodiments, the binding affinity of the antigen binding region to the antigen is increased in the CAR construct having the spacer domain. In embodiments, the activity of the CAR having the spacer domain is higher than the CAR without the spacer domain. In embodiments, the flexibility of the antigen binding region of the CAR is increased by the presence of the spacer domain.

[0130] The term "intracellular domain" refers to the portion of the receptor or protein that interacts with the interior of a cell or cell organelle via protein-protein interactions. In embodiments, the recombinant protein (e.g., the intracellular domain) further includes one or more intracellular co-stimulatory signaling domains. An "intracellular co-stimulatory signaling domain" as provided herein includes amino acid sequences capable of providing co-stimulatory signaling in response to binding of an antigen to the antibody region provided herein including embodiments thereof. In embodiments, the signaling of the co-stimulatory signaling domain results in production of cytokines and proliferation of the T cell expressing the same. In embodiments, the intracellular co-stimulatory signaling domain comprises at least one or more of a CD28 intracellular co-stimulatory signaling domain, a 4-1BB (CD137) intracellular co-stimulatory signaling domain, an ICOS intracellular co-stimulatory signaling domain, an OX-40 intracellular co-stimulatory signaling domain, or any combinations thereof. For example, a preferred intracellular co-stimulatory signaling domain comprises or consists of at least a portion of CD28 intracellular co-stimulatory signaling domain, or at least a portion of a 4-1BB (CD137) intracellular co-stimulatory signaling domain. Another preferred intracellular co-stimulatory signaling domain comprises or consists of at least a portion of CD28 intracellular co-stimulatory signaling domain coupled with at least a portion of a 4-1BB (CD137) intracellular co-stimulatory signaling domain. In embodiments, at least a portion of the CD28 intracellular domain comprises or consists of the amino acid sequence of SEQ ID NO:32 or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:32. In embodiments, at least a portion of the CD28 intracellular domain comprises or consists of the amino acid sequence of SEQ ID NO:32 or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:32. In embodiments, at least a portion of the 4-1BB intracellular co-stimulatory signaling domain comprises or consists of the amino acid sequence of SEQ ID NO:33 or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:33. In embodiments, at least a portion of the 4-1BB intracellular co-stimulatory signaling domain comprises or consists of the amino acid sequence of SEQ ID NO:33 or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:29. In embodiments, the chimeric antigen receptor disclosed herein or the recombinant protein includes an amino acid sequence of a combination of SEQ ID NO: 32 and SEQ ID NO:33 (either SEQ ID NO: 32 present at the N'-terminus of SEQ ID NO: 33, or SEQ ID NO: 33 present at the N'-terminus of SEQ ID NO: 32), or an amino acid sequence at

least 80%, 85%, 90%, or 95% identical to a combination of SEQ ID NO: 32 and SEQ ID NO:33 (either SEQ ID NO: 32 present at the N'-terminus of SEQ ID NO: 33, or SEQ ID NO: 33 present at the N'-terminus of SEQ ID NO: 32).

[0131] In embodiments, the recombinant protein further includes an intracellular T-cell signaling domain. An "intracellular T-cell signaling domain" as provided herein includes amino acid sequences capable of providing primary signaling in response to binding of an antigen to the antibody region provided herein including embodiments thereof. In embodiments, the signaling of the intracellular T-cell signaling domain results in activation of the T cell expressing the chimeric antigen receptor. In embodiments, the signaling of the intracellular T-cell signaling domain results in proliferation (cell division) of the T cell expressing the same. In embodiments, the signaling of the intracellular T-cell signaling domain results in the expression of proteins by the T cell that are known in the art to be characteristic of activated T cell such as, for example, CTLA-4, PD-1, CD28, Cand D69. In embodiments, the intracellular T-cell signaling domain is a CD3ζ intracellular T-cell signaling domain.

[0132] In embodiments, the CD3ζ intracellular T-cell signaling domain includes the amino acid sequence of SEQ ID NO:34 or an amino acid sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:34 that generates a CD3ζ intracellular T-cell signaling domain having at least 80%, 85%, 90%, or 95% activity of the CD3ζ intracellular T-cell signaling domain having SEQ ID NO:34. In embodiments, the CD3ζ intracellular T-cell signaling domain has the amino acid sequence of SEQ ID NO:34 or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:34 that generates a peptide having at least 80%, 85%, 90%, or 95% activity of the CD3ζ intracellular T-cell signaling domain having SEQ ID NO:34.

[0133] In embodiments, the ROR-1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95%

identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and CH2 and CH3 domain, iii) CD28 transmembrane domain, iv) 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0134] Alternatively, in embodiments, the ROR1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and CH2 domain, iii) CD28 transmembrane domain, iv) 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0135] Alternatively, in embodiments, the ROR1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and CH3 domain, iii) CD28 transmembrane domain, iv) 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0136] Alternatively, in embodiments, the ROR1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and a portion of CH3 domain (e.g., a half of CH3 domain, N-terminal 43 amino acids of CH3 domain, etc.), iii) CD28 transmembrane domain, iv) 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0137] Alternatively, in embodiments, the ROR1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge domain, iii) CD28 transmembrane domain, iv) 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0138] Alternatively, in embodiments, the ROR1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%,

90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and CH2 and CH3 domain, iii) CD28 transmembrane domain, iv) CD28 costimulatory domain coupled to 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0139] Alternatively, in embodiments, the ROR-1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and CH2 domain, iii) CD28 transmembrane domain, iv) CD28 costimulatory domain coupled to 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0140] Alternatively, in embodiments, the ROR-1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3

(SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and CH3 domain, iii) CD28 transmembrane domain, iv) CD28 costimulatory domain coupled to 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0141] Alternatively, in embodiments, the ROR-1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge and a portion of CH3 domain (e.g., a half of CH3 domain, N-terminal 43 amino acids of CH3 domain, etc.), iii) CD28 transmembrane domain, iv) CD28 costimulatory domain coupled to 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0142] Alternatively, in embodiments, the ROR-1 CAR disclosed herein includes or consists of i) ROR1 scFv (having CDR L1 (SEQ ID NO:43), CDR L2 (SEQ ID NO:44), and CDR L3 (SEQ ID NO:45), CDR H1 (SEQ ID NO:46), CDR H2 (SEQ ID NO:47), and CDR H3 (SEQ ID NO:48), or VL domain having the sequence of SEQ ID NO:21, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:21 and the VH domain having the sequence of SEQ ID NO:27, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:27) or alternatively ROR1 scFv (CDR L1 (SEQ ID NO:49), CDR L2 (SEQ ID NO:50), and CDR L3 (SEQ ID NO:51), CDR H1 (SEQ ID NO:52), CDR H2 (SEQ ID NO:53), and CDR H3 (SEQ ID NO:54), or VL domain having the sequence of SEQ ID NO:19, or a sequence at least 80%, 85%,

90%, or 95% identical to SEQ ID NO:19 and the VH domain having the sequence of SEQ ID NO:20, or a sequence at least 80%, 85%, 90%, or 95% identical to SEQ ID NO:20), ii) a spacer domain having a hinge domain, iii) CD28 transmembrane domain, iv) CD28 costimulatory domain coupled to 4-1BB (CD137) costimulatory domain, and v) CD3Z T cell activation domain.

[0143] It is contemplated that the chimeric antigen receptor described here binds to amino acids 130-160 of ROR-1 or a fragment thereof, preferably to a peptide including a glutamic acid at a position corresponding to position 138 of ROR-1 polypeptide. Alternatively and/or additionally, the chimeric antigen receptor described herein specifically binds either the 3' or middle Ig-like region of the extracellular domain of the ROR-1 protein, preferably to 3' end of the Ig-like region of the extracellular domain of ROR-1 protein from position 1-147.

[0144] Consequently, the ROR-1 CAR disclosed herein binds to a ROR-1 expressing cells and can initiate or induce immune response against the ROR-1 expressing cells, including a neuroendocrine cancer cell, such as, for example, a carcinoid tumor, an islet cell tumor, a medullary thyroid cancer, a pheochromocytoma, a neuroendocrine carcinoma of the skin, small cell lung cancer, large cell neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), or metastatic castration-resistant prostate cancer (CRPC).

[0145] In embodiments, the recombinant protein provided herein, including embodiments thereof, further includes a detectable domain. A "detectable domain" as provided herein is a peptide moiety detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, a detectable domain as provided herein may be a protein or other entity which can be made detectable, e.g., by incorporating a radiolabel or being reactive to an antibody specifically. Any appropriate method known in the art for conjugating an antibody to the label may be employed, e.g., using methods described in Hermanson, Bioconjugate Techniques 1996, Academic Press, Inc., San Diego. In the present invention, a detectable domain is used to confirm transfection of T cells.

[0146] In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 500 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 550 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 600 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding

affinity of about 650 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 700 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 750 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 800 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 850 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 900 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 950 pM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 1 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 1 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 1.5 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 2 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 2.5 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 3 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 3.5 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 4 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 4.5 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 5 nM to about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 5.5 nM to about 6 nM.

[0147] In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 500 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 500 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 550 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 550 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 600 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 600 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of

about 650 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 650 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 700 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 700 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 750 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 750 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 800 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 800 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 850 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 850 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 900 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 900 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 950 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 950 pM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 1 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 1 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 1 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 1.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 1.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 2 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 2 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 2.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 2.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 3 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 3 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 3.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 3.5 nM. In embodiments, the recombinant protein or

chimeric antigen receptor has a binding affinity of about 4 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 4 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 4.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 4.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 5.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 5.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor has a binding affinity of 6 nM.

[0148] In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 40 nM (e.g., 35, 30, 25, 20, 15, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, 0.5, 0.25, 0.1 nM). In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 40 nM (e.g., 35, 30, 25, 20, 15, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, 0.5, 0.25, 0.1 nM). In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 35 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 35 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 30 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 30 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 25 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 25 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 20 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 20 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 15 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 15 nM. In embodiments, the recombinant protein or chimeric antigen

receptor binds to an ROR-1 protein with a KD of less than about 10 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 10 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 9 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 9 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 8 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 8 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 7 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 7 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 6 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 5 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 5 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 4 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 4 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 3 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 3 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 2 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 2 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 1 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 1 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 0.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 0.5 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an

ROR-1 protein with a KD of less than about 0.25 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 0.25 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than about 0.1 nM. In embodiments, the recombinant protein or chimeric antigen receptor binds to an ROR-1 protein with a KD of less than 0.1 nM.

[0149] Further provided herein are recombinant nucleic acids encoding the recombinant protein or chimeric antigen receptor provided herein including embodiments thereof. In some embodiments, the chimeric antigen receptor is encoded by a single recombinant nucleic acid that forms part of an expression vector. Any suitable expression vector that is capable of being transfected into and expressed in an immune cells (e.g., CD8+ T cells, CD4+ T cells, CD56+ immune cells, NK cells, or genetically modified or engineered NK cells) are contemplated. Exemplary and/or preferred expression vectors may include a viral expression vector (e.g., expression vectors for adenovirus, adeno-associated viruses, alphaviruses, herpes viruses, lentiviruses, etc.). In some embodiments, an adenovirus is a replication deficient and non-immunogenic virus, which is typically accomplished by targeted deletion of selected viral proteins (e.g., E1, E2b, E3 proteins). For example, the recombinant nucleic acid can be placed in a non-viral vector (e.g., mammalian expression vector) and transfected to the T cells using any generally used transfection method. For other example, the recombinant nucleic acid in a viral vector such that the viral particle including recombinant nucleic acid infect the T cells to deliver the recombinant nucleic acid into the T cells. For still other example, where the recombinant nucleic acid is a self-replicating RNA-based vector, self-replicating RNA-based vector can be formulated with a pharmaceutically acceptable carrier (e.g., in a buffer or cell culture medium, preferably with RNAase inhibitors)) such that the self-replicating RNA-based vector can be delivered in a naked form to the cell by contacting directly to the cell membrane. In some embodiments, the self-replicating RNA-based vector can be coupled to a carrier molecule. Exemplary carrier molecules includes protein A, protein G, protein Z, albumin, refolded albumin, a nanoparticle (e.g., quantum dots, gold nanoparticles, magnetic nanoparticles, nanotubes, polymeric nanoparticles, dendrimers, etc.), or a bead (e.g., polystyrene bead, latex bead, dynabead, etc.). Preferably, the nanoparticle and/or beads have a dimension below 1 μm, preferably below 100 nm. In other embodiments, the self-replicating RNA-based vector can be coupled with a micro particle (e.g., PLG RG503 (50:50 lactide/glycolide molar ratio), where the

self-replicating RNA-based vector can be absorbed to the micro particle for further delivery to the cell. In still other embodiments, the self-replicating RNA-based vector can be encapsulated in a liposome (e.g., PEG-based liposome, etc.) to protect the self-replicating RNA-based vector from RNAase digestion and deliver the RNA-based vector by fusing the liposome to the target cell membrane.

[0150] In embodiments, the recombinant nucleic acids encoding the recombinant protein or chimeric antigen receptor provided herein can be inserted into a vector having a cassette for gene editing (e.g., CRISPR-CAS expression vector). Another exemplary expression vectors may include transposon-based expression system (e.g., Sleeping Beauty system, as disclosed in Deninger et al., PLOS ONE, June 1, 2015).

CELLS AND PHARMACEUTICAL COMPOSITIONS THEREOF

[0151] Provided herein is a cell expressing a recombinant protein as described herein, which includes a chimeric antigen receptor (CAR) comprising a ROR-1-binding antibody or antibody fragment region, a linker domain, a transmembrane domain, and an intracellular domain. In embodiments, the ROR-1 binding domain is an antibody.

[0152] The chimeric antigen receptor described herein is expressed on the surface of T lymphocytes or T cells, such as, for example, CD8+ T cells and CD4+ T cells isolated from an individual afflicted with neuroendocrine cancer by genetically engineering the cells to express the heterologous nucleic acid sequences encoding the chimeric nucleic acid receptor. Such generated CAR-T cells are then re-administered to the individual. Once administered, the CAR-T cells specifically bind to ROR-1-expressing cells, such as neuroendocrine cancer cells expressing ROR-1, to elicit an immune response against the neuroendocrine cancer cells.

[0153] In embodiments, the chimeric antigen receptor described herein is expressed on the surface of natural killer cells isolated from an individual afflicted with neuroendocrine cancer and then genetically modified to express the ROR-1 CAR. In certain embodiments, the NK cells are CD56 positive cells. CD56 positivity can be determined by for example flow cytometry analysis of acell population and defined as cells at least 10x, 100x, or 1,000x compared to cells stained with an isotype control antibody. In certain embodiments, the NK cells are primary NK cells. In embodiments, the NK cells comprise an NK cell line. In certain embodiments, the NK cells are autologous to an individual being treated with a CAR expressing NK cell of this disclosure. In embodiments, the NK cells are heterologous to an individual being treated with a

CAR expressing NK cell of this disclosure. In embodiments, the NK cells are allogeneic to an individual being treated with a CAR expressing NK cell of this disclosure. NK cells can be derived from any suitbale source bone marrow, induced pluripotent stem cells, peripheral blood mononuvlear cells, fetal or placental cells.

[0154] In embodiments, the cell is administered as part of a pharmaceutical composition. The pharmaceutical composition comprises a pharmaceutical acceptable excipient, diluent or carrier in addition to the cell that expresses the CAR comprising a ROR-1-binding antibody region.

[0155] The chimeric antigen receptor(s) and/or the recombinant nucleic acid encoding the chimeric antigen receptor(s) may be formulated as a pharmaceutical composition, optionally with any pharmaceutically acceptable carrier (e.g., as a sterile injectable composition for immune cells expressing chimeric antigen receptor(s), a pharmaceutically acceptable salt for recombinant nucleic acid encoding the chimeric antigen receptor(s), etc.). While the dose or cell titer of the pharmaceutical composition may vary depending on the treatment protocols, treatment regimens, treatment conditions, etc., one example of the dose or cell titer of the pharmaceutical composition may include a cell titer of at least 1 × 103 cells/ml, preferably at least 1 × 105 cells/ml, more preferably at least 1 × 106 cells/ml, and at least 1 ml, preferably at least 5ml, more preferably and at least 20 ml per dosage unit.

[0156] In some embodiments, the pharmaceutical composition may include a homogenous cell or plurality thereof (e.g., CD8+ T cells expressing the chimeric antigen receptor, CD4+ T cells expressing the chimeric antigen receptor NK cells expressing the chimeric antigen receptor, etc.). In other embodiments, the composition can comprise a mixture of heterogeneous cells (e.g., mixture of CD8+ T cells expressing the chimeric antigen receptor and NK cells expressing the chimeric antigen receptor, etc., in a ratio of 1:1, 1:2, 1:3, 1:4, 4:1, 3:1, 2:1, etc.). The ratio of different types of cells may vary based on the type of neuroendocrine cancer, age, gender, or health status of the patient, size of tumor, and the cell counts of the patient. The actual amount effective for a particular application will depend, *inter alia*, on the condition being treated. When administered in methods to treat a disease, the recombinant proteins described herein will contain an amount of active ingredient effective to achieve the desired result, e.g., modulating the activity of a target molecule, and/or reducing, eliminating, or slowing the progression of disease symptoms. Determination of a therapeutically effective amount of a compound of the

invention is well within the capabilities of those skilled in the art, especially in light of the detailed disclosure herein.

[0157] The dosage and frequency (single or multiple doses) administered to a mammal can vary depending upon a variety of factors, for example, whether the mammal suffers from another disease, and its route of administration; size, age, sex, health, body weight, body mass index, and diet of the recipient; nature and extent of symptoms of the disease being treated (e.g., symptoms of cancer and severity of such symptoms), kind of concurrent treatment, complications from the disease being treated or other health-related problems. Other therapeutic regimens or agents can be used in conjunction with the methods and compounds of the invention. Adjustment and manipulation of established dosages (e.g., frequency and duration) are well within the ability of those skilled in the art.

[0158] For any composition (e.g., recombinant protein, nucleic acid) provided herein, the therapeutically effective amount can be initially determined from cell culture assays. Target concentrations will be those concentrations of active compound(s) that are capable of achieving the methods described herein, as measured using the methods described herein or known in the art. As is well known in the art, effective amounts for use in humans can also be determined from animal models. For example, a dose for humans can be formulated to achieve a concentration that has been found to be effective in animals. The dosage in humans can be adjusted by monitoring effectiveness and adjusting the dosage upwards or downwards, as described above. Adjusting the dose to achieve maximal efficacy in humans based on the methods described above and other methods is well within the capabilities of the ordinarily skilled artisan.

[0159] Dosages may be varied depending upon the requirements of the patient and the compound being employed. The dose administered to a patient, in the context of the present invention should be sufficient to affect a beneficial therapeutic response in the patient over time. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects. Determination of the proper dosage for a particular situation is within the skill of the practitioner. Generally, treatment is initiated with smaller dosages which are less than the optimum dose of the compound. Thereafter, the dosage is increased by small increments until the optimum effect under circumstances is reached.

[0160] Dosage amounts and intervals can be adjusted individually to provide levels of the administered compound effective for the particular clinical indication being treated. This will provide a therapeutic regimen that is commensurate with the severity of the individual's disease state.

[0161] Utilizing the teachings provided herein, an effective prophylactic or therapeutic treatment regimen can be planned that does not cause substantial toxicity and yet is effective to treat the clinical symptoms demonstrated by the particular patient. This planning should involve the careful choice of active compound by considering factors such as compound potency, relative bioavailability, patient body weight, presence and severity of adverse side effects, and the like.

[0162] "Pharmaceutically acceptable excipient" and "pharmaceutically acceptable carrier" refer to a substance that aids the administration of an active agent to and absorption by a subject and can be included in the compositions of the present invention without causing a significant adverse toxicological effect on the patient. Non limiting examples of pharmaceutically acceptable excipients include water, NaCl, normal saline solutions, lactated Ringer's, normal sucrose, normal glucose, binders, fillers, disintegrants, lubricants, coatings, sweeteners, flavors, salt solutions (such as Ringer's solution), alcohols, oils, gelatins, carbohydrates such as lactose, amylose or starch, fatty acid esters, hydroxymethycellulose, polyvinyl pyrrolidine, and colors, and the like. Such preparations can be sterilized and, if desired, mixed with auxiliary agents such as lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, and/or aromatic substances and the like that do not deleteriously react with the compounds of the invention. One of skill in the art will recognize that other pharmaceutical excipients are useful in the present invention.

[0163] The term "pharmaceutically acceptable salt" refers to salts derived from a variety of organic and inorganic counter ions well known in the art and include, by way of example only, sodium, potassium, calcium, magnesium, ammonium, tetraalkylammonium, and the like; and when the molecule contains a basic functionality, salts of organic or inorganic acids, such as hydrochloride, hydrobromide, tartrate, mesylate, acetate, maleate, oxalate and the like.

[0164] The term "preparation" is intended to include the formulation of the active compound with encapsulating material as a carrier providing a capsule in which the active component with or without other carriers, is surrounded by a carrier, which is thus in association with it.

Similarly, cachets and lozenges are included. Tablets, powders, capsules, pills, cachets, and lozenges can be used as solid dosage forms suitable for oral administration.

[0165] The pharmaceutical preparation is optionally in unit dosage form. In such form the preparation is subdivided into unit doses containing appropriate quantities of the active component. The unit dosage form can be a packaged preparation, the package containing discrete quantities of preparation, such as packeted tablets, capsules, and powders in vials or ampoules. Also, the unit dosage form can be a capsule, tablet, cachet, or lozenge itself, or it can be the appropriate number of any of these in packaged form. The unit dosage form can be of a frozen dispersion.

METHODS OF TREATMENT

[0166] The CAR-T cell compositions described herein are useful for treating a neuroendocrine cancer in an individual in need thereof, and for preventing or treating a metastasis originating from a neuroendocrine cancer.

[0167] Thus, described herein are methods of treating a neuroendocrine cancer and methods of preventing or treating metastasis originating from a neuroendocrine cancer, that comprise the administration of cells that express chimeric antigen receptors that target human ROR-1. The chimeric antigen receptors described herein are expressed by T lymphocytes or natural killer cells isolated from an individual afflicted with neuroendocrine cancer and re-administered to the individual. Administration of T cells expressing the CARs described herein serves as an effective therapeutic treatment for neuroendocrine cancers that express ROR-1 and metastases thereof.

[0168] The chimeric antigen receptors comprise i) an antigen binding region, wherein the antigen binding region specifically binds ROR-1 and wherein the antigen binding region comprises a light chain variable domain and a heavy chain variable domain, ii) a spacer domain, iii) a transmembrane domain, and iv) an intracellular domain. The light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45, and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48. Alternatively, the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51, and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ

ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54.

[0169] In some instances, the light chain variable domain is covalently linked to the heavy chain variable domain through a polypeptide linker. In some embodiments, the polypeptide linker comprises an amino acid sequence of SEQ ID NO: 24.

[0170] In embodiments, the spacer domain comprises an antibody domain. In some embodiments, the antibody domain comprises an immunoglobulin hinge domain, an immunoglobulin constant heavy chain 3 (CH3) domain, an immunoglobulin constant heavy chain 2 (CH2) domain, or a combination thereof.

[0171] In embodiments, the spacer domain comprises an amino acid sequence represented by SEQ ID NO: 29, SEQ ID NO: 41 or SEQ ID NO: 42.

[0172] In embodiments, the light chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 21.

[0173] In embodiments, the heavy chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 27.

[0174] In embodiments, the transmembrane domain comprises a CD8α transmembrane domain, a CD28 transmembrane domain, a CD4 transmembrane domain, a CD3ζ transmembrane domain, or any combination thereof. In some aspects, the transmembrane domain is a CD28 transmembrane domain.

[0175] In embodiments, the intracellular domain comprises an intracellular co-stimulatory signaling domain, an intracellular T-cell signaling domain, or a combination thereof. The intracellular co-stimulatory signaling domain is a 4-1BB intracellular co-stimulatory signaling domain, a CD28 intracellular co-stimulatory signaling domain, a ICOS intracellular co-stimulatory signaling domain, an OX-40 intracellular co-stimulatory signaling domain, or any combination thereof. In some embodiments, the intracellular costimulatory signaling domain comprises a 41-BB intracellular co-stimulatory signaling domain. In other embodiments, the intracellular costimulatory signaling domain comprises a CD28 intracellular co-stimulatory signaling domain and a 41-BB intracellular co-stimulatory signaling domain.

[0176] In embodiments, the intracellular costimulatory signaling domain further comprises an intracellular T-cell signaling domain. In some embodiments, the intracellular T-cell signaling domain is a CD3ζ intracellular T-cell signaling domain.

[0177] In embodiments, the chimeric antigen receptor binds to a cell expressing ROR-1. In some embodiments, the cell expressing ROR-1 is a neuroendocrine cancerous cell.

[0178] In embodiments, the cell is a T lymphocyte. In some embodiments, the T lymphocyte is a CD4+ T lymphocyte or a CD8 + T lymphocyte.

[0179] In embodiments, the cell is a natural killer cell. In some embodiments, the natural killer cell is autologous to the subject. In other embodiments, the natural killer cell is heterologous to the subject. In yet other embodiments, the natural killer cell is allogeneic to the subject.

[0180] Neuroendocrine cancers that may be treated by the methods provided herein include, but are not limited to, carcinoid tumors, islet cell tumors, medullary thyroid cancers, pheochromocytoma, neuroendocrine carcinoma of the skin, small cell lung cancer, large cell neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), and metastatic castration-resistant prostate cancer (CRPC). In some aspects, the neuroendocrine cancer is metastatic castration-resistant prostate cancer (CRPC).

[0181] In embodiments, the neuroendocrine cancerous cells express ROR-1. In some instances, the subject has failed to respond to androgen deprivation therapy. In some instances, the neuroendocrine cancer has metastasized to bone.

[0182] In embodiments, the methods provided herein further comprise administering cirmtuzumab to the subject. In some embodiments, the cirmtuzumab and the cells expressing the disclosed chimeric antigen receptors are administered separately. In other embodiments, the cirmtuzumab and the cells are administered together.

[0183] In embodiments, the methods provided herein further comprise administering to the subject platinum-based chemotherapy. Suitable platinum-based chemotherapy includes, but it is not limited to, carboplatin, cisplatin, etoposide, a taxane, and any combination thereof.

[0184] Treatment refers to a method that seeks to improve or ameliorate the condition being treated. With respect to neuroendocrine cancer, treatment includes, but is not limited to, reduction of tumor volume, reduction in growth of tumor volume, increase in progression-free survival, or overall life expectancy. In certain embodiments, treatment will effect remission of a neuroendocrine cancer being treated. In certain embodiments, treatment encompasses use as a prophylactic or maintenance dose intended to prevent reoccurrence or progression of a previously treated neuroendocrine cancer or tumor. It is understood by those of skill in the art

that not all individuals will respond equally or at all to a treatment that is administered, nevertheless these individuals are considered to be treated.

[0185] The anti-ROR-1 CAR T-cells and anti-ROR-1 CAR-T cell compositions can be administered to a subject in need thereof by any route suitable for the administration of cell-containing pharmaceutical compositions, such as, for example, subcutaneous, intraperitoneal, intravenous, intramuscular, intratumoral, or intracerebral, etc. In certain embodiments, the antibodies are administered intravenously. In certain embodiments, the antibodies are administered subcutaneously. In certain embodiments, the antibodies are administered intratumorally.

[0186] The anti-ROR-1 CAR T-cells and anti-ROR-1 CAR-T cell compositions can be administered according to a suitable dosage schedule. In certain embodiments, the CAR T-cells are administered once, with subsequent doses depending on clinical criteria. If an individual does not respond or only partially responds said patient can have an anti-ROR-1 CAR-T cell composition administered a second, third, or fourth time until the desired clinical response is observed. A dosage of CAR-T cells will generally comprise at least 1x106 cells, but no more than 5x108 cells. Cells can be administered based upon a total amount of an individual's viable PBMC that were transduced with a CAR construct. In certain embodiments, a single dosage comprises 1 million transduced PBMCs to 100 million transduced PBMCs. In certain embodiments, a single dosage comprises 1 million transduced PBMCs to 2 million transduced PBMCs, 1 million transduced PBMCs to 3 million transduced PBMCs, 1 million transduced PBMCs to 4 million transduced PBMCs, 1 million transduced PBMCs to 5 million transduced PBMCs, 1 million transduced PBMCs to 6 million transduced PBMCs, 1 million transduced PBMCs to 7 million transduced PBMCs, 1 million transduced PBMCs to 8 million transduced PBMCs, 1 million transduced PBMCs to 9 million transduced PBMCs, 1 million transduced PBMCs to 10 million transduced PBMCs, 1 million transduced PBMCs to 50 million transduced PBMCs, 1 million transduced PBMCs to 100 million transduced PBMCs, 2 million transduced PBMCs to 3 million transduced PBMCs, 2 million transduced PBMCs to 4 million transduced PBMCs, 2 million transduced PBMCs to 5 million transduced PBMCs, 2 million transduced PBMCs to 6 million transduced PBMCs, 2 million transduced PBMCs to 7 million transduced PBMCs, 2 million transduced PBMCs to 8 million transduced PBMCs, 2 million transduced PBMCs to 9 million transduced PBMCs, 2 million transduced PBMCs to 10 million transduced

PBMCs, 2 million transduced PBMCs to 50 million transduced PBMCs, 2 million transduced PBMCs to 100 million transduced PBMCs, 3 million transduced PBMCs to 4 million transduced PBMCs, 3 million transduced PBMCs to 5 million transduced PBMCs, 3 million transduced PBMCs to 6 million transduced PBMCs, 3 million transduced PBMCs to 7 million transduced PBMCs, 3 million transduced PBMCs to 8 million transduced PBMCs, 3 million transduced PBMCs to 9 million transduced PBMCs, 3 million transduced PBMCs to 10 million transduced PBMCs, 3 million transduced PBMCs to 50 million transduced PBMCs, 3 million transduced PBMCs to 100 million transduced PBMCs, 4 million transduced PBMCs to 5 million transduced PBMCs, 4 million transduced PBMCs to 6 million transduced PBMCs, 4 million transduced PBMCs to 7 million transduced PBMCs, 4 million transduced PBMCs to 8 million transduced PBMCs, 4 million transduced PBMCs to 9 million transduced PBMCs, 4 million transduced PBMCs to 10 million transduced PBMCs, 4 million transduced PBMCs to 50 million transduced PBMCs, 4 million transduced PBMCs to 100 million transduced PBMCs, 5 million transduced PBMCs to 6 million transduced PBMCs, 5 million transduced PBMCs to 7 million transduced PBMCs, 5 million transduced PBMCs to 8 million transduced PBMCs, 5 million transduced PBMCs to 9 million transduced PBMCs, 5 million transduced PBMCs to 10 million transduced PBMCs, 5 million transduced PBMCs to 50 million transduced PBMCs, 5 million transduced PBMCs to 100 million transduced PBMCs, 6 million transduced PBMCs to 7 million transduced PBMCs, 6 million transduced PBMCs to 8 million transduced PBMCs, 6 million transduced PBMCs to 9 million transduced PBMCs, 6 million transduced PBMCs to 10 million transduced PBMCs, 6 million transduced PBMCs to 50 million transduced PBMCs, 6 million transduced PBMCs to 100 million transduced PBMCs, 7 million transduced PBMCs to 8 million transduced PBMCs, 7 million transduced PBMCs to 9 million transduced PBMCs, 7 million transduced PBMCs to 10 million transduced PBMCs, 7 million transduced PBMCs to 50 million transduced PBMCs, 7 million transduced PBMCs to 100 million transduced PBMCs, 8 million transduced PBMCs to 9 million transduced PBMCs, 8 million transduced PBMCs to 10 million transduced PBMCs, 8 million transduced PBMCs to 50 million transduced PBMCs, 8 million transduced PBMCs to 100 million transduced PBMCs, 9 million transduced PBMCs to 10 million transduced PBMCs, 9 million transduced PBMCs to 50 million transduced PBMCs, 9 million transduced PBMCs to 100 million transduced PBMCs, 10 million transduced PBMCs to 50 million transduced PBMCs, 10 million transduced PBMCs to 100 million transduced PBMCs, or

50 million transduced PBMCs to 100 million transduced PBMCs. In certain embodiments, a single dosage comprises 1 million transduced PBMCs, 2 million transduced PBMCs, 3 million transduced PBMCs, 4 million transduced PBMCs, 5 million transduced PBMCs, 6 million transduced PBMCs, 7 million transduced PBMCs, 8 million transduced PBMCs, 9 million transduced PBMCs, 10 million transduced PBMCs, 50 million transduced PBMCs, or 100 million transduced PBMCs. In certain embodiments, a single dosage comprises at least 1 million transduced PBMCs, 2 million transduced PBMCs, 3 million transduced PBMCs, 4 million transduced PBMCs, 5 million transduced PBMCs, 6 million transduced PBMCs, 7 million transduced PBMCs, 8 million transduced PBMCs, 9 million transduced PBMCs, 10 million transduced PBMCs, or 50 million transduced PBMCs. In certain embodiments, a single dosage comprises at most 2 million transduced PBMCs, 3 million transduced PBMCs, 4 million transduced PBMCs, 5 million transduced PBMCs, 6 million transduced PBMCs, 7 million transduced PBMCs, 8 million transduced PBMCs, 9 million transduced PBMCs, 10 million transduced PBMCs, 50 million transduced PBMCs, or 100 million transduced PBMCs.

[0187] More or less cells may be used depending on the transduction efficiency of an individual's T cells on a case by case basis. In certain embodiments, a single dosage comprises 1 million CAR-T cells to 100 million CAR-T cells. In certain embodiments, a single dosage comprises 1 million CAR-T cells to 2 million CAR-T cells, 1 million CAR-T cells to 3 million CAR-T cells, 1 million CAR-T cells to 4 million CAR-T cells, 1 million CAR-T cells to 5 million CAR-T cells, 1 million CAR-T cells to 6 million CAR-T cells, 1 million CAR-T cells to 7 million CAR-T cells, 1 million CAR-T cells to 8 million CAR-T cells, 1 million CAR-T cells to 9 million CAR-T cells, 1 million CAR-T cells to 10 million CAR-T cells, 1 million CAR-T cells to 50 million CAR-T cells, 1 million CAR-T cells to 100 million CAR-T cells, 2 million CAR-T cells to 3 million CAR-T cells, 2 million CAR-T cells to 4 million CAR-T cells, 2 million CAR-T cells to 5 million CAR-T cells, 2 million CAR-T cells to 6 million CAR-T cells, 2 million CAR-T cells to 7 million CAR-T cells, 2 million CAR-T cells to 8 million CAR-T cells, 2 million CAR-T cells to 9 million CAR-T cells, 2 million CAR-T cells to 10 million CAR-T cells, 2 million CAR-T cells to 50 million CAR-T cells, 2 million CAR-T cells to 100 million CAR-T cells, 3 million CAR-T cells to 4 million CAR-T cells, 3 million CAR-T cells to 5 million CAR-T cells, 3 million CAR-T cells to 6 million CAR-T cells, 3 million CAR-T cells to 7 million CAR-T cells, 3 million CAR-T cells to 8 million CAR-T cells, 3 million CAR-T

cells to 9 million CAR-T cells, 3 million CAR-T cells to 10 million CAR-T cells, 3 million CAR-T cells to 50 million CAR-T cells, 3 million CAR-T cells to 100 million CAR-T cells, 4 million CAR-T cells to 5 million CAR-T cells, 4 million CAR-T cells to 6 million CAR-T cells, 4 million CAR-T cells to 7 million CAR-T cells, 4 million CAR-T cells to 8 million CAR-T cells, 4 million CAR-T cells to 9 million CAR-T cells, 4 million CAR-T cells to 10 million CAR-T cells, 4 million CAR-T cells to 50 million CAR-T cells, 4 million CAR-T cells to 100 million CAR-T cells, 5 million CAR-T cells to 6 million CAR-T cells, 5 million CAR-T cells to 7 million CAR-T cells, 5 million CAR-T cells to 8 million CAR-T cells, 5 million CAR-T cells to 9 million CAR-T cells, 5 million CAR-T cells to 10 million CAR-T cells, 5 million CAR-T cells to 50 million CAR-T cells, 5 million CAR-T cells to 100 million CAR-T cells, 6 million CAR-T cells to 7 million CAR-T cells, 6 million CAR-T cells to 8 million CAR-T cells, 6 million CAR-T cells to 9 million CAR-T cells, 6 million CAR-T cells to 10 million CAR-T cells, 6 million CAR-T cells to 50 million CAR-T cells, 6 million CAR-T cells to 100 million CAR-T cells, 7 million CAR-T cells to 8 million CAR-T cells, 7 million CAR-T cells to 9 million CAR-T cells, 7 million CAR-T cells to 10 million CAR-T cells, 7 million CAR-T cells to 50 million CAR-T cells, 7 million CAR-T cells to 100 million CAR-T cells, 8 million CAR-T cells to 9 million CAR-T cells, 8 million CAR-T cells to 10 million CAR-T cells, 8 million CAR-T cells to 50 million CAR-T cells, 8 million CAR-T cells to 100 million CAR-T cells, 9 million CAR-T cells to 10 million CAR-T cells, 9 million CAR-T cells to 50 million CAR-T cells, 9 million CAR-T cells to 100 million CAR-T cells, 10 million CAR-T cells to 50 million CAR-T cells, 10 million CAR-T cells to 100 million CAR-T cells, or 50 million CAR-T cells to 100 million CAR-T cells . In certain embodiments, a single dosage comprises 1 million CAR-T cells, 2 million CAR-T cells, 3 million CAR-T cells, 4 million CAR-T cells, 5 million CAR-T cells, 6 million CAR-T cells, 7 million CAR-T cells, 8 million CAR-T cells, 9 million CAR-T cells, 10 million CAR-T cells, 50 million CAR-T cells, or 100 million CAR-T cells . In certain embodiments, a single dosage comprises at least 1 million CAR-T cells, 2 million CAR-T cells, 3 million CAR-T cells, 4 million CAR-T cells, 5 million CAR-T cells, 6 million CAR-T cells, 7 million CAR-T cells, 8 million CAR-T cells, 9 million CAR-T cells, 10 million CAR-T cells, or 50 million CAR-T cells . In certain embodiments, a single dosage comprises at most 2 million CAR-T cells, 3 million CAR-T cells, 4 million CAR-T cells, 5 million CAR-T cells, 6 million

CAR-T cells, 7 million CAR-T cells, 8 million CAR-T cells, 9 million CAR-T cells, 10 million CAR-T cells, 50 million CAR-T cells, or 100 million CAR-T cells.

[00187] In certain embodiments, a population of the anti-ROR-1 CAR-T cells of the current disclosure are included in a pharmaceutical composition comprising one or more pharmaceutically acceptable excipients, carriers, and diluents. In certain embodiments, the CAR-T cells of the current disclosure are administered suspended in a sterile isotonic solution. In certain embodiments, the solution comprises about 0.9% NaCl. In certain embodiments, the solution comprises about 5.0% dextrose. In certain embodiments, the solution further comprises one or more of: buffers, for example, acetate, citrate, histidine, succinate, phosphate, bicarbonate and hydroxymethylaminomethane (Tris); surfactants, for example, polysorbate 80 (Tween 80), polysorbate 20 (Tween 20), and poloxamer 188; polyol/disaccharide/polysaccharides, for example, glucose, dextrose, mannose, mannitol, sorbitol, sucrose, trehalose, and dextran 40; amino acids, for example, glycine or arginine; antioxidants, for example, ascorbic acid, methionine; or chelating agents, for example, EDTA or EGTA. The CAR-T cells when formulated, can be buffered at a certain pH, generally between about 7.0 and about 8.0. In certain embodiments, the cells are buffered at a physiological pH of about 7.4 (averaging between about 7.35 and 7.45.

[0188] Also described herein are methods of treating an individual that has developed one or more serious adverse events associated with CAR T-cell treatment comprising administering a bolus injection of cirmtuzumab. Such an administration blocks CAR T-cells from interacting with their targets and can attenuate their activity.

EXAMPLES

[0189] The following illustrative examples are representative of embodiments of compositions and methods described herein and are not meant to be limiting in any way.

EXAMPLE 1: CHIMERIC ANTIGEN RECEPTOR MODIFIED T-CELLS (CAR-T) THAT TARGET NEUROENDOCRINE CANCER CELLS EXPRESSING ROR-1

[0190] Pre-clinical studies involving the use of anti-human ROR1 T-cell CARS against a wide variety of solid and liquid tumor cancers have been previously described. However, when used clinically (NCT02706392 and NCT02194374), these same ROR1 CARS had minimal activity in

treating patient ROR1^{pos} hematological and solid tumor cancers. The lack of therapeutic effect in these studies is due to the use of T-cell CARS comprising rabbit/human chimeric ROR1 targeting domains. These domains present the potential for off target binding, are recognized as foreign antigens by the immune system, and are therefore rapidly inactivated.

[0191] The anti-ROR1 T-cell CARs constructed and tested in these examples employ a scFv antigen targeting domain that is generated from fully humanized cirmtuzumab (Figure 2), and which comprises the complementarity determining regions (CDRs) and variable regions (V_H/V_L) of the cirmtuzumab antibody. The examples presented herein show that T-cell CAR employing cirmtuzumab as the antigen binding component are effective in treating ROR1^{pos} neuroendocrine cancers that are resistant to other therapies.

[0192] Treatment Failures

[0193] The use of potent therapies aimed at inhibiting critical oncogenic pathways active in epithelial cancers has led to multiple resistance mechanisms, including the development of highly aggressive neuroendocrine cancers, such as small cell neuroendocrine carcinoma (SCNC). SCNC can arise from almost all epithelial organs including the prostate and lung. Metastatic castration resistant prostate cancer (CRPC) is one of several lethal neuroendocrine cancers. Small cell prostate cancer (SCPC) is a type of neuroendocrine prostate cancer (NEPC), a particularly malignant form of CRPC.

[0194] One in six men is diagnosed with prostate cancer (PCa), and up to one quarter of PCa patients develop advanced prostate cancer with poor prognosis and five-year survival. The main treatment for these types of prostate cancers is androgen deprivation therapy (ADT) which targets androgen receptor (AR) signaling. Inevitably, however, the cancer progresses to ADT resistance and patients develop lethal castration resistant prostate cancer (CRPC) and metastasis. NEPC is emerging with increasing frequency in patients treated with ADT.

[0195] Most PCa metastasize to bone where it typically develops therapy resistance and there is no cure. ROR1 is an attractive therapeutic target, since it is expressed on a number of highly malignant hematological and solid tumor cancer cells, including CRPC and NEPC cells. However, despite the recent development of several novel therapies that have improved survival for patients, nearly all individuals with CRPC develop resistance to therapy and disease progression.

[0196] Innovation

[0197] Because mCRPC and NEPC remain an urgent un-met medical need, we have produced a series of 2nd generation T-cell CAR constructs that when transduced into human T-cells demonstrated highly potent and specific anti-neuroendocrine tumoral activity and specificity in *in vitro* and *in vivo* test systems. As shown in Figure 2, the CARs of this disclosure include light chain CDRs of the anti-human ROR-1 mAbs 4A5 or UC-961 attached to the heavy chain CDRs of the same mAbs by specific linkers that generate high-affinity single-chain (scFv) molecules that specifically bind human ROR-1 with a sufficient affinity to activate intracellular signaling and cytotoxicity in the transduced T-lymphocytes. To attach the scFv to a transmembrane domain, a series of protein spacers generated from IgG4 have been created. These spacers allow the anti-ROR-1 scFv binding domain sufficient flexibility to optimally bind the target ROR-1 antigen.

[0198] The extracellular antigen binding domain from the CARs is bound to a CD28 transmembrane domain. This transmembrane domain is then attached to an intracellular activating domain derived from CD28 and/or CD137, which are employed singularly (2nd-gen CAR) or in combination (3rd-gen CAR). These activating domains are then attached to the T-cell receptor activating domain contained within the CD3 zeta chain (CD3 ζ-chain). Therefore, the anti-ROR-1 CARs constructed and tested in these examples are expressed as a single polypeptide that from the N-terminal end contains in order: a leader that directs the construct to the cell surface, the light chain CDR of either the 4A5 or UC-961 mAbs, a linker that attaches the light and heavy chains, the heavy chain CDR of 4A5 or UC-961 mAbs that are complimented by the corresponding light chain molecules, a spacer of defined length generated from IgG4 including the IgG4 hinge region, the CD28 transmembrane region, the intracellular activation domains of CD28 and 41-BB (CD137)-individually or in tandem attached to the T-cell ζ-chain which extends to the carboxy terminus of the molecule. Employing clinical grade procedures and processes, we have now produced anti-ROR1 T-cell CAR products from over 20 normal human donor and chronic lymphocytic leukemia (CLL) patient products from subjects ranging in age from 31 to 83.

[0199] Figure 3 present graphs showing *in vitro* cell killing activity of ROR1 CAR T-cells in a 4h chromium release assay (left panel) and 120h ACEA impedance assay (right panel) from T cells of two healthy donors, that were tranduced with ROR1 at the indicated effect to target (E:T) ratios against leukemic Mec1 ROR1pos cells in the left panel and an ACEA impedance assay

against MB 231 ROR1pos breast cancer cells in the right panel. The anti-ROR1 CAR T-cells demonstrated high and specific cytotoxicity without significant killing of ROR1-negative target cells. In *in vitro* studies, both the normal and patient derived T-cell CAR products demonstrated dose dependent activity against a wide-variety of ROR1pos solid and liquid tumor cell lines with little off-target activity (Figure 3).

[0200] To confirm the activity of these products, we have also tested our anti-ROR1 T-cell CARs against a murine leukemia model that employed a human $ROR1^{pos}$ CLL derived cells as targets (Figures 4 and 5).

[0201] Figure 4 shows bioluminescence imaging of mice inoculated with MEC1-ROR1 cells and with ROR1 CAR T-Cells. Animals treated with CAR-T cells had reduced disease burden compared to controls. The highest dose ($3x10^6$ CAR-T cells) cohort showed reduction of the leukemic burden to background levels by day 30, and had only minimal amounts of disease for the duration of the study. Animals in the control groups (untreated, mock transduced) had to be sacrificed on day 20. The right panel shows the total bioluminescent product collected from the mice. Blue square and circle are controls and green triangles ROR1-CAR T treated mice.

[0202] Figure 5 shows ROR-1 CAR T cell expression in mouse tissues at various times. Following ROR-1 CAR-T administration, animals were sacrificed on days 11 (top panels) and day 25 (bottom panels). Blood and organs were collected and subjected to flow analysis for CAR expression and confirmatory ROR1 binding activity. The ROR-1 CAR-T cell number was substantially greater in mice bearing MEC-1 ROR1 cells (CAR + MEC1-ROR-1) vs control (CAR only), demonstrating elevated expansion of ROR-1 CAR-T cells in animals with tumor burden. Bars represent the mean values from the five mice in each group and error bars represent the S.E of the mean.

[0203] These results indicated that cirmtuzumab-based anti-ROR1 T cell CARS are highly potent and specific against tumor cells.

[0204] The CARs described herein can be included in a transposon-based or lentiviral vector, and introduced into target lymphocytes or natural killer cells employing standard transfection or transduction techniques. To maximize stable transduction and long-term expression of the CAR product, retroviral delivery systems are used including murine gamma and human lentivirus. Currently, a third generation lentiviral, four plasmid system (Addgene, Inc.) is used to render T lymphocytes transgenic for an ROR-1 expressing CAR. This third-generation system is based on

the lentiviral vector system described in Naldini et al, "Efficient transfer, integration, and sustained long-term expression of the transgene in adult rat brains injected with a lentiviral vector" *Proc Natl Acad Sci* USA. 1996 Oct 15; 93(21): 11382–11388. This four-plasmid system comprises: plasmid 1-gag/pol; plasmid 2-rev; plasmid 3 VSV-G protein; and plasmid 4, the transfer plasmid, which comprises a nucleic acid sequence encoding an anti-ROR1 CAR, which has been inserted using the restriction sites in the poly-linker.

EXAMPLE 2: ROR-1 IS EXPRESSED IN PRIMARY HUMAN PROSTATE CANCER CELLS

[0205] A study aimed at elucidating the expression of ROR1 in human neuroendocrine cancers including prostate cancer was performed.

[0206] *Tissue Microarray Analysis*

[0207] Tissue microarray evaluation revealed that ninety percent (n=19/21) of prostate cancers had moderate to strong staining for ROR1 on the plasma membrane (Table 1). Additionally, expression was associated with AKT activation and silencing of ROR1 expression impaired cell growth *in vitro*. Figure 6 shows the results obtained from the analysis of tumor RNA sequences obtained from 66 prostate cancer samples, expressed as association of single-sample Gene Set Enrichment Analysis profiles of non-canonical WNT and stem cell gene sets with the expression of ROR1 (mRNA). The analysis shows a significant enrichment of WNT non-canonical and stem cell gene sets against ROR1 mRNA expression

[0208] *Prostate Cancer Patient-Derived Xenograft Models*

[0209] Despite the challenges presented by PCa bone metastases, which are not typically surgically removed or biopsied, we established a Biobank and new patient- derived xenografts (PDX) and organoid models, which are used as pre-clinical models to accurately represent the patient disease and perform drug testing predictive of the patient response and drug efficacy.

[0210] Figure 4 shows the results obtained from whole human genome HTA2.0 Affymetrix microarray and RNASeq gene expression profiling. These results demonstrate that Wnt5A was highly expressed in a patient prostatic adenocarcinoma bone metastasis specimen and in its corresponding PDX, PCSD1. Figure 7A shows that RNASeq analysis of another patient PCa bone metastasis-derived PDX, PCSD13, a small cell prostate cancer, showed significant ROR1 expression (Figure 4). These data are indicative of the interplay between Wnt5A, ROR-1, ROR-

2, and bone metastatic prostate cancer, as advanced CRPC is associated with Wnt5A and ROR1 expression.

[0211] FACS analysis revealed that ROR1 protein was highly expressed in PCSD13 cells as well as in PC3 and DU145 PCa cell lines (Figure 7B). We noted the reciprocal expression of Wnt5a and ROR1 in the bone metastases from the prostate adenocarcinoma, PCSD1, compared to small cell prostate cancer, PCSD13. While PCSD1, was PSMA+WNT5A+ROR1^{low}ROR2^{low}, PCSD13, was PSMA^{-}WNT5A^{-}ROR1+ROR2+. This may reflect a fundamental difference in prostate adenocarcinoma and prostate small cell carcinoma, or NEPC. Our findings underscore the importance of ROR1 expression characterization at differential stages in prostate cancer to better understand the role of ROR1 in prostate cancer disease progression and the emergence of neuroendocrine prostate cancer (NEPC), and identify the most suitable patient population for ROR1 targeting with cirmtuzumab-CART cells.

[0212] *PDX-Derived Organoid Cultures*

[0213] Three-dimensional (3D) organoid cell cultures from patient-derived xenograft (PDX) and primary patient tumor cells were established. Figure 8 shows PCSD1 PDX tumors cells from three-dimensional organoids that replicate histomorphology of the xenografts growing in the femur bone. The 3D cultures consisted of two main cell masses: spheroids and epithelial cysts similar to gland-like structures seen in sections from xenografts growing within the femur bone displacing bone marrow and in the patient. Spheroids were resistant to androgen deprivation-induced death. Spheroid masses contained cyst-like structures surrounded by tumor cells that were similar to gland-like structures. Black Arrows point to the cyst structures. Organoids are GFP+. PDXs were obtained from prostate cancer bone metastases. PCSD1 expressing GFP-Luciferase formed different morphologies under 3D-culture conditions. Figure 8 also shows that enzalutamide treatment of PCSD1 reduced lumen size and number of epithelial cysts. Transcriptome analysis showed that AR-responsive genes such as PSA (KLK3) and TMPRSS2 were downregulated under ADT while stem-cell transcription factors, steroidogenic and neurogenic pathway genes were upregulated. Thus, anti-androgens could still suppress canonical AR-responsive genes, but the tumor and organoid growth were resistant to ADT including the anti-androgen, enzalutamide.

EXAMPLE 3: ANTI-ROR-1 T-CELL CARS ARE HIGHLY POTENT IN TARGETING AND KILLING NEUROENDOCRINE CANCER CELL LINES EXPRESSING ROR-1

[0214] PCa is highly heterogenous, exhibits a high recurrence rate following standard treatments and therefore, new therapeutic approaches are needed. We have generated a cirmtuzumab-based T-cell CAR to target treatment resistant ROR1^{pos} cancers. To test and demonstrate the activity of this CAR product, we have produced a series of 2nd generation T-cell CAR constructs that when transduced into human T-cells demonstrated highly potent and specific anti-tumoral activity and specificity in *in vitro* and *in vivo* test systems of hematological and human solid tumor cancers.

[0215] The aim of these studies is to determine the efficacy of human ROR1 CAR-T cells against PCa cell lines, PDX models and organoids of mCRPC and NEPC in combination with standard-of-care therapies including androgen deprivation therapy, and docetaxel, to determine efficacy and define the use of adjunctive therapies in conjunction with the CAR T cells. A further goal is to evaluate ROR1 expression and signaling in differing clinical states of malignant prostate cancer and define PCa cell types that express the ROR-1 oncoprotein. An additional goal is to determine efficacy of ROR1 CART cells against patient biopsy-derived organoids *in vitro* using ROR1 CAR engineered into TILs and PBMCs from the same patient.

[0216] As shown in Figure 9, the generated anti-ROR1 T-cell CARs are highly potent in targeting and killing ROR1 expressing NEPC cell lines even at low effector to target (E:T) ratios. Figure 10 shows that anti-ROR1 CAR-T cells specifically killed the ROR1^{POS} PDX cells in Effector: Target (E:T) dose-dependent manner. Thus, the anti-ROR1 T-cell CAR is highly potent in targeting and killing ROR1 expressing NEPC cell lines even at low effector to target (E:T) ratios.

[0217] *Pilot Study*

[0218] A pilot study was conducted to determine the effect of the CAR T cells provided herein on a prostate cancer cell line implanted subcutaneously. PC3 cells transduced with luciferase were implanted sub-cutaneously into the flanks of immuno-deficient NSG mice. For treatment groups, we administered the ROR1 T-cell CAR both intravenously and by direct injection into the tumor. The control animals received mock transduced activated T-cells generated from the same donor leukapheresed product. As shown in Figure 11, the PC3 cells rapidly expanded in the backs of these animals and by week 4 had expanded into large bulky tumors and the mice had to

be sacrificed. In contrast, the CAR-T treated mice that received a single intravenous or intra-tumoral injection had reduced disease burden when compared to control animals, and had only minimal amounts of disease at the end of the study.

[0219] To determine the efficacy of ROR1 CART cells in PCa cell lines and PDX models of mCRPC and NEPC *in vivo* alone and in combination, with docetaxel, the effect of the anti-ROR-1 CAR T cells on tumor growth inhibition is examined in PCa cell lines and PDX PCSD1, and PCSD13 organoids.

[0220] The anti-ROR-1 CAR T cells are tested in PCa Cell lines and PCa organoids *in vitro* and in sub-cutaneous, intra-femoral bone and intra-cardiac injected PCa cell line xenografts and PDXs *in vivo*.

[0221] The outline of these experiments in pre-clinical models for metastatic prostate cancer is shown below:

[0222] **Cells:** Prostate cancer cell lines: AR+ROR1^{low}: LNCaP; ARV7+: VCaP; AR - ROR1^{high}; PC3; AR - ROR1^{high}: DU145, PCa cells lines all stably express RFP-luciferase and cytotoxicity assay will be performed in Incucyte. Prostate Cancer Bone Metastasis PDX Organoids AR+ROR1^{low}: PCSD1 and AR+ROR1^{high} PCSD13.

[0223] **Therapy:** cirmtuzumab-based anti-ROR1 CART cells.

[0224] ***In vitro Experiment 1.*** Perform titration of Effector:Target (E:T) ratios of CART cell experiments on four PCa cell lines alone or in combination with Docetaxel. Four Effector to Target (E:T) ratios are tested: 30:1, 10:1, 3:1, 1:1 ROR1 CART or control T cells alone +/- anti-androgen +/- docetaxel in triplicate per 96-well plate x 2 plates per cell line) x 4 prostate cancer cell lines. Cell Viability is measured using Incucyte for RFP-labeled cells in 96-well plate assays. Cytotoxic killing is measured in LDH-release assay.

[0225] ***In vitro Experiment 2***. Titration of E:T experiments is performed on PCSD1-GFP-luciferase, PCSD13-GFP-luciferase for CART as above in Incucyte assay. Test 3D cultures of 2 PDOs (PCSD1 and PCSD13) in groups: Vehicle control, E:T ratios 30:1. 10:1, 3:1, 1:1 CART or control T cells +/-Enzalutamide +/- Docetaxel in triplicate 24- well plates (see FIG. 1) = 2 PDOs x one 24-well plate x 2 experiments (duplicates) = 4 plates . Weekly digital microscope imaging and analysis of organoid cell number (viability) and size (proliferation). Determine AR protein levels and organoid differentiation using Immunohistochemistry (IHC) of AR and Immunofluorescence (IFC) analysis of prostate markers: Cytokeratin (CK) 5, CK8, p63;

Proliferation: Ki67 and Apoptosis: Cleaved Caspase 3. Measure effects on AR expression and AR-dependent gene expression using qRT-PCR and RNAseq. Experiment are performed in triplicate plates. Dose titration treatment starting at Week 1 after doming organoids. Images at pre-treatment vs. 3 h post-treatment (hrs.), 6 h, 12 h, 24 h. Collect cells for RNA, lysate after 24 h for AR degradation analysis by IHC and FFPE sections for IHC and IFC.

[0226] *In vivo* PCa cell line Xenograft and Patient derived xenograft (PDX) Experiments:

[0227] **Mice**: NSG (NOD.Cg-*Prkdcscid Il2rgtm1Wjl*/SzJ, Jackson Labs Stock # 005557), 6-8 weeks old, male.

[0228] **Cells: LNCaP** (AR+, enzalutamide sensitive) a.) sub-cutaneous (s.c.), b.) intra-cardiac (i.c.) injection**., 2. PC3** (AR negative, enzalutamide resistant) a.) sub-cutaneous (s.c.), b.) intra-cardiac (i.c.) injection, **3. DU145** (AR negative, enzalutamide resistant) a.) sub-cutaneous (s.c.), b.) intra-cardiac (i.c.) injection, **4. VCaP** (AR+, enzalutamide resistant) a.) sub-cutaneous (s.c.), b.) intra-cardiac (i.c.) injection, **5. PCSD1** PDX cells from bone metastasis of prostate adenoma carcinoma (AR+, enzalutamide resistant in the femur bone environment) a.) sub- cutaneous (s.c.), b.) intra-femoral (i.f.) injection, **6. PCSD13** PDX cells bone metastasis of prostate small cell carcinoma (AR+, enzalutamide resistant in the femur bone environment) a.) sub-cutaneous (s.c.), b.) intra- femoral (i.f.) injection.

[0229] **Therapy:** Cirmtuzumab-based Anti-ROR1 CART cells Treatments start when tumors are at least 100 mm^3. For CART treatment group n= 10 mice (depending in tumor size at start of treatment): 1. Control T cells (no CAR), Vehicle (n= 10), 2. CART cells, Vehicle (n= 10), 3. Control T cells, Docetaxel, (n= 10),4. CART cells, Docetaxel, (n= 10).

[0230] Total n= 40 mice x 6 Xenograft (LNCaP, PC3, DU145, VCaP, PCSD1, PCSD13) models = 240 mice.

[0231] For CART compared to control T cells each treatment group n= 8-10 mice (depending in tumor size at start of treatment):1. Control T cells, Vehicle (n=8-10), 2. CART cells, Vehicle (n=8-10), 3. Control T cells, Enzalutamide, (n= 8-10),4. CART cells, Enzalutamide, (n= 8-10) Total n= 40 mice x 4 (LNCaP, VCaP, PCSD1, PCSD13) Xenograft mouse models = 240 mice.

[0232] Monitor clinical signs daily + caliper measurements of tumor volumes, body weights and health report twice weekly. After 4 weeks of treatment the experiments are terminated for collection of a.) peripheral blood: plasma for drug concentration (PK/PD), serum (PSA), b. Tumors from all mice: Fixing (¼ of tumor) in 4% PFA, Flash freezing (¼) in liquid nitrogen for

DNA, RNA, protein analysis, Half of tumor dissociated to single cells for organoids, cryopreservation in 10%DMSO, 90%FBS for FACS on tumor cells, future re-transplantation to measure tumor-initiating cancer stem cells. Injected and contra-lateral non-injected Femurs with surrounding tissue will be formalin fixed and de-calcified for IHC and IFC.

[0233] Characterization and improved efficacy of ROR1 CART cells in PCa cell line xenograft and PDX models of mCRPC and NEPC alone or subsequent therapy with docetaxel in vivo**.**

[0234] The ability of ROR-1 CAR T cells to eradicate a range of different types of already established PCa tumors is tested in vivo. Human PCa cell lines are implanted sub-cutaneously (s.c.) in immunodeficient mice (NSG). Human patient-derived PCa bone metastasis xenografts (PDX) are directly injected intra-femorally (i.f.) into the endosteal bone marrow space of the right femur to test the efficacy of the CARTs against bone metastases or sub-cutaneously (s.c.) for comparison to the PCa cell lines. Tumor growth inhibition by CART cells alone is compared to SOC therapies: docetaxel and the ADT, enzalutamide, alone and in combination.

[0235] In vivo PCa cell line Xenograft and Patient derived xenograft (PDX) Experiments Outline:

[0236] Mice: NSG (NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ, Jackson Labs Stock # **005557**), 6-8 weeks old, male.

[0237] Cells: 1. PC3 (AR^{neg}, $ROR1^{pos}$ enzalutamide resistant) sub-cutaneous (s.c.), **2. DU145** (AR^{neg}, $ROR1^{pos}$, enzalutamide-resistant) sub-cutaneous (s.c.), 3. **PCSD13** PDX cells bone metastasis of prostate small cell carcinoma (AR^{pos}, $ROR1^{pos}$ enza resistant in the femur bone environment) a.) sub-cutaneous (s.c.), b.) intra- femoral (i.f.).

[0238] Therapy: Cirmtuzumab Anti-ROR1 CART cells Treatments will start when tumors are at least 100 mm^3. 4. LNCaP (AR^{pos}, $ROR1^{low}$ enzalutamide sensitive), sub-cutaneous (s.c

[0239] In vivo Expt 1: CART plus docetaxel: For CART treatment group n= 10 mice (depending in tumor size at start of treatment): 1. Control T cells (no CAR), Vehicle (n= 10), 2. CART cells, Vehicle (n= 10), 3. Control T cells, docetaxel, (n= 10),4. CART cells, docetaxel, (n= 10).

[0240] Test ROR1+ cells: Total n= 40 mice x 4 Xenograft PC3 s.c., DU145 s.c., PCSD13 s.c., i.f. models = 160 mice

[0241] In vivo Expt 2: CART plus enzalutamide: For CART compared to control T cells each treatment group n= 10 mice (depending in tumor size at start of treatment):1. Control T

cells, Vehicle (n=10), 2. CART cells, Vehicle (n=10), 3. Control T cells, enzalutamide, (n= 10),4. CART cells, enzalutamide, (n= 10).

[0242] Test AR+ , ROR1+ cells: 1. LNCaP (s.c.), 2. PCSD13 (s.c.) and 3. PCSD13 (i.f.),

[0243] Total n= 40 mice x 3 (LNCaP AR^{pos}, $ROR1^{low}$sc, PCSD13 s.c., PCSD13 i.f.) xenograft mouse models = 120 mice

[0244] Primary Endpoints:

[0245] Tumor growth inhibition: Caliper measurements of tumor volumes, body weights and health report twice weekly plus weekly in vivo bioluminescence (IVIS).

[0246] Serum collection weekly: PSA and ALP assays.

[0247] Termination Endpoint: After 4 weeks of treatment, peripheral blood, spleen and bone marrow are collected and analyzed for CART presence using FACS, plasma for drug concentration (PK/PD), serum (PSA). Tumors from all mice: Fix ($^1/_4$ of tumor) in 4% PFA, flash freezing ($^1/_4$) in liquid nitrogen for DNA, RNA, protein analysis, Half of tumor will be dissociated into single cells for organoids, FACS on tumor cells, and tumor infiltrating CART cells, cryopreservation in 10%DMSO, 90%FBS for future re-transplantation to measure tumor-initiating cancer stem cells. Injected and contra-lateral non-injected Femurs with surrounding tissue are formalin fixed and decalcified for IHC and IFC. Flash frozen samples are used for extraction of DNA, RNA for RNASeq, qPCR of PSA, AR, and protein for immunoblotting analysis of signaling pathways: WNT5A, ROR1, ROR2, Phospho-Tyrosines, AKT and ERK. Femur bone plus periosteal tumor tissue: Formalin fixed for MicroCT, then paraffin-embedded for FFPE sections, immunohistochemistry (PSA, ROR1 and ROR2, other Frizzled proteins) and immunofluorescence (AR, CK5, CK8, Ki67, cleaved caspase3).

[0248] *In vivo testing of anti-ROR1-CAR T cells in de novo bone metastasis models using intra-cardiac or intra-iliac artery injection models of bone metastasis alone or in combination with ADT (enzalutamide) and/or docetaxel.*

[0249] The efficacy of the cirmtuzumab-based CAR T cells is tested against de novo metastasis. alone or subsequent to therapy with docetaxel in treating mice engrafted with ROR1 expressing cell lines, PC3, DU145 and PDX PCSD13 via intra-cardiac and intra-iliac xenograft artery injections. Mice are first treated with docetaxel or enzalutamide for at least 28 days to de-bulk tumors. Following chemotherapy treatment and washout, the PCa is treated with the CART cells.

[0250] Primary Endpoints:

[0251] Tumor growth inhibition: weekly IVIS body weight, weekly IVIS, weekly serum collection, and weekly PSA and ALP assays.

[0252] Termination Endpoint: Collect tumor tissue to be flash frozen for subsequent extraction of DNA, RNA for RNASeq, qPCR of PSA, AR, and ROR1 and protein for immunoblotting analysis of signaling pathways: WNT5A, ROR1, ROR2, Phospho-Tyrosines, AKT, ERK.

[0253] Outcome**:** cirmtuzumab-based CAR T cells inhibit tumor cell growth of ROR1+ metastatic prostate cancer lines and PDX *in vitro* and *in vivo* alone or in combination with prior SOCs docetaxel or enzalutamide.

[0254] *Development of a Companion Diagnostic to detect ROR1 expressing CSCs in patients that have CRPC.*

[0255] The aim of this study is to develop a CLIA-certified IHC assay that can be employed to detect ROR-1 in neuroendocrine cancers, such as CPRC.

[0256] The anti-ROR1 antibody employed in the development of this assay is mAb (4A5). In this process 4A5 is tested using Tissue Microarrays (TMAs) of normal, inflammatory, and neoplastic (benign and malignant) tissues provided by the Biorepository Tissue Technology Shared Resource (BTTSR) facility at UC San Diego. Both frozen and paraffin embedded TMAs from the relevant pathologies are used, including patient-derived prostate tumor samples collected at various pathological states and matching normal tissue controls. For validation purposes, the antibody is tested using two standard IHC techniques, the standard and highly sensitive ABC technique (Vector, CA), as described, and the ImmPRESS™ HRP Polymer Detection Kit, as well as standard indirect immune- fluorescence.

[0257] **TMA selection**: The prostate tissue TMAs is constructed as described, using the MicaArray GEN 3.0 manual arrayer (Micatu Inc, New York). A cohort of de-identified paraffin blocks is selected from the BTTSR, representing a range of non-malignant and malignant prostate tumors. Negative tissue controls are arrayed together with known positives samples previously detected on $ROR1^{pos}$ cancers of the ovary, colon, lung, skin, and pancreas.

[0258] **Analysis of Protein Expression**: The Study Pathologist and a pathologist blinded to the results or the techniques evaluate all TMAs and individual tissues before IHC analysis using H&E-stained slides, for relevancy and tissue preservation. The number of positive cells is visually evaluated for each core and the results are expressed as a percentage of stained

cells/total number of cells. Based on their immunoreactivity, the TMA cores are divided and scored in five categories: 0, less the 10% of stained cells; 1, between 10% and 25%; 2, between 25% and 50%; 3, 50% to 75%; and 4, 75% to 100% of cells stained. Quantitative automated image analysis are explored.

[0259] Statistical analysis: Pearson's correlation coefficient is used to quantify agreement between measurements, as described by Anagnostou et al. Cohen's weighted kappa is also used to measure agreement between antibody pairs.

[0260] CLIA Assay Validation-including: specificity, sensitivity, reproducibility and limits. A set of samples from the CRPC TMAs is analyzed by a study pathologist on consecutive days to determine the day-to-day variability, reproducibility and robustness of assay performance. In a second set of studies, two independent pathologists read 40 specimens from $ROR1^{pos}$ and ^{neg} samples. Inter-rater agreement are quantified by Pearson's correlation and Cohen's weighted kappa, together with their 95% confidence limits. Based on the results of these studies, a CLIA validated IHC companion assay is developed to allow enrollment of patients with $ROR1^{pos}$ CRPC into clinical studies with the cirmtuzumab-based T-cell CAR.

[0261] *Biosystem Cultures*

[0262] The aim of this study was to determine the efficacy of ROR1 CART cells against patient biopsy-derived organoids *in vitro* using ROR1 CAR engineered into TILs and PBMCs from the same patient. Personalized mini-tumors in cell cultures have been successfully generated from tumor tissues of prostate cancer (PCa) patients (Lee et al, 2020). Samples of each patient's tumor tissues were collected immediately after surgical removal and used to establish 3D-organoids, or ***mini-tumors.*** In parallel, we expanded each patient's own immune cells that were residing within the tumor tissue known as *tumor infiltrating lymphocytes (TILs).* We then combined each patient's mini-tumors with their own TILs to establish personalized 3D-Biosystem cultures as shown in Figure13. These personal patient-derived mini-tumors are being used to determine responses to immunotherapies in combination with current and novel tumor targeting therapies.

[0263] Organoids are established and TILs are expanded from n=5-10 patient biopsies from prostate cancer metastases. Cirmtuzumab-based CART cells are generated from TILs and PBMCs from the same patients as the organoids using our lentiviral construct that we used in our CART product. Organoids and patient- derived cirmtuzumab-based CARTs aree co-cultured.

Cytotoxic killing is measured in digital microscope daily imaging at time points: day1-7. Single cell RNA sequencing (UCSD IGM core, 10X Genomics) and immunofluorescence cytochemistry of co-cultures with immune cell and prostate markers.

[0264] The results of this study allow for the development of a strategy to tailor immune therapy for individual patients through a better understanding of the mechanisms of response and resistance.

[0265] *Evaluation of ROR1 expression and signaling in differing clinical states of malignant prostate cancer and definition of PCa cell types that express ROR-1.*

[0266] ROR1 expression patterns and signaling are studied in samples derived from patients with localized prostate cancer of differing Gleason score, metastatic hormone sensitive prostate cancer, metastatic CRPC, and neuroendocrine prostate cancer to determine wheether ROR1 expression is increased in higher grade and castrate resistant tumors.

[0267] FFPE tissue from standard of care radical prostatectomy, prostate biopsy, and metastasis biopsy archived in the UCSD Pathology Biorepository are analyzed. IHC staining is performed with optimal commercially available anti-ROR1 antibody, such as 4A5 (BD) or Protein Tech, a rabbit polyclonal in the UCSD Tissue Technology Shared Resource histology core. IHC-stained slides are reviewed, and the areas of tumor are manually identified and marked. All slides are scanned in the Tissue Technology Shared Resource using the Aperio ScanScope XT system (Aperio®; Vista, CA). The Spectrum Analysis algorithm package and ImageScope analysis software are applied to quantify IHC staining using a color deconvolution algorithm as previously described. (60,61).

[0268] Clinical specimens are also reviewed to determine Gleason score and presence of neuroendocrine differentiation. Clinical parameters including age, race, ethnicity, PSA, stage, and prior treatment status are captured and linked to pathologic and ROR1 expression data. The expression of ROR1 is assessed and graded as follows: 0: No positive cancer cells, 1: Low-moderate staining to <50% of cancer cells, 2: Intense staining of <50% of cancer cells or moderate staining to >50% of cancer cells; 3: Intense staining on >50% of cancer cells. All staining is evaluated and ROR1 levels are correlated with disease parameters including imaging response of measurable disease, PSA response (PSA decline ≥50% from baseline), or stable disease ≥ 6 months. In addition, the effect of cirmtuzumab-based CART inhibition of ROR1

signaling is evaluated using antibodies to phospho-SRC, phospho-AKT, phospho-CREB, YAP/TAZ, and BMI1 in serial sections of the biopsies.

[0269] Statistical analysis: Table 1 details the number of archived specimens available for use. For the primary analysis, we investigate comparisons in ROR1 expression and downstream signaling between castration resistant disease (n=20) and hormone sensitive disease (n=70). We define positive ROR1 expression as an IHC grading of 1 to 3. We compute the proportion of ROR1 positive specimens for each clinical state and its 95% CIs. Fisher's exact test is used to compare the proportion of ROR1 positivity between castrate resistant and hormone sensitive clinical states.

[0270] The results indicate that ROR1 expression rate is 20% in hormone sensitive specimens and 60% in castrate resistant specimens with a power of 90% and a two-sided alpha of 0.05, with our current sample size.

Table 1. Archived specimens to be procured from UCSD Pathology Biorepository

Clinical State	**Number of Specimens Available for Use**
Radical Prostatectomy – Gleason 6	10
Radical Prostatectomy – Gleason 7	20
Radical Prostatectomy – Gleason 8-10	30
Metastasis Biopsy – Hormone sensitive	10
Metastasis Biopsy – Castration resistant	20
Neuroendocrine	10

[0271] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention.

[0272] All publications, patent applications, issued patents, and other documents referred to in this specification are herein incorporated by reference as if each individual publication, patent application, issued patent, or other document was specifically and individually indicated to be incorporated by reference in its entirety. Definitions that are contained in text incorporated by reference are excluded to the extent that they contradict definitions in this disclosure.

EMBODIMENTS

[0273] Embodiment 1. A chimeric antigen receptor (CAR) comprising:

i. an antibody binding region, wherein the antibody binding region specifically binds ROR-1 and wherein the antibody binding region comprises a light chain variable domain and a heavy chain variable domain;

wherein the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO: 43, a CDR L2 as set forth in SEQ ID NO: 44 and a CDR L3 as set forth in SEQ ID NO: 45; and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ ID NO: 46, a CDR H2 as set forth in SEQ ID NO: 47, and a CDR H3 as set forth in SEQ ID NO: 48;

ii. a spacer domain;

iii. a transmembrane domain; and

iv. an intracellular domain.

[0274] Embodiment 2. A chimeric antigen receptor (CAR) comprising:

v. an antibody binding region, wherein the antibody binding region specifically binds ROR-1 and wherein the antibody binding region comprises a light chain variable domain and a heavy chain variable domain;

wherein the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO: 49, a CDR L2 as set forth in SEQ ID NO: 50 and a CDR L3 as set forth in SEQ ID NO: 51; and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ ID NO: 52, a CDR H2 as set forth in SEQ ID NO: 53, and a CDR H3 as set forth in SEQ ID NO: 54;

vi. a spacer domain;

vii. a transmembrane domain; and

viii. an intracellular domain.

[0275] Embodiment 3. The chimeric antigen receptor of any one of embodiments 1-2, wherein the spacer domain is between 14 and 120 amino acids in length.

[0276] Embodiment 4. The chimeric antigen receptor of any one of embodiments 1-3, wherein the light chain variable domain is linked to the N-terminus or the C-terminus of the heavy chain variable domain.

[0277] Embodiment 5. The chimeric antigen receptor of any one of embodiments 1-4, wherein the light chain variable domain is covalently linked to the heavy chain variable domain through a polypeptide linker.

[0278] Embodiment 6. The chimeric antigen receptor of embodiment 5, wherein the polypeptide linker comprises an amino acid sequence of SEQ ID NO: 24.

[0279] Embodiment 7. The chimeric antigen receptor of any one of embodiments 1-6, wherein the spacer domain comprises an antibody domain.

[0280] Embodiment 8. The chimeric antigen receptor of embodiment 7, wherein the antibody domain comprises an immunoglobulin hinge domain, an immunoglobulin constant heavy chain 3 (CH3) domain, an immunoglobulin constant heavy chain 2 (CH2) domain, or a combination thereof.

[0281] Embodiment 9. The chimeric antigen receptor of any one of embodiments 1-8, wherein the spacer domain comprises an amino acid sequence of SEQ ID NO: 29, SEQ ID NO: 41 or SEQ ID NO: 42.

[0282] Embodiment 10. The chimeric antigen receptor of any one of embodiments 1-9, wherein the light chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 21.

[0283] Embodiment 11. The chimeric antigen receptor of any one of embodiments 1-10, wherein the heavy chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 27.

[0284] Embodiment 12. The chimeric antigen receptor of any one of embodiments 1-11, wherein the transmembrane domain comprises a CD8α transmembrane domain, a CD28 transmembrane domain, a CD4 transmembrane domain, a CD3ζ transmembrane domain, or any combination thereof.

[0285] Embodiment 13. The chimeric antigen receptor of embodiment 12, wherein the transmembrane domain is a CD28 transmembrane domain.

[0286] Embodiment 14. The chimeric antigen receptor of any one of embodiments 1-13, wherein the intracellular domain comprises an intracellular co-stimulatory signaling domain, an intracellular T-cell signaling domain, or a combination thereof.

[0287] Embodiment 15. The chimeric antigen receptor of embodiment 14, wherein the intracellular co-stimulatory signaling domain is a 4-1BB intracellular co-stimulatory signaling domain, a CD28 intracellular co-stimulatory signaling domain, a ICOS intracellular co-stimulatory signaling domain, an OX-40 intracellular co-stimulatory signaling domain, or any combination thereof.

[0288] Embodiment 16. The chimeric antigen receptor of embodiment 15, wherein the intracellular costimulatory signaling domain comprises a 41-BB intracellular co-stimulatory signaling domain.

[0289] Embodiment 17. The chimeric antigen receptor of embodiment 16, wherein the intracellular costimulatory signaling domain comprises a CD28 intracellular co-stimulatory signaling domain and a 41-BB intracellular co-stimulatory signaling domain.

[0290] Embodiment 18. The chimeric antigen receptor of any one of embodiments 15-17, wherein the intracellular costimulatory signaling domain further comprises an intracellular T-cell signaling domain.

[0291] Embodiment 19. The chimeric antigen receptor of embodiment 18, wherein the intracellular T-cell signaling domain is a CD3ζ intracellular T-cell signaling domain.

[0292] Embodiment 20. The chimeric antigen receptor of any one of embodiments 1-19, wherein the chimeric antigen receptor binds to a cell.

[0293] Embodiment 21. The chimeric antigen receptor of embodiment 20, wherein the cell is a neuroendocrine cancer cell.

[0294] Embodiment 22. The chimeric antigen receptor of embodiment 21, wherein the neuroendocrine cancer cell is a carcinoid tumor cell, an islet cell tumor cell, a medullary thyroid cancer cell, a pheochromocytoma cell, a neuroendocrine carcinoma of the skin cell, small cell lung cancer cell, large cell neuroendocrine carcinoma cell, neuroendocrine prostate cancer (NEPC) cell, or metastatic castration-resistant prostate cancer (CRPC) cell.

[0295] Embodiment 23. The chimeric antigen receptor of any one of embodiments 1-22, wherein the chimeric antigen receptor forms part of a cell.

[0296] Embodiment 24. The chimeric antigen receptor of any one of embodiments 1-23, wherein the chimeric antigen receptor forms part of a T cell.

[0297] Embodiment 25. An isolated nucleic acid encoding a chimeric antigen receptor of any one of embodiments 1-24.

[0298] Embodiment 26. A pharmaceutical composition comprising a therapeutically effective amount of a chimeric antigen receptor of any one of embodiments 1-25, and a pharmaceutically acceptable excipient.

[0299] Embodiment 27. A method of treating a neuroendocrine cancer in a subject in need thereof, wherein the method comprises administering to the subject an effective amount of the pharmaceutical composition of embodiment 26.

[0300] Embodiment 28. The method of embodiment 27, wherein the chimeric antigen receptor (CAR) binds to a neuroendocrine cancerous cell.

[0301] Embodiment 29. The method of any one of embodiments 27-28, wherein the cell is a T lymphocyte.

[0302] Embodiment 30. The method of embodiment 29, wherein the T lymphocyte is a CD4+ T lymphocyte or a CD8 + T lymphocyte.

[0303] Embodiment 31. The method of any one of embodiments 27-30, wherein the cell is a natural killer cell.

[0304] Embodiment 32. The method of embodiment 31, wherein the natural killer cell is autologous to the subject.

[0305] Embodiment 33. The method of embodiment 31, wherein the natural killer cell is heterologous to the subject.

[0306] Embodiment 34. The method of embodiment 31, wherein the natural killer cell is allogenic to the subject.

[0307] Embodiment 35. The method of any one of embodiments 27-34, wherein the neuroendocrine cancer is a carcinoid tumor, an islet cell tumor, a medullary thyroid cancer, a pheochromocytoma, a neuroendocrine carcinoma of the skin, small cell lung cancer, large cell neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), or metastatic castration-resistant prostate cancer (CRPC).

[0308] Embodiment 36. The method of any one of embodiments 27-35, wherein the neuroendocrine cancer is metastatic castration-resistant prostate cancer (CRPC).

[0309] Embodiment 37. The method of any one of embodiments 27-36, wherein neuroendocrine cancerous cells express ROR-1.

[0310] Embodiment 38. The method of any one of embodiments 27-37, wherein the subject has failed to respond to androgen deprivation therapy.

[0311] Embodiment 39. The method of any one of embodiments 27-38, wherein the neuroendocrine cancer has metastasized to bone.

[0312] Embodiment 40. The method of any one of embodiments 27-39, wherein the method further comprises administering cirmtuzumab to the subject.

[0313] Embodiment 41. The method of embodiment 40, wherein the cirmtuzumab and the cell are administered separately.

[0314] Embodiment 42. The method of embodiment 40, wherein the cirmtuzumab and the cell are administered together.

[0315] Embodiment 43. The method of any one of embodiments 27-42, wherein the method further comprises administering to the subject platinum-based chemotherapy.

[0316] Embodiment 44. The method of embodiment 43, wherein the platinum-based chemotherapy comprises carboplatin, cisplatin, etoposide, a taxane, or any combination thereof.

[0317] Embodiment 45. A method of preventing or treating metastasis in a subject with a neuroendocrine cancer, wherein the method comprises administering to the subject an effective amount of the pharmaceutical composition of embodiment 26.

[0318] Embodiment 46. The method of embodiment 45, wherein the chimeric antigen receptor (CAR) binds to a neuroendocrine cancerous cell.

[0319] Embodiment 47. The method of any one of embodiments 45-46, wherein the cell is a T lymphocyte.

[0320] Embodiment 48. The method of embodiment 47, wherein the T lymphocyte is a CD4+ T lymphocyte or a CD8 + T lymphocyte.

[0321] Embodiment 49. The method of any one of embodiments 45-48, wherein the cell is a natural killer cell.

[0322] Embodiment 50. The method of embodiment 49, wherein the natural killer cell is autologous to the subject.

[0323] Embodiment 51. The method of embodiment 49, wherein the natural killer cell is heterologous to the subject.

[0324] Embodiment 52. The method of embodiment 49, wherein the natural killer cell is allogenic to the subject.

[0325] Embodiment 53. The method of any one of embodiments 45-52, wherein the neuroendocrine cancer is a carcinoid tumor, an islet cell tumor, a medullary thyroid cancer, a pheochromocytoma, a neuroendocrine carcinoma of the skin, small cell lung cancer, large cell

neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), or metastatic castration-resistant prostate cancer (CRPC).

[0326] Embodiment 54. The method of any one of embodiments 45-53, wherein the neuroendocrine cancer is metastatic castration-resistant prostate cancer (CRPC).

[0327] Embodiment 55. The method of any one of embodiments 45-54, wherein neuroendocrine cancerous cells express ROR-1.

[0328] Embodiment 56. The method of any one of embodiments 45-55, wherein the subject has failed to respond to androgen deprivation therapy.

[0329] Embodiment 57. The method of any one of embodiments 45-56, wherein the neuroendocrine cancer has metastasized to bone.

[0330] Embodiment 58. The method of any one of embodiments 45-57, wherein the method further comprises administering cirmtuzumab to the subject.

[0331] Embodiment 59. The method of embodiment 58, wherein the cirmtuzumab and the cell are administered separately.

[0332] Embodiment 60. The method of embodiment 58, wherein the cirmtuzumab and the cell are administered together.

[0333] Embodiment 61. The method of any one of embodiments 45-60, wherein the method further comprises administering to the subject platinum-based chemotherapy.

[0334] Embodiment 62. The method of embodiment 61, wherein the platinum-based chemotherapy comprises carboplatin, cisplatin, etoposide, a taxane, or any combination thereof.

[0335] Embodiment 63. The method of any one of embodiments 43 and 61, wherein the platinum-based chemotherapy comprises administering an antibody-drug conjugate.

REFERENCES

[0336] 1. Siegel R, Ma J, Zou Z, & Jemal A. Cancer statistics. CA Cancer J Clin 2014: 64(1):9-29.

[0337] 2. Oster G, Lamerato L, Glass AG, Richert-Boe KE, Lopez A, Chung K, Richhariya A, Dodge T, Wolff GG, Balakumaran A, Edelsberg J. Natural history of skeletal-related events in patients with breast, lung, or prostate cancer and metastases to bone: a 15-year study in two large US health systems. Support Care in Cancer. 2013 Dec 21(12):3279-3286.

[0338] 3. Logothetis C, Morris MJ, Den R, Coleman RE. Current perspectives on bone metastases in castrate-resistant prostate cancer. Cancer Metastasis Rev. 2018 Mar;37(1):189-196. doi: 10.1007/s10555-017-9719-4. Review. PMID:29380085

[0339] 4. Garnero P, Buchs N, Zekri J, Rizzoli R, Coleman RE, Delmas PD. Markers of bone turnover for the management of patients with bone metastases from prostate cancer. Br J Cancer. 2000 82(4):858-864.

[0340] 5. Shiao SL, Chu GC, Chung LW. Regulation of prostate cancer progression by the tumor microenvironment. Cancer Lett. 2016 Jan 28. pii: S0304-3835(15)00773-9. doi: 10.1016/j.canlet.2015.12.022. [Epub ahead of print].

[0341] 6. Vargas HA, Wassberg C, Fox JJ, Wibmer A, Goldman DA, Kuk D, Gonen M, Larson SM, Morris MJ, Scher HI, Hricak H. Bone metastases in castration-resistant prostate cancer: associations between morphologic CT patterns, glycolytic activity, and androgen receptor expression on PET and overall survival. Radiology. 2014 Apr;271(1):220-9. doi: 10.1148/radiol.13130625. Epub 2013 Nov 18. PMID:24475817

[0342] 7. Amend SR1, Roy S2, Brown JS3, Pienta KJ2. Ecological paradigms to understand the dynamics of metastasis. Cancer Lett. 2016 Sep 28;380(1):237-42. doi: 10.1016/j.canlet.2015.10.005. Epub 2015 Oct 10.

[0343] 8. Shiozawa Y1,2, Berry JE1, Eber MR1,2, Jung Y1, Yumoto K1, Cackowski FC1, Yoon HJ3, Parsana P4,5, Mehra R6, Wang J1, McGee S1, Lee E1, Nagrath S3, Pienta KJ4, Taichman RS1. The marrow niche controls the cancer stem cell phenotype of disseminated prostate cancer. Oncotarget. 2016 Jul 5;7(27):41217-41232. doi: 10.18632/oncotarget.9251.

[0344] 9. Nguyen HM, Vessella RL, Morrissey C, Brown LG, Coleman IM, Higano CS, Mostaghel EA, Zhang X, True LD, Lam HM, Roudier M, Lange PH, Nelson PS, Corey E. LuCaP Prostate Cancer Patient-Derived Xenografts Reflect the Molecular Heterogeneity of

Advanced Disease an--d Serve as Models for Evaluating Cancer Therapeutics. Prostate. 2017 May;77(6):654-671. doi: 10.1002/pros.23313. Epub 2017 Feb 3. PMID:28156002

[0345] 10. Kleb B, Estécio MR, Zhang J, Tzelepi V, Chung W, Jelinek J, Navone NM, Tahir S, Marquez VE, Issa JP, Maity S, Aparicio A. Differentially methylated genes and androgen receptor re-expression in small cell prostate carcinomas. Epigenetics. 2016 Mar 3;11(3):184-93. doi: 10.1080/15592294.2016.1146851. Epub 2016 Feb 18. PMID:26890396

[0346] 11. Hao J, Ci X, Xue H, Wu R, Dong X, Choi SYC, He H, Wang Y, Zhang F, Qu S, Zhang F, Haegert AM, Gout PW, Zoubeidi A, Collins C, Gleave ME, Lin D, Wang Y. Patient-derived Hormone-naive Prostate Cancer Xenograft Models Reveal Growth Factor Receptor Bound Protein 10 as an Androgen Receptor-repressed Gene Driving the Development of Castration-resistant ProstateCancer.Eur Urol. 2018 Mar 12. pii: S0302-2838(18)30162-3. doi: 10.1016/j.eururo.2018.02.019. [Epub ahead of print] PMID:29544736

[0347] 12. Robinson D, Van Allen EM, Wu YM, Schultz N, Lonigro RJ, Mosquera JM, Montgomery B, Taplin ME, Pritchard CC, Attard G, Beltran H, Abida W, Bradley RK, Vinson J, Cao X, Vats P, Kunju LP, Hussain M, Feng FY, Tomlins SA, Cooney KA, Smith DC, Brennan C, Siddiqui J, Mehra R, Chen Y, Rathkopf DE, Morris MJ, Solomon SB, Durack JC, Reuter VE, Gopalan A, Gao J, Loda M, Lis RT, Bowden M, Balk SP, Gaviola G, Sougnez C, Gupta M, Yu EY, Mostaghel EA, Cheng HH, Mulcahy H, True LD, Plymate SR, Dvinge H, Ferraldeschi R, Flohr P, Miranda S, Zafeiriou Z, Tunariu N, Mateo J, Perez-Lopez R, Demichelis F, Robinson BD, Sboner A, Schiffman M, Nanus DM, Tagawa ST, Sigaras A, Eng KW, Elemento O, Sboner A, Heath EI, Scher HI, Pienta KJ, Kantoff P, de Bono JS, Rubin MA, Nelson PS, Garraway LA, Sawyers CL, Chinnaiyan AM. Integrative Clinical Genomics of Advanced Prostate Cancer. Cell. 2015 May 21;161(5):1215-1228. doi: 10.1016/j.cell.2015.05.001. Erratum in: Cell. 2015 Jul 16;162(2):454.

[0348] 13. Beltran H, Wyatt AW, Chedgy EC, Donoghue A, Annala M, Warner EW, Beja K, Sigouros M, Mo F, Fazli L, Collins CC, Eastham J, Morris M, Taplin ME, Sboner A, Halabi S, Gleave ME. Impact of Therapy on Genomics and Transcriptomics in High-Risk Prostate Cancer Treated with Neoadjuvant Docetaxel and Androgen Deprivation Therapy. Clin Cancer Res. 2017 Nov 15;23(22):6802-6811. doi: 10.1158/1078-0432.CCR-17-1034. Epub 2017 Aug 25. PMID: 28842510

[0349] 14. Pritchard CC, Mateo J, Walsh MF, De Sarkar N, Abida W, Beltran H, Garofalo A, Gulati R, Carreira S, Eeles R, Elemento O, Rubin MA, Robinson D, Lonigro R, Hussain M, Chinnaiyan A, Vinson J, Filipenko J, Garraway L, Taplin ME, AlDubayan S, Han GC, Beightol M, Morrissey C, Nghiem B, Cheng HH, Montgomery B, Walsh T, Casadei S, Berger M, Zhang L, Zehir A, Vijai J, Scher HI, Sawyers C, Schultz N, Kantoff PW, Solit D, Robson M, Van Allen EM, Offit K, de Bono J, Nelson PS. Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. N Engl J Med. 2016 Aug 4;375(5):443-53. doi: 10.1056/NEJMoa1603144. Epub 2016 Jul 6. PMID:27433846

[0350] 15. Luo J, Attard G, Balk SP, Bevan C, Burnstein K, Cato L, Cherkasov A, De Bono JS, Dong Y, Gao AC, Gleave M, Heemers H, Kanayama M, Kittler R, Lang JM, Lee RJ, Logothetis CJ, Matusik R, Plymate S, Sawyers CL, Selth LA, Soule H, Tilley W, Weigel NL, Zoubeidi A, Dehm SM, Raj GV. Role of Androgen Receptor Variants in Prostate Cancer: Report from the 2017 Mission Androgen Receptor Variants Meeting.Eur Urol. 2018 May;73(5):715-723. doi: 10.1016/j.eururo.2017.11.038. Epub 2017 Dec 16. PMID:29258679

[0351] 16. Armenia J, Wankowicz SAM, Liu D, Gao J, Kundra R, Reznik E, Chatila WK, Chakravarty D, Han GC, Coleman I, Montgomery B, Pritchard C, Morrissey C, Barbieri CE, Beltran H, Sboner A, Zafeiriou Z, Miranda S, Bielski CM, Penson AV, Tolonen C, Huang FW, Robinson D, Wu YM, Lonigro R, Garraway LA, Demichelis F, Kantoff PW, Taplin ME, Abida W, Taylor BS, Scher HI, Nelson PS, de Bono JS, Rubin MA, Sawyers CL, Chinnaiyan AM; PCF/SU2C International Prostate Cancer Dream Team, Schultz N, Van Allen EM; PCF/SU2C International Prostate Cancer Dream Team. The long tail of oncogenic drivers in prostate cancer. Nat Genet. 2018 Apr 2. doi: 10.1038/s41588-018-0078-z. [Epub ahead of print] PMID:29610475

[0352] 17. Carlsson A, Kuhn P, Luttgen MS, Dizon KK, Troncoso P, Corn PG, Kolatkar A, Hicks JB, Logothetis CJ, Zurita AJ. Paired High-Content Analysis of Prostate Cancer Cells in Bone Marrow and Blood Characterizes Increased Androgen Receptor Expression in Tumor Cell Clusters. Clin Cancer Res. 2017 Apr 1;23(7):1722-1732. doi: 10.1158/1078-0432.CCR-16-1355. Epub 2016 Oct 4. PMID:27702818

[0353] 18. Don-Doncow N1, Marginean F2, Coleman I3, Nelson PS3, Ehrnström R4, Krzyzanowska A1, Morrissey C5, Hellsten R1, Bjartell A6. Expression of STAT3 in Prostate

Cancer Metastases. Eur Urol. 2017 Mar;71(3):313-316. doi: 10.1016/j.eururo.2016.06.018. Epub 2016 Jun 22.

[0354] 19. Wu Y, Schoenborn JR, Morrissey C, Xia J, Larson S, Brown LG, Qu X, Lange PH, Nelson PS, Vessella RL, Fang M. High-Resolution Genomic Profiling of Disseminated Tumor Cells in Prostate Cancer.J Mol Diagn. 2016 Jan;18(1):131-43. doi: 10.1016/j.jmoldx.2015.08.004. Epub 2015 Nov 20.PMID:26607774

[0355] 20. Haider M, Zhang X, Coleman I, Ericson N, True LD, Lam HM, Brown LG, Ketchanji M, Nghiem B, Lakely B, Coleman R, Montgomery B, Lange PH, Roudier M, Higano CS, Bielas JH, Nelson PS, Vessella RL, Morrissey C. Epithelial mesenchymal-like transition occurs in a subset of cells in castration resistant prostate cancer bone metastases. Clin Exp Metastasis. 2016 Mar;33(3):239-48. doi: 10.1007/s10585-015-9773-7. Epub 2015 Dec 14.

[0356] 21. Bluemn EG, Coleman IM, Lucas JM, Coleman RT, Hernandez-Lopez S, Tharakan R, Bianchi-Frias D, Dumpit RF, Kaipainen A, Corella AN, Yang YC, Nyquist MD, Mostaghel E, Hsieh AC, Zhang X, Corey E, Brown LG, Nguyen HM, Pienta K, Ittmann M, Schweizer M, True LD, Wise D, Rennie PS, Vessella RL, Morrissey C, Nelson PS. Androgen Receptor Pathway-Independent Prostate Cancer Is Sustained through FGF Signaling. Cancer Cell. 2017 Oct 9;32(4):474-489.e6. doi: 10.1016/j.ccell.2017.09.003. PMID:29017058

[0357] 22. Cho WJ, Oliveira DS, Najy AJ, Mainetti LE, Aoun HD, Cher ML, Heath E, Kim HR, Bonfil RD. Gene expression analysis of bone metastasis and circulating tumor cells from metastatic castrate-resistant prostate cancer patients. J Transl Med. 2016 Mar 15;14:72. doi: 10.1186/s12967-016-0829-5. PMID:26975354.

[0358] 23. Davies AH, Beltran H, Zoubeidi A. Cellular plasticity and the neuroendocrine phenotype in prostate cancer. Nat Rev Urol. 2018 Feb 20. doi: 10.1038/nrurol.2018.22. [Epub ahead of print] Review.PMID: 29460922

[0359] 24. Bishop JL, Thaper D, Vahid S, Davies A, Ketola K, Kuruma H, Jama R, Nip KM, Angeles A, Johnson F, Wyatt AW, Fazli L, Gleave ME, Lin D, Rubin MA, Collins CC, Wang Y, Beltran H, Zoubeidi A. The Master Neural Transcription Factor BRN2 Is an Androgen Receptor-Suppressed Driver of Neuroendocrine Differentiation in Prostate Cancer. Cancer Discov. 2017 Jan;7(1):54-71. doi: 10.1158/2159-8290.CD-15-1263. Epub 2016 Oct 26. PMID:2778470

[0360] 25. Dardenne E, Beltran H, Benelli M, Gayvert K, Berger A, Puca L, Cyrta J, Sboner A, Noorzad Z, MacDonald T, Cheung C, Yuen KS, Gao D, Chen Y, Eilers M, Mosquera JM, Robinson BD, Elemento O, Rubin MA, Demichelis F, Rickman DS. N-Myc Induces an EZH2-Mediated Transcriptional Program Driving Neuroendocrine Prostate Cancer. Cancer Cell. 2016 Oct 10;30(4):563-577. doi: 10.1016/j.ccell.2016.09.005.PMID: 27728805

[0361] 26. Zhang W, Liu B, Wu W, Li L, Broom BM, Basourakos SP, Korentzelos D, Luan Y, Wang J, Yang G, Park S, Azad AK, Cao X, Kim J, Corn PG, Logothetis CJ, Aparicio AM, Chinnaiyan AM, Navone N, Troncoso P, Thompson TC. Targeting the MYCN-PARP-DNA Damage Response Pathway in Neuroendocrine Prostate Cancer. Clin Cancer Res. 2018 Feb 1;24(3):696-707. doi: 10.1158/1078-0432.CCR-17-1872. Epub 2017 Nov 14. PMID:2913834

[0362] 27. Lee JK, Phillips JW, Smith BA, Park JW, Stoyanova T, McCaffrey EF, Baertsch R, Sokolov A, Meyerowitz JG, Mathis C, Cheng D, Stuart JM, Shokat KM, Gustafson WC, Huang J, Witte ON. N-Myc Drives Neuroendocrine Prostate Cancer Initiated from Human Prostate Epithelial Cells.Cancer Cell. 2016 Apr 11;29(4):536-547. doi: 10.1016/j.ccell.2016.03.001. Epub 2016 Mar 31.PMID:27050099

[0363] 28. Singhal U, Wang Y, Henderson J, Niknafs YS, Qiao Y, Gursky A, Zaslavsky A, Chung JS, Smith DC, Karnes RJ, Chang SL, Feng FY, Palapattu GS, Taichman RS, Chinnaiyan AM, Tomlins SA, Morgan TM. Multigene Profiling of CTCs in mCRPC Identifies a Clinically Relevant Prognostic Signature. Mol Cancer Res. 2018 Apr;16(4):643-654. doi: 10.1158/1541-7786.MCR-17-0539. Epub 2018 Feb 16. PMID:29453313

[0364] 29. Spratt DE, Zhang J, Santiago-Jiménez M, Dess RT, Davis JW, Den RB, Dicker AP, Kane CJ, Pollack A, Stoyanova R, Abdollah F, Ross AE, Cole A, Uchio E, Randall JM, Nguyen H, Zhao SG, Mehra R, Glass AG, Lam LLC, Chelliserry J, du Plessis M, Choeurng V, Aranes M, Kolisnik T, Margrave J, Alter J, Jordan J, Buerki C, Yousefi K, Haddad Z, Davicioni E, Trabulsi EJ, Loeb S, Tewari A, Carroll PR, Weinmann S, Schaeffer EM, Klein EA, Karnes RJ, Feng FY, Nguyen PL. Development and Validation of a Novel Integrated Clinical-Genomic Risk Group Classification for Localized Prostate Cancer. J Clin Oncol. 2018 Feb 20;36(6):581-590. doi: 10.1200/JCO.2017.74.2940. Epub 2017 Nov 29.PMID:29185869

[0365] 30. Nguyen PL, Haddad Z, Ross AE, Martin NE, Deheshi S, Lam LLC, Chelliserry J, Tosoian JJ, Lotan TL, Spratt DE, Stoyanova RS, Punnen S, Ong K, Buerki C, Aranes M, Kolisnik T, Margrave J, Yousefi K, Choeurng V, Davicioni E, Trock BJ, Kane CJ, Pollack A,

Davis JW, Feng FY, Klein EA. Ability of a Genomic Classifier to Predict Metastasis and Prostate Cancer-specific Mortality after Radiation or Surgery based on Needle Biopsy Specimens. Eur Urol. 2017 Nov;72(5):845-852. doi: 10.1016/j.eururo.2017.05.009. Epub 2017 May 19. PMID:28528811

[0366] 31. Klaassen Z, Howard LE, de Hoedt A, Amling CL, Aronson WJ, Cooperberg MR, Kane CJ, Terris MK, Freedland SJ. Factors predicting skeletal-related events in patients with bone metastatic castration-resistant prostate cancer.Cancer. 2017 May 1;123(9):1528-1535. doi: 10.1002/cncr.30505. Epub 2016 Dec 27. PMID:28026865

[0367] 32. Kohli M, Wang L, Xie F, Sicotte H, Yin P, Dehm SM, Hart SN, Vedell PT, Barman P, Qin R, Mahoney DW, Carlson RE, Eckel-Passow JE, Atwell TD, Eiken PW, McMenomy BP, Wieben ED, Jha G, Jimenez RE, Weinshilboum R, Wang L. Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy.PLoS One. 2015 Dec 22;10(12):e0145176. doi: 10.1371/journal.pone.0145176. eCollection 2015.PMID:26695660

[0368] 33. Lee GT, Kang DI, Ha YS, Jung YS, Chung J, Min K, Kim TH, Moon KH, Chung JM, Lee DH, Kim WJ, Kim IY. Prostate cancer bone metastases acquire resistance to androgen deprivation via WNT5A-mediated BMP-6 induction. Br J Cancer. 2014 Mar 18;110(6):1634-44. doi: 10.1038/bjc.2014.23. Epub 2014 Feb 11. PMID:24518599

[0369] 34. Lee GT, Kwon SJ, Kim J, Kwon YS, Lee N, Hong JH, Jamieson C, Kim WJ, Kim IY. WNT5A induces castration-resistant prostate cancer via CCL2 and tumour-infiltrating macrophages. Br J Cancer. 2018 Mar 6;118(5):670-678. doi: 10.1038/bjc.2017.451. Epub 2018 Jan 30. PMID:29381686

[0370] 35. Miyamoto DT, Zheng Y, Wittner BS, Lee RJ, Zhu H, Broderick KT, Desai R, Fox DB, Brannigan BW, Trautwein J, Arora KS, Desai N, Dahl DM, Sequist LV, Smith MR, Kapur R, Wu CL, Shioda T, Ramaswamy S, Ting DT, Toner M, Maheswaran S, Haber DA. RNA-Seq of single prostate CTCs implicates noncanonical Wnt signaling in antiandrogen resistance. Science. 2015 Sep 18;349(6254):1351-6. doi: 10.1126/science.aab0917. PMID: 26383955

[0371] 36. F. Jin et al., "Regulation of prostate cancer cell migration toward bone marrow stromal cell-conditioned medium by Wnt5a signaling.," Mol. Med. Rep., vol. 8, no. 5, pp. 1486–92, Nov. 2013.

[0372] 37. Tamura K, Furihata M, Satake H, Hashida H, Kawada C, Osakabe H, Fukuhara H, Kumagai N, Iiyama T, Shuin T, Inoue K.SHISA2 enhances the aggressive phenotype in prostate cancer through the regulation of WNT5A expression. Oncol Lett. 2017 Dec;14(6):6650-6658. doi: 10.3892/ol.2017.7099. Epub 2017 Sep 28. PMID: 29344118

[0373] 38. Huang L, Pu Y, Hu WY, Birch L, Luccio-Camelo D, Yamaguchi T, Prins GS. The role of Wnt5a in prostate gland development. Dev Biol. 2009 Apr 15;328(2):188-99. doi: 10.1016/j.ydbio.2009.01.003. Epub 2009 Jan 14. PMID: 19389372

[0374] 39. M. Okamoto et al., "Noncanonical Wnt5a enhances Wnt/β-catenin signaling during osteoblastogenesis.," Sci. Rep., vol. 4, no. 1, p. 4493, Mar. 2014.

[0375] 40. Hosseini-Farahabadi S, Gignac SJ, Danescu A, Fu K, Richman JM. Abnormal WNT5A Signaling Causes Mandibular Hypoplasia in Robinow Syndrome.J Dent Res. 2017 Oct;96(11):1265-1272. doi: 10.1177/0022034517716916. Epub 2017 Jun 29. PMID:28662348

[0376] 41. Choi MY, Widhopf GF 2nd, Wu CC, Cui B, Lao F, Sadarangani A, Cavagnaro J, Prussak C, Carson DA, Jamieson C, Kipps TJ. Pre-clinical Specificity and Safety of UC-961, a First-In-Class Monoclonal Antibody Targeting ROR1. Clin Lymphoma Myeloma Leuk. 2015 Jun;15 Suppl:S167-9. doi: 10.1016/j.clml.2015.02.010. Review. PMID: 26297272

[0377] 42. Yu J, Chen L, Cui B, Wu C, Choi MY, Chen Y, Zhang L, Rassenti LZ, Widhopf Ii GF, Kipps TJ. Cirmtuzumab inhibits Wnt5a-induced Rac1 activation in chronic lymphocytic leukemia treated with ibrutinib. Leukemia. 2017 Jun;31(6):1333-1339. doi: 10.1038/leu.2016.368. Epub 2016 Dec 1. PMID: 27904138

[0378] 43. Jamieson, CH, (PI), and Choi, M (Co-PI), Kipps, TJ (Responsible Party), ClinicalTrials.gov Identifier: NCT02222688, A Phase I Clinical Trial to Determine the Safety and Tolerability of UC-961 (Cirmtuzumab), an Anti-ROR1 Monoclonal Antibody, for the Treatment of Patients With Relapsed or Refractory Chronic Lymphocytic Leukemia Who Are Ineligible for Chemotherapy. https://clinicaltrials.gov/ct2/show/NCT02222688

[0379] 44. Bauer M, Bénard J, Gaasterland T, Willert K, Cappellen D. WNT5A encodes two isoforms with distinct functions in cancers. PLoS One. 2013 8 (11): e80526. doi:10.1371/journal.pone.0080526. PMID 24260410.

[0380] 45. Raheem, O., A.A. Kulidjian, C. Wu, Y.B. Jeong, T. Yamaguchi, K.M. Smith, D. Goff, H. Leu, S.R. Morris, N.A. Cacalano, K. Masuda, C.H. Jamieson, C.J. Kane, and C.A. Jamieson, A novel patient-derived intra-femoral xenograft model of bone metastatic

prostate cancer that recapitulates mixed osteolytic and osteoblastic lesions. J Transl Med, 2011. 9: p. 185.

[0381] 46. Godebu, E., M. Muldong, A. Strasner, C.N. Wu, S.C. Park, J.R. Woo, W. Ma, M.A. Liss, T. Hirata, O. Raheem, N.A. Cacalano, A.A. Kulidjian, and C.A. Jamieson, PCSD1, a new patient-derived model of bone metastatic prostate cancer, is castrate-resistant in the bone-niche. J Transl Med, 2014. 12: p. 275.

[0382] 47. Hirata, T., S.C. Park, M.T. Muldong, C.N. Wu, T. Yamaguchi, A. Strasner, O. Raheem, H. Kumon, R.L. Sah, N.A. Cacalano, C.H.M. Jamieson, C.J. Kane, K. Masuda, A.A. Kulidjian, and C.A.M. Jamieson, Specific bone region localization of osteolytic versus osteoblastic lesions in a patient-derived xenograft model of bone metastatic prostate cancer. Asian J Urol, 2016. 3(4): p. 229-239

[0383] 48. CAM Jamieson, Kulidjian, A.A., Muldong, M, Wu, C., Lee, S., Mendoza, T., Park, SC, Park, JS, Raheem, O., Woo, JR, Godebu, E., Strasner, A., Kane, CJ, Gaasterland, T. Genomic analysis of a longitudinal series of surgical prostate cancer bone metastases and xenografts from the same patient with progressively therapy-resistant cancer revealed selection of metastatic clone. (Research completed, Manuscript in Preparation).

[0384] 49. Ritter KE, Wang Z, Vezina CM, Bjorling DE, Southard-Smith EM1.Serotonin Receptor 5-HT3A Affects Development of Bladder Innervation and Urinary Bladder Function. Front Neurosci. 2017 Dec 12;11:690. doi: 10.3389/fnins.2017.00690. eCollection 2017.

[0385] 50. Hu WY, Hu DP, Xie L, Li Y, Majumdar S, Nonn L, Hu H, Shioda T, Prins GS. Isolation and functional interrogation of adult human prostate epithelial stem cells at single cell resolution. Stem Cell Res. 2017 Aug;23:1-12. doi: 10.1016/j.scr.2017.06.009. Epub 2017 Jun 16. PMID: 28651114

[0386] 51. Sarin S, Zuniga-Sanchez E, Kurmangaliyev YZ, Cousins H, Patel M, Hernandez J, Zhang KX, Samuel MA, Morey M, Sanes JR, Zipursky SL. Role for Wnt Signaling in Retinal Neuropil Development: Analysis via RNA-Seq and In Vivo Somatic CRISPR Mutagenesis. Neuron. 2018 Apr 4;98(1):109-126.e8. doi: 10.1016/j.neuron.2018.03.004. Epub 2018 Mar 22. PMID:29576390

[0387] 52. Yu J, Chen L, Chen Y, Hasan MK, Ghia EM, Zhang L, Wu R, Rassenti LZ, Widhopf GF, Shen Z, Briggs SP, Kipps TJ. Wnt5a induces ROR1 to associate with 14-3-3ζ for

enhanced chemotaxis and proliferation of chronic lymphocytic leukemia cells. Leukemia. 2017 Dec;31(12):2608-2614. doi: 10.1038/leu.2017.132. Epub 2017 May 3. PMID:28465528

[0388] 53. Zhang S, Zhang H, Ghia EM, Huang J, Wu L, Zhang J, Lam S, Lei Y, He J, Cui B, Widhopf GF 2nd, Yu J, Schwab R, Messer K, Jiang W, Parker BA, Carson DA, Kipps TJ. Inhibition of chemotherapy resistant breast cancer stem cells by a ROR1 specific antibody. Proc Natl Acad Sci U S A. 2019 Jan 22;116(4):1370-1377. doi: 10.1073/pnas.1816262116. Epub 2019 Jan 8.PMID:30622177

[0389] 54. Yu J, Chen L, Cui B, Widhopf GF 2nd, Shen Z, Wu R, Zhang L, Zhang S, Briggs SP, Kipps TJ. Wnt5a induces ROR1/ROR2 heterooligomerization to enhance leukemia chemotaxis and proliferation. J Clin Invest. 2016 Feb;126(2):585-98. PMID:26690702

[0390] 55. Hasan MK, Rassenti L, Widhopf GF 2nd, Yu J, Kipps TJ. Wnt5a causes ROR1 to complex and activate cortactin to enhance migration of chronic lymphocytic leukemia cells. Leukemia. 2019 Mar;33(3):653-661. doi: 10.1038/s41375-018-0306-7. Epub 2018 Dec 19. PMID:30568170

[0391] 56. Choi MY, Widhopf GF 2nd, Ghia EM, Kidwell RL, Hasan MK, Yu J, Rassenti LZ, Chen L, Chen Y, Pittman E, Pu M, Messer K, Prussak CE, Castro JE, Jamieson C, Kipps TJ. Phase I Trial: Cirmtuzumab Inhibits ROR1 Signaling and Stemness Signatures in Patients with Chronic Lymphocytic Leukemia. Cell Stem Cell. 2018 Jun 1;22(6):951-959.e3. doi: 10.1016/j.stem.2018.05.018.PMID:29859176

[0392] 57. Zhang S, Chen L, Wang-Rodriguez J, Zhang L, Cui B, Frankel W, Wu R, Kipps TJ. The onco-embryonic antigen ROR1 is expressed by a variety of human cancers. Am J Pathol. 2012 Dec;181(6):1903-10. doi: 10.1016/j.ajpath.2012.08.024. Epub 2012 Oct 4. PMID:23041612

[0393] 58. Li C, Wang S, Xing Z, Lin A, Liang K, Song J, Hu Q, Yao J, Chen Z, Park PK, Hawke DH, Zhou J, Zhou Y, Zhang S, Liang H, Hung MC, Gallick GE, Han L, Lin C, Yang L. A ROR1-HER3-lncRNA signalling axis modulates the Hippo-YAP pathway to regulate bone metastasis. Nat Cell Biol. 2017 Feb;19(2):106-119. doi: 10.1038/ncb3464. Epub 2017 Jan 23.PMID:28114269

[0394] 59. Woo JR, Liss MA, Muldong MT, Palazzi K, Strasner A, Ammirante M, Varki N, Shabaik A, Howell S, Kane CJ, Karin M, Jamieson CA. Tumor infiltrating B-cells are increased

in prostate cancer tissue. J Transl Med. 2014 Jan 30;12:30. doi: 10.1186/1479-5876-12-30. PMID:24475900

INFORMAL SEQUENCE LISTING

[0395] **UC961 VL:**

DIVMTQTPLSLPVTPGEPASISCRASKSISKYLAWYQQKPGQAPRLLIYSGSTLQSGIPPRF SGSGYGTDFTLTINNIESEDAAYYFCQQHDESPYTFGEGTKVEIK (SEQ ID NO:21)

[0396] Linker #3:

GGGGSGSTSGSGKPGSGEGSTKGGGGGS (SEQ ID NO:24)

[0397] **UC961 VH:**

QVQLQESGPGLVKPSQTLSLTCTVSGYAFTAYNIHWVRQAPGQGLEWMGSFDPYDGGS SYNQKFKDRLTISKDTSKNQVVLTMTNMDPVDTATYYCARGWYYFDYWGHGTLVTVS S (SEQ ID NO:27)

[0398] **Spacer #3 (or "Hinge/Short")**:

VDESKYGPPCPPCP (SEQ ID NO:29)

[0399] **Spacer CH3:**

VDESKYGPPCPPCPLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO:41)

[0400] **Spacer CH2CH3 (or "Long/Full"):**

VDESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFN WYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO:42)

[0401] **UC961 CDR L1:**

KSISKY (SEQ ID NO:43)

[0402] **UC961 CDR L2:**

SGS (SEQ ID NO:44)

[0403] **UC961 CDR L3:**

QQHDESPY (SEQ ID NO:45)

[0404] **UC961 CDR H1:**

GYAFTAYN (SEQ ID NO:46)

[0405] **UC961 CDR H2**:

FDPYDGGS (SEQ ID NO:47)

[0406] **UC961 CDR H3**:

GWYYFDY (SEQ ID NO:48)

[0407] **4A5 CDR L1**:

PDINSY (SEQ ID NO:49)

[0408] **4A5 CDR L2**:

RAN (SEQ ID NO:50)

[0075] **4A5 CDR L3:**

LQYDEFPYT (SEQ ID NO:51)

[0409] **4A5 CDR H1**:

GFTFSSYA (SEQ ID NO:52)

[0410] **4A5 CDR H2**:

ISRGGTT (SEQ ID NO:53)

[0411] **4A5 CDR H3**:

YDYDGYYAMDY (SEQ ID NO:54)

[0412] **Full-length human ROR-1 Protein** (SEQ ID NO:55):

MHRPRRRGTRPPLLALLAALLLAARGAAAQETELSVSAELVPTSSWNISSELNKDSYLTL
DEPMNNITTSLGQTAELHCKVSGNPPPTIRWFKNDAPVVQEPRRLSFRSTIYGSRLRIRNL
DTTDTGYFQCVATNGKEVVSSTGVLFVKFGPPPTASPGYSDEYEEDGFCQPYRGIACAR
FIGNRTVYMESLHMQGEIENQITAAFTMIGTSSHLSDKCSQFAIPSLCHYAFPYCDETSSV
PKPRDLCRDECEILENVLCQTEYIFARSNPMILMRLKLPNCEDLPQPESPEAANCIRIGIPM
ADPINKNHKCYNSTGVDYRGTVSVTKSGRQCQPWNSQYPHTHTFTALRFPELNGGHSY
CRNPGNQKEAPWCFTLDENFKSDLCDIPACDSKDSKEKNKMEILYILVPSVAIPLAIALLF
FFICVCRNNQKSSSAPVQRQPKHVRGQNVEMSMLNAYKPKSKAKELPLSAVRFMEELG
ECAFGKIYKGHLYLPGMDHAQLVAIKTLKDYNNPQQWMEFQQEASLMAELHHPNIVCL
LGAVTQEQPVCMLFEYINQGDLHEFLIMRSPHSDVGCSSDEDGTVKSSLDHGDFLHIAIQ
IAAGMEYLSSHFFVHKDLAARNILIGEQLHVKISDLGLSREIYSADYYRVQSKSLLPIRW
MPPEAIMYGKFSSDSDIWSFGVVLWEIFSFGLQPYYGFSNQEVIEMVRKRQLLPCSEDCP

PRMYSLMTECWNEIPSRRPRFKDIHVRLRSWEGLSSHTSSTTPSGGNATTQTTSLSASPV
SNLSNPRYPNYMFPSQGITPQGQIAGFIGPPIPQNQRFIPINGYPIPPGYAAFPAAHYQPTG
PPRVIQHCPPPKSRSPSSASGSTSTGHVTSLPSSGSNQEANIPLLPHMSIPNHPGGMGITVF
GNKSQKPYKIDSKQASLLGDANIHGHTESMISAEL

[0413] **21 amino acid stretch of human ROR-1 including glutamic acid at position 138**

(SEQ ID NO:56): VATNGKEVVSSTGVLFVKFGP

[0414] **15 amino acid stretch of human ROR-1 including glutamic acid at position 138**

(SEQ ID NO:57): EVVSSTGVLFVKFGP

CLAIMS

1. A method of treating a neuroendocrine cancer in a subject in need thereof, wherein the method comprises administering to the subject an effective amount of a cell that expresses a chimeric antigen receptor (CAR) comprising a ROR-1-binding antibody region.

2. The method of claim 1, wherein the chimeric antigen receptor comprises:

i. an antigen binding region, wherein the antigen binding region specifically binds ROR-1 and wherein the antigen binding region comprises a light chain variable domain and a heavy chain variable domain;

(a) wherein the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45; and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48; or

(b) wherein the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51; and the heavy chain variable domain comprising a CDR H1 as set forth in SEQ ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54;

ii. a spacer domain;

iii. a transmembrane domain; and

iv. an intracellular domain.

3. The method of claim 2, wherein the spacer domain is between 14 and 120 amino acids in length.

4. The method of claim 3, wherein the light chain variable domain is linked to the N-terminus or the C-terminus of the heavy chain variable domain.

5. The method of claim 4, wherein the light chain variable domain is covalently linked to the heavy chain variable domain through a polypeptide linker.

6. The method of claim 5, wherein the polypeptide linker comprises an amino acid sequence of SEQ ID NO: 24.
7. The method of claim 3, wherein the spacer domain comprises an antibody domain.
8. The method of claim 7, wherein the antibody domain comprises an immunoglobulin hinge domain, an immunoglobulin constant heavy chain 3 (CH3) domain, an immunoglobulin constant heavy chain 2 (CH2) domain, or a combination thereof.
9. The method of claim 2, wherein the spacer domain comprises an amino acid sequence of SEQ ID NO: 29, SEQ ID NO: 41 or SEQ ID NO: 42.
10. The method of claim 2, wherein the light chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 21.
11. The method of claim 2, wherein the heavy chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 27.
12. The method of claim 2, wherein the transmembrane domain comprises a CD8α transmembrane domain, a CD28 transmembrane domain, a CD4 transmembrane domain, a CD3ζ transmembrane domain, or any combination thereof.
13. The method of claim 12, wherein the transmembrane domain is a CD28 transmembrane domain.
14. The method of claim 2, wherein the intracellular domain comprises an intracellular co-stimulatory signaling domain, an intracellular T-cell signaling domain, or a combination thereof.
15. The method of claim 14, wherein the intracellular co-stimulatory signaling domain is a 4-1BB intracellular co-stimulatory signaling domain, a CD28 intracellular co-stimulatory signaling domain, a ICOS intracellular co-stimulatory signaling domain, an OX-40 intracellular co-stimulatory signaling domain, or any combination thereof.
16. The method of claim 15, wherein the intracellular costimulatory signaling domain comprises a 41-BB intracellular co-stimulatory signaling domain.
17. The method of claim 15, wherein the intracellular costimulatory signaling domain comprises a CD28 intracellular co-stimulatory signaling domain and a 41-BB intracellular co-stimulatory signaling domain.

18. The method of claim 15, wherein the intracellular costimulatory signaling domain further comprises an intracellular T-cell signaling domain.
19. The method of claim 18, wherein the intracellular T-cell signaling domain is a CD3ζ intracellular T-cell signaling domain.
20. The method of claim 1, wherein the chimeric antigen receptor (CAR) binds to a neuroendocrine cancerous cell.
21. The method of claim 1, wherein the cell is a T lymphocyte.
22. The method of claim 21, wherein the T lymphocyte is a CD4+ T lymphocyte or a CD8 + T lymphocyte.
23. The method of claim 1, wherein the cell is a natural killer cell.
24. The method of claim 23, wherein the natural killer cell is autologous to the subject.
25. The method of claim 23, wherein the natural killer cell is heterologous to the subject.
26. The method of claim 23, wherein the natural killer cell is allogeneic to the subject.
27. The method of claim 1, wherein the neuroendocrine cancer is a carcinoid tumor, an islet cell tumor, a medullary thyroid cancer, a pheochromocytoma, a neuroendocrine carcinoma of the skin, small cell lung cancer, large cell neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), or metastatic castration-resistant prostate cancer (CRPC).
28. The method of claim 1, wherein the neuroendocrine cancer is metastatic castration-resistant prostate cancer (CRPC).
29. The method of claim 28, wherein neuroendocrine cancerous cells express ROR-1.
30. The method of claim 28, wherein the subject has failed to respond to androgen deprivation therapy.
31. The method of claim 30, wherein the neuroendocrine cancer has metastasized to bone.
32. The method of claim 27, further comprising administering cirmtuzumab to the subject.
33. The method of claim 32, wherein the cirmtuzumab and the cell are administered separately.
34. The method of claim 32, wherein the cirmtuzumab and the cell are administered together.
35. The method of claim 32, wherein the method further comprises administering to the subject platinum-based chemotherapy.

36. The method of claim 35, wherein the platinum-based chemotherapy comprises carboplatin, cisplatin, etoposide, a taxane, or any combination thereof.
37. The method of claim 35, wherein the platinum-based chemotherapy comprises administering an antibody-drug conjugate.
38. A method of preventing or treating metastasis in a subject with a neuroendocrine cancer, wherein the method comprises administering to the subject an effective amount of a cell that expresses a chimeric antigen receptor (CAR) comprising a ROR-1-binding antibody region.
39. The method of claim 38, wherein the chimeric antigen receptor comprises:
    i. an antigen binding region, wherein the antigen binding region specifically binds ROR-1 and wherein the antigen binding region comprises a light chain variable domain and a heavy chain variable domain;
        (a) wherein the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:43, a CDR L2 as set forth in SEQ ID NO:44 and a CDR L3 as set forth in SEQ ID NO:45; and the heavy chain variable domain comprises a CDR H1 as set forth in SEQ ID NO:46, a CDR H2 as set forth in SEQ ID NO:47, and a CDR H3 as set forth in SEQ ID NO:48; or
        (b) wherein the light chain variable domain comprises a CDR L1 as set forth in SEQ ID NO:49, a CDR L2 as set forth in SEQ ID NO:50 and a CDR L3 as set forth in SEQ ID NO:51; and the heavy chain variable domain comprising a CDR H1 as set forth in SEQ ID NO:52, a CDR H2 as set forth in SEQ ID NO:53, and a CDR H3 as set forth in SEQ ID NO:54;
    ii. a spacer domain;
    iii. a transmembrane domain; and
    iv. an intracellular domain.
40. The method of claim 39, wherein the spacer domain is between 14 and 120 amino acids in length.
41. The method of claim 39, wherein the light chain variable domain is linked to the N-terminus or the C-terminus of the heavy chain variable domain.

42. The method of claim 39, wherein the light chain variable domain is covalently linked to the heavy chain variable domain through a polypeptide linker.
43. The method of claim 42, wherein the polypeptide linker comprises an amino acid sequence of SEQ ID NO: 24.
44. The method of claim 39, wherein the spacer domain comprises an antibody domain.
45. The method of claim 39, wherein the antibody domain comprises an immunoglobulin hinge domain, an immunoglobulin constant heavy chain 3 (CH3) domain, an immunoglobulin constant heavy chain 2 (CH2) domain, or a combination thereof.
46. The method of claim 45, wherein the spacer domain comprises an amino acid sequence of SEQ ID NO: 29, SEQ ID NO: 41 or SEQ ID NO: 42.
47. The method of claim 39, wherein the light chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 21.
48. The method of claim 39, wherein the heavy chain variable domain comprises an amino acid sequence at least about 90%, 95%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 27.
49. The method of claim 39, wherein the transmembrane domain comprises a CD8α transmembrane domain, a CD28 transmembrane domain, a CD4 transmembrane domain, a CD3ζ transmembrane domain, or any combination thereof.
50. The method of claim 49, wherein the transmembrane domain is a CD28 transmembrane domain.
51. The method of claim 39, wherein the intracellular domain comprises an intracellular co-stimulatory signaling domain, an intracellular T-cell signaling domain, or a combination thereof.
52. The method of claim 51, wherein the intracellular co-stimulatory signaling domain is a 41-BB intracellular co-stimulatory signaling domain, a CD28 intracellular co-stimulatory signaling domain, a ICOS intracellular co-stimulatory signaling domain, an OX-40 intracellular co-stimulatory signaling domain, or any combination thereof.
53. The method of claim 52, wherein the intracellular costimulatory signaling domain comprises a 41-BB intracellular co-stimulatory signaling domain.

54. The method of claim 52, wherein the intracellular costimulatory signaling domain comprises a CD28 intracellular co-stimulatory signaling domain and a 4-1BB intracellular co-stimulatory signaling domain.
55. The method of claim 52, wherein the intracellular costimulatory signaling domain further comprises an intracellular T-cell signaling domain.The method of claim 54, wherein the intracellular T-cell signaling domain is a CD3ζ intracellular T-cell signaling domain.
56. The method of claim 38, wherein the chimeric antigen receptor (CAR) binds to an endocrine cancerous cell.
57. The method of claim 38, wherein the cell is a T lymphocyte.
58. The method of claim 57, wherein the T lymphocyte is a CD4+ T lymphocyte or a CD8 + T lymphocyte.
59. The method of claim 38, wherein the cell is a natural killer cell.
60. The method of claim 59, wherein the natural killer cell is autologous to the subject.
61. The method of claim 59, wherein the natural killer cell is heterologous to the subject.
62. The method of claim 59, wherein the natural killer cell is allogeneic to the subject.
63. The method of claim 38, wherein the neuroendocrine cancer is a carcinoid tumor, an islet cell tumor, a medullary thyroid cancer, a pheochromocytoma, a neuroendocrine carcinoma of the skin, small cell lung cancer, large cell neuroendocrine carcinoma, neuroendocrine prostate cancer (NEPC), or metastatic castration-resistant prostate cancer (CRPC).
64. The method of claim 38, wherein the neuroendocrine cancer is metastatic castration-resistant prostate cancer (CRPC).
65. The method of claim 64, wherein neuroendocrine cancerous cells express ROR-1.
66. The method of claim 65, wherein the subject has failed to respond to androgen deprivation therapy.
67. The method of claim 66, wherein the neuroendocrine cancer has metastasized to bone.
68. The method of claim 65, further comprising administering cirmtuzumab to the subject.
69. The method of claim 68, wherein the cirmtuzumab and the cell are administered separately.
70. The method of claim 68, wherein the the cirmtuzumab and the cell are administered together.

71. The method of claim 68, wherein the method further comprises administering to the subject platinum-based chemotherapy.
72. The method of claim 71, wherein the platinum-based chemotherapy comprises carboplatin, cisplatin, etoposide, a taxane, or any combination thereof.
73. The method of claim 71, wherein the platinum-based chemotherapy comprises administering an antibody-drug conjugate.

FIGURE 1

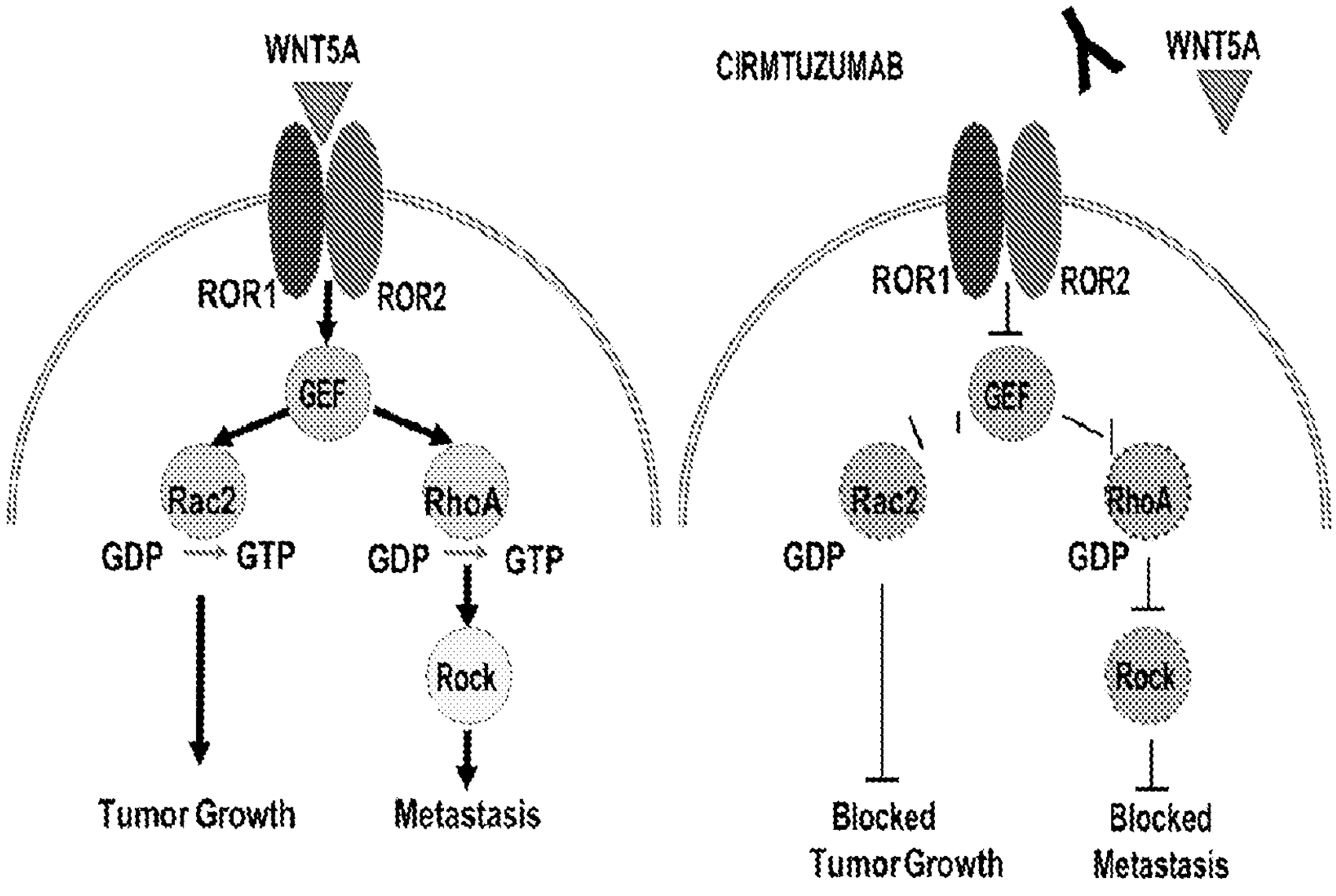

WNT5A
ROR1
ROR2
GEF
Rac2
RhoA
GDP
GTP
GDP
GTP
Rock
Tumor Growth
Metastasis
CIRMTUZUMAB
WNT5A
ROR1
ROR2
GEF
Rac2
RhoA
GDP
GDP
Rock
Blocked
Tumor Growth
Blocked
Metastasis

FIGURE 2

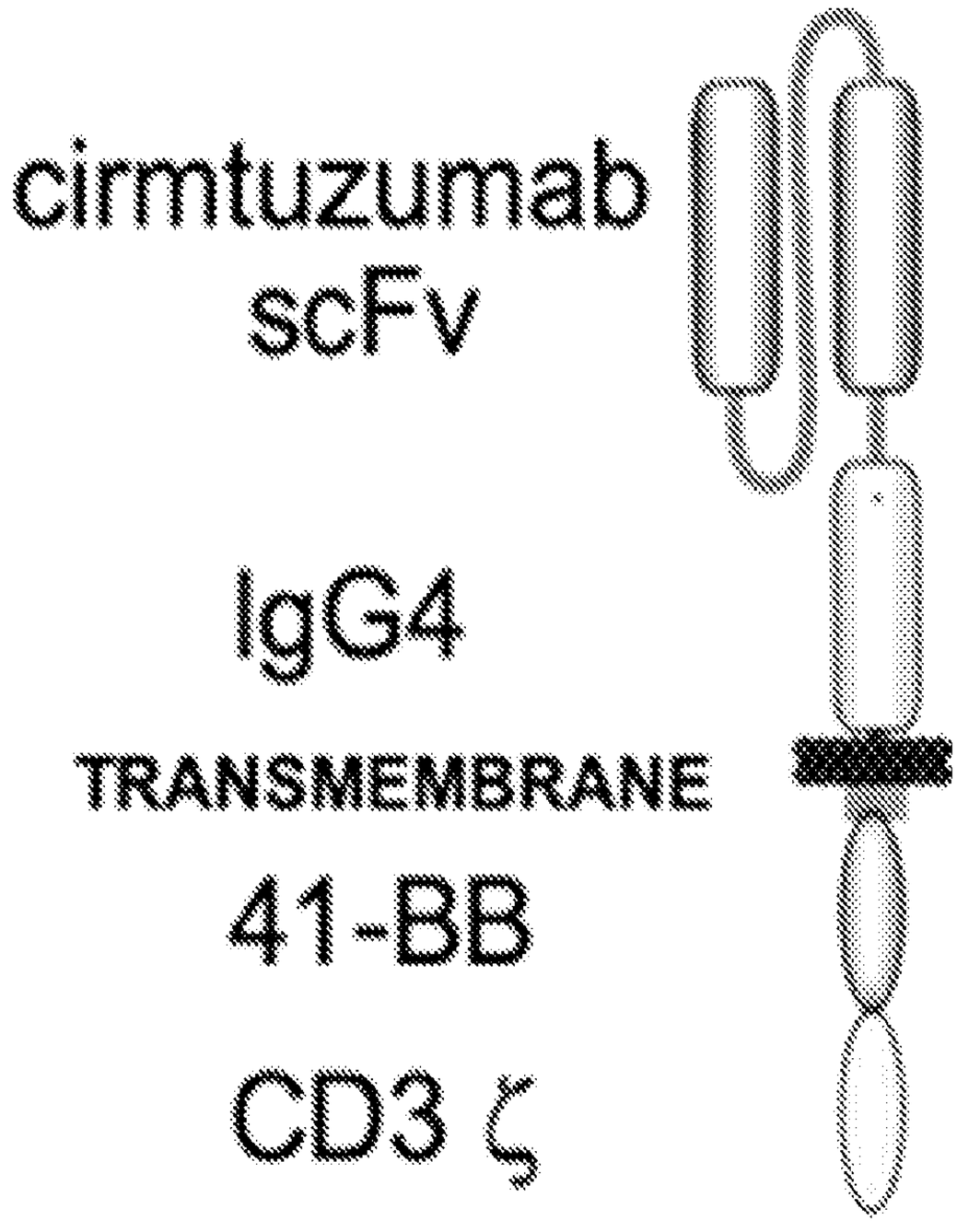


FIGURE 3

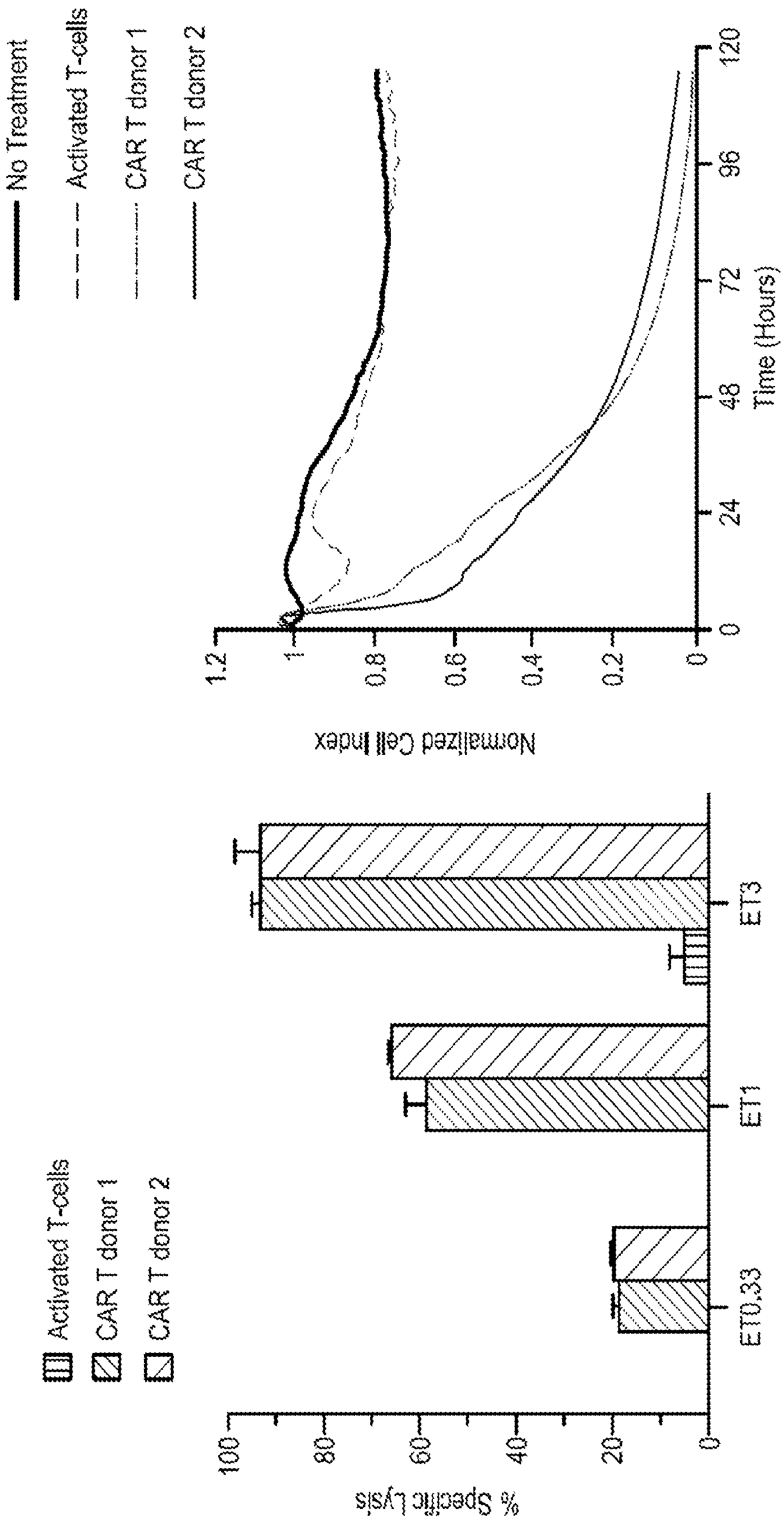

No Treatment
Activated T-cells
CAR T donor 1
CAR T donor 2
Normalized Cell Index
Time (Hours)
0
24
48
72
96
120
0.2
0.4
0.6
0.8
1
1.2
E:T 3
E:T 1
E:T 0.33
% Specific Lysis
0
20
40
60
80
100

FIGURE 4

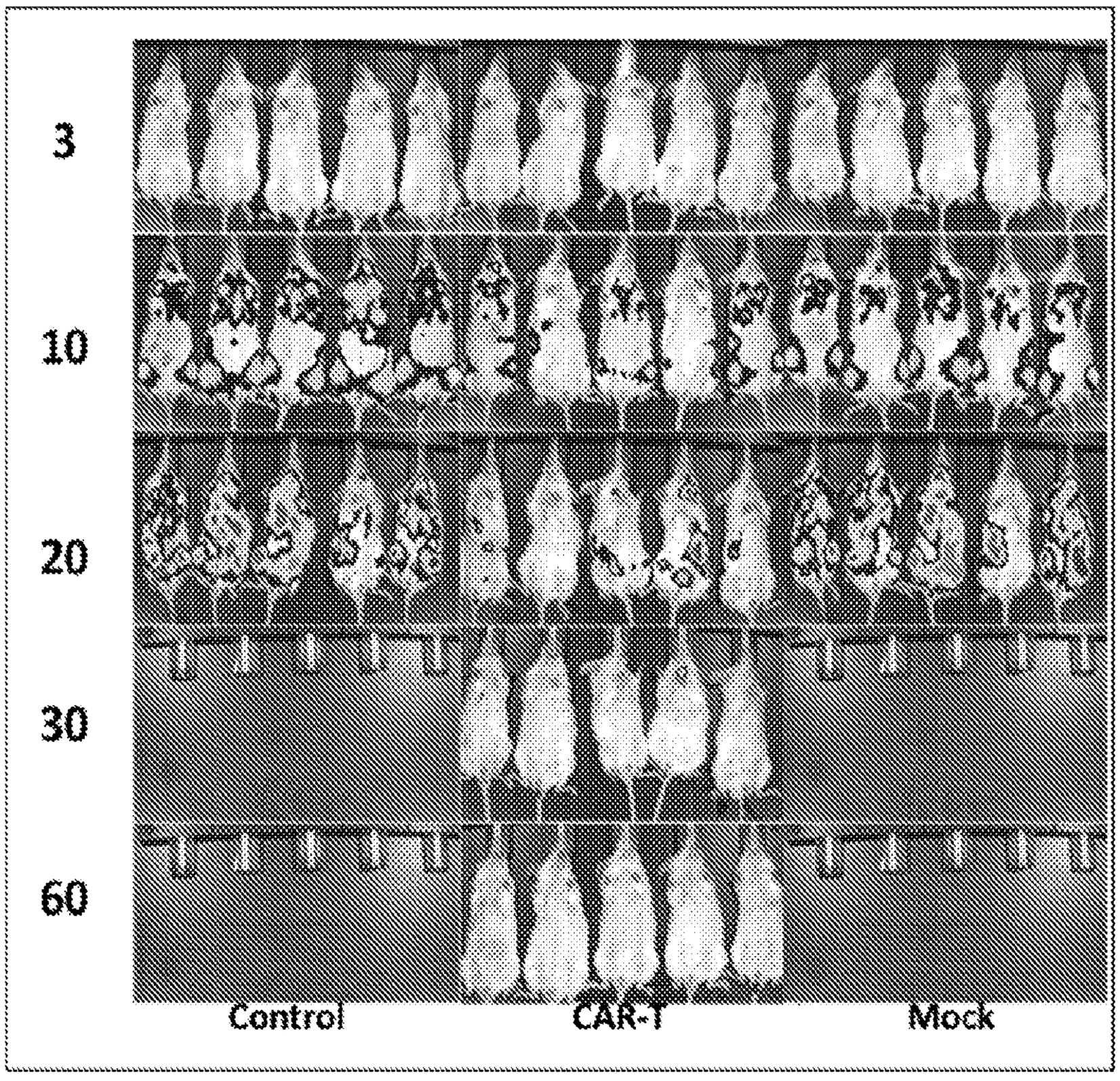
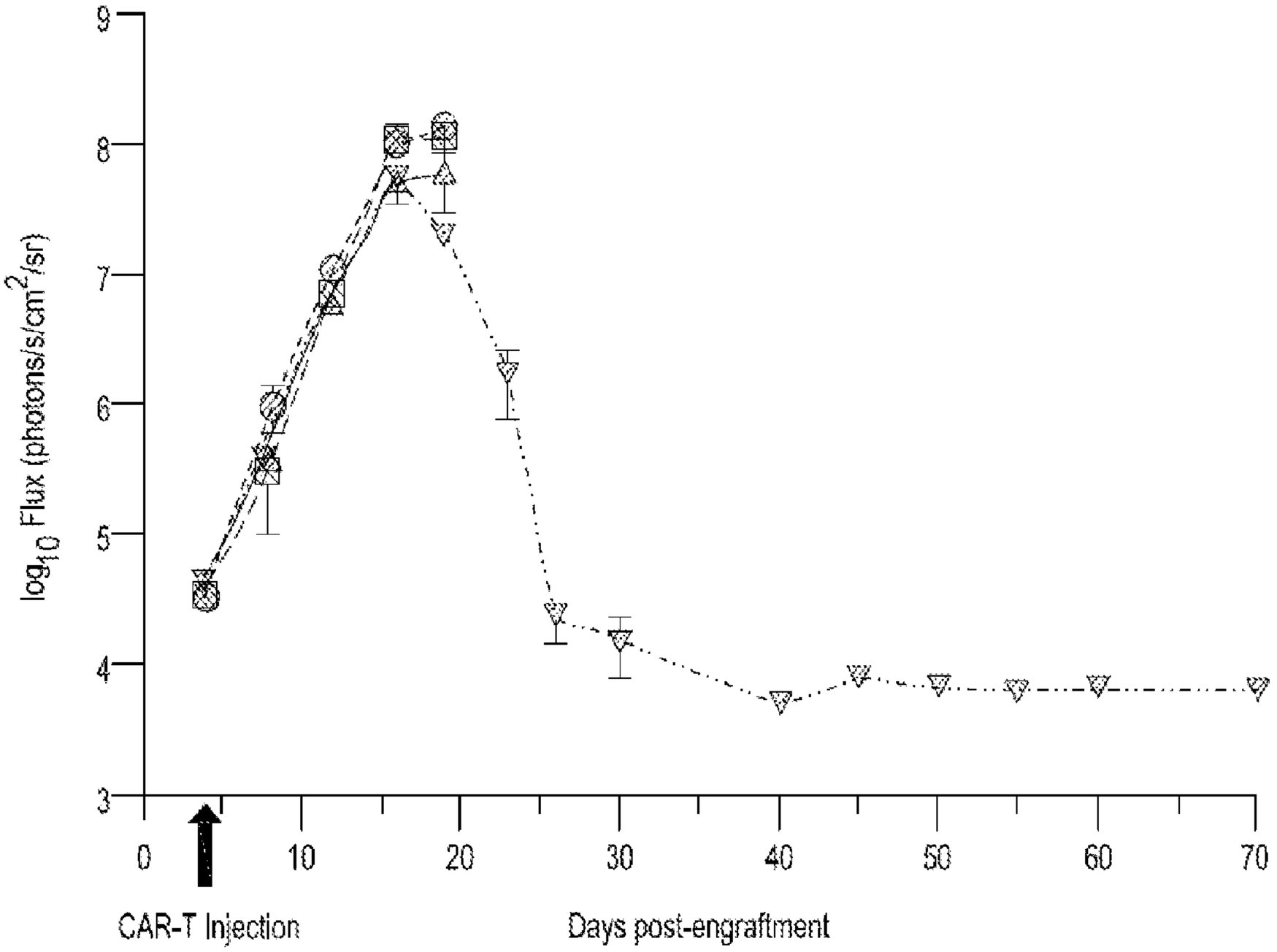


FIGURE 4 (continued)



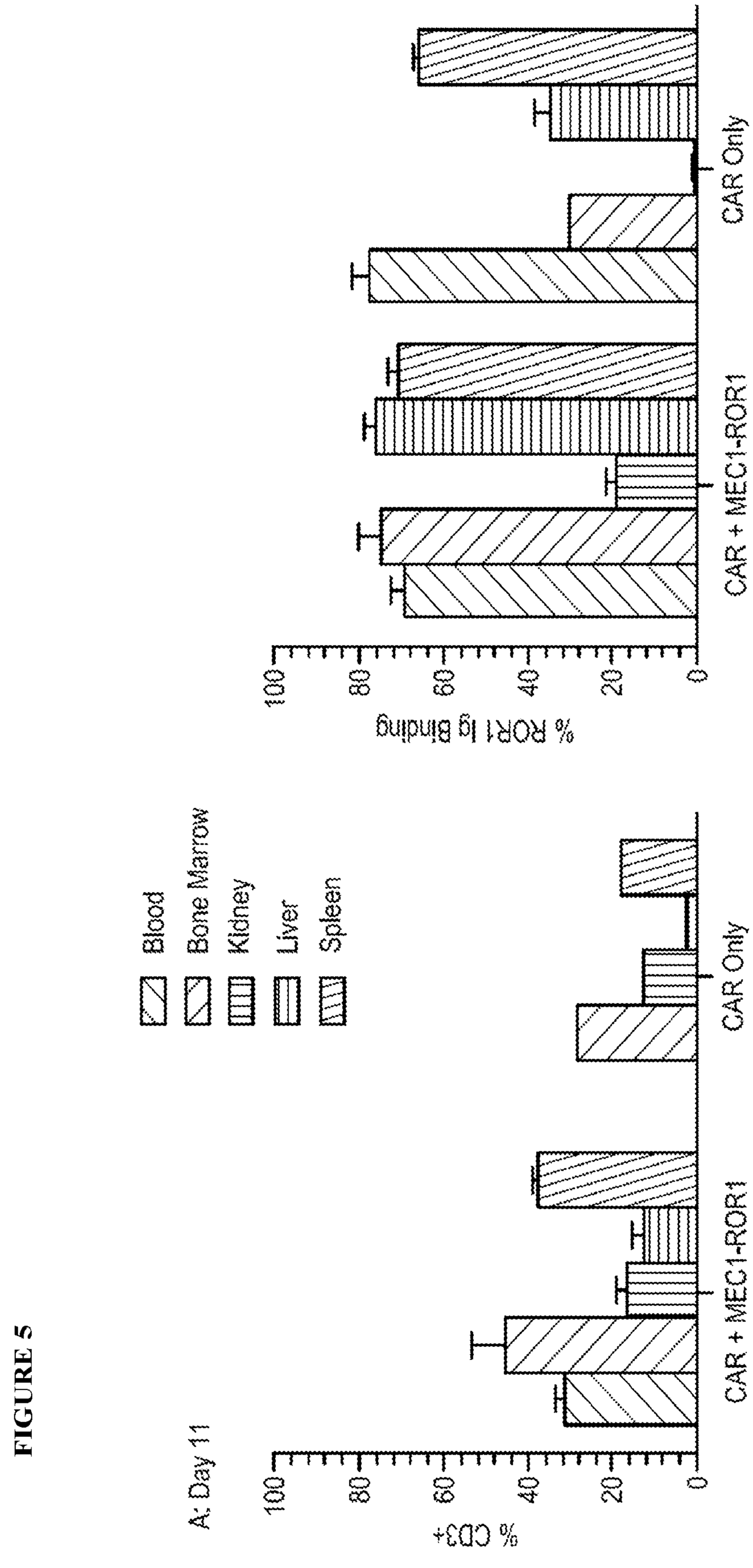

Blood
Bone Marrow
Kidney
Liver
Spleen
% ROR1 Ig Binding
100
80
60
40
20
0
CAR Only
CAR + MEC1-ROR1
A: Day 11
% CD3+
100
80
60
40
20
0
CAR Only
CAR + MEC1-ROR1

FIGURE 5

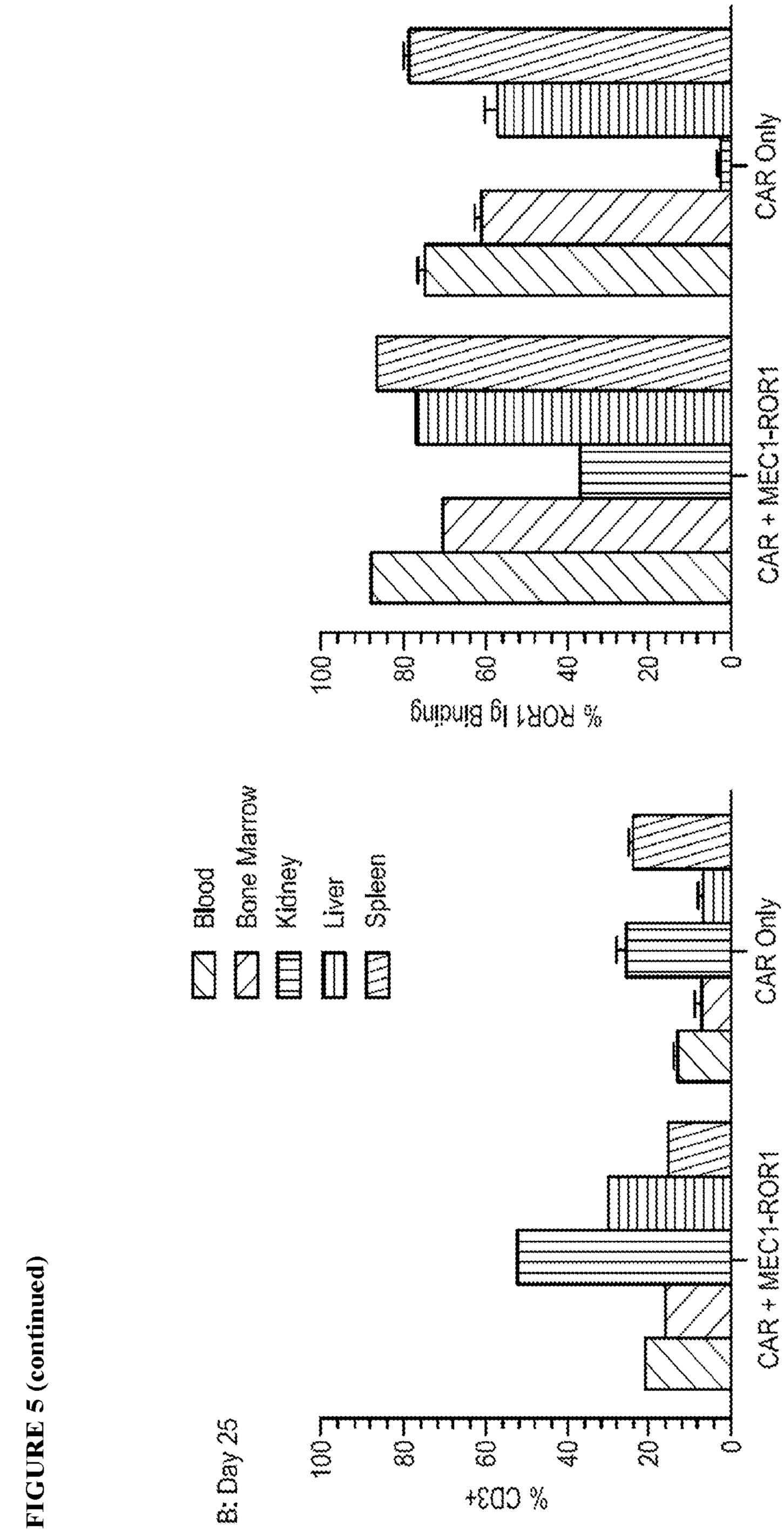


FIGURE 5 (continued)

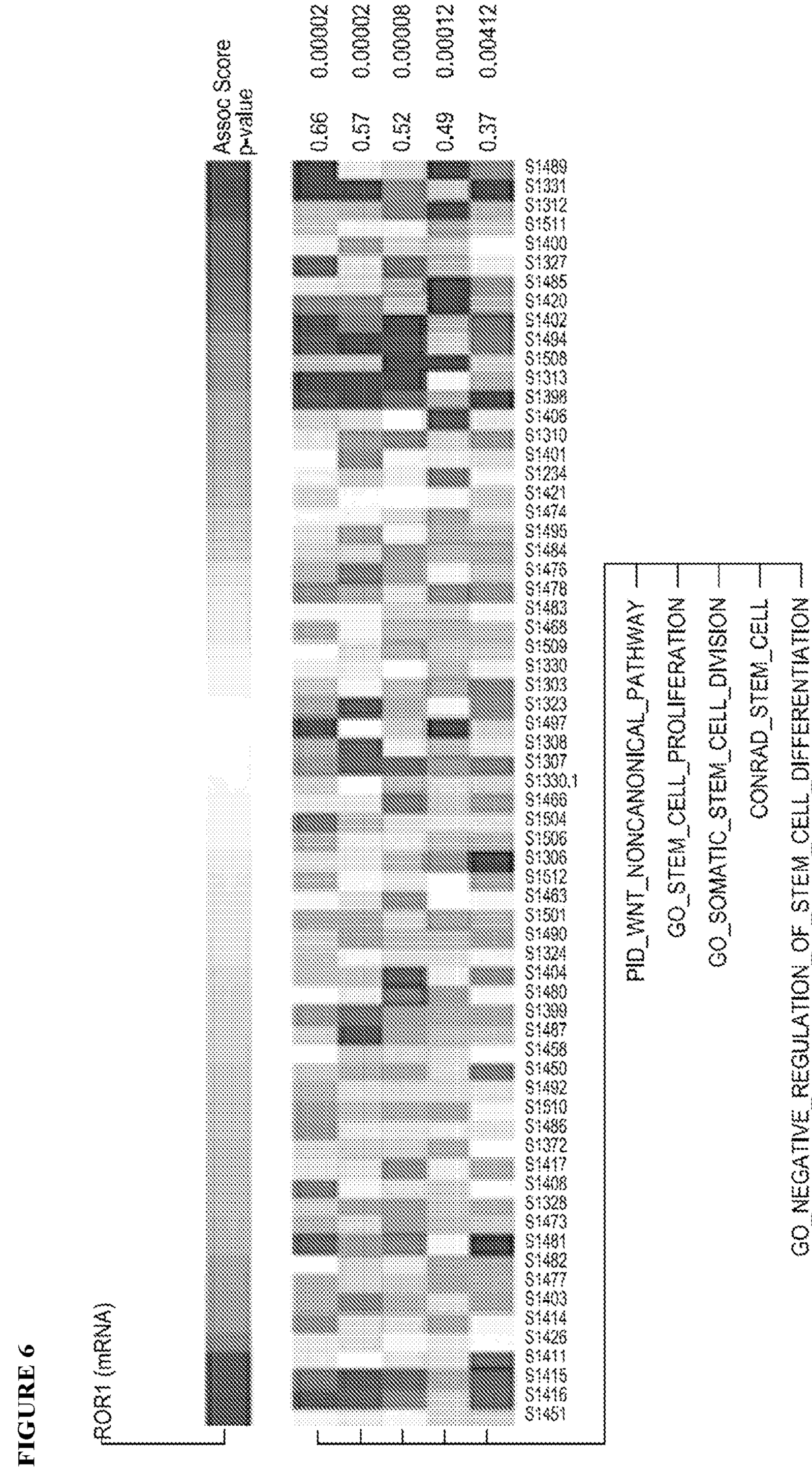
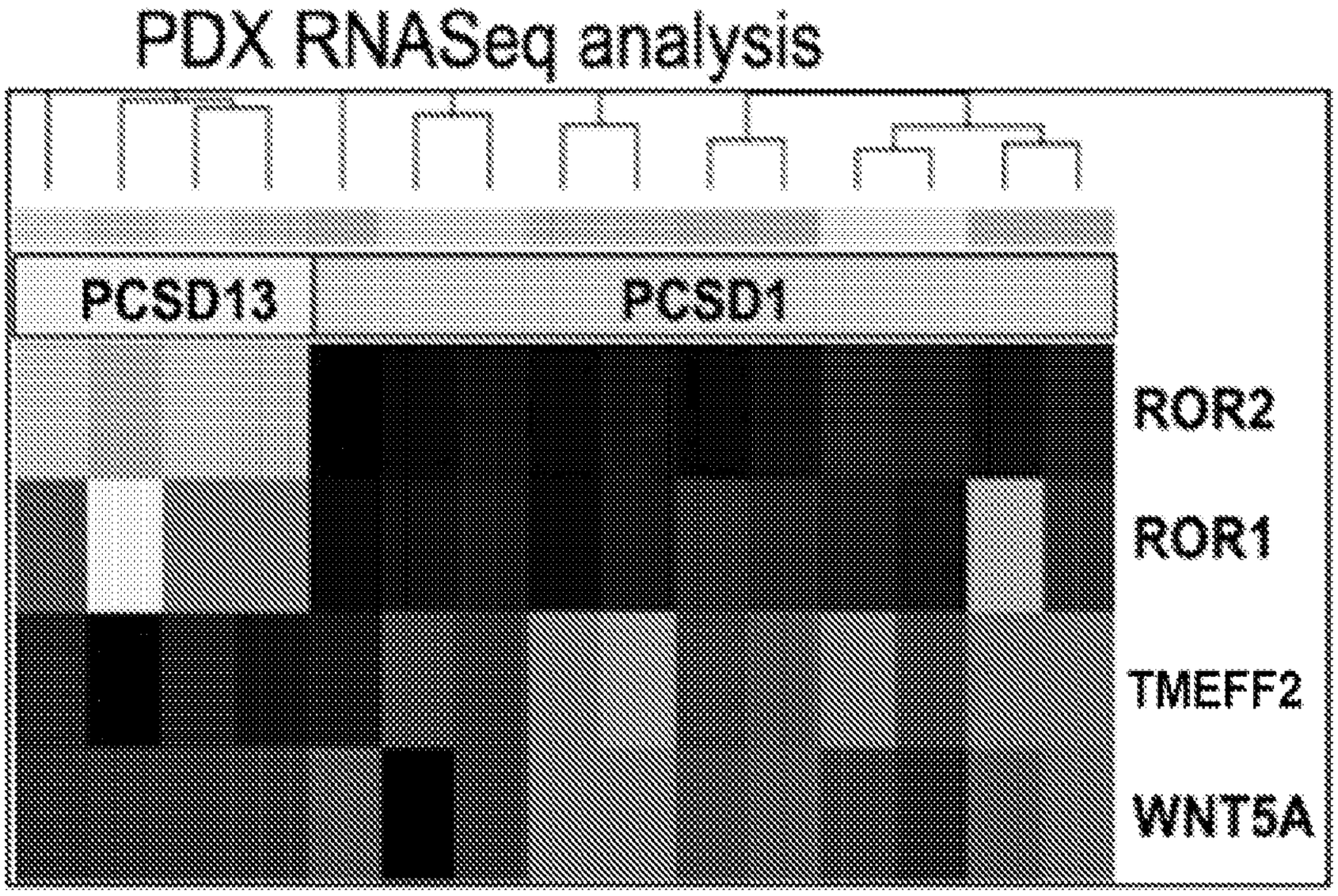

Assoc Score
p-value
0.66
0.57
0.52
0.49
0.37
0.00002
0.00002
0.00008
0.00012
0.00412
ROR1 (mRNA)
PID_WNT_NONCANONICAL_PATHWAY
GO_STEM_CELL_PROLIFERATION
GO_SOMATIC_STEM_CELL_DIVISION
CONRAD_STEM_CELL
GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION

FIGURE 6

FIGURE 7A



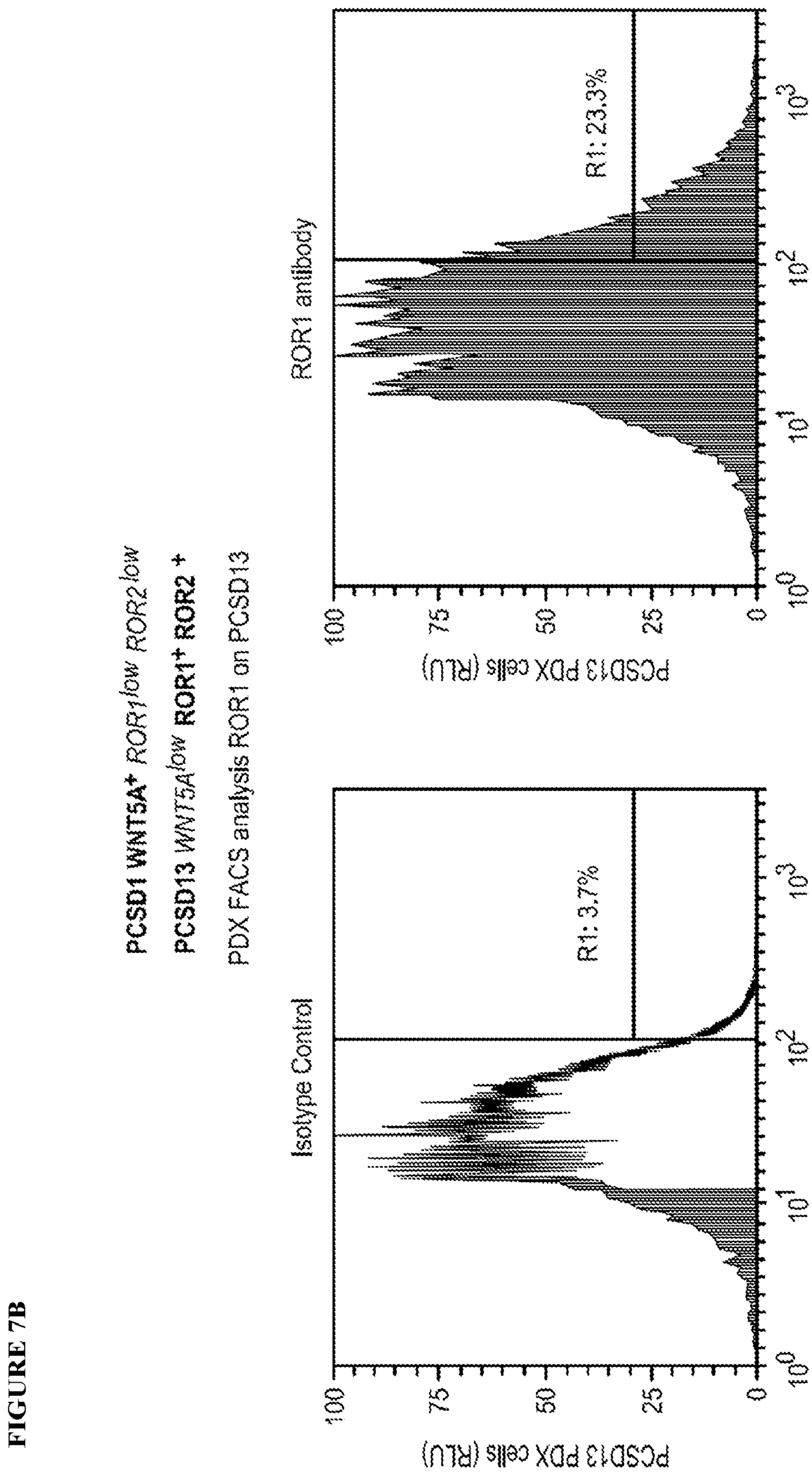

PCSD1 WNT5A+ ROR1low ROR2low
PCSD13 WNT5A+ ROR1low ROR2low ROR1+ ROR2+
PDX FACS analysis ROR1 on PCSD13
ROR1 antibody
R1: 23.3%
PCSD13 PDX cells (RLU)
100
75
50
25
0
10^0
10^1
10^2
10^3
Isotype Control
R1: 3.7%
PCSD13 PDX cells (RLU)

FIGURE 7B

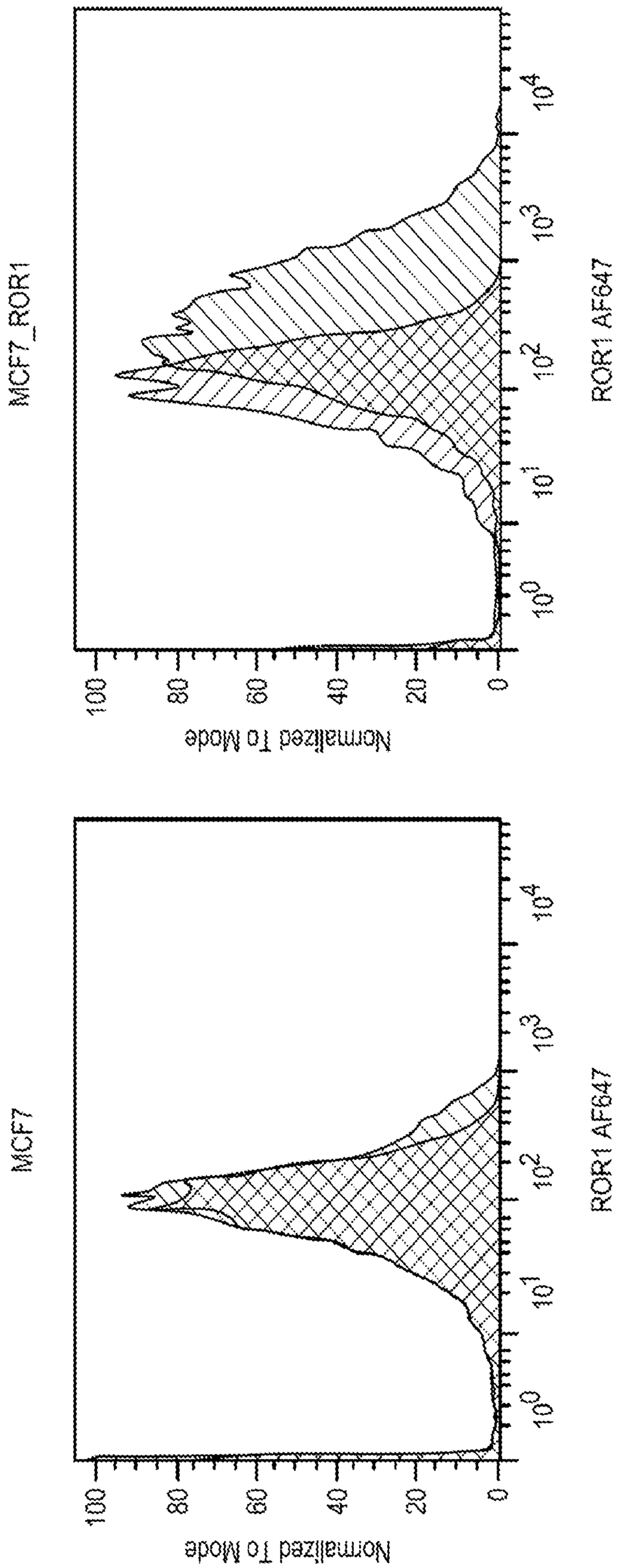

MCF7_ROR1
ROR1 AF647
Normalized To Mode
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
MCF7
ROR1 AF647
Normalized To Mode
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4

FIGURE 7C

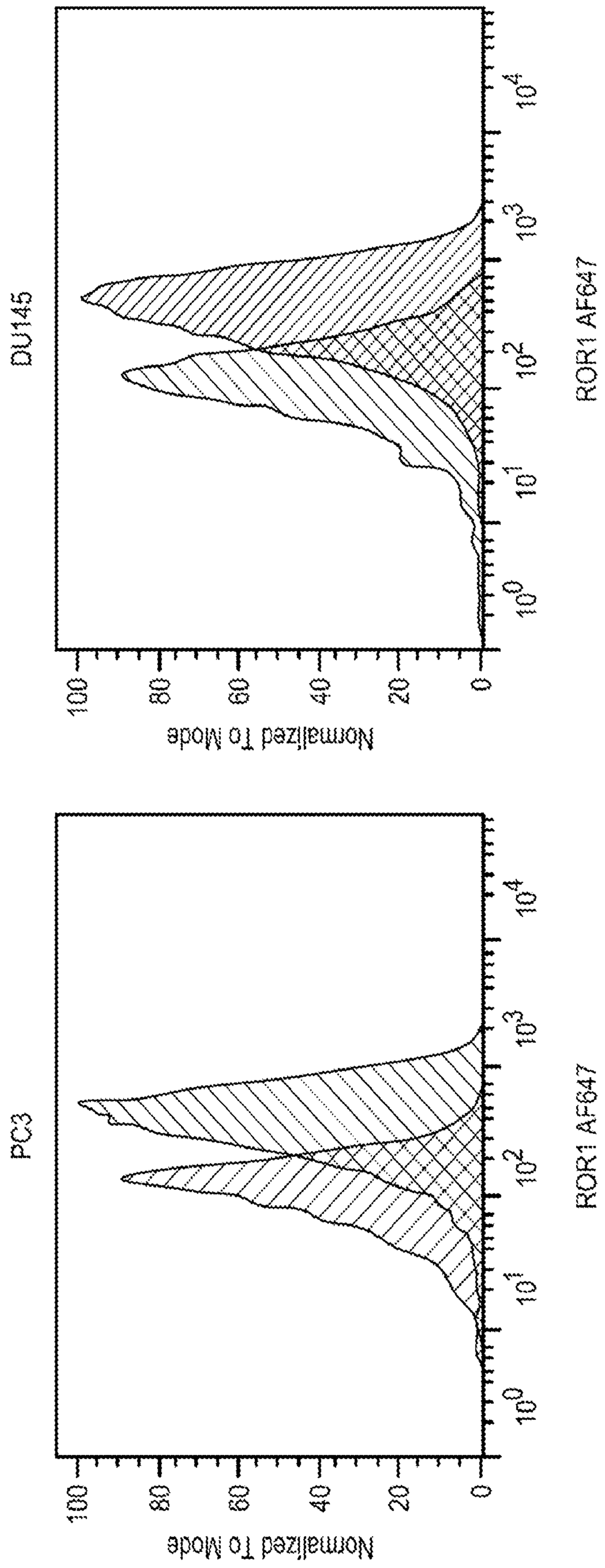


FIGURE 7C (continued)

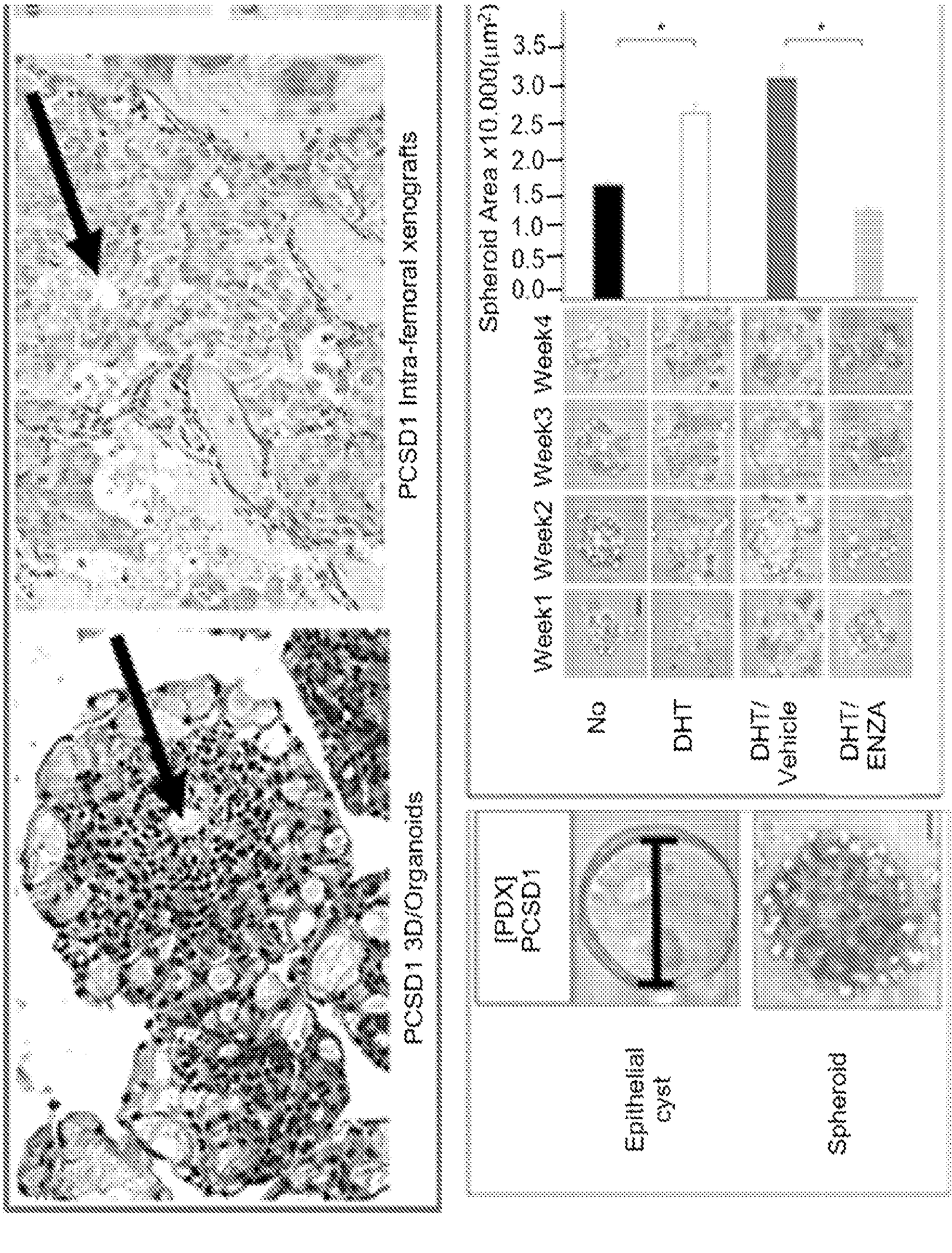

PCSD1 Intra-femoral xenografts
PCSD1 3D/Organoids
[PDX]
PCSD1
Epithelial cyst
Spheroid
Spheroid Area x10,000(μm²)
0.0 0.5 1.0 1.5 2.0 2.5 3.0 3.5
Week1 Week2 Week3 Week4
No
DHT
DHT/ Vehicle
DHT/ ENZA

FIGURE 8

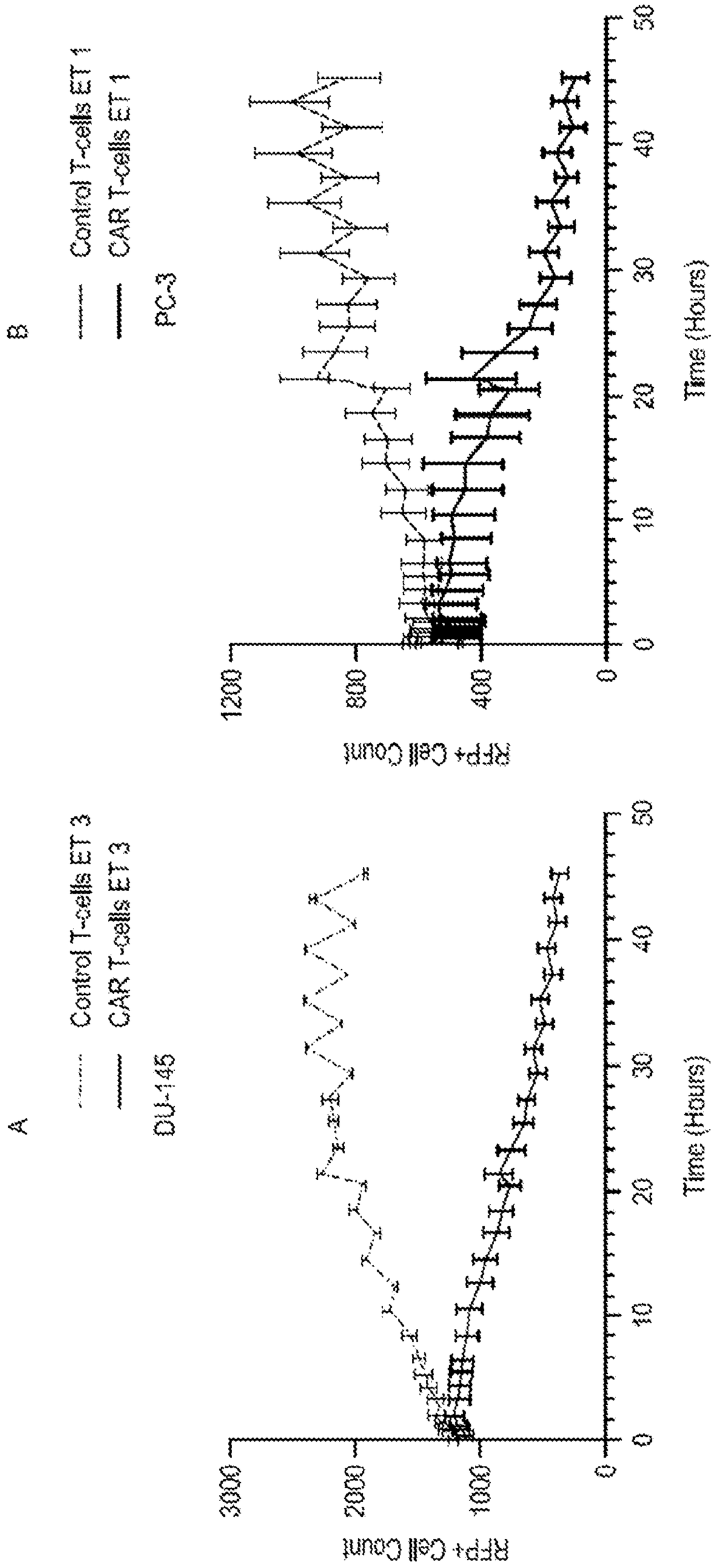

A
Control T-cells ET 3
CAR T-cells ET 3
DU-145
RFP+ Cell Count
3000
2000
1000
0
0
10
20
30
40
50
Time (Hours)
B
Control T-cells ET 1
CAR T-cells ET 1
PC-3
RFP+ Cell Count
1200
800
400
0
0
10
20
30
40
50
Time (Hours)

FIGURE 9

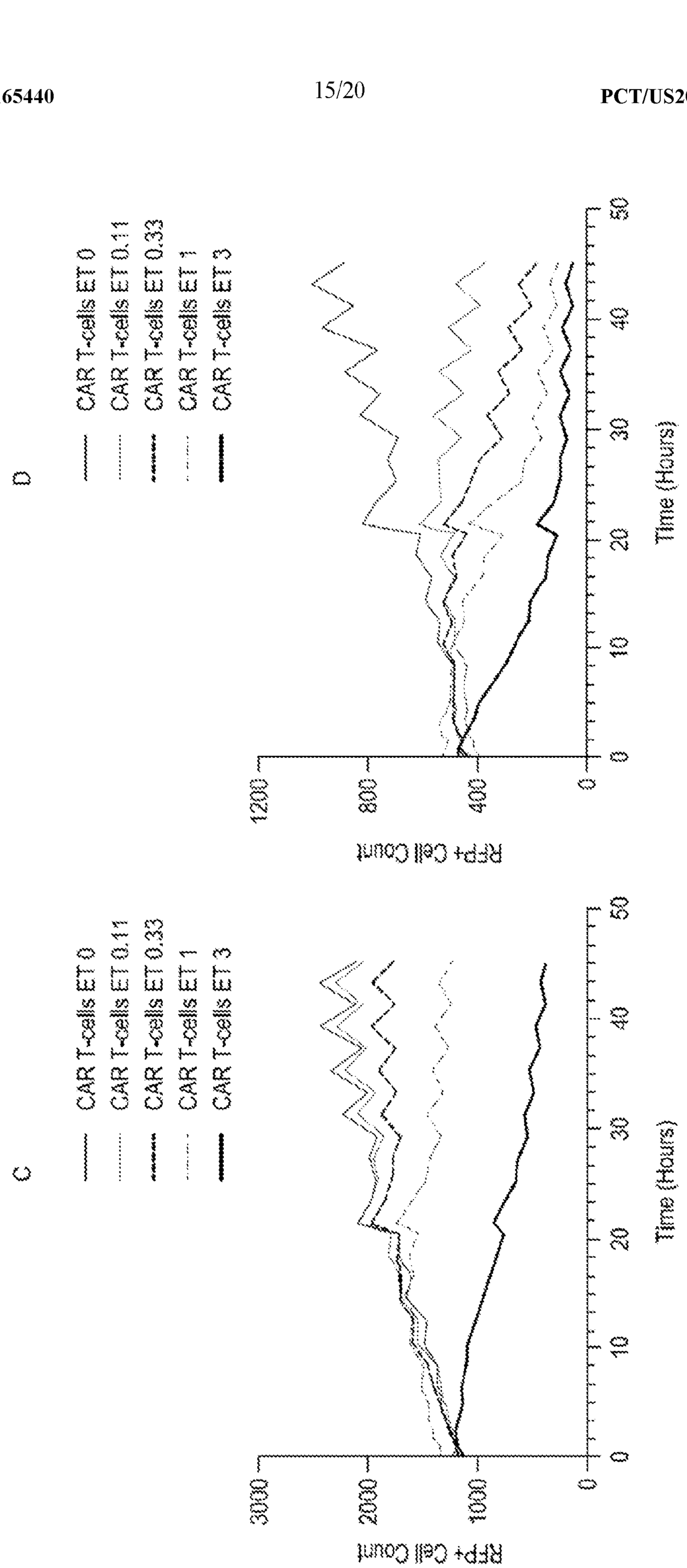


FIGURE 9 (continued)

FIGURE 10

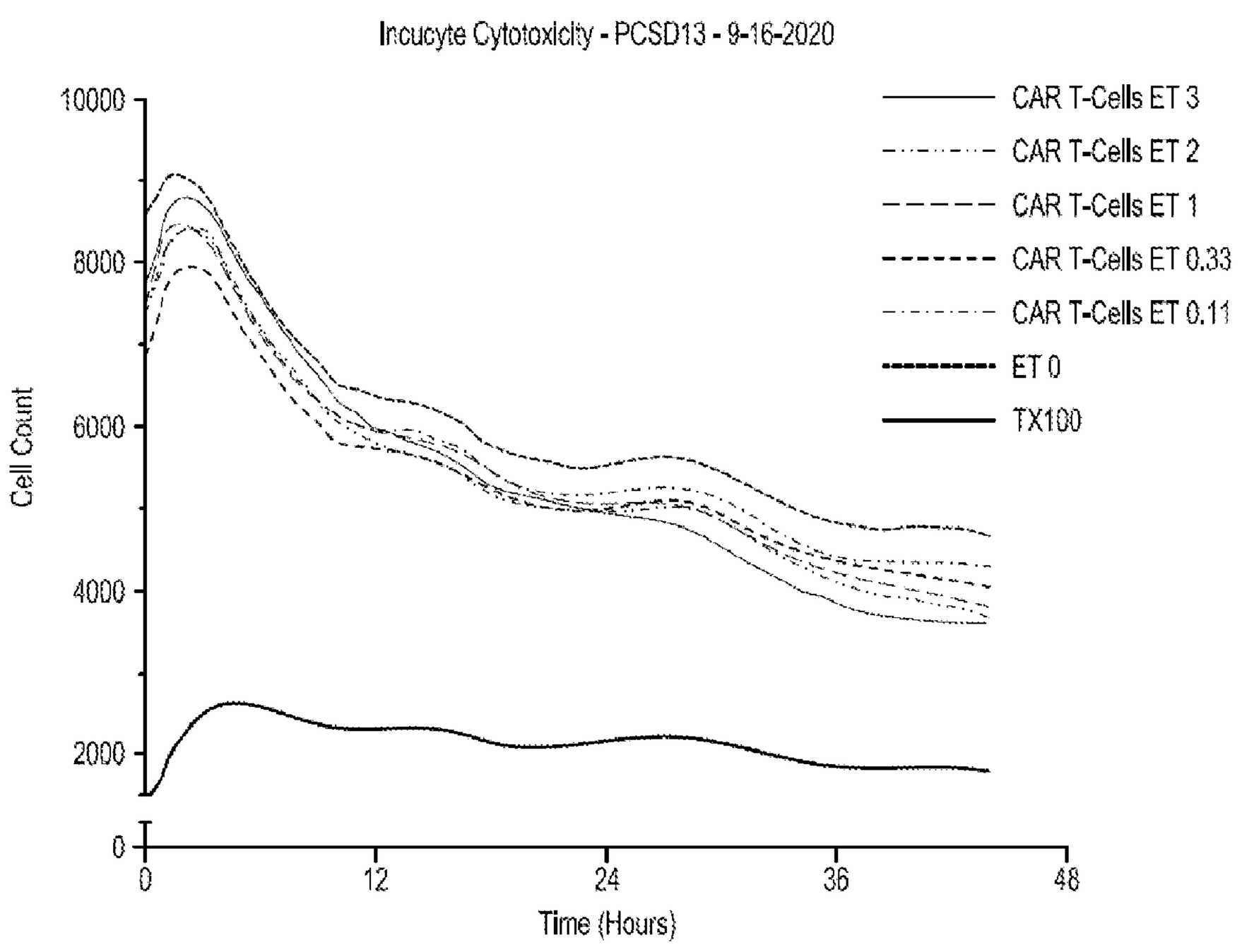

A
Incucyte Cytotoxicity - PCSD13 - 9-16-2020
Cell Count
10000
8000
6000
4000
2000
0
0
12
24
36
48
Time (Hours)
CAR T-Cells ET 3
CAR T-Cells ET 2
CAR T-Cells ET 1
CAR T-Cells ET 0.33
CAR T-Cells ET 0.11
ET 0
TX100

FIGURE 10 (continued)

B

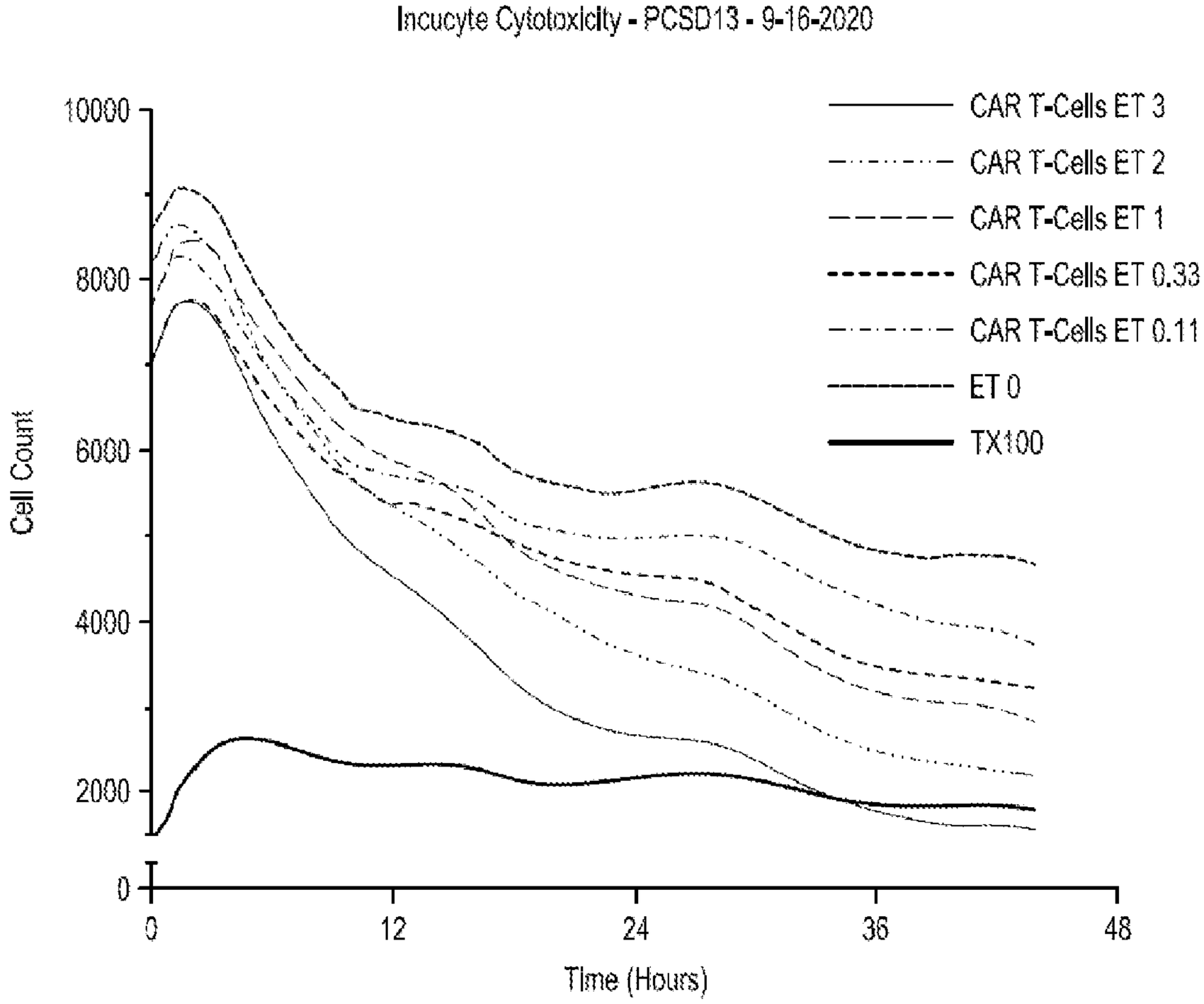


FIGURE 11

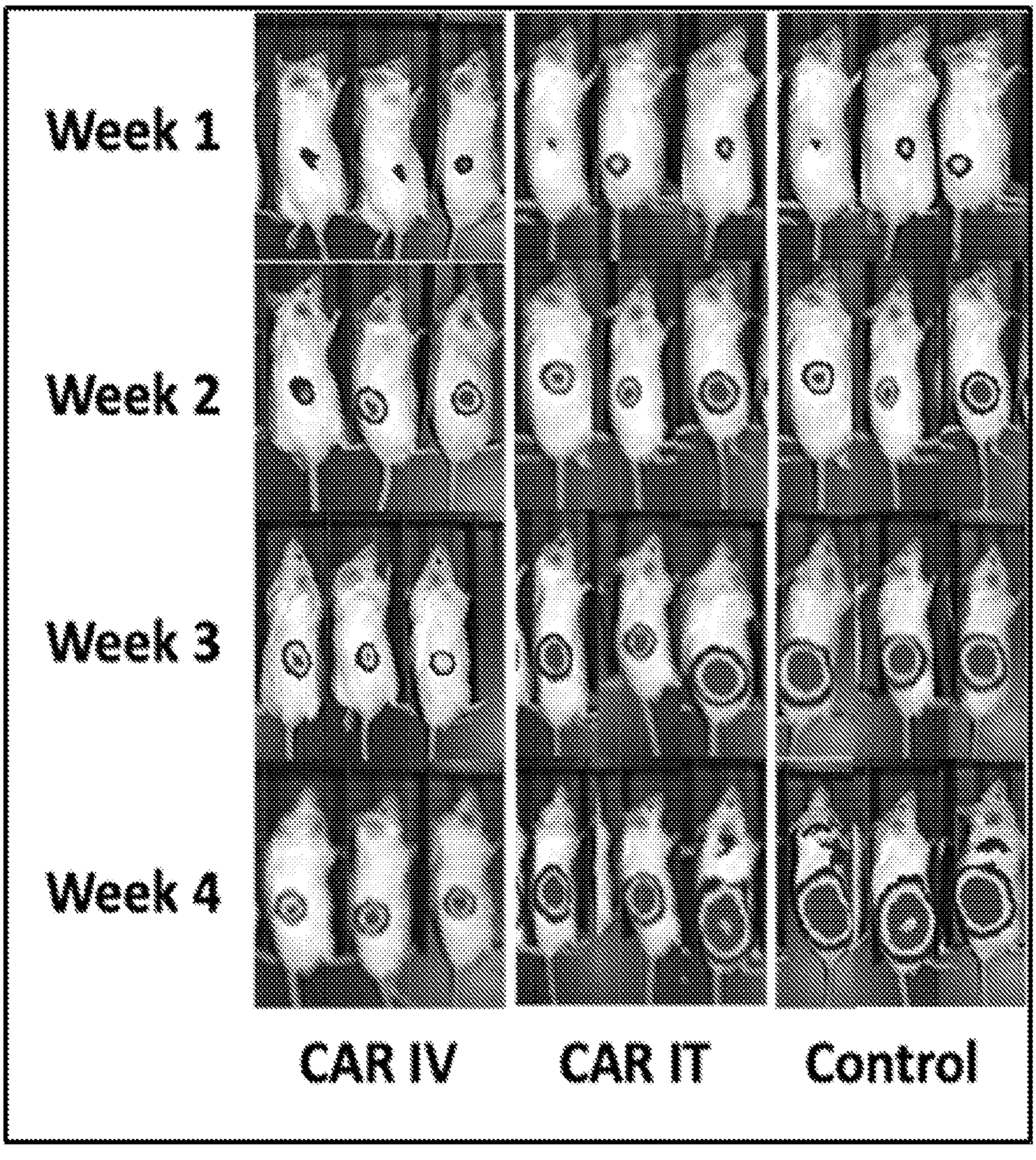


FIGURE 12

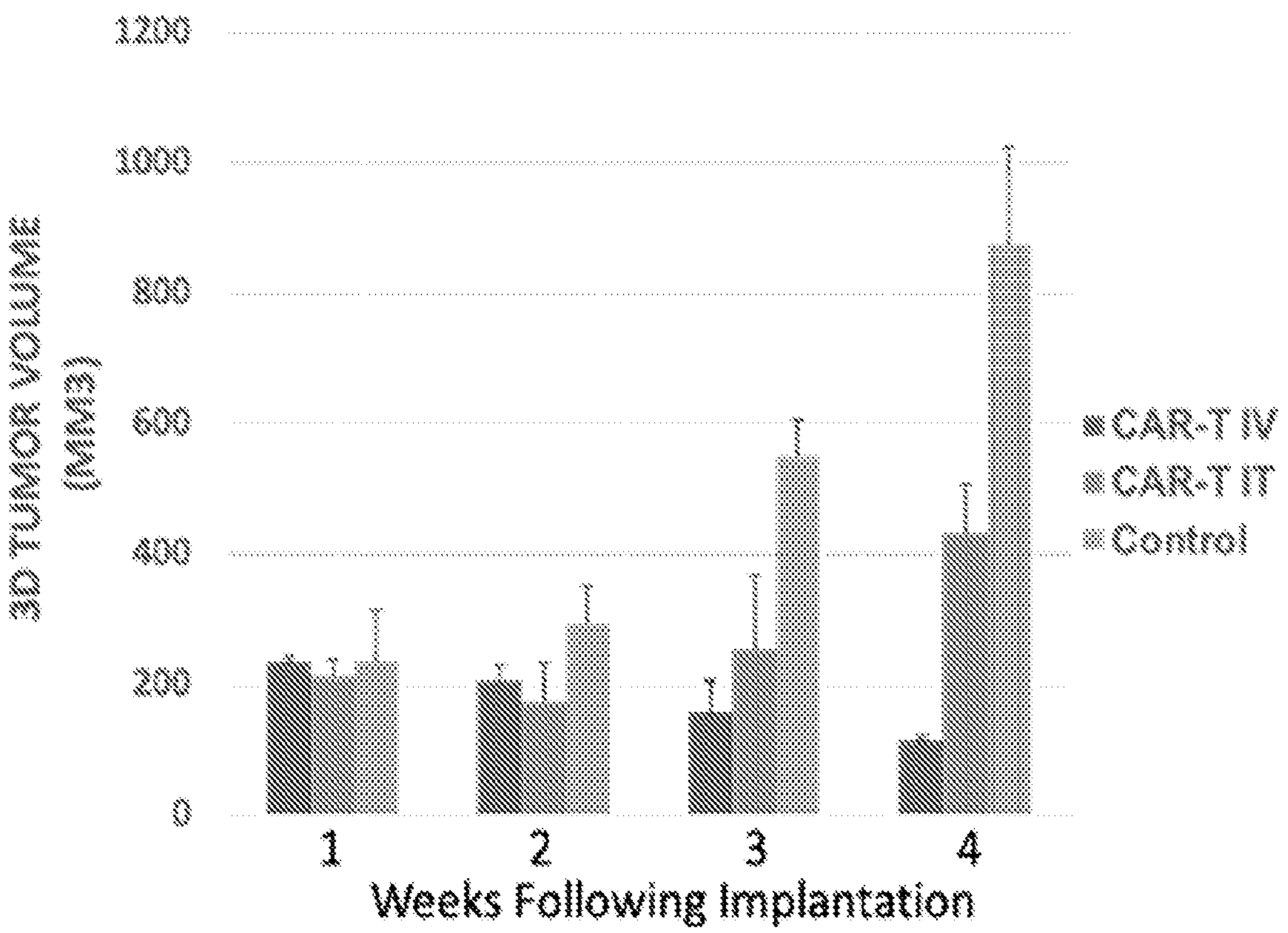
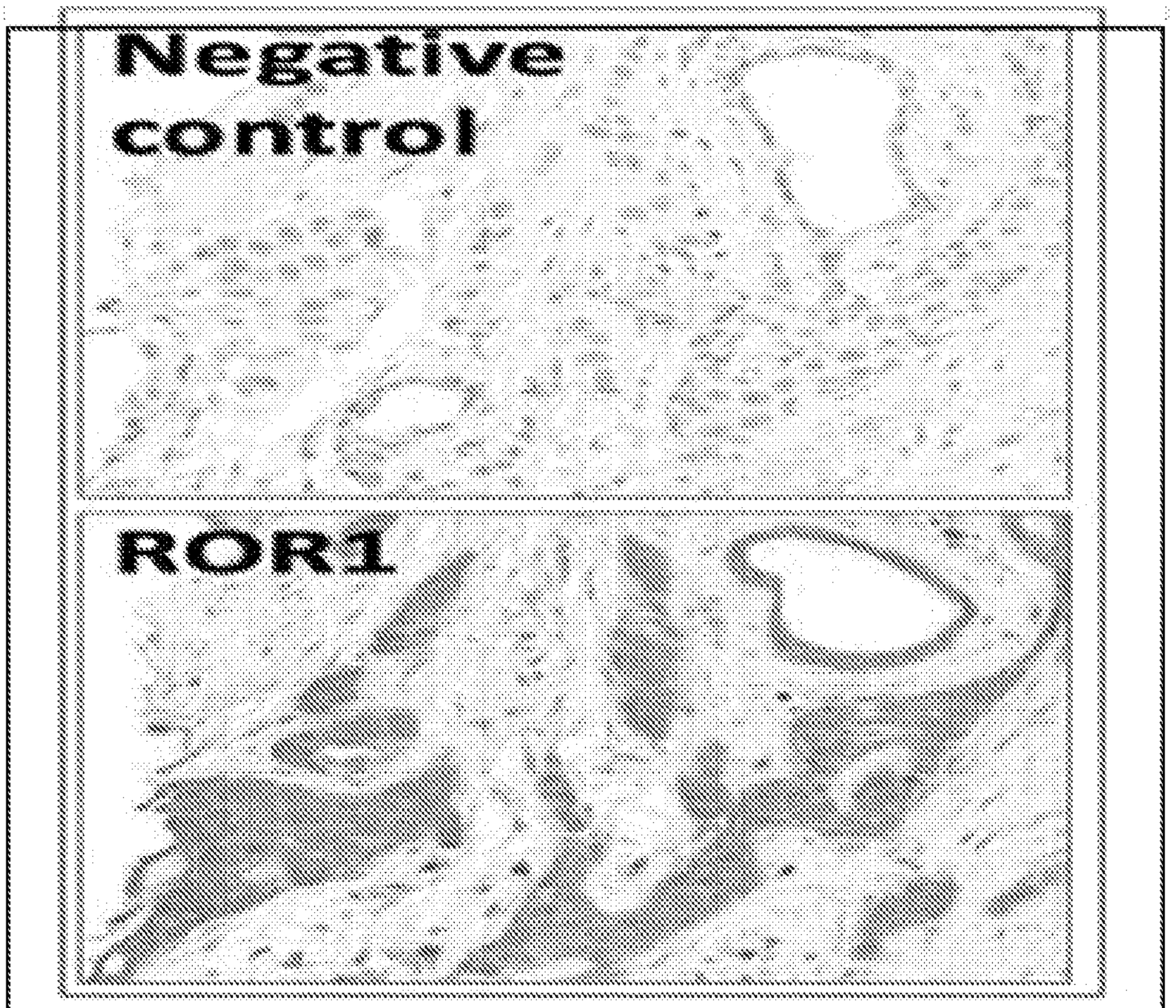

1200
1000
800
600
400
200
0
3D TUMOR VOLUME (mm3)
1
2
3
4
Weeks Following Implantation
CAR-T IV
CAR-T IT
Control

FIGURE 13



Optimized ROR1 protein IHC analysis.
Right Panels: ROR1 IHC breast adenocarcinoma formalin-fixed paraffin

SEQUENCE LISTING

<110> The Regents of the University of California

<120> Treatment of Neuroendocrine Cancers

<130> 048537-640001WO

<150> US 63/144,337
<151> 2021-02-01

<160> 57

<170> PatentIn version 3.5

<210> 1
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 1
atgggatggt catgtatcat ccttttttcta gtagcaactg caaccggtgt acattcc 57

<210> 2
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 2
gacatcaaga tgacccagtc tccatcttcc atgtatgcat ctctaggaga gagagtcact 60

atcacttgca aggcgagtcc ggacattaat agctatttaa gctggttcca gcagaaacca 120

gggaaatctc ctaagaccct gatctatcgt gcaaacagat tggttgatgg ggtcccatca 180

aggttcagtg gcggtggatc tgggcaagat tattctctca ccatcaacag cctggagtat 240

gaagatatgg gaatttatta ttgtctacag tatgatgaat ttccgtacac gttcggaggg 300

gggaccaagc tggaaatgaa a 321

<210> 3

<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 3
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca aggcgagtcc ggacattaat agctatttaa gctggtttca gcagaggcca 120

ggccaatctc caaggcgcct aatttatcgt gcaaacagat tggttgatgg ggtcccagac 180

aggttcagtg gcagtgggtc aggcactgat ttcacactga aaatcagcag ggtggaggct 240

gaggatgttg gagtttatta ctgtctacag tatgatgaat ttccgtacac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 4
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 4
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca gggcaagtaa gagcattagc aaatatttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctattct ggatccactt tgcaatctgg gatcccacct 180

cgattcagtg gcagcgggta tggaacagat tttaccctca caattaataa catagaatct 240

gaggatgctg catattactt ctgtcaacag catgatgaat ccccgtacac gttcggcgag 300

gggaccaagg tggaaatcaa a 321

<210> 5
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 5
ggctccacct ctggatccgg caagcccgga tctggcgagg gatccaccaa gggc 54

<210> 6
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 6
ggctccacct ctggatccgg caagcccgga tctggcgagg gatccaccaa gggc 54

<210> 7
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 7
ggtggtggtg gtagcggctc cacctctgga tccggcaagc ccggatctgg cgagggatcc 60

accaagggcg gaggaggagg aagt 84

<210> 8
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 8
gaagtgaaac tagtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt agctatgcca tgtcttgggt tcgccagatt 120

ccagagaaga ggctggagtg ggtcgcatcc attagtcgtg gtggtaccac ctactatcca 180

gacagtgtga agggccgatt caccatctcc agagataatg tcaggaacat cctgtacctg 240

caaatgagca gtctgaggtc tgaggacacg gccatgtatt actgtggaag atatgattac 300

gacgggtact atgcaatgga ctactggggt caaggaacct cagtcaccgt ctcctca 357

<210> 9
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 9
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggatt cactttcagt agctatgcca tgtcttggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggttcc attagtcgtg gtggtaccac ctactatcca 180

gacagtgtga agggcagatt caccatctcc agagacaacg ccaagaactc actgtatctg 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtggaag atatgattac 300

gacgggtact atgcaatgga ctactggggc cagggaacgc tggtcaccgt cagctca 357

<210> 10
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 10
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggtta tgcattcact gcctacaaca tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggttct tttgatcctt acgatggtgg tagtagttac 180

aaccagaagt tcaaggacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagagggtgg 300

tactactttg actactgggg ccacggaacc ctggtcaccg tctcctca 348

<210> 11
<211> 42
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 11
gtcgacgagt ccaaatatgg tcccccatgc ccaccatgcc ca 42

<210> 12
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 12
ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cgtcctccat cgagaaaacc 60

atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccag 120

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 180

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 240

cccgtgctgg actccgacgg ctccttcttc ctctacagca ggctaaccgt ggacaagagc 300

aggtggcagg aggggaatgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 360

tacacacaga agagcctctc cctgtcccta ggtaaaatg 399

<210> 13
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 13
gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 60

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 120

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 180

ccgcgggagg agcagttcaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 240

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 300

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 360

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 420

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 480

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 540

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 600

gctctgcaca accactacac acagaagagc ctctccctgt ccctaggtaa aatg 654

<210> 14
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 14
ttttgggtgc tggtggtggt tggtggagtc ctggcttgct atagcttgct agtaacagtg 60

gcctttatta ttttctgggt gaggagtaag aggagcaggg gcggacacag tgactacatg 120

aacatgactc cccgccgccc tgggcccacc cgcaagcatt accagcccta tgccccacca 180

cgcgacttcg cagcctatcg ctcc 204

<210> 15
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 15
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60

actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 16

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 16
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgctga 339

<210> 17
<211> 7489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 17
gtccgaaatc aacctctgga ttacaaaatt tgtgaaagat tgactggtat tcttaactat 60

gttgctcctt ttacgctatg tggatacgct gctttaatgc ctttgtatca tgctattgct 120

tcccgtatgg ctttcatttt ctcctccttg tataaatcct ggttgctgtc tctttatgag 180

gagttgtggc ccgttgtcag gcaacgtggc gtggtgtgca ctgtgtttgc tgacgcaacc 240

cccactggtt ggggcattgc caccacctgt cagctccttt ccgggacttt cgctttcccc 300

ctccctattg ccacggcgga actcatcgcc gcctgccttg cccgctgctg gacaggggct 360

cggctgttgg gcactgacaa ttccgtggtg ttgtcgggga agctgacgtc ctttccatgg 420

ctgctcgcct gtgttgccac ctggattctg cgcgggacgt ccttctgcta cgtcccttcg 480

gccctcaatc cagcggacct tccttcccgc ggcctgctgc cggctctgcg gcctcttccg 540

cgtcttcgcc ttcgccctca gacgagtcgg atctcccttt gggccgcctc cccgcctgga 600

attcgagctc ggtaccttta agaccaatga cttacaaggc agctgtagat cttagccact 660

ttttaaaaga aaaggggga ctggaagggc taattcactc ccaacgaaga caagatctgc 720

tttttgcttg tactgggtct ctctggttag accagatctg agcctgggag ctctctggct 780

aactagggaa cccactgctt aagcctcaat aaagcttgcc ttgagtgctt caagtagtgt 840

gtgcccgtct gttgtgtgac tctggtaact agagatccct cagacccttt tagtcagtgt 900

ggaaaatctc tagcagtagt agttcatgtc atcttattat tcagtattta taacttgcaa 960

agaaatgaat atcagagagt gagaggaact tgtttattgc agcttataat ggttacaaat 1020

aaagcaatag catcacaaat ttcacaaata aagcattttt ttcactgcat tctagttgtg 1080

gtttgtccaa actcatcaat gtatcttatc atgtctggct ctagctatcc cgcccctaac 1140

tccgcccatc ccgcccctaa ctccgcccag ttccgcccat tctccgcccc atggctgact 1200

aatttttttt atttatgcag aggccgaggc cgcctcggcc tctgagctat tccagaagta 1260

gtgaggaggc ttttttggag gcctagggac gtacccaatt cgccctatag tgagtcgtat 1320

tacgcgcgct cactggccgt cgttttacaa cgtcgtgact gggaaaaccc tggcgttacc 1380

caacttaatc gccttgcagc acatcccccc ttcgccagct ggcgtaatag cgaagaggcc 1440

cgcaccgatc gcccttccca acagttgcgc agcctgaatg gcgaatggga cgcgccctgt 1500

agcggcgcat taagcgcggc gggtgtggtg gttacgcgca gcgtgaccgc tacacttgcc 1560

agcgccctag cgcccgctcc tttcgctttc ttcccttcct ttctcgccac gttcgccggc 1620

tttccccgtc aagctctaaa tcgggggctc cctttagggt tccgatttag tgctttacgg 1680

cacctcgacc ccaaaaaact tgattagggt gatggttcac gtagtgggcc atcgccctga 1740

tagacggttt ttcgcccttt gacgttggag tccacgttct ttaatagtgg actcttgttc 1800

caaactggaa caacactcaa ccctatctcg gtctattctt ttgatttata agggattttg 1860

ccgatttcgg cctattggtt aaaaaatgag ctgatttaac aaaaatttaa cgcgaatttt 1920

aacaaaatat taacgcttac aatttaggtg gcacttttcg gggaaatgtg cgcggaaccc 1980

ctatttgttt atttttctaa atacattcaa atatgtatcc gctcatgaga caataaccct 2040

gataaatgct tcaataatat tgaaaaagga agagtatgag tattcaacat ttccgtgtcg 2100

```
cccttattcc ctttttgcg gcattttgcc ttcctgtttt tgctcaccca gaaacgctgg     2160

tgaaagtaaa agatgctgaa gatcagttgg gtgcacgagt gggttacatc gaactggatc     2220

tcaacagcgg taagatcctt gagagttttc gccccgaaga acgttttcca atgatgagca     2280

cttttaaagt tctgctatgt ggcgcggtat tatcccgtat tgacgccggg caagagcaac     2340

tcggtcgccg catacactat tctcagaatg acttggttga gtactcacca gtcacagaaa     2400

agcatcttac ggatggcatg acagtaagag aattatgcag tgctgccata accatgagtg     2460

ataacactgc ggccaactta cttctgacaa cgatcggagg accgaaggag ctaaccgctt     2520

ttttgcacaa catgggggat catgtaactc gccttgatcg ttgggaaccg gagctgaatg     2580

aagccatacc aaacgacgag cgtgacacca cgatgcctgt agcaatggca acaacgttgc     2640

gcaaactatt aactggcgaa ctacttactc tagcttcccg gcaacaatta atagactgga     2700

tggaggcgga taaagttgca ggaccacttc tgcgctcggc ccttccggct ggctggttta     2760

ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca gcactggggc     2820

cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag gcaactatgg     2880

atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat tggtaactgt     2940

cagaccaagt ttactcatat atactttaga ttgatttaaa acttcatttt taatttaaaa     3000

ggatctaggt gaagatcctt tttgataatc tcatgaccaa aatcccttaa cgtgagtttt     3060

cgttccactg agcgtcagac cccgtagaaa agatcaaagg atcttcttga gatccttttt     3120

ttctgcgcgt aatctgctgc ttgcaaacaa aaaaaccacc gctaccagcg gtggtttgtt     3180

tgccggatca agagctacca actcttttc cgaaggtaac tggcttcagc agagcgcaga     3240

taccaaatac tgttcttcta gtgtagccgt agttaggcca ccacttcaag aactctgtag     3300

caccgcctac atacctcgct ctgctaatcc tgttaccagt ggctgctgcc agtggcgata     3360

agtcgtgtct taccgggttg gactcaagac gatagttacc ggataaggcg cagcggtcgg     3420

gctgaacggg gggttcgtgc acacagccca gcttggagcg aacgacctac accgaactga     3480

gatacctaca gcgtgagcta tgagaaagcg ccacgcttcc cgaagggaga aaggcggaca     3540

ggtatccggt aagcggcagg gtcggaacag gagagcgcac gagggagctt ccagggggaa     3600
```

acgcctggta tctttatagt cctgtcgggt ttcgccacct ctgacttgag cgtcgatttt 3660

tgtgatgctc gtcaggggg cggagcctat ggaaaaacgc cagcaacgcg gccttttac 3720

ggttcctggc cttttgctgg ccttttgctc acatgttctt tcctgcgtta tcccctgatt 3780

ctgtggataa ccgtattacc gcctttgagt gagctgatac cgctcgccgc agccgaacga 3840

ccgagcgcag cgagtcagtg agcgaggaag cggaagagcg cccaatacgc aaaccgcctc 3900

tccccgcgcg ttggccgatt cattaatgca gctggcacga caggtttccc gactggaaag 3960

cgggcagtga gcgcaacgca attaatgtga gttagctcac tcattaggca ccccaggctt 4020

tacactttat gcttccggct cgtatgttgt gtggaattgt gagcggataa caatttcaca 4080

caggaaacag ctatgaccat gattacgcca agcgcgcaat taaccctcac taaagggaac 4140

aaaagctgga gctgcaagct taatgtagtc ttatgcaata ctcttgtagt cttgcaacat 4200

ggtaacgatg agttagcaac atgccttaca aggagagaaa aagcaccgtg catgccgatt 4260

ggtggaagta aggtggtacg atcgtgcctt attaggaagg caacagacgg gtctgacatg 4320

gattggacga accactgaat tgccgcattg cagagatatt gtatttaagt gcctagctcg 4380

atacataaac gggtctctct ggttagacca gatctgagcc tgggagctct ctggctaact 4440

agggaaccca ctgcttaagc ctcaataaag cttgccttga gtgcttcaag tagtgtgtgc 4500

ccgtctgttg tgtgactctg gtaactagag atccctcaga ccctttttagt cagtgtggaa 4560

aatctctagc agtggcgccc gaacagggac ttgaaagcga aagggaaacc agaggagctc 4620

tctcgacgca ggactcggct tgctgaagcg cgcacggcaa gaggcgaggg gcggcgactg 4680

gtgagtacgc caaaaatttt gactagcgga ggctagaagg agagagatgg gtgcgagagc 4740

gtcagtatta agcgggggag aattagatcg cgatgggaaa aaattcggtt aaggccaggg 4800

ggaaagaaaa aatataaatt aaaacatata gtatgggcaa gcagggagct agaacgattc 4860

gcagttaatc ctggcctgtt agaaacatca gaaggctgta gacaaatact gggacagcta 4920

caaccatccc ttcagacagg atcagaagaa cttagatcat tatataatac agtagcaacc 4980

ctctattgtg tgcatcaaag gatagagata aaagacacca aggaagcttt agacaagata 5040

gaggaagagc aaaacaaaag taagaccacc gcacagcaag cggccgctga tcttcagacc 5100

tggaggagga gatatgaggg acaattggag aagtgaatta tataaatata aagtagtaaa 5160

aattgaacca ttaggagtag cacccaccaa ggcaaagaga agagtggtgc agagagaaaa 5220

aagagcagtg ggaataggag ctttgttcct tgggttcttg ggagcagcag gaagcactat 5280

gggcgcagcg tcaatgacgc tgacggtaca ggccagacaa ttattgtctg gtatagtgca 5340

gcagcagaac aatttgctga gggctattga ggcgcaacag catctgttgc aactcacagt 5400

ctggggcatc aagcagctcc aggcaagaat cctggctgtg gaaagatacc taaaggatca 5460

acagctcctg gggatttggg gttgctctgg aaaactcatt tgcaccactg ctgtgccttg 5520

gaatgctagt tggagtaata aatctctgga acagatttgg aatcacacga cctggatgga 5580

gtgggacaga gaaattaaca attacacaag cttaatacac tccttaattg aagaatcgca 5640

aaaccagcaa gaaaagaatg aacaagaatt attggaatta gataaatggg caagtttgtg 5700

gaattggttt aacataacaa attggctgtg gtatataaaa ttattcataa tgatagtagg 5760

aggcttggta ggtttaagaa tagtttttgc tgtactttct atagtgaata gagttaggca 5820

gggatattca ccattatcgt ttcagaccca cctcccaacc ccgaggggac ccgacaggcc 5880

cgaaggaata gaagaagaag gtggagagag agacagagac agatccattc gattagtgaa 5940

cggatctcga cggtatcggt taacttttaa aagaaaaggg gggattgggg ggtacagtgc 6000

aggggaaaga atagtagaca taatagcaac agacatacaa actaaagaat tacaaaaaca 6060

aattacaaaa ttcaaaattt tatcgatgcc tccccgtcac cacccccccc aacccgcccc 6120

gaccggagct gagagtaatt catacaaaag gactcgcccc tgccttgggg aatcccaggg 6180

accgtcgtta aactcccact aacgtagaac ccagagatcg ctgcgttccc gccccctcac 6240

ccgcccgctc tcgtcatcac tgaggtggag aagagcatgc gtgaggctcc ggtgcccgtc 6300

agtgggcaga gcgcacatcg cccacagtcc ccgagaagtt gggggggaggg gtcggcaatt 6360

gaaccggtgc ctagagaagg tggcgcgggg taaactggga aagtgatgtc gtgtactggc 6420

tccgcctttt tcccgagggt gggggagaac cgtatataag tgcagtagtc gccgtgaacg 6480

ttctttttcg caacgggttt gccgccagaa cacaggtaag tgccgtgtgt ggttcccgcg 6540

ggcctggcct ctttacgggt tatggccctt gcgtgccttg aattacttcc acgcccctgg 6600

ctgcagtacg tgattcttga tcccgagctt cgggttggaa gtgggtggga gagttcgagg 6660

ccttgcgctt aaggagcccc ttcgcctcgt gcttgagttg aggcctggcc tgggcgctgg 6720

ggccgccgcg tgcgaatctg gtggcacctt cgcgcctgtc tcgctgcttt cgataagtct 6780

ctagccattt aaaatttttg atgatatcct gcgacgcttt ttttctggca agatagtctt 6840

gtaaatgcgg gccaagatct gcacactggt atttcggttt ttggggccgc gggcggcgac 6900

ggggcccgtg cgtcccagcg cacatgttcg gcgaggcggg gcctgcgagc gcggccaccg 6960

agaatcggac gggggtagtc tcaagctggc cggcctgctc tggtgcctgg cctcgcgccg 7020

ccgtgtatcg ccccgccctg ggcggcaagg ctggcccggt cggcaccagt tgcgtgagcg 7080

gaaagatggc cgcttcccgg ccctgctgca gggagctcaa aatggaggac gcggcgctcg 7140

ggagagcggg cgggtgagtc acccacacaa aggaaaaggg cctttccgtc ctcagccgtc 7200

gcttcatgtg actccacgga gtaccgggcg ccgtccaggc acctcgatta gttctcgagc 7260

ttttggagta cgtcgtcttt aggttggggg gaggggtttt atgcgatgga gtttccccac 7320

actgagtggg tggagactga agttaggcca gcttggcact tgatgtaatt ctccttggaa 7380

tttgcccttt ttgagtttgg atcttggttc attctcaagc ctcagacagt ggttcaaagt 7440

ttttttcttc catttcaggt gtcgtgaaaa ctacccctct agagccacc 7489

<210> 18
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 18

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 19

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 19

Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15

Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Pro Asp Ile Asn Ser Tyr
20 25 30

Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45

Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Gly Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Tyr
65 70 75 80

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Met Lys
100 105

<210> 20
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 20

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Pro Asp Ile Asn Ser Tyr
            20                  25                  30

Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
        35                  40                  45

Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Asp Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
65                  70                  75                  80

Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Tyr
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 21
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 21

```
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1               5                   10                  15

Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Pro Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Glu Ser
65 70 75 80

Glu Asp Ala Ala Tyr Tyr Phe Cys Gln Gln His Asp Glu Ser Pro Tyr
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys
100 105

<210> 22
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 22

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 23
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 23

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 24

<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 24

Gly Gly Gly Gly Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser
1 5 10 15

Gly Glu Gly Ser Thr Lys Gly Gly Gly Gly Gly Ser
20 25

<210> 25
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 25

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Glu Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Gly
85 90 95

Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
115

<210> 26
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 26

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly
85 90 95

Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 27
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 27

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ala Phe Thr Ala Tyr
20 25 30

Asn Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ser Phe Asp Arg Tyr Asp Gly Gly Ser Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65 70 75 80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 29
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 29

Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 30
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 30

Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 31
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 31

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

```
            20                  25                  30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35                  40                  45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys Met
    210                 215
```

<210> 32
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 32

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
20 25 30

Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
50 55 60

Ala Tyr Arg Ser
65

<210> 33
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 33

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu

35 40

<210> 34
<211> 112
<212> PRT
<213> Homo sapiens

<400> 34

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 35
<211> 2148
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 35
atgggatggt catgtatcat ccttttttcta gtagcaactg caaccggtgt acattccgac 60

atcaagatga cccagtctcc atcttccatg tatgcatctc taggagagag agtcactatc 120

acttgcaagg cgagtccgga cattaatagc tatttaagct ggttccagca gaaaccaggg 180

aaatctccta agaccctgat ctatcgtgca aacagattgg ttgatggggt cccatcaagg 240

ttcagtggcg gtggatctgg gcaagattat tctctcacca tcaacagcct ggagtatgaa 300

gatatgggaa tttattattg tctacagtat gatgaatttc cgtacacgtt cggaggggg 360

accaagctgg aaatgaaagg ctccacctct ggatccggca agcccggatc tggcgaggga 420

tccaccaagg gcgaagtgaa actagtggag tctgggggag gcttagtgaa gcctggaggg 480

tccctgaaac tctcctgtgc agcctctgga ttcactttca gtagctatgc catgtcttgg 540

gttcgccaga ttccagagaa gaggctggag tgggtcgcat ccattagtcg tggtggtacc 600

acctactatc cagacagtgt gaagggccga ttcaccatct ccagagataa tgtcaggaac 660

atcctgtacc tgcaaatgag cagtctgagg tctgaggaca cggccatgta ttactgtgga 720

agatatgatt acgacgggta ctatgcaatg gactactggg gtcaaggaac ctcagtcacc 780

gtctcctcag agtccaaata tggtccccca tgcccaccat gcccagcacc tgagttcctg 840

gggggaccat cagtcttcct gttcccccca aaacccaagg acactctcat gatctcccgg 900

acccctgagg tcacgtgcgt ggtggtggac gtgagccagg aagaccccga ggtccagttc 960

aactggtacg tggatggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

ttcaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaac 1080

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cgtcctccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccag 1200

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca ggctaaccgt ggacaagagc 1380

aggtggcagg aggggaatgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacacaga agagcctctc cctgtcccta ggtaaaatgt tttgggtgct ggtggtggtt 1500

ggtggagtcc tggcttgcta tagcttgcta gtaacagtgg cctttattat tttctgggtg 1560

aggagtaaga ggagcagggg cggacacagt gactacatga acatgactcc ccgccgccct 1620

gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 1680

tccaaacggg gcagaaagaa actcctgtat atattcaaac aaccatttat gagaccagta 1740

caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga agaaggagga 1800

tgtgaactga gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag 1860

aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag 1920

agacgtggcc gggaccctga gatgggggga aagccgagaa ggaagaaccc tcaggaaggc 1980

ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa 2040

ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc 2100

aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgctga 2148

<210> 36
<211> 2154
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 36
atgggatggt catgtatcat ccttttttcta gtagcaactg caaccggtgt acattccgac 60

atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 120

acttgcaagg cgagtccgga cattaatagc tatttaagct ggtttcagca gaggccaggc 180

caatctccaa ggcgcctaat ttatcgtgca aacagattgg ttgatggggt cccagacagg 240

ttcagtggca gtgggtcagg cactgatttc acactgaaaa tcagcagggt ggaggctgag 300

gatgttggag tttattactg tctacagtat gatgaatttc cgtacacgtt cggccaaggg 360

accaaggtgg aaatcaaagg ctccacctct ggatccggca agcccggatc tggcgaggga 420

tccaccaagg gcgaagtgca gctggtgcag tctggagcag aggtgaaaaa gcccggggag 480

tctctgagga tctcctgtaa gggttctgga ttcactttca gtagctatgc catgtcttgg 540

atcaggcagt ccccatcgag aggccttgag tggctgggtt ccattagtcg tggtggtacc 600

acctactatc cagacagtgt gaagggcaga ttcaccatct ccagagacaa cgccaagaac 660

tcactgtatc tgcaaatgaa cagcctgaga gccgaggaca cggctgtgta ttactgtgga 720

agatatgatt acgacgggta ctatgcaatg gactactggg gccagggaac gctggtcacc 780

gtcagctcag tcgacgagtc caaatatggt cccccatgcc caccatgccc agcacctgag 840

ttcctggggg gaccatcagt cttcctgttc cccccaaaac ccaaggacac tctcatgatc 900

tcccggaccc ctgaggtcac gtgcgtggtg gtggacgtga gccaggaaga ccccgaggtc 960

cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020

gagcagttca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080

ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccgtc ctccatcgag 1140

aaaaccatct ccaaagccaa agggcagccc cgagagccac aggtgtacac cctgccccca 1200

tcccaggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctac 1260

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaggct aaccgtggac 1380

aagagcaggt ggcaggaggg gaatgtcttc tcatgctccg tgatgcatga ggctctgcac 1440

aaccactaca cacagaagag cctctccctg tccctaggta aaatgttttg ggtgctggtg 1500

gtggttggtg gagtcctggc ttgctatagc ttgctagtaa cagtggcctt tattattttc 1560

tgggtgagga gtaagaggag caggggcgga cacagtgact acatgaacat gactccccgc 1620

cgccctgggc ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc 1680

tatcgctcca aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga 1740

ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa 1800

ggaggatgtg aactgagagt gaagttcagc aggagcgcag acgccccgc gtaccagcag 1860

ggccagaacc agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg 1920

gacaagagac gtggccggga ccctgagatg gggggaaagc cgagaaggaa gaaccctcag 1980

gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg 2040

atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca 2100

gccaccaagg acacctacga cgcccttcac atgcaggccc tgcccctcg ctga 2154

<210> 37
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 37
atgggatggt catgtatcat ccttttttcta gtagcaactg caaccggtgt acattccgat 60

attgtgatga cccagactcc actctccctg cccgtcaccc ctggagagcc ggcctccatc 120

tcctgcaggg caagtaagag cattagcaaa tatttagcct ggtaccagca gaaacctggc 180

caggctccca ggctcctcat ctattctgga tccactttgc aatctgggat cccacctcga 240

ttcagtggca gcgggtatgg aacagatttt accctcacaa ttaataacat agaatctgag 300

gatgctgcat attacttctg tcaacagcat gatgaatccc cgtacacgtt cggcgagggg 360

accaaggtgg aaatcaaagg tggtggtggt agcggctcca cctctggatc cggcaagccc 420

ggatctggcg agggatccac caagggcgga ggaggaggaa gtcaggtgca gctgcaggag 480

tcgggcccag gactggtgaa gccttcacag accctgtccc tcacctgcac tgtctctggt 540

tatgcattca ctgcctacaa catacactgg gtgcgacagg cccctggaca agggcttgag 600

tggatgggtt cttttgatcc ttacgatggt ggtagtagtt acaaccagaa gttcaaggac 660

agactcacca tctccaagga cacctccaaa aaccaggtgg tccttacaat gaccaacatg 720

gaccctgtgg acacagccac gtattactgt gcaagagggt ggtactactt tgactactgg 780

ggccacggaa ccctggtcac cgtctcctca gtcgacgagt ccaaatatgg tcccccatgc 840

ccaccatgcc cagcacctga gttcctgggg ggaccatcag tcttcctgtt cccccccaaaa 900

cccaaggaca ctctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 960

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 1020

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 1080

accgtcctgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 1140

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1200

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1260

tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1320

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380

tacagcaggc taaccgtgga caagagcagg tggcaggagg ggaatgtctt ctcatgctcc 1440

gtgatgcatg aggctctgca caaccactac acacagaaga gcctctccct gtccctaggt 1500

aaaatgtttt gggtgctggt ggtggttggt ggagtcctgg cttgctatag cttgctagta 1560

acagtggcct ttattatttt ctgggtgagg agtaagagga gcaggggcgg acacagtgac 1620

tacatgaaca tgactccccg ccgccctggg cccacccgca agcattacca gccctatgcc 1680

ccaccacgcg acttcgcagc ctatcgctcc aaacggggca gaaagaaact cctgtatata 1740

ttcaaacaac catttatgag accagtacaa actactcaag aggaagatgg ctgtagctgc 1800

cgatttccag aagaagaaga aggaggatgt gaactgagag tgaagttcag caggagcgca 1860

gacgcccccg cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga 1920

agagaggagt acgatgtttt ggacaagaga cgtggccggg accctgagat ggggggaaag 1980

ccgagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg 2040

gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 2100

ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc 2160

ctgccccctc gctga 2175

<210> 38
<211> 715
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 38

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

```
Val His Ser Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala
            20                  25                  30

Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Pro Asp Ile
        35                  40                  45

Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys
    50                  55                  60

Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg
65                  70                  75                  80

Phe Ser Gly Gly Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn Ser
                85                  90                  95

Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu
            100                 105                 110

Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Met Lys Gly Ser
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
145                 150                 155                 160

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
                165                 170                 175

Ala Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
            180                 185                 190

Ala Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
        195                 200                 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu
    210                 215                 220
```

```
Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Gly
225                 230                 235                 240

Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Ser Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro
            260                 265                 270

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    290                 295                 300

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
305                 310                 315                 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                325                 330                 335

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            340                 345                 350

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        355                 360                 365

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
    370                 375                 380

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
385                 390                 395                 400

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                405                 410                 415
```

```
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            420                 425                 430

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        435                 440                 445

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
    450                 455                 460

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465                 470                 475                 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val
                485                 490                 495

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
            500                 505                 510

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly
        515                 520                 525

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
    530                 535                 540

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
545                 550                 555                 560

Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
                565                 570                 575

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
            580                 585                 590

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
        595                 600                 605

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
    610                 615                 620
```

```
Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
625                 630                 635                 640


Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
                645                 650                 655


Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
            660                 665                 670


Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
        675                 680                 685


His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
    690                 695                 700


Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
705                 710                 715


<210>  39
<211>  717
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic construct

<400>  39

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1               5                   10                  15


Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
            20                  25                  30


Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Pro Asp Ile
        35                  40                  45


Asn Ser Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg
    50                  55                  60
```

```
Arg Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Asp Arg
65                  70                  75                  80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
                85                  90                  95

Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Tyr Asp Glu
            100                 105                 110

Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
145                 150                 155                 160

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Thr Phe Ser Ser Tyr
                165                 170                 175

Ala Met Ser Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
            180                 185                 190

Gly Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
        195                 200                 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
    210                 215                 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly
225                 230                 235                 240

Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255
```

```
Thr Leu Val Thr Val Ser Ser Val Asp Glu Ser Lys Tyr Gly Pro Pro
            260                 265                 270

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
        275                 280                 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    290                 295                 300

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
305                 310                 315                 320

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                325                 330                 335

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
            340                 345                 350

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        355                 360                 365

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
    370                 375                 380

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
385                 390                 395                 400

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                405                 410                 415

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            420                 425                 430

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        435                 440                 445

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
    450                 455                 460
```

```
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465                 470                 475                 480

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe
                485                 490                 495

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
            500                 505                 510

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
        515                 520                 525

Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
    530                 535                 540

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
545                 550                 555                 560

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
                565                 570                 575

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
            580                 585                 590

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
        595                 600                 605

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
    610                 615                 620

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
625                 630                 635                 640

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
                645                 650                 655
```

```
Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
            660                 665                 670


Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
        675                 680                 685


Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
    690                 695                 700


Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
705                 710                 715
```

<210> 40
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 40

```
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1               5                   10                  15


Val His Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30


Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Ser Ile
        35                  40                  45


Ser Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
    50                  55                  60


Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Pro Arg
65                  70                  75                  80


Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn
                85                  90                  95
```

```
Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys Gln Gln His Asp Glu
            100                 105                 110

Ser Pro Tyr Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Gly Gly
        115                 120                 125

Gly Gly Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
    130                 135                 140

Gly Ser Thr Lys Gly Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
145                 150                 155                 160

Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys
                165                 170                 175

Thr Val Ser Gly Tyr Ala Phe Thr Ala Tyr Asn Ile His Trp Val Arg
            180                 185                 190

Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ser Phe Asp Pro Tyr
        195                 200                 205

Asp Gly Gly Ser Ser Tyr Asn Gln Lys Phe Lys Asp Arg Leu Thr Ile
    210                 215                 220

Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met
225                 230                 235                 240

Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Gly Trp Tyr Tyr
                245                 250                 255

Phe Asp Tyr Trp Gly His Gly Thr Leu Val Thr Val Ser Ser Val Asp
            260                 265                 270

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
        275                 280                 285

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290                 295                 300
```

```
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305                 310                 315                 320

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
                325                 330                 335

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
            340                 345                 350

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355                 360                 365

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
    370                 375                 380

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
                405                 410                 415

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
    450                 455                 460

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495
```

```
Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val Val Val Gly Gly Val
            500                 505                 510

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
        515                 520                 525

Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met
    530                 535                 540

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
545                 550                 555                 560

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys
                565                 570                 575

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
            580                 585                 590

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
        595                 600                 605

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
    610                 615                 620

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
625                 630                 635                 640

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
                645                 650                 655

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
            660                 665                 670

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
        675                 680                 685

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
    690                 695                 700
```

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
705 710 715 720

Leu Pro Pro Arg

<210> 41
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 41

Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Leu Pro
1 5 10 15

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
20 25 30

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
35 40 45

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
50 55 60

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
65 70 75 80

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
85 90 95

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
100 105 110

<210> 42
<211> 231

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 42

```
Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
1               5                  10                  15


Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            20                  25                  30


Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        35                  40                  45


Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
    50                  55                  60


Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
65                  70                  75                  80


Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                85                  90                  95


Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
            100                 105                 110


Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        115                 120                 125


Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
    130                 135                 140


Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145                 150                 155                 160


Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                165                 170                 175
```

```
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            180                 185                 190


Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
        195                 200                 205


Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210                 215                 220


Leu Ser Leu Ser Leu Gly Lys
225                 230


<210>  43
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic construct

<400>  43

Lys Ser Ile Ser Lys Tyr
1               5


<210>  44
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic construct

<400>  44

Ser Gly Ser
1


<210>  45
<211>  8
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> Synthetic construct

<400> 45

Gln Gln His Asp Glu Ser Pro Tyr
1   5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 46

Gly Tyr Ala Phe Thr Ala Tyr Asn
1   5

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 47

Phe Asp Pro Tyr Asp Gly Gly Ser
1   5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 48

Gly Trp Tyr Tyr Phe Asp Tyr
1   5

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 49

Pro Asp Ile Asn Ser Tyr
1   5

<210> 50
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 50

Arg Ala Asn
1

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 51

Leu Gln Tyr Asp Glu Phe Pro Tyr Thr
1   5

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 52

Gly Phe Thr Phe Ser Ser Tyr Ala
1   5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 53

Ile Ser Arg Gly Gly Thr Thr
1   5

<210> 54
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 54

Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr
1   5   10

<210> 55
<211> 937
<212> PRT
<213> Homo sapiens

<400> 55

Met His Arg Pro Arg Arg Arg Gly Thr Arg Pro Pro Leu Leu Ala Leu
1   5   10   15

Leu Ala Ala Leu Leu Leu Ala Ala Arg Gly Ala Ala Ala Gln Glu Thr
            20   25   30

```
Glu Leu Ser Val Ser Ala Glu Leu Val Pro Thr Ser Ser Trp Asn Ile
        35                  40                  45

Ser Ser Glu Leu Asn Lys Asp Ser Tyr Leu Thr Leu Asp Glu Pro Met
    50                  55                  60

Asn Asn Ile Thr Thr Ser Leu Gly Gln Thr Ala Glu Leu His Cys Lys
65                  70                  75                  80

Val Ser Gly Asn Pro Pro Pro Thr Ile Arg Trp Phe Lys Asn Asp Ala
                85                  90                  95

Pro Val Val Gln Glu Pro Arg Arg Leu Ser Phe Arg Ser Thr Ile Tyr
            100                 105                 110

Gly Ser Arg Leu Arg Ile Arg Asn Leu Asp Thr Thr Asp Thr Gly Tyr
        115                 120                 125

Phe Gln Cys Val Ala Thr Asn Gly Lys Glu Val Val Ser Ser Thr Gly
    130                 135                 140

Val Leu Phe Val Lys Phe Gly Pro Pro Pro Thr Ala Ser Pro Gly Tyr
145                 150                 155                 160

Ser Asp Glu Tyr Glu Glu Asp Gly Phe Cys Gln Pro Tyr Arg Gly Ile
                165                 170                 175

Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Val Tyr Met Glu Ser Leu
            180                 185                 190

His Met Gln Gly Glu Ile Glu Asn Gln Ile Thr Ala Ala Phe Thr Met
        195                 200                 205

Ile Gly Thr Ser Ser His Leu Ser Asp Lys Cys Ser Gln Phe Ala Ile
    210                 215                 220

Pro Ser Leu Cys His Tyr Ala Phe Pro Tyr Cys Asp Glu Thr Ser Ser
```

```
225                 230                 235                 240

Val Pro Lys Pro Arg Asp Leu Cys Arg Asp Glu Cys Glu Ile Leu Glu
                245                 250                 255

Asn Val Leu Cys Gln Thr Glu Tyr Ile Phe Ala Arg Ser Asn Pro Met
            260                 265                 270

Ile Leu Met Arg Leu Lys Leu Pro Asn Cys Glu Asp Leu Pro Gln Pro
        275                 280                 285

Glu Ser Pro Glu Ala Ala Asn Cys Ile Arg Ile Gly Ile Pro Met Ala
    290                 295                 300

Asp Pro Ile Asn Lys Asn His Lys Cys Tyr Asn Ser Thr Gly Val Asp
305                 310                 315                 320

Tyr Arg Gly Thr Val Ser Val Thr Lys Ser Gly Arg Gln Cys Gln Pro
                325                 330                 335

Trp Asn Ser Gln Tyr Pro His Thr His Thr Phe Thr Ala Leu Arg Phe
            340                 345                 350

Pro Glu Leu Asn Gly Gly His Ser Tyr Cys Arg Asn Pro Gly Asn Gln
        355                 360                 365

Lys Glu Ala Pro Trp Cys Phe Thr Leu Asp Glu Asn Phe Lys Ser Asp
    370                 375                 380

Leu Cys Asp Ile Pro Ala Cys Asp Ser Lys Asp Ser Lys Glu Lys Asn
385                 390                 395                 400

Lys Met Glu Ile Leu Tyr Ile Leu Val Pro Ser Val Ala Ile Pro Leu
                405                 410                 415

Ala Ile Ala Leu Leu Phe Phe Phe Ile Cys Val Cys Arg Asn Asn Gln
            420                 425                 430
```

```
Lys Ser Ser Ser Ala Pro Val Gln Arg Gln Pro Lys His Val Arg Gly
        435                 440                 445

Gln Asn Val Glu Met Ser Met Leu Asn Ala Tyr Lys Pro Lys Ser Lys
    450                 455                 460

Ala Lys Glu Leu Pro Leu Ser Ala Val Arg Phe Met Glu Glu Leu Gly
465                 470                 475                 480

Glu Cys Ala Phe Gly Lys Ile Tyr Lys Gly His Leu Tyr Leu Pro Gly
                485                 490                 495

Met Asp His Ala Gln Leu Val Ala Ile Lys Thr Leu Lys Asp Tyr Asn
            500                 505                 510

Asn Pro Gln Gln Trp Met Glu Phe Gln Gln Glu Ala Ser Leu Met Ala
        515                 520                 525

Glu Leu His His Pro Asn Ile Val Cys Leu Leu Gly Ala Val Thr Gln
    530                 535                 540

Glu Gln Pro Val Cys Met Leu Phe Glu Tyr Ile Asn Gln Gly Asp Leu
545                 550                 555                 560

His Glu Phe Leu Ile Met Arg Ser Pro His Ser Asp Val Gly Cys Ser
                565                 570                 575

Ser Asp Glu Asp Gly Thr Val Lys Ser Ser Leu Asp His Gly Asp Phe
            580                 585                 590

Leu His Ile Ala Ile Gln Ile Ala Ala Gly Met Glu Tyr Leu Ser Ser
        595                 600                 605

His Phe Phe Val His Lys Asp Leu Ala Ala Arg Asn Ile Leu Ile Gly
    610                 615                 620

Glu Gln Leu His Val Lys Ile Ser Asp Leu Gly Leu Ser Arg Glu Ile
```

625 630 635 640

Tyr Ser Ala Asp Tyr Tyr Arg Val Gln Ser Lys Ser Leu Leu Pro Ile
645 650 655

Arg Trp Met Pro Pro Glu Ala Ile Met Tyr Gly Lys Phe Ser Ser Asp
660 665 670

Ser Asp Ile Trp Ser Phe Gly Val Val Leu Trp Glu Ile Phe Ser Phe
675 680 685

Gly Leu Gln Pro Tyr Tyr Gly Phe Ser Asn Gln Glu Val Ile Glu Met
690 695 700

Val Arg Lys Arg Gln Leu Leu Pro Cys Ser Glu Asp Cys Pro Pro Arg
705 710 715 720

Met Tyr Ser Leu Met Thr Glu Cys Trp Asn Glu Ile Pro Ser Arg Arg
725 730 735

Pro Arg Phe Lys Asp Ile His Val Arg Leu Arg Ser Trp Glu Gly Leu
740 745 750

Ser Ser His Thr Ser Ser Thr Thr Pro Ser Gly Gly Asn Ala Thr Thr
755 760 765

Gln Thr Thr Ser Leu Ser Ala Ser Pro Val Ser Asn Leu Ser Asn Pro
770 775 780

Arg Tyr Pro Asn Tyr Met Phe Pro Ser Gln Gly Ile Thr Pro Gln Gly
785 790 795 800

Gln Ile Ala Gly Phe Ile Gly Pro Pro Ile Pro Gln Asn Gln Arg Phe
805 810 815

Ile Pro Ile Asn Gly Tyr Pro Ile Pro Pro Gly Tyr Ala Ala Phe Pro
820 825 830

```
Ala Ala His Tyr Gln Pro Thr Gly Pro Pro Arg Val Ile Gln His Cys
        835                 840                 845


Pro Pro Pro Lys Ser Arg Ser Pro Ser Ser Ala Ser Gly Ser Thr Ser
    850                 855                 860


Thr Gly His Val Thr Ser Leu Pro Ser Ser Gly Ser Asn Gln Glu Ala
865                 870                 875                 880


Asn Ile Pro Leu Leu Pro His Met Ser Ile Pro Asn His Pro Gly Gly
                885                 890                 895


Met Gly Ile Thr Val Phe Gly Asn Lys Ser Gln Lys Pro Tyr Lys Ile
            900                 905                 910


Asp Ser Lys Gln Ala Ser Leu Leu Gly Asp Ala Asn Ile His Gly His
        915                 920                 925


Thr Glu Ser Met Ile Ser Ala Glu Leu
    930                 935


<210>  56
<211>  21
<212>  PRT
<213>  Homo sapiens

<400>  56

Val Ala Thr Asn Gly Lys Glu Val Val Ser Ser Thr Gly Val Leu Phe
1               5                   10                  15


Val Lys Phe Gly Pro
            20


<210>  57
<211>  15
<212>  PRT
<213>  Homo sapiens

<400>  57
```

```
Glu Val Val Ser Ser Thr Gly Val Leu Phe Val Lys Phe Gly Pro
1               5                   10                  15
```