ANTI-KRAS-G12D T CELL RECEPTORS

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This patent application claims the benefit of U.S. Provisional Patent Application No. 62/369,883, filed August 2, 2016, which is incorporated by reference in its entirety herein.

INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

[0002] Incorporated by reference in its entirety herein is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: One 60,828 Byte ASCII (Text) file named "728242_ST25.txt" dated July 26, 2017.

BACKGROUND OF THE INVENTION

[0003] Some cancers may have very limited treatment options, particularly when the cancer becomes metastatic and unresectable. Despite advances in treatments such as, for example, surgery, chemotherapy, and radiation therapy, the prognosis for many cancers, such as, for example, pancreatic, colorectal, lung, endometrial, ovarian, and prostate cancers, may be poor. Accordingly, there exists an unmet need for additional treatments for cancer.

BRIEF SUMMARY OF THE INVENTION

[0004] An embodiment of the invention provides an isolated or purified TCR comprising the amino acid sequences of: (a) SEQ ID NOs: 9-14; (b) SEQ ID NOs: 17-22; (c) SEQ ID NOs: 25-30; or (d) SEQ ID NOs: 33-38.

[0005] Another embodiment of the invention provides an isolated or purified polypeptide comprising the amino acid sequences of: (a) SEQ ID NOs: 9-14; (b) SEQ ID NOs: 17-22; (c) SEQ ID NOs: 25-30; or (d) SEQ ID NOs: 33-38.

[0006] Another embodiment of the invention provides an isolated or purified protein comprising: (a) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 9-11 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 12-14; (b) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 17-19 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 20-22; (c) a first polypeptide chain comprising the amino acid sequences of SEQ ID

NOs: 25-27 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 28-30; or (d) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 33-35 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 36-38.

[0007] The invention further provides related nucleic acids, recombinant expression vectors, host cells, populations of cells, and pharmaceutical compositions relating to the TCRs, polypeptides, and proteins of the invention.

[0008] Methods of detecting the presence of cancer in a mammal and methods of treating or preventing cancer in a mammal are further provided by the invention.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWING(S)

[0009] Figure 1A is a graph showing IFN-γ production (spots/2e4 cells) as determined by ELISPOT assay of 24 individual TIL cultures after co-culture with autologous dendritic cells transfected with an irrelevant tandem minigene (TMG) RNA (closed circles), or the indicated TMG construct encoding the 61 mutations identified by whole-exomic and transcriptome sequencing (TMG-1 (stars), TMG-2 (△), TMG-3 (▽), TMG-4 (open diamond), TMG-5 (closed diamond)).

[0010] Figure 1B is a graph showing IFN-γ production (spots/2e4 cells) as determined by ELISPOT assay (left axis; unshaded bars), and flow cytometric analysis of 4-1BB expression on CD8+ T cells (%) (right axis; shaded bars) of TIL culture #6 after co-culture with dendritic cells (DCs) transfected with an irrelevant TMG RNA or TMG-1, or incubated overnight with the mutated long peptides encoded by TMG-1.

[0011] Figure 1C is a graph showing IFN-γ production as determined by ELISPOT assay (left axis; unshaded bars), and flow cytometric analysis of 4-1BB expression on CD8+ T cells (%) (right axis; shaded bars) of the infusion product (TIL culture #6 after undergoing clinical scale rapid expansion) after co-culture with DCs transfected with the indicated TMG RNA, or incubated overnight with the 24-AA long KRAS-wild type (WT) or $KRAS^{G12D}$ peptides.

[0012] Figures 2A-2D are graphs showing the results of a TCR-Vβ deep sequencing analysis quantitating the frequency of each of the four identified $KRAS^{G12D}$-reactive T-cell clones in the infusion product (Rx1, filled bar), three metastatic lung samples prior to cell transfer (Tu-1, diamond; Tu-2A, square; and Tu-2B, triangle), the one progressing lesion after cell transfer (Tu-Pro, inverted triangle), and the peripheral blood of the patient before and at various times after cell infusion (circles). Numbers in parentheses indicate the rank of

the TCR sequence in the given sample. ⊗ and ND, not detected (< 0.0002%). A (TRAV4/TRBV5-6(A)). B (TRAV12-2/TRBV10-2). C (TRAV4/TRBV5-6(B)). D (TRAV4/TRBV5-6 (C)).

[0013] Figures 3A-3D are graphs showing the expression of the T-cell activation marker 4-1BB on T cells engineered with the TCR comprising the amino acid sequences of SEQ ID NOs: 50 and 51 (TRAV4/TRBV5-6 (A)) (Fig. 3A), SEQ ID NOs: 56 and 57 (TRAV12-2/TRBV10-2) (Fig. 3B), SEQ ID NOs: 54 and 55 (TRAV4/TRBV5-6 (B)) (Fig. 3C), or SEQ ID NOs: 52 and 53 (TRAV4/TRBV5-6 (C)) (Fig. 3D) after overnight coculture with autologous PBMCs incubated with titrating amounts of KRAS wild-type (WT) 9-mer (open circles), G12D mutant KRAS 9mer (closed circles), KRAS WT 10-mer (open triangle), or KRAS G12D mutant KRAS 10-mer peptide (closed triangle).

[0014] Figures 4A and 4B are graphs showing IFN-γ production (spots/2e4 cells) (A) and 4-1BB expression (B) of T cells genetically engineered with the indicated TCR after overnight coculture with two $KRAS^{G12D}$-positive pancreatic cancer cells lines not expressing (Mock) or expressing the HLA-C*08:02 allele. TRBV5-6(A) TCR (unshaded bars); TRBV10-02 TCR (shaded bars); TRBV5-6(B) TCR (horizontal stripes); TRBV5-6(C) TCR (diagonal stripes). MD, MDA-Panc48; HP, HPAC. Flow cytometry data are gated on CD8+ $KRAS^{G12D}$-specific TCR+ cells. ">" greater than ~ 500 spots not accurate.

[0015] Figures 5A-5D are graphs showing 4-1BB expression (%) of T cells genetically engineered with the indicated TCR after overnight coculture with target COS cells transduced with full length wild-type (wt) KRAS (unshaded bars) or KRAS-G12D gene (shaded bar) and the indicated HLA allele. TRBV5-6(A) TCR (Fig. 5A); TRBV10-02 TCR (Fig. 5B); TRBV5-6(B) TCR (Fig. 5C); TRBV5-6(C) TCR (Fig. 5D).

DETAILED DESCRIPTION OF THE INVENTION

[0016] Kirsten rat sarcoma viral oncogene homolog (KRAS), also referred to as GTPase KRas, V-Ki-Ras2 Kirsten rat sarcoma viral oncogene, or KRAS2, is a member of the small GTPase superfamily. There are two transcript variants of KRAS: KRAS variant A and KRAS variant B. Hereinafter, references to "KRAS" (mutated or unmutated) refer to both variant A and variant B, unless specified otherwise. Without being bound to a particular theory or mechanism, it is believed that, when mutated, KRAS may be involved in signal transduction early in the oncogenesis of many human cancers. A single amino acid substitution may activate the protein. When activated, mutated KRAS binds to guanosine-5'-

triphosphate (GTP) and converts GTP to guanosine 5′-diphosphate (GDP). The mutated KRAS protein product may be constitutively activated. Mutated KRAS protein may be expressed in any of a variety of human cancers such as, for example, pancreatic (e.g., pancreatic carcinoma), colorectal, lung (e.g., lung adenocarcinoma), endometrial, ovarian (e.g., epithelial ovarian cancer), and prostate cancers.

[0017] An embodiment of the invention provides an isolated or purified TCR having antigenic specificity for mutated human KRAS (hereinafter, "mutated KRAS"). Hereinafter, references to a "TCR" also refer to functional portions and functional variants of the TCR, unless specified otherwise. The inventive TCR may have antigenic specificity for any KRAS (protein, polypeptide or peptide) with a G12D mutation.

[0018] In an embodiment of the invention, the TCR has antigenic specificity for a KRAS protein with the G12D mutation, the KRAS protein comprising or consisting of the amino acid sequence of SEQ ID NO: 3 or 4. The mutated KRAS variant A protein amino acid sequence of SEQ ID NO: 3 generally corresponds to positions 1-189 of the unmutated, wild-type (WT) KRAS protein variant A amino acid sequence of SEQ ID NO: 1 with the exception that in SEQ ID NO: 3, the glycine at position 12 is substituted with aspartic acid. The mutated KRAS variant B protein amino acid sequence of SEQ ID NO: 4 generally corresponds to positions 1-188 of the unmutated, WT KRAS protein variant B amino acid sequence of SEQ ID NO: 2 with the exception that in SEQ ID NO: 4, the glycine at position 12 is substituted with aspartic acid.

[0019] In an embodiment of the invention, the TCR has antigenic specificity for a KRAS peptide with the G12D mutation described above, the KRAS peptide having any length. For example, the TCR may have antigenic specificity for a KRAS peptide with the G12D mutation, the KRAS peptide having a length of about 8 to about 24 amino acid residues, preferably about 9 to about 11 amino acid residues. In an embodiment of the invention, the TCR may have antigenic specificity for a KRAS peptide with the G12D mutation, the KRAS peptide having a length of about 8 amino acid residues, about 9 amino acid residues, about 10 amino acid residues, about 11 amino acid residues, about 12 amino acid residues, or about 24 amino acid residues. For example, the TCR may have antigenic specificity for a $KRAS_{10-18}$ peptide with the G12D mutation, the peptide comprising or consisting of the amino acid sequence of GADGVGKSA (SEQ ID NO: 8). The mutated KRAS peptide amino acid sequence of SEQ ID NO: 8 with the G12D mutation generally corresponds to positions 1-9 of

the unmutated, WT $KRAS_{10-18}$ peptide amino acid sequence of SEQ ID NO: 7 with the exception that in SEQ ID NO: 8, the glycine at position 3 is substituted with aspartic acid.

[0020] In still another embodiment of the invention, the TCR may have antigenic specificity for a KRAS peptide with the G12D mutation, the mutated KRAS peptide comprising or consisting of the amino acid sequence of GADGVGKSA (mutated $KRAS_{10-18}$; SEQ ID NO: 8) or GADGVGKSAL (mutated $KRAS_{10-19}$; SEQ ID NO: 6). In an exemplary embodiment, the TCR has antigenic specificity for a mutated KRAS epitope, the mutated KRAS epitope comprising or consisting of the amino acid sequence of GADGVGKSA (mutated $KRAS_{10-18}$; SEQ ID NO: 8) or GADGVGKSAL (mutated $KRAS_{10-19}$; SEQ ID NO: 6).

[0021] In an embodiment of the invention, the inventive TCRs are able to recognize mutated KRAS within the context of an HLA-Cw8 molecule. In this regard, the TCR may elicit an immune response upon binding to mutated KRAS within the context of an HLA-Cw8 molecule. The inventive TCRs are able to recognize mutated KRAS that is presented by an HLA-Cw8 molecule and may bind to the HLA-Cw8 molecule in addition to mutated KRAS. Exemplary HLA-Cw8 molecules, in the context of which the inventive TCRs recognize mutated KRAS, include those encoded by the HLA-Cw*0801, HLA-Cw*0802, HLA-Cw*0803, HLA-Cw*0804, HLA-Cw*0805, HLA-Cw*0806, HLA-Cw*0807, HLA-Cw*0808, and HLA-Cw*0809 alleles. In a preferred embodiment, the TCRs recognize mutated KRAS within the context of an HLA-Cw*0802 molecule.

[0022] In an embodiment of the invention, in addition to having the ability to recognize mutated KRAS within the context of an HLA-Cw8 molecule, one of the inventive TCRs (TRAV12-2/TRBV10-2 (Table 5)) is also able to recognize mutated KRAS within the context of an HLA-Cw5 molecule. In this regard, the TCR may elicit an immune response upon binding to mutated KRAS within the context of an HLA-Cw5 molecule. The inventive TCR is able to recognize mutated KRAS that is presented by an HLA-Cw5 molecule and may bind to the HLA-Cw5 molecule in addition to mutated KRAS. Exemplary HLA-Cw5 molecules, in the context of which the inventive TCR recognizes mutated KRAS, include those encoded by the HLA-Cw*0501, HLA-Cw*0502, HLA-Cw*0503, HLA-Cw*0504, HLA-Cw*0505, HLA-Cw*0506, HLA- HLA-Cw*0508, HLA-Cw*0509, and HLA-Cw*0510 alleles. In a preferred embodiment, the TCR recognizes mutated KRAS within the context of an HLA-Cw*0501 molecule. The amino acid sequences of HLA-Cw*0802 and HLA-Cw*0501 differ from one another by only two amino acid residues. Without being

bound to a particular theory or mechanism, it is believed that the TRAV12-2/TRBV10-2 TCR may also recognize mutated KRAS that is presented by other HLA molecules that are similar to one or both of HLA-Cw*0802 and HLA-Cw*0501.

[0023] The TCRs of the invention provide many advantages, including when expressed by cells used for adoptive cell transfer. Mutated KRAS is expressed by cancer cells and is not expressed by normal, noncancerous cells. Without being bound to a particular theory or mechanism, it is believed that the inventive TCRs advantageously target the destruction of cancer cells while minimizing or eliminating the destruction of normal, non-cancerous cells, thereby reducing, for example, by minimizing or eliminating, toxicity. Moreover, the inventive TCRs may, advantageously, successfully treat or prevent mutated KRAS-positive cancers that do not respond to other types of treatment such as, for example, chemotherapy, surgery, or radiation. Additionally, the inventive TCRs may provide highly avid recognition of mutated KRAS, which may provide the ability to recognize unmanipulated tumor cells (e.g., tumor cells that have not been treated with interferon (IFN)-γ, transfected with a vector encoding one or both of mutated KRAS and HLA-Cw*0802, pulsed with a KRAS peptide with the G12D mutation, or a combination thereof). Moreover, the HLA-Cw*0802 allele is expressed in up to about 8% and about 11% of American Caucasian and African American ethnicities, respectively. Accordingly, the inventive TCRs may increase the number of immunotherapy-eligible cancer patients to include those patients that express the HLA-Cw*0802 allele who may not be eligible for immunotherapy using TCRs that recognize antigen in the context of other MHC molecules.

[0024] The phrase "antigenic specificity," as used herein, means that the TCR can specifically bind to and immunologically recognize mutated KRAS with high avidity. For example, a TCR may be considered to have "antigenic specificity" for mutated KRAS if about 1 x 10^4 to about 1 x 10^5 T cells expressing the TCR secrete at least about 200 pg/mL or more (e.g., 200 pg/mL or more, 300 pg/mL or more, 400 pg/mL or more, 500 pg/mL or more, 600 pg/mL or more, 700 pg/mL or more, 1000 pg/mL or more, 5,000 pg/mL or more, 7,000 pg/mL or more, 10,000 pg/mL or more, 20,000 pg/mL or more, or a range defined by any two of the foregoing values) of IFN-γ upon co-culture with (a) antigen-negative HLA-Cw*0802$^+$ target cells pulsed with a low concentration of mutated KRAS peptide (e.g., about 0.05 ng/mL to about 10 ng/mL, 1 ng/mL, 2 ng/mL, 5 ng/mL, 8 ng/mL, 10 ng/mL, or a range defined by any two of the foregoing values) or (b) antigen-negative HLA-Cw*0802$^+$ target cells into which a nucleotide sequence encoding mutated KRAS has been introduced such

that the target cell expresses mutated KRAS. Cells expressing the inventive TCRs may also secrete IFN-γ upon co-culture with antigen-negative HLA-Cw*0802$^+$ target cells pulsed with higher concentrations of mutated KRAS peptide.

[0025] Alternatively or additionally, a TCR may be considered to have "antigenic specificity" for mutated KRAS if T cells expressing the TCR secrete at least twice as much IFN-γ upon co-culture with (a) antigen-negative HLA-Cw*0802$^+$ target cells pulsed with a low concentration of mutated KRAS peptide or (b) antigen-negative HLA-Cw*0802$^+$ target cells into which a nucleotide sequence encoding mutated KRAS has been introduced such that the target cell expresses mutated KRAS as compared to the amount of IFN-γ expressed by a negative control. The negative control may be, for example, (i) T cells expressing the TCR, co-cultured with (a) antigen-negative HLA-Cw*0802$^+$ target cells pulsed with the same concentration of an irrelevant peptide (e.g., some other peptide with a different sequence from the mutated KRAS peptide) or (b) antigen-negative HLA-Cw*0802$^+$ target cells into which a nucleotide sequence encoding an irrelevant peptide has been introduced such that the target cell expresses the irrelevant peptide, or (ii) untransduced T cells (e.g., derived from PBMC, which do not express the TCR) co-cultured with (a) antigen-negative HLA-Cw*0802$^+$ target cells pulsed with the same concentration of mutated KRAS peptide or (b) antigen-negative HLA-Cw*0802$^+$ target cells into which a nucleotide sequence encoding mutated KRAS has been introduced such that the target cell expresses mutated KRAS. IFN-γ secretion may be measured by methods known in the art such as, for example, enzyme-linked immunosorbent assay (ELISA).

[0026] Alternatively or additionally, a TCR may be considered to have "antigenic specificity" for mutated KRAS if at least twice as many of the numbers of T cells expressing the TCR secrete IFN-γ upon co-culture with (a) antigen-negative HLA-Cw*0802$^+$ target cells pulsed with a low concentration of mutated KRAS peptide or (b) antigen-negative HLA-Cw*0802$^+$ target cells into which a nucleotide sequence encoding mutated KRAS has been introduced such that the target cell expresses mutated KRAS as compared to the numbers of negative control T cells that secrete IFN-γ. The concentration of peptide and the negative control may be as described herein with respect to other aspects of the invention. The numbers of cells secreting IFN-γ may be measured by methods known in the art such as, for example, ELISPOT.

[0027] Alternatively or additionally, a TCR may be considered to have "antigenic specificity" for mutated KRAS if T cells expressing the TCR upregulate expression of one or

more T-cell activation markers as measured by, for example, flow cytometry after stimulation with target cells expressing mutated KRAS. Examples of T-cell activation markers include 4-1BB, OX40, CD107a, CD69, and cytokines that are upregulated upon antigen stimulation (e.g., tumor necrosis factor (TNF), interleukin (IL)-2, etc.).

[0028] The invention provides a TCR comprising two polypeptides (i.e., polypeptide chains), such as an alpha (α) chain of a TCR, a beta (β) chain of a TCR, a gamma (γ) chain of a TCR, a delta (δ) chain of a TCR, or a combination thereof. The polypeptides of the inventive TCR can comprise any amino acid sequence, provided that the TCR has antigenic specificity for mutated KRAS.

[0029] In an embodiment of the invention, the TCR comprises two polypeptide chains, each of which comprises a variable region comprising a complementarity determining region (CDR)1, a CDR2, and a CDR3 of a TCR. In an embodiment of the invention, the TCR comprises a first polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 9 (CDR1 of α chain), a CDR2 comprising the amino acid sequence of SEQ ID NO: 10 (CDR2 of α chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 11 (CDR3 of α chain), and a second polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 12 (CDR1 of β chain), a CDR2 comprising the amino acid sequence of SEQ ID NO: 13 (CDR2 of β chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 14 (CDR3 of β chain).

[0030] In another embodiment of the invention, the TCR comprises a first polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 17 (CDR1 of α chain), a CDR2 comprising the amino acid sequence of SEQ ID NO: 18 (CDR2 of α chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 19 (CDR3 of α chain), and a second polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 20 (CDR1 of β chain), a CDR2 comprising the amino acid sequence of SEQ ID NO: 21 (CDR2 of β chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 22 (CDR3 of β chain).

[0031] In another embodiment of the invention, the TCR comprises a first polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 25 (CDR1 of α chain), a CDR2 comprising the amino acid sequence of SEQ ID NO: 26 (CDR2 of α chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 27 (CDR3 of α chain), and a second polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 28 (CDR1 of β chain), a CDR2 comprising the amino acid sequence of SEQ ID NO:

29 (CDR2 of β chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 30 (CDR3 of β chain).

[0032] In another embodiment of the invention, the TCR comprises a first polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 33 (CDR1 of α chain), a CDR2 comprising the amino acid sequence of SEQ ID NO: 34 (CDR2 of α chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 35 (CDR3 of α chain), and a second polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 36 (CDR1 of β chain), a CDR2 comprising the amino acid sequence of SEQ ID NO: 37 (CDR2 of β chain), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 38 (CDR3 of β chain).

[0033] In this regard, the inventive TCR can comprise any one or more of the amino acid sequences selected from the group consisting of SEQ ID NOs: 9-14, 17-22, 25-30, and 33-38. In an embodiment of the invention, the TCR comprises the amino acid sequences of: (i) SEQ ID NO: 9-11; (ii); SEQ ID NOs: 12-14; (iii) SEQ ID NOs: 17-19; (iv) SEQ ID NOs: 20-22; (v) SEQ ID NOs: 25-27; (vi) SEQ ID NOs: 28-30; (vii) SEQ ID NOs: 33-35; or (viii) SEQ ID NOs: 36-38. In an especially preferred embodiment, the TCR comprises the amino acid sequences of: (a) all of SEQ ID NOs: 9-14; (b) all of SEQ ID NOs: 17-22; (c) all of SEQ ID NOs: 25-30; or (d) all of SEQ ID NOs: 33-38.

[0034] In an embodiment of the invention, the TCR comprises an amino acid sequence of a variable region of a TCR comprising the CDRs set forth above. In this regard, the TCR can comprise the amino acid sequence of: SEQ ID NO: 15 (variable region of α chain); SEQ ID NO: 23 (variable region of α chain); SEQ ID NO: 31 (variable region of α chain); SEQ ID NO: 39 (variable region of α chain); SEQ ID NO: 16 (variable region of β chain); SEQ ID NO: 24 (variable region of β chain); SEQ ID NO: 32 (variable region of β chain); SEQ ID NO: 40 (variable region of β chain); both SEQ ID NOs: 15 and 16; both SEQ ID NOs: 23 and 24; both SEQ ID NOs: 31 and 32; or both SEQ ID NOs: 39 and 40. Preferably, the inventive TCR comprises the amino acid sequences of (i) both of SEQ ID NOs: 15-16; (ii) both of SEQ ID NOs: 23-24; (iii) both of SEQ ID NOs: 31-32; or (iv) both of SEQ ID NOs: 39-40.

[0035] The inventive TCRs may further comprise an α chain constant region and a β chain constant region. The constant region may be derived from any suitable species such as, e.g., human or mouse. In an embodiment of the invention, the TCRs further comprise a murine α and β chain constant regions or human α and β chain constant regions. As used

herein, the term "murine" or "human," when referring to a TCR or any component of a TCR described herein (e.g., complementarity determining region (CDR), variable region, constant region, α chain, and/or β chain), means a TCR (or component thereof) which is derived from a mouse or a human, respectively, i.e., a TCR (or component thereof) that originated from or was, at one time, expressed by a mouse T cell or a human T cell, respectively.

[0036] In an embodiment of the invention, the TCRs further comprise human α and β chain constant regions. In this regard, the TCR can comprise the amino acid sequence of SEQ ID NO: 41, wherein X at position 1 is any naturally occurring amino acid residue (the constant region of a human α chain), SEQ ID NO: 42 (the constant region of a human β chain), SEQ ID NO: 43 (the constant region of a human β chain), both SEQ ID NOs: 41 and 42, or both SEQ ID NOs: 41 and 43. In an embodiment of the invention, the TCR comprises any of the human constant regions described herein in combination with any of the CDR regions described herein. In this regard, the TCR may comprise the amino acid sequences of: (a) all of SEQ ID NOs: 9-14, 41, and 42; (b) all of SEQ ID NOs: 17-22, 41, and 42; (c) all of SEQ ID NOs: 25-30, 41, and 42; (d) all of SEQ ID NOs: 33-38, 41, and 42; (e) all of SEQ ID NOs: 9-14, 41, and 43; (f) all of SEQ ID NOs: 17-22, 41, and 43; (g) all of SEQ ID NOs: 25-30, 41, and 43; or (h) all of SEQ ID NOs: 33-38, 41, and 43. In an embodiment of the invention, the TCR comprises any of the human constant regions described herein in combination with any of the variable regions described herein. In this regard, the TCR may comprise the amino acid sequences of: (i) all of SEQ ID NOs: 15-16, 41, and 42; (ii) all of SEQ ID NOs: 23-24, 41, and 42; (iii) all of SEQ ID NOs: 31-32, 41, and 42; (iv) all of SEQ ID NOs: 39-42; (v) all of SEQ ID NOs: 15-16, 41, and 43; (vi) all of SEQ ID NOs: 23-24, 41, and 43; (vii) all of SEQ ID NOs: 31-32, 41, and 43; or (viii) all of SEQ ID NOs: 39-40, 41, and 43.

[0037] An embodiment of the invention provides a chimeric TCR comprising a human variable region and a murine constant region, wherein the TCR has antigenic specificity for mutated KRAS presented in the context of an HLA-Cw8 molecule. The murine constant region may provide any one or more advantages. For example, the murine constant region may diminish mispairing of the inventive TCR with the endogenous TCRs of the host cell into which the inventive TCR is introduced. Alternatively or additionally, the murine constant region may increase expression of the inventive TCR as compared to the same TCR with a human constant region. The chimeric TCR may comprise the amino acid sequence of SEQ ID NO: 44 (wild-type (WT) murine α chain constant region), SEQ ID NO: 45 (WT

murine β chain constant region), or both SEQ ID NOs: 44 and 45. Preferably, the inventive TCR comprises the amino acid sequences of both SEQ ID NOs: 44 and 45. The chimeric TCR may comprise any of the murine constant regions described herein in combination with any of the CDR regions as described herein with respect to other aspects of the invention. In this regard, the TCR may comprise the amino acid sequences of: (a) all of SEQ ID NOs: 9-14, 44, and 45; (b) all of SEQ ID NOs: 17-22, 44, and 45; (c) all of SEQ ID NOs: 25-30, 44, and 45; or (d) all of SEQ ID NOs: 33-38, 44, and 45. In another embodiment of the invention, the chimeric TCR may comprise any of the murine constant regions described herein in combination with any of the variable regions described herein with respect to other aspects of the invention. In this regard, the TCR may comprise the amino acid sequences of: (i) SEQ ID NOs: 15-16, 44, and 45; (ii) SEQ ID NOs: 23-24, 44, and 45; (iii) SEQ ID NOs: 31-32, 44, and 45; or (iv) SEQ ID NOs: 39-40, 44, and 45;

[0038] In an embodiment of the invention, the TCR comprises a substituted constant region. In this regard, the TCR may comprise the amino acid sequence of any of the TCRs described herein with one, two, three, or four amino acid substitution(s) in the constant region of one or both of the α and β chain. Preferably, the TCR comprises a murine constant region with one, two, three, or four amino acid substitution(s) in the murine constant region of one or both of the α and β chains. In an especially preferred embodiment, the TCR comprises a murine constant region with one, two, three, or four amino acid substitution(s) in the murine constant region of the α chain and one amino acid substitution in the murine constant region of the β chain. In some embodiments, the TCRs comprising the substituted constant region advantageously provide one or more of increased recognition of mutated $KRAS^+$ targets, increased expression by a host cell, diminished mispairing with endogenous TCRs, and increased anti-tumor activity as compared to the parent TCR comprising an unsubstituted (wild-type) constant region. In general, the substituted amino acid sequences of the murine constant regions of the TCR α and β chains, SEQ ID NOs: 46 and 47, respectively, correspond with all or portions of the unsubstituted murine constant region amino acid sequences SEQ ID NOs: 44 and 45, respectively, with SEQ ID NO: 46 having one, two, three, or four amino acid substitution(s) when compared to SEQ ID NO: 44 and SEQ ID NO: 47 having one amino acid substitution when compared to SEQ ID NO: 45. In this regard, an embodiment of the invention provides a TCR comprising the amino acid sequences of (a) SEQ ID NO: 46 (constant region of α chain), wherein (i) X at position 48 is Thr or Cys; (ii) X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; (iii) X at position 114 is Met,

Ala, Val, Leu, Ile, Pro, Phe, or Trp; and (iv) X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; and (b) SEQ ID NO: 47 (constant region of β chain), wherein X at position 57 is Ser or Cys. In an embodiment of the invention, the TCR comprising SEQ ID NO: 46 does not comprise SEQ ID NO: 44 (unsubstituted murine constant region of α chain). In an embodiment of the invention, the TCR comprising SEQ ID NO: 47 does not comprise SEQ ID NO: 45 (unsubstituted murine constant region of β chain).

[0039] In an embodiment of the invention, the substituted constant region includes cysteine substitutions in the constant region of one or both of the α and β chains to provide a cysteine-substituted TCR. Opposing cysteines in the α and the β chains provide a disulfide bond that links the constant regions of the α and the β chains of the substituted TCR to one another and which is not present in a TCR comprising the unsubstituted murine constant regions. In this regard, the TCR may be a cysteine-substituted TCR in which one or both of the native Thr at position 48 (Thr48) of SEQ ID NO: 44 and the native Ser at position 57 (Ser57) of SEQ ID NO: 45 may be substituted with Cys. Preferably, both of the native Thr48 of SEQ ID NO: 44 and the native Ser57 of SEQ ID NO: 45 are substituted with Cys. In an embodiment, the cysteine-substituted TCR comprises an α chain constant region comprising the amino acid sequence of SEQ ID NO: 46, wherein X at position 48 is Cys, X at position 112 is the native Ser, X at position 114 is the native Met, and X at position 115 is the native Gly, and a β chain constant region comprising the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 is Cys. The cysteine-substituted TCRs of the invention may include the substituted constant region in addition to any of the CDRs or variable regions described herein.

[0040] In an embodiment of the invention, the substituted amino acid sequence includes substitutions of one, two, or three amino acids in the transmembrane (TM) domain of the constant region of one or both of the α and β chains with a hydrophobic amino acid to provide a hydrophobic amino acid-substituted TCR. The hydrophobic amino acid substitution(s) in the TM domain of the TCR may increase the hydrophobicity of the TM domain of the TCR as compared to a TCR that lacks the hydrophobic amino acid substitution(s) in the TM domain. In this regard, the TCR is a hydrophobic amino acid-substituted TCR in which one, two, or three of the native Ser112, Met114, and Gly115 of SEQ ID NO: 44 may, independently, be substituted with Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; preferably with Leu, Ile, or Val. Preferably, all three of the native Ser112, Met114, and Gly115 of SEQ ID NO: 44 may, independently, be substituted with Ala, Val, Leu, Ile, Pro,

Phe, Met, or Trp; preferably with Leu, Ile, or Val. In an embodiment, the hydrophobic amino acid-substituted TCR comprises an α chain constant region comprising the amino acid sequence of SEQ ID NO: 46, wherein X at position 48 is the native Thr, X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp, X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp, and X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp, and a β chain constant region comprising the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 is the native Ser, wherein the hydrophobic amino acid-substituted TCR comprising SEQ ID NO: 46 does not comprise SEQ ID NO: 44 (unsubstituted murine constant region of α chain). In a preferred embodiment, the hydrophobic amino acid-substituted TCR comprises an α chain constant region comprising the amino acid sequence of SEQ ID NO: 46, wherein X at position 48 is the native Thr, X at position 112 is Leu, X at position 114 is Ile, and X at position 115 is Val, and a β chain constant region comprising the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 is the native Ser. The hydrophobic amino acid-substituted TCRs of the invention may include the substituted constant region in addition to any of the CDRs or variable regions described herein.

[0041] In an embodiment of the invention, the substituted amino acid sequence includes the cysteine substitutions in the constant region of one or both of the α and β chains in combination with the substitution(s) of one, two, or three amino acids in the transmembrane (TM) domain of the constant region of one or both of the α and β chains with a hydrophobic amino acid (also referred to herein as "cysteine-substituted, hydrophobic amino acid-substituted TCR"). In this regard, the TCR is a cysteine-substituted, hydrophobic amino acid-substituted TCR in which the native Thr48 of SEQ ID NO: 46 is substituted with Cys; one, two, or three of the native Ser112, Met114, and Gly115 of SEQ ID NO: 46 are, independently, substituted with Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; preferably with Leu, Ile, or Val; and the native Ser57 of SEQ ID NO: 47 is substituted with Cys. Preferably, all three of the native Ser112, Met114, and Gly115 of SEQ ID NO: 46 may, independently, be substituted with Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; preferably with Leu, Ile, or Val. In an embodiment, the cysteine-substituted, hydrophobic amino acid-substituted TCR comprises an α chain comprising the amino acid sequence of SEQ ID NO: 46, wherein X at position 48 is Cys, X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp, X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp, and X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp, and a β chain comprising the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 is Cys, wherein SEQ ID NO: 46 does not comprise SEQ ID NO: 44

(unsubstituted α chain) and SEQ ID NO: 47 does not comprise SEQ ID NO: 45 (unsubstituted β chain). Preferably, the cysteine-substituted, hydrophobic amino acid-substituted TCR comprises an α chain comprising the amino acid sequence of SEQ ID NO: 46, wherein X at position 48 is Cys, X at position 112 is Leu, X at position 114 is Ile, X at position 115 is Val, and a β chain comprising the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 is Cys. In this regard, the cysteine-substituted, hydrophobic amino acid-substituted TCR comprises an α chain constant region comprising the amino acid sequence of SEQ ID NO: 48 and a β chain constant region comprising the amino acid sequence of SEQ ID NO: 49. The cysteine-substituted, hydrophobic amino acid-substituted TCRs of the invention may include the substituted constant region in addition to any of the CDRs or variable regions described herein.

[0042] In an embodiment of the invention, the inventive cysteine-substituted, hydrophobic amino acid-substituted TCR can comprise an α chain of a TCR and a β chain of a TCR. Each of the α chain and β chain of the inventive TCR can independently comprise any amino acid sequence. In this regard, the α chain of the inventive TCR can comprise the amino acid sequence of SEQ ID NO: 50, 52, 54, or 56. An α chain of this type can be paired with any β chain of a TCR. In this regard, the β chain of the inventive TCR can comprise the amino acid sequence of SEQ ID NO: 51, 53, 55, or 57. The inventive TCR, therefore, can comprise the amino acid sequence of SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, both SEQ ID NOs: 50 and 51, both SEQ ID NOs: 52 and 53, both SEQ ID NO: 54 and 55, or both SEQ ID NOs: 56 and 57. Preferably, the inventive TCR comprises the amino acid sequences of (1) both of SEQ ID NOs: 50-51; (2) both of SEQ ID NOs: 52-53; (3) both of SEQ ID NOs: 54-55; or (4) both of SEQ ID NOs: 56-57.

[0043] Also provided by the invention is a polypeptide comprising a functional portion of any of the TCRs described herein. The term "polypeptide," as used herein, includes oligopeptides and refers to a single chain of amino acids connected by one or more peptide bonds.

[0044] With respect to the inventive polypeptides, the functional portion can be any portion comprising contiguous amino acids of the TCR of which it is a part, provided that the functional portion specifically binds to mutated KRAS. The term “functional portion,” when used in reference to a TCR, refers to any part or fragment of the TCR of the invention, which part or fragment retains the biological activity of the TCR of which it is a part (the parent

TCR). Functional portions encompass, for example, those parts of a TCR that retain the ability to specifically bind to mutated KRAS (e.g., within the context of an HLA-Cw*0802 molecule), or detect, treat, or prevent cancer, to a similar extent, the same extent, or to a higher extent, as the parent TCR. In reference to the parent TCR, the functional portion can comprise, for instance, about 10%, 25%, 30%, 50%, 68%, 80%, 90%, 95%, or more, of the parent TCR.

[0045] The functional portion can comprise additional amino acids at the amino or carboxy terminus of the portion, or at both termini, which additional amino acids are not found in the amino acid sequence of the parent TCR. Desirably, the additional amino acids do not interfere with the biological function of the functional portion, e.g., specifically binding to mutated KRAS; and/or having the ability to detect cancer, treat or prevent cancer, etc. More desirably, the additional amino acids enhance the biological activity, as compared to the biological activity of the parent TCR.

[0046] The polypeptide can comprise a functional portion of either or both of the α and β chains of the TCRs of the invention, such as a functional portion comprising one or more of the CDR1, CDR2, and CDR3 of the variable region(s) of the α chain and/or β chain of a TCR of the invention. In an embodiment of the invention, the polypeptide can comprise the amino acid sequence of SEQ ID NO: 9 (CDR1 of α chain), SEQ ID NO: 10 (CDR2 of α chain), SEQ ID NO: 11 (CDR3 of α chain), SEQ ID NO: 12 (CDR1 of β chain), SEQ ID NO: 13 (CDR2 of β chain), SEQ ID NO: 14 (CDR3 of β chain), or a combination thereof. In another embodiment of the invention, the polypeptide can comprise the amino acid sequence of SEQ ID NO: 17 (CDR1 of α chain), SEQ ID NO: 18 (CDR2 of α chain), SEQ ID NO: 19 (CDR3 of α chain), SEQ ID NO: 20 (CDR1 of β chain), SEQ ID NO: 21 (CDR2 of β chain), SEQ ID NO: 22 (CDR3 of β chain), or a combination thereof. In another embodiment of the invention, the polypeptide can comprise the amino acid sequence of SEQ ID NO: 25 (CDR1 of α chain), SEQ ID NO: 26 (CDR2 of α chain), SEQ ID NO: 27 (CDR3 of α chain), SEQ ID NO: 28 (CDR1 of β chain), SEQ ID NO: 29 (CDR2 of β chain), SEQ ID NO: 30 (CDR3 of β chain), or a combination thereof. In another embodiment of the invention, the polypeptide can comprise the amino acid sequence of SEQ ID NO: 33 (CDR1 of α chain), SEQ ID NO: 34 (CDR2 of α chain), SEQ ID NO: 35 (CDR3 of α chain), SEQ ID NO: 36 (CDR1 of β chain), SEQ ID NO: 37 (CDR2 of β chain), SEQ ID NO: 38 (CDR3 of β chain), or a combination thereof. Preferably, the polypeptide comprises the amino acid sequences of (a)

both of SEQ ID NOs: 9-14; (b) both of SEQ ID NOs: 17-22; (c) both of SEQ ID NOs: 25-30; or (d) both of SEQ ID NOs: 33-38.

[0047] In an embodiment of the invention, the inventive polypeptide can comprise, for instance, the variable region of the inventive TCR comprising a combination of the CDR regions set forth above. In this regard, the polypeptide can comprise the amino acid sequence of SEQ ID NO: 15 (variable region of α chain), SEQ ID NO: 16 (variable region of β chain), both SEQ ID NOs: 15 and 16, SEQ ID NO: 23 (variable region of α chain), SEQ ID NO: 24 (variable region of β chain), both SEQ ID NOs: 23 and 24, SEQ ID NO: 31 (variable region of α chain), SEQ ID NO: 32 (variable region of β chain), both SEQ ID NOs: 31 and 32, SEQ ID NO: 39 (variable region of α chain), SEQ ID NO: 40 (variable region of β chain), or both SEQ ID NOs: 39 and 40. Preferably, the polypeptide comprises the amino acid sequences of (i) both SEQ ID NOs: 15 and 16, (ii) both SEQ ID NOs: 23 and 24, (iii) both SEQ ID NOs: 31 and 32, or (iv) both SEQ ID NOs: 39 and 40.

[0048] In an embodiment of the invention, the inventive polypeptide can further comprise the constant region of the inventive TCR set forth above. In this regard, the polypeptide can further comprise the amino acid sequence of SEQ ID NO: 41 (human constant region of α chain), SEQ ID NO: 42 (human constant region of β chain), SEQ ID NO: 43 (human constant region of β chain), SEQ ID NO: 44 (WT murine constant region of α chain), SEQ ID NO: 45 (WT murine constant region of β chain), SEQ ID NO: 46 (substituted murine constant region of α chain), SEQ ID NO: 47 (substituted murine constant region of β chain), SEQ ID NO: 48 (cysteine-substituted, hydrophobic amino acid-substituted murine constant region of α chain), SEQ ID NO: 49 (cysteine-substituted, hydrophobic amino acid-substituted murine constant region of α chain), both SEQ ID NOs: 44 and 45, both SEQ ID NOs: 46 and 47, or both SEQ ID NOs: 48 and 49, both SEQ ID NOs: 41 and 42, or both SEQ ID NOs: 41 and 43. Preferably, the polypeptide further comprises the amino acid sequences of (i) both SEQ ID NOs: 44 and 45, (ii) both SEQ ID NOs: 46 and 47, (iii) both SEQ ID NOs: 48 and 49, (iv) both SEQ ID NOs: 41 and 42, or (v) both SEQ ID NOs: 41 and 43 in combination with any of the CDR regions or variable regions described herein with respect to other aspects of the invention.

[0049] In an embodiment of the invention, the inventive polypeptide can comprise the entire length of an α or β chain of the TCR described herein. In this regard, the inventive polypeptide can comprise the amino acid sequence of SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, or SEQ ID

NO: 57. Alternatively, the polypeptide of the invention can comprise both chains of the TCRs described herein. For example, the polypeptide of the invention can comprise both amino acid sequences of SEQ ID NOs: 50 and 51, both SEQ ID NOs: 52 and 53, both SEQ ID NOs: 54 and 55, or both SEQ ID NOs: 56 and 57. Preferably, the polypeptide comprises the amino acid sequences of (1) both SEQ ID NOs: 50-51; (2) both SEQ ID NOs: 52-53; (3) both SEQ ID NOs: 54-55; or (4) both SEQ ID NOs: 56-57.

[0050] The invention further provides a protein comprising at least one of the polypeptides described herein. By "protein" is meant a molecule comprising one or more polypeptide chains.

[0051] In an embodiment, the protein of the invention can comprise (a) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 9-11 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NOs: 12-14; (b) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 17-19 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 20-22; (c) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 25-27 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 28-30; or (d) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 33-35 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 36-38.

[0052] In another embodiment of the invention, the protein may comprise (i) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 15 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 16; (ii) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 23 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 24; (iii) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 31 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 32; or (iv) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 39 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 40.

[0053] The inventive protein may further comprise any of the constant regions described herein with respect to other aspects of the invention. In this regard, in an embodiment of the invention, the first polypeptide chain may further comprise the amino acid sequence of SEQ ID NO: 46, wherein: (i) X at position 48 of SEQ ID NO: 46 is Thr or Cys; (ii) X at position 112 of SEQ ID NO: 46 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; (iii) X at position 114 of SEQ ID NO: 46 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; and (iv) X at position 115 of

SEQ ID NO: 46 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; and (B) the second polypeptide chain may further comprise the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 of SEQ ID NO: 47 is Ser or Cys. In another embodiment of the invention, the first polypeptide chain may further comprise the amino acid sequence of SEQ ID NO: 41 (constant region of human α chain), SEQ ID NO: 44 (WT constant region of murine α chain), or SEQ ID NO: 48 (cysteine-substituted, hydrophobic amino acid-substituted murine constant region of α chain), and the second polypeptide chain may further comprise the amino acid sequence of SEQ ID NO: 42 (constant region of human β chain), SEQ ID NO: 43 (constant region of human β chain), SEQ ID NO: 45 (WT constant region of murine β chain), or SEQ ID NO: 49 (cysteine-substituted, hydrophobic amino acid-substituted murine constant region of β chain).

[0054] Alternatively or additionally, the protein of the invention can comprise (1) a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 50 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 51; (2) a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 52 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 53; (3) a first polypeptide chain comprising the amino acid sequence of SEQ ID NOs: 54 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 55; or (4) a first polypeptide chain comprising the amino acid sequence of SEQ ID NOs: 56 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 57. In this instance, the protein of the invention can be a TCR. Alternatively, if, for example, the protein comprises a single polypeptide chain comprising the amino acid sequences of both SEQ ID NOs: 50 and 51, both SEQ ID NOs: 52 and 53, both SEQ ID NOs: 54 and 55, or both SEQ ID NOs: 55 and 56, or if the first and/or second polypeptide chain(s) of the protein further comprise(s) other amino acid sequences, e.g., an amino acid sequence encoding an immunoglobulin or a portion thereof, then the inventive protein can be a fusion protein. In this regard, the invention also provides a fusion protein comprising at least one of the inventive polypeptides described herein along with at least one other polypeptide. The other polypeptide can exist as a separate polypeptide of the fusion protein, or can exist as a polypeptide, which is expressed in frame (in tandem) with one of the inventive polypeptides described herein. The other polypeptide can encode any peptidic or proteinaceous molecule, or a portion thereof, including, but not limited to an immunoglobulin, CD3, CD4, CD8, an MHC molecule, a CD1 molecule, e.g., CD1a, CD1b, CD1c, CD1d, etc.

[0055] The fusion protein can comprise one or more copies of the inventive polypeptide and/or one or more copies of the other polypeptide. For instance, the fusion protein can comprise 1, 2, 3, 4, 5, or more, copies of the inventive polypeptide and/or of the other polypeptide. Suitable methods of making fusion proteins are known in the art, and include, for example, recombinant methods.

[0056] In some embodiments of the invention, the TCRs, polypeptides, and proteins of the invention may be expressed as a single protein comprising a linker peptide linking the α chain and the β chain. In this regard, the TCRs, polypeptides, and proteins of the invention may further comprise a linker peptide. The linker peptide may advantageously facilitate the expression of a recombinant TCR, polypeptide, and/or protein in a host cell. The linker peptide may comprise any suitable amino acid sequence. For example, the linker peptide may comprise SEQ ID NO: 58. Upon expression of the construct including the linker peptide by a host cell, the linker peptide may be cleaved, resulting in separated α and β chains. In an embodiment of the invention, the TCR, polypeptide, or protein may comprise an amino acid sequence comprising a full-length α chain, a full-length β chain, and a linker peptide positioned between the α and β chains.

[0057] The protein of the invention can be a recombinant antibody, or an antigen binding portion thereof, comprising at least one of the inventive polypeptides described herein. As used herein, "recombinant antibody" refers to a recombinant (e.g., genetically engineered) protein comprising at least one of the polypeptides of the invention and a polypeptide chain of an antibody, or an antigen binding portion thereof. The polypeptide of an antibody, or antigen binding portion thereof, can be a heavy chain, a light chain, a variable or constant region of a heavy or light chain, a single chain variable fragment (scFv), or an Fc, Fab, or $F(ab)_2'$ fragment of an antibody, etc. The polypeptide chain of an antibody, or an antigen binding portion thereof, can exist as a separate polypeptide of the recombinant antibody. Alternatively, the polypeptide chain of an antibody, or an antigen binding portion thereof, can exist as a polypeptide, which is expressed in frame (in tandem) with the polypeptide of the invention. The polypeptide of an antibody, or an antigen binding portion thereof, can be a polypeptide of any antibody or any antibody fragment, including any of the antibodies and antibody fragments described herein.

[0058] Included in the scope of the invention are functional variants of the inventive TCRs, polypeptides, or proteins described herein. The term "functional variant," as used herein, refers to a TCR, polypeptide, or protein having substantial or significant sequence

identity or similarity to a parent TCR, polypeptide, or protein, which functional variant retains the biological activity of the TCR, polypeptide, or protein of which it is a variant. Functional variants encompass, for example, those variants of the TCR, polypeptide, or protein described herein (the parent TCR, polypeptide, or protein) that retain the ability to specifically bind to mutated KRAS for which the parent TCR has antigenic specificity or to which the parent polypeptide or protein specifically binds, to a similar extent, the same extent, or to a higher extent, as the parent TCR, polypeptide, or protein. In reference to the parent TCR, polypeptide, or protein, the functional variant can, for instance, be at least about 30%, 50%, 75%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or more identical in amino acid sequence to the parent TCR, polypeptide, or protein, respectively.

[0059] The functional variant can, for example, comprise the amino acid sequence of the parent TCR, polypeptide, or protein with at least one conservative amino acid substitution. Conservative amino acid substitutions are known in the art, and include amino acid substitutions in which one amino acid having certain physical and/or chemical properties is exchanged for another amino acid that has the same chemical or physical properties. For instance, the conservative amino acid substitution can be an acidic amino acid substituted for another acidic amino acid (e.g., Asp or Glu), an amino acid with a nonpolar side chain substituted for another amino acid with a nonpolar side chain (e.g., Ala, Gly, Val, Ile, Leu, Met, Phe, Pro, Trp, Val, etc.), a basic amino acid substituted for another basic amino acid (Lys, Arg, etc.), an amino acid with a polar side chain substituted for another amino acid with a polar side chain (Asn, Cys, Gln, Ser, Thr, Tyr, etc.), etc.

[0060] Alternatively or additionally, the functional variants can comprise the amino acid sequence of the parent TCR, polypeptide, or protein with at least one non-conservative amino acid substitution. In this case, it is preferable for the non-conservative amino acid substitution to not interfere with or inhibit the biological activity of the functional variant. Preferably, the non-conservative amino acid substitution enhances the biological activity of the functional variant, such that the biological activity of the functional variant is increased as compared to the parent TCR, polypeptide, or protein.

[0061] The TCR, polypeptide, or protein can consist essentially of the specified amino acid sequence or sequences described herein, such that other components of the TCR, polypeptide, or protein, e.g., other amino acids, do not materially change the biological activity of the TCR, polypeptide, or protein. In this regard, the inventive TCR, polypeptide, or protein can, for example, consist essentially of the amino acid sequence of SEQ ID NO:

50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, (1) both of SEQ ID NOs: 50-51; (2) both of SEQ ID NOs: 52-53; (3) both of SEQ ID NOs: 54-55; or (4) both of SEQ ID NOs: 56-57. Also, for instance, the inventive TCRs, polypeptides, or proteins can consist essentially of the amino acid sequence(s) of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 39, SEQ ID NO: 40, (i) both of SEQ ID NOs: 15-16; (ii) both of SEQ ID NOs: 23-24; (iii) both of SEQ ID NOs: 31-32; or (iv) both of SEQ ID NOs: 39-40. Furthermore, the inventive TCRs, polypeptides, or proteins can consist essentially of the amino acid sequences of (a) all of SEQ ID NOs: 9-14; (b) all of SEQ ID NOs: 17-22; (c) all of SEQ ID NOs: 25-30; or (d) all of SEQ ID NOs: 33-38.

[0062] The TCRs, polypeptides, and proteins of the invention can be of any length, i.e., can comprise any number of amino acids, provided that the TCRs, polypeptides, or proteins retain their biological activity, e.g., the ability to specifically bind to mutated KRAS; detect cancer in a mammal; or treat or prevent cancer in a mammal, etc. For example, the polypeptide can be in the range of from about 50 to about 5000 amino acids long, such as 50, 70, 75, 100, 125, 150, 175, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more amino acids in length. In this regard, the polypeptides of the invention also include oligopeptides.

[0063] The TCRs, polypeptides, and proteins of the invention can comprise synthetic amino acids in place of one or more naturally-occurring amino acids. Such synthetic amino acids are known in the art, and include, for example, aminocyclohexane carboxylic acid, norleucine, α-amino n-decanoic acid, homoserine, S-acetylaminomethyl-cysteine, trans-3- and trans-4-hydroxyproline, 4-aminophenylalanine, 4-nitrophenylalanine, 4-chlorophenylalanine, 4-carboxyphenylalanine, β-phenylserine β-hydroxyphenylalanine, phenylglycine, α-naphthylalanine, cyclohexylalanine, cyclohexylglycine, indoline-2-carboxylic acid, 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid, aminomalonic acid, aminomalonic acid monoamide, N'-benzyl-N'-methyl-lysine, N',N'-dibenzyl-lysine, 6-hydroxylysine, ornithine, α-aminocyclopentane carboxylic acid, α-aminocyclohexane carboxylic acid, α-aminocycloheptane carboxylic acid, α-(2-amino-2-norbornane)-carboxylic acid, α,γ-diaminobutyric acid, α,β-diaminopropionic acid, homophenylalanine, and α-tert-butylglycine.

[0064] The TCRs, polypeptides, and proteins of the invention can be glycosylated, amidated, carboxylated, phosphorylated, esterified, N-acylated, cyclized via, e.g., a disulfide

bridge, or converted into an acid addition salt and/or optionally dimerized or polymerized, or conjugated.

[0065] The TCR, polypeptide, and/or protein of the invention can be obtained by methods known in the art such as, for example, *de novo* synthesis. Also, polypeptides and proteins can be recombinantly produced using the nucleic acids described herein using standard recombinant methods. See, for instance, Green and Sambrook, Molecular Cloning: A Laboratory Manual, 4th ed., Cold Spring Harbor Press, Cold Spring Harbor, NY (2012). Alternatively, the TCRs, polypeptides, and/or proteins described herein can be commercially synthesized by companies, such as Synpep (Dublin, CA), Peptide Technologies Corp. (Gaithersburg, MD), and Multiple Peptide Systems (San Diego, CA). In this respect, the inventive TCRs, polypeptides, and proteins can be synthetic, recombinant, isolated, and/or purified.

[0066] Included in the scope of the invention are conjugates, e.g., bioconjugates, comprising any of the inventive TCRs, polypeptides, or proteins (including any of the functional portions or variants thereof), nucleic acids, recombinant expression vectors, host cells, populations of host cells, or antibodies, or antigen binding portions thereof. Conjugates, as well as methods of synthesizing conjugates in general, are known in the art.

[0067] An embodiment of the invention provides a nucleic acid comprising a nucleotide sequence encoding any of the TCRs, polypeptides, or proteins described herein. "Nucleic acid," as used herein, includes "polynucleotide," "oligonucleotide," and "nucleic acid molecule," and generally means a polymer of DNA or RNA, which can be single-stranded or double-stranded, which can contain natural, non-natural or altered nucleotides, and which can contain a natural, non-natural or altered internucleotide linkage, such as a phosphoroamidate linkage or a phosphorothioate linkage, instead of the phosphodiester found between the nucleotides of an unmodified oligonucleotide. In an embodiment, the nucleic acid comprises complementary DNA (cDNA). It is generally preferred that the nucleic acid does not comprise any insertions, deletions, inversions, and/or substitutions. However, it may be suitable in some instances, as discussed herein, for the nucleic acid to comprise one or more insertions, deletions, inversions, and/or substitutions.

[0068] Preferably, the nucleic acids of the invention are recombinant. As used herein, the term "recombinant" refers to (i) molecules that are constructed outside living cells by joining natural or synthetic nucleic acid segments to nucleic acid molecules that can replicate in a

living cell, or (ii) molecules that result from the replication of those described in (i) above. For purposes herein, the replication can be *in vitro* replication or *in vivo* replication.

[0069] The nucleic acids can be constructed based on chemical synthesis and/or enzymatic ligation reactions using procedures known in the art. See, for example, Green and Sambrook et al., *supra*. For example, a nucleic acid can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed upon hybridization (e.g., phosphorothioate derivatives and acridine substituted nucleotides). Examples of modified nucleotides that can be used to generate the nucleic acids include, but are not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N^6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N^6-substituted adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N^6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, 3-(3-amino-3-N-2-carboxypropyl) uracil, and 2,6-diaminopurine. Alternatively, one or more of the nucleic acids of the invention can be purchased from companies, such as Macromolecular Resources (Fort Collins, CO) and Synthegen (Houston, TX).

[0070] The nucleic acid can comprise any nucleotide sequence which encodes any of the TCRs, polypeptides, or proteins described herein. In an embodiment of the invention, the nucleic acid may comprise the nucleotide sequences of any one of SEQ ID NOs: 63-70 (Table 1). In an embodiment of the invention, the nucleic acid comprises the nucleotide sequences of both of SEQ ID NOs: 63-64, both of SEQ ID NOs: 65-66, both of SEQ ID NOs: 67-68, or both of SEQ ID NOs: 69-70.

TABLE 1

TCR ID	TCR chain	Nucleotide sequence of the indicated TCR chain variable region
1	Alpha (TRAV4*01)	SEQ ID NO: 63 (wild-type)

TCR ID	TCR chain	Nucleotide sequence of the indicated TCR chain variable region
	Beta (TRBV5-6*01) (A)	SEQ ID NO: 64 (wild-type)
2	Alpha (TRAV4*01)	SEQ ID NO: 65 (codon-optimized)
	Beta (TRBV5-6*01) (C)	SEQ ID NO: 66 (codon-optimized)
3	Alpha (TRAV4*01)	SEQ ID NO: 67 (wild-type)
	Beta (TRBV5-6*01) (B)	SEQ ID NO: 68 (wild-type)
4	Alpha (TRAV12-2*01)	SEQ ID NO: 69 (wild-type)
	Beta (TRBV10-2*01)	SEQ ID NO: 70 (wild-type)

[0071] In an embodiment of the invention, the nucleic acid comprises a codon-optimized nucleotide sequence encoding any of the TCRs, polypeptides, or proteins described herein. Without being bound to any particular theory or mechanism, it is believed that codon optimization of the nucleotide sequence increases the translation efficiency of the mRNA transcripts. Codon optimization of the nucleotide sequence may involve substituting a native codon for another codon that encodes the same amino acid, but can be translated by tRNA that is more readily available within a cell, thus increasing translation efficiency. Optimization of the nucleotide sequence may also reduce secondary mRNA structures that would interfere with translation, thus increasing translation efficiency.

[0072] The invention also provides a nucleic acid comprising a nucleotide sequence which is complementary to the nucleotide sequence of any of the nucleic acids described herein or a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of any of the nucleic acids described herein.

[0073] The nucleotide sequence which hybridizes under stringent conditions preferably hybridizes under high stringency conditions. By "high stringency conditions" is meant that the nucleotide sequence specifically hybridizes to a target sequence (the nucleotide sequence of any of the nucleic acids described herein) in an amount that is detectably stronger than non-specific hybridization. High stringency conditions include conditions which would distinguish a polynucleotide with an exact complementary sequence, or one containing only a few scattered mismatches from a random sequence that happened to have a few small regions (e.g., 3-10 bases) that matched the nucleotide sequence. Such small regions of

complementarity are more easily melted than a full-length complement of 14-17 or more bases, and high stringency hybridization makes them easily distinguishable. Relatively high stringency conditions would include, for example, low salt and/or high temperature conditions, such as provided by about 0.02-0.1 M NaCl or the equivalent, at temperatures of about 50-70 °C. Such high stringency conditions tolerate little, if any, mismatch between the nucleotide sequence and the template or target strand, and are particularly suitable for detecting expression of any of the inventive TCRs. It is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide.

[0074] The invention also provides a nucleic acid comprising a nucleotide sequence that is at least about 70% or more, e.g., about 80%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to any of the nucleic acids described herein. In this regard, the nucleic acid may consist essentially of any of the nucleotide sequences described herein.

[0075] The nucleic acids of the invention can be incorporated into a recombinant expression vector. In this regard, the invention provides a recombinant expression vector comprising any of the nucleic acids of the invention. In an embodiment of the invention, the recombinant expression vector comprises a nucleotide sequence encoding the α chain, the β chain, and linker peptide.

[0076] For purposes herein, the term "recombinant expression vector" means a genetically-modified oligonucleotide or polynucleotide construct that permits the expression of an mRNA, protein, polypeptide, or peptide by a host cell, when the construct comprises a nucleotide sequence encoding the mRNA, protein, polypeptide, or peptide, and the vector is contacted with the cell under conditions sufficient to have the mRNA, protein, polypeptide, or peptide expressed within the cell. The vectors of the invention are not naturally-occurring as a whole. However, parts of the vectors can be naturally-occurring. The inventive recombinant expression vectors can comprise any type of nucleotide, including, but not limited to DNA and RNA, which can be single-stranded or double-stranded, synthesized or obtained in part from natural sources, and which can contain natural, non-natural or altered nucleotides. The recombinant expression vectors can comprise naturally-occurring, non-naturally-occurring internucleotide linkages, or both types of linkages. Preferably, the non-naturally occurring or altered nucleotides or internucleotide linkages do not hinder the transcription or replication of the vector.

[0077] The recombinant expression vector of the invention can be any suitable recombinant expression vector, and can be used to transform or transfect any suitable host cell. Suitable vectors include those designed for propagation and expansion or for expression or both, such as plasmids and viruses. The vector can be selected from the group consisting of the pUC series (Fermentas Life Sciences), the pBluescript series (Stratagene, LaJolla, CA), the pET series (Novagen, Madison, WI), the pGEX series (Pharmacia Biotech, Uppsala, Sweden), and the pEX series (Clontech, Palo Alto, CA). Bacteriophage vectors, such as λGT10, λGT11, λZapII (Stratagene), λEMBL4, and λNM1149, also can be used. Examples of plant expression vectors include pBI01, pBI101.2, pBI101.3, pBI121 and pBIN19 (Clontech). Examples of animal expression vectors include pEUK-Cl, pMAM and pMAMneo (Clontech). Preferably, the recombinant expression vector is a viral vector, e.g., a retroviral vector. In an especially preferred embodiment, the recombinant expression vector is an MSGV1 vector.

[0078] The recombinant expression vectors of the invention can be prepared using standard recombinant DNA techniques described in, for example, Green and Sambrook et al., *supra*. Constructs of expression vectors, which are circular or linear, can be prepared to contain a replication system functional in a prokaryotic or eukaryotic host cell. Replication systems can be derived, e.g., from ColEl, 2 μ plasmid, λ, SV40, bovine papillomavirus, and the like.

[0079] Desirably, the recombinant expression vector comprises regulatory sequences, such as transcription and translation initiation and termination codons, which are specific to the type of host cell (e.g., bacterium, fungus, plant, or animal) into which the vector is to be introduced, as appropriate and taking into consideration whether the vector is DNA- or RNA-based.

[0080] The recombinant expression vector can include one or more marker genes, which allow for selection of transformed or transfected host cells. Marker genes include biocide resistance, e.g., resistance to antibiotics, heavy metals, etc., complementation in an auxotrophic host cell to provide prototrophy, and the like. Suitable marker genes for the inventive expression vectors include, for instance, neomycin/G418 resistance genes, hygromycin resistance genes, histidinol resistance genes, tetracycline resistance genes, and ampicillin resistance genes.

[0081] The recombinant expression vector can comprise a native or nonnative promoter operably linked to the nucleotide sequence encoding the TCR, polypeptide, or protein, or to

the nucleotide sequence which is complementary to or which hybridizes to the nucleotide sequence encoding the TCR, polypeptide, or protein. The selection of promoters, e.g., strong, weak, inducible, tissue-specific and developmental-specific, is within the ordinary skill of the artisan. Similarly, the combining of a nucleotide sequence with a promoter is also within the skill of the artisan. The promoter can be a non-viral promoter or a viral promoter, e.g., a cytomegalovirus (CMV) promoter, an SV40 promoter, an RSV promoter, and a promoter found in the long-terminal repeat of the murine stem cell virus.

[0082] The inventive recombinant expression vectors can be designed for either transient expression, for stable expression, or for both. Also, the recombinant expression vectors can be made for constitutive expression or for inducible expression.

[0083] Further, the recombinant expression vectors can be made to include a suicide gene. As used herein, the term "suicide gene" refers to a gene that causes the cell expressing the suicide gene to die. The suicide gene can be a gene that confers sensitivity to an agent, e.g., a drug, upon the cell in which the gene is expressed, and causes the cell to die when the cell is contacted with or exposed to the agent. Suicide genes are known in the art and include, for example, the Herpes Simplex Virus (HSV) thymidine kinase (TK) gene, cytosine deaminase, purine nucleoside phosphorylase, nitroreductase, and the inducible caspase 9 gene system.

[0084] Another embodiment of the invention further provides a host cell comprising any of the recombinant expression vectors described herein. As used herein, the term "host cell" refers to any type of cell that can contain the inventive recombinant expression vector. The host cell can be a eukaryotic cell, e.g., plant, animal, fungi, or algae, or can be a prokaryotic cell, e.g., bacteria or protozoa. The host cell can be a cultured cell or a primary cell, i.e., isolated directly from an organism, e.g., a human. The host cell can be an adherent cell or a suspended cell, i.e., a cell that grows in suspension. Suitable host cells are known in the art and include, for instance, DH5α *E. coli* cells, Chinese hamster ovarian cells, monkey VERO cells, COS cells, HEK293 cells, and the like. For purposes of amplifying or replicating the recombinant expression vector, the host cell is preferably a prokaryotic cell, e.g., a DH5α cell. For purposes of producing a recombinant TCR, polypeptide, or protein, the host cell is preferably a mammalian cell. Most preferably, the host cell is a human cell. While the host cell can be of any cell type, can originate from any type of tissue, and can be of any developmental stage, the host cell preferably is a peripheral blood lymphocyte (PBL) or a peripheral blood mononuclear cell (PBMC). More preferably, the host cell is a T cell.

[0085] For purposes herein, the T cell can be any T cell, such as a cultured T cell, e.g., a primary T cell, or a T cell from a cultured T cell line, e.g., Jurkat, SupT1, etc., or a T cell obtained from a mammal. If obtained from a mammal, the T cell can be obtained from numerous sources, including but not limited to blood, bone marrow, lymph node, the thymus, or other tissues or fluids. T cells can also be enriched for or purified. Preferably, the T cell is a human T cell. The T cell can be any type of T cell and can be of any developmental stage, including but not limited to, $CD4^+/CD8^+$ double positive T cells, $CD4^+$ helper T cells, e.g., Th_1 and Th_2 cells, $CD4^+$ T cells, $CD8^+$ T cells (e.g., cytotoxic T cells), tumor infiltrating lymphocytes (TILs), memory T cells (e.g., central memory T cells and effector memory T cells), naïve T cells, and the like.

[0086] Also provided by the invention is a population of cells comprising at least one host cell described herein. The population of cells can be a heterogeneous population comprising the host cell comprising any of the recombinant expression vectors described, in addition to at least one other cell, e.g., a host cell (e.g., a T cell), which does not comprise any of the recombinant expression vectors, or a cell other than a T cell, e.g., a B cell, a macrophage, a neutrophil, an erythrocyte, a hepatocyte, an endothelial cell, an epithelial cells, a muscle cell, a brain cell, etc. Alternatively, the population of cells can be a substantially homogeneous population, in which the population comprises mainly of host cells (e.g., consisting essentially of) comprising the recombinant expression vector. The population also can be a clonal population of cells, in which all cells of the population are clones of a single host cell comprising a recombinant expression vector, such that all cells of the population comprise the recombinant expression vector. In one embodiment of the invention, the population of cells is a clonal population comprising host cells comprising a recombinant expression vector as described herein.

[0087] In an embodiment of the invention, the numbers of cells in the population may be rapidly expanded. Expansion of the numbers of T cells can be accomplished by any of a number of methods as are known in the art as described in, for example, U.S. Patent 8,034,334; U.S. Patent 8,383,099; U.S. Patent Application Publication No. 2012/0244133; Dudley et al., *J. Immunother.*, 26:332-42 (2003); and Riddell et al., *J. Immunol. Methods*, 128:189-201 (1990). In an embodiment, expansion of the numbers of T cells is carried out by culturing the T cells with OKT3 antibody, IL-2, and feeder PBMC (e.g., irradiated allogeneic PBMC).

[0088] The inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, and host cells (including populations thereof), can be isolated and/or purified. The term "isolated" as used herein means having been removed from its natural environment. The term "purified" as used herein means having been increased in purity, wherein "purity" is a relative term, and not to be necessarily construed as absolute purity. For example, the purity can be at least about 50%, can be greater than 60%, 70%, 80%, 90%, 95%, or can be 100%.

[0089] The inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, and host cells (including populations thereof), all of which are collectively referred to as "inventive TCR materials" hereinafter, can be formulated into a composition, such as a pharmaceutical composition. In this regard, the invention provides a pharmaceutical composition comprising any of the TCRs, polypeptides, proteins, nucleic acids, expression vectors, and host cells (including populations thereof), described herein, and a pharmaceutically acceptable carrier. The inventive pharmaceutical compositions containing any of the inventive TCR materials can comprise more than one inventive TCR material, e.g., a polypeptide and a nucleic acid, or two or more different TCRs. Alternatively, the pharmaceutical composition can comprise an inventive TCR material in combination with another pharmaceutically active agent(s) or drug(s), such as a chemotherapeutic agents, e.g., asparaginase, busulfan, carboplatin, cisplatin, daunorubicin, doxorubicin, fluorouracil, gemcitabine, hydroxyurea, methotrexate, paclitaxel, rituximab, vinblastine, vincristine, etc.

[0090] Preferably, the carrier is a pharmaceutically acceptable carrier. With respect to pharmaceutical compositions, the carrier can be any of those conventionally used for the particular inventive TCR material under consideration. Methods for preparing administrable compositions are known or apparent to those skilled in the art and are described in more detail in, for example, *Remington: The Science and Practice of Pharmacy*, 22nd Ed., Pharmaceutical Press (2012). It is preferred that the pharmaceutically acceptable carrier be one which has no detrimental side effects or toxicity under the conditions of use.

[0091] The choice of carrier will be determined in part by the particular inventive TCR material, as well as by the particular method used to administer the inventive TCR material. Accordingly, there are a variety of suitable formulations of the pharmaceutical composition of the invention. Suitable formulations may include any of those for parenteral, subcutaneous, intravenous, intramuscular, intraarterial, intrathecal, intratumoral, or interperitoneal administration. More than one route can be used to administer the inventive

TCR materials, and in certain instances, a particular route can provide a more immediate and more effective response than another route.

[0092] Preferably, the inventive TCR material is administered by injection, e.g., intravenously. When the inventive TCR material is a host cell expressing the inventive TCR, the pharmaceutically acceptable carrier for the cells for injection may include any isotonic carrier such as, for example, normal saline (about 0.90% w/v of NaCl in water, about 300 mOsm/L NaCl in water, or about 9.0 g NaCl per liter of water), NORMOSOL R electrolyte solution (Abbott, Chicago, IL), PLASMA-LYTE A (Baxter, Deerfield, IL), about 5% dextrose in water, or Ringer's lactate. In an embodiment, the pharmaceutically acceptable carrier is supplemented with human serum albumen.

[0093] For purposes of the invention, the amount or dose (e.g., numbers of cells when the inventive TCR material is one or more cells) of the inventive TCR material administered should be sufficient to effect, e.g., a therapeutic or prophylactic response, in the subject or animal over a reasonable time frame. For example, the dose of the inventive TCR material should be sufficient to bind to a cancer antigen (e.g., mutated KRAS), or detect, treat or prevent cancer in a period of from about 2 hours or longer, e.g., 12 to 24 or more hours, from the time of administration. In certain embodiments, the time period could be even longer. The dose will be determined by the efficacy of the particular inventive TCR material and the condition of the animal (e.g., human), as well as the body weight of the animal (e.g., human) to be treated.

[0094] Many assays for determining an administered dose are known in the art. For purposes of the invention, an assay, which comprises comparing the extent to which target cells are lysed or IFN-γ is secreted by T cells expressing the inventive TCR, polypeptide, or protein upon administration of a given dose of such T cells to a mammal among a set of mammals of which each is given a different dose of the T cells, could be used to determine a starting dose to be administered to a mammal. The extent to which target cells are lysed or IFN-γ is secreted upon administration of a certain dose can be assayed by methods known in the art.

[0095] The dose of the inventive TCR material also will be determined by the existence, nature and extent of any adverse side effects that might accompany the administration of a particular inventive TCR material. Typically, the attending physician will decide the dosage of the inventive TCR material with which to treat each individual patient, taking into consideration a variety of factors, such as age, body weight, general health, diet, sex,

inventive TCR material to be administered, route of administration, and the severity of the cancer being treated. In an embodiment in which the inventive TCR material is a population of cells, the number of cells administered per infusion may vary, e.g., from about 1 x 10^6 to about 1 x 10^{12} cells or more. In certain embodiments, fewer than 1 x 10^6 cells may be administered.

[0096] One of ordinary skill in the art will readily appreciate that the inventive TCR materials of the invention can be modified in any number of ways, such that the therapeutic or prophylactic efficacy of the inventive TCR materials is increased through the modification. For instance, the inventive TCR materials can be conjugated either directly or indirectly through a bridge to a chemotherapeutic agent. The practice of conjugating compounds to a chemotherapeutic agent is known in the art. One of ordinary skill in the art recognizes that sites on the inventive TCR materials, which are not necessary for the function of the inventive TCR materials, are ideal sites for attaching a bridge and/or a chemotherapeutic agent, provided that the bridge and/or chemotherapeutic agent, once attached to the inventive TCR materials, do(es) not interfere with the function of the inventive TCR materials, i.e., the ability to bind to mutated KRAS or to detect, treat, or prevent cancer.

[0097] It is contemplated that the inventive pharmaceutical compositions, TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, and populations of cells can be used in methods of treating or preventing cancer. Without being bound to a particular theory, the inventive TCRs are believed to bind specifically to mutated KRAS, such that the TCR (or related inventive polypeptide or protein), when expressed by a cell, is able to mediate an immune response against a target cell expressing mutated KRAS. In this regard, the invention provides a method of treating or preventing cancer in a mammal, comprising administering to the mammal any of the pharmaceutical compositions, TCRs, polypeptides, or proteins described herein, any nucleic acid or recombinant expression vector comprising a nucleotide sequence encoding any of the TCRs, polypeptides, proteins described herein, or any host cell or population of cells comprising a recombinant vector which encodes any of the TCRs, polypeptides, or proteins described herein, in an amount effective to treat or prevent cancer in the mammal.

[0098] An embodiment of the invention provides any of the pharmaceutical compositions, TCRs, polypeptides, or proteins described herein, any nucleic acid or recombinant expression vector comprising a nucleotide sequence encoding any of the TCRs, polypeptides, proteins described herein, or any host cell or population of cells comprising a

recombinant vector which encodes any of the TCRs, polypeptides, or proteins described herein, for use in the treatment or prevention of cancer in a mammal.

[0099] The terms "treat," and "prevent" as well as words stemming therefrom, as used herein, do not necessarily imply 100% or complete treatment or prevention. Rather, there are varying degrees of treatment or prevention of which one of ordinary skill in the art recognizes as having a potential benefit or therapeutic effect. In this respect, the inventive methods can provide any amount of any level of treatment or prevention of cancer in a mammal. Furthermore, the treatment or prevention provided by the inventive method can include treatment or prevention of one or more conditions or symptoms of the cancer being treated or prevented. For example, treatment or prevention can include promoting the regression of a tumor. Also, for purposes herein, "prevention" can encompass delaying the onset of the cancer, or a symptom or condition thereof. Alternatively or additionally, "prevention" may encompass preventing or delaying the recurrence of cancer, or a symptom or condition thereof.

[0100] Also provided is a method of detecting the presence of cancer in a mammal. The method comprises (i) contacting a sample comprising one or more cells from the mammal with any of the inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, populations of cells, or pharmaceutical compositions described herein, thereby forming a complex, and detecting the complex, wherein detection of the complex is indicative of the presence of cancer in the mammal.

[0101] With respect to the inventive method of detecting cancer in a mammal, the sample of cells can be a sample comprising whole cells, lysates thereof, or a fraction of the whole cell lysates, e.g., a nuclear or cytoplasmic fraction, a whole protein fraction, or a nucleic acid fraction.

[0102] For purposes of the inventive detecting method, the contacting can take place *in vitro* or *in vivo* with respect to the mammal. Preferably, the contacting is *in vitro*.

[0103] Also, detection of the complex can occur through any number of ways known in the art. For instance, the inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, or populations of cells, described herein, can be labeled with a detectable label such as, for instance, a radioisotope, a fluorophore (e.g., fluorescein isothiocyanate (FITC), phycoerythrin (PE)), an enzyme (e.g., alkaline phosphatase, horseradish peroxidase), and element particles (e.g., gold particles).

[0104] For purposes of the inventive methods, wherein host cells or populations of cells are administered, the cells can be cells that are allogeneic or autologous to the mammal. Preferably, the cells are autologous to the mammal.

[0105] With respect to the inventive methods, the cancer can be any cancer, including any of acute lymphocytic cancer, acute myeloid leukemia, alveolar rhabdomyosarcoma, bone cancer, brain cancer, breast cancer, cancer of the anus, anal canal, or anorectum, cancer of the eye, cancer of the intrahepatic bile duct, cancer of the joints, cancer of the neck, gallbladder, or pleura, cancer of the nose, nasal cavity, or middle ear, cancer of the oral cavity, cancer of the vagina, cancer of the vulva, chronic lymphocytic leukemia, chronic myeloid cancer, colon cancer, colorectal cancer, endometrial cancer, esophageal cancer, uterine cervical cancer, gastrointestinal carcinoid tumor, glioma, Hodgkin lymphoma, hypopharynx cancer, kidney cancer, larynx cancer, liver cancer, lung cancer, malignant mesothelioma, melanoma, multiple myeloma, nasopharynx cancer, non-Hodgkin lymphoma, cancer of the oropharynx, ovarian cancer, cancer of the penis, pancreatic cancer, peritoneum, omentum, and mesentery cancer, pharynx cancer, prostate cancer, rectal cancer, renal cancer, skin cancer, small intestine cancer, soft tissue cancer, stomach cancer, testicular cancer, thyroid cancer, cancer of the uterus, ureter cancer, and urinary bladder cancer. A preferred cancer is cancer is pancreatic, colorectal, lung, endometrial, ovarian, or prostate cancer. Preferably, the lung cancer is lung adenocarcinoma, the ovarian cancer is epithelial ovarian cancer, and the pancreatic cancer is pancreatic adenocarcinoma. In another preferred embodiment, the cancer is a cancer that expresses the mutated KRAS amino acid sequence with the G12D mutation.

[0106] The mammal referred to in the inventive methods can be any mammal. As used herein, the term "mammal" refers to any mammal, including, but not limited to, mammals of the order Rodentia, such as mice and hamsters, and mammals of the order Logomorpha, such as rabbits. It is preferred that the mammals are from the order Carnivora, including Felines (cats) and Canines (dogs). It is more preferred that the mammals are from the order Artiodactyla, including Bovines (cows) and Swines (pigs) or of the order Perssodactyla, including Equines (horses). It is most preferred that the mammals are of the order Primates, Ceboids, or Simoids (monkeys) or of the order Anthropoids (humans and apes). An especially preferred mammal is the human.

[0107] The following examples further illustrate the invention but, of course, should not be construed as in any way limiting its scope.

EXAMPLES

Next-generation sequencing

[0108] Genomic DNA (gDNA) and total RNA was purified from various tumors and matched normal apheresis samples using the QIAGEN ALLPREP DNA/RNA kit (Qiagen, Venlo, Netherlands) following the manufacturer's suggestions. One sample (Tu-Pri) was formalin-fixed, paraffin-embedded (FFPE) and gDNA was extracted using the Covaris TRUXTRACTM FFPE DNA kit, as directed by the manufacturer (Covaris, Woburn, MA). Whole-exome library construction and exon capture of approximately 20,000 coding genes was prepared using Agilent Technologies SURESELECTXT target enrichment system for paired-end libraries coupled with Human ALL EXON V6 RNA bait (Agilent Technologies, Santa Clara, CA, USA). Whole-exome sequencing (WES) libraries were subsequently sequenced on a NEXTSEQ 500 desktop sequencer (Illumina, San Diego, CA, USA). The library was prepped using 3 μg gDNA from fresh tumor tissue samples and 200 ng gDNA from the FFPE tumor sample following manufacturer's protocol. Paired-end sequencing was done with an ILLUMINA high-output flow cell kit (300 cycles) using initially v1 of the reagent/flow cell kit followed by a subsequent run of the same library prep on v2 of reagent/flow cell kit. RNA-seq libraries were prepared using 2 μg of total RNA with the ILLUMINA TRUSEQ RNA stranded library prep kit following the manufacturer's protocol. RNA-seq libraries were paired-end sequenced on a NEXTSEQ 500 desktop sequencer (Illumina, San Diego, CA, USA).

Alignment, processing and variant calling

[0109] For WES, alignments were performed using NOVOALIGN MPI program from Novocraft (Selangor, Malaysia) (novocraft.com/) to human genome build hg19. Duplicates were marked using Picard's MARKDUPLICATES tool. In/del realignment and base recalibration was carried out according to the GATK best practices workflow (broadinstitute.org/gatk/). Post cleanup of data, SAMTOOLS utility (samtools.sourceforge.net) was used to create pileup files and VARSCAN2 platform-independent mutation caller (varscan.sourceforge.net) was used to call somatic variants using the following criteria: tumor and normal read counts of 10 or greater, variant allele frequency of 10% or greater and tumor variant reads of 4 or more. These variants were then annotated using ANNOVAR software tool (annovar.openbioinformatics.org).

[0110] For RNA-seq, alignments were performed using the STAR (github.com/alexdobin/STAR) two pass method to human genome build hg19. Duplicates were marked using Picard's MARKDUPLICATES tool. Reads were split and trimmed using GATK SPLITNTRIM tool. After which In/del realignment and base recalibration were performed using GATK toolbox. A pileup file was created using the final recalibrated bam file and SAMTOOLS MPILEUP tool. Finally, variants were called using VARSCAN2 platform-independent mutation caller.

[0111] WES and RNA-seq was carried out on three metastatic fresh tumor samples (Tu-1, Tu-2A, and Tu-2B). Variants with a minimum exome frequency of 7% and a minimum of three alternate reads were then manually curated using the Integrated Genomics Viewer (IGV) tool (Broad Institute, Cambridge, MA) in order to remove false positive calls that appeared to result from sequencing or mapping errors. In an attempt to focus on mutations that were likely to be clonal or represented in dominant clonal populations, 61 mutations were chosen for further analysis based upon their detection in more two or more tumor samples. One of these 61 mutations was KRAS (Table 2). These included 29 that were identified in a minimum of one WES and one RNA-seq library, and 32 that were identified in WES libraries from two or more of the metastatic lesions.

TABLE 2

Gene Symbol	**KRAS**
Transcript ID	NM_004985
Mutation Position	chr12:25398284
Mutation Type*	NS SNV
cDNA Change	c.G35A
Amino Acid Change	p.G12D
% Mutant Reads† (Exome)	27
% Mutant Reads† (RNA)	38
FPKM‡	7.94

Generation of tumor infiltrating lymphocytes (TILs), infusion TILs, and antigen presenting dendritic cells (DCs)

[0112] TILs, infusion TILs, and dendritic cells were generated as described in Tran et al., *Science*, 350: 1387-90 (2015). Briefly, to generate TILs, surgically resected tumors were cut into twenty-four fragments approximately 1-2 mm in size and each fragment was placed into a separate well of a 24-well plate containing 2 ml of complete media (CM) containing high dose IL-2 (6000 IU/ml, Chiron, Emeryville, CA). CM contained RPMI media supplemented with 10% in-house human serum, 2 mM L-glutamine, 25 mM HEPES and 10 μg/ml gentamicin. TIL fragment culture #6 was selected for treatment and thus underwent a rapid expansion procedure in gas-permeable G-REX100 flasks using irradiated PBMC at a ratio of 1 to 100 in 400 ml of 50/50 medium, supplemented with 5% human AB serum, 3000 IU/ml of IL-2, and 30 ng/ml of OKT3 antibody (Miltenyi Biotec, Bergisch Gladbach, Germany). 50/50 media contained a 1 to 1 mixture of CM with AIM-V media. All cells were cultured at 37 °C with 5% CO_2.

[0113] Immature DCs were generated from peripheral blood monocytes using the plastic adherence method. Briefly, patient apheresis was thawed, washed, set to 7.5-10e6 cells/ml with AIM-V media (Life Technologies, Carlsbad, CA) and then incubated at approximately 1e6 cells/cm^2 in tissue culture flasks (162 cm^2 surface area) and incubated at 37 °C, 5% CO_2. After 90 minutes (min), the non-adherent cells were collected and the adherent cells in the flasks were vigorously washed with AIM-V media, and then further incubated with AIM-V media for 60 min. The media and non-adherent cells were removed and the adherent cells in the flasks were then vigorously washed again with AIM-V media and then incubated with DC media. DC media contained RPMI containing 5% human serum, 100 U/ml penicillin and 100 μg/ml streptomycin, 2 mM L-glutamine, 800 IU/ml GM-CSF (LEUKINE (sargramostim)) and 200 U/ml IL-4 (Peprotech, Rocky Hill, NJ). On day 2-3, fresh DC media was added to the cultures. DCs were cryopreserved on day 4 or 5 after initiation of the culture. DCs were used in experiments between day 4 and day 6 post initiation of the cultures.

Identification of mutation-reactive T cells and co-culture experiments

[0114] The detailed methods are described in Tran et al., *Science*, 350: 1387-90 (2015). Briefly, sixty-one mutations were identified by whole-exome and transcriptome sequencing. One of these 61 mutations was KRAS (Table 2). For each mutation, a minigene encoding the

mutation flanked by 12 amino acids on either side with the parent protein was generated and synthesized in tandem to create tandem minigene (TMG) constructs. Five TMGs (TMGs 1-5) encoding the 61 mutations were made, *in vitro* transcribed into RNA, and then electroporated into autologous antigen presenting DCs allowing for the processing and presentation of all mutations in the context of the patient's own HLA-I and HLA-II molecules (Table 4). The TMGs for wild-type and mutated KRAS are shown in Table 3. The HLA data shown in Table 4 was determined from next generation sequencing data using the algorithm PHLAT as described in Bai et al., *BMC Genomics*, 15: 325 (2014). Twenty-four individual TIL cultures from the patient were then cocultured with these TMG-expressing DCs, and T-cell reactivity was determined by IFN-γ enzyme-linked immunospot (ELISPOT) assay (Fig. 1A) and flow cytometric analysis of the T-cell activation markers 4-1BB and OX40. Multiple TIL cultures that were reactive against TMG-1 were identified. To identify which mutated antigen in TMG-1 was being recognized by TIL culture #6, the peptides that were encoded in TMG-1 were synthesized (ThermoFisher Scientific (Waltham, MA) and GenScript Inc. (Piscataway Township, NJ)) and then individually pulsed onto DCs overnight followed by co-culture with TIL culture #6 (Fig. 1B).

TABLE 3

Gene Symbol	KRAS
Amino Acid Change	p.G12D
Wild-Type Minigene (Amino Acid)	MTEYKLVVVGAGGVGKSALTIQLI (SEQ ID NO: 61)
Mutated Minigene (Amino Acid)	MTEYKLVVVGADGVGKSALTIQLI (SEQ ID NO: 62)
TMG Construct	1

TABLE 4

HLA-I						**HLA-II**					
A	A	B	B	C	C	DRB1	DRB1	DQA1	DQA1	DQB1	DQB1
02:01	03:01	14:01	44:03	08:02	16:01	07:01		02:01		02:02	

[0115] The following HPLC purified peptides (GenScript Inc.) were used in peptide titration experiments: wild-type (WT)-9mer: GAGGVGKSA (SEQ ID NO: 7); mutated (G12D)-9mer: GADGVGKSA (SEQ ID NO: 8); WT-10mer: GAGGVGKSAL (SEQ ID NO: 5); G12D-10mer: GADGVGKSAL (SEQ ID NO: 6).

[0116] Intracellular cytokine staining (ICS) and flow cytometry was used to determine the expression of the cytokines IFN-γ, TNF, and IL-2, and the degranulation marker CD107a as described in Tran et al., *Science*, 344: 641-5 (2014). Briefly, target and effector cells were combined in the wells of a 96-well plate and both GOLGISTOP and GOLGIPLUG protein transport inhibitors (both at ½ the recommended concentrations) were added to the culture (BD Biosciences, Franklin Lakes, NJ). At t = 6 h post stimulation, cells were processed using the CYTOFIX/CYTOPERM kit (BD Biosciences) according to the manufacturer's instructions. Cells were acquired on a FACSCANTOII flow cytometer and data were analyzed using FLOWJO software (TreeStar Inc., Ashland, OR). Boolean gate analysis was used to determine the percentage of cells expressing the indicated number of effector functions (cytokines and degranulation marker).

Identification of $KRAS^{G12D}$-reactive T-cell clones

[0117] Four $KRAS^{G12D}$-reactive TCRs were identified using various methods. The dominant TRBV5-6 (Vβ5.2) clone in the infusion bag was isolated from TIL fragment culture #6 prior to rapid expansion. Briefly, TIL culture #6 was stained with the anti-Vβ5.2-PE (phycoerythrin) antibody (Beckman Coulter, Schaumburg, IL) and the Vβ5.2+ cells were enriched using anti-PE specific antibodies conjugated to magnetic microbeads as directed by the manufacturer (Miltenyi Biotec). Total RNA was isolated from the Vβ5.2+ T cells (RNEASY MINI kit, Qiagen) and then underwent 5'RACE as directed by manufacturer (SMARTER RACE cDNA amplification kit, Clontech) using TCR-alpha and beta chain constant primers. The sequences of the alpha and beta chain constant primers were: TCR-alpha, 5'— GCC ACA GCA CTG TTG CTC TTG AAG TCC —3' (SEQ ID NO: 59); TCR-beta, 5'— CAG GCA GTA TCT GGA GTC ATT GAG —3 (SEQ ID NO: 60). Program 1 of the kit was used for the PCR, with a modification to the extension time (2 min instead of 3 min). TCR PCR products were then isolated by standard agarose gel electrophoresis and gel extraction (zymogen) and products were then sequenced (Macrogen, Seoul, Korea).

[0118] The second and third ranked TCRs in the infusion bag were also $KRAS^{G12D}$-reactive and were isolated by first stimulating the day 40 post-cell transfer apheresis sample with DCs pulsed overnight with $KRAS^{G12D}$ long peptides. Vβ5.2-positive and negative CD8+ T cells that upregulated the T-cell activation marker 4-1BB after overnight stimulation were then sorted separately by FACS. The Vβ5.2+ cells were further expanded prior to undergoing 5'RACE as described above, followed by TOPO-TA cloning of the TCR PCR

products and sequencing of individual colonies to identify the TCR-alpha and beta chains. The Vβ5.2-negative cells underwent single-cell, multiplex TCR PCR to identify the TCR-alpha and beta chains as described in Pasetto et al., *Cancer Immunol. Res.*, (2016).

[0119] The fourth $KRAS^{G12D}$-reactive TCR (ranked 45th in the infusion bag) was identified from a different TIL fragment (TIL fragment #5) using another single-cell technology approach. Briefly, TIL culture #5 was co-cultured with DCs transfected with TMG-1 (which encodes for $KRAS^{G12D}$) and after 4 hours (h), the TILs were harvested and subjected to the FLUIDIGM C1 system (Fluidigm, San Francisco, CA) to prepare single-cell RNA-seq samples according to the manufacturer's protocol. Single-cell RNA-seq samples were then sequenced by the ILLUMINA MISEQ system and the data were analyzed by an in-house bioinformatics program. TCR-alpha and beta sequences were extracted from samples that demonstrated an upregulation of IFN-γ transcripts upon stimulation.

In vivo tracking of $KRAS^{G12D}$-reactive T cells

[0120] To determine the frequencies of the $KRAS^{G12D}$-reactive T cells in the samples, the TCR sequences of the $KRAS^{G12D}$-reactive T-cell clones were first identified, and these sequences were interrogated against the TCR-Vβ deep sequencing data from the indicated samples. The number of in-frame productive TCR reads in the samples ranged between 522,499 to 1,990,345.

Flow cytometry antibodies

[0121] The following anti-human flow cytometry antibodies were used in this report: CD3-AF700 (clone: UCHT1, BioLegend), CD8-PE-Cy7 (clone: SK1, BD Biosciences), CD4-APC-Cy7 (clone: SK3, BioLegend), OX40-FITC (clone: Ber-ACT35, BD Biosciences), 4-1BB-APC (clone: 4B4-1, BioLegend), and Vβ5.2-PE (Beckman Coulter). Fluorochrome conjugated anti-mouse TCR-beta constant region antibody (H57-597, eBioscience) was used to evaluate transduction efficiency of the TCRs. The IO TEST Beta Mark TCR V kit was used to assess the TCR-Vβ repertoire (Beckman Coulter).

Identification of mutation-reactive T cells and generation of infusion product

[0122] A previously described method (Lu et al., *Clin. Cancer Res.*, 20: 3401-10 (2014); Tran et al., *Science*, 344: 641-5 (2014); Tran et al., *Science,* 350: 1387-90 (2015)) was used to

test whether TILs from patient 4095 recognized somatic mutations expressed by her metastatic lung tumors. TIL culture #6 contained the highest frequency of $KRAS^{G12D}$-reactive CD8+ T cells and thus underwent a two-week rapid expansion procedure prior to cell infusion as described in Tran et al., *Science*, 344: 641-5 (2014).

In vivo tracking of $KRAS^{G12D}$-specific T-cell clones

[0123] T-cell receptor (TCR)-Vβ deep sequencing was performed on gDNA isolated from the patient's infusion product, 3 separate lung nodules prior to treatment, the progressing lesion (Lesion 3), and on peripheral blood prior to and at various times after cell infusion (Adaptive Biotechnologies, Seattle WA) to interrogate the frequency of $KRAS^{G12D}$-reactive TCR sequences.

Assessing Reactivity of $KRAS^{G12D}$-Specific TCRs

[0124] Four $KRAS^{G12D}$-reactive TCRs were identified, and the TCR-alpha and beta chain sequences were synthesized and then cloned into the MSGV1 retroviral vector (GenScript Inc.). Retroviral supernatants encoding the TCRs were generated and used to transduce autologous peripheral blood T cells as described in Tran et al., *Science,* 344: 641-5 (2014). TCR-transduced T cells were then co-cultured with autologous peripheral blood mononuclear cells (PBMCs) loaded with titrating doses of various KRAS peptides, or $KRAS^{G12D}$-positive pancreatic cancer cell lines stably expressing or not expressing the restricting HLA-C*08:02 allele (Tran et al., *Science,* 350: 1387-90 (2015)). T-cell reactivity was determined the next day by IFN-γ ELISPOT assay and flow cytometric analysis of the T-cell activation markers 4-1BB and OX40 (Tran et al., *Science,* 350: 1387-90 (2015)).

EXAMPLE 1

[0125] This example demonstrates the *in vivo* frequency of $KRAS^{G12D}$ mutation-reactive CD8+ T cells.

[0126] The patient was a 49-year old female with colorectal adenocarcinoma and multiple bilateral pulmonary metastases. She previously received 12 cycles of FOLFOX chemotherapy after a sigmoid colectomy and partial cystectomy, followed by 4182 cGy radiation to the bladder suture line. Shortly after this, she experienced an increase in the number and size of FDG avid bilateral pulmonary nodules. Biopsy of a right lower lobe nodule was consistent with metastatic colorectal adenocarcinoma.

[0127] The patient was enrolled on the institutional review board-approved phase II clinical trial (ClinicalTrials.gov number, NCT01174121) designed to test whether the adoptive transfer of *ex vivo* expanded tumor-infiltrating lymphocytes (TILs) containing T cells targeting cancer mutations can mediate regression of metastatic solid cancers. Baseline CT scans revealed lung disease as the sole source of cancer progression. Three lung lesions were resected using video-assisted thoracoscopic surgery (VATS) and 24 individual TIL cultures were generated from multiple tumor fragments. The 3 lesions also underwent whole-exomic and transcriptome sequencing to identify mutations expressed by the tumors (Table 2). Each TIL culture was evaluated for reactivity against these mutations. It was found that the patient's TILs contained CD8+ T cells that specifically recognized the $KRAS^{G12D}$ mutation (Fig. 1A and B). The TIL culture that displayed the highest frequency of $KRAS^{G12D}$-reactive CD8+ T cells was selected. The numbers of selected cells were expanded for treatment (Fig. 1B and C). Prior to cell infusion, the patient underwent a non-myeloablative, lymphodepleting chemotherapy regimen including 60 mg/kg cyclophosphamide for 2 days, followed by 25 mg/m^2 fludarabine for 5 days (Dudley et al., *J. Clin. Oncol.*, 23: 2346-57 (2005)). The patient received a single infusion of 1.48×10^{11} TILs, followed by 5 doses of interleukin-2 (IL-2) at 720,000 IU/kg, stopping for fatigue. The therapy was well tolerated and the patient was sent home two weeks after cell infusion. Approximately 75% of the infusion product contained CD8+ T cells that specifically recognized the $KRAS^{G12D}$ mutation, and the majority of these T cells produced multiple effector cytokines (IFN-γ, TNF, and IL-2) and displayed cytolytic potential. All 7 metastatic lung lesions regressed at the first follow up 40 days-post cell transfer, and 6/7 lesions continued to regress or completely respond until one lesion (Lesion 3) progressed at approximately 9 months-post therapy. A VATS resection of the left lower lung was performed at approximately 9 months-post cell transfer to remove the sole progressing lesion (Lesion 3) as well as a responding lesion (Lesion 2) that was PET negative and completely necrotic with no live tumor cells on pathologic analysis. The patient remains clinically disease free 3 months after the lung resection.

[0128] The infusion TIL product contained at least four $KRAS^{G12D}$-reactive T-cell clonotypes of varying frequencies. The three highest frequency TCRs in the infusion product were reactive against $KRAS^{G12D}$, comprising of 49.5%, 19.1%, and 6.9% of the infusion bag, while a fourth $KRAS^{G12D}$-reactive TCR was the 45^{th} most frequent and was present at only 0.04% of the infusion bag (Figs. 2A-2D and Table 5). None of these $KRAS^{G12D}$-reactive

TCRs were detected (frequency < 0.0002%) in the peripheral blood of the patient one week prior to infusion (Figs. 2A-2D). After cell transfer, dramatic differences in the engraftment of the $KRAS^{G12D}$-reactive TCRs were observed. The most dominant infused T-cell clonotype (~7.3 x 10^{10} cells) was not detected in the blood 40 days-post cell transfer, while the remaining $KRAS^{G12D}$-reactive T-cell clones were detected at this time point (Figs. 2A-2D). The $KRAS^{G12D}$-reactive T-cell clones persisting in the peripheral blood represented 10.4%, 4.5%, and 0.005% of all peripheral blood T cells at approximately 9 months-post cell transfer, and the most dominant T-cell clone in the peripheral blood at that time was the TRBV10-02 mutant $KRAS^{G12D}$-reactive TCR (Figs. 2A-2D and Table 5). There did not appear to be an enrichment of the $KRAS^{G12D}$-reactive T-cell clones in the progressing tumor relative to the peripheral blood (Figs. 2A-2D).

TABLE 5

Patient ID	TCR-α/TCR-β Gene Name	TCR-α/TCR-β CDR3 Amino Acid Sequence	Frequency in Tumor Samples†	Rank in Tumor Samples†	Frequency in Infusion Product	Rank in Infusion Product	Frequency in Blood on d+266	Rank in Blood on d+266
4095	TRAV4/ TRBV5-6 (A)	CLVGDMDQAGTALIF (SEQ ID NO: 11)/ CASSLGEGRVDGYTF (SEQ ID NO: 14)	0.21 0.20 0.16	20 26 33	49.5	1	Not detected	Not applicable
4095	TRAV12-2/ TRBV10-2	CAAAMDSSYKLIF (SEQ ID NO: 35)/ CASSDPGTEAFF (SEQ ID NO: 38)	2.7 3.0 2.9	1 1 2	19.1	2	10.4	1
4095	TRAV4/ TRBV5-6 (B)	CLVGDRDQAGTALIF (SEQ ID NO: 27)/ CASSFGQSSTYGYTF (SEQ ID NO: 30)	Not detected	NA	6.9	3	4.5	5
4095	TRAV4/ TRBV5-6 (C)	CLVGDMDQAGTALIF (SEQ ID NO: 19)/ CASSLGRASNQPQHF (SEQ ID NO: 22)	0.02 0.01 0.008	917 1589 2243	0.04	45	0.005	1784

† Three different metastatic tumor fragments were evaluated for patient 4095.

d+266 =266 days after cell transfer.

EXAMPLE 2

[0129] This example demonstrates the specificity and sensitivity of the $KRAS^{G12D}$–reactive TCRs.

[0130] The nucleotide sequence encoding the TCR was cloned from each of the four $KRAS^{G12D}$-reactive T-cell clonotypes of Example 1. Each TCR was cloned into an MSGV1-retroviral vector. The amino acid sequences of the alpha and beta chains of each of the four TCRs is shown in Table 6.

TABLE 6

TCR-α/TCR-β Gene Name	Variable Region Alpha Chain Amino Acid Sequence	Variable Region Beta Chain Amino Acid Sequence
TRAV4/ TRBV5-6 (A)	SEQ ID NO: 15	SEQ ID NO: 16
TRAV12-2/ TRBV10-2	SEQ ID NO: 39	SEQ ID NO: 40
TRAV4/ TRBV5-6 (B)	SEQ ID NO: 31	SEQ ID NO: 32
TRAV4/ TRBV5-6 (C)	SEQ ID NO: 23	SEQ ID NO: 24

[0131] The nucleotide sequence cloned into the MSGV1-retroviral vector encoded the variable region of the TCR alpha chain (shown in Table 6) and the murine TCR alpha chain constant region, followed by a P2A linker sequence (SEQ ID NO: 58) and a nucleotide sequence encoding the variable region of the TCR beta chain (shown in Table 6) and the murine TCR beta chain constant region. The TCR was further modified to include cysteine substitutions in the murine constant region of both of the α and β chains in combination with a substitution(s) of three amino acids in the TM domain of the murine constant region of the alpha chain with a hydrophobic amino acid. The full-length amino acid sequence of each of the four TCRs is shown in Table 7. Without being bound to a particular theory or mechanism, it is believed that the murine TCR alpha and beta constant chains may diminish mispairing with endogenous TCRs and may promote the expression of the introduced TCRs by the host cells. It is also believed that enhanced expression and pairing of the introduced TCR alpha and beta chains may be achieved by incorporating hydrophobic amino acids in the

TCR alpha constant chain, and introducing a second disulfide bond between the alpha and beta chain constant regions.

TABLE 7

TCR-α/TCR-β Gene Name	Alpha Chain Amino Acid Sequence	Beta Chain Amino Acid Sequence
TRAV4/ TRBV5-6 (A)	SEQ ID NO: 50	SEQ ID NO: 51
TRAV12-2/ TRBV10-2	SEQ ID NO: 56	SEQ ID NO: 57
TRAV4/ TRBV5-6 (B)	SEQ ID NO: 54	SEQ ID NO: 55
TRAV4/ TRBV5-6 (C)	SEQ ID NO: 52	SEQ ID NO: 53

[0132] Autologous peripheral blood T cells were genetically modified to express one of these four TCRs. Cell surface expression of the introduced TCRs was evaluated on day 10 post-TCR gene modification by flow cytometric analysis for the murine TCR-β constant region (mTCR-β) since the TCRs were designed with the murine TCR-alpha and beta constant regions. Vector transduced cells served as a negative control. The data are gated were gated on CD8+ T cells. The percentage of cells expressing the murine TCR-β constant region are shown in Table 8.

TABLE 8

Vector Transduced	%
TRAV4/ TRBV5-6 (A)	83
TRAV12-2/ TRBV10-2	83
TRAV4/ TRBV5-6 (B)	83
TRAV4/ TRBV5-6 (C)	79
Empty Vector(Control)	0

[0133] The TCR-engineered T cells were co-cultured overnight with autologous PBMCs incubated with titrating amounts of KRAS wild-type (WT) or G12D mutant 9mer or 10mer peptides. The percentage of cells expressing the T-cell activation marker 4-1BB was measured. The results are shown in Figures 3A-3D. Three of the four TCRs were

preferentially reactive against the 9 amino acid long $KRAS^{G12D}$ peptide GA**D**GVGKSA (SEQ ID NO: 8), while one TCR was reactive only against the 10 amino acid long $KRAS^{G12D}$ peptide GA**D**GVGKSAL (SEQ ID NO: 6) (Figs. 3A-3D). All TCRs were specific for the mutation and did not recognize the wild type KRAS peptides (Figs. 3A-3D). Peptide titration experiments demonstrated that the TCRs were able to recognize peptides at concentrations between 1-10 nM when pulsed onto autologous PBMCs (Figs. 3A-3D).

[0134] The TCR-engineered T cells were co-cultured overnight with one of two $KRAS^{G12D}$-positive pancreatic cancer cells lines (MDA-Panc48 or HPAC) not expressing or expressing the HLA-C*08:02 allele. IFN-γ secretion was measured by ELISPOT assay and 4-1BB expression was measured by flow cytometry. The results are shown in Figures 4A-4B. The TCRs specifically recognized the pancreatic cancer cells lines only when they expressed both the $KRAS^{G12D}$ mutation and the HLA-C*08:02 allele (Figs. 4A-4B).

EXAMPLE 3

[0135] This example demonstrates that cells transduced to express the TRAV12-2/TRBV10-2 TCR (SEQ ID NOs: 56 and 57) recognize mutated KRAS in the context of HLA allele C*08:02 or C*05:01.

[0136] Autologous peripheral blood T cells were genetically modified to express one of the four TCRs as described in Example 2. COS7 cells were co-transfected with full length wild-type (wt) KRAS or KRAS-G12D genes and the HLA allele C*07:01, C*08:02, or C*05:01, followed by co-culture with the indicated $KRAS^{G12D}$-reactive TCR transduced cells. Cells were analyzed for 4-1BB expression by flow cytometry the next day. The results are shown in Figures 5A-5D. Data were gated on TCR-transduced (mouse TCRβ+) CD8+ T cells. HLA-C*07:01 served as a negative control HLA allele.

[0137] All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.

[0138] The use of the terms "a" and "an" and "the" and "at least one" and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The use of the term "at least one"

followed by a list of one or more items (for example, "at least one of A and B") is to be construed to mean one item selected from the listed items (A or B) or any combination of two or more of the listed items (A and B), unless otherwise indicated herein or clearly contradicted by context. The terms "comprising," "having," "including," and "containing" are to be construed as open-ended terms (i.e., meaning "including, but not limited to,") unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

[0139] Preferred embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Variations of those preferred embodiments may become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventors expect skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

CLAIM(S):

1. An isolated or purified TCR comprising the amino acid sequences of:

(a) SEQ ID NOs: 9-14;

(b) SEQ ID NOs: 17-22;

(c) SEQ ID NOs: 25-30; or

(d) SEQ ID NOs: 33-38.

2. The isolated or purified TCR of claim 1, comprising the amino acid sequences of:

(i) SEQ ID NOs: 15-16;

(ii) SEQ ID NOs: 23-24;

(iii) SEQ ID NOs: 31-32; or

(iv) SEQ ID NOs: 39-40.

3. The isolated or purified TCR of claim 1 or 2, further comprising:

(A) the amino acid sequence of SEQ ID NO: 46, wherein:

(i) X at position 48 of SEQ ID NO: 46 is Thr or Cys;

(ii) X at position 112 of SEQ ID NO: 46 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp;

(iii) X at position 114 of SEQ ID NO: 46 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp;

and

(iv) X at position 115 of SEQ ID NO: 46 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp;

and

(B) the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 of SEQ ID NO: 47 is Ser or Cys.

4. The isolated or purified TCR of any one of claims 1-3, comprising the amino acid sequences of:

(1) SEQ ID NOs: 50-51;

(2) SEQ ID NOs: 52-53;

(3) SEQ ID NOs: 54-55; or

(4) SEQ ID NOs: 56-57.

5. An isolated or purified polypeptide comprising the amino acid sequences of:

(a) SEQ ID NOs: 9-14;

(b) SEQ ID NOs: 17-22;

(c) SEQ ID NOs: 25-30; or

(d) SEQ ID NOs: 33-38.

6. The isolated or purified polypeptide of claim 5, comprising the amino acid sequences of:

(i) SEQ ID NOs: 15-16;

(ii) SEQ ID NOs: 23-24;

(iii) SEQ ID NOs: 31-32; or

(iv) SEQ ID NOs: 39-40.

7. The isolated or purified polypeptide of claim 5 or 6, further comprising:

(A) the amino acid sequence of SEQ ID NO: 46, wherein:

(i) X at position 48 of SEQ ID NO: 46 is Thr or Cys;

(ii) X at position 112 of SEQ ID NO: 46 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp;

(iii) X at position 114 of SEQ ID NO: 46 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp;

and

(iv) X at position 115 of SEQ ID NO: 46 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp;

and

(B) the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 of SEQ ID NO: 47 is Ser or Cys.

8. The isolated or purified polypeptide of any one of claims 5-7, comprising the amino acid sequences of:

(1) SEQ ID NOs: 50-51;

(2) SEQ ID NOs: 52-53;

(3) SEQ ID NOs: 54-55; or

(4) SEQ ID NOs: 56-57.

9. An isolated or purified protein comprising:

(a) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 9-11 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 12-14;

(b) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 17-19 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 20-22;

(c) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 25-27 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 28-30; or

(d) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 33-35 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 36-38.

10. The isolated or purified protein of claim 9 comprising:

(i) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 15 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 16;

(ii) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 23 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 24;

(iii) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 31 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 32; or

(iv) a first polypeptide chain comprising the amino acid sequences of SEQ ID NO: 39 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NO: 40.

11. The isolated or purified protein of claim 9 or 10, wherein:

(A) the first polypeptide chain further comprises the amino acid sequence of SEQ ID NO: 46, wherein:

(i) X at position 48 of SEQ ID NO: 46 is Thr or Cys;

(ii) X at position 112 of SEQ ID NO: 46 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp;

(iii) X at position 114 of SEQ ID NO: 46 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp;

and

(iv) X at position 115 of SEQ ID NO: 46 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp;

and

(B) the second polypeptide chain further comprises the amino acid sequence of SEQ ID NO: 47, wherein X at position 57 of SEQ ID NO: 47 is Ser or Cys.

12. The isolated or purified protein of any one of claims 9-11, wherein:

(1) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 50 and the second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 51;

(2) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 52 and the second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 53;

(3) the first polypeptide chain comprises the amino acid sequence of SEQ ID NOs: 54 and the second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 55; or

(4) the first polypeptide chain comprises the amino acid sequence of SEQ ID NOs: 56 and the second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 57.

13. An isolated or purified nucleic acid comprising a nucleotide sequence encoding the TCR of any one of claims 1-4, the polypeptide of any one of claims 5-8, or the protein of any one of claims 9-12.

14. A recombinant expression vector comprising the nucleic acid of claim 13.

15. An isolated or purified host cell comprising the recombinant expression vector of claim 14.

16. A population of cells comprising at least one isolated or purified host cell of claim 15.

17. A pharmaceutical composition comprising the TCR of any one of claims 1-4, the polypeptide of any one of claims 5-8, the protein of any one of claims 9-12, the nucleic acid

of claim 13, the recombinant expression vector of claim 14, the host cell of claim 15, or the population of host cells of claim 16, and a pharmaceutically acceptable carrier.

18. A method of detecting the presence of cancer in a mammal, the method comprising:

(a) contacting a sample comprising cells of the cancer with the TCR of any one of claims 1-4, the polypeptide of any one of claims 5-8, the protein of any one of claims 9-12, the nucleic acid of claim 13, the recombinant expression vector of claim 14, the host cell of claim 15, the population of host cells of claim 16, or the pharmaceutical composition of claim 17, thereby forming a complex; and

(b) detecting the complex,

wherein detection of the complex is indicative of the presence of cancer in the mammal.

19. The method of claim 18, wherein the cancer is pancreatic, colorectal, lung, endometrial, ovarian, or prostate cancer.

20. The TCR of any one of claims 1-4, the polypeptide of any one of claims 5-8, the protein of any one of claims 9-12, the nucleic acid of claim 13, the recombinant expression vector of claim 14, the host cell of claim 15, the population of host cells of claim 16, or the pharmaceutical composition of claim 17 for use in the treatment or prevention of cancer in a mammal.

21. The TCR, polypeptide, protein, nucleic acid, recombinant expression vector, host cell, population of host cells, or pharmaceutical composition for the use of claim 20, wherein the cancer is pancreatic, colorectal, lung, endometrial, ovarian, or prostate cancer.