TRANSGENE GENETIC TAGS AND METHODS OF USE

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims the benefit of priority to U.S. Provisional Patent Application No. 62/058,973, filed October 2, 2014, U.S. Provisional Patent Application No. 61/977,751, filed April 10, 2014, U.S. Provisional Patent Application No. 61/986,479, filed April 30, 2014, U.S. Provisional Patent Application No. 62/089,730 filed December 9, 2014, U.S. Provisional Patent Application No. 62/090845, filed December 11, 2014, and U.S. Provisional Patent Application No. 62/088,363, filed December 5, 2014. The entire disclosures of the aforementioned applications are expressly incorporated by reference in their entireties.

REFERENCE TO SEQUENCE LISTING, TABLE, OR COMPUTER PROGRAM LISTING

[0002] The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled SCRI-066WO-SEQUENCE_LISTING.TXT created April 7, 2015, which is 47kb in size. The information is the electronic format of the Sequence Listing is incorporated herein by reference in its entirety

FIELD OF THE INVENTION

[0003] The present invention relates to the compositions and methods useful for detecting transgene expression in cells.

BACKGROUND OF THE INVENTION

[0004] Expression of transgenes in cells is becoming an important therapeutic approach for a variety of conditions. For example, in adoptive immunotherapy, human T lymphocytes are engineered by gene transfer to express chimeric antigen receptors (CARs) specific for surface molecules expressed on tumor cells. Chimeric receptors are synthetic receptors that include an extracellular ligand binding domain, most commonly a single chain

variable fragment of a monoclonal antibody (scFv) linked to intracellular signaling components, most commonly CD3ζ alone or combined with one or more costimulatory domains. Other examples of conditions treated with transgene modified cells include thalassemia, hemophilia, myocardial infarction, and severe combined immunodeficiency. However, a major issue remains with obtaining stable expression of transgene expression at levels comparable to endogenous genes. There is a need to identify compositions and methods for selecting and/or detecting cells that express transgenes at high levels.

SUMMARY OF THE INVENTION

[0005] The use and selection of homogenous products has been a limiting factor to the clinical success and reproducibility of gene therapy strategies. As provided herein, a candidate genetic tag and tool for cellular engineering was designed. In some alternatives, a genetic tag comprises an epitope based on human Her2, designated Her2t. In a specific alternative, Her2t is devoid of all Her2 intracellular components, yet contains the Her2 transmembrane region, a conformationally intact epitope recognized by the monoclonal antibody trastuzumab (Herceptin) and a peptide to facilitate surface expression. Three variants of the Her2t construct, one containing the full Her2 Domain IV and two conformational epitopes that were designed based on the three-dimensional structure of Her2 in complex with Herceptin (Garrett et al J. Immunology 178:7120 (2007); Cho et al 2003), were incorporated into the lentiviral packaging plasmid epHIV7 and characterized in CHO cells.

[0006] In some aspects, utilization of Her2t as a genetic tag allows for the *ex vivo* selection and purification of homogenous populations of cellular therapeutics that express a transgene of interest. In addition, Her2t can be used to track cellular therapeutics *in vivo*; for instance, Her2t can be used as a target for Herceptin staining of blood, bone marrow and cerebrospinal fluid aspirates to check for the persistence of transgene-expressing cellular therapeutics to follow cancer remission to therapeutic persistence in a patient. Her2t extends the therapeutic reach of CAR therapy by allowing for the concerted purification of cells expressing multiple transgenes when used with another genetic tag such as EGFRt.

[0007] In some alternatives, the disclosure provides an isolated polypeptide comprising at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an

extracellular domain of HER2 polypeptide having a sequence of amino acids of 511 to 652 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. Nucleic acids coding for the isolated polypeptide are included herein.

[0008] In other alternatives, host cells are provided comprising the nucleic acid coding for an isolated polypeptide comprising at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511to 562 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, and wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2. Host cells can be selected from the group consisting of CD8 T cells, CD4 T cells, CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, CD4 central memory cells, and combinations thereof. Host cells can further comprise a second nucleic acid coding for a second chimeric antigen receptor linked to a second genetic tag. In some alternatives, the second nucleic acid can be introduced into the same host cells as a nucleic acid coding for an isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 562 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2. In other alternatives, the second nucleic acid is introduced into a second host cell population and at least the two host cell populations are combined into a single composition. In some alternatives, the T cells comprise precursor T cells. In some alternatives, the precursor T cells are hematopoietic stem cells.

[0009] Another aspect of the disclosure provides methods of manufacturing compositions comprising host cells as described herein. In some alternatives, a method comprises introducing an isolated nucleic acid, such as a nucleic acid coding for an isolated polypeptide comprising at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain (ECD) of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, into a host cell; and culturing the host cells in a medium comprising at

least one growth factor. In some alternatives, a method further comprises selecting the host cells for expression of ECD before or after or both before and after the culturing step. In other alternatives, a method of manufacturing further comprises introducing a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag into the host cell. In some alternatives, the method further comprises selecting the host cells for expression of the second genetic tag before or after or both before and after the culturing step.

[0010] In other alternatives, a method is provided wherein the method comprises introducing a first isolated nucleic acid, such as a nucleic acid coding for an isolated polypeptide comprising at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, into a first host cell; selecting first host cells that express ECD, introducing a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag into a second host cell, selecting second host cells for expression of the second genetic tag, and optionally, culturing the first and second host cells in a medium comprising at least one growth factor. In some alternatives, a composition comprises a first and second host cell population.

[0011] Another aspect of the disclosure relates to methods and uses of the compositions for treating cancer, tracking the cells of the composition *in vivo*, and killing the cells of the composition *in vivo*. In some alternatives, a method is provided wherein the method comprises treating a patient having cancer and expressing a tumor antigen, wherein the method further comprises administering an effective amount of a composition of host cells comprising one or more nucleic acids coding for a chimeric antigen receptor linked to a genetic tag. In some alternatives, the host cells of the composition comprise a first nucleic acid coding for a first chimeric antigen receptor linked to a first genetic tag and a second nucleic acid coding for a second chimeric antigen receptor linked to a second genetic tag. In some alternatives, the method further comprises administering an antibody or antigen binding fragment thereof that specifically binds to the genetic tag. In some alternatives, an antibody is administered that binds to the first genetic tag, an antibody is administered that

specifically binds to the second genetic tag, or both administered. In some alternatives, the antibody is labelled with a detectable label, a cytotoxic agent, or both.

[0012] In some alternatives, an isolated polypeptide is provided, wherein the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab.

[0013] In some alternatives, an isolated polypeptide is provided, wherein the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab.

[0014] In some alternatives, an isolated nucleic acid is provided wherein the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide

encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of LEGGGEGRGSLLTCG (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25 (CD20CAR).

[0015] In some alternatives, a host cell is provided wherein the host cell comprises an isolated nucleic acid, wherein the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a

transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25 (CD20CAR). In some alternatives, the host cell is selected from the group consisting of CD8 T cells, CD4 T cells, CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, CD4 central memory cells, and combinations thereof. In some alternatives, the host cell is autologous. In some

alternatives, the host cell is antigen specific. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0016] In some alternatives, a composition comprising host cells is provided wherein the host cells comprise an isolated nucleic acid, wherein the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID

NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25 (CD20CAR). In some alternatives, the host cell is selected from the group consisting of CD8 T cells, CD4 T cells, CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, CD4 central memory cells, and combinations thereof. In some alternatives, the host cell is autologous. In some alternatives, the host cell is antigen specific. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0017] In some alternatives, a method of manufacturing a composition is provided, wherein the method comprises introducing an isolated nucleic acid into a host cell and culturing the host cells in a medium comprising at least one growth factor. In some alternatives, the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some

alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain,

wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25 (CD20CAR). In some alternatives, the host cell is selected from the group consisting of CD8 T cells, CD4 T cells, CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, CD4 central memory cells, and combinations thereof. In some alternatives, the host cell is autologous. In some alternatives, the host cell is antigen specific. In some alternatives, the growth factor is selected from the group consisting of IL-15, IL-7, IL-21, IL-2, and combinations thereof. In some alternatives, the method further comprises selecting cells that express the Her2t polypeptide. In some alternatives, the cells are selected before culturing the cells in the medium. In some alternatives, the cells are selected using an antibody that binds to Domain IV of Her2. In some alternatives, the antibody is trastuzumab. In some alternatives, the method further comprises introducing a second isolated nucleic acid coding for a chimeric antigen receptor linked to a second genetic tag. In some alternatives, the method further comprises selecting cells expressing the second genetic tag. In some alternatives, the second genetic tag comprises EGFRt. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

BRIEF DESCRIPTION OF THE DRAWINGS

[0018] **Figure 1. Structural schematic of Her2t.** (**Panel A**) Molecular model of the extracellular and transmembrane regions of Her2t (middle) versus Her2 (ErbB2; left). Her2t in complex with Herceptin Fab (right). (**Panel B**) Schematic of Her2t containing leader peptide composed of the GMCSF receptor-α chain signal sequence (GMCSFRss) to allow for surface expression. The remaining Her2t sequence is composed of an epitope of Her2 (ErbB2) Domain IV (89 aa) and a 23-aa transmembrane region. (**Panel C**) Her2t was cloned in frame downstream to the CAR and T2A to allow for co-expression.

[0019] **Figure 2. Her2t partners with trastuzumab (Herceptin) to immunomagnetically enrich Her2t-expressing cells.** (**Panel A**) Titration of biotinylated Herceptin against a Her2-expressing cell line. (**Panel B**) Her2t-transduced K562 cells pre- and post-selection using biotinylated Herceptin and anti-biotin microbeads (Miltenyi). Cells purified up to 95% Her2t positive. (**Panel C**) The epitope of Her2t is specifically recognized by Herceptin and goes unrecognized by commercial Her2t antibodies. (**Panel D**) Western blot analysis using a commercial antibody (top) or biotinylated Herceptin (bottom) exemplifying the difference in kDa size between Her2t (25kDa) and ErbB2 (250kDa). Lanes from left to right (1-4): MW ladder, K562 parental, K562 Her2t, K562 ErbB2 (Her2).

[0020] **Figure 3. Her2t is an effective selection marker in concert with EGFRt in central memory T cells (Tcm).** (**Panel A**) Purification of CD8 Tcm from PBMC using a two-step column purification scheme. CD8+CD45RA- cells are initially selected using a CD8 isolation kit (to enrich for CD8 positive cells) and CD45RA microbeads (to remove CD45RA positive cells). Cells are then positively selected using CD62L microbeads. (**Panel B**) CD8 Tcm transduced with CD19CAR-T2A-Her2, CD20CAR-T2A-EGFRt, or both selected using biotinylated Herceptin or Erbitux and anti-biotin microbeads. CD8 Tcm transduced with CD19CAR-T2A-Her2t and CD20CAR-T2A-EGFRt (Both) can be sequentially purified allowing for a dual-specific T cell for CAR therapy. The fifth panel goes with the dual purified Tcm histogram (Both). The top histogram shows Herceptin SA-PE staining (Her2t+) and the bottom histogram shows Erbitux SA-PE staining (EGFRt+) for the dual purified Tcm. (**Panel C**) Western blot analysis using a CD3ζ specific antibody on cell lysates of Her2t or EGFRt purified CD8 Tcm. Lanes from left to right (1-4): MW ladder, Mock transduced, CD19CAR-T2A-Her2t transduced, CD19CAR-T2A-EGFRt transduced. Band intensities demonstrate that while the MFI in (**Panel B**) is lower for Her2t stained cells, Her2t purified cells have higher transgene expression levels than EGFRt purified cells. Upper bands = CD19CAR ; Lower bands = endogenous CD3ζ. A comparison of band intensities between the CAR zeta chain (Upper panel-50kDa) and the internal zeta chain of the host T Cells (lower panel -15kDa) shows that the cells expressing CARher2t construct had about 2 fold higher expression of the CAR as compared to the CAREGFRt construct.

[0021] **Figure 4. Her2t and Her2t/EGFRt transduced cells maintain effector phenotype and target specificity.** (**Panel A**) characterization of K562 target panel left to

right: K562 parental, K562 CD19, K562 CD20, and K562 CD19/CD20 (X-axis: CD19+; Y-axis: CD20+). (**Panel B**) 4-hour chromium release assay showing CD19- and CD20-CAR T cell specificity against K562 target panel cells. CD8 Tcm were co-cultured with K562 target cells at a 50:1, 25:1, 12.5:1 or 6.25:1 ratio. Only the dual transduced T cells were able to target all antigen expressing K562 cells. The CD19CAR-T2A-Her2t and CD19CAR-T2A-EGFRt CD8 Tcm demonstrate similar lytic capacity. (**Panel C**) 24-hour cytokine release assay. CD8 Tcm were co-cultured with K562 target cells at a 2:1 T cell-to-target ratio for 24 hours and then supernatant was analyzed for the presence of effector cytokines. CD19CAR-T2A-Her2t transduced CD8 Tcm produced a more diverse repertoire and higher levels of effector cytokines relative to CD19CAR-T2A-EGFRt transduced CD8 Tcm. The panels are the same as A and B (Left to right: K562 parental, K562 CD19, K562 CD20 and K562 CD19/CD20). Similar results were seen for CD4 Tcm (data not shown). (**Panel D**) Representative fold cytokine production from 24hr cytokine release assay. CD8 Tcm purified by Her2t (CD19CAR-Her2t) produce significantly higher IL2, IFNy and TNFa effector cytokine levels when co-cultured with CD19 expressing K562 (above) as compared to CD19CAR-EGFRt. Student's t test $p > 0.05$.

[0022] Figure 5. Use of Her2t as a marker for in vivo detection and fluorescent staining of engineered cells. (**Panel A**) CD19CAR-T2A-Her2t or CD19CAR-T2A-EGFRt-expressing CD4 and CD8 Tcm (10^7) were injected intravenously into NOD/scid IL-2RγC null mice alongside a subcutaneous injection of 5×10^6 NSØ-IL15 cells to provide systemic supply of human IL-15. Bone marrow was harvested 14 days post injection and cell suspensions were analyzed by flow cytometry. (**Panel B**) three panels showing cells gated for viable (93.6% lymphocytes), single (98.8%), and alive cells (99.9%). (B) CD8 and CD45 staining of left to right (Mock, CD19CAR-T2A-Her2t, CD19CAR-T2A-EGFRt Tcm). At least $1x10^7$ cells were recorded inside of the viable, single cell and alive gates. So although the CD45+ cells represent around 1% of the population, it is equivalent to $1x10^5$ cells. The remaining cells are mouse bone marrow cells. (**Panel C**) Human CD45+ cells were co-stained with biotinylated Herceptin or Erbitux and SA-APC. Her2t- or EGFRt-expressing Tcm from bone marrow were identified. (**Panel D**) TM-LCL parental, Her2(ErbB2) or Her2t expressing cells were adhered to slides using poly-L-lysine and then stained using

biotinylated Herceptin and SA-AF647. Staining was only present for cells expressing Her2 or Her2t when stained with biotinylated Herceptin and SA-AF647.

[0023] Figure 6. Multisort purification of Her2t and EGFRt positive T cells. H9 cells ($5x10^6$ parental, $Her2t^+$, $EGFRt^+$, or $Her2t^+/EGFRt^+$) were mixed together and then subjected to purification. The cells were initially purified based on biotinylated Herceptin and anti-biotin multisort beads. The multisort beads were then removed and the positive fraction subsequently subjected to purification based on Erbitux-APC and anti-APC microbeads. The final positive fraction was dual positive for Her2t and EGFRt.

[0024] Figure 7. Three variants of Her2t (CD28hinge, IgG4hinge or Her2tG) were designed to enhance binding to the antibody Herceptin. Shown is a general schematic indicating where the new sequences were inserted into Her2t.

[0025] Figure 8. Her2tG displays enhanced binding to Herceptin. H9 cells were transduced with lentivirus at an MOI of 1 with Her2t or Her2tG. Transduced cells were then purified by biotinylated Herceptin and anti-biotin microbeads according to the manufacturers' protocol. The purified populations were later stained for Her2t or Her2tG using biotinylated Herceptin and streptavidin-PE. Histograms display greater binding to Her2tG.

[0026] Figure 9. Her2tG displays the greatest ability to bind Herceptin. H9 cells were transduced with lentivirus at 0.05, 0.1, 0.25, 0.5, 1 and 3ul (left to right) and then analyzed for Herceptin binding five days later. The Her2t variant Her2t(CD28hinge) was able to bind Herceptin at levels similar to the original Her2t (Her2t staining not shown but based on prior experience). Her2t(IgG4hinge) enhanced Herceptin binding relative to Her2t or Her2t(CD28hinge), while the Her2tG variant had the greatest capacity to bind Herceptin and stain transduced H9 cells.

Definitions.

[0027] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains.

[0028] "About" as used herein when referring to a measurable value is meant to encompass variations of ±20% or ±10%, more preferably ±5%, even more preferably ±1%, and still more preferably ±0.1 % from the specified value.

[0029] "Antigen" or "Ag" as used herein refers to a molecule that provokes an immune response. This immune response can involve either antibody production, or the activation of specific immunologically-competent cells, or both. It is readily apparent that an antigen can be generated, synthesized, produced recombinantly or can be derived from a biological sample. Such a biological sample can include, but is not limited to a tissue sample, a tumor sample, a cell or a biological fluid, such as, for example, blood, plasma, and ascites fluid.

[0030] "Anti-tumor effect" as used herein, refers to a biological effect, which can be manifested by a decrease in tumor volume, a decrease in the number of tumor cells, a decrease in the number of metastases, an increase in life expectancy, or a decrease of various physiological symptoms associated with the cancerous condition. An "anti-tumor effect" can also be manifested by a decrease in recurrence or an increase in the time before recurrence. In some alternatives, a method of treating a patient is provided wherein the method comprises administering an effective amount of a composition, wherein the composition comprises cells, wherein the cells of the composition express a chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a genetic tag. In some alternatives, the composition has an anti-tumor effect.

[0031] "Chimeric receptor" as used herein refers to a synthetically designed receptor comprising a ligand binding domain of an antibody or other protein sequence that binds to a molecule associated with the disease or disorder and is linked via a spacer domain to one or more intracellular signaling domains of a T cell or other receptors, such as a costimulatory domain. Chimeric receptor can also be referred to as artificial T cell receptors, chimeric T cell receptors, chimeric immunoreceptors, and chimeric antigen receptors (CARs). These CARs are engineered receptors that can graft an arbitrary specificity onto an immune receptor cell. Chimeric antigen receptors or "CARs" are referred to by some investigators to include the antibody or antibody fragment, the spacer, signaling domain, and transmembrane region. However, due to the surprising effects of modifying the different components or domains of the CAR, such as the epitope binding region (for example, antibody fragment, scFv, or portion thereof), spacer, transmembrane domain, and/ or signaling domain), the components of the CAR are described in some contexts herein as

independent elements. The variation of the different elements of the CAR can, for example, lead to stronger binding affinity for a \specific epitope.

[0032] "Co-stimulatory domain," as the term is used herein refers to a signaling moiety that provides to T cells a signal which, in addition to the primary signal provided by for instance the CD3 zeta chain of the TCR/CD3 complex, mediates a T cell response, including, but not limited to, activation, proliferation, differentiation, cytokine secretion, and the like. A co-stimulatory domain can include all or a portion of, but is not limited to, CD27, CD28, 4-1BB, OX40, CD30, CD40, ICOS, lymphocyte function-associated antigen-l (LFA-l), CD2, CD7, LIGHT, NKG2C, B7-H3, and/or a ligand that specifically binds with CD83. In some alternatives, the co-stimulatory domain is an intracellular signaling domain that interacts with other intracellular mediators to mediate a cell response including activation, proliferation, differentiation and cytokine secretion, and the like. In some alternatives described herein, the chimeric antigen receptor comprises a co-stimulatory domain.

[0033] "Coding for" as used herein refers to the property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other macromolecules such as a defined sequence of amino acids. Coding for can be used interchangeably with the term, "encoding." Thus, a gene codes for a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. A "nucleic acid sequence coding for a polypeptide" includes all nucleotide sequences that are degenerate versions of each other and that code for the same amino acid sequence.

[0034] "Cytotoxic T lymphocyte" (CTL) as used herein, refers to a T lymphocyte that expresses CD8 on the surface thereof (i.e., a $CD8^+$ T cell). In some alternatives, such cells are preferably "memory" T cells (T_M cells) that are antigen-experienced.

[0035] "Central memory" T cell (or "T_{CM}") as used herein, refers to an antigen experienced CTL that expresses CD62L or CCR-7 and CD45RO on the surface thereof, and does not express or has decreased expression of CD45RA as compared to naive cells. In some alternatives, central memory cells are positive for expression of CD62L, CCR7, CD28, CD127, CD45RO, and/or CD95, and/or have decreased expression of CD54RA as compared to naïve cells. In some alternatives, a host cell is provided wherein the host cell is antigen specific. In some alternatives, the cell is a central memory T cell.

[0036] "Effector memory" T cell (or "T_{EM}") as used herein refers to an antigen experienced T cell that does not express or has decreased expression of CD62L on the surface thereof as compared to central memory cells, and does not express or has decreased expression of CD45RA as compared to naïve cell. In some alternatives, effector memory cells are negative for expression of CD62L and CCR7, compared to naïve cells or central memory cells, and have variable expression of CD28 and CD45RA. In some alternatives, a host cell is provided wherein the host cell is antigen specific. In some alternatives, the cell is an effector memory T cell.

[0037] "Naïve " T cells as used herein refers to a non-antigen experienced T lymphocyte that expresses CD62L and CD45RA, and does not express CD45RO- as compared to central or effector memory cells. In some alternatives, naïve CD8+ T lymphocytes are characterized by the expression of phenotypic markers of naïve T cells including CD62L, CCR7, CD28, CD127, and/or CD45RA. In some alternatives, a host cell is provided wherein the host cell is antigen specific. In some alternatives, the cell is a naive T cell.

[0038] "Effector " "T_E" T cells as used herein, refers to an antigen experienced cytotoxic T lymphocyte cells that do not express or have decreased expression of CD62L, CCR7, and/or CD28, and are positive for granzyme B and/or perforin as compared to central memory or naïve T cells. In some alternatives, a host cell is provided wherein the host cell is antigen specific. In some alternatives, the cell is an effector T cell.

[0039] "T cell precursors" as described herein refers to lymphoid precursor cells that can migrate to the thymus and become T cell precursors, which do not express a T cell receptor. All T cells originate from hematopoietic stem cells in the bone marrow. Hematopoietic progenitors (lymphoid progenitor cells) from hematopoietic stem cells populate the thymus and expand by cell division to generate a large population of immature thymocytes. The earliest thymocytes express neither CD4 nor CD8, and are therefore classed as double-negative ($CD4^-CD8^-$) cells. As they progress through their development, they become double-positive thymocytes ($CD4^+CD8^+$), and finally mature to single-positive ($CD4^+CD8^-$ or $CD4^-CD8^+$) thymocytes that are then released from the thymus to peripheral tissues.

[0040] About 98% of thymocytes die during the development processes in the thymus by failing either positive selection or negative selection, whereas the other 2% survive and leave the thymus to become mature immunocompetent T cells.

[0041] The double negative (DN) stage of the precursor T cell is focused on producing a functional β-chain whereas the double positive (DP) stage is focused on producing a functional α-chain, ultimately producing a functional αβ T cell receptor. As the developing thymocyte progresses through the four DN stages (DN1, DN2, DN3, and DN4), the T cell expresses an invariant α-chain but rearranges the β-chain locus. If the rearranged β-chain successfully pairs with the invariant α-chain, signals are produced which cease rearrangement of the β-chain (and silence the alternate allele) and result in proliferation of the cell. Although these signals require this pre-TCR at the cell surface, they are dependent on ligand binding to the pre-TCR. These thymocytes will then express both CD4 and CD8 and progresses to the double positive (DP) stage where selection of the α-chain takes place. If a rearranged β-chain does not lead to any signaling (e.g. as a result of an inability to pair with the invariant α-chain), the cell may die by neglect (lack of signaling).

[0042] "Hematopoietic stem cells" or "HSC" as described herein, are precursor cells that can give rise to myeloid cells such as, for example, macrophages, monocytes, macrophages, neutrophils, basophils, eosinophils, erythrocytes, megakaryocytes/platelets, dendritic cells and lymphoid lineages (such as, for example, T-cells, B-cells, NK-cells). HSCs have a heterogeneous population in which three classes of stem cells exist, which are distinguished by their ratio of lymphoid to myeloid progeny in the blood (L/M).

[0043] "Enriched" and "depleted" as used herein to describe amounts of cell types in a mixture, refers to the subjecting of the mixture of the cells to a process or step which results in an increase in the number of the "enriched" type and a decrease in the number of the "depleted" cells. Thus, depending upon the source of the original population of cells subjected to the enriching process, a mixture or composition can contain 60, 70, 80, 90, 95, or 99 percent or more (in number or count) of the "enriched" cells, including any integer between any two endpoints of any of the listed values and 40, 30, 20, 10, 5 or 1 percent or less (in number or count) of the "depleted" cells, including any integer between any two endpoints of any of the listed values.

[0044] "Epitope" as used herein refers to a part of an antigen or molecule that is recognized by the immune system including antibodies, T cells, and/ or B cells. Epitopes usually have at least 7 amino acids and can be linear or conformational.

[0045] "Her2" or "ERBB2" refers to a membrane bound protein kinase receptor that needs a co-receptor for ligand binding. An exemplary polypeptide reference sequence for Her2 is found at Uniprot record P04626 and SEQ ID NO: 23.(Table 8) The full length reference sequence has 1255 amino acids including 1-22 amino acid signal sequence, 23-652 amino acid extracellular domain, 653-675 amino acid transmembrane domain, and 676-1255 amino acid cytoplasmic domain as shown in Table 8. The full length mature polypeptide sequence has 1233 amino acids as the leader sequence is not included in the mature polypeptide. A number of naturally occurring variants and isoforms are known. A nucleic reference sequence is found at Genbank X03363/gI 31197. The extracellular domain has 4 regions that correspond to: Domain I amino acids 23-217; domain II amino acids 218 to 341; domain III amino acids 342 to 510; and Domain IV amino acids 511 to 562 of SEQ ID NO: 23.

[0046] "Her2t" refers to a fragment of the sequence of Her2, and is useful as a genetic tag for transgene expression. In some alternatives, Her2t comprises domain IV of the extracellular domain of Her2 and excludes full length Her2. In some alternatives, Her2t specifically binds to an antibody specific for Domain IV of Her2. In other alternatives, Her2t comprises amino acids 511 to 562 or 563-652 of SEQ ID NO: 23.

[0047] "Isolated," is used to describe the various polypeptides disclosed herein, and means polypeptide or nucleic acid that has been identified and separated and/or recovered from a component of its natural environment. Preferably, the isolated polypeptide or nucleic acid is free of association with all components with which it is naturally associated. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide or nucleic acid, and can include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes.

[0048] "Intracellular signaling domain" as used herein refers to all or a portion of one or more domains of a molecule (here the chimeric receptor molecule) that provides for activation of a lymphocyte. Intracellular domains of such molecules mediate a signal by interacting with cellular mediators to result in proliferation, differentiation, activation and

other effector functions. In some alternatives, such molecules include all or portions of CD28, CD3, and/or 4-1BB, or combinations thereof.

[0049] "Ligand" as used herein refers to a substance that binds specifically to another substance to form a complex. Examples of ligands include epitopes on antigens, molecules that bind to receptors, substrates, inhibitors, hormones, and activators. "Ligand binding domain" as used herein refers to a substance or portion of a substance that binds to a ligand. Examples of ligand binding domains include antigen binding portions of antibodies, extracellular domains of receptors, and active sites of enzymes.

[0050] "Operably linked" as used herein, refers to functional linkage between a regulatory sequence and a heterologous nucleic acid sequence resulting in expression of the latter. For example, a first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary, it is to join two protein coding regions, in the same reading frame.

[0051] "Percent (%) amino acid sequence identity" with respect to the genetic tag polypeptide sequences identified herein, is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For example, % amino acid sequence identity values generated using the WU-BLAST-2 computer program [Altschul et al., Methods in Enzymology, 266:460-480 (1996)] uses several search parameters, most of which are set to the default values. Those that are not set to default values (i.e., the adjustable parameters) are set with the following values: overlap span=1,

overlap fraction=0.125, word threshold (T)=11 and scoring matrix=BLOSUM62. A % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between each or all of the polypeptide amino acid sequence of the reference Her2 sequence provided in SEQ ID NO: 15 or amino acids 563-652 of SEQ ID NO: 23 and the comparison amino acid sequence of interest as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the polypeptide of interest.

[0052] "Genetic tag variant polynucleotide" as used herein refers to a polypeptide-encoding nucleic acid molecule as defined below having at least about 80% nucleic acid sequence identity with the polynucleotide acid sequence shown in SEQ ID NO: 15 or nucleotides or a specifically derived fragment thereof. Ordinarily, a variant of polynucleotide or fragment thereof will have at least about 80% nucleic acid sequence identity, more preferably at least about 81% nucleic acid sequence identity, more preferably at least about 82% nucleic acid sequence identity, more preferably at least about 83% nucleic acid sequence identity, more preferably at least about 84% nucleic acid sequence identity, more preferably at least about 85% nucleic acid sequence identity, more preferably at least about 86% nucleic acid sequence identity, more preferably at least about 87% nucleic acid sequence identity, more preferably at least about 88% nucleic acid sequence identity, more preferably at least about 89% nucleic acid sequence identity, more preferably at least about 90% nucleic acid sequence identity, more preferably at least about 91% nucleic acid sequence identity, more preferably at least about 92% nucleic acid sequence identity, more preferably at least about 93% nucleic acid sequence identity, more preferably at least about 94% nucleic acid sequence identity, more preferably at least about 95% nucleic acid sequence identity, more preferably at least about 96% nucleic acid sequence identity, more preferably at least about 97% nucleic acid sequence identity, more preferably at least about 98% nucleic acid sequence identity and yet more preferably at least about 99% nucleic acid sequence identity with the nucleic acid sequence as shown in SEQ ID NO: 14 or a derived fragment thereof, or any percent nucleic acid sequence identity between any two of the values of percent nucleic acid sequence identity listed. Variants do not encompass the native nucleotide sequence. In this regard, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of chimeric receptor variant polynucleotides having at least about 80% nucleic acid sequence identity to the

nucleotide sequence of SEQ ID No: 14 or nucleotides that encodes a polypeptide having an amino acid sequence of SEQ ID NO: 18.

[0053] "Substantially purified" refers to a molecule that has 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% or less other molecule types or other cell types, or any value between any two of the percent purification values listed. A substantially purified cell also refers to a cell, which has been separated from other cell types with which it is normally associated in its naturally occurring state. In some instances, a population of substantially purified cells refers to a homogenous population of cells.

[0054] "Not substantially found" when used in reference the presence of a tumor antigen or other molecules on normal cells refers to the percentage of a normal cell type that has the antigen or molecule, and/or the density of the antigen on the cells. In some alternatives, not substantially found means that the antigen or molecule is found on less than 50% of normal cell type and/or at a 50% less density as compared to the amount of cells or antigen found on a tumor cell or other diseased cell.

[0055] "T cells" or "T lymphocytes" as used herein can be from any mammalian, preferably primate, species, including monkeys, dogs, and humans. In some alternatives, the T cells are allogeneic (from the same species but different donor) as the recipient subject; in some alternatives, the T cells are autologous (the donor and the recipient are the same); in some alternatives, the T cells are syngeneic (the donor and the recipients are different but are identical twins).

[0056] "Vector" or "construct" is a nucleic acid used to introduce heterologous nucleic acids into a cell that has regulatory elements to provide expression of the heterologous nucleic acids in the cell. Vectors include but are not limited to plasmid, minicircles, yeast, and viral genomes.

DETAILED DESCRIPTION

[0057] This disclosure provides for a genetic tag polypeptide or variant thereof and a nucleic acid coding for the genetic tag useful to provide a selection marker and/or an identification marker for transgene expressing cells.

Transgene Genetic Tag and Polypeptides and Variants.

[0058] One aspect of the disclosure provides a genetic tag for transgene expression that provides stable expression of the transgene expression in cells. In some alternatives, the genetic tag provides for selection of transduced cells that express the transgene at levels comparable to endogenous genes. In some alternatives, the genetic tag is expressed on the cell surface, has decreased immunogenicity, does not substantially increase the genetic payload in a vector, and/or provides for transgene expression in a variety of cells.

[0059] In some alternatives, the genetic tag is a fragment of Her2 designated as Her2t that at least includes an epitope recognized by an anti-Her2 antibody. In some alternatives, the antibody specifically binds to Domain IV of Her2. In other alternatives, the antibody specifically binds to Domain IV of Her2 and does not bind to epitopes in domains I, II, and/or III of Her2. In some alternatives, the anti-Her2 antibody is an antibody therapeutically useful for treating cancer. In some alternatives, the epitope is recognized by trastuzumab (Herceptin). In some alternatives, the epitope is recognized by trastuzumab and/or antibodies that compete for binding with trastuzumab but no other anti- Her2 antibodies that bind for example, to epitopes in domains I, II, and/or III of Her2.

[0060] In a specific alternative, the epitope includes amino acids as determined by the crystal structure of Her2 in complex with Herceptin Fab (Cho et al., Nature (2003) 421:756). The interaction between Her2 and Herceptin occurs between three loop regions (two electrostatic and one hydrophobic) in Domain IV. Key interactive amino acids in HER2 towards Herceptin are as follows: loop 1 (electrostatic), which includes amino acid sequence 580-584 EADQC (including Glu 580 and Asp 582) (SEQ ID NO: 42), loop 2 (hydrophobic) which includes amino acid sequence 592-595 DPPF (including Asp 592 and Phe 595) (SEQ ID NO: 43), and loop 3 (electrostatic) which includes amino acid sequence 616-625 FPDEEGACQP (Including Gln 624) (SEQ ID NO: 44) (aa numbering system is based off of the entire ErbB2(Her2) sequence of SEQ ID NO:23, including the signaling sequence and as shown in Table 8). Using the numbering system of Cho et al. which removes the 22aa from the signal sequence resulting in the following amino acids of HER2 involved with Herceptin : loop 1 Glu 558 and Asp 560, loop 2 Asp 570 and Phe 573, and loop 3 Gln 602. In some alternatives, a fragment of Her2 contains at least these amino acid residues and is further selected for binding to trastuzumab or an antibody that competes for binding with

trastuzumab when expressed on a cell surface. While not meant to limit the scope of the disclosure, it is believed that a Her2t fragment containing at least amino acids 563-652 includes an epitope that can bind trastuzumab as a smaller epitope containing amino acids 578 to 652 did not bind to trastuzumab. In some alternatives, the Her2t fragment comprises the amino acids 563-652 of Her2t. In some alternatives, the Her2t fragment comprises the amino acid sequences 580-584 of Her2t, amino acid sequences 592-595 of Her2t and amino acid sequences 616-625 of Her2t.

[0061] In a specific alternative, a fragment of Her2 comprises, consists essentially of, or consists of amino acids 511-652 (Domain IV) or 563-652 as shown in Table 6 (SEQ ID NO:18). In some alternatives, a variant of the Her2 fragment has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity with the sequence of SEQ ID NO:18 or a percentage sequence identity that is between a range defined by any two of the aforementioned percentages, and when expressed on the cell surface binds to trastuzumab. In some alternatives, the variant fragment has at least 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid substitutions, preferably conservative amino acid substitutions. Such substitutions can be identified using the crystal structure of Her2 in complex with Herceptin Fab (Cho et al., Nature (2003)). In some alternatives, the variant fragment does not include amino acid substitution in the residues involved in binding to trastuzumab as described herein. In some alternatives, the fragment includes residues in Domain IV of Her2 and excludes one or more other domains of Her2 including domain 1, domain II, domain III, and/or intracellular domains.

[0062] In some alternatives, the genetic tag generates little or no immune response. In some alternatives, a genetic tag is selected from endogenously occurring proteins in order to take advantage of the subject's tolerance to endogenous proteins. In some alternatives, the genetic tag is analyzed with software for predicting antigenic epitopes such as MHC-I antigenic peptide processing prediction algorithm. A sequence: MLLLVTSLLLCELPHPAFLLIPCHPECQPQNGSVT (SEQ ID NO: 16) is analyzed for antigenic determinants. In some alternatives, the nucleic acid sequence of the genetic tag is derived from and/or modified from the germ line sequence for incorporation in an artificial or synthetic transgene construct.

[0063] In some alternatives, a genetic tag further includes a transmembrane domain. The transmembrane domain can be derived either from a natural or a synthetic source. When the source is natural, the domain can be derived from any membrane-bound or transmembrane protein. Transmembrane regions comprise at least the transmembrane region(s) of) the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3, CD45, CD4, CD8, CD9, CD16, CD22; CD33, CD37, CD64, CD80, CD86, CD134, CD137 and/or CD154. In a specific alternative, the transmembrane domain comprises the amino acid sequence of the Her2 transmembrane domain as shown in Table 6 (e.g. amino acids 653-675 (SEQ ID NO: 20). A representative polynucleotide sequence coding for the Her2 transmembrane domain (SEQ ID NO: 19) is shown in Table 6.

[0064] In some alternatives, synthetic or variant transmembrane domains comprise predominantly hydrophobic residues, such as leucine and valine. In some alternatives, a transmembrane domain can have at least 80%, 85%, 90%, 95%, or 100% amino acid sequence identity with a transmembrane domain as shown in Table 6 or percentage sequence identity that is between a range defined by any two of the aforementioned percentages. Variant transmembrane domains preferably have a hydrophobic score of at least 50 as calculated by Kyte Doolittle.

[0065] In some alternatives, a genetic tag includes a peptide that enhances surface expression of the genetic tag. Such peptides include, for example, including the granulocyte macrophage stimulating factor signal sequence, endogenous Her2 leader peptide (aa 1-22), type I signal peptides, IgGκ signal peptide, and/or CD8 leader sequence. In some alternatives, the leader sequence has a sequence of SEQ ID NO: 17.

[0066] In a specific alternative, a genetic tag comprises a fragment of Her2 that binds trastuzumab, and a transmembrane domain as exemplified by SEQ ID NO: 20. In another specific alternative, a genetic tag comprises a peptide that enhances surface expression, a fragment of Her2 that binds trastuzumab, and a transmembrane domain as exemplified by SEQ ID NO: 15. In some alternatives, a variant of the genetic tag has 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity with the sequence of SEQ ID NO:16 or SEQ ID NO:20 or a percentage sequence identity that is between a range defined by any two of the aforementioned percentages, and when expressed on the cell surface binds to trastuzumab. In some alternatives, the variant fragment has at least 9, 8, 7, 6,

5, 4, 3, 2, or 1 amino acid substitutions, preferably conservative amino acid substitutions. In some alternatives, the variant fragment does not include amino acid substitution in the residues involved in binding to trastuzumab.

[0067] Optionally, a linker sequence can precede the genetic tag sequence and/or separate one or more functional domains (e.g. peptide to enhance surface expression, genetic tag, transmembrane domain) of the genetic tag. Linker sequences are optionally cleavable, for example, T2A sequences (as shown in Table 1) or IRES sequences. Cleavable linker sequences are typically placed to precede the genetic tag sequence in a nucleic acid construct. Other linker sequences are typically short peptides, of about 2 to 15 amino acids and are located between functional domains of the genetic tag including the peptide to enhance surface expression, genetic tag, and transmembrane domain. In some alternatives, the linkers are between 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids and are located between functional domains of the genetic tag including the peptide to enhance surface expression, genetic tag, and transmembrane domain. In some alternatives the linker is a cleavable linker. In some alternatives the linker is a cleavable T2A sequence. In some alternatives, the linker comprises IRES sequences.

[0068] In some alternatives, the system further comprises one or more additional genetic tags. In an alternative, the additional genetic tag sequence is a fragment of an epidermal growth factor receptor (EGFRt) sequence. An example of such a sequence is provided in Table 7. Typically a genetic tag sequence has a functional characteristic that allows for selection of transduced cells and/or detection of transduced cells. In some alternatives, the genetic tag sequence is compatible with transduction of human lymphocytes.

[0069] In other alternatives, an additional genetic tag is a positive selectable marker. A positive selectable genetic tag can be a gene, which upon being introduced into the host cell, expresses a dominant phenotype permitting positive selection of cells carrying the gene. Genes of this type are known in the art, and include, inter alia, hygromycin-B phosphotransferase gene (hph) which confers resistance to hygromycin B, the amino glycoside phosphotransferase gene (neo or aph) from Tn5 which codes for resistance to the antibiotic G418, the dihydrofolate reductase (DHFR) gene which provides resistance to methotrexate, DHFR dm, the pac gene that provides resistance to puromycin, Sh ble gene which inactivates zeocin, the adenosine deaminase gene (ADA), and the multi-drug

resistance (MDR) gene. Transduced cells cultured in the presence of these agents will survive and be selected. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0070] In an alternative, a first nucleic acid further comprises a polynucleotide coding for a genetic tag sequence. In some alternatives, the genetic tag sequence is a Her2t sequence. An exemplary polynucleotide and amino acid for the Her2t sequences is shown in Table 6 and provided by SEQ ID NO:14 and SEQ ID NO:15, respectively. In an alternative, the genetic tag sequence is an epidermal growth factor receptor fragment (EGFRt) as shown in Table 7. An exemplary polynucleotide for the truncated epidermal growth factor receptor is SEQ ID NO: 22.

[0071] A polynucleotide coding for genetic tag can be readily prepared by synthetic or recombinant methods from the amino acid sequence. In some alternatives, a polynucleotide coding for a genetic tag sequence is operably linked to a polynucleotide coding for a linker sequence. In some alternatives, the polynucleotide coding for a genetic tag sequence can also have one or more restriction enzyme sites at the 5' and/or 3' ends of the coding sequence in order to provide for easy excision and replacement of the polynucleotide coding for a tag sequence with another polynucleotide coding for a different genetic tag sequence. In some alternatives, the polynucleotide coding for a marker sequence is codon optimized for expression in mammalian cells, preferably humans.

[0072] In some alternatives, two or more genetic tag sequences can be employed. In some alternatives, a first genetic tag sequence is operably linked to a first chimeric antigen receptor and provides for an indication that the transduced cell is expressing the first CAR. In other alternatives, a second genetic tag sequence is operably linked to a second and different CAR and provides an indication that the transduced cell is expressing the second CAR.

Nucleic Acids, and Vectors.

[0073] Another aspect of the disclosure includes nucleic acid constructs and variants thereof coding for the genetic tags as described herein.

[0074] In some alternatives, a nucleic acid codes for an amino acid sequence of a fragment Her2 or a variant thereof. In a specific alternative, a nucleic acid codes for a

polypeptide having an amino acid sequence of SEQ ID NO: 18. In a specific alternative, a nucleic acid codes for a polypeptide having an amino acid sequence of SEQ ID NO: 15. In an alternative, the genetic tag sequence is an epidermal growth factor receptor fragment (EGFRt) as shown in Table 7. An exemplary polynucleotide for the truncated epidermal growth factor receptor is SEQ ID NO: 21. Nucleic acids include nucleic acid sequences that are codon optimized for expression in humans, degenerate sequences, and variant sequences.

Vectors.

[0075] In some alternatives, a vector comprises a nucleic acid coding for a genetic tag. A nucleic acid coding for a genetic tag can be packaged in a vector as a separate construct or linked to a nucleic acid coding for a transgene. In some alternatives, a nucleic acid coding for a genetic tag is packaged in a vector as a separate construct or linked to a nucleic acid coding for a transgene

[0076] A variety of vector combinations can be constructed to provide for efficiency of transduction and transgene expression. In some alternatives, the vector is a dual packaged or single (all in one) viral vector. In other alternatives, the vectors can include a combination of viral vectors and plasmid vectors. Other viral vectors include foamy virus, adenoviral vectors, retroviral vectors, and lentiviral vectors. In alternatives, the vector is a lentiviral vector.

[0077] In some alternatives, a plasmid vector or a viral vector comprises a nucleic acid comprising a polynucleotide coding for a genetic tag. In some alternatives, the genetic tag comprises a polynucleotide coding for Her2t, and further comprises a promoter, a polynucleotide coding for a peptide to enhance surface expression and/or a polynucleotide coding for a transmembrane domain. In a specific alternative, the first nucleic acid codes for a polypeptide having a sequence of SEQ ID NO: 18 or SEQ ID NO: 20 or SEQ ID NO: 15 or variant thereof operably linked to a promoter.

[0078] In some alternatives, a plasmid or viral vector comprises a promoter operably linked to a polynucleotide coding for a chimeric antigen receptor operably linked to a polynucleotide coding for a genetic tag. In some alternatives, the chimeric antigen receptor

is directed to CD19 or CD20 and the genetic tag comprises Her2t fragment. In some alternatives, the polynucleotide coding for the CAR is operably linked to the genetic tag with a self-cleavable linker. In other alternatives, a plasmid or viral vector comprises a promoter operably linked to a polynucleotide coding for a CD19 chimeric antigen receptor operably linked to a polynucleotide coding for Her2t or EGFRt. In other alternatives, a plasmid or viral vector comprises a promoter operably linked to a polynucleotide coding for a CD20 chimeric antigen receptor operably linked to a polynucleotide coding for Her2t or EGFRt.

[0079] Each element of the nucleic acid can be separated from one another with a linker sequence, preferably, a self-cleaving linker such as a T2A self-cleaving sequence.

[0080] In other alternatives, the heterogeneous (heterogeneous to the vector, e,g, lentiviral vector) nucleic acid sequence is limited by the amount of additional genetic components that can be packaged in the vector. In some alternatives, a construct contains at least two genes heterogenous to the viral vector. In some alternatives, the construct contains no more than 4 genes heterogenous to the viral vector. The number of genes heterogenous to the viral vector that can be packaged in the vector can be determined by detecting the expression of one or more transgenes, and selecting vector constructs that provide for transduction of at least 10% of the cells and/or detectable expression levels of the transgene in at least 10% of the cells.

[0081] In some alternatives, a lentivirus is a dual packaged virus. A dual packaged virus contains at least one nucleic acid comprising a polynucleotide coding for a chimeric antigen receptor and a first genetic tag. Optionally the nucleic acid further comprises a polynucleotide coding for a cytokine, and/or a chemokine receptor. A dual packaged virus contains at least one nucleic acid comprising a polynucleotide coding for a chimeric antigen receptor and a second genetic tag. Optionally the nucleic acid further comprises a polynucleotide coding for a cytokine, and/or a chemokine receptor. In some alternatives of a system with two constructs, each construct can be packaged in a separate viral vector and the viral vectors can be mixed together for transduction in a cell population. In some alternatives, the first and second genetic tags are different from one another.

[0082] In some alternatives, the dual packaged virus provides for expression of at least two different transgenes, (e.g. CAR constructs) in a single cell type. Using different genetic tags provides for selection of dual transduced cells. In a specific alternative, a

plasmid or viral vector comprises a promoter operably linked to a polynucleotide coding for a CD19 chimeric antigen receptor operably linked to a polynucleotide coding for Her2t. In other alternatives, the plasmid or viral vector further comprises a promoter operably linked to a polynucleotide coding for a CD20 chimeric antigen receptor operably linked to a polynucleotide coding for EGFRt.

[0083] In some alternatives, the vector is a minicircle. Minicircles are episomal DNA vectors that are produced as circular expression cassettes devoid of any bacterial plasmid DNA backbone. Their smaller molecular size enables more efficient transfections and offers sustained expression over a period of weeks as compared to standard plasmid vectors that only work for a few days. In some alternatives, a minicircle comprises a promoter linked to a polynucleotide coding for a chimeric antigen receptor operably linked to a genetic tag. One or more minicircles can be employed. In some alternatives, a minicircle comprises a promoter linked to a polynucleotide coding for a chimeric antigen receptor and first genetic tag, another minicircle comprises a promoter linked to a polynucleotide coding for a chimeric antigen receptor and a second and different genetic tag. In some alternatives, each element of the constructs is separated by a nucleic acid, such as one coding for a self-cleaving T2A sequence. In some alternatives, each minicircle differs from one another in the chimeric antigen receptor including but not limited to the spacer length and sequence, the intracellular signaling domain, and/or the genetic tag sequence.

[0084] In some alternatives, the vector is a PiggyBac transposon. The PiggyBac (PB) transposon is a mobile genetic element that efficiently transposes between vectors and chromosomes via a "cut and paste" mechanism. During transposition, the PB transposase recognizes transposon-specific inverted terminal repeat sequences (ITRs) located on both ends of the transposon vector and efficiently moves the contents from the original sites and efficiently integrates them into TTAA chromosomal sites. The powerful activity of the PiggyBac transposon system enables genes of interest between the two ITRs in the PB vector to be easily mobilized into target genomes.

[0085] In some alternatives, a PB contains a promoter linked to a polynucleotide coding for a chimeric antigen receptor operably linked to a genetic tag. One or more PB transposons can be employed. In some alternatives, a PB comprises a promoter linked to a polynucleotide coding for a chimeric antigen receptor and a first genetic tag, another PB

comprises a promoter linked to a polynucleotide coding for a chimeric antigen receptor, and a second and different genetic tag. Each element of the constructs is separated by a nucleic acid, such as that coding for a self-cleaving T2A sequence. In some alternatives, each PB differs from one another in the chimeric antigen receptor including but not limited to the spacer length and sequence, the intracellular signaling domain, and/or the genetic tag sequence.

[0086] In some alternatives, a first nucleic acid comprises a first promoter operably linked to a polynucleotide coding for chimeric antigen receptor comprising a ligand binding domain, wherein the ligand binding domain binds to a ligand, wherein the ligand is a tumor specific molecule, viral molecule, or any other molecule expressed on a target cell population that is suitable to mediate recognition and elimination by a lymphocyte; a polynucleotide coding for a polypeptide spacer, wherein the spacer provides for increased T cell proliferation and/or cytokine production in response to the ligand as compared to a reference chimeric receptor; a polynucleotide coding for a transmembrane domain; and d) a polynucleotide coding for an intracellular signaling domain. In some alternatives, the first nucleic acid further comprises a genetic tag.

[0087] In some alternatives, a second nucleic acid comprises a polynucleotide coding for a second and different chimeric antigen receptor. The first and second chimeric antigen receptor can differ from one another in the ligand binding domain, the target antigen, an epitope of the target antigen, the spacer domain in length and sequence (short medium or long), and in the intracellular signaling domains. In some alternatives, the second nucleic acid further comprises a second and different genetic tag from that of the first nucleic acid.

[0088] In some alternatives, in a single lentivirus construct the first and second nucleic acids can be separated by a genomic insulator nucleic acid such as the sea urchin insulator chromatin domain.

[0089] In some alternatives, promoters used herein can be inducible or constitutive promoters. Inducible promoters include a tamoxifen inducible promoter, tetracycline inducible promoter, and doxocycline inducible promoter (e.g. tre) promoter. Constitutive promoters include SV40, CMV, UBC, EF1alpha, PGK, and CAGG.

[0090] One or more of these vectors can be used in conjunction with one another to transduce target cells and provide for expression of a chimeric antigen receptor.

Transgenes.

[0091] Severeal transgenes are also aspects of the invention.

[0092] The genetic tags as described herein are useful for the selection, tracking, and killing of cells transduced with and expressing a transgene. The genetic tags can be utilized with any number of different transgenes. In this disclosure, chimeric antigen receptor transgenes are exemplified but similar principals apply to the design, identification and selection of other transgenes expressed in transduced cells.

Chimeric Antigen Receptors.

[0093] Several chimeric antigen receptors can be utilized in the alternatives described herein.

[0094] A system for expression of chimeric antigen receptor comprises: a first nucleic acid comprising a first promoter linked to a polynucleotide coding for a chimeric antigen receptor, the chimeric antigen receptor comprising a ligand binding domain, wherein the ligand binding domain binds to a ligand, wherein the ligand is a tumor specific molecule, viral molecule, or any other molecule expressed on a target cell population that is suitable to mediate recognition and elimination by a lymphocyte; a polynucleotide coding for a polypeptide spacer, wherein the spacer provides for increased T cell proliferation and/or cytokine production in response to the ligand as compared to a reference chimeric receptor; a polynucleotide coding for a transmembrane domain; and d) a polynucleotide coding for an intracellular signaling domain. In other alternatives, another polynucleotide coding for a chimeric antigen receptor is under the control of a constitutive promoter.

Ligand binding domain.

[0095] Many ligand binding domains can be utilized in the alternatives described herein.

[0096] In some alternatives, the chimeric receptor nucleic acid comprises a polynucleotide coding for a ligand binding domain. In some alternatives, the ligand binding domain specifically binds to a tumor or viral specific antigen. In some alternatives, a ligand

binding domain, includes without limitation, receptors or portions thereof, small peptides, peptidomimetics, substrates, cytokines, and the like. In some alternatives, the ligand binding domain is an antibody or fragment thereof. A nucleic acid sequence coding for an antibody or antibody fragment can readily be determined. In a specific alternative, the polynucleotide codes for a single chain Fv that specifically binds CD19. In other specific some alternatives, the polynucleotide codes for a single chain Fv that specifically binds CD20, HER2, CE7, hB7H3, or EGFR. The sequences of these antibodies are known to or can readily be determined by those of skill in the art.

[0097] Tumor antigens are proteins that are produced by tumor cells that elicit an immune response. The selection of the ligand binding domain of the disclosure will depend on the type of cancer to be treated, and can target tumor antigens or other tumor cell surface molecules. A tumor sample from a subject can be characterized for the presence of certain biomarkers or cell surface markers. For example, breast cancer cells from a subject can be positive or negative for each of Her2Neu, Estrogen receptor, and/or the Progesterone receptor. A tumor antigen or cell surface molecule is selected that is found on the individual subject's tumor cells. Tumor antigens and cell surface molecules are well known in the art and include, for example, carcinoembryonic antigen (CEA), prostate specific antigen, PSMA, Her2/neu, estrogen receptor, progesterone receptor, ephrinB2, CD19, CD171, EGFR, CD20, CD22, CD23, CD123, CS-1, CE7, hB7H3, ROR1, mesothelin, c-Met, GD-2, and/or MAGE A3 TCR. In some alternatives a target molecule is a cell surface molecule that is found on tumor cells and is not substantially found on normal tissues, or restricted in its expression to non-vital normal tissues.

[0098] In one alternative, the target molecule on the tumor comprises one or more epitopes associated with a malignant tumor. Malignant tumors express a number of proteins that can serve as target antigens for T cell receptor or chimeric receptor mediated recognition. Other target molecules belong to the group of cell transformation-related molecules such as CD19 or CD20. In some alternatives, the tumor antigen is selectively expressed or overexpressed on the tumor cells as compared to control cells of the same tissue type. In other alternatives, the tumor antigen is a cell surface polypeptide.

[0099] Once a tumor cell surface molecule that might be targeted with a chimeric receptor is identified, an epitope of the target molecule is selected and characterized.

Antibodies that specifically bind a tumor cell surface molecule can be prepared using methods of obtaining monoclonal antibodies, methods of phage display, methods to generate human or humanized antibodies, or methods using a transgenic animal or plant engineered to produce human antibodies. Phage display libraries of partially or fully synthetic antibodies are available and can be screened for an antibody or fragment thereof that can bind to the target molecule. Phage display libraries of human antibodies are also available. In some alternatives, antibodies specifically bind to a tumor cell surface molecule and do not cross react with nonspecific components such as bovine serum albumin or other unrelated antigens. Once identified, the amino acid sequence or polynucleotide sequence coding for the antibody can be isolated and/or determined. In some alternatives, phage display libraries of partially or fully synthetic antibodies are screened for an antibody or fragment thereof that can bind to a target molecule.

[0100] Antibodies or antigen binding fragments include all or a portion of polyclonal antibodies, a monoclonal antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a bispecific antibody, a minibody, and a linear antibody. Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody and can readily be prepared. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0101] In some alternatives, a number of different antibodies that bind to particular tumor cell surface molecules can be isolated and characterized. In some alternatives, the antibodies are characterized based on epitope specificity of the targeted molecule. In addition, in some alternatives, antibodies that bind to the same epitope can be selected based on the affinity of the antibody for that epitope. In some alternatives, an antibody has an affinity of at least 1 mM, and preferably <50 nM. In some alternatives, an antibody is selected that has a higher affinity for the epitope as compared to other antibodies. For example, an antibody is selected that has at least a 2 fold, at least a 5 fold, at least a 10 fold, at least a 20 fold, at least a 30 fold, at least a 40 fold, or at least a 50 fold greater affinity than a reference antibody that binds to the same epitope. In some alternatives, an antibody is selected that has at least a 2 fold, at least a 5 fold, at least a 10 fold, at least a 20 fold, at least

a 30 fold, at least a 40 fold, or at least a 50 fold greater affinity, than a reference antibody that binds to the same epitope or any value of greater affinity between any of the defined values listed.

[0102] In some alternatives, target molecules are selected from CD19, CD20, CD22, CD23, CE7, hB7H3, EGFR, CD123, CS-1, ROR1, mesothelin, Her2, c-Met, PSMA, GD-2, and/or MAGE A3 TCR and combinations thereof. In some alternatives, when a Her2 CAR construct is desired, the genetic tag comprises an epitope that does not bind to the scFv for Her2 used in the CAR construct. In some alternatives, when a EGFR CAR construct is desired, the genetic tag comprises an epitope that does not bind to the scFv for EGFR used in the CAR construct.

[0103] In specific alternatives, the target antigen is CD19. A number of antibodies specific for CD19 are known to those of skill in the art and can be readily characterized for sequence, epitope binding, and affinity. In a specific alternative, the chimeric receptor construct includes a scFV sequence from FMC63 antibody. In other alternatives, the scFV is a human or humanized ScFv comprising a variable light chain comprising a CDRL1 sequence of RASQDISKYLN (SEQ ID NO: 27), CDRL2 sequence of SRLHSGV (SEQ ID NO:28), and a CDRL3 sequence of GNTLPYTFG (SEQ ID NO: 29). In other alternatives, the scFV is a human or humanized ScFv comprising a variable heavy chain comprising CDRH1 sequence of DYGVS (SEQ ID NO: 30), CDRH2 sequence of VIWGSETTYYNSALKS (SEQ ID NO: 31), and a CDRH3 sequence of YAMDY (SEQ ID NO: 32). The disclosure also contemplates variable regions that have at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity to that of the scFv for FMC63 or a percentage sequence identity that is between a range defined by any two of the aforementioned percentages and that have at least the same affinity for CD19.

[0104] In some alternatives, CDR regions are found within antibody regions as numbered by Kabat as follows: for the light chain; CDRL1 amino acids 24-34;CDRL2 amino acids 50-56; CDRL3 at amino acids 89-97; for the heavy chain at CDRH1 at amino acids 31-35; CDRH2 at amino acids 50-65; and for CDRH3 at amino acids 95-102. CDR regions in antibodies can be readily determined.

[0105] In specific alternatives, the target antigen is CD20. A number of antibodies specific for CD20 are known to those of skill in the art and can be readily

characterized for sequence, epitope binding, and affinity. In a specific alternative, the chimeric receptor construct includes a scFV sequence as shown in Table 9. In other alternatives, the scFV is a human or humanized ScFv comprising a variable light chain comprising a CDRL1 sequence of R A S S S V N Y M D (SEQ ID NO: 33), CDRL2 sequence of A T S N L A S (SEQ ID NO: 34), and a CDRL3 sequence of Q Q W S F N P P T (SEQ ID NO: 35). In other alternatives, the scFV is a human or humanized ScFv comprising a variable heavy chain comprising CDRH1 sequence of S Y N M H (SEQ ID NO: 36), CDRH2 of A I Y P G N G D T S Y N Q K F K G (SEQ ID NO: 37), and a CDRH3 sequence of S N Y Y G S S Y W F F D V (SEQ ID NO: 38). The CDR sequences can readily be determined from the amino acid sequence of the scFv. The disclosure also contemplates variable regions that have at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity to that of the scFv for CD20 or a percentage sequence identity that is between a range defined by any two of the aforementioned percentages and that have at least the same affinity for CD20.

[0106] In some alternatives, a polynucleotide coding for a ligand binding domain is operably linked to a polynucleotide coding for a spacer region. In some alternatives, the polynucleotide coding for a ligand binding domain can also have one or more restriction enzyme sites at the 5' and/or 3' ends of the coding sequence in order to provide for easy excision and replacement of the polynucleotide with another polynucleotide coding for a ligand binding domain coding for a different antigen or that has different binding characteristics. For example, a restriction site, NheI, is encoded upstream of the leader sequence; and a 3' RsrII located within the hinge region allows sub-cloning of any desirable scFv into a chimeric receptor vector. In some alternatives, the polynucleotide is codon optimized for expression in mammalian cells. In some alternatives, the polynucleotide is codon optimized for expression in human cells.

[0107] In some alternatives, the polynucleotide coding for a ligand binding domain is operably linked to a signal peptide. In some alternatives the signal peptide is a signal peptide for granulocyte colony stimulating factor. Polynucleotides coding for other signal peptides such as CD8 alpha can be utilized.

[0108] In some alternatives, the polynucleotide coding for a ligand binding domain is operably linked to a promoter. A promoter is selected that provides for expression

of the chimeric antigen receptor in a mammalian cell. In a specific alternative the promoter is an inducible promoter.

[0109] A specific alternative of a polynucleotide coding for a ligand binding domain is shown in Table 1 as the scFv from an antibody that specifically binds CD19, such as FMC63. A polynucleotide encoding for a flexible linker including the amino acids GSTSGSGKPGSGEGSTKG (SEQ ID NO: 39) separates the VH and VL chains in the scFV. The amino acid sequence of the scFv including the linker is shown in Table 1. (SEQ ID NO: 2) Other CD19-targeting antibodies such as SJ25C1 and HD37 are known. (SJ25C1: Bejcek et al. Cancer Res 2005, PMID 7538901; HD37: Pezutto et al. JI 1987, PMID 2437199).

[0110] A specific alternative of a polynucleotide coding for a ligand binding domain is shown in Table 9 as the scFv from an antibody that specifically binds CD20. A polynucleotide encoding for a flexible linker including the amino acids GSTSGSGKPGSGEGSTKG (SEQ ID NO: 39) separates the VH and VL chains in the scFV. The amino acid sequence of the scFv is shown in Table 9 (SEQ ID NO: 25). Other CD20-targeting antibodies such as 1F5 (Budde *et al.* 2013, PLOS One) are known.

Spacer.

[0111] In some alternatives, the chimeric receptor nucleic acid comprises a polynucleotide coding for a spacer region. Typically a spacer region is found between the ligand binding domain and the transmembrane domain of the chimeric receptor. In some alternatives, a spacer region provides for flexibility of the ligand binding domain, allows for high expression levels in lymphocytes. A CD19-specific chimeric receptor having a spacer domain of about 229 amino acids had less antitumor activity than a CD19-specific chimeric receptor with a short spacer region comprised of the modified IgG4 hinge only.

[0112] In some alternatives, a spacer region has at least 10 to 229 amino acids, 10 to 200 amino acids, 10 to 175 amino acids, 10 to 150 amino acids, 10 to 125 amino acids, 10 to 100 amino acids, 10 to 75 amino acids, 10 to 50 amino acids, 10 to 40 amino acids, 10 to 30 amino acids, 10 to 20 amino acids, or 10 to 15 amino acids, or a length that is within a range defined by any two of the aforementioned amino acid lengths. In some alternatives, a

spacer region has 12 amino acids or less but greater than 1 amino acid, 119 amino acids or less but greater than 1 amino acid, or 229 amino acids or less but greater than 1 amino acid.

[0113] In some alternatives, the spacer region is derived from a hinge region of an immunoglobulin like molecule. In some alternatives, a spacer region comprises all or a portion of the hinge region from a human IgG1, human IgG2, a human IgG3, or a human IgG4, and can contain one or more amino acid substitutions. Exemplary sequences of the hinge regions are provided in Table 5. In some alternatives, a portion of the hinge region includes the upper hinge amino acids found between the variable heavy chain and the core, and the core hinge amino acids including a polyproline region.

[0114] In some alternatives, hinge region sequences can be modified in one or more amino acids in order to avoid undesirable structural interactions such as dimerization. In a specific alternative, the spacer region comprises a portion of a modified human hinge region from IgG4, for example, as shown in Table 1 or Table 5 (SEQ ID NO: 10). A representative of a polynucleotide coding for a portion of a modified IgG4 hinge region is provided in Table 1. (SEQ ID NO: 1). In some alternatives, a hinge region can have at least about 90%, 92%, 95%, or 100% sequence identity with a hinge region amino acid sequence identified in Table 1 or Table 5. In a specific alternative, a portion of a human hinge region from IgG4 has an amino acid substitution in the core amino acids from CPSP to CPPC.

[0115] In some alternatives, all or a portion of the hinge region is combined with one or more domains of a constant region of an immunoglobulin. For example, a portion of a hinge region can be combined with all or a portion of a CH2 or CH3 domain or variant thereof. In some alternatives, the spacer region does not include the 47-48 amino acid hinge region sequence from CD8 alpha or the spacer region comprising an extracellular portion of the CD28 molecule.

[0116] In some alternatives, a short spacer region has about 12 amino acids or less but greater than 1 amino acid and comprises all or a portion of a IgG4 hinge region sequence or variant thereof, an intermediate spacer region has about 119 amino acids or less but greater than 1 amino acid and comprises all or a portion of a IgG4 hinge region sequence and a CH3 region or variant thereof, and a long spacer has about 229 amino acids or less but greater than 1 amino acid and comprises all or a portion of a IgG4 hinge region sequence, a CH2 region, and a CH3 region or variant thereof.

[0117] A polynucleotide coding for a spacer region can be readily prepared by synthetic or recombinant methods from the amino acid sequence. In some alternatives, a polynucleotide coding for a spacer region is operably linked to a polynucleotide coding for a transmembrane region. In some alternatives, the polynucleotide coding for the spacer region can also have one or more restriction enzyme sites at the 5' and/or 3' ends of the coding sequence in order to provide for easy excision and replacement of the polynucleotide with another polynucleotide coding for a different spacer region. In some alternatives, the polynucleotide coding for the spacer region is codon optimized for expression in mammalian cells. In some alternatives, the polynucleotide coding for the spacer region is codon optimized for expression in human cells.

[0118] In an alternative, the spacer region is selected from a hinge region sequence from IgG1, IgG2, IgG3, or IgG4 or portion thereof, a hinge region sequence from IgG1, IgG2, IgG3, or IgG4 in combination with all or a portion of a CH2 region or variant thereof, a hinge region sequence from IgG1, IgG2, IgG3, or IgG4 in combination with all or a portion of a CH3 region or variant thereof, and a hinge region sequence from IgG1, IgG2, IgG3, or IgG4 in combination with all or a portion of a CH2 region or variant thereof, and a CH3 region or variant thereof. In some alternatives, a short spacer region is a modified IgG4 hinge sequence (SEQ ID NO:10) having 12 amino acids or less but greater than 1 amino acid, an intermediate sequence is a IgG4 hinge sequence with a CH3 sequence having 119 amino acids or less but greater than 1 amino acid; or a IgG4 hinge sequence with a CH2 and CH3 region having 229 amino acids or less but greater than 1 amino acid. In some alternatives, a short spacer region has 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acids or a size within a range defined by any two of the aforementioned amino acid lengths. In some alternatives, a medium spacer region has 13, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110 or 119 amino acids or a size within a range defined by any two of the aforementioned amino acid lengths. In some alternatives, a spacer region has 120, 130, 140, 150, 160, 170, 180, 190, 200, 210 or 219 amino acids or a size within a range defined by any two of the aforementioned amino acid lengths.

Transmembrane domain.

[0119] In some alternatives, the chimeric receptor nucleic acid comprises a polynucleotide coding for a transmembrane domain. The transmembrane domain provides

for anchoring of the chimeric receptor in the membrane. In some alternatives, the transmembrane domain of the chimeric antigen receptor is different than that of the genetic tag.

[0120] In an alternative, the transmembrane domain that naturally is associated with one of the domains in the chimeric receptor is used. In some cases, the transmembrane domain can be selected or modified by amino acid substitution to avoid binding of such domains to the transmembrane domains of the same or different surface membrane proteins to minimize interactions with other members of the receptor complex.

[0121] The transmembrane domain can be derived either from a natural or a synthetic source. When the source is natural, the domain can be derived from any membrane-bound or transmembrane protein. Transmembrane regions comprise at least the transmembrane region(s) of the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3, CD45, CD4, CD8, CD9, CD16, CD22; CD33, CD37, CD64, CD80, CD86, CD134, CD137 and/or CD154. In a specific alternative, the transmembrane domain comprises the amino acid sequence of the CD28 transmembrane domain as shown in Table 2. A representative polynucleotide sequence coding for the CD28 transmembrane domain is shown in Table 1 (within SEQ ID NO: 2).

[0122] A transmembrane domain can be synthetic or a variant of a naturally occurring transmembrane domain. In some alternatives, synthetic or variant transmembrane domains comprise predominantly hydrophobic residues such as leucine and valine. In some alternatives, a transmembrane domain can have at least 80%, 85%, 90%, 95%, or 100% amino acid sequence identity with a transmembrane domain as shown in Table 2 or Table 6 or a sequence identity that is a percentage within a range defined by any two of the aforementioned percentages. Variant transmembrane domains preferably have a hydrophobic score of at least 50 as calculated by Kyte Doolittle.

[0123] A polynucleotide coding for a transmembrane domain can be readily prepared by synthetic or recombinant methods. In some alternatives, a polynucleotide coding for a transmembrane domain is operably linked to a polynucleotide coding for an intracellular signaling region. In some alternatives, the polynucleotide coding for a transmembrane domain can also have one or more restriction enzyme sites at the 5' and/or 3' ends of the coding sequence in order to provide for easy excision and replacement of the

polynucleotide coding for a transmembrane domain with another polynucleotide coding for a different transmembrane domain. In some alternatives, the polynucleotide coding for a transmembrane domain is codon optimized for expression in mammalian cells, preferably human cells.

Intracellular signaling domain.

[0124] In some alternatives, the chimeric receptor nucleic acid comprises a polynucleotide coding for an intracellular signaling domain. The intracellular signaling domain provides for activation of one function of the transduced cell expressing the chimeric receptor upon binding to the ligand expressed on tumor cells. In some alternatives, the intracellular signaling domain contains one or more intracellular signaling domains. In some alternatives, the intracellular signaling domain is a portion of and/or a variant of an intracellular signaling domain that provides for activation of at least one function of the transduced cell.

[0125] Examples of intracellular signaling domains for use in a chimeric receptor of the disclosure include the cytoplasmic sequences of the CD3 zeta chain, and/or co-receptors that act in concert to initiate signal transduction following chimeric receptor engagement, as well as any derivative or variant of these sequences and any synthetic sequence that has the same functional capability. T cell activation can be said to be mediated by two distinct classes of cytoplasmic signaling sequence: those that initiate antigen-dependent primary activation and provide a T cell receptor like signal (primary cytoplasmic signaling sequences) and those that act in an antigen-independent manner to provide a secondary or co-stimulatory signal (secondary cytoplasmic signaling sequences). Primary cytoplasmic signaling sequences that act in a stimulatory manner can contain signaling motifs which are known as receptor tyrosine-based activation motifs or ITAMs. Examples of ITAM containing primary cytoplasmic signaling sequences include those derived from CD3 zeta, FcR gamma, CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b, and/or CD66d. In some alternatives, the primary signaling intracellular domain can have at least 80%, 85%, 90%, or 95% sequence identity to CD3zeta having a sequence provided in Table 4 or a percentage sequence identity that is within a range defined by any two of the

aforementioned percentages. In some alternatives variants of CD3 zeta retain at least one, two, three or all ITAM regions as shown in Table 4.

[0126] In a preferred alternative, the intracellular signaling domain of the chimeric receptor can be designed to comprise the CD3-zeta signaling domain by itself or combined with any other desired cytoplasmic domain(s). For example, the intracellular signaling domain of the chimeric receptor can comprise a CD3zeta chain and a costimulatory signaling region.

[0127] The co-stimulatory signaling region refers to a portion of the chimeric receptor comprising the intracellular domain of a costimulatory molecule. A co-stimulatory molecule is a cell surface molecule other than an antigen receptor or their ligands that is required for a response of lymphocytes to an antigen. Examples of such molecules include CD27, CD28, 4-1BB (CD 137), OX40, CD30, CD40, lymphocyte function-associated antigen-1 (LFA-l), CD2, CD7, LIGHT, NKG2C, B7-H3, zeta chain associated protein kinase (ZAP70), and/or a ligand that specifically binds with CD83. In some alternatives, the co-stimulatory signaling domain can have at least 80%, 85%, 90%, or 95% amino acid sequence identity to the intracellular domain of CD28 as shown in Table 2 or to 4-1BB having a sequence provided in Table 3 or any percent sequence identity that is within a range defined by any two of the aforementioned percentages. In an alternative, a variant of the CD28 intracellular domain comprises an amino acid substitution at positions 186-187, wherein LL is substituted with GG.

[0128] The intracellular signaling sequences of the chimeric receptor can be linked to each other in a random or specified order. Optionally, a short oligo- or polypeptide linker, preferably between 2 and 10 amino acids in length can form the linkage. In some alternatives, a short oligo- or polypeptide linker comprise 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids or a size that is within a range defined by any two of the aforementioned sizes. In one alternative, the intracellular signaling domains comprises all or a portion of the signaling domain of CD3-zeta or variant thereof and all or a portion of the signaling domain of CD28 or a variant thereof. In another alternative, the intracellular signaling domain comprises all or a portion of the signaling domain of CD3-zeta or variant thereof and all or a portion of the signaling domain of 4-lBB or variant thereof. In yet another alternative, the intracellular signaling domain comprises all or a portion of the signaling domain of CD3-zeta or variant

thereof, all or a portion of the signaling domain of CD28 or variant thereof, and all or a portion of the signaling domain of 4-1BB or variant thereof. In a specific alternative, the amino acid sequence of the intracellular signaling domain comprising a variant of CD3zeta and a portion of the 4-1BB intracellular signaling domain is provided in Table 1. A representative nucleic acid sequence is provided in Table 1(within SEQ ID NO: 2).

[0129] In an alternative, a polynucleotide coding for an intracellular signaling domain comprises a 4-1BB intracellular domain linked to a portion of a CD3zeta domain. In other alternatives, a 4-1BB intracellular domain and a CD28 intracellular domain are linked to a portion of a CD3 zeta domain.

[0130] A polynucleotide coding for an intracellular signaling domain can be readily prepared by synthetic or recombinant methods from the amino acid sequence. In some alternatives, the polynucleotide coding for an intracellular signaling domain can also have one or more restriction enzyme sites at the 5' and/or 3' ends of the coding sequence in order to provide for easy excision and replacement of the polynucleotide coding for an intracellular signaling domain with another polynucleotide coding for a different intracellular signaling domain. In some alternatives, the polynucleotide coding for an intracellular signaling domain is codon optimized for expression in mammalian cells. In some alternatives, the polynucleotide coding for an intracellular signaling domain is codon optimized for expression in human cells.

Linker domains.

[0131] In some alternatives a linker domain is provided for flexibility between domains in a CAR construct. As shown below, a linker (SEQ ID NO: 45) between Domain IV and the transmembrane domain of Her2t led to the construct Her2tG. The linker is used to induce flexibility between protein domains. In other examples, the scFv of many CARs contain four consecutive G3S subunits placed between the Vh and Vl domains of the CAR's scFv. This allows for flexibility in folding of the two scFv domains. In an exemplary alternative, the rational of using two G3S linker subunits would suffice in being able to induce an increased amount of flexibility for Her2tG.

[0132] Two G3S linker subunits linked as one (SEQ ID NO: 45) was also used to mimic the spacer length of the CD28hinge and IgG4 hinge. Both the CD28 hinge and IgG4

hinge have been used as spacers previously between the scFv and transmembrane region in CARs that are functional. Both the CD28hinge and IgG4hinge contain a cysteine that facilitate dimerization. While helpful for CARs, this dimerization may inhibit the flexibility of Her2t and therefore not allow for as significant recognition to Herceptin. The advantage of using two G3S linkers (SEQ ID NO: 45) over three or four was to limit vector payload, eliminate potentially unnecessary sequences and at the same time achieve enhanced functionality.

[0133] In some alternatives, an isolated polypeptide is provided, wherein the isolated polypeptide comprises at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab.

Host Cells and Compositions: T lymphocyte populations.

[0134] The compositions described herein provide for genetically modified host cells with the vectors and/or constructs as described herein. In some alternatives, the host cells are CD4+ and/or CD8+ T lymphocytes. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0135] T lymphocytes can be collected in accordance with known techniques and enriched or depleted by known techniques such as affinity binding to antibodies such as flow

cytometry and/or immunomagnetic selection. After enrichment and/or depletion steps, in vitro expansion of the desired T lymphocytes can be carried out in accordance with known techniques or variations thereof that will be apparent to those skilled in the art. In some alternatives, the T cells are autologous T cells obtained from the patient.

[0136] For example, the desired T cell population or subpopulation can be expanded by adding an initial T lymphocyte population to a culture medium in vitro, and then adding to the culture medium feeder cells, such as non-dividing peripheral blood mononuclear cells (PBMC), (e.g., such that the resulting population of cells contains at least 5, 10, 20, or 40 or more PBMC feeder cells or an amount that is within a range defined by any two of the aforementioned amounts for each T lymphocyte in the initial population to be expanded); and incubating the culture (e.g. for a time sufficient to expand the numbers of T cells). The non-dividing feeder cells can comprise gamma-irradiated PBMC feeder cells. In some alternatives, the PBMC are irradiated with gamma rays in the range of 3000 to 3600 rads to prevent cell division. In some alternatives, the PBMC are irradiated with gamma rays of 3000, 3100, 3200, 3300, 3400, 3500 or 3600 rads or any value of rads between any two endpoints of any of the listed values to prevent cell division. The order of addition of the T cells and feeder cells to the culture media can be reversed if desired. The culture can typically be incubated under conditions of temperature and the like that are suitable for the growth of T lymphocytes. For the growth of human T lymphocytes, for example, the temperature will generally be at least 25 degrees Celsius, preferably at least 30 degrees, more preferably about 37 degrees. In some alternatives, the temperature for the growth of human T lymphocytes is 22, 24, 26, 28, 30, 32, 34, 36, 37 degrees Celsius or any other temperature between any two endpoints of any of the listed values.

[0137] The T lymphocytes expanded include $CD8^+$ cytotoxic T lymphocytes (CTL) and $CD4^+$ helper T lymphocytes that can be specific for an antigen present on a human tumor or a pathogen.

[0138] Optionally, the expansion method can further comprise the step of adding non-dividing EBV-transformed lymphoblastoid cells (LCL) as feeder cells. LCL can be irradiated with gamma rays in the range of 6000 to 10,000 rads. In some alternatives, the LCL are irradiated with gamma rays in of 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500 or 10,000 rads or any amount of rads between two endpoints of any of the listed values. The

LCL feeder cells can be provided in any suitable amount, such as a ratio of LCL feeder cells to initial T lymphocytes of at least about 10:1.

[0139] Optionally, the expansion method can further comprise the step of adding anti-CD3 and/or anti CD28 antibody to the culture medium (*e.g.*, at a concentration of at least about 0.5 ng/ml). Optionally, the expansion method can further comprise the step of adding IL-2 and/or IL-15 to the culture medium (*e.g.*, wherein the concentration of IL-2 is at least about10 units/ml).

[0140] After isolation of T lymphocytes both cytotoxic and helper T lymphocytes can be sorted into naïve, memory, and effector T cell subpopulations either before or after expansion.

[0141] CD8+ cells can be obtained by using standard methods. In some alternatives, CD8+ cells are further sorted into naïve, central memory, and effector memory cells by identifying cell surface antigens that are associated with each of those types of CD8+ cells. In some alternatives, memory T cells are present in both CD62L+ and CD62L- subsets of CD8+ peripheral blood lymphocytes. PBMC are sorted into CD62L-CD8+ and CD62L+CD8+ fractions after staining with anti-CD8 and anti-CD62L antibodies. In some alternatives, the expression of phenotypic markers of central memory T_{CM} include CD45RO, CD62L, CCR7, CD28, CD3, and CD127 and are negative or low for granzyme B. In some alternatives, central memory T cells are CD45RO+, CD62L+, CD8+ T cells. In some alternatives, effector T_E are negative for CD62L, CCR7, CD28, and CD127, and positive for granzyme B and perforin. In some alternatives, naïve CD8+ T lymphocytes are characterized by the expression of phenotypic markers of naïve T cells including CD62L, CCR7, CD28, CD3, CD127, and CD45RA.

[0142] CD4+ T helper cells are sorted into naïve, central memory, and effector cells by identifying cell populations that have cell surface antigens. CD4+ lymphocytes can be obtained by standard methods. In some alternatives, naïve CD4+ T lymphocytes are CD45RO-, CD45RA+, CD62L+, CD4+ T cells. In some alternatives, central memory CD4+ cells are CD62L+ and CD45RO+. In some alternatives, effector CD4+ cells are CD62L- and CD45RO-.

[0143] Whether a cell or cell population is positive for a particular cell surface marker can be determined by flow cytometry using staining with a specific antibody for the

surface marker and an isotype matched control antibody. A cell population negative for a marker refers to the absence of significant staining of the cell population with the specific antibody above the isotype control, positive refers to uniform staining of the cell population above the isotype control. In some alternatives, a decrease in expression of one or markers refers to loss of 1 log10 in the mean fluorescence intensity and/or decrease of percentage of cells that exhibit the marker of at least 20% of the cells, 25% of-the cells, 30% of the cells, 35% of the cells, 40% of the cells, 45% of the cells, 50% of the cells, 55% of the cells, 60% of the cells, 65% of the cells, 70% of the cells, 75% of the cells, 80% of the cells, 85% of the cells, 90% of the cell, 95% of the cells, and 100% of the cells and any % between 20 and 100% when compared to a reference cell population or any percent range of cells between the percent values of any of the aforementioned values when compared to a reference cell population. In some alternatives, a cell population positive for one or markers refers to a percentage of cells that exhibit the marker of at least 50% of the cells, 55% of the cells, 60% of the cells, 65% of the cells, 70% of the cells, 75% of the cells, 80% of the cells, 85% of the cells, 90% of the cell, 95% of the cells, and 100% of the cells and any percentage within a range defined by any two of the aforementioned percentages when compared to a reference cell population.

[0144] In some alternatives, populations of CD4+ and CD8+ that are antigen specific can be obtained by stimulating naïve or antigen specific T lymphocytes with antigen. For example, antigen-specific T cell lines or clones can be generated to Cytomegalovirus antigens by isolating T cells from infected subjects and stimulating the cells in vitro with the same antigen. Naïve T cells can also be used. Any number of antigens from tumor cells can be utilized as targets to elicit T cell responses. In some alternatives, the adoptive cellular immunotherapy compositions are useful in the treatment of a disease or disorder including a solid tumor, hematologic malignancy, breast cancer or melanoma.

Modification of T lymphocyte populations.

[0145] In some alternatives, it can be desired to introduce functional genes into the T cells to be used in immunotherapy in accordance with the present disclosure. For example, the introduced gene or genes can improve the efficacy of therapy by promoting the

viability and/or function of transferred T cells; or they can provide a genetic marker to permit selection and/or evaluation of in vivo survival or migration; or they can incorporate functions that improve the safety of immunotherapy, for example, by making the cell susceptible to controlled expression of the transgene. This can be carried out in accordance with known techniques that will be apparent to those skilled in the art based upon the present disclosure.

[0146] In some alternatives, T cells are modified with vector coding for genetic tags as described herein. In some alternatives, cells are modified with a vector comprising a polynucleotide coding for a chimeric antigen receptor operably linked to a genetic tag. In other alternatives, cells are modified with a vector comprising a polynucleotide coding for a genetic tag alone. In some alternatives, the T cells are obtained from the subject to be treated, in other alternatives, the lymphocytes are obtained from allogeneic human donors, preferably healthy human donors.

[0147] Chimeric receptors can be constructed with a specificity for any cell surface marker by utilizing antigen binding fragments or antibody variable domains of, for example, antibody molecules. The antigen binding molecules can be linked to one or more cell signaling modules. In some alternatives, cell signaling modules include CD3 transmembrane domain, CD3 intracellular signaling domains, and CD28 transmembrane domains. In some alternatives, the intracellular signaling domain comprises a CD28 transmembrane and signaling domain linked to a CD3 zeta intracellular domain.

[0148] In some alternatives, the same or a different chimeric receptor can be introduced into each of population of CD4+ and CD8+ T lymphocytes. In some alternatives, the chimeric receptor in each of these populations has a ligand binding domain that specifically binds to the same ligand on the tumor or infected cell or a different antigen or epitope. The cellular signaling modules can differ. In some alternatives, the intracellular signaling domain of the CD8+ cytotoxic T cells is the same as the intracellular signaling domain of the CD4+ helper T cells. In other alternatives, the intracellular signaling domain of the CD8+ cytotoxic T cells is different than the intracellular signaling domain of the CD4+ helper T cells. Each chimeric receptor is operably linked to a different genetic tag allowing for selection and identification of transduced cells expressing both chimeric antigen receptors.

[0149] Alternatives include methods of manufacturing compositions comprising host cells as described herein. In some alternatives, a method comprises introducing an isolated nucleic acid, such as a nucleic acid coding for isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, into a host cell; and culturing the host cells in a medium comprising at least one growth factor. In some alternatives, a method further comprises selecting the host cells for expression of Her2t before or after or both before and after the culturing step. In other alternatives, a method of manufacturing further comprises introducing a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag into the host cell. In some alternatives, the method further comprises selecting the host cells for expression of the second genetic tag before or after or both before and after the culturing step. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0150] In other alternatives, a method comprises introducing a first isolated nucleic acid, such as a nucleic acid coding for isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, into a first host cell; selecting first host cells that express Her2t, introducing a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag into a second host cell, selecting second host cells for expression of the second genetic tag, and optionally, culturing the first and second host cells in a medium comprising at least one growth factor. In some alternatives, a composition comprises a first and second host cell population. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0151] In some alternatives each of the CD4 or CD8 T lymphocytes can be sorted in to naïve, central memory, effector memory or effector cells prior to transduction as described herein. In some alternatives, each of the CD4 or CD8 T lymphocytes can be sorted into naïve, central memory, effector memory, or effector cells after transduction.

[0152] As described herein, in some alternatives, naïve CD4+ cells are CD45RO-, CD45RA+, CD62L+, and/or CD4+ positive T cells. In some alternatives, central memory CD4+ cells are CD62L positive and/or CD45RO positive. In some alternatives, effector CD4+ cells are CD62L negative and/or CD45RO positive. Each of these populations can be independently modified with a chimeric receptor.

[0153] As described herein, in some alternatives, memory T cells are present in both CD62L+ and/or CD62L- subsets of CD8+ peripheral blood lymphocytes. PBMC are sorted into CD62L-CD8+ and/or CD62L+CD8+ fractions after staining with anti-CD8 and anti-CD62L antibodies. In some alternatives, the expression of phenotypic markers of central memory T cells (TCM) include CD62L, CCR7, CD28, CD3, and/or CD127 and are negative or low for granzyme B. In some alternatives, central memory T cells are CD45RO+, CD62L+, and/or CD8+ T cells. In some alternatives, effector T cells (T_E) are negative for CD62L, CCR7, CD28, and/or CD127, and positive for granzyme B and/or perforin. In some alternatives, naïve CD8+ T lymphocytes are characterized by CD8+, CD62L+, CD45RO+, CCR7+, CD28+ CD127+, and/or CD45RO+. Each of these populations can be independently modified with a chimeric receptor.

[0154] Various transduction techniques have been developed which utilize recombinant infectious virus particles for gene delivery. This represents a currently preferred approach to the transduction of T lymphocytes of the present invention. The viral vectors which have been used in this way include virus vectors derived from simian virus 40, adenoviruses, adeno-associated virus (AAV), lentiviral vectors, and retroviruses. Thus, gene transfer and expression methods are numerous but essentially function to introduce and express genetic material in mammalian cells. Several of the above techniques have been used to transduce hematopoietic or lymphoid cells, including calcium phosphate transfection, protoplast fusion, electroporation, and infection with recombinant adenovirus, adeno-associated virus and retrovirus vectors. Primary T lymphocytes have been successfully transduced by electroporation and by retroviral or lentiviral infection.

[0155] Retroviral and lentiviral vectors provide a highly efficient method for gene transfer into eukaryotic cells. Moreover, retroviral or lentiviral integration takes place in a controlled fashion and results in the stable integration of one or a few copies of the new

genetic information per cell. In some alternatives, retroviral or lentiviral vectors are used for gene transfer into eukaryotic cells. In some alternatives, the cells are human cells.

[0156] It is contemplated that overexpression of a stimulatory factor (for example, a lymphokine or a cytokine) can be toxic to the treated individual. Therefore, it is within the scope of the invention to include gene segments that cause the T cells of the invention to be susceptible to negative selection in vivo. By "negative selection" it is meant that the infused cell can be eliminated as a result of a change in the in vivo condition of the individual. The negative selectable phenotype can result from the insertion of a gene that confers sensitivity to an administered agent, for example, a compound. In some alternatives, the genetic tag Her2t also provides for negative selection in vivo. For example, if it was desired to eliminate CAR expressing cells with the genetic tag Her2t, an antibody that binds to Domain IV of Her2 (e.g.trastuzumab) or an antibody that competes for binding with an antibody that binds to Domain IV of Her2, is administered to the subject. In preferred alternatives for eliminating the transduced cells the antibodies, the antibodies contain an Fc region in order to activate antibody dependent cellular cytotoxicity reaction to kill the transduced cells. In other alternatives, the antibody or fragment thereof is linked to a cytotoxic agent. The cytotoxic conjugate binds to cells expressing CAR and her2t and kills the cells. This method provides a way to ablate administered cells that are associated with toxicity or adverse side effects.

[0157] Other negative selectable genes are known in the art, and include, inter alia the following: the Herpes simplex virus type I thymidine kinase (HSV-I TK) gene, which confers ganciclovir sensitivity; the cellular hypoxanthine phosphribosyltransferase (HPRT) gene, the cellular adenine phosphoribosyltransferase (APRT) gene, and bacterial cytosine deaminase.

[0158] A variety of methods can be employed for transducing T lymphocytes, as is well known in the art. In some alternatives, transduction is carried out using lentiviral vectors.

[0159] In some alternatives, CD4+ and CD8+ cells each can separately be modified with an expression vector encoding a chimeric receptor to form defined populations. In some alternatives, cells can be separately modified with a vector comprising a polynucleotide coding for a CAR and first genetic tag and/or and a vector comprising a

polynucleotide coding for a CAR and second and different genetic tag. In some alternatives, the CAR constructs can be the same or different. For example, CD8 T cells are transduced with a CAR construct having the first genetic tag and CD4 T cells are tranduced with the same CAR with second genetic tag.

[0160] In some alternatives, these cells are then further sorted into subpopulations of naïve, central memory and effector cells as described above by sorting for cell surface antigens unique to each of those cell populations. In addition, CD4+ or CD8+ cell populations can be selected by their cytokine profile or proliferative activities. For example, CD4+ T lymphocytes that have enhanced production of cytokines such as IL-2, IL-4, IL-10, TNFα, and/or IFNγ as compared to sham transduced cells or transduced CD8+ cells when stimulated with antigen can be selected. In other alternatives, naïve or central memory CD4+ T cells that have enhanced production of IL-2 and/or TNFα are selected. Likewise, CD8+ cells that have enhanced IFNγ production are selected as compared to sham transduced CD8+ cells. In some alternatives, CD4+ or CD8+ cell populations are selected by their cytokine profile or proliferative activities. In some alternatives, CD4+ T lymphocytes that have enhanced production of cytokines such as IL-2, IL-4, IL-10, TNFα, and/or IFNγ as compared to sham transduced cells or transduced CD8+ cells when stimulated with antigen are selected.

[0161] In some alternatives, CD4+ and CD8+ cells are selected that are cytotoxic for antigen bearing cells. In some alternatives, CD4+ are expected to be weakly cytotoxic as compared to CD8+ cells. In a preferred alternative, transduced lymphocytes, such as CD8+ central memory cells, are selected that provide for tumor cell killing *in vivo* using an animal model established for the particular type of cancer.

[0162] In yet other alternatives, transduced cells are selected for the expression of a genetic tag. In some alternatives, after transduction, cells expressing, for example, Her2t or EGFRt are selected using antibodies that bind to the genetic tags. In some alternatives, the antibodies provide for selection of cell population containing at least 80-100% cells positive for the genetic tag.

[0163] Selected cells can be evaluated for transgene expression using techniques such as Western blot or flow cytometry. In some alternatives the cells selected for expression of a genetic tag are also further characterized for expression of the CAR by analyzing, for

example, the amount of the stimulatory domain (e.g. CD3zeta), Protein L, and T2A. In some alternatives, cells having a ratio of about 1:0.1 to 10:0.1 of expression of the CAR to the genetic tag are selected. In some alternatives, cells having a ratio of about 1:0.1, 2: 0.1, 3: 0.1, 4: 0.1, 5:01, 6:0.1, 7:0.1, 8:0.1, 9:01, or 10:0.1 of expression of the CAR to the genetic tag, or any other ratio of the CAR to the genetic tag that is between any of the listed ratios, are selected. In some alternatives, the Her2t genetic tag can be utilized in cases where the expression of the CAR is low as it provides better transgene expression levels than EGFRt. In some alternatives, a Her2t genetic tag provides for at least a 1.5 fold, 2 fold, 5 fold, or 10 fold increase in transgene expression as compared to EGFRt genetic tag, or any other fold increase between any two of the listed values.

[0164] In yet other alternatives, transduced chimeric receptor expressing T cells are selected that can persist in vivo using an animal model established for the particular type of cancer. In some alternatives, transduced chimeric receptor CD8+ central memory cells have been shown to persist in vivo after introduction into the animal for about 3 day or more, 10 days or more, 20 days or more, 30 days or more, 40 days or more, or 50 days or more, or any other time between any two of the listed values. Persistence in vivo can be determined by imaging with a detectably labeled antibody that binds to a genetic tag, such as Her2t or EGFRt.

[0165] The disclosure contemplates that combinations of CD4+ and CD8+ T cells will be utilized in the compositions. In one alternative, combinations of chimeric receptor transduced CD4+ cells can be combined with chimeric receptor transduced CD8+ cells of the same ligand specificity or combined with $CD8^+$ T cells that are specific for a distinct tumor ligand and different genetic tag. In other alternatives, chimeric receptor transduced CD8+ cells are combined with chimeric receptor transduced CD4+ cells specific for a different ligand expressed on the tumor. In yet another alternative, chimeric receptor modified CD4+ and CD8+ cells are combined. In some alternatives CD8+ and CD4+ cells can be combined in different ratios for example, a 1:1 ratio of CD8+ and CD4+, a ratio of 10:1 of CD8+ to CD4+, or a ratio of 100:1 of CD8+ to CD4+, or any other ratio of CD8+ to CD4+ that is between any two of the listed ratio values. In some alternatives, the combined population is tested for cell proliferation *in vitro* and/or *in vivo*, and the ratio of cells that provides for proliferation of cells is selected.

[0166] Before or after transduction and/or selection for chimeric receptor bearing cells, the cell populations are preferably expanded in vitro until a sufficient number of cells are obtained to provide for at least one infusion into a human subject, typically around 10^4 cells/kg to 10^9 cells/kg. In some alternatives, the transduced cells are cultured in the presence of antigen bearing cells, anti CD3, anti CD28, and IL 2, IL-7, IL 15, and/or IL-21 and combinations thereof.

[0167] Each of the subpopulations of CD4+ and CD8+ cells can be combined with one another. In a specific alternative, modified naïve or central memory CD4+ cells are combined with modified central memory CD8+ T cells to provide a synergistic cytotoxic effect on antigen bearing cells, such as tumor cells.

Compositions.

[0168] The disclosure provides for an adoptive cellular immunotherapy composition comprising a genetically modified T lymphocyte cell preparation as described herein.

[0169] In some alternatives, the T lymphocyte cell preparation comprises CD4 + T cells that have a chimeric receptor comprising an extracellular antibody variable domain specific for a ligand associated with the disease or disorder, a spacer region, a transmembrane domain, and an intracellular signaling domain of a T cell receptor and a genetic tag as described herein. In other alternatives, an adoptive cellular immunotherapy composition further comprises a chimeric receptor modified tumor-specific CD8+ cytotoxic T lymphocyte cell preparation that provides a cellular immune response, wherein the cytotoxic T lymphocyte cell preparation comprises CD8+ T cells that have a chimeric receptor comprising an extracellular single chain antibody specific for a ligand associated with the disease or disorder, a spacer region, a transmembrane domain, and an intracellular signaling domain of a T cell receptor and a genetic tag as described herein. In some alternatives, the chimeric receptor modified T cell population of the disclosure can persist *in vivo* for at least about 3 days or longer. In alternative each of these populations can be combined with one another or other cell types to provide a composition.

[0170] Alternatives include CD4 and/or CD8 host cells as described herein. In some alternatives, a host cell comprises an isolated nucleic acid, such as a nucleic acid

coding for an isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO:23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0171] In other alternatives, a composition comprises a first host cell comprising a first isolated nucleic acid, such as a nucleic acid coding for an isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO:23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and a second host cell comprising a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag. In some alternatives, the first host cell and the second host cell can be the same or different type of host cells, for example, the first host cell can be a CD8 central memory cells and the second host cell can be a naïve CD4 cell. In some alternatives, first and second host cells are each selected from the group consisting of CD8 T cells, CD4 T cells,CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, CD4 central memory cells, and combinations thereof.

[0172] In some alternatives, the CD4+ T helper lymphocyte cell is selected from the group consisting of naïve CD4+ T cells, central memory CD4+ T cells, effector memory CD4+ T cells, or bulk CD4+ T cells. In some alternatives, CD4+ helper lymphocyte cell is a naïve CD4+ T cell, wherein the naïve CD4+ T cell comprises a CD45RO-, CD45RA+, CD62L+ CD4+ T cell.

[0173] In some alternatives, the CD8+ T cytotoxic lymphocyte cell is selected from the group consisting of naïve CD8+ T cells, central memory CD8+ T cells, effector memory CD8+ T cells or bulk CD8+ T cells. In some alternatives, the CD8+ cytotoxic T lymphocyte cell is a central memory T cell wherein the central memory T cell comprises a CD45RO+, CD62L+, CD8+ T cell. In yet other alternatives, the CD8+ cytotoxic T

lymphocyte cell is a central memory T cell and the CD4+ helper T lymphocyte cell is a naïve or central memory CD4+ T cell.

Methods.

[0174] The disclosure provides methods of making adoptive immunotherapy compositions and uses or methods of using these compositions for performing cellular immunotherapy in a subject having a disease or disorder.

[0175] Alternatives include methods of manufacturing compositions comprising host cells as described herein. In some alternatives, a method comprises introducing an isolated nucleic acid, such as a nucleic acid coding for isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, into a host cell; and culturing the host cells in a medium comprising at least one growth factor. In some alternatives, a method further comprises selecting the host cells for expression of Her2t before or after or both before and after the culturing step. In other alternatives, a method of manufacturing further comprises introducing a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag into the host cell. In some alternatives, the method further comprises selecting the host cells for expression of the second genetic tag before or after or both before and after the culturing step. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0176] In other alternatives, a method comprises introducing a first isolated nucleic acid, such as a nucleic acid coding for isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 511 to 652 or 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, into a first host cell; selecting first host cells that express Her2t, introducing a second nucleic acid coding for a second chimeric antigen receptor and a second genetic tag into a second host cell, selecting second host cells for expression of the second genetic tag, and optionally, culturing the first and second host cells

in a medium comprising at least one growth factor. In some alternatives, a composition comprises a first and second host cell population.

[0177] In some alternatives, a method of manufacturing the compositions comprises obtaining a modified naïve or central memory CD4+ T helper cell, wherein the modified helper T lymphocyte cell preparation comprises CD4+ T cells that have a chimeric receptor comprising a ligand binding domain specific for a tumor cell surface molecule, a spacer domain, a transmembrane domain, and an intracellular signaling domain and a genetic tag as described herein.

[0178] In another alternative, a method further comprises obtaining a modified CD8+ central memory T cell, wherein the modified central memory CD8 T lymphocyte cell preparation comprises CD8+ cells that have a chimeric receptor comprising a ligand binding domain specific for a tumor cell surface molecule, a spacer domain, a transmembrane domain, and an intracellular signaling domain and a genetic tag as described herein. In other alternatives, CD8+ cells have a cytokine or chemokine receptor under the control of an inducible promoter.

[0179] The chimeric antigen receptor and genetic tag in both modified CD4+ T cells and modified CD8+ cytotoxic T cell can be the same or different. For example, modified CD4+ T cells that have a first CAR and first genetic tag, while the CD8+ cytotoxic T cell comprises CD8+ cells that have a second and different CAR and second and different genetic tag. In some alternatives, the polynucleotide can code for a chimeric antigen receptor that is the same in both the CD4+ and the CD8+ cell population. The difference between the two CAR constructs can include the specificity or affinity of the ligand binding domain for an antigen or epitope, the length and sequence of the spacer region, and the intracellular signaling components.

[0180] The preparation of the CD4+ and CD8+ cells that are modified with a chimeric receptor has been described above as well as in the examples. Antigen specific T lymphocytes can be obtained from a patient having the disease or disorder or can be prepared by *in vitro* stimulation of T lymphocytes in the presence of antigen. Subpopulations of CD4+ and CD8+ T lymphocytes that are not selected for antigen specificity can also be isolated as described herein and combined in the methods of manufacturing. Cell populations are

advantageously selected for expression of one or more genetic tags, such as Her2t and/or EGFRt.

[0181] In some alternatives, the combination of cell populations can be evaluated for uniformity of cell surface makers, the ability to proliferate through at least two generations, to have a uniform cell differentiation status. Quality control can be performed by determining the ratio of expression of CAR to the expression of the genetic tag. Cell differentiation status and cell surface markers on the chimeric receptor modified T cells can be determined by flow cytometry. In some alternatives, the markers and cell differentiation status on the CD8+ cells include CD3, CD8, CD62L, CD28, CD27, CD69, CD25, PD-1, CTLA-4, CD45RO, and/or CD45RA. In some alternatives, the markers and the cell differentiation status on the CD4+ cells include CD3, CD4, CD62L, CD28, CD27, CD69, CD25, PD-1, CTLA-4 CD45RO, and/or CD45RA.

[0182] In some alternatives, the chimeric receptor modified T cells as described herein are able to persist *in vivo* for at least 3 days, or at least 10 days. In some alternatives, the chimeric receptor modified T cells as described herein are able to persist *in vivo* for at least 3 days, 4 days, 5, days, 6 days, 7 days, 8 days, 9 days, or 10 days or any time within a range defined by any two of the aforementioned time points. In some alternatives, the chimeric receptor modified T cells can proliferate *in vivo* through at least 2, or at least 3 generations as determined by CFSE dye dilution. Proliferation and persistence of the chimeric receptor modified T cells can be determined by using an animal model of the disease or disorder and administering the cells and determining persistence and/ or proliferative capacity of the transferred cells by detecting the cells using a detectably labeled antibody that binds to the genetic tag such as Erbitux(EGFRt) and/or Herceptin (Her2t). When using antibodies or antigen binding fragments to detect transgene expressing cells in vivo, and antibody or antigen binding fragment preferably does not include a Fc portion in order to minimize any ADCC reaction. In other some alternatives, proliferation and activation can be tested *in vitro* by going through multiple cycles of activation with antigen bearing cells.

[0183] The disclosure also provides methods of performing cellular immunotherapy in a subject having a disease or disorder comprising: administering a composition of lymphocytes expressing one or more chimeric antigen receptor and genetic

tag as described herein. In some alternatives, a method of performing cellular immunotherapy in a subject having a disease or disorder is provided, wherein the method comprises administering a composition of lymphocytes expressing one or more chimeric antigen receptor and genetic tag.

[0184] Alternatives include a method of treating patient having cancer expressing a tumor antigen comprises administering an effective amount of a compositions as described herein, wherein the cells of the composition express a chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a genetic tag. In some alternatives, the cancer has a tumor antigen recognized by the chimeric antigen receptor on the cells. In some alternatives, the cancer is selected from the group consisting of breast cancer, diffuse large B cell lymphoma, lymphoma, ALL, CLL, and multiple myeloma.

[0185] In some alternatives, a method of treating patient having cancer expressing a tumor antigen comprises administering an effective amount of a compositions as described herein, wherein the cells of the composition express a first chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a first genetic tag and a second chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a second genetic tag.

[0186] In some alternatives, a method of treating patient having cancer expressing a tumor antigen comprises administering an effective amount of a composition comprising a first host cell that expresses a first chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a first genetic tag and a second host cell comprising a second chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a second genetic tag. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells.

[0187] In other alternatives, a method of treating a patient having cancer and/or expressing a tumor antigen is provided, wherein the method comprises administering an effective amount of a composition as described herein and an antibody that specifically binds to the genetic tag, wherein the cells of the composition express a chimeric antigen receptor

that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a genetic tag. In some alternatives, the antibody binds to Domain IV of Her2, or binds to EGFRt. In some alternatives, the antibodies are Herceptin or Erbitux.

[0188] In some alternatives, if a toxic effect of the composition is observed, an antibody that binds the genetic tag is administered. The antibody can bind to and kill the CAR expressing cells of the composition in order to avoid toxic and/or fatal side effects. In some alternatives, the antibody or antigen binding fragment preferable contains a Fc fragment in order to activate ADCC reactions. In other alternatives, the antibody or antigen binding fragment is conjugated to a cytotoxic agent. Cytotoxic agents include cantansinoids, calicheamicin and/or auristatins. In some alternatives, the cytotoxic agents comprise cantansinoids, calicheamicin and/or auristatins.

[0189] In some alternatives, an antibody is detectably labelled in order to allow tracking of the cells in vivo. In some alternatives, when the antibody is used for detection in vivo, it is preferred that the antibody or antigen binding fragment lacks all or a portion of the Fc region in order to avoid ADCC reactions. Detectable labels include biotin, His tags, myc tags, radiolabels, and/or fluorescent labels. In some alternatives the detectable labels comprise biotin, His tags, myc tags, radiolabels, and/or fluorescent labels.

[0190] In other alternatives, a method comprises administering to the subject a genetically modified cytotoxic T lymphocyte cell preparation that provides a cellular immune response, wherein the cytotoxic T lymphocyte cell preparation comprises CD8 + T cells that have a chimeric receptor comprising a ligand binding domain specific for a tumor cell surface molecule, a spacer domain, a transmembrane domain, and an intracellular signaling domain and a first genetic tag as described herein, and/or a genetically modified helper T lymphocyte cell preparation that elicits direct tumor recognition and augments the genetically modified cytotoxic T lymphocyte cell preparations ability to mediate a cellular immune response, wherein the helper T lymphocyte cell preparation comprises CD4+ T cells that have a chimeric receptor comprising a ligand binding domain specific for a tumor cell surface molecule, a spacer domain, a transmembrane domain, and an intracellular signaling domain and a second genetic tag.

[0191] Another alternative describes a method of performing cellular immunotherapy in a subject having a disease or disorder comprising: analyzing a biological

sample of the subject for the presence of a target molecule associated with the disease or disorder and administering the adoptive immunotherapy compositions described herein, wherein the chimeric receptor specifically binds to the target molecule.

[0192] Subjects that can be treated by the present invention are, in general, human and other primate subjects, such as monkeys and apes for veterinary medicine purposes. The subjects can be male or female and can be any suitable age, including infant, juvenile, adolescent, adult, and geriatric subjects. In some alternatives, the subject is a primate subject or a human.

[0193] The methods are useful in the treatment of, for example, hematologic malignancy, melanoma, breast cancer, and other epithelial malignancies or solid tumors. In some alternatives, the molecule associated with the disease or disorder is selected from the group consisting of orphan tyrosine kinase receptor ROR1, Her2, EGFR, CE7, hB7H3, CD19, CD20, CD22, mesothelin, CEA, and hepatitis B surface antigen.

[0194] Subjects that can be treated include subjects afflicted with cancer, including but not limited to colon, lung, liver, breast, renal, prostate, ovarian, skin (including melanoma), bone, and brain cancer, etc. In some alternatives, the tumor associated antigens or molecules are known, such as melanoma, breast cancer, squamous cell carcinoma, colon cancer, leukemia, myeloma, and prostate cancer. In other alternatives the tumor associated molecules can be targeted with genetically modified T cells expressing an engineered chimeric receptor. Examples include but are not limited to B cell lymphoma, breast cancer, prostate cancer, and leukemia. In some alternatives, the subject has B cell lymphoma, breast cancer, prostate cancer, and/or leukemia.

[0195] Cells prepared as described above can be utilized in methods and compositions for adoptive immunotherapy in accordance with known techniques, or variations thereof that will be apparent to those skilled in the art based on the instant disclosure.

[0196] In some alternatives, the cells are formulated by first harvesting them from their culture medium, and then washing and concentrating the cells in a medium and container system suitable for administration (a "pharmaceutically acceptable" carrier) in a treatment-effective amount. Suitable infusion medium can be any isotonic medium formulation, typically normal saline, Normosol R (Abbott) or Plasma-Lyte A (Baxter), but

also 5% dextrose in water or Ringer's lactate can be utilized. The infusion medium can be supplemented with human serum albumin, fetal bovine serum or other human serum components.

[0197] In some alternatives, a treatment effective amount of cells in the composition is a transduced CD4 or CD8 cell or at least 2 cell subsets (for example, 1 CD8+ central memory T cell subset and 1 CD4+ helper T cell subset) or is more typically greater than 10^2 cells, and up to 10^6, up to and including 10^8 or 10^9 cells and can be more than 10^{10} cells or any amount of cells defined between any two endpoints of any of the listed values.

[0198] The number of cells will depend upon the ultimate use for which the composition is intended, as will the type of cells included therein. For example, if cells that are specific for a particular antigen are desired, then the population will contain greater than 70%, generally greater than 80%, 85% and 90-95% of such cells or any percent amount of cells within a range defined by any two of the aforementioned percentages.

[0199] For uses provided herein, the cells are generally in a volume of a liter or less but greater than 1nl, can be 500 mls or less but greater than 1nl, even 250 mls or 100 mls or less but greater than 1nl, or any volume defined between two endpoints of any of the listed values.

[0200] Hence the density of the desired cells is typically greater than 10^4 cells/ml and generally is greater than 10^7 cells/ml, generally 10^8 cells/ml or greater. The clinically relevant number of immune cells can be apportioned into multiple infusions that cumulatively equal or exceed 10^6, 10^7, 10^8, 10^8, 10^9, 10^{10} or 10^{11} cells or any amount of cells within a range defined by two of the aforementioned amounts.

[0201] In some alternatives, the lymphocytes can be used to confer immunity to individuals. By "immunity" is meant a lessening of one or more physical symptoms associated with a response to infection by a pathogen, or to a tumor, to which the lymphocyte response is directed. The amount of cells administered is usually in the range present in normal individuals with immunity to the pathogen. Thus, the cells are usually administered by infusion, with each infusion in a range of from 2 cells, up to at least 10^6 to $3x10^{10}$ cells, preferably in the range of at least 10^7 to 10^9 cells or any amount of cells within a range defined by two of the aforementioned amounts.

[0202] The T cells can be administered by a single infusion, or by multiple infusions over a range of time. However, since different individuals are expected to vary in responsiveness, the type and amount of cells infused, as well as the number of infusions and the time range over which multiple infusions are given are determined by the attending physician, and can be determined by routine examination. The generation of sufficient levels of T lymphocytes (including cytotoxic T lymphocytes and/or helper T lymphocytes) is readily achievable using the rapid expansion method of the present invention, as exemplified herein.

[0203] In some alternatives, the composition as described herein are administered intravenously, intraperitoneally, intratumorly, into the bone marrow, into the lymph node, and/or into cerebrospinal fluid. In some alternatives, the chimeric receptor engineered compositions are delivered to the site of the tumor. Alternatively, the compositions as described herein can be combined with a compound that targets the cells to the tumor or the immune system compartments and avoid sites such as the lung.

[0204] In some alternatives, the compositions as described herein are administered with chemotherapeutic agents and/or immunosuppressants. In an alternative, a patient is first treated with a chemotherapeutic agent that inhibits or destroys other immune cells followed by the compositions described herein. In some cases, chemotherapy can be avoided entirely. The present invention is illustrated further in the examples set forth below.

Additional Alternatives.

[0205] In some alternatives, an isolated polypeptide is provided, wherein the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that

provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab.

[0206] In some alternatives, an isolated polypeptide is provided wherein the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab.

[0207] In some alternatives, an isolated nucleic acid is provided wherein the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO:

17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25

(CD20CAR). In some alternatives, the size of the isolated nucleic acid comprises a size of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 14.9 Kb, or any size in between any two of the construct size listed.

[0208] In some alternatives, a host cell is provided wherein the host cell comprises an isolated nucleic acid, wherein the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide

comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25 (CD20CAR). In some alternatives, the host cell is selected from the group consisting of CD8 T cells, CD4 T cells, CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, and CD4 central memory cells, or combinations thereof. In some alternatives, the host cell is autologous. In some alternatives, the host cell is antigen specific. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells. In some alternatives, the size of the isolated nucleic acid comprises a size of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 14.9 Kb, or any size in between any two of the construct size listed.

[0209] In some alternatives, a composition comprising host cells is provided wherein the host cells comprise an isolated nucleic acid, wherein the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes

the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a

sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25 (CD20CAR). In some alternatives, the host cell is selected from the group consisting of CD8 T cells, CD4 T cells, CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, and CD4 central memory cells, or combinations thereof. In some alternatives, the host cell is autologous. In some alternatives, the host cell is antigen specific. In some alternatives, the host cells are precursor T cells. In some alternatives, the host cells are hematopoietic stem cells. In some alternatives, the size of the isolated nucleic acid comprises a size of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 14.9 Kb, or any size in between any two of the construct size listed.

[0210] In some alternatives, a method of manufacturing a composition is provided, wherein the method comprises introducing an isolated nucleic acid into a host cell and culturing the host cells in a medium comprising at least one growth factor. In some alternatives, the isolated nucleic acid encodes a polypeptide. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide has the sequence of SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity

to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45). In some alternatives, the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO: 23. In some alternatives, the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23. In some alternatives, the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23. In some alternatives, the isolated polypeptide further comprises a leader peptide that provides for cell surface expression. In some alternatives, the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17. In some alternatives, the antibody is trastuzumab. In some alternatives, the isolated nucleic acid further comprises a promoter. In some alternatives, the isolated nucleic acid further comprises a transgene. In some alternatives, the transgene comprises a polynucleotide encoding a chimeric antigen receptor. In some alternatives, the chimeric antigen receptor comprises an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain. In some alternatives, the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide with a self-cleaving linker. In some alternatives, the HER2 polypeptide comprises at least 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2. In some alternatives, the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26). In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 2. In some alternatives, the chimeric antigen receptor comprises the amino acid sequence of SEQ ID NO: 25 (CD20CAR). In some alternatives, the host cell is selected from the group consisting of CD8 T cells, CD4 T cells, CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, and

CD4 central memory cells, or combinations thereof. In some alternatives, the host cell is autologous. In some alternatives, the host cell is antigen specific. In some alternatives, the growth factor is selected from IL-15, IL-7, IL-21, or IL-2, and combinations thereof. In some alternatives, the method further comprises selecting cells that express the Her2t polypeptide. In some alternatives, the cells are selected before culturing the cells in the medium. In some alternatives, the cells are selected using an antibody that binds to Domain IV of Her2. In some alternatives, the antibody is trastuzumab. In some alternatives, the method further comprises introducing a second isolated nucleic acid coding for a chimeric antigen receptor linked to a second genetic tag. In some alternatives, the method further comprises selecting cells expressing the second genetic tag. In some alternatives, the second genetic tag comprises EGFRt.

[0211] The preparation of transduced cells containing a CAR with a her2t marker sequence is described in the following.

Antibodies and flow cytometry.

[0212] Fluorochrome-conjugated isotype controls, anti-CD3, CD4, CD8, CD45, Her2, and streptavidin were obtained from BD Biosciences. Cetuximab (Erbitux) and trastuzumab (Herceptin) were purchased from the Seattle Children's Hospital. Erbitux and Herceptin were biotinylated (Pierce) or directly conjugated to APC (Solulink), according to manufacturer's instructions. Data acquisition was performed on an LSRFortessa (BD Biosciences), and the percentage of cells in a region of analysis was calculated using FlowJo data analysis software.

Cell lines.

[0213] All cell lines were maintained in RPMI 1640 supplemented with 2 mM L-glutamine, 25 mM HEPES (Irvine Scientific), and 10% heat-inactivated fetal bovine serum (Hyclone or Atlas), unless otherwise noted. K562 erythroleukemia target cell lines were kindly provided by Dr. Stanley Riddell (Fred Hutchinson Cancer Research Center). Other cell lines H9 T lymphoblast, Raji (human Burkitt's lymphoma), and 293T (highly transfectable derivative of human embryonic kidney 293 cells) were supplied by the American Type Culture Collection. Epstein-Barr virus-transformed lymphoblastoid cell lines

(TM-LCLs) were made from peripheral blood mononuclear cells (PBMCs) as previously described (Pelloquin *et al.* 1986). GFP:ffluc-expressing cell lines were transduced with GFP:ffluc_epHIV7 and sorted using the BD FACSJazz sorter.

Vector construction and preparation of Her2t or EGFRt-encoding lentivirus.

[0214] The second-generation 41BB-zeta CD19CAR-T2A-EGFRt_epHIV7 lentiviral construct was previously described (Hudecek *et al.* 2013). (**Table 1**)

[0215] The CD20CAR-T2A-EGFRt_epHIV7 contains a Leu16 (murine anti-human CD20) scFv fused to the human IgG4Hinge-CH3 (119 aa) spacer domain portion of IgG4 along with the same signaling components of the CD19CAR (4-1BB-zeta). (**Table 9**)

[0216] Her2t was synthesized by PCR, using pDONR223-ErbB2 (Addgene) as a template and the epHIV7 lentiviral vector as a recipient.(Tables 6 and 8) The final product, Her2t_epHIV7, contains the human granulocyte-macrophage colony stimulating factor receptor leader peptide (GMCSFRss) fused in frame to domain IV (aa 563-652) and the transmembrane spanning components of Her2 (aa 653-675). Her2t replaced EGFRt in the CD19CAR-T2A-EGFRt_epHIV7 construct by PCR and Gibson cloning. EGFRt was synthesized as previously described (Wang *et al.* 2011). (Table 7)

[0217] The CD19CAR-T2A-Her2t-, CD19CAR-T2A-EGFRt-, CD20CAR-T2A-EGFRt-, Her2t-, and EGFRt-encoding lentiviruses were produced in 293T cells using the packaging vectors pCHGP-2, pCMV-Rev2, and pCMV-G.

Generation of CAR-, Her2t-, and/or EGFRt-expressing cell lines.

[0218] To generate CD4 or CD8 central memory T cells, human PBMCs were isolated over Ficoll-Paque (Pharmacia Biotech) from blood discard kits of healthy donors (Puget Sound Blood Center). PBMCs from each donor were split into two groups (CD4 or CD8 central memory T cell isolation) and subsequently AutoMACS depleted using CD4 or CD8 isolation kits and anti-CD45RA microbeads (Miltenyi Biotec), per the manufacturer's protocol. The depleted fraction was then positively selected on AutoMACS using anti-CD62L microbeads to produce $CD4^+CD45RO^+CD62L^+$ or $CD8^+CD45RO^+CD62L^+$ central memory T cells. Isolated cells were then stimulated with 50U/ml interleukin-2 (IL-2), 2 ng/ml interleukin-15 (IL-15), and anti-CD3/CD28 beads (Life Technologies). Primary

T cell lines were transduced on day 3 after activation using protamine sulfate (1:100 dilution) and a virus MOI of 1 followed by centrifugation at 800 × *g* for 45 minutes at 32°C. All other cell lines were similarly transduced at a low cell passage number.

[0219] The $Her2t^+$ or $EGFRt^+$ subset of each cell line was enriched by immunomagnetic selection with biotin-conjugated Herceptin or Erbitux and anti-biotin microbeads (Miltenyi). Selected CD19 or $CD20CAR^+$ T cells were expanded 12-18 days post transduction by stimulation with irradiated (8000 rad) TM-LCLs at a T cell:TM-LCL ratio of 1:7 in the presence of 50U/ml IL-2 and 2ng/ml of IL-15. CD19CAR-T2A-$Her2t^+$ /CD20CAR-T2A-$EGFRt^+$ T cells were sorted using biotinylated Herceptin and anti-biotin multisort microbeads (Miltenyi) followed by bead removal, Erbitux-APC cell labeling, and anti-APC microbeads (Miltenyi).

Protein analysis.

[0220] Cell lysis was carried out in RIPA buffer containing protease inhibitor cocktail. Cell lysates were analyzed by BCA assay (Pierce), equally loaded onto gels and western blots were probed with the primary antibodies Her2 and phospho-Her2 (Cell Signaling Technology), anti CD247 (CD3ζ), biotinylated Herceptin, or anti–β-actin (loading control). Secondary IRDye 800CW conjugated Streptavidin or goat anti-mouse or rabbit (LI-COR) was added as per the manufacturer's instructions. Blots were imaged on the Odyssey Infrared Imaging System (LI-COR).

Cytotoxicity, cytokine secretion, and proliferation assays.

[0221] *Cytotoxicity:* Four-hour chromium release assays were performed as previously described (Wang *et al.* 2011). Antibody-dependent cell-mediated cytotoxicity (ADCC) was determined using up to 2.5×10^5 Tcm cells expressing CD19CAR with Her2t marker, CD20CAR with EGFRt marker, CD19CAR-Her2t and CD20CAREGFRt, and CD19CAR with EGFRt as a marker sequence as effector cells in co-cultures with 5×10^3 Cr^{51}-labeled K562 cell expressing either CD19 or CD20.

[0222] *Cytokine secretion:* T cells (5×10^5) were plated in triplicate with target cells at an E:T ratio of 2:1 in a 96-well plate and supernatants were analyzed by cytometric bead array using a Bio-Plex Human Cytokine Panel (Bio-Rad), according to the manufacturer's instructions.

[0223] *Proliferation:* T cells were labeled with 0.2 μM carboxyfluorescein succinimidyl ester (CFSE; Invitrogen), washed, and plated in triplicate with stimulator cells in medium without exogenous cytokines. After 72 hours of incubation, cells were labeled with anti-CD3 and live/dead stain, and subsequently analyzed by flow cytometry to assess cell division of viable $CD3^+$ cells.

***In vivo* T-cell engraftment and ADCC.**

[0224] All mouse experiments were approved by the Animal Care and Use Committee of Seattle Children's Research Institute. NOD/Scid IL2RγCnull mice were obtained from The Jackson Laboratory or bred in-house.

[0225] *Engraftment:* Six- to 10-week old NOD/Scid IL2RγCnull mice were injected intravenously on day 0 with 10^7 of either Her2t/EGFRt-negative (Mock) or Her2t or EGFRt-selected T cells and subcutaneously with 5×10^6 viable NS0-IL15 cells to provide a systemic supply of human IL-15 in vivo. Bone marrow was harvested from killed animals 14 days later, and cell suspensions were analyzed by flow cytometry using anti-CD45, live/dead, CD4, CD8, biotinylated Herceptin or Erbitux, and streptavidin-APC provided by BD Biosciences. Alternatively, femurs were fixed in 10% formalin for 24 hours, decalcified for 2 hours (Richard-Allan Scientific), and embedded in paraffin for immunohistochemical staining with anti-CD45 (DAKO), anti-EGFR (clone 31G7; Invitrogen) according to the manufacturer's instructions, or biotinylated Herceptin and SA-AF647 followed by counterstain with Hoechst. Similarly, $Her2^-$ or $Her2t^+$ cell lines were adhered to slides using poly-L-Lysine and then stained using biotinylated Herceptin and SA-AF647. Fluorescent images were acquired using the Nuance FX Biomarker Imaging System.

Statistical analyses.

[0226] Statistical analyses were conducted using Prism Software (GraphPad). Student's *t*-tests were conducted as two-sided paired tests with a confidence interval of 95%, and results with a *P* value less than 0.05 were considered significant. Statistical analyses of survival were conducted by log-rank testing, and results with a *P* value less than 0.05 were considered significant.

Design and initial characterization of a multifunctional surface epitope based on human ErbB2 (Her2).

[0227] The use and selection of homogenous immune cell products has been a limiting factor to the clinical success and reproducibility of adoptive therapy strategies. To this end, a non-immunogenic epitope based on human Her2, coined Her2t was designed, as a candidate genetic tag and tool for cellular engineering (**Figure 1 panel A**). Her2t is devoid of all Her2 intracellular components, yet contains the Her2 transmembrane region, a conformationally intact binding epitope recognized by the monoclonal antibody trastuzumab (Herceptin) and a GMCSFRss to facilitate surface expression (**Figure 1 panel B**). Three variants of the Her2t construct, one containing the full Her2 Domain IV and two minimal conformational epitopes designed based on the three dimensional structure of Her2 in complex with Herceptin (Garrett et al 2007; Cho et al 2003), were initially incorporated into the lentiviral packaging plasmid epHIV7 and characterized in CHO cells. The Her2t construct including amino acids 563-652 outlined in **Figure 1 panel B** displayed the greatest transient surface expression based on flow analysis using biotinylated Herceptin and a streptavidin-conjugated fluorophore and was therefore chosen for further downstream characterization (data not shown).

Her2t is a viable and functionally inert genetic tag.

[0228] Following initial transient expression analysis, the Her2t-containing epHIV7 was subjected to VSV-g pseudotyped self-inactivating lentivirus production. The resultant virus was then transduced into multiple cell types resulting in 8.2-65% $Her2t^+$ populations (data not shown), with transduced K562 erythroleukemia cells (13.8% $Her2t^+$) as a representative (**Figure 2 panel A**). To assess the utility of Her2t as a target for the selective enrichment of transgene-endowed cell populations, the transduced K562 population was subjected to a two-step immunomagnetic purification process using biotinylated Herceptin and anti-biotin microbeads. This process consistently resulted in cell populations that were $\geq$95% $Her2t^+$ (**Figure 2 panel B**). Later titration experiments revealed that 1.2ng or lower of biotinylated Herceptin was sufficient to maximally label 10^6 $Her2t^+$ cells.(**Figure 2 panel A**).

[0229] As displayed in our molecular model (**Figure 1 panel A**), Her2t is devoid of extracellular Domains I-III and contains a Domain IV binding epitope necessary for antibody recognition. It was therefore predicted that Her2t would be incapable of binding to

commercial Her2 antibodies and would be uniquely recognized by Herceptin. Flow analyses confirmed that Herceptin could efficiently recognize and stain Her2t and full Her2-expressing K562 cells, while a commercial antibody was only able to recognize full Her2 (**Figure 2 panel C**).

[0230] Western immunoblot analyses for Her2t and full Her2 were similarly carried out on Herceptin-selected $Her2t^+$ or full $Her2^+$ expressing cells, respectively. As expected, when a commercial Her2 antibody was used the full 185kDa Her2 protein was only detected in lysates from full Her2-expressing cells. Likewise, Her2 phosphorylation was only detected in lysates from full Her2-expressing cells that were treated with neuregulin. A band for Her2t was only detected in $Her2t^+$ cell lysates when probed with biotinylated Herceptin (**Figure 2 panel D**).

Her2t is a highly stringent and complementary selection epitope for T cell therapy.

[0231] A highly efficient selection epitope for chimeric antigen receptor (CAR) expressing T cell therapeutics coined EGFRt was previously identified (Wang et al 2011). It was examined whether the coordinate expression of Her2t in CAR-containing viral vectors might facilitate the clinical use of *ex vivo* engineered, broad-scope CAR therapeutics. Furthermore, Her2t diversifies the repertoire of available, non-immunogenic selection markers for CAR-redirected T cell therapeutics and can act as an alternative or supplement to EGFRt selection strategies (i.e. rendering a T cell bispecific against multiple candidate tumor antigens).

[0232] To evaluate the utility of Her2t in CAR therapy, a multidomain DNA construct composed of the previously described CD19CAR (Hudecek et al 2013) and a ribosomal skip T2A sequence to direct co-expression with Her2t was constructed (**Figure 1 panel C**). The resultant CD19CAR-T2A-Her2t construct was subsequently incorporated into epHIV7 and subjected to viral production as described earlier.

[0233] To assess the functionality of Her2t as a selection marker relative or in concert to EGFRt expression, $CD4^+$ or $CD8^+$ central memory (Tcm) cells (**Figure 3 panel A**) were transduced with a panel of CAR-T2A-Her2t and/or CAR-T2A-EGFRt containing viral vectors (**Figure 3 panel B**). The $CD4^+$ or $CD8^+$ Tcm transduced with a single CAR-

containing vector were 22-72% Her2t$^+$ or EGFRt$^-$ pre-immunomagnetic selection using biotinylated Herceptin (Her2t) or Erbitux (EGFRt) and anti-biotin microbeads, but were consistently enriched to uniform purity (>90%) post-selection (**Figure 3 B**). Dual Her2t$^+$ and EGFRt$^+$ transduced cells were alternatively immunomagnetically sorted using a combination of multisort and anti-APC beads (Materials and Methods) resulting in >90% dual transgene-positive cells (**Figure 6**).

[0234] Alternatively, dual-transduced cell lines can be sorted using free biotin or streptavidin as an alternative to bead removal. Since flow mean fluorescence intensity (MFI) analyses indicated that Her2t-selected Tcm populations might express lower transgene levels relative to EGFRt-selected populations (**Figure 3 panel B**), we next asked whether Her2t levels directly correlated with lower CAR expression. To do this, CD19CAR-expressing Tcm that were selected by Her2t or EGFRt were lysed and cell lysates analyzed by CD3ζ targeted western blot analysis. Results demonstrate that Her2t-appended transgenes are selected at a higher expression level (e.g. about 2 fold) than EGFRt-appended transgenes (**Figure 3 panel C**). These results denote that Her2t allows for a more stringent selection process relative to EGFRt selection. The western blot analysis also demonstrated CD19CAR and CD20CAR co-expression in dual-selected Tcm (**Figure 3 panel C**).

Dual-selected Tcm maintain effector phenotype and target specificity *in vitro*.

[0235] Multiple cancer types downregulate or mutate target antigens as a means to escape therapy. The simultaneous targeting of multiple tumor-associated antigens is therefore a promising therapeutic approach to overcome tumor escape and can broaden the therapeutic reach of T cell therapeutics. To assess whether the co-expression of two CARs (CD19- and CD20-CAR) mediated by surface marker (Her2t and EGFRt) selection could enhance the functional attributes of CAR redirected T cells, the *in vitro* function of dual CAR-expressing Tcm relative to their single CAR-expressing counterparts was analyzed. Cytotoxicity analyses showed that each CAR-redirected Tcm subset (CD19-, CD20- or CD19- and CD20-CAR expressing) conferred similar levels of specific lysis against K562 cells that express CD19, CD20, or both (**Figure 4 panel A**) but did not mediate recognition of the CD19$^-$/CD20$^-$ parental K562 targets (**Figure 4 panel B**).

[0236] The paired functionality of the dual CAR-expressing Tcm against a K562 target panel was next tested (**Figure 4 panel B**) and demonstrate that only the dual CAR-expressing Tcm were able to confer specific lysis against all target expressing K562 cells. In contrast, the CD19- or CD20-specific CAR expressing Tcm cells were only able to trigger cytolytic activity against K562 cells expressing their cognate target antigens (**Figure 4 panel B**).

[0237] Quantitative analysis of cytokine production in response to stimulation with the K562 target panel demonstrate similar specificity. While no CAR-expressing Tcm was able to produce cytokines in response to co-culture with K562 parental cells, the dual CAR-expressing Tcm produced IL2, IFNγ and TNFα in response to co-culture with all target-expressing cells and cytokine production was restricted to K562/CD19-CD20 and K562/CD19 or K562/CD20 targets cells for single CAR-expressing Tcm. (**Figure 4 panel C**). These results indicate that only the dual CAR-expressing Tcm is bispecific for CD19 and CD20 and mediates activation and targeting of T cells upon encounter of either antigen alone. Interestingly, Her2t-selected CD19CAR-expressing Tcm produced a more diverse and enhanced cytokine profile (e.g. about 2-3 fold greater) relative to their EGFRt-selected counterpart. (**Figure 3 panel D**)This can be due to the stringent nature of Her2t selection and the resultant enhancement of total CAR expression in Her2t-selected Tcm.

[0238] Since CAR antitumor activity correlates with the proliferation and survival of transferred T cells, we chose to perform a CFSE dilution assay to analyze proliferation of CAR modified Tcm after engagement with their respective target(s). It was found that dual CAR expression promoted Tcm proliferation following stimulation at similar levels to CD19CAR-expressing Tcm.

Tracking of adoptively transferred Her2t$^+$ T cells by flow cytometry and immunohistochemistry.

[0239] The majority of CAR therapy clinical trials to date have relied on PCR-based techniques to quantify gene-modified cell persistence post therapeutic dosing. The use of therapy specific genetic tags, such as Her2t, can further permit multiparameter phenotypic analysis and identify infused CAR T cell subsets that can correlate with therapeutic responses.

[0240] To test the utility of Her2t as a tracking agent *in vivo*, bone marrow specimens from NOD/*Scid* IL-2RγC^{null} mice engrafted with CD19CAR^{+}Her2t^{+} CD4 and CD8 Tcm was harvested and subjected the processed samples to flow cytometric analysis. (**Figure 5 panel A**). Similar levels of CD45^{+} T cell engraftment were found in mice administered with marker-negative, Her2t^{+}, and EGFRt^{+} cells (**Figure 5 panel B**). Of the CD45^{+} T cell subset, 11.7-45.7% were double stained for CD8 indicating a preferential expansion of CD4^{+} T cells. Furthermore, co-staining for Her2t using biotinylated Herceptin and APC-conjugated streptavidin allowed for the resolution of Her2t^{+} T cells from their Her2t-negative counterparts (**Figure 5 panel C**). These results demonstrate that Her2t is a viable tracking marker for adoptively transferred T cells.

[0241] It was next determined whether Her2t was a viable target for immunohistochemical (IHC) staining. As a preliminary study, Her2t^{+} cells were adhered to slides and stained with biotinylated Herceptin and a fluorochrome-conjugated streptavidin (**Figure 5 panel D**).

Herceptin binding to Her2t sensitizes human T cells to ADCC.

[0242] Incorporating a safety mechanism in administered T cells is a valuable feature should an adverse clinical event occur during therapy. An in vitro cytotoxicity analysis of Her2t^{+} or EGFRt^{+} T cells when co-cultured with GMCSF stimulated PBMCs and either Herceptin or Erbitux will be conducted.

[0243] H9 (T cells) cells ($5x10^{6}$ parental, Her2t^{+}, EGFRt^{+}, or Her2t^{+}/EGFRt^{+}) were mixed together and then subjected to purification. (**Figure 6**). The cells were initially purified based on biotinylated Herceptin and anti-biotin multisort beads. The multisort beads were then removed and the positive fraction subsequently subjected to purification based on Erbitux-APC and anti-APC microbeads. The final positive fraction was dual positive for Her2t and EGFRt.(**Figure 6**).

[0244] In this system, stimulated PBMCs will act as a source of effectors able to induce antibody dependent cellular cytotoxicity in the presence of antibody. The goal would be to selectively eliminate Her2t^{+} or EGFRt^{+} cells when Herceptin or Erbitux is added to the co-culture, respectively. These tests will be expanded in vivo using ffluc^{+} Tcm that co-express Her2t or EGFRt. In this setting, Tcm will be engrafted into NOD/Scid IL-2RγC^{null}

mice followed by the administration of Herceptin or Erbitux and freshly activated PBMCs. The in vivo engraftment and antibody-mediated elimination of transferred Tcm will be measured by in vivo biophotonic imaging. Herceptin or Erbitux-mediated elimination should be specific to Tcm expressing Her2t, EGFRt or both markers.

Combined Her2t and EGFRt selection confers dual CAR specificity *in vivo*.

[0245] The goal for these experiments is to show selective antitumor activity in vivo. K562 ffluc^{+} tumor cells that are CD19^{+}, CD20^{+} or CD19/CD20^{+} will be established by s.c. injection into the left or right flank of NOD/Scid IL-2RγC^{null} mice. CD19CAR-Her2t, CD19CAR-EGFRt, CD20CAR-EGFRt or CD19CAR-Her2t and CD20CAR expressing Tcm will be injected intravenously following tumor establishment and T cell specificity will be determined by biophotonic imaging. Loss of tumor luciferase activity (total photon flux) will indicate tumor regression.

[0246] Tumor regression should occur for all tumor targets when mice are treated with the dual CAR-expressing Tcm, while only CD19 or CD20-expressing K562 tumors should regress when mice are treated with Tcm expressing their cognate CAR. Alternatively, CD19^{-}, CD20^{+} or CD19/CD20^{+} K562 cells will be established as before and ffluc^{+}CAR^{+} Tcm will be administered post tumor establishment. Tcm localization based on CAR-specificity will be determined by biophotonic imaging. The dual-selected Her2t^{+}EGFRt^{+} T cells should localize to both flanks irrespective of target antigen on the K562 tumors, while CD19 or CD20CAR expressing cells should localized to their target antigen specific K562 tumor.

Introduction of a linker domain (Her2tG) between the Her2 domain IV and the transmembrane domain allows for enhanced binding to the antibody Herceptin.

[0247] As shown in **Figure 7,** are schematics of the primary sequence of Her2t and Her2tG. Her2tG differs from Her2t with the addition of a linker sequence between the Her2 domain IV and the transmembrane region and comprises the sequence GGGSGGGS (SEQ ID NO: 45) and the construct is designated as Her2tG. H9 cells were transduced with lentivirus at an MOI of 1 with Her2t or Her2tG. Transduced cells were then purified by biotinylated Herceptin and anti-biotin microbeads according to the manufacturers' protocol.

The purified populations were later stained for Her2t or Her2tG using biotinylated Herceptin and streptavidin-PE. Histograms display greater binding to Her2tG (**Figure 8**). As shown in **Figure 9**, H9 cells were transduced with lentivirus at 0.05, 0.1, 0.25, 0.5, 1 and 3ul (left to right) and then analyzed for Herceptin binding five days later. The Her2t variant Her2t(CD28hinge) was able to bind Herceptin at levels similar to the original Her2t (Her2t staining not shown but based on prior experience). Her2t(IgG4hinge) enhanced Herceptin binding relative to Her2t or Her2t(CD28hinge), while the Her2tG variant had the greatest capacity to bind Herceptin and stain transduced H9 cells.

[0248] As shown from the experiments, a linker (SEQ ID NO: 45) between Domain IV and the transmembrane domain of Her2t led to the construct Her2tG. The linker is used to induce flexibility between protein domains. In other examples, the scFv of many CARs contain four consecutive G3S subunits placed between the Vh and Vl domains of the CAR's scFv. This allows for flexibility in folding of the two scFv domains. The rational here is that two G3S linker subunits would suffice in being able to induce the same amount of flexibility for Her2tG.

[0249] Two G3S linker subunits (SEQ ID NO: 45) was also used to mimic the spacer length of the CD28hinge and IgG4hinge. Both the CD28hinge and IgG4hinge have been used as spacers between the scFv and transmembrane region in CARs that are functional. Both the CD28hinge and IgG4hinge contain a cysteine that help in dimerization. While helpful for CARs, this dimerization may inhibit the flexibility of Her2t and therefore not allow for as significant recognition to Herceptin. The advantage of using two G3S linkers (SEQ ID NO: 45) over three or four was to limit vector payload, eliminate potentially unnecessary sequences and at the same time achieve enhanced functionality.

[0250] A multi-purpose cell surface marker designated Her2t is described. This novel marker contains only 113 of the 1255 amino acids that compose full-length Her2 and is devoid of all extra or intracellular domains responsible for intact Her2 cell signaling. Hematopoietic cells lack Her2 expression making Her2t a prime candidate transgene selection marker that by design is rendered functionally inert yet able to refine donor T cells into homogenous, transgene-expressing therapeutic products. The design of Her2t comprises fusion of the N-terminal Her2t fragment to the leader peptide of the human GM-CSF receptor-α chain. This fusion helps facilitate Her2t surface expression and allows for the

minimal binding epitope to be uniquely recognized by the pharmaceutical grade monoclonal antibody trastuzumab (Herceptin).

[0251] It was demonstrated that due to its minimal cDNA footprint Her2t can be expressed alone or coordinately incorporated into self-inactivating lentiviral vectors alongside biologically active transgenes, namely a chimeric antigen receptor (CAR). Coordinate transgene expression levels were attained by appending Her2t to the CAR via a T2A ribosomal skip linker and were verified by flow and western blot analysis of Her2t-purified CD8 central memory T cells. Furthermore, it was also demonstrated that Her2t is a highly stringent selection epitope that, in comparison to EGFRt selection strategies, allows for the *ex vivo* selection of T cells with greater CAR expression and effector cytokine production. This characteristic can be advantageous when higher transgene expression levels are desired, as can be the case when expanding CAR therapy to the treatment of multiple tumor types.

[0252] In addition to equipping T cells with elevated transgene expression levels, rendering an individual T cell bispecific against multiple tumor antigens can prove clinically beneficial. Indeed, the down regulation or mutation of target antigens is commonly observed in multiple cancer types necessitating the implementation of strategies beyond therapy driven by a single CAR. Along these lines, it was demonstrated that Her2t is a complementary selection epitope to EGFRt that, when each selection epitope is appended to a CAR, can facilitate the multisort purification of dual-CAR expressing T cells. Similar cytotoxic activity and effector cytokine production between single and dual-CAR expressing T cells demonstrate that the individual or concerted expression of Her2t and EGFRt does not result in any overt functional impairment.

[0253] Herceptin is amenable to biotinylation or chemical conjugation. As formulated for commercial use, Herceptin is reconstituted in clinical grade H_2O and retains Her2-specific high affinity binding post biotinylation. This, combined with the availability of cGMP grade anti-biotin microbeads (Miltenyi Biotec), enables the selection of therapeutically relevant $Her2t^+$ cells on a CliniMACS device. It was demonstrated that cells as low as 13.8% positive for Her2t can be immunomagnetically enriched to >90% purity. Furthermore, the results demonstrate that biotinylated Herceptin can be coupled with

antibodies targeted against T cell markers to permit multiparameter phenotypic analysis and track the *in vivo* distribution of therapeutic, CAR expressing T cells.

[0254] The therapeutic reach of CAR immunotherapy is rapidly expanding beyond its initial success with the treatment of blood borne tumors. Alternative genetic tags that are inherently non-immunogenic, unique to T cell populations and highly efficient at selection are clearly needed. Her2t encompasses these aforementioned characteristics and diversifies the repertoire of selection epitopes to be used for CAR therapy. Furthermore, Her2t is a prime candidate for the concerted selection of CAR therapeutics equipped with multiplexed genetic systems.

[0255] An advantage of using Her2t is for its diminutive size. As such Her2t has the advantage of packing efficiency with even bigger constructs. In order to take advantage of the system it is preferred to have the construct less than 5kb. In some alternatives, the size of the construct is 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 14.9 Kb, or any size in between any two of the construct size listed. The low size is necessary as constructs above 15kb may run the risk of having low titers.

[0256] The foregoing is illustrative of the present invention, and is not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein. All references and documents referred to herein are hereby incorporated by reference.

Table 1 **CD19CAR**

GMCSFRss

```
DNA: ATGCTGCTGCTGGTGACCAGCCTGCTGCTGTGCGAGCTGCCCCACCCCGCC
 AA: M  L  L  L  V  T  S  L  L  L  C  E  L  P  H  P  A
```

CD19scFv

```
DNA: TTTCTGCTGATCCCC:GACATCCAGATGACCCAGACCACCTCCAGCCTGAGC
 AA: F  L  L  I  P   D  I  Q  M  T  Q  T  T  S  S  L  S

DNA: GCCAGCCTGGGCGACCGGGTGACCATCAGCTGCCGGGCCAGCCAGGACATC
 AA: A  S  L  G  D  R  V  T  I  S  C  R  A  S  Q  D  I

DNA: AGCAAGTACCTGAACTGGTATCAGCAGAAGCCCGACGGCACCGTCAAGCTG
 AA: S  K  Y  L  N  W  Y  Q  Q  K  P  D  G  T  V  K  L

DNA: CTGATCTACCACACCAGCCGGCTGCACAGCGGCGTGCCCAGCCGGTTTAGC
 AA: L  I  Y  H  T  S  R  L  H  S  G  V  P  S  R  F  S
```

```
DNA: GGCAGCGGCTCCGGCACCGACTACAGCCTGACCATCTCCAACCTGGAACAG
 AA: G  S  G  S  G  T  D  Y  S  L  T  I  S  N  L  E  Q

DNA: GAAGATATCGCCACCTACTTTTGCCAGCAGGGCAACACACTGCCCTACACC
 AA: E  D  I  A  T  Y  F  C  Q  Q  G  N  T  L  P  Y  T

DNA: TTTGGCGGCGGAACAAAGCTGGAAATCACCGGCAGCACCTCCGGCAGCGGC
 AA: F  G  G  G  T  K  L  E  I  T  G  S  T  S  G  S  G

DNA: AAGCCTGGCAGCGGCGAGGGCAGCACCAAGGGCGAGGTGAAGCTGCAGGAA
 AA: K  P  G  S  G  E  G  S  T  K  G  E  V  K  L  Q  E

DNA: AGCGGCCCTGGCCTGGTGGCCCCCAGCCAGAGCCTGAGCGTGACCTGCACC
 AA: S  G  P  G  L  V  A  P  S  Q  S  L  S  V  T  C  T

DNA: GTGAGCGGCGTGAGCCTGCCCGACTACGGCGTGAGCTGGATCCGGCAGCCC
 AA: V  S  G  V  S  L  P  D  Y  G  V  S  W  I  R  Q  P

DNA: CCCAGGAAGGGCCTGGAATGGCTGGGCGTGATCTGGGGCAGCGAGACCACC
 AA: P  R  K  G  L  E  W  L  G  V  I  W  G  S  E  T  T

DNA: TACTACAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGC
 AA: Y  Y  N  S  A  L  K  S  R  L  T  I  I  K  D  N  S

DNA: AAGAGCCAGGTGTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCC
 AA: K  S  Q  V  F  L  K  M  N  S  L  Q  T  D  D  T  A

DNA: ATCTACTACTGCGCCAAGCACTACTACTACGGCGGCAGCTACGCCATGGAC
 AA: I  Y  Y  C  A  K  H  Y  Y  Y  G  G  S  Y  A  M  D
```

IgG4hinge

```
DNA: TACTGGGGCCAGGGCACCAGCGTGACCGTGAGCAGC:GAGAGCAAGTACGGA
 AA: Y  W  G  Q  G  T  S  V  T  V  S  S   E  S  K  Y  G
```

CD28tm

```
DNA: CCGCCCTGCCCCCCTTGCCCT:ATGTTCTGGGTGCTGGTGGTGGTCGGAGGC
 AA: P  P  C  P  P  C  P   M  F  W  V  L  V  V  V  G  G


DNA: GTGCTGGCCTGCTACAGCCTGCTGGTCACCGTGGCCTTCATCATCTTTTGG
 AA: V  L  A  C  Y  S  L  L  V  T  V  A  F  I  I  F  W
```

41BB

```
DNA: GTG:AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATG
 AA: V   K  R  G  R  K  K  L  L  Y  I  F  K  Q  P  F  M

DNA: AGACCAGTACAAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCA
 AA: R  P  V  Q  T  T  Q  E  E  D  G  C  S  C  R  F  P
```

CD3Zeta

```
DNA: GAAGAAGAAGAAGGAGGATGTGAACTGCGGGTGAAG:TTCAGCAGAAGCGCC
 AA: E  E  E  E  G  G  C  E  L  R  V  K   F  S  R  S  A

DNA: GACGCCCCTGCCTACCAGCAGGGCCAGAATCAGCTGTACAACGAGCTGAAC
 AA: D  A  P  A  Y  Q  Q  G  Q  N  Q  L  Y  N  E  L  N

DNA: CTGGGCAGAAGGGAAGAGTACGACGTCCTGGATAAGCGGAGAGGCCGGGAC
 AA: L  G  R  R  E  E  Y  D  V  L  D  K  R  R  G  R  D
```

DNA: CCTGAGATGGGCGGCAAGCCTCGGCGGAAGAACCCCCAGGAAGGCCTGTAT
AA: P E M G G K P R R K N P Q E G L Y

DNA: AACGAACTGCAGAAAGACAAGATGGCCGAGGCCTACAGCGAGATCGGCATG
AA: N E L Q K D K M A E A Y S E I G M

DNA: AAGGGCGAGCGGAGGCGGGGCAAGGGCCACGACGGCCTGTATCAGGGCCTG
AA: K G E R R R G K G H D G L Y Q G L

DNA: TCCACCGCCACCAAGGATACCTACGACGCCCTGCACATGCAGGCCCTGCCC
AA: S T A T K D T Y D A L H M Q A L P

T2A
DNA: CCAAGG:CTCGAGGGCGGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGT (SEQ ID NO: 46)
AA: P R L E G G G E G R G S L L T C G (SEQ ID NO: 2)

DNA: GACGTGGAGGAGAATCCCGGCCCTAGG (SEQ ID NO:1)

Table 2 Uniprot P10747 CD28 (SEQ ID NO:3)

```
10         20         30         40         50         60
MLRLLLALNL FPSIQVTGNK ILVKQSPMLV AYDNAVNLSC KYSYNLFSRE FRASLHKGLD

        70         80         90        100        110        120
SAVEVCVVYG NYSQQLQVYS KTGFNCDGKL GNESVTFYLQ NLYVNQTDIY FCKIEVMYPP

       130        140        150        160        170        180
PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR

       190        200        210        220
SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS
```

1-18 signal peptide

19-152 extracellular domain

153-179 transmembrane domain

180-220 intracellular domain

Position 186-187 LL→GG

Table 3 Uniprot Q07011 4-1BB (SEQ ID NO:4)

```
    10         20         30         40         50         60
MGNSCYNIVA TLLLVLNFER TRSLQDPCSN CPAGTFCDNN RNQICSPCPP NSFSSAGGQR

        70         80         90        100        110        120
TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS MCEQDCKQGQ ELTKKGCKDC

       130        140        150        160        170        180
CFGTFNDQKR GICRPWTNCS LDGKSVLVNG TKERDVVCGP SPADLSPGAS SVTPPAPARE

       190        200        210        220        230        240
PGHSPQIISF FLALTSTALL FLLFFLTLRF SVVKRGRKKL LYIFKQPFMR PVQTTQEEDG

       250
CSCRFPEEEE GGCEL
```

1-23 signal peptide

24-186 extracellular domain

187-213 transmembrane domain

214-255 intracellular domain

Table 4 Uniprot P20963 human CD3ζ isoform 3 (SEQ ID NO: 5)

```
10         20         30         40         50         60
MKWKALFTAA ILQAQLPITE AQSFGLLDPK LCYLLDGILF IYGVILTALF LRVKFSRSAD

        70         80         90        100        110        120
APAYQQGQNQ LYNELNLGRR EEYDVLDKRR GRDPEMGGKP QRRKNPQEGL YNELQKDKMA

       130        140        150        160
EAYSEIGMKG ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR
```

1-21 signal peptide

22-30 extracellular

31-51 transmembrane

52-164 intracellular domain

61-89 ITAM1

100-128 ITAM2

131-159 ITAM3

Table 5 Exemplary Hinge region Sequences

Human IgG1 EPKSCDKTHTCPPCP (SEQ ID NO: 6)

Human IgG2 ERKCCVECPPCP (SEQ ID NO:7)

Human IgG3 ELKTPLGDTHTCPRCP $(EPKSCDTPPPCPRCP)_3$ (SEQ ID NO:8)

Human IgG4 ESKYGPPCPSCP (SEQ ID NO:9)

Modified Human IgG4 ESKYGPPCPPCP (SEQ ID NO:10)

Modified Human IgG4 YGPPCPPCP (SEQ ID NO:11)

Modified Human IgG4 KYGPPCPPCP (SEQ ID NO:12)

Modified Human IgG4 EVVKYGPPCPPCP (SEQ ID NO:13)

Table 6 Her2t nucleic acid (SEQ ID NO:14) and amino acid sequence (SEQ ID NO:15)

HER2T (CHP) Nucleotide and Amino Acid Sequence

```
                                                  M  L  L  V  T  S  L  L  L  C  E  L  P  H
                                                  ATGCT TCTCCTGGTG ACAAGCCTTC TGCTCTGTGA GTTACCACAC
                                                  TACGA AGAGGACCAC TGTTCGGAAG ACGAGACACT CAATGGTGTG

 P  A  F  L  L  I  P  C  H  P  E  C  Q  P  Q  N  G  S  V  T  C  F  G  P  E  A  D  Q  C  V  A  C  A  H
CCAGCATTCC TCCTGATCCC ATGCCACCCT GAGTGTCAGC CCCAGAATGG CTCAGTGACC TGTTTTGGAC CGGAGGCTGA CCAGTGTGTG GCCTGTCCCC
GGTCGTAAGG AGGACTAGGG TACGGTGGGA CTCACAGTCG GGGTCTTACC GAGTCACTGG ACAAAACCTG GCCTCCGACT GGTCACACAC CGGACACGGG

 Y  K  D  P  P  F  C  V  A  R  C  P  S  G  V  K  P  D  L  S  Y  M  P  I  W  K  F  P  D  E  E  G  A
ACTATAAGGA CCCTCCCTTC TGCGTGGCCC GCTGCCCCAG CGGTGTGAAA CCTGACCTCT CCTACATGCC CATCTGGAAG TTTCCAGATG AGGAGGGCGC
TGATATTCCT GGGAGGGAAG ACGCACCGGG CGACGGGGTC GCCACACTTT GGACTGGAGA GGATGTACGG GTAGACCTTC AAAGGTCTAC TCCTCCCGCG

 C  Q  P  C  P  I  N  C  T  H  S  C  V  D  L  D  D  K  G  C  P  A  E  Q  R  A  S  P  L  T  S  I  I
ATGCCAGCCT TGCCCCATCA ACTGCACCCA CTCCTGTGTG GACCTGGATG ACAAGGGCTG CCCCGCCGAG CAGAGGGCCA GCCCTCTGAC GTCCATCATC
TACGGTCGGA ACGGGGTAGT TGACGTGGGT GAGGACACAC CTGGACCTAC TGTTCCCGAC GGGGCGGCTC GTCTCTGGGT CGGGAGACTG CAGGTAGTAG

 S  A  V  V  G  I  L  L  V  V  V  L  G  V  V  F  G  I  L  I  *
TCTGCGGTGG TTGGCATTCT GCTGGTCGTG GTCTTGGGGG TGGTCTTTGG GATCCTCATC TGA
AGACGCCACC AACCGTAAGA CGACCAGCAC CAGAACCCCC ACCAGAAACC CTAGGAGTAG ACT
```

1-MLLLVTSLLLCELPHPAFLLIP-22 (GMCSFRss) (SEQ ID NO:17)

563 - C H P E C Q P Q N G S V T C F G P **E** A **D** Q C V A C A H Y K **D** P P **F** C V A R C P S G V K P D L S Y
M P I W K F P D E E G A C **Q** P C P I N C T H S C V D L D D K G C P A E Q R A S P L T 652

(Her2 sequence-residues in bold identified as binding to Herceptin) (SEQ ID NO:18)

653- SIISAVVGILLVVVLGVVFGILI I – 675 (SEQ ID NO:19)

563 - C H P E C Q P Q N G S V T C F G P **E** A **D** Q C V A C A H Y K **D** P P **F** C V A R C P S G V K P D L S Y
M P I W K F P D E E G A C **Q** P C P I N C T H S C V D L D D K G C P A E Q R A S P L T S I I S A V V G I L
L V V V L G V V F G I L I – 675 (SEQ ID NO:20)

Table 7 EGFRt Nucleotide (SEQ ID NO:21) and Amino Acid (SEQ ID NO:22)

```
DNA:   ATGCTTCTCCTGGTGACAAGCCTT
 AA:    M  L  L  L  V  T  S  L

DNA: CTGCTCTGTGAGTTACCACACCCAGCATTCCTCCTGATCCCACGCAAAGTG
 AA: L  L  C  E  L  P  H  P  A  F  L  L  I  P  R  K  V

DNA: TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACTCTCCATAAATGCT
 AA: C  N  G  I  G  I  G  E  F  K  D  S  L  S  I  N  A

DNA: ACGAATATTAAACACTTCAAAAACTGCACCTCCATCAGTGGCGATCTCCAC
 AA: T  N  I  K  H  F  K  N  C  T  S  I  S  G  D  L  H

DNA: ATCCTGCCGGTGGCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG
 AA: I  L  P  V  A  F  R  G  D  S  F  T  H  T  P  P  L

DNA: GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGGAAATCACAGGGTTT
 AA: D  P  Q  E  L  D  I  L  K  T  V  K  E  I  T  G  F

DNA: TTGCTGATTCAGGCTTGGCCTGAAAACAGGACGGACCTCCATGCCTTTGAG
 AA: L  L  I  Q  A  W  P  E  N  R  T  D  L  H  A  F  E

DNA: AACCTAGAAATCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCTCTT
 AA: N  L  E  I  I  R  G  R  T  K  Q  H  G  Q  F  S  L

DNA: GCAGTCGTCAGCCTGAACATAACATCCTTGGGATTACGCTCCCTCAAGGAG
 AA: A  V  V  S  L  N  I  T  S  L  G  L  R  S  L  K  E

DNA: ATAAGTGATGGAGATGTGATAATTTCAGGAAACAAAAATTTGTGCTATGCA
 AA: I  S  D  G  D  V  I  I  S  G  N  K  N  L  C  Y  A

DNA: AATACAATAAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAAACCAAA
 AA: N  T  I  N  W  K  K  L  F  G  T  S  G  Q  K  T  K

DNA: ATTATAAGCAACAGAGGTGAAAACAGCTGCAAGGCCACAGGCCAGGTCTGC
 AA: I  I  S  N  R  G  E  N  S  C  K  A  T  G  Q  V  C

DNA: CATGCCTTGTGCTCCCCCGAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGC
 AA: H  A  L  C  S  P  E  G  C  W  G  P  E  P  R  D  C

DNA: GTCTCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGGACAAGTGCAAC
 AA: V  S  C  R  N  V  S  R  G  R  E  C  V  D  K  C  N

DNA: CTTCTGGAGGGTGAGCCAAGGGAGTTTGTGGAGAACTCTGAGTGCATACAG
 AA: L  L  E  G  E  P  R  E  F  V  E  N  S  E  C  I  Q

DNA: TGCCACCCAGAGTGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACGG
 AA: C  H  P  E  C  L  P  Q  A  M  N  I  T  C  T  G  R
```

DNA: GGACCAGACAACTGTATCCAGTGTGCCCACTACATTGACGGCCCCCACTGC
AA: G P D N C I Q C A H Y I D G P H C

DNA: GTCAAGACCTGCCCGGCAGGAGTCATGGGAGAAAACAACACCCTGGTCTGG
AA: V K T C P A G V M G E N N T L V W

DNA: AAGTACGCAGACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTGCACC
AA: K Y A D A G H V C H L C H P N C T

DNA: TACGGATGCACTGGGCCAGGTCTTGAAGGCTGTCCAACGAATGGGCCTAAG
AA: Y G C T G P G L E G C P T N G P K

DNA: ATCCCGTCCATCGCCACTGGGATGGTGGGGGCCCTCCTCTTGCTGCTGGTG
AA: I P S I A T G M V G A L L L L L V

DNA: GTGGCCCTGGGGATCGGCCTCTTCATG*TGA* (SEQ ID NO:21)
AA: V A L G I G L F M * (SEQ ID NO:22)

Table 8 **Full length Her2 isoform 1 (Uniprot PO4626-1)(SEQ ID NO:23)**

```
MELAALCRWG LLLALLPPGA ASTQVCTGTD MKLRLPASPE THLDMLRHLY     50
QGCQVVQGNL ELTYLPTNAS LSFLQDIQEV QGYVLIAHNQ VRQVPLQRLR    100
IVRGTQLFED NYALAVLDNG DPLNNTTPVT GASPGGLREL QLRSLTEILK    150
GGVLIQRNPQ LCYQDTILWK DIFHKNNQLA LTLIDTNRSR ACHPCSPMCK    200
GSRCWGESSE DCQSLTRTVC AGGCARCKGP LPTDCCHEQC AAGCTGPKHS    250
DCLACLHFNH SGICELHCPA LVTYNTDTFE SMPNPEGRYT FGASCVTACP    300
YNYLSTDVGS CTLVCPLHNQ EVTAEDGTQR CEKCSKPCAR VCYGLGMEHL    350
REVRAVTSAN IQEFAGCKKI FGSLAFLPES FDGDPASNTA PLQPEQLQVF    400
ETLEEITGYL YISAWPDSLP DLSVFQNLQV IRGRILHNGA YSLTLQGLGI    450
SWLGLRSLRE LGSGLALIHH NTHLCFVHTV PWDQLFRNPH QALLHTANRP    500
EDECVGEGLA CHQLCARGHC WGPGPTQCVN CSQFLRGQEC VEECRVLQGL    550
PREYVNARHC LPCHPECQPQ NGSVTCFGPE ADQCVACAHY KDPPFCVARC    600
PSGVKPDLSY MPIWKFPDEE GACQPCPINC THSCVDLDDK GCPAEQRASP    650
LTSIISAVVG ILLVVVLGVV FGILIKRRQQ KIRKYTMRRL LQETELVEPL    700
TPSGAMPNQA QMRILKETEL RKVKVLGSGA FGTVYKGIWI PDGENVKIPV    750
AIKVLRENTS PKANKEILDE AYVMAGVGSP YVSRLLGICL TSTVQLVTQL    800
MPYGCLLDHV RENRGRLGSQ DLLNWCMQIA KGMSYLEDVR LVHRDLAARN    850
VLVKSPNHVK ITDFGLARLL DIDETEYHAD GGKVPIKWMA LESILRRRFT    900
HQSDVWSYGV TVWELMTFGA KPYDGIPARE IPDLLEKGER LPQPPICTID    950
VYMIMVKCWM IDSECRPRFR ELVSEFSRMA RDPQRFVVIQ NEDLGPASPL   1000
DSTFYRSLLE DDDMGDLVDA EEYLVPQQGF FCPDPAPGAG GMVHHRHRSS   1050
STRSGGGDLT LGLEPSEEEA PRSPLAPSEG AGSDVFDGDL GMGAAKGLQS   1100
LPTHDPSPLQ RYSEDPTVPL PSETDGYVAP LTCSPQPEYV NQPDVRPQPP   1150
SPREGPLPAA RPAGATLERP KTLSPGKNGV VKDVFAFGGA VENPEYLTPQ   1200
GGAAPQPHPP PAFSPAFDNL YYWDQDPPER GAPPSTFKGT PTAENPEYLG   1250
LDVPV                                                    1255
```

1-22-signal peptide

23-652-extracellular domain

653-675 transmembrane domain

676-1255 cytoplasmic

Table 9 CD20CAR Nucleic acid (SEQ ID NO:24) and polypeptide (SEQ ID No:25)

CD20 scFV NA

Atggagacagacacactcctgctatgggtgctgctgctctgggttccaggttccacaggtgacattgtgctgacccaatctccagct
atcctgtctgcatctccaggggagaaggtcacaatgacttgcagggccagctcaagtgtaaattacatggactggtaccagaagaa
gccaggatcctccccaaaccctggatttatgccacatccaacctggcttctggagtccctgctcgcttcagtggcagtgggtctggg
acctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttttaatccacccacgt
tcggaggggggaccaagctggaaataaaaggcagtactagcggtggtggctccgggggcggttccggtgggggcggcagcagcg
aggtgcagctgcagcagtctggggctgagctggtgaagcctggggcctcagtgaagatgtcctgcaaggcttctggctacacattta
ccagttacaatatgcactgggtaaagcagacacctggacagggcctggaatggattggagctatttatccaggaaatggtgatact
tcctacaatcagaagttcaaaggcaaggccacattgactgcagacaaatcctccagcacagcctacatgcagctcagcagcctga
catctgaggactctgcggactattactgtgcaagatctaattattacggtagtagctactggttcttcgatgtctggggcgcagggac
cacggtcaccgtctcctca

IgG4-Hinge **(SEQ ID NO: 47)**

Gagagcaagtacggaccgccctgccccccttgccct

CH3 **(SEQ ID NO: 48)**

Ggccagcctcgcgagccccaggtgtacaccctgcctccctcccaggaagagatgaccaagaaccaggtgtccctgacctgcctgg
tgaagggcttctaccccagcgacatcgccgtggagtgggagagcaacggccagcctgagaacaactacaagaccacccctcccgt
gctggacagcgacggcagcttcttcctgtacagccggctgaccgtggacaagagccggtggcaggaaggcaacgtctttagctgca
gcgtgatgcacgaggccctgcacaaccactacacccagaagagcctgagcctgtccctgggcaag

CD20 scFV Protein (SEQ ID NO: 25)

M E T D T L L L W V L L L W V P G S T G D I V L T Q S P A I L S A S P G E K V T M T C ***R A S S S V***
N Y M D W Y Q K K P G S S P K P W I Y ***A T S N L A S*** G V P A R F S G S G S G T S Y S L T I S R V E
A E D A A T Y Y C ***Q Q W S F N P P T*** F G G G T K L E I K G S T S G G G S G G G S G G G G S S E V
Q L Q Q S G A E L V K P G A S V K M S C K A S G Y T F T ***S Y N M H*** W V K Q T P G Q G L E W I G
A I Y P G N G D T S Y N Q K F K G K A T L T A D K S S S T A Y M Q L S S L T S E D S A D Y Y C A R
S N Y Y G S S Y W F F D V W G A G T T V T V S S

IgG4-Hinge **(SEQ ID NO: 49)**

E S K Y G P P C P P C P

CH3 **(SEQ ID NO: 50)**

G Q P R E P Q V Y T L P P S Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S R L T V D K S R W Q E G N V F S C S V M H E A L H N H Y T Q K S L S L S L G K

The rest of the CD20CAR construct (CD28tm-41BB-zeta-T2A-EGFRt) is the same as the CD19CAR-T2A-EGFRt construct.

WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563 to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER2.

2. The isolated polypeptide of claim 1, wherein the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO:23.

3. The isolated polypeptide of claim 2, wherein the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23.

4. The isolated polypeptide of any one of claims 1-3 wherein the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23.

5. The isolated polypeptide of any one of claims 1-4, further comprising a leader peptide that provides for cell surface expression.

6. The isolated polypeptide of claim 5, wherein the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17.

7. The isolated polypeptide of any one of claims 1-6, wherein the antibody is trastuzumab.

8. An isolated nucleic acid encoding the polypeptide of any one of claims 1-7 or 38-44.

9. The isolated nucleic acid of claim 8 further comprising a promoter.

10. The isolated nucleic acid of claim 8 or claim 9 further comprising a transgene.

11. The isolated nucleic acid of claim 10, wherein the transgene comprises a polynucleotide encoding a chimeric antigen receptor.

12. The isolated nucleic acid of claim 11, wherein the chimeric antigen receptor comprising an antigen binding domain, a spacer domain, a transmembrane domain and at least one stimulatory domain.

13. The isolated nucleic acid of any one of claims 10 to 12, wherein the polynucleotide encoding the transgene is linked to the nucleic acid encoding the HER2 polypeptide of claim 1 with a self-cleaving linker.

14. The isolated nucleic acid of claim 13, wherein the self-cleaving linker is a T2A linker having the sequence of L E G G G E G R G S L L T C G (SEQ ID NO: 26).

15. The isolated nucleic acid of any one of claims 11-14, wherein the chimeric antigen receptor comprises the amino acid sequence set forth in SEQ ID NO: 2.

16. The isolated nucleic acid of any one of claims 11-14, wherein the chimeric antigen receptor comprises the amino acid sequence set forth in SEQ ID NO: 25. (CD20CAR).

17. A host cell comprising the isolated nucleic acid of any one claims 8-16.

18. The isolated host cell of claim 17, wherein the host cell is selected from the group consisting of CD8 T cells, CD4 T cells,CD4 naïve T cells, CD8 naïve T cells, CD8 central memory cells, CD4 central memory cells, and combinations thereof.

19. The isolated host cell of claims 17 or claim 18, wherein the host cell is autologous.

20. The isolated host cell of any one of claims 17-19 wherein the host cell is antigen specific.

21. A composition comprising the host cells of any one of claims 17-20 or 45 -46.

22. A method of manufacturing a composition comprising:
    a) Introducing an isolated nucleic acid of any one of claims 8-16 into a host cell; and
    b) Culturing the host cells in a medium comprising at least one growth factor.

23. The method of claim 22, wherein the growth factor is selected from the group consisting of IL-15, IL-7, IL-21, IL-2, and combinations thereof.

24. The method of claim 22 or claim 23, further comprising selecting cells that express the Her2t polypeptide.

25. The method of any one of claims 22-24, wherein the cells are selected before culturing the cells in the medium.

26. The method of any one of claims 24-25, wherein the cells are selected using an antibody that binds to Domain IV of Her2.

27. The method of claim 26, wherein the antibody is trastuzumab.

28. The method of any one of claims 22-27, further comprising introducing a second isolated nucleic acid coding for a chimeric antigen receptor linked to a second genetic tag.

29. The method of claim 28, further comprising selecting cells expressing the second genetic tag.

30. The method of any one of claims 28-29 wherein the second genetic tag comprises EGFRt.

31. A method of treating patient having cancer expressing a tumor antigen comprising administering an effective amount of a composition of claim 21,wherein the cells of the composition express a chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a genetic tag.

32. A use of a composition of claim 21 for treating a cancer having a tumor antigen recognized by the chimeric antigen receptor on the cells.

33. A method of treating patient having cancer expressing a tumor antigen comprising administering an effective amount of a composition of claim 21 and an antibody that specifically binds to the genetic tag, wherein the cells of the composition express a chimeric antigen receptor that comprises an antigen binding domain that binds to the tumor antigen expressed on the cancer cell and a genetic tag.

34. A use of a composition of claim 21 for treating a cancer having a tumor antigen recognized by the chimeric antigen receptor on the cells of the composition and an antibody that specifically binds the genetic tag.

35. The method or use of any one of claims 31 to 34 where the antibody is Herceptin or Erbitux.

36. The method or use of any one of claims 31-35, wherein the antibody is conjugated to a cytotoxic agent.

37. The method or use of any one of claims 31-35, wherein the antibody is detectably labelled.

38. An isolated polypeptide comprising at least 95% sequence identity to a polypeptide of an extracellular domain of HER2 polypeptide having a sequence of amino acids 563

to 652 of SEQ ID NO: 23 linked to a transmembrane domain, wherein the isolated polypeptide specifically binds to an antibody that binds to an epitope in Domain IV of Her2, and wherein the isolated polypeptide excludes the full length mature HER, and wherein the extracellular domain of HER2 polypeptide having the sequence of amino acids 563 to 652 of SEQ ID NO: 23 is linked to the transmembrane domain by a sequence comprising amino acids GGGSGGGS (SEQ ID NO: 45).

39. The isolated polypeptide of claim 38, wherein the HER2 polypeptide comprises amino acids glutamic acid 580, aspartic acid 582, aspartic acid 592, phenylalanine 595, and glutamine 624 of SEQ ID NO:23.

40. The isolated polypeptide of claim 39, wherein the HER2 polypeptide comprises amino acids 563-652 of SEQ ID NO: 23.

41. The isolated polypeptide of any one of claims 38-40 wherein the transmembrane domain comprises amino acids 653-675 of SEQ ID NO: 23.

42. The isolated polypeptide of any one of claims 38-41, further comprising a leader peptide that provides for cell surface expression.

43. The isolated polypeptide of claim 42, wherein the leader peptide comprises an amino acid sequence set forth in SEQ ID NO: 17.

44. The isolated polypeptide of any one of claims 38-43, wherein the antibody is trastuzumab.
45. The host cell of claim 17, wherein the host cell is a precursor T cell.
46. The host cell of claim 17, wherein the host cell is a hematopoietic stem cell.
47. The host cell of any one of claims 22-30, wherein the host cell is a precursor T cell.
48. The host cell of any one of claims 22-30, wherein the host cell is a hematopoietic stem cell.