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(54) **COMPOSITIONS AND METHODS FOR TREATING ACUTE MYELOID LEUKEMIA**

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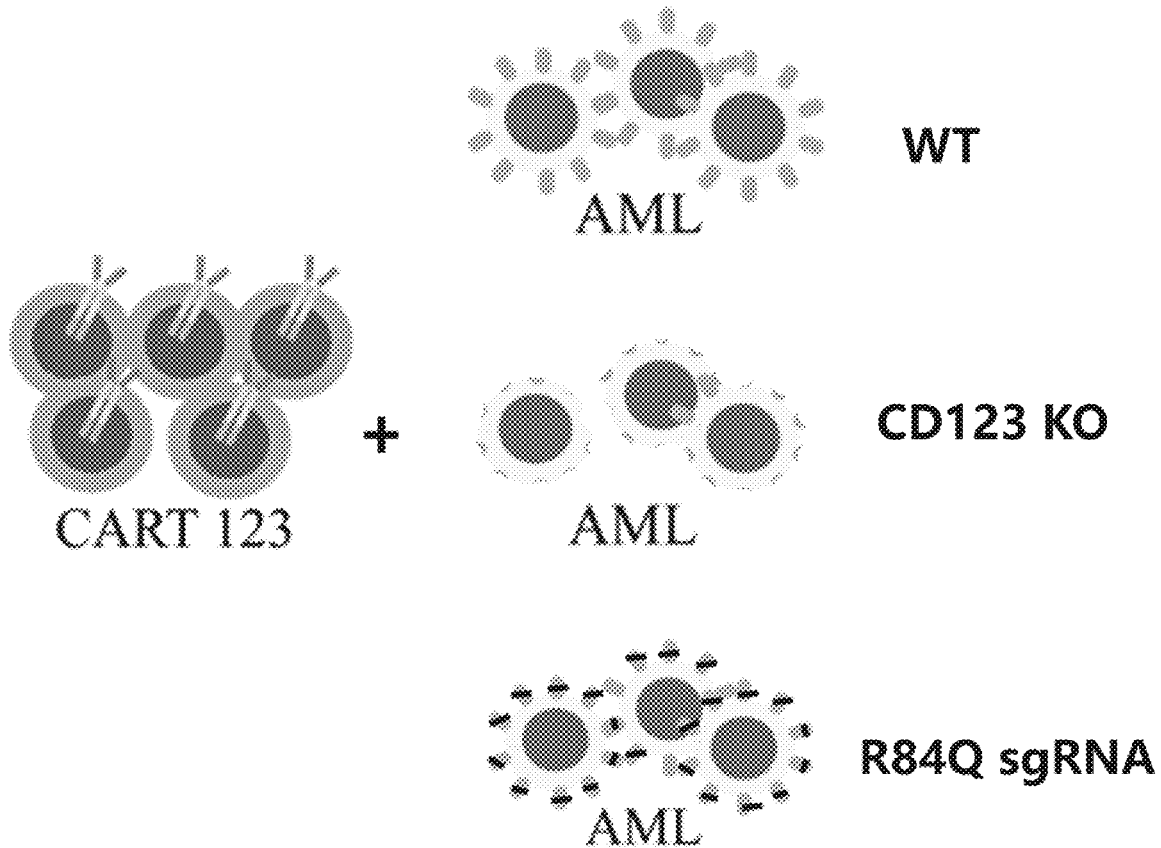
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(57) **ABSTRACT**

The present disclosure describes compositions and methods for treating cancers such as acute myeloid leukemia (AML), in particular relapsed and refractory AML. The method entails administering to the patient an antibody or a chimeric antigen receptor (CAR)-expressing immune cell targeting a molecule such as CD33, CD123, CD117 or CLL-1 following, or concurrently with, transplanting to the patient an engineered stem cell expressing the same molecule but with a mutation disrupting the epitope to the antibody or CAR. Due to the mutation, the engineered stem cell, unlike endogenous hematopoietic cells, is not targeted by the therapy and thus can supply the patient with functional hematopoietic cells and antigens.

Specification includes a Sequence Listing.

A



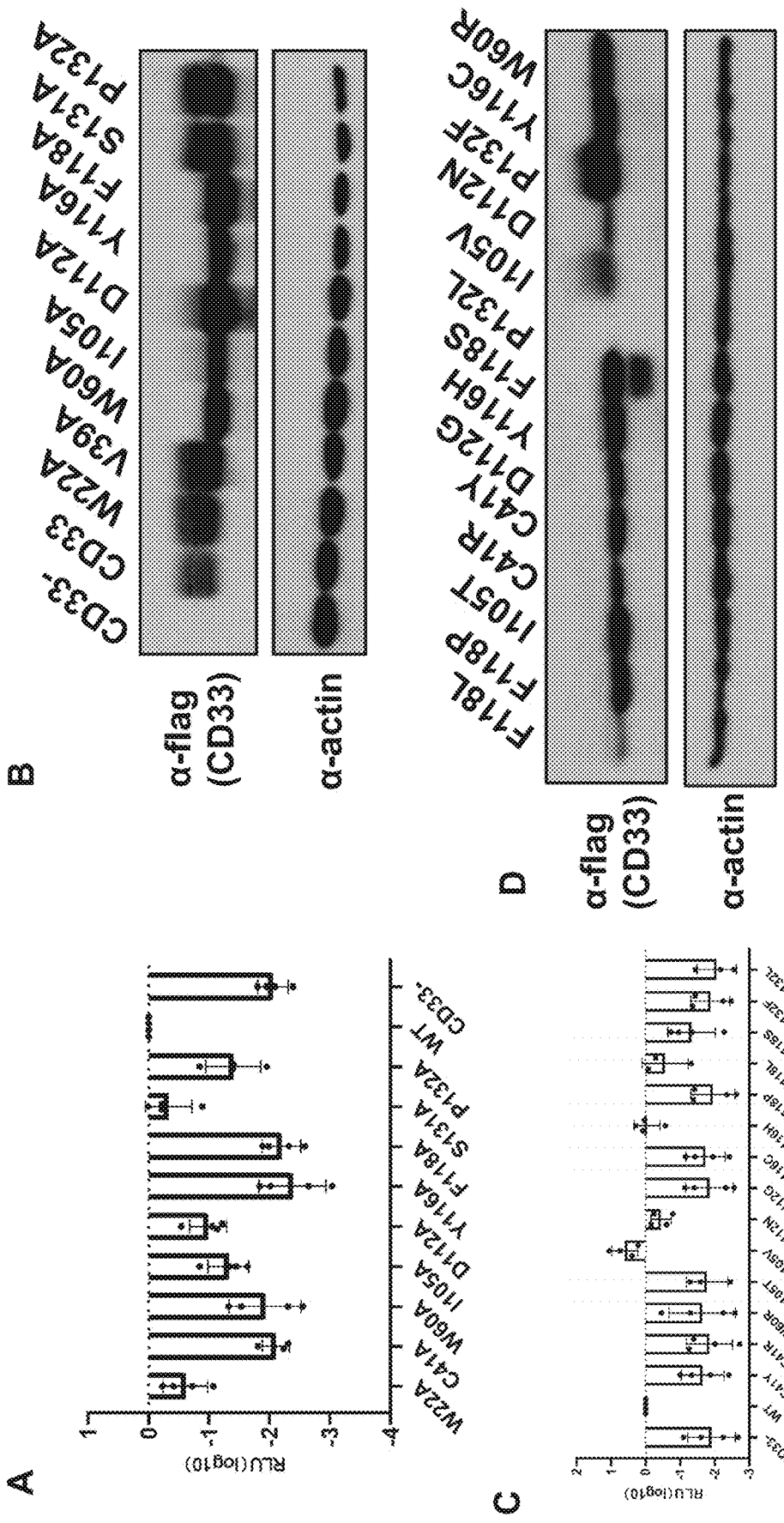
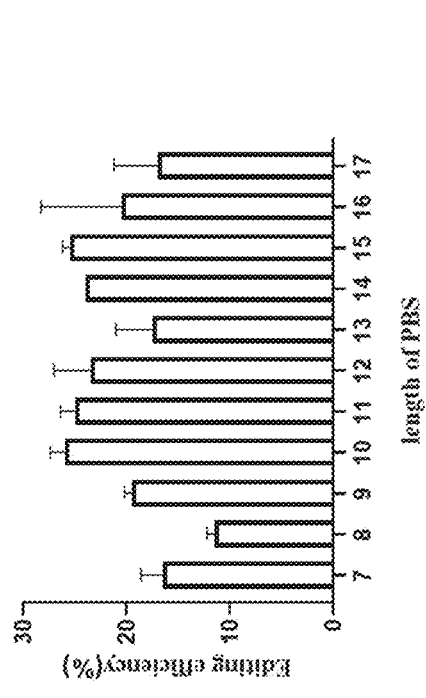
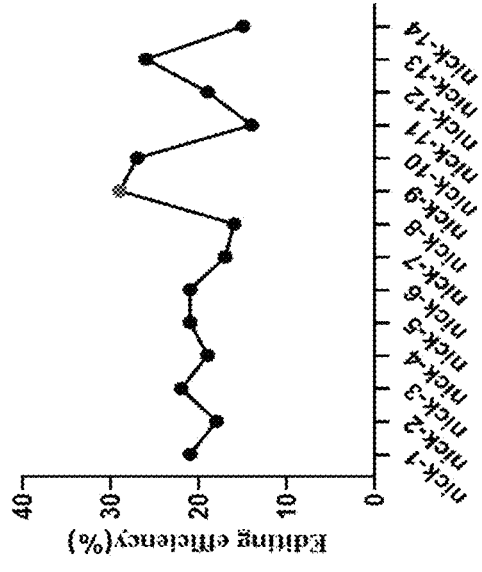


FIG. 1A-D

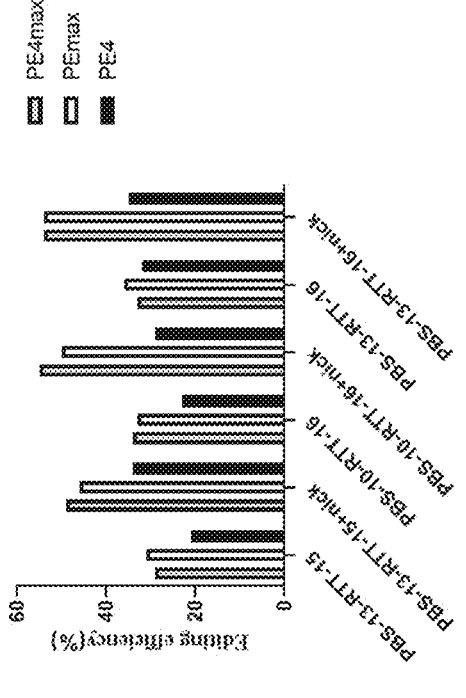
E



D



G



F

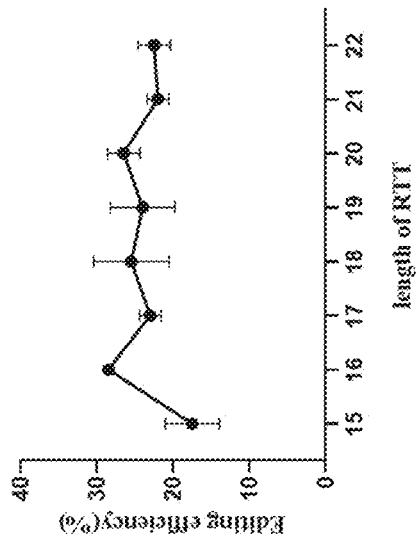


FIG. 2D-G

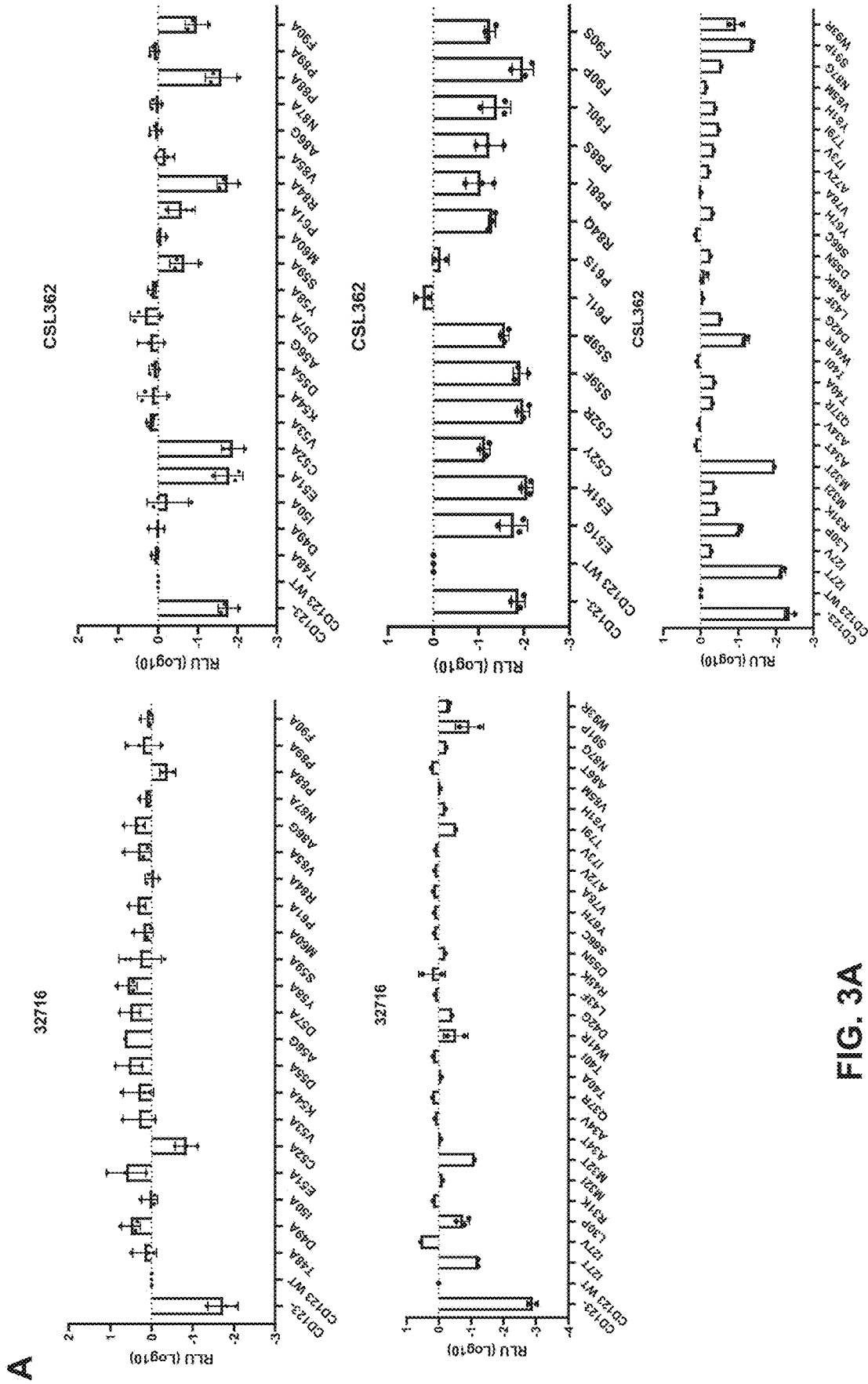


FIG. 3A

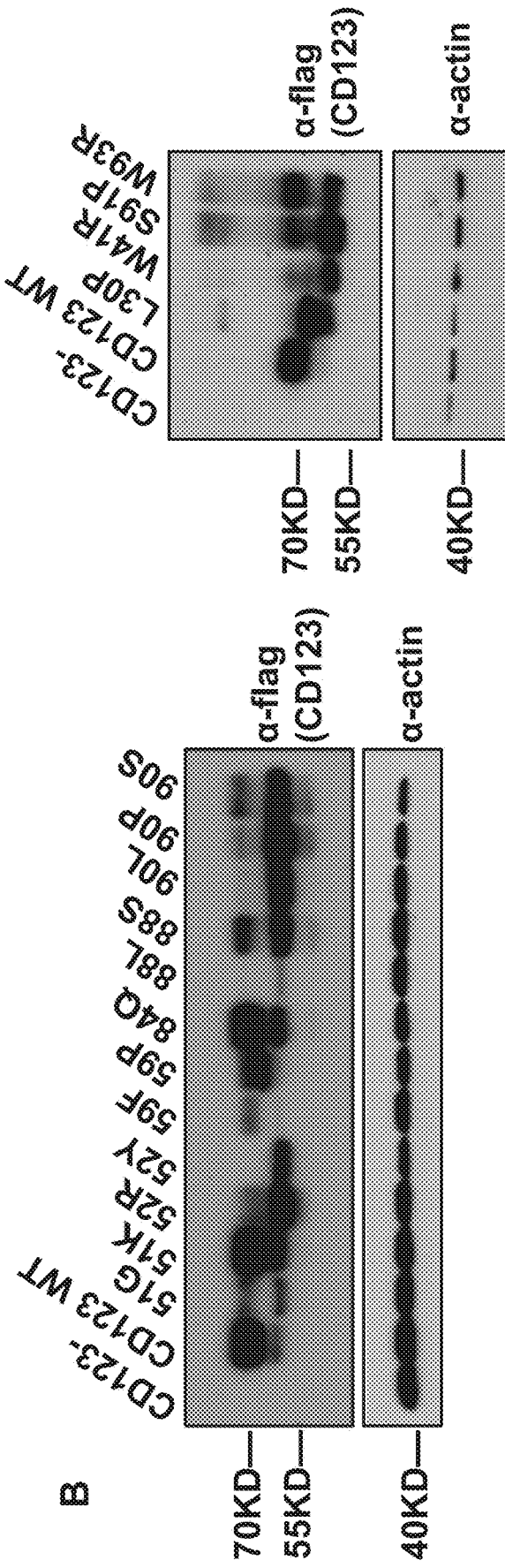


FIG. 3B

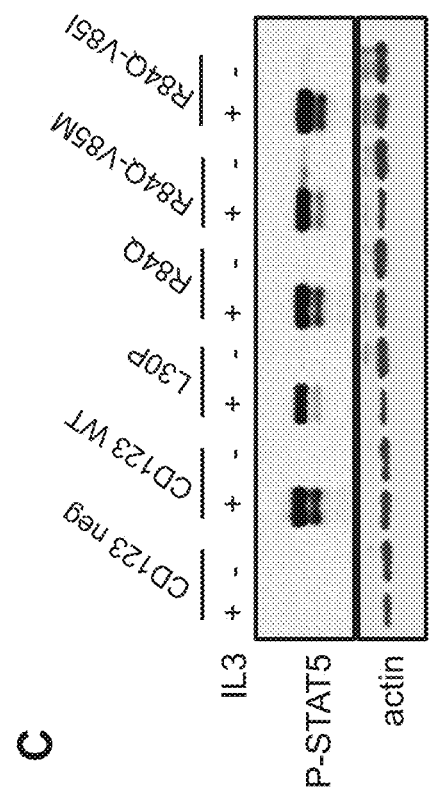
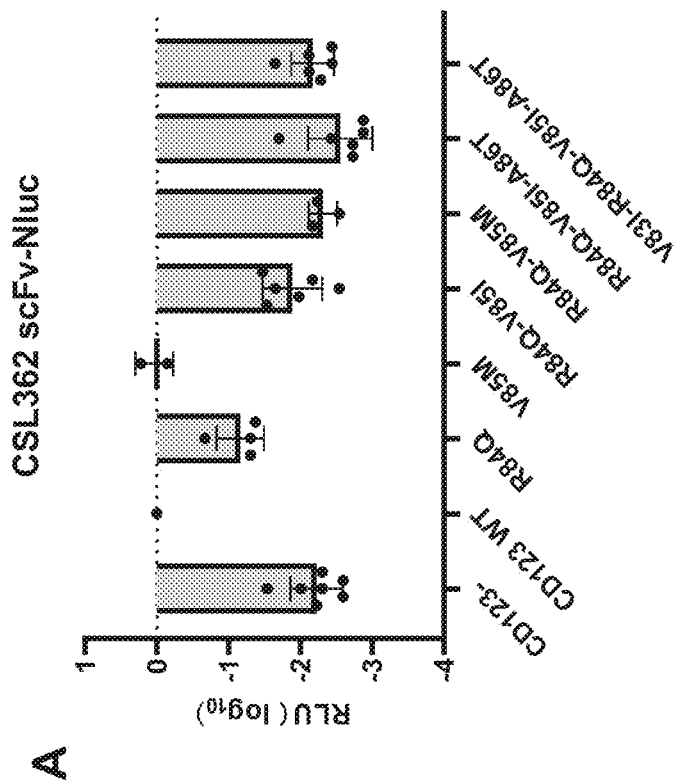
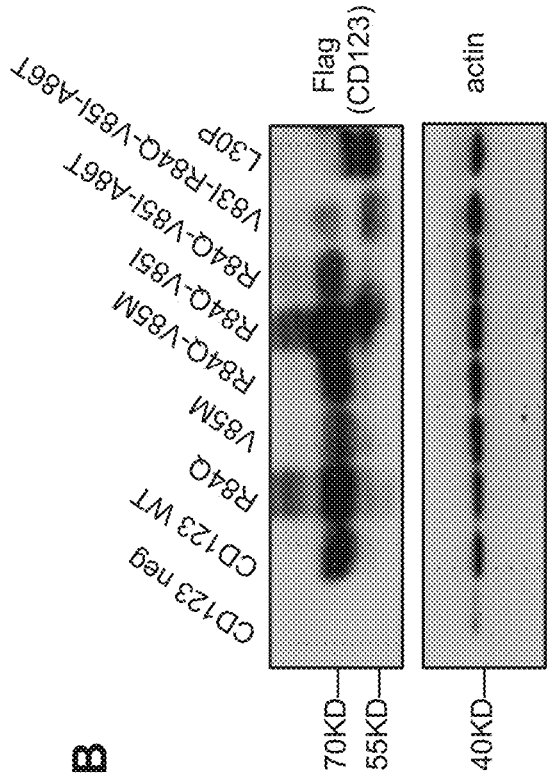


FIG. 4A-C

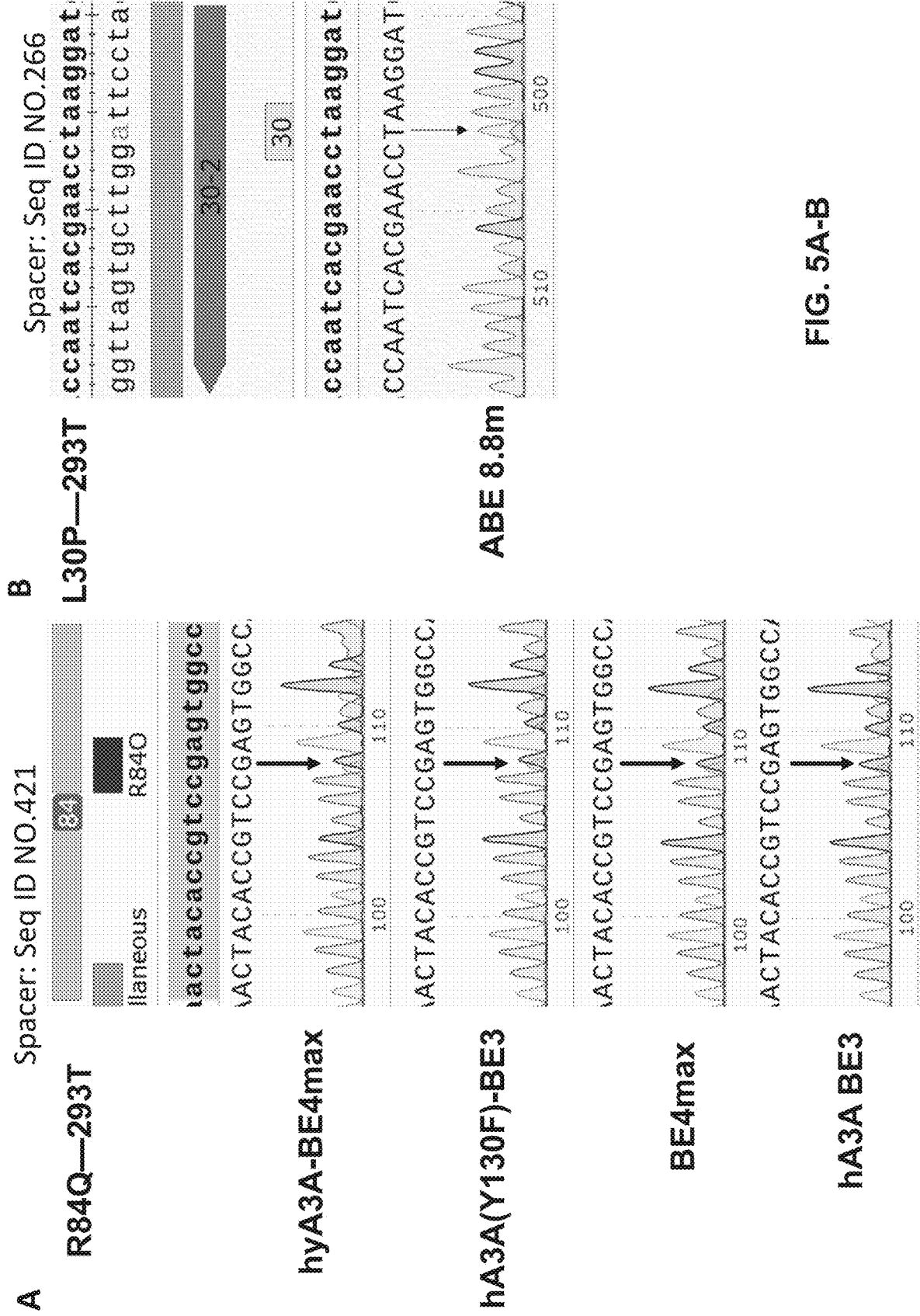
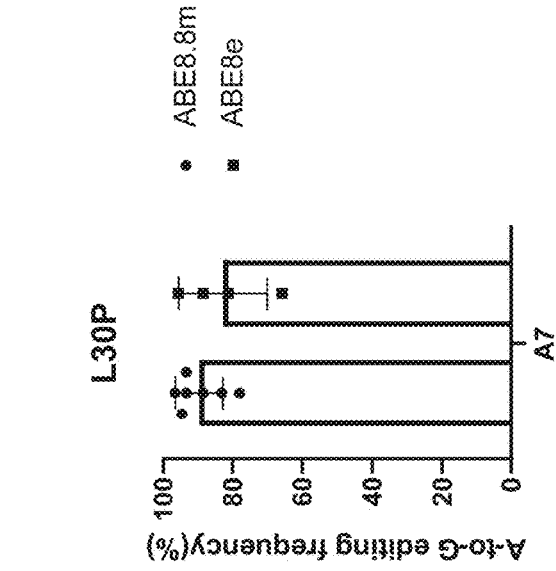
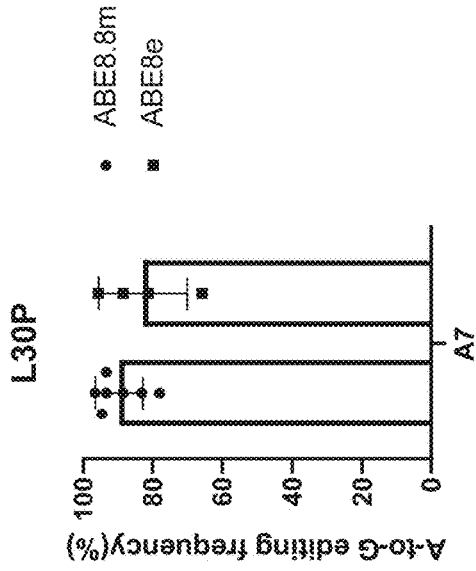


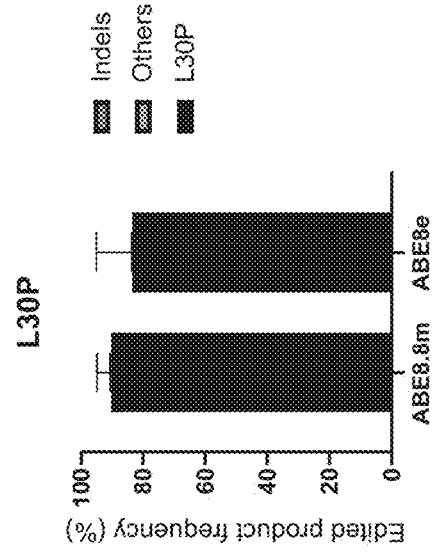
FIG. 5A-B



E



F



D

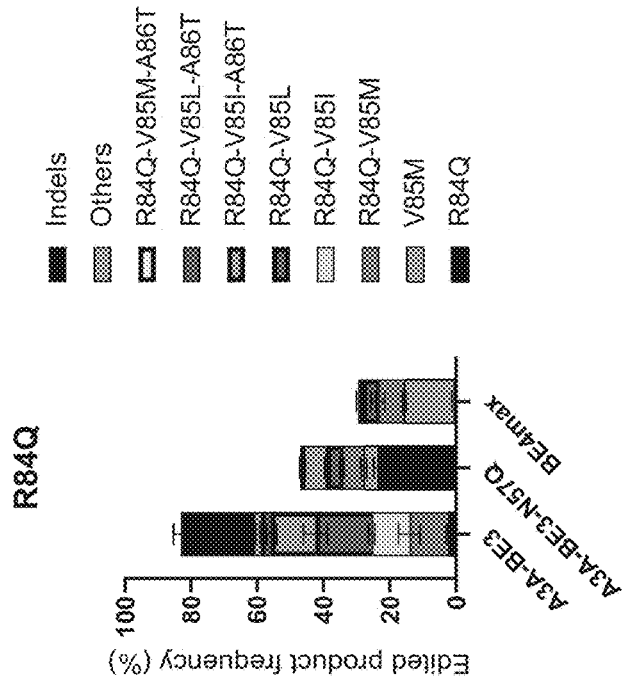
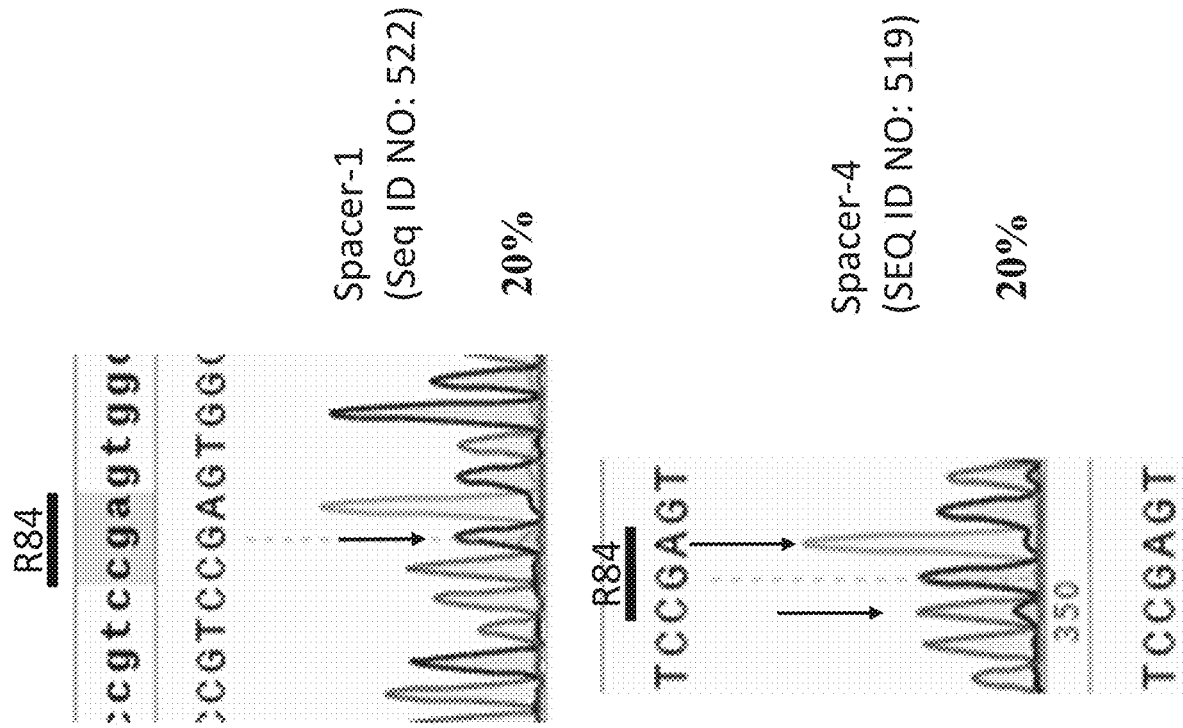


FIG. 5C-F



H

G

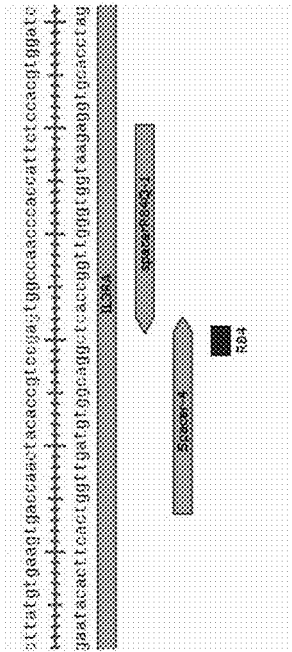


FIG. 5G-H

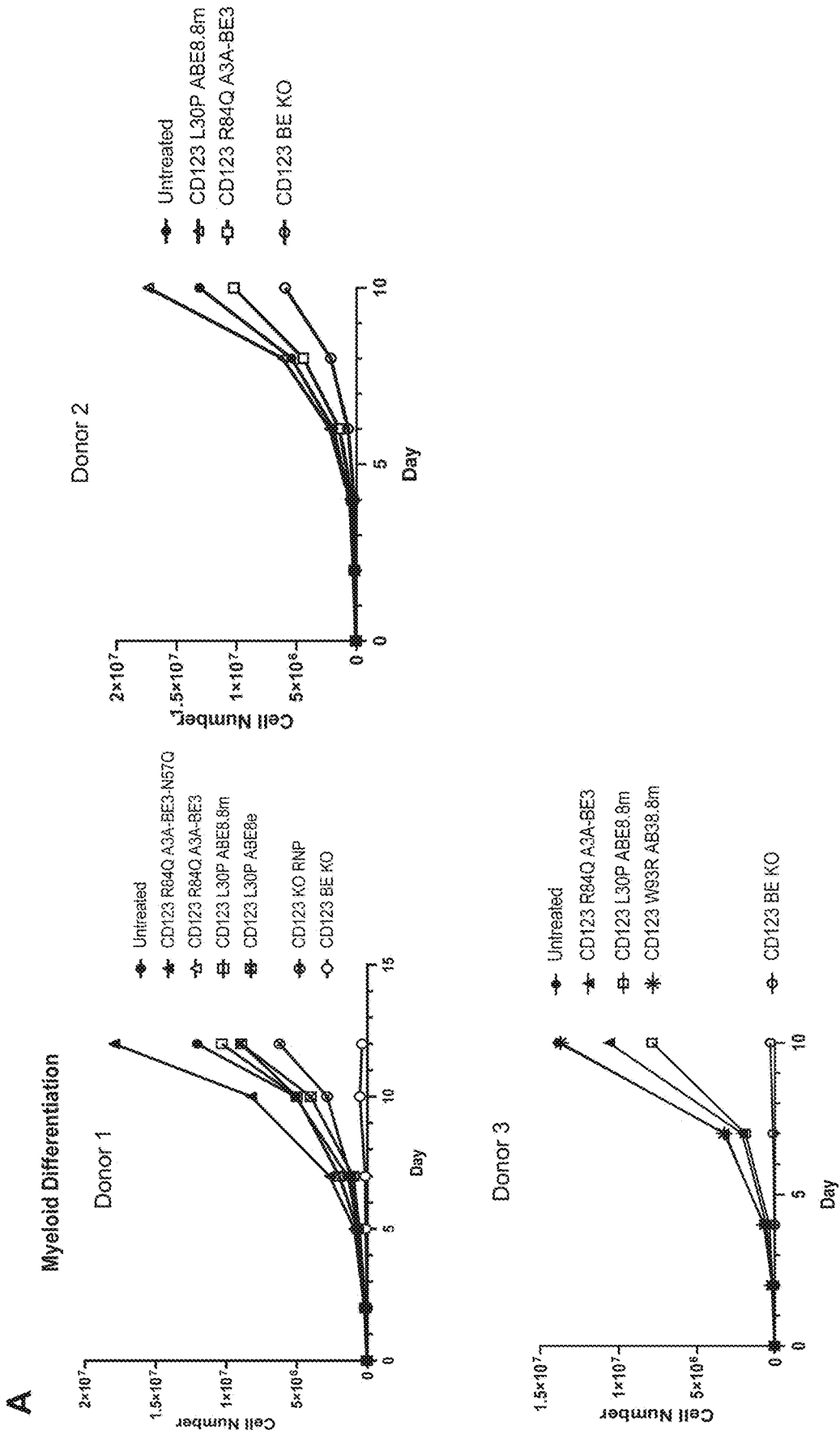


FIG. 6A

B

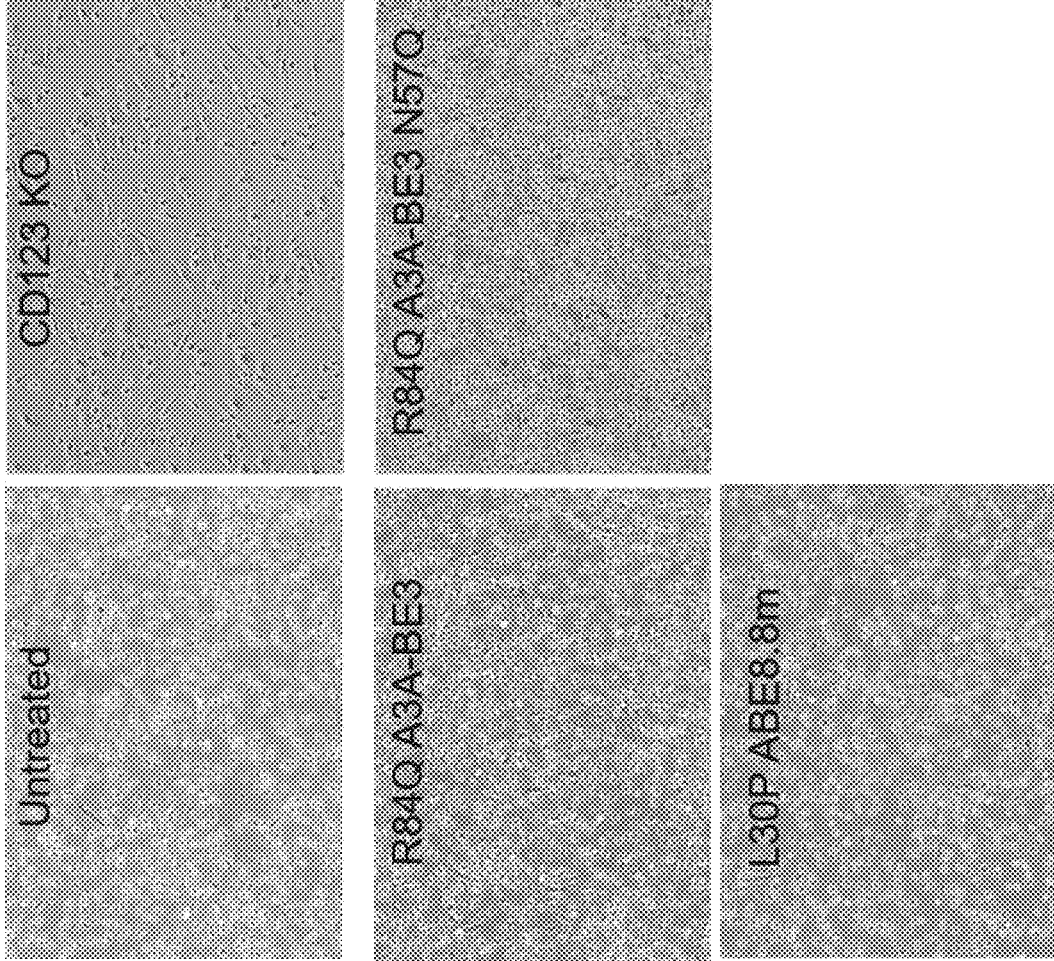


FIG. 6B

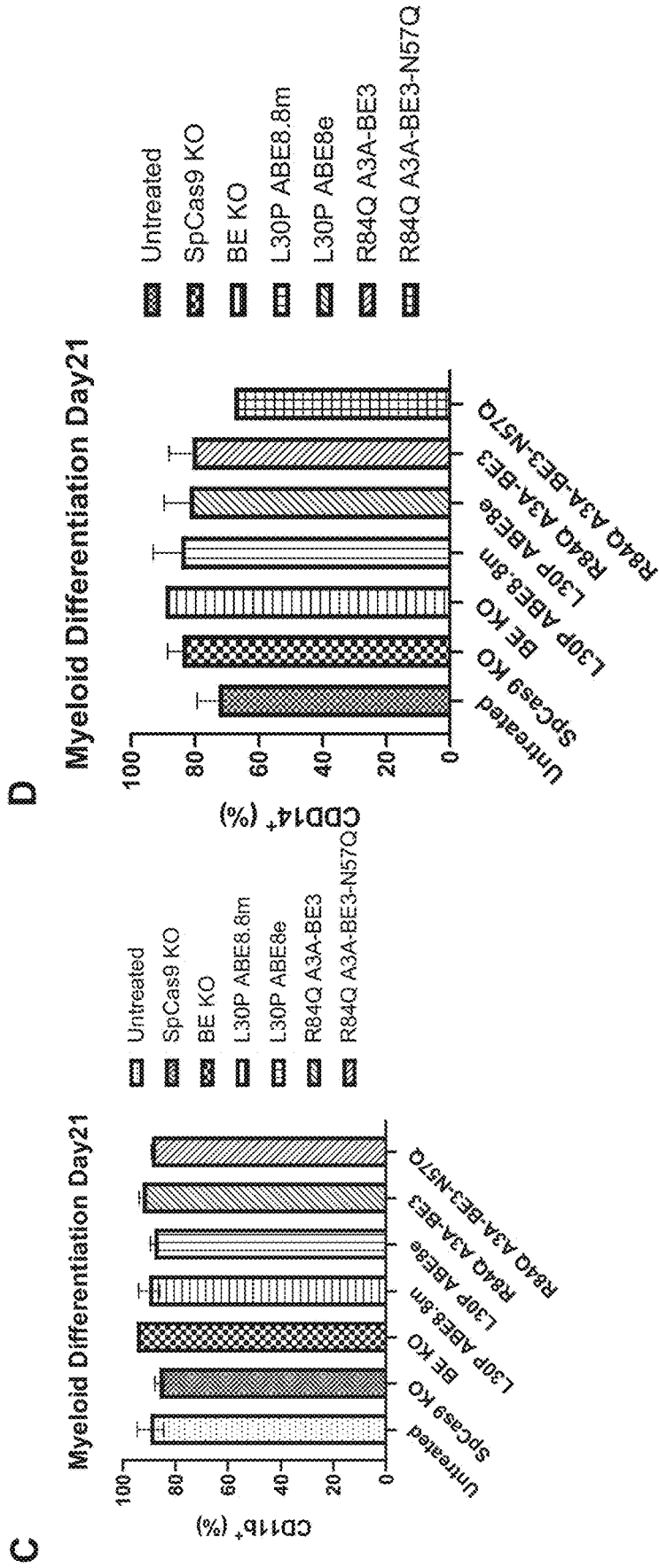


FIG. 6C-D

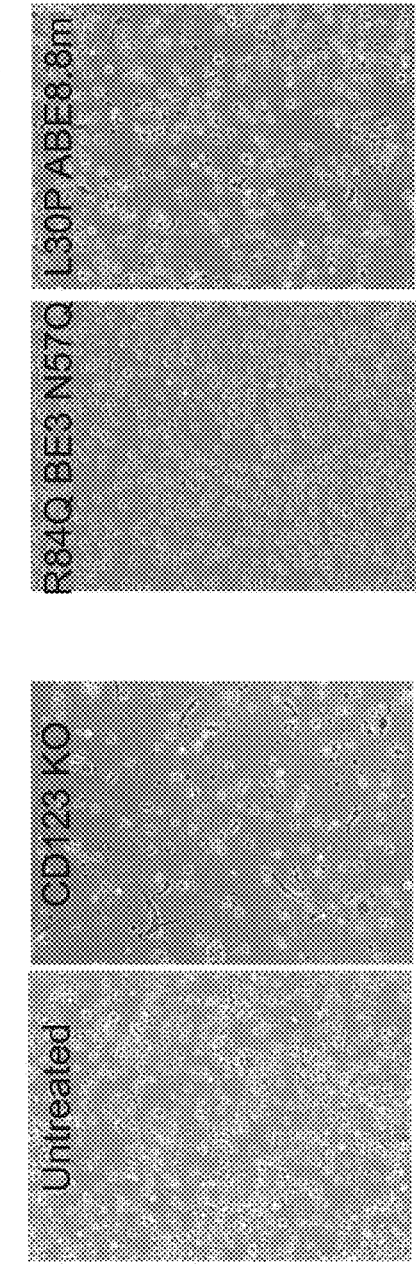
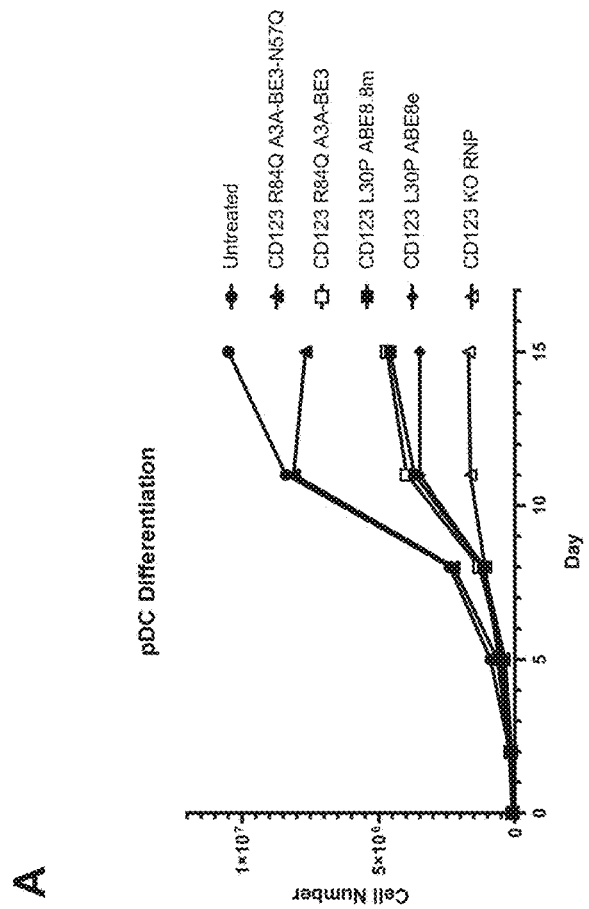
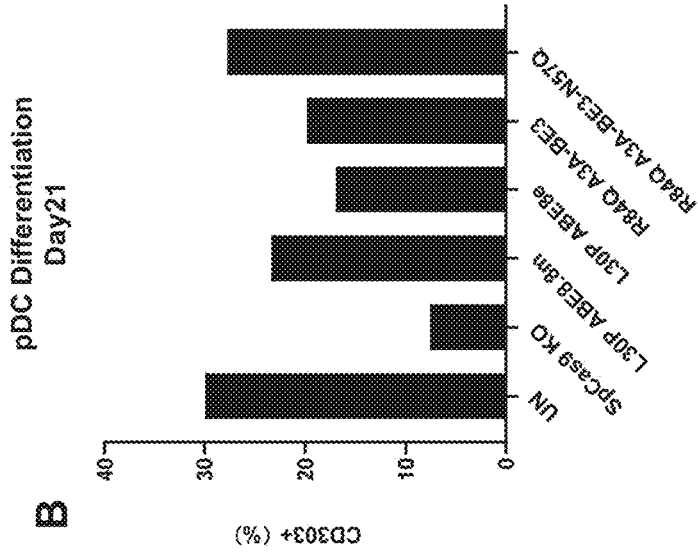


FIG. 7A-C

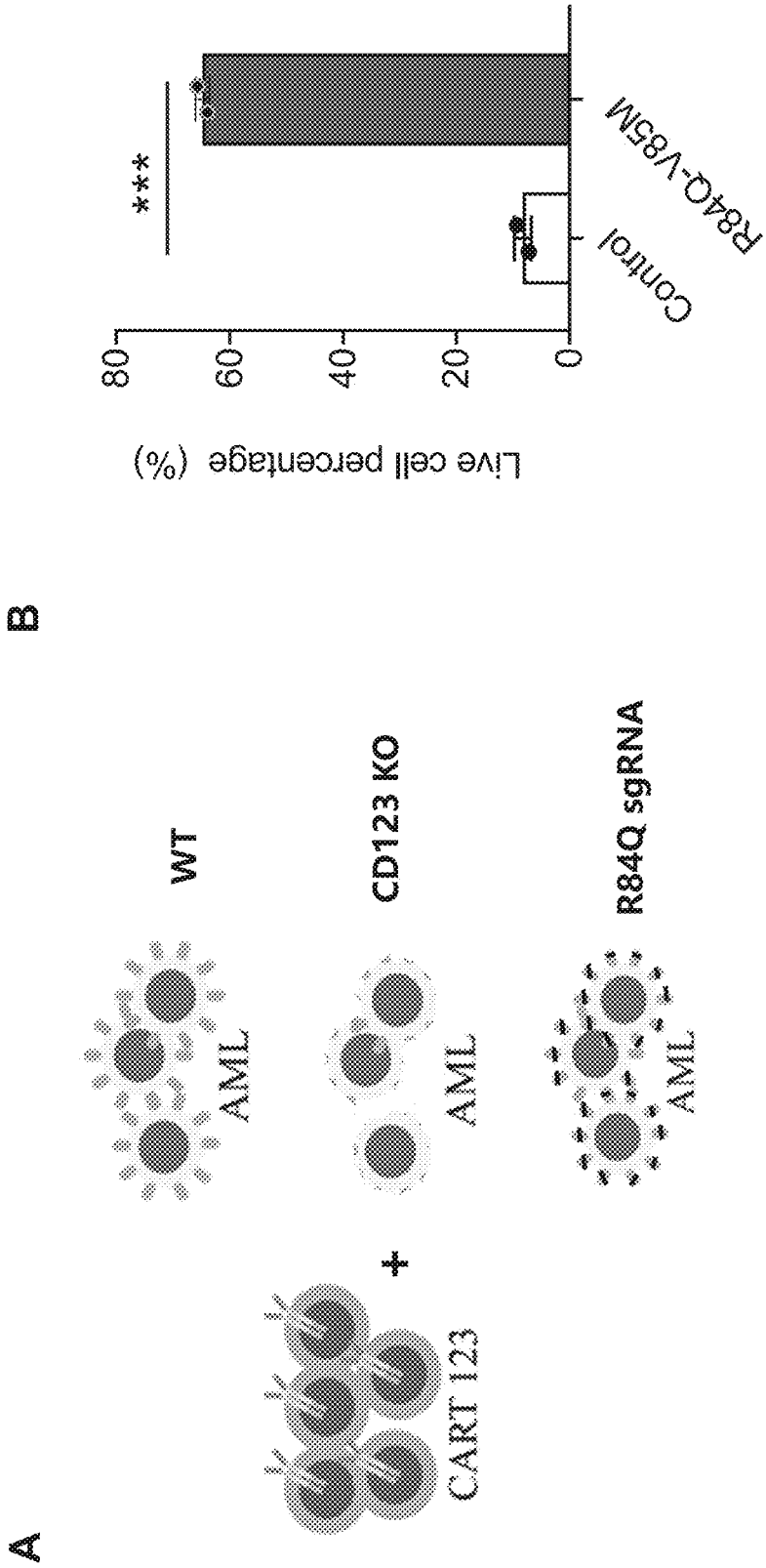


FIG. 8A-B

COMPOSITIONS AND METHODS FOR TREATING ACUTE MYELOID LEUKEMIA

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of Chinese application No. PCT/CN2023/072703, filed Jan. 17, 2023, and CN202311057422.8, filed Aug. 22, 2023, the content of each of which is hereby incorporated by reference in its entirety.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0002] The content of the electronic sequence listing (366244.xml: Size: 797,237 bytes; and Date of Creation: Jan. 16, 2024) is herein incorporated by reference in its entirety.

BACKGROUND

[0003] Acute myeloid leukemia (AML) is a hematological malignancy caused by accumulated mutations in myeloid progenitor cells that cause hyperproliferation and blockage of differentiation, resulting in the accumulation of myeloid blasts in hematopoietic tissues. Despite a high initial response to standard chemotherapy, relapse is common and the prognosis is poor in most AML patients. The conventional chemotherapy drugs cannot fundamentally solve the high occurrences of relapse and drug resistance, and there is a possibility of relapse after hematopoietic stem cell transplantation. Therefore, it is urgent to develop new and improved therapeutic methods.

[0004] Chimeric antigen receptor (CAR) T cell therapy uses genetically modified T cells to target and kill cancer cells more specifically and effectively. After T cells are collected from the blood, the cells are engineered to express CARs on their surfaces. CARs can be introduced into T cells using CRISPR/Cas9 gene editing technology. When these allogeneic CAR T cells are injected into patients, the receptors enable the T cells to kill cancer cells.

[0005] CD33 (also known as Siglec3, sialic acid-binding Ig-like lectin 3, gp67, or p67) is a member of the Siglec lectin family whose expression is restricted to normal monocytes, granulocytes, hematopoietic progenitors, and immunophenotype-defined hematopoiesis stem cells in the stem cell population. It is expressed on the AML cells of most acute myeloid leukemia patients at both onset and relapse. It functions by binding sialic acid residues of glycoproteins and glycolipids. Anti-CD33 CAR-T cells represent an effective therapeutic option for CD33-expressing malignancies.

[0006] CD123 is the alpha chain of interleukin-3 receptor, and CD123 can specifically recognize and bind interleukin-3 (IL-3). IL-3 is mainly produced by helper T cells activated by antigen stimulation, which can promote cell growth and proliferation. It is related to the occurrence of tumors, allergic inflammation, and autoimmune diseases. CD123 is expressed in AML cells from most patients with acute myeloid leukemia. CD123 is also expressed in normal hematopoietic stem cells, functionally related to the differentiation of hematopoietic stem cells. Anti-CD123 CAR-T cells represent an effective therapeutic option for CD123-expressing malignancies.

[0007] CD117, also known as mast/stem cell growth factor receptor (SCFR), proto-oncogene c-Kit, tyrosine protein

kinase Kit, is a 145-kd transmembrane glycoprotein. Studies in mice with inactivating mutations of c-kit or its ligand, stem cell factor (SCF), have shown that normal functional activity of c-kit is essential for maintaining normal hematopoiesis, melanogenesis, gametogenesis, and cell growth and differentiation. CD117 is expressed on hematopoietic progenitor cells, mast cells, germ cells, interstitial cells of Cajal (ICC), and also highly expressed in AML cells from most AML patients, and thus anti-CD117 CAR-T cells represent an effective treatment for CD117-expressing malignancies.

[0008] C-type lectin-like 1 (CLL-1) is also known as MICL, CLEC12A, CLEC-1, dendritic cell-associated lectin 1, and DCAL-2. CLL-1 is a glycoprotein receptor that is a member of a large family of C-type lectin-like receptors involved in immune regulation. Members of this family have diverse functions such as cell adhesion, intercellular signaling, glycoprotein turnover, and roles in inflammation and immune responses. CLL-1 is expressed on hematopoietic cells and primarily on innate immune cells, including monocytes, DCs, pDCs, and granulocyte and myeloid progenitor cells. CLL-1 is also expressed in cancer cells of most acute myeloid leukemia (AML) and myelodysplastic syndrome (MDS) patients. CLL-1 is a leukemia stem cell (LSC)-related surface antigen. Anti-CLL-1 CAR-T cells represent an effective therapeutic option for CLL-1-expressing malignancies.

SUMMARY

[0009] The present disclosure describes compositions and methods for treating cancers such as acute myeloid leukemia (AML). The method entails administering to the patient an antibody drug conjugates or a chimeric antigen receptor (CAR)-expressing immune cell targeting a molecule such as CD33, CD123, CD117 or CLL-1 following, or concurrently with, transplanting to the patient an engineered stem cell expressing the same molecule but with a mutation disrupting the epitope to the antibody or CAR. Due to the mutation, the engineered stem cell, unlike endogenous hematopoietic cells, is not targeted by the therapy and thus can supply the patient with functional hematopoietic cells and antigens.

[0010] One embodiment of the present disclosure provides a method for preparing a cancer patient for a therapy, comprising administering to the patient a stem cell expressing a mutant CD33 protein comprising a mutation in an epitope recognized by an anti-CD33 antibody which has reduced binding to the mutant CD33 protein as compared to the corresponding wild-type CD33 protein, wherein the therapy comprises the antibody, an antigen-binding fragment of the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

[0011] Another embodiment of the present disclosure provides a method for preparing a cancer patient for a therapy, comprising administering to the patient a stem cell expressing a mutant CD123 protein comprising a mutation in an epitope recognized by an anti-CD123 antibody which has reduced binding to the mutant CD123 protein as compared to the corresponding wild-type CD123 protein, wherein the therapy comprises the antibody, an antigen-binding fragment of the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

[0012] Another embodiment of the present disclosure provides a method for preparing a cancer patient for a therapy, comprising administering to the patient a stem cell expressing a mutant CD117 protein comprising a mutation in an epitope recognized by an anti-CD117 antibody which has reduced binding to the mutant CD117 protein as compared to the corresponding wild-type CD117 protein, wherein the therapy comprises the antibody, an antigen-binding fragment of the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

[0013] Another embodiment of the present disclosure provides a method for preparing a cancer patient for a therapy, comprising administering to the patient a stem cell expressing a mutant CLL-1 protein comprising a mutation in an epitope recognized by an anti-CLL-1 antibody which has reduced binding to the mutant CLL-1 protein as compared to the corresponding wild-type CLL-1 protein, wherein the therapy comprises the antibody, an antigen-binding fragment of the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

[0014] In some embodiments, the cancer is leukemia. In some embodiments, the cancer is acute myeloid leukemia (AML).

[0015] In some embodiments, the stem cell is a hematopoietic stem and progenitor cell (HSPC).

[0016] In some embodiments, the mutant CD33 protein comprises a mutation at one or more residues selected from the group consisting of C41, W60, I105, D112, Y116, F118, P132, W22, G34, R89, N100, N113, and S131 according to SEQ ID NO:1, wherein the mutation is preferably non-conservative. In some embodiments, the anti-CD33 antibody is my9.6 or an antigen-binding fragment thereof.

[0017] In some embodiments, the mutant CD33 protein comprises a mutation at one or more residues selected from the group consisting of C41, W60, I105, Y116, and F118 according to SEQ ID NO:1, wherein the mutation is preferably non-conservative. In some embodiments, the anti-CD33 antibody is HM195 or an antigen-binding fragment thereof.

[0018] In some embodiments, mutation is introduced to the stem cell with a base editor comprising a gRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO: 19-144. In some embodiments, mutation is introduced to the stem cell with a prime editor and a pegRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:145-228.

[0019] In some embodiments, the mutant CD123 protein comprises a mutation at one or more residues selected from the group consisting of 127, L30, M32, W41, E51, C52, S59, P61, R84, P88, F90, S91, and W93 according to SEQ ID NO:2, wherein the mutation is preferably non-conservative. In some embodiments, the anti-CD123 antibody is CSL362 or 32716, or an antigen-binding fragment thereof.

[0020] In some embodiments, mutation is introduced to the stem cell with a base editor comprising a gRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:229-516. In some embodiments, mutation is introduced to the stem cell with a prime editor and a pegRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:517-541.

[0021] In some embodiments, the mutant CD117 protein comprises a mutation at one or more residues selected from

the group consisting of T67, K69, T71, S81, Y83, T114, T119, and K129 according to SEQ ID NO:3, wherein the mutation is preferably non-conservative. In some embodiments, the anti-CD117 antibody is Ab85 or an antigen-binding fragment thereof.

[0022] In some embodiments, the mutant CD117 protein comprises a mutation at one or more residues selected from the group consisting of S236, H238, Y244, S273, T277, and T279 according to SEQ ID NO:3, wherein the mutation is preferably non-conservative. In some embodiments, the anti-CD117 antibody is Ab67 or an antigen-binding fragment thereof.

[0023] In some embodiments, mutation is introduced to the stem cell with a base editor comprising a gRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:542-758. In some embodiments, mutation is introduced to the stem cell with a prime editor and a pegRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:759-801.

[0024] In some embodiments, the mutant CLL-1 protein comprises a mutation at one or more residues selected from amino acid residues 142-158 according to SEQ ID NO:4, wherein the mutation is preferably non-conservative. In some embodiments, the anti-CLL-1 antibody is Hu6E7, N54A, or an antigen-binding fragment thereof.

[0025] In some embodiments, is introduced to the stem cell with a base editor comprising a gRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:802-879. In some embodiments, mutation is introduced to the stem cell with a prime editor and a pegRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:880-893.

[0026] In some embodiments, the therapy comprises the immune cell that comprises the CAR. In some embodiments, the immune cell is a T cell, an NK cell, or a macrophage.

[0027] In some embodiments, the method further comprises administering the therapy to the patient. In some embodiments, the therapy is administered after the stem cell is administered.

[0028] In some embodiments, the stem cell is autologous or allogeneic to the patient.

[0029] In some embodiments, the patient expresses CD33, CD123, CD117 or CLL-1 in cancer cells.

[0030] Also provided, in one embodiment, is a method for treating acute myeloid leukemia (AML) in a patient in need thereof, comprising: (a) editing the genome of a stem cell to introduce a mutation to an epitope of the CD33 protein recognized by an anti-CD33 antibody which has reduced binding to the mutated CD33 protein as compared to the corresponding wild-type CD33 protein, wherein the mutation is at one or more residues selected from the group consisting of C41, W60, I105, D112, Y116, F118, P132, W22, G34, R89, N100, N113, and S131 according to SEQ ID NO:1, and is preferably a non-conservative mutation, (b) transplanting to the patient the edited stem cell, and (c) administering to the patient the antibody, an antigen-binding fragment of the antibody, an antibody-drug conjugate comprising the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

[0031] Also provided, in one embodiment, is a method for treating acute myeloid leukemia (AML) in a patient in need thereof, comprising: (a) editing the genome of a stem cell to introduce a mutation to an epitope of the CD123 protein

recognized by an anti-CD123 antibody which has reduced binding to the mutated CD123 protein as compared to the corresponding wild-type CD123 protein, wherein the mutation is at one or more residues selected from the group consisting of 127, L30, M32, W41, E51, C52, S59, P61, R84, P88, F90, S91, and W93 according to SEQ ID NO:2, and is preferably a non-conservative mutation, (b) transplanting to the patient the edited stem cell, and (c) administering to the patient the antibody, an antigen-binding fragment of the antibody, an antibody-drug conjugate comprising the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

[0032] Also provided, in one embodiment, is a method for treating acute myeloid leukemia (AML) in a patient in need thereof, comprising: (a) editing the genome of a stem cell to introduce a mutation to an epitope of the CD117 protein recognized by an anti-CD117 antibody which has reduced binding to the mutated CD117 protein as compared to the corresponding wild-type CD117 protein, wherein the mutation is at one or more residues selected from the group consisting of T67, K69, T71, S81, Y83, T114, T119, K129, S236, H238, Y244, S273, T277, and T279 according to SEQ ID NO:3, and is preferably a non-conservative mutation, (b) transplanting to the patient the edited stem cell, and (c) administering to the patient the antibody, an antigen-binding fragment of the antibody, an antibody-drug conjugate comprising the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

[0033] Also provided, in one embodiment, is a method for treating acute myeloid leukemia (AML) in a patient in need thereof, comprising: (a) editing the genome of a stem cell to introduce a mutation to an epitope of the CLL-1 protein recognized by an anti-CLL-1 antibody which has reduced binding to the mutated CLL-1 protein as compared to the corresponding wild-type CLL-1 protein, wherein the mutation is at one or more residues selected from amino acid residues 142 to 158 according to SEQ ID NO:4, and is preferably a non-conservative mutation, (b) transplanting to the patient the edited stem cell, and (c) administering to the patient the antibody, an antigen-binding fragment of the antibody, an antibody-drug conjugate comprising the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

BRIEF DESCRIPTION OF THE DRAWINGS

[0034] FIG. 1A-D. Determination of epitopes of CD33 that mediate the interaction by anti-CD33 scFv clone my9.6 or HM195. (A) Binding affinity of indicated CD33 mutations with anti-CD33 scFV clone my9.6. HEK 293T cells were transfected with wildtype or indicated CD33 mutant and then incubated with anti-CD33 scFV-luciferase fusion proteins, RLU: relative luminescence units. (B) Western blot of CD33 expression. HEK293T cells were transfected with flag tagged wild-type or indicated CD33 mutants. (C) Binding affinity of additional CD33 mutations. RLU: relative luminescence units (D) Western blot of CD33 expression. HEK293T cells were transfected with flag tagged wild-type or indicated CD33 mutants.

[0035] FIG. 2A-G. Mutating endogenous CD33 epitopes in HEK 293T cells and human CD34+ HSPCs by base editors and prime editor. (A) Sanger sequencing of base

editors targeting W60 of CD33 in CD34+ HSPCs. Red arrow pointed at desired mutation site. (B) Deep sequencing of editing efficiency and editing products. (C) Illustration of Prime editing design and editing efficiency of in HEK293T cells. PE4 was used to target P132 site of CD33. (D-F) Optimization of PE4 with variable nick site (D), PBS lengths (E), RT template lengths (F). (G) Comparison of PE4, PE4max and PEmax in editing P132 into A132 of CD33. HSPCs: hematopoietic stem and progenitor cells

[0036] FIG. 3A-B. Determination of epitopes of CD123 that mediate the recognition by scFv clone 32716 or CSL362. (A) Binding affinity of indicated CD123 mutations with anti-CD123 scFv clone 32716 (left panels) or clone CSL362 (right panels). HEK 293T cells were transfected with wildtype or indicated CD123 mutant and then incubated with anti-CD123 scFv-luciferase fusion proteins. (B) Western blot of CD123 expression. HEK293T cells were transfected with flag tagged wild-type or indicated CD123 mutants.

[0037] FIG. 4A-C. CD123 combined mutation R84-V85 can reduce the affinity of the CSL362 antibody without affecting expression and the CD123 downstream signaling pathway. (A) Combined mutations at different sites and their binding affinity with CSL362. (B) Immunoprecipitation to detect the expression levels of different combined mutation variants. (C) Immunoprecipitation to detect CD123 downstream signaling pathway pSTAT5. The results show that combined mutations do not affect the normal function of CD123.

[0038] FIG. 5A-H. Mutation of endogenous CD123 sites in HEK 293T cells using base editors and prime editors. (A-B) Editing of CD123-R84 (A) or L30 (B) in HEK 293T cells targeted by BE. Arrows indicate the desired mutation sites. (C-E) Deep sequencing of edited efficiency (C, E) and edited products (D, F) in human hematopoietic stem progenitor cells. (E-F) ABE8.8m-mediated single-base editing products have a purity exceeding 90%, while CBE has more off-target products (C-D). (G) Precise editing of the CD123-R84 site using a prime editor. The schematic shows the design of pegRNA. (H) First-generation sequencing shows that both pegRNAs can effectively edit the R84 site. Arrows point to the editing site.

[0039] FIG. 6A-D. Hematopoietic stem cells after precise editing of antigen sites have normal myeloid differentiation and proliferative capacity. (A) Myeloid cell count. Cells with precise editing of CD123 R84Q or L30P antigen sites have better cell viability compared to CD123 knockout cells. (B) Myeloid cell morphology. Cells with precise editing of CD123 R84Q or L30P have consistent morphology with the control, while direct knockout of CD123 affects cell morphological changes. (C-D) Myeloid differentiation ratio. Edited hematopoietic stem progenitor cells were subjected to in vitro myeloid differentiation, and differentiation ability was verified using myeloid surface molecules CD11b (C) and CD14 (D). Precise editing of cells does not affect myeloid differentiation.

[0040] FIG. 7A-C. Hematopoietic stem cells after precise editing of antigen sites can differentiate into plasmacytoid dendritic cells. (A) Number of plasmacytoid dendritic cells. Cells with precise editing of CD123 R84Q or L30P antigen sites have more plasmacytoid dendritic cells compared to CD123 knockout cells. (B) Ratio of plasmacytoid dendritic cell differentiation. Edited hematopoietic stem progenitor cells were subjected to in vitro differentiation into plasma-

cytoid dendritic cells, and differentiation ability was verified using CD303 surface molecules. (C) Morphology of plasmacytoid dendritic cells. pDC: plasmacytoid dendritic cell.

[0041] FIG. 8A-B. CD123-CAR-T cell targeting experiment. (A) Preparation of CAR-T cells containing CSL362 monoclonal antibody, and co-culturing CAR-T cells with wild-type AML tumor cells, CD123 knockout AML cells, or cells containing CD123-R84Q mutation. (B) The co-cultivation results of hematopoietic stem cells after precise editing through the guide editor and undergoing myeloid differentiation with CAR-T CD123 in vitro were obtained. Compared to the unedited control group, cells after precise editing showed resistance to CAR-T killing, significantly improving cell survival rates.

DETAILED DESCRIPTION

Definitions

[0042] The term “allogeneic” refers to any material derived from one individual which is then introduced to another individual of the same species, e.g., allogeneic T cell transplantation.

[0043] The term “autologous” refers to any material derived from the same individual to which it is later to be re-introduced. For example, the engineered autologous cell therapy (eACT™) method described herein involves collection of lymphocytes from a patient, which are then engineered to express, e.g., a CAR construct, and then administered back to the same patient.

[0044] The term “antibody” (Ab) includes, without limitation, a glycoprotein immunoglobulin which binds specifically to an antigen. In general, an antibody can comprise at least two heavy (H) chains and two light (L) chains interconnected by disulfide bonds, or an antigen-binding molecule thereof. Each H chain comprises a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region comprises three constant domains, CH1, CH2 and CH3. Each light chain comprises a light chain variable region (abbreviated herein as VL) and a light chain constant region. The light chain constant region comprises one constant domain, CL. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL comprises three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the Abs may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (e.g., effector cells) and the first component (C1q) of the classical complement system. In general, human antibodies are approximately 150 kD tetrameric agents composed of two identical heavy (H) chain polypeptides (about 50 kD each) and two identical light (L) chain polypeptides (about 25 kD each) that associate with each other into what is commonly referred to as a “Y-shaped” structure. The heavy and light chains are linked or connected to one another by a single disulfide bond; two other disulfide bonds connect the heavy chain hinge regions to one another, so that the dimers are connected to one

another and the tetramer is formed. Naturally-produced antibodies are also glycosylated, e.g., on the CH2 domain.

[0045] The term “variable region” or “variable domain” is used interchangeably. The variable region typically refers to a portion of an antibody, generally, a portion of a light or heavy chain, typically about the amino-terminal 110 to 120 amino acids in the mature heavy chain and about 90 to 115 amino acids in the mature light chain, which differ extensively in sequence among antibodies and are used in the binding and specificity of a particular antibody for its particular antigen. The variability in sequence is concentrated in those regions called complementarity determining regions (CDRs) while the more highly conserved regions in the variable domain are called framework regions (FR). Without wishing to be bound by any particular mechanism or theory, it is believed that the CDRs of the light and heavy chains are primarily responsible for the interaction and specificity of the antibody with antigen. In certain embodiments, the variable region is a human variable region. In certain embodiments, the variable region comprises rodent or murine CDRs and human framework regions (FRs). In particular embodiments, the variable region is a primate (e.g., non-human primate) variable region. In certain embodiments, the variable region comprises rodent or murine CDRs and primate (e.g., non-human primate) framework regions (FRs).

[0046] The terms “VL” and “VL domain” are used interchangeably to refer to the light chain variable region of an antibody or an antigen-binding molecule thereof.

[0047] The terms “VH” and “VH domain” are used interchangeably to refer to the heavy chain variable region of an antibody or an antigen-binding molecule thereof.

[0048] “Chimeric antigen receptor” or “CAR” refers to a molecule engineered to comprise a binding motif and a means of activating immune cells (for example T cells such as naive T cells, central memory T cells, effector memory T cells or combination thereof) upon antigen binding. CARs are also known as artificial T cell receptors, chimeric T cell receptors or chimeric immunoreceptors. In some embodiments, a CAR comprises a binding motif, an extracellular domain, a transmembrane domain, one or more co-stimulatory domains, and an intracellular signaling domain. A T cell that has been genetically engineered to express a chimeric antigen receptor may be referred to as a CAR T cell. “Extracellular domain” (or “ECD”) refers to a portion of a polypeptide that, when the polypeptide is present in a cell membrane, is understood to reside outside of the cell membrane, in the extracellular space.

[0049] The term “extracellular ligand-binding domain,” as used herein, refers to an oligo- or polypeptide that is capable of binding a ligand, e.g., a cell surface molecule. For example, the extracellular ligand-binding domain may be chosen to recognize a ligand that acts as a cell surface marker on target cells associated with a particular disease state (e.g., cancer). Examples of cell surface markers that may act as ligands include those associated with viral, bacterial and parasitic infections, autoimmune disease and cancer cells.

[0050] The binding domain of the CAR may be followed by a “spacer,” or, “hinge,” which refers to the region that moves the antigen binding domain away from the effector cell surface to enable proper cell/cell contact, antigen binding and activation (Patel et al., *Gene Therapy*, 1999; 6: 412-419). The hinge region in a CAR is generally between

the transmembrane (TM) and the binding domain. In certain embodiments, a hinge region is an immunoglobulin hinge region and may be a wild type immunoglobulin hinge region or an altered wild type immunoglobulin hinge region. Other exemplary hinge regions used in the CARs described herein include the hinge region derived from the extracellular regions of type 1 membrane proteins such as CD8alpha, CD4, CD28 and CD7, which may be wild-type hinge regions from these molecules or may be altered.

[0051] The “transmembrane” region or domain is the portion of the CAR that anchors the extracellular binding portion to the plasma membrane of the immune effector cell, and facilitates binding of the binding domain to the target antigen. The transmembrane domain may be a CD3zeta transmembrane domain, however other transmembrane domains that may be employed include those obtained from CD8alpha, CD4, CD28, CD45, CD9, CD16, CD22, CD33, CD64, CD80, CD86, CD134, CD137, and CD154. In one embodiment, the transmembrane domain is the transmembrane domain of CD137. In certain embodiments, the transmembrane domain is synthetic in which case it would comprise predominantly hydrophobic residues such as leucine and valine.

[0052] The “intracellular signaling domain” or “signaling domain” refers to the part of the chimeric antigen receptor protein that participates in transducing the message of effective CAR binding to a target antigen into the interior of the immune effector cell to elicit effector cell function, e.g., activation, cytokine production, proliferation and cytotoxic activity, including the release of cytotoxic factors to the CAR-bound target cell, or other cellular responses elicited with antigen binding to the extracellular CAR domain. The term “effector function” refers to a specialized function of the cell. Effector function of the T cell, for example, may be cytolytic activity or help or activity including the secretion of a cytokine. Thus, the terms “intracellular signaling domain” or “signaling domain,” used interchangeably herein, refer to the portion of a protein which transduces the effector function signal and that directs the cell to perform a specialized function. While usually the entire intracellular signaling domain can be employed, in many cases it is not necessary to use the entire domain. To the extent that a truncated portion of an intracellular signaling domain is used, such truncated portion may be used in place of the entire domain as long as it transduces the effector function signal. The term intracellular signaling domain is meant to include any truncated portion of the intracellular signaling domain sufficient to transducing effector function signal. The intracellular signaling domain is also known as the, “signal transduction domain,” and is typically derived from portions of the human CD3 or FcRy chains.

[0053] It is known that signals generated through the T cell receptor alone are insufficient for full activation of the T cell and that a secondary, or costimulatory signal is also required. Thus, T cell activation can be said to be mediated by two distinct classes of cytoplasmic signaling sequences: those that initiate antigen dependent primary activation through the T cell receptor (primary cytoplasmic signaling sequences) and those that act in an antigen independent manner to provide a secondary or costimulatory signal (secondary cytoplasmic signaling sequences). Cytoplasmic signaling sequences that act in a costimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motif or ITAMs.

[0054] Examples of ITAM containing primary cytoplasmic signaling sequences that are of particular use in the disclosure include those derived from TCRzeta, FcRgamma, FcRbeta, CD3gamma, CD3delta, CD3epsilon, CD5, CD22, CD79a, CD79b and CD66d.

[0055] As used herein, the term, “costimulatory signaling domain,” or “costimulatory domain”, refers to the portion of the CAR comprising the intracellular domain of a costimulatory molecule. Costimulatory molecules are cell surface molecules other than antigen receptors or Fc receptors that provide a second signal required for efficient activation and function of T lymphocytes upon binding to antigen. Examples of such co-stimulatory molecules include CD27, CD28, 4-1 BB (CD137), OX40 (CD134), CD30, CD40, PD-1, ICOS (CD278), LFA-1, CD2, CD7, LIGHT, NKD2C, B7-H2 and a ligand that specifically binds CD83. Accordingly, while the present disclosure provides exemplary costimulatory domains derived from CD3zeta and 4-1 BB, other costimulatory domains are contemplated for use with the CARs described herein. The inclusion of one or more co stimulatory signaling domains may enhance the efficacy and expansion of T cells expressing CAR receptors. The intracellular signaling and costimulatory signaling domains may be linked in any order in tandem to the carboxyl terminus of the transmembrane domain.

[0056] Although scFv-based CARs engineered to contain a signaling domain from CD3 or FcRgamma have been shown to deliver a potent signal for T cell activation and effector function, they are not sufficient to elicit signals that promote T cell survival and expansion in the absence of a concomitant costimulatory signal. Other CARs containing a binding domain, a hinge, a transmembrane and the signaling domain derived from CD3zeta or FcRgamma together with one or more costimulatory signaling domains (e.g., intracellular costimulatory domains derived from CD28, CD137, CD134 and CD278) may more effectively direct antitumor activity as well as increased cytokine secretion, lytic activity, survival and proliferation in CAR expressing T cells in vitro, and in animal models and cancer patients.

[0057] A “conservative amino acid substitution” is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a nonessential amino acid residue in an immunoglobulin polypeptide is preferably replaced with another amino acid residue from the same side chain family. In another embodiment, a string of amino acids can be replaced with a structurally similar string that differs in order and/or composition of side chain family members.

[0058] Non-limiting examples of conservative amino acid substitutions are provided in the tables below, where a similarity score of 0 or higher indicates conservative substitution between the two amino acids.

[0059] A substitution or mutation that is not considered a conservative amino acid substitution/mutation can be referred to as a non-conservative substitution/mutation.

TABLE A

Amino Acid Similarity Matrix																				
	C	G	P	S	A	T	D	E	N	Q	H	K	R	V	M	I	L	F	Y	W
W	-8	-7	-6	-2	-6	-5	-7	-7	-4	-5	-3	-3	2	-6	-4	-5	-2	0	0	17
Y	0	-5	-5	-3	-3	-3	-4	-4	-2	-4	0	-4	-5	-2	-2	-1	-1	7	10	
F	-4	-5	-5	-3	-4	-3	-6	-5	-4	-5	-2	-5	-4	-1	0	1	2	9		
L	-6	-4	-3	-3	-2	-2	-4	-3	-3	-2	-2	-3	-3	2	4	2	6			
I	-2	-3	-2	-1	-1	0	-2	-2	-2	-2	-2	-2	-2	4	2	5				
M	-5	-3	-2	-2	-1	-1	-3	-2	0	-1	-2	0	0	2	6					
V	-2	-1	-1	-1	0	0	-2	-2	-2	-2	-2	-2	-2	4						
R	-4	-3	0	0	-2	-1	-1	-1	0	1	2	3	6							
K	-5	-2	-1	0	-1	0	0	0	1	1	0	5								
H	-3	-2	0	-1	-1	-1	1	1	2	3	6									
Q	-5	-1	0	-1	0	-1	2	2	1	4										
N	-4	0	-1	1	0	0	2	1	2											
E	-5	0	-1	0	0	0	3	4												
D	-5	1	-1	0	0	0	4													
T	-2	0	0	1	1	3														
A	-2	1	1	1	2															
S	0	1	1	1																
P	-3	-1	6																	
G	-3	5																		
C	12																			

[0060] A “patient” includes any human who is afflicted with a cancer (e.g., a leukemia). The terms “subject” and “patient” are used interchangeably herein.

[0061] A “therapeutically effective amount,” “effective dose,” “effective amount,” or “therapeutically effective dosage” of a therapeutic agent, e.g., engineered CAR T cells, is any amount that, when used alone or in combination with another therapeutic agent, protects a subject against the onset of a disease or promotes disease regression evidenced by a decrease in severity of disease symptoms, an increase in frequency and duration of disease symptom-free periods, or a prevention of impairment or disability due to the disease affliction. The ability of a therapeutic agent to promote disease regression can be evaluated using a variety of methods known to the skilled practitioner, such as in human subjects during clinical trials, in animal model systems predictive of efficacy in humans, or by assaying the activity of the agent in in vitro assays.

[0062] “Treatment” or “treating” of a subject refers to any type of intervention or process performed on, or the administration of an active agent to, the subject with the objective of reversing, alleviating, ameliorating, inhibiting, slowing down or preventing the onset, progression, development, severity or recurrence of a symptom, complication or condition, or biochemical indicia associated with a disease. In one embodiment, “treatment” or “treating” includes a partial remission. In another embodiment, “treatment” or “treating” includes a complete remission. In some embodiments, treatment may be of a subject who does not exhibit signs of the relevant disease, disorder and/or condition and/or of a subject who exhibits only early signs of the disease, disorder, and/or condition. In some embodiments, such treatment may be of a subject who exhibits one or more established signs of the relevant disease, disorder and/or condition. In some embodiments, treatment may be of a subject who has been diagnosed as suffering from the relevant disease, disorder, and/or condition. In some embodiments, treatment may be of a subject known to have one or more susceptibility factors that are statistically correlated with increased risk of development of the relevant disease, disorder, and/or condition.

[0063] A “zinc finger DNA binding protein” (or binding domain) is a protein, or a domain within a larger protein, that binds DNA in a sequence-specific manner through one or more zinc fingers, which are regions of amino acid sequence within the binding domain whose structure is stabilized through coordination of a zinc ion. Thus, each zinc finger of a multi-finger ZFP includes a recognition helix region for binding to DNA within a backbone. The term zinc finger DNA binding protein is often abbreviated as zinc finger protein or ZFP. The term “zinc finger nuclease” includes one ZFN as well as a pair of ZFNs (the members of the pair are referred to as “left and right” or “first and second” or “pair”) that dimerize to cleave the target gene.

[0064] A “TALE DNA binding domain” or “TALE” is a polypeptide comprising one or more TALE repeat domains/units. The repeat domains, each comprising a repeat variable diresidue (RVD), are involved in binding of the TALE to its cognate target DNA sequence. A single “repeat unit” (also referred to as a “repeat”) is typically 33-35 amino acids in length and exhibits at least some sequence homology with other TALE repeat sequences within a naturally occurring TALE protein. TALE proteins may be designed to bind to a target site using canonical or non-canonical RVDs within the repeat units. See, e.g., U.S. Pat. Nos. 8,586,526 and 9,458,205. Zinc finger and TALE DNA-binding domains can be “engineered” to bind to a predetermined nucleotide sequence, for example via engineering (altering one or more amino acids) of the recognition helix region of a naturally occurring zinc finger protein or by engineering of the amino acids involved in DNA binding (the repeat variable diresidue or RVD region). Therefore, engineered zinc finger proteins or TALE proteins are proteins that are non-naturally occurring. Non-limiting examples of methods for engineering zinc finger proteins and TALEs are design and selection. A designed protein is a protein not occurring in nature whose design/composition results principally from rational criteria. Rational criteria for design include application of substitution rules and computerized algorithms for processing information in a database storing information of existing ZFP or TALE designs (canonical and non-canonical RVDs) and binding data. See, for example, U.S. Pat. Nos. 9,458,205:

8,586,526; 6,140,081; 6,453,242; and 6,534,261: see also International Patent Publication Nos. WO 98/53058; WO 98/53059; WO 98/53060; WO 02/016536; and WO 03/016496. The term "TALEN" includes one TALEN as well as a pair of TALENs (the members of the pair are referred to as "left and right" or "first and second" or "pair") that dimerize to cleave the target gene.

[0065] CRISPR/Cas (Clustered regularly interspaced short palindromic repeats/CRISPR-associated protein) system has been the most powerful genomic editing tool since its conception for its unparalleled editing efficiency, convenience and the potential applications in living organism. Directed by guide RNA (gRNA), a Cas nuclease can generate DNA double strand breaks (DSBs) at the targeted genomic sites in various cells (both cell lines and cells from living organisms). These DSBs are then repaired by the endogenous DNA repair system, which could be utilized to perform desired genome editing.

[0066] Base editors (BE), which integrate the CRISPR/Cas system with the APOBEC (apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like) cytosine deaminase family, were recently developed that greatly enhanced the efficiency of CRISPR/Cas9-mediated gene correction. Through fusion with Cas9 nickase (nCas9) or catalytically dead Cas9 (dCas9), the cytosine (C) deamination activity of rat APOBEC1 (rA1) can be purposely directed to the target bases in genome and to catalyze C to Thymine (T) substitutions at these bases.

[0067] Prime editing (PE) is a genome editing technology by which the genome of living organisms may be modified. Prime editing directly writes new genetic information into a targeted DNA site. It uses a fusion protein, consisting of a catalytically impaired endonuclease (e.g., Cas9) fused to an engineered reverse transcriptase enzyme, and a prime editing guide RNA (pegRNA), capable of identifying the target site and providing the new genetic information to replace the target DNA nucleotides. Prime editing mediates targeted insertions, deletions, and base-to-base conversions without the need for double strand breaks (DSBs) or donor DNA templates.

Transplantation of Engineered Tumor Antigen-Expressing Cells

[0068] Tumor-associated antigens are commonly targeted for cancer therapies. Ideally, non-cancer cells do not express these antigens and thus would not be killed by the therapies. However, frequently other tissues can also have expression, albeit lower expression sometimes, of these antigens. Such cells therefore can be targeted by the therapy, causing undesired adverse effects.

[0069] Example therapies targeting a tumor associated antigen include antibodies, either directly, or through antibody-dependent cellular cytotoxicity (ADCC) or antibody-dependent cellular phagocytosis (ADCP). Another example is chimeric antigen receptor (CAR) T cell therapy which uses genetically modified T cells to target and kill cancer cells.

[0070] The present disclosure provides compositions and methods for treating a cancer while reducing adverse effects associated with non-cancerous cells expressing a tumor associated antigen targeted by a therapy. In an illustrative example, a genome editing tool is used to modify the target epitope in a hematopoietic stem and progenitor cell (HSPC) such that the HSPC cannot be bound by the therapeutic

antibody or CAR cell, while retaining the normal biological function. When the engineered HSPC is transplanted to a patient that receives the therapy, even if the patient's own HSPC is targeted by the therapy, the transplanted engineered HSPC can supplement the required activity of the HSPC, reducing or avoid the associated toxicities.

[0071] According to one embodiment of the present disclosure, provided is a method for preparing a cancer (e.g., leukemia, in particular AML) patient for a therapy. The therapy is designed to specifically target an antigen expressed by the cancer cells, which may include an antibody, an antigen-binding fragment, a chimeric antigen receptor (CAR), or an immune cells (e.g., T cells, NK cells, macrophages, monocytes), or their respective coding sequences. Example tumor associated antigens are known. In some embodiments, the cancer is leukemia. In some embodiments, the leukemia is AML, in particular relapsed and/or refractory AML. For acute myeloid leukemia (AML), the antigen may be CD33, CD123, CD117 or CLL-1, without limitation. In some embodiments, the cancer patient has cancer cells expressing CD33. In some embodiments, the cancer patient has cancer cells expressing CD123. In some embodiments, the cancer patient has cancer cells expressing CD117. In some embodiments, the cancer patient has cancer cells expressing CLL-1.

[0072] In some embodiments, the method entails administering to the patient a stem cell that expresses a mutant form of the antigen. In some embodiments, the mutation is at one or more amino acid residues within the epitope of the antigen targeted by the therapy, or at one or more amino acid residues that impact such binding, such by determining the conformation of the epitope. In some embodiments, the mutation does not affect, or at least does not significantly change, the activities of the antigen.

[0073] Amino acid residues that are important for the antibody binding have been identified for each of CD33, CD123, CD117 or CLL-1, for a number of commonly used antibodies.

[0074] For instance, for CD33, important residues for the binding by antibody my9.6 include C41, W60, I105, D112, Y116, F118, P132, W22, G34, R89, N100, N113, and S131 (residue positions according to CD33 protein sequence as shown in SEQ ID NO: 1). As publicly known, antibody my9.6 has a VH sequence of SEQ ID NO:5 and a VL sequence of SEQ ID NO:6. It is appreciated that an antigen-binding fragment of my9.6 or a CAR molecule that includes the antigen-binding fragment also has the same binding characteristics.

[0075] Also for CD33, important residues for the binding by antibody HM195 include C41, W60, I105, Y116, and F118 (residue positions according to CD33 protein sequence as shown in SEQ ID NO:1). As publicly known, antibody HM195 has a VH sequence of SEQ ID NO:7 and a VL sequence of SEQ ID NO:8. It is appreciated that an antigen-binding fragment of HM195 or a CAR molecule that includes the antigen-binding fragment also has the same binding characteristics.

[0076] For CD123, important residues for the binding by antibody CSL362 or 32716 include I27, L30, M32, W41, E51, C52, S59, P61, R84, P88, F90, S91, and W93 (residue positions according to CD123 protein sequence as shown in SEQ ID NO:2). As publicly known, antibody CSL362 has a VH sequence of SEQ ID NO:9 and a VL sequence of SEQ ID NO:10; and antibody 32716 has a VH sequence of SEQ

ID NO:11 and a VL sequence of SEQ ID NO:12. It is appreciated that an antigen-binding fragment of CSL362 or 32716 or a CAR molecule that includes the antigen-binding fragment also has the same binding characteristics.

[0077] For CD117, important residues for the binding by antibody Ab85 include T67, K69, T71, S81, Y83, T114, T119, and K129 (residue positions according to CD117 protein sequence as shown in SEQ ID NO:3). As publicly known, antibody Ab85 has a VH sequence of SEQ ID NO: 13 and a VL sequence of SEQ ID NO:14. It is appreciated that an antigen-binding fragment of Ab85 or a CAR molecule that includes the antigen-binding fragment also has the same binding characteristics.

[0078] Also for CD117, important residues for the binding by antibody Ab67 include S236, H238, Y244, S273, T277, and T279 (residue positions according to CD117 protein sequence as shown in SEQ ID NO:3). As publicly known, antibody Ab67 has a VH sequence of SEQ ID NO:15 and a VL sequence of SEQ ID NO:16. It is appreciated that an antigen-binding fragment of Ab67 or a CAR molecule that includes the antigen-binding fragment also has the same binding characteristics.

[0079] For CLL-1, important residues for the binding by antibody Hu6E7.N54A include residues 142 to 158 (DSCYFLSDDVQWTWQESK) of the CD117 protein sequence as shown in SEQ ID NO:4). As publicly known, antibody Hu6E7.N54A has a VH sequence of SEQ ID NO: 17 and a VL sequence of SEQ ID NO: 18. It is appreciated that an antigen-binding fragment of Hu6E7.N54A or a CAR molecule that includes the antigen-binding fragment also has the same binding characteristics.

[0080] In some embodiments, the mutation eliminates or reduces binding of the antigen by a corresponding antibody, antigen-binding fragment or AR. In some embodiments, the mutation is a non-conservative mutation. Examples of non-conservative mutations are provided in Table A, indicated by a negative (<0) similarity score. In some embodiments, only amino acid residues having a similarity score of <-1 are used. In some embodiments, only amino acid residues having a similarity score of <-2, or <-3, or <-4 are used. In some embodiment, the mutation (for a residue that is not alanine) is to alanine. In some embodiments, the mutation is not to alanine. In some embodiments, the mutation is not to cysteine. Example mutations are provided in Table B.

TABLE B

Example Mutations					
	Example mutations	Preferred	More preferred	Even more preferred	Most preferred
W	C/G/P/S/A/T/D/E/N/Q/H/ K/V/M/I/L	G/P/S/A/T/D/E/N/Q/ H/K/V/M/I/L/F/Y	G/P/A/T/D/E/N/ Q/H/K/V/M/I	G/P/A/T/D/E/ N/Q/V/M/I	G/P/A/T/D/E/ Q/V/I
Y	G/P/S/A/T/D/E/N/Q/K/R/ V/M/I/L	G/P/S/A/T/D/E/N/Q/ H/K/R/V/M/I/L/W	G/P/S/A/T/D/E/ Q/K/R	G/P/D/E/Q/K/ R	G/P/R
F	C/G/P/S/A/T/D/E/N/Q/H/ K/R/V	G/P/S/A/T/D/E/N/Q/ H/K/R/V/M/W	G/P/S/A/T/D/E/ N/Q/K/R	G/P/A/D/E/N/ Q/K/R	G/P/D/E/Q/K
L	C/G/P/S/A/T/D/E/N/Q/H/ K/R/Y/W	G/P/S/A/T/D/E/N/Q/ H/K/R/Y/W	G/P/S/D/E/N/K/ R	G/D	
I	C/G/P/S/A/D/E/N/Q/H/K/ R/Y/W	G/P/S/A/T/D/E/N/Q/ H/K/R/Y/W	G/W	W	W
M	C/G/P/S/A/T/D/E/Q/H/Y/ W	G/P/S/A/T/D/E/N/Q/ H/K/R/F/Y/W	G/D/W	W	
V	C/G/P/S/D/E/N/Q/H/K/R/ F/Y/W	G/P/S/A/T/D/E/N/Q/ H/K/R/F/Y/W	W	W	W
R	C/G/A/T/D/E/V/I/L/F/Y	G/P/S/A/T/D/E/N/V/ M/I/L/F/Y	G/L/F/Y	F/Y	Y
K	C/G/P/A/V/I/L/F/Y/W	G/P/S/A/T/D/E/H/V/ M/I/L/F/Y/W	L/F/Y/W	F/Y	F
H	C/G/S/A/T/V/M/I/L/F/W	G/P/S/A/T/K/V/M/I/L/ F/Y/W	W		
Q	C/G/S/T/V/M/I/L/F/Y/W	G/P/S/A/T/V/M/I/L/F/ Y/W	F/Y/W	F/Y/W	F/W
N	C/P/V/I/L/F/Y/W	G/P/A/T/R/V/M/I/L/F/ Y/W	L/F/W	F/W	
E	C/P/R/V/M/I/L/F/Y/W	G/P/S/A/T/K/R/V/M/I/ L/F/Y/W	L/F/Y/W	F/Y/W	F/W
D	C/P/R/V/M/I/L/F/Y/W	P/S/A/T/K/R/V/M/I/L/ F/Y/W	M/L/F/Y/W	L/F/Y/W	F/W
T	C/Q/H/R/M/L/F/Y/W	G/P/D/E/N/Q/H/K/R/ V/M/I/L/F/Y/W	F/Y/W	W	W
A	C/H/K/R/M/I/L/F/Y/W	D/E/N/Q/H/K/R/V/M/ I/L/F/Y/W	F/Y/W	F/W	W
S	Q/H/V/M/I/L/F/Y/W	D/E/Q/H/K/R/V/M/I/L/ F/Y/W	L/F/Y		
P	C/G/D/E/N/K/V/M/I/L/F/Y/ W	G/T/D/E/N/Q/H/K/R/ V/M/I/L/F/Y/W	L/F/Y/W	F/Y/W	F/Y/W
G	C/P/Q/H/K/R/V/M/I/L/F/Y/ W	P/T/E/N/Q/H/K/R/V/ M/I/L/F/Y/W	R/M/I/L/F/Y/W	L/F/Y/W	F/Y/W
C	G/P/A/T/D/E/N/Q/H/K/R/ V/M/I/L/F/W	G/P/S/A/T/D/E/N/Q/ H/K/R/V/M/I/L/F/Y/W	G/P/D/E/N/Q/H/ K/R/M/L/F/W	D/E/N/Q/K/R/ M/L/F/W	D/E/Q/K/M/L/ W

[0081] The stem cell being engineered and transplanted can be any stem cell that is able to replace the endogenous cells that can be targeted by the therapy. For AML, for instance, the stem cell may be a hematopoietic stem and progenitor cell (HSPC) or an induced pluripotent stem cell (iPSC), without limitation. Prior to the transplantation, the stem cell may be cultured and/or differentiated. The stem cell, without limitation, may be obtained or derived from a donor subject, or from the patient.

[0082] In some embodiments, the therapy includes an corresponding antibody, an antigen-binding fragment of the antibody, a chimeric antigen receptor (CAR) that includes the antigen-binding fragment, or an immune cell that includes the CAR. Methods of preparing antibodies, fragments and CARs are known in the art, such as DNA synthesis, transduction, and expression.

[0083] In some embodiments, the CAR is expressed and enclosed in an immune cell for form a CAR-immune cell. In some embodiments, the immune cell is a T cell, an NK cell, or a macrophage, without limitation.

[0084] Administration of the therapy is preferably after the stem cell transplantation. In another embodiment, they can be done concurrently. In some embodiments, administration of the therapy, at least one, two or more of the administrations, take place before the stem cell transplantation.

[0085] One of ordinary skill in the art would recognize that multiple administrations of the compositions of the disclosure may be required to effect the desired therapy. For example a composition may be administered 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more times over a span of 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 1 year, 2 years, 5, years, 10 years, or more.

[0086] The methods for administering the cell compositions described herein includes any method which is effective to result in reintroduction of ex vivo genetically modified immune effector cells that either directly express a CAR in the subject or on reintroduction of the genetically modified progenitors of immune effector cells that on introduction into a subject differentiate into mature immune effector cells that express the CAR. One method comprises transducing peripheral blood T cells ex vivo with a nucleic acid construct in accordance with the present disclosure and returning the transduced cells into the subject.

[0087] Although the foregoing disclosure has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings of this disclosure that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims. The following examples are provided by way of illustration only and not by way of limitation. Those skilled in the art will readily recognize a variety of noncritical parameters that could be changed or modified to yield similar results.

Gene Editing Methods and Edited Cells

[0088] The mutations can be introduced to the stem cell with methods known in the art, such as with a zinc finger DNA binding protein, the TALEN technology, a transposon, a retrotransposon, or a CRISPR-based technology, such as base editors and prime editors.

[0089] It is commonly known that based editors and prime editors have target sequence requirements and thus it is challenging to design suitable guide RNA sequences.

Through trials and errors, the instant inventors were able to design and confirm a number of guide RNA sequences capable to introducing the desired mutations.

[0090] A base editor (BE) integrates the CRISPR/Cas system with the APOBEC (apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like) AID (activation-induced cytidine deaminase) family. Through the fusion with the Cas9 nickase (nCas9) or a catalytically dead Cpf1 (dCpf1 also known as dCas12a), the nucleobase deaminase activity of APOBEC/AID family members can be purposely directed to the target bases in the genome and to catalyze base substitutions.

[0091] The term “nucleobase deaminase” as used herein, refers to a group of enzymes that catalyze the hydrolytic deamination of nucleobases such as cytidine, deoxycytidine, adenosine and deoxyadenosine. Non-limiting examples of nucleobase deaminases include cytidine deaminases and adenosine deaminases.

[0092] “Cytidine deaminase” refers to enzymes that catalyze the irreversible hydrolytic deamination of cytidine and deoxycytidine to uridine and deoxyuridine, respectively. Cytidine deaminases maintain the cellular pyrimidine pool. A family of cytidine deaminases is APOBEC (“apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like”). Members of this family are C-to-U editing enzymes. Some APOBEC family members have two domains, one domain of APOBEC like proteins is the catalytic domain, while the other domain is a pseudocatalytic domain. More specifically, the catalytic domain is a zinc dependent cytidine deaminase domain and is important for cytidine deamination. RNA editing by APOBEC-1 requires homodimerisation and this complex interacts with RNA binding proteins to form the editosome.

[0093] Non-limiting examples of APOBEC proteins include APOBEC1, APOBEC2, APOBEC3A, APOBEC3B, APOBEC3C, APOBEC3D, APOBEC3F, APOBEC3G, APOBEC3H, APOBEC4, and activation-induced (cytidine) deaminase (AID).

[0094] “Adenosine deaminase”, also known as adenosine aminohydrolase, or ADA, is an enzyme (EC 3.5.4.4) involved in purine metabolism. It is needed for the breakdown of adenosine from food and for the turnover of nucleic acids in tissues.

[0095] Non-limiting examples of adenosine deaminases include tRNA-specific adenosine deaminase (TadA), adenosine deaminase tRNA specific 1 (ADAT1), adenosine deaminase tRNA specific 2 (ADAT2), adenosine deaminase tRNA specific 3 (ADAT3), adenosine deaminase RNA specific B1 (ADARB1), adenosine deaminase RNA specific B2 (ADARB2), adenosine monophosphate deaminase 1 (AMPD1), adenosine monophosphate deaminase 2 (AMPD2), adenosine monophosphate deaminase 3 (AMPD3), adenosine deaminase (ADA), adenosine deaminase 2 (ADA2), adenosine deaminase like (ADAL), adenosine deaminase domain containing 1 (ADAD1), adenosine deaminase domain containing 2 (ADAD2), adenosine deaminase RNA specific (ADAR) and adenosine deaminase RNA specific B1 (ADARB1).

[0096] Prime editing is a genome editing technology by which the genome of living organisms may be modified. Prime editing directly writes new genetic information into a targeted DNA site. It uses a fusion protein, consisting of a catalytically impaired endonuclease (e.g., Cas9) fused to an engineered reverse transcriptase enzyme, and a prime edit-

ing guide RNA (pegRNA), capable of identifying the target site and providing the new genetic information to replace the target DNA nucleotides. Prime editing mediates targeted insertions, deletions, and base-to-base conversions without the need for double strand breaks (DSBs) or donor DNA templates.

[0097] The pegRNA is capable of identifying the target nucleotide sequence to be edited, and encodes new genetic information that replaces the targeted sequence. The pegRNA consists of an extended single guide RNA (sgRNA) containing a primer binding site (PBS) and a reverse transcriptase (RT) template sequence. During genome editing, the primer binding site allows the 3' end of the nicked DNA strand to hybridize to the pegRNA, while the RT template serves as a template for the synthesis of edited genetic information.

[0098] The fusion protein, in some embodiments, includes a nickase fused to a reverse transcriptase. An example nickase is Cas9 H840A. The Cas9 enzyme contains two nuclease domains that can cleave DNA sequences, a RuvC domain that cleaves the non-target strand and a HNH domain that cleaves the target strand. The introduction of a H840A substitution in Cas9, through which the histidine residue at 840 is replaced by an alanine, inactivates the HNH domain. With only the RuvC functioning domain, the catalytically impaired Cas9 introduces a single strand nick, hence a nickase.

[0099] Non-limiting examples of reverse-transcriptases include human immunodeficiency virus (HIV) reverse-transcriptase, moloney murine leukemia virus (M-MLV) reverse-transcriptase and avian myeloblastosis virus (AMV) reverse-transcriptase.

[0100] In some embodiments, the prime editing system further includes a single guide RNA (sgRNA) that directs the Cas9 H840A nickase portion of the fusion protein to nick the non-edited DNA strand.

[0101] Example gRNA for base editors and example pegRNA for prime editors are provided in Tables 1-4. For instance, for CD33, a gRNA can include a spacer sequence selected from SEQ ID NO:19-144, and pegRNA can include a spacer sequence selected from SEQ ID NO:145-228. For CD123, a gRNA can include a spacer sequence selected from SEQ ID NO: 229-516, and pegRNA can include a spacer sequence selected from SEQ ID NO: 517-541. For CD117, a gRNA can include a spacer sequence selected from SEQ ID NO: 542-758, and pegRNA can include a spacer sequence selected from SEQ ID NO: 759-801. For CLL-1, a gRNA can include a spacer sequence selected from SEQ ID NO: 802-879, and pegRNA can include a spacer sequence selected from SEQ ID NO: 880-893.

[0102] In some embodiments, to introduce a mutation at C41 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:19-33. In some embodiments, to introduce a mutation at W60 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:34-46. In some embodiments, to introduce a mutation at I105 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:47-58. In some embodiments, to introduce a mutation at D112 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:59-65. In some embodiments, to introduce a mutation at Y116 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:66-72.

[0103] In some embodiments, to introduce a mutation at F118 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:73-80. In some embodiments, to introduce a mutation at P132 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:81-89. In some embodiments, to introduce a mutation at W22 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:90-99. In some embodiments, to introduce a mutation at G34 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:101-110. In some embodiments, to introduce a mutation at R89 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:111-118.

[0104] In some embodiments, to introduce a mutation at N100 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:119-128. In some embodiments, to introduce a mutation at N113 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:129-133. In some embodiments, to introduce a mutation at S131 of CD33, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:134-144.

[0105] In some embodiments, to introduce a mutation at W22, G34, or C41 of CD33, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO: 145-180. In some embodiments, to introduce a mutation at W60 of CD33, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:181-186. In some embodiments, to introduce a mutation at R89, N100, or I105 of CD33, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:187-212. In some embodiments, to introduce a mutation at D112, N113, Y116, or F118 of CD33, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:213-216. In some embodiments, to introduce a mutation at S131 or P132 of CD33, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:217-228.

[0106] In some embodiments, to introduce a mutation at I27 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:229-263. In some embodiments, to introduce a mutation at L30 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:264-298. In some embodiments, to introduce a mutation at M32 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:299-330. In some embodiments, to introduce a mutation at W41 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:331-345.

[0107] In some embodiments, to introduce a mutation at E51 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:346-376. In some embodiments, to introduce a mutation at C52 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:377-391. In some embodiments, to introduce a mutation at S59 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:392-420. In some embodiments, to introduce a mutation at R84 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:421-435.

[0108] In some embodiments, to introduce a mutation at P88 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:436-450. In some embodiments, to introduce a mutation at F90 of CD123, the

gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:451-466. In some embodiments, to introduce a mutation at S91 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:467-497. In some embodiments, to introduce a mutation at W93 of CD123, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:498-516.

[0109] In some embodiments, to introduce a mutation at R84, P88, F90, S91, or W93 of CD123, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:517-533. In some embodiments, to introduce a mutation at E51, C52, S59, or P61 of CD123, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:534-537.

[0110] In some embodiments, to introduce a mutation at L27, L30, M32 or W41 of CD123, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:538-539. In some embodiments, to introduce a mutation at L27, L30, or M32 of CD123, the pegRNA sequence can include a spacer of SEQ ID NO:540. In some embodiments, to introduce a mutation at L27 or L30 of CD123, the pegRNA sequence can include a spacer of SEQ ID NO:541.

[0111] In some embodiments, to introduce a mutation at T67 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:542-554. In some embodiments, to introduce a mutation at K69 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:555-561. In some embodiments, to introduce a mutation at T71 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:562-566. In some embodiments, to introduce a mutation at S81 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:567-583.

[0112] In some embodiments, to introduce a mutation at Y83 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:584-595. In some embodiments, to introduce a mutation at T114 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:596-610. In some embodiments, to introduce a mutation at T119 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:611-623. In some embodiments, to introduce a mutation at K129 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:624-641.

[0113] In some embodiments, to introduce a mutation at S236 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:642-661. In some embodiments, to introduce a mutation at H238 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:662-666. In some embodiments, to introduce a mutation at Y244 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:667-701. In some embodiments, to introduce a mutation at S273 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:702-738. In some embodiments, to introduce a mutation at T277 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:739-751. In some embodiments, to introduce a mutation at T279 of CD117, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:752-758.

[0114] In some embodiments, to introduce a mutation at T67, K69, T71, S81, or Y83 of CD117, the pegRNA sequence can include a spacer of a sequence selected from

SEQ ID NO:759-769. In some embodiments, to introduce a mutation at T114, T119, or K129 of CD117, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:770-791.

[0115] In some embodiments, to introduce a mutation at S236, H238, or Y244 of CD117, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:792-796. In some embodiments, to introduce a mutation at S273, T277, or T279 of CD117, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:797-801.

[0116] In some embodiments, to introduce a mutation at one of the residue of 142 to 158 (DSCYFLSDDVQTWQESK: of SEQ ID NO:4, such as D142, S143, C144, Y145, F146, L147, S148, D149, D150, V151, Q152, T153, W154, Q155, E156, S157, or K158) of CLL-1, the gRNA sequence can include a spacer of a sequence selected from SEQ ID NO:802-879.

[0117] In some embodiments, to introduce a mutation at one of the residue of 142 to 158 (DSCYFLSDDVQTWQESK: of SEQ ID NO:4, such as D142, S143, C144, Y145, F146, L147, S148, D149, D150, V151, Q152, T153, W154, Q155, E156, S157, or K158) of CLL-1, the pegRNA sequence can include a spacer of a sequence selected from SEQ ID NO:880-893.

[0118] One embodiment provides a mutant CD123 protein comprising a mutation at residue R84 (position according to SEQ ID NO:2). In some embodiments, the mutation is to an amino acid residue that is not lysine. In some embodiments, the mutation is non-conservative. In some embodiments, the mutation is to glutamine (Q), asparagine (N) or histidine (H). In some embodiments, the mutant CD123 protein has reduced binding to an anti-CD123 antibody as disclosed herein, as compared to the wild-type CD123 protein.

[0119] In some embodiments, the mutation is R84Q. In some embodiments, the mutation is R84N. In some embodiments, the mutation is R84H.

[0120] In some embodiments, the mutant CD123 protein further comprises a mutation at residue V85 (position according to SEQ ID NO:2). In some embodiments, the mutation at residue V85 is to methionine (M), isoleucine (I), leucine (L), alanine (A), cysteine (C), glycine (G), or threonine (T). In some embodiments, the mutation is V85I. In some embodiments, the mutation is V85M.

[0121] In some embodiments, the mutations in CD123 are selected from the group consisting of R84Q and V85I, R84Q and V85M, R84H and V85I, and R84H and V85M. In some embodiments, the mutant CD123 protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 894, 895, 896 and 897.

[0122] Also provided are polynucleotides encoding the mutant CD123 protein of the present disclosure, and cells comprising the mutant CD123 protein or a polynucleotide encoding the mutant CD123 protein.

EXAMPLES

Example 1. Identification and Editing of CD33 Epitope

[0123] This example identified the potential epitope of the CD33 protein for antibodies my9.6 or HM195, and designed mutants that abolished the antibody binding.

[0124] HEK 293T cells were transfected with wildtype or certain CD33 mutants and then incubated with anti-CD33

scFV-luciferase fusion proteins. The mutated residues included W22, C41, W60, I105, D112, Y116, F118, S131, and P132. The tested antibodies included my9.6 and HM195. FIGS. 1A and 1C show the binding affinity of the indicated CD33 mutations with anti-CD33 scFV of antibody my9.6 (RLU: relative luminescence units). FIGS. 1B and 2D present Western blot images of CD33 expression from the transfected cells. These figures clearly show that some of the mutations significantly reduced the binding and thus are within the epitope.

[0125] CRISPR-based base editors and prime editors were used to generate mutation at W60 of the CD33 protein. Sanger sequencing confirmed the W60R mutation in the CD34+ HSPCs. In FIG. 2A, red arrow pointed at desired mutation site. The editing efficiency for editing products is shown in FIG. 2B, including Y59h/W60R/F61L, Y59H/W60R/F61P, W60R/F61P, W60R/F61S, W60R/F61L, Y59H/F61L, Y59H/F61L, Y69H/W60R, F61P and W60R. It is clear that the vast majority of the products contained the desired W60R mutation.

[0126] FIG. 2C illustrates the prime editing design (locations of spacers for PE4 for mutating P132 to A) and their editing efficiency in HEK293T cells. The editing was further optimized with variable nick sites (FIG. 2D), PBS lengths (FIG. 2E), or RT template lengths (FIG. 2F). In FIG. 2G, the editing efficiencies of PE4, PE4max and PEmax in editing P132 into A of CD33 were compared, all of which were high.

Example 2. Identification and Editing of CD123 Epitope

[0127] Like in Example 1, the epitopes of CD123 that mediate the recognition by scFv of clone 32716 or CSL362 were determined. HEK 293T cells were transfected with wildtype or indicated CD123 mutant and then incubated with anti-CD123 scFv-luciferase fusion proteins. The binding affinity of indicated CD123 mutations with anti-CD123 scFv clone 32716 (left panels) or clone CSL362 (right panels) is shown in FIG. 3A. The expression of these mutants was confirmed by Western blot (FIG. 3B).

[0128] Further reduction of affinity with the scFv was effectively achieved by introducing combined mutations, such as R84Q-V85I or R84Q-V85M, resulting in a 100-fold decrease (FIG. 4A). The introduction of combined mutations did not affect the normal folding and expression of the CD123 protein (FIG. 4B). Validation of downstream functions of the CD123 protein revealed that both combined mutations and single-point mutations did not affect the activation of downstream signaling pathways (FIG. 4C), suggesting that these mutations can specifically reduce interaction with antibodies without affecting the normal protein function.

[0129] Precise editing of the CD123 antigen site was performed in HEK 293T cells and human hematopoietic stem progenitor cells using base editors and prime editors, respectively. Editing efficiency was confirmed through Sanger sequencing (R84 in FIG. 5A or L30 in FIG. 4B). Deep sequencing results showed the editing efficiency of each editing product (FIG. 5C-F). As shown in FIG. 5G-H, prime editors efficiently and precisely edited the CD123-R84 site. Arrows indicate the editing sites.

[0130] Further validation in hematopoietic stem progenitor cells confirmed that precise editing of the CD123 antigen site does not affect stem cell differentiation and function.

Compared to CD123 knockout cells, cells with precise editing of CD123 R84Q or L30P antigen sites showed better cell viability (FIG. 6A), and their cell morphology was consistent with the unedited control (FIG. 6B). Flow cytometry analysis of myeloid differentiation and plasmacytoid dendritic cell differentiation proportions were consistent with the control (FIG. 6C and FIG. 7).

[0131] In CD123-CAR-T cell targeting experiments, cells with precise mutations could evade CAR-T cell killing. (A) CAR-T cells containing CSL362 monoclonal antibody were prepared and co-cultured with wild-type AML tumor cells, CD123 knockout AML cells, or cells containing CD123-R84Q mutation. CAR-T efficiently killed wild-type tumor cells expressing CD123, while the killing efficiency was significantly reduced for cells containing CD123-R84Q mutation (FIG. 8A-C).

[0132] Additional similar testing was conducted for other epitope residues in CD33 and CD123, as well as for CD117 and CLL-1. The target residues and their corresponding spacer sequences used in gRNA for base editors or pegRNA for prime editors are summarized in Table 1 below.

TABLE 1A

Epitope Residues in CD33	
Antibody	Target Residues in Epitope
my9.6	C41, W60, I105, D112, Y116, F118, P132, W22, G34, R89, N100, N113, S131
HM195	C41, W60, I105, Y116, F118

TABLE 1B

CD33 Protein Sequence (SEQ ID NO: 1)	
MPLLLLLLPLLWAGALAMDPNFWLQVQESVTVQEGLCVLVPC TF FFHP I PYY	
DKNSPVHGYW F REGAII SRD S PVATNKL D QEVQ E ETQGR F RL L GD P SR R N	
CSLS I VDARRR D NGS Y F F RMER G STKYSYK S PQLSVH V TD L THR P K I L I P	
GTLEPGH S KNL T CSVSWACEQGT P PI F SWLSAAPT S LG P R I TH S SVL I I T	
PRPQDHGTN L TCQVKFAGAGV T TERTIQ L NV T YV P QNP T TG I FP G D S G S GK	
QETRAGV V HGAIGGAGV T ALLALCLCLIFFIVK T HR R KAAR T AVGR N D T H	
PTTGSASPKHQK S KLHG P TETSSCSGAAPT V EMDEELHYASL N FNHGM N P	
SKD T ST E YSE V RTQ	

TABLE 1C

VH/VL of my9.6		SEQ ID NO:
Region	Sequence	
VH	QVQLQQPGA E VVKPGASVKMSCKASGYTFTSY I HWI KQTPGQGLEWVGV I YPGND D ISYNQK F Q G KATL T ADK SSTTAYMQLSSL T SEDSAVYYCAREVRL R Y F PDVWGQ G TTVT V SS	5

TABLE 1C-continued

VH/VL of my9.6		SEQ ID NO:
Region	Sequence	
VL	EIVLTQSPGSLAVSPGERVTMSCKSSQVFFSSSQKN YLAWYQQIPGQSPRLLIYWASTRESGVPDRPTGSGSG TDFTLTISVVQPEDLAIYYCHQYLSRRTFGQGTKLEI KR	6

TABLE 1D

VH/VL of HM195		SEQ ID NO:
Region	Sequence	
VH	QVQLVQSGAEVKKPGSSVKVSKASGYTFDYNMHVVR QAPGGLEWIGYIYPYNGGTGYNQKFKSKATITADEST NTAYMELSSLRSEDTAVYYCARGRPAMDYWGQGLVTV SS	7
VL	DIQMTQSPSSLSASVGDRTITCRASEVDNYGISFMN WFOQKPKGKAPKLLIYAASNQSGVPSRFSGSGSGLDFT LTISLQPDFATYYCQQSKEVPWFVFGQGTKVEIK	8

TABLE 1E

Example spacer sequences of gRNA for editing CD33 epitope					
Residue	Editor	Cas	Spacer	SEQ ID NO:	
C41	ABE/CBE	Sp cas9	gtgcagggcacgaggacgca	19	
			aagtgcagggcacgaggacg	20	
	CBE		gaaagtgcagggcacgagga	21	
			aagaaagtgcagggcacgag	22	
			gaagaaagtgcagggcacga	23	
			ggaagaaagtgcagggcacg	24	
			tggaagaaagtgcagggcac	25	
			tcagggcacgaggacgcac	26	
			atggaagaaagtgcagggca	27	
			ggatggaagaaagtgcaggg	28	
			tgggatggaagaaagtgcag	29	
			At cas9	atggaagaaagtgcagggcacg	30
			ggaagaaagtgcagggcacgag	31	
			aagaaagtgcagggcacgagga	32	
			gaagaaagtgcagggcacgagg	33	
			W60	ABE	Sp cas9
ggaaccagtaaacatgaact	35				
gaaccagtaaacatgaactg	36				
accagtaaacatgaactggg	37				
aaccagtaaacatgaactgg	38				
ccagtaaacatgaactgggg	39				
cttcccgaaccagtaacca	40				
tcccgaaccagtaaacatg	41				
ttcccgaaccagtaaacat	42				
tccttcccgaaccagtaaac	43				
ggctccttcccgaaccagt	44				
At cas9	aaccagtaaacatgaactgggg	45			
ttcccgaaccagtaaacatga	46				
1105	ABE	Sp cas9	tacgatgctcagggagcagt	47	
			gtctacgatgctcagggagc	48	
			cgtctacgatgctcagggag	49	
			ggcgtctacgatgctcaggg	50	

TABLE 1E-continued

Example spacer sequences of gRNA for editing CD33 epitope							
Residue	Editor	Cas	Spacer	SEQ ID NO:			
		At cas9	tggcgtctacgatgctcagg	51			
			ctggcgtctacgatgctcag	52			
			cctggcgtctacgatgctca	53			
			tcctggcgtctacgatgctc	54			
			ctcctggcgtctacgatgct	55			
			tctacgatgctcagggagcagt	56			
			ctacgatgctcagggagcagtt	57			
			cgatgctcagggagcagttgtt	58			
D112	ABE	At cas9	ggagggataatggttcatactt	59			
			ggaggaggataatggttcata	60			
			aggaggaggataatggttcata	61			
			Sp cas9	ataatggttcatacttcttt	62		
			gacgccaggaggaggataaa	63			
			ggaggaggataatggttca	64			
Y116	ABE	Sp cas9	caggaggaggataatggtt	65			
			ttcatacttcttccggatgg	66			
F118	ABE	Sp cas9	tcatacttcttccggatgga	67			
			gttcatacttcttccggatg	68			
			ccgaaagaagtatgaacct	69			
			At cas9	aatggttcatacttcttccgga	70		
			ggttcatacttcttccggatgg	71			
			catacttcttccggatggagag	72			
					At cas9	ccgaaagaagtatgaacct	73
						catccgaaagaagtatgaac	74
						ctctctccatccgaaagaag	75
						catccgaaagaagtatgaacca	76
						atccgaaagaagtatgaacct	77
						tccgaaagaagtatgaacct	78
cgaaagaagtatgaacctat	79						
ctctccatccgaaagaagtatg	80						
P132	CBE	Sp cas9	caaatctcccagctctctg	81			
			tctcccagctctctctgtgca	82			
			aatctcccagctctctgtg	83			
			tacaaatctcccagctctc	84			
			At cas9	atctcccagctctctgtgcat	85		
			gttacaaatctcccagctctc	86			
			atacagttacaaatctcccag	87			
			aaatctcccagctctctgtg	88			
acaaatctcccagctctctgt	89						
W22	ABE	Sp cas9	agaaatttggatccatagcc	90			
			tgcaacttgagccagaaatt	91			
			agccagaaatttggatccat	92			
			cagccagaaatttggatcca	93			
			tgagccagaaatttggatc	94			
			cacttgagccagaaatttgg	95			
G34	ABE	Sp cas9	gcacttgagccagaaattt	96			
			At cas9	tgcaacttgagccagaaattt	97		
			tgagccagaaatttggatcca	98			
			ccagaaatttggatccatagcc	99			
			cttgagccagaaatttggatc	100			
				CBE	At cas9	aaacctcctgtaccgtcac	101
						cacaaacctcctgtaccgt	102
						acgcacaaacctcctgtac	103
aggagcgcacaaacctcctg	104						
cgaggagcgcacaaacctcc	105						
gagcgcacaaacctcctgtacc	106						
aaacctcctgtaccgtcactg	107						
caaaacctcctgtaccgtca	108						
cacaaacctcctgtaccgtca	109						
cgaggagcgcacaaacctcctg	110						

TABLE 1E-continued

Example spacer sequences of gRNA for editing CD33 epitope						
Residue	Editor	Cas	Spacer	SEQ ID NO:		
R89	CBE	Sp cas9	aggaggcggaatctgcctg	111		
			aaggaggcggaatctgcct	112		
		At cas9	aggcggaatctgcctgagct	113		
			gaatctgcctgagctcctcc	114		
			gaggcggaatctgcctgagtc	115		
			aggaggcggaatctgcctgag	116		
			aaggaggcggaatctgcctga	117		
			ccaaggaggcggaatctgcct	118		
N100	ABE/CBE	Sp cas9	aacaactgctccctgagcat	119		
			aggaacaactgctccctgag	120		
			gtaggaacaactgctccctg	121		
			agtaggaacaactgctccct	122		
			cagtaggaacaactgctccc	123		
			gggatcccagtaggaacaactg	124		
	At cas9	agtaggaacaactgctccctga	125			
		cccagtaggaacaactgctccc	126			
		ggggatcccagtaggaacaact	127			
		atcccagtaggaacaactgctc	128			
		N113	ABE	Sp cas9	ataatggttcataacttcttt	129
					ggaggaggataatggttca	130
At cas9	ggaggataatggttcataact		131			
	aggaggaggataatggttcat		132			
			ataatggttcataacttctttcg	133		
S131	ABE	Sp cas9	gggagatttgaactgtatt	134		
			gagctggggagatttgaact	135		
			gctggggagatttgaactg	136		
			tctccccagctctctgtgca	137		
	CBE	caaatctccccagctctctg	138			
		tacaaaatctccccagctctc	139			
		aatctccccagctctctgtg	140			
		CBE	At cas9	atctccccagctctctgtgcat	141	
				acaaaatctccccagctctctgt	142	
		ABE	aaatctccccagctctctgtgc	143		
	agctggggagatttgaactgt		144			

TABLE 1F-continued

Example spacer sequences of pegRNA for editing CD33 epitope			
Residue	Spacer	SEQ ID NO:	
R89, N100, 1105	GTGAGTGGCTGTGGGAGAGGGG	164	
	GGTGAGTGGCTGTGGGAGAGGG	165	
	AGGTGAGTGGCTGTGGGAGAGG	166	
	GGGAGTTCTTGTCTAGTAGGG	167	
	TGGGAGTTCTTGTCTAGTAGG	168	
	GTTCTTGTCTAGTAGGGTATGG	169	
	TTCTTGTCTAGTAGGGTATGG	170	
	TGGAGAGTCCCTGGATATAATGG	171	
	GAACCACTAACCATGAAGTGGG	172	
	TGTCTAGTAGGGTATGGGATGG	173	
	TGGATATAATGGCTCCTTCCCGG	174	
	TGTGGCCACTGGAGAGTCCCTGG	175	
	CGGAACCACTAACCATGAAGTGG	176	
	GGAAGAAAGTGCAGGGCAGAGG	177	
	ATGGGATGGAGAAAGTGCAGGG	178	
	TATGGATGGAGAAAGTGCAGG	179	
	GGAACCACTAACCATGAAGTGGG	180	
	W60	GACAAGAAGTCCCGATTCATGG	181
TGGAGAGTCCCTGGATATAATGG		182	
TGGATATAATGGCTCCTTCCCGG		183	
CTAGCTGTCTTGTGGCCACTGG		184	
TTCTTGATCTAGCTTGTGGTGG		185	
TGTGGCCACTGGAGAGTCCCTGG		186	
R89, N100, 1105		GGGAAGGAGCCATTATATCCAGG	187
		GCCTCCTTGGGGATCCCACTAGG	188
		GGGAAGGAGCCATTATATCCAGG	189
		GCTAGATCAAGAAGTACAGGAGG	190
		TATATCCAGGGACTCTCCAGTGG	191
		GAACTACAGGAGGAGACTCAGGG	192
	AGAAGTACAGGAGGAGACTCAGG	193	
	CATGGTTACTGGTCCGGGAAGG	194	
	CAAGCTAGATCAAGAAGTACAGG	195	
	AGGGCAGATTCGGCTCCTTGGG	196	
	CAGTTATGGTTACTGGTCCCGG	197	
	GGGCAGATTCGGCTCCTTGGGG	198	
	AGTTATGGTTACTGGTCCCGG	199	
	CAGGGCAGATTCGGCTCCTTGG	200	
	AGGGAGCAGTTGTCTACTGGG	201	
	GGGAGATTTGTAAGTGTATTGG	202	
	CAGGGAGCAGTTGTCTACTGG	203	
	TGTCTACTGGGATCCCAAGG	204	
	TGAACCATATCCCTCCTCTGG	205	
	TCCTACTGGGATCCCAAGGAGG	206	
	TCCTGGCGTCTACGATGCTCAGG	207	
	TACTGGGATCCCAAGGAGGCGG	208	
	CCTGGCGTCTACGATGCTCAGG	209	
	TGTCACATGCACAGAGAGCTGGG	210	
GTCCATGCACAGAGAGCTGGG	211		
CTGTCCATGCACAGAGAGCTGG	212		
D112, N113, Y116, F118	GGGAGATTTGTAAGTGTATTGG	213	
	TGTCACATGCACAGAGAGCTGGG	214	
	GTCCATGCACAGAGAGCTGGG	215	
	CTGTCCATGCACAGAGAGCTGG	216	
	S131, P132	TGGTTACTACTTCTTTCGGATGG	217
		GACGCCAGGAGGGGATAATGG	218
		GCATCGTAGACGCCAGGAGGAGG	219
		CCCTGAGCATCTAGACGCCAGG	220
		CATCGTAGACGCCAGGAGGAGG	221
		TGAGCATCTAGACGCCAGGAGG	222
		ATAATGGTTACTACTTCTTTCGG	223
		TACTTCTTTCGGATGGAGAGG	224
GTACCATGAAGTCCCTTGGCG		225	
TGTCACATGCACAGAGAGCTGGG		226	
GTCCATGCACAGAGAGCTGGG		227	
CTGTCCATGCACAGAGAGCTGG		228	

TABLE 1F

Example spacer sequences of pegRNA for editing CD33 epitope		
Residue	Spacer	SEQ ID NO:
W22, G34, C41	TGGCTATGGATCCAAATTTCTGG	145
	AAATTTCTGGCTGCAAGTGCAGG	146
	GCAGGAGTCAAGTGCAGGACAGG	147
	GGAGTCAAGTGCAGGACAGGAGG	148
	GAGTCAAGTGCAGGACAGGAGG	149
	GGGAGAGGGGTGTCCGGCTGGG	150
	GTGGGAGGGGTGTCCGGCTGGG	151
	GGGGAGAGGGGTGTCCGGCTGG	152
	TCGTTTCCCAACAGGGCCCTGG	153
	CTGTGGGGAGAGGGTTGTCCGG	154
	CCCCACAGGGCCCTGGCTATGG	155
	GCAAGTGCAGGAGTCAAGTGCAGG	156
	GCTGACCCCTCGTTTCCCAACAGG	157
	TGACCCCTCGTTTCCCAACAGGG	158
	CTGACCCCTCGTTTCCCAACAGGG	159
	TGTGGGCAGGTGAGTGGCTGTGG	160
	TGGGCAGGTGAGTGGCTGTGGG	161
	GCTGTGGGGAGAGGGTTGTCCG	162
	CCCTGTGTGGGCAGGTGAGTGG	163

TABLE 2A

Epitope Residues in CD123	
Antibody	Target Residues in Epitope
CSL362 or 32716	I27, L30, M32, W41, E51, C52, S59, P61, R84, P88, F90, S91, W93

TABLE 2B

CD123 Protein Sequence (SEQ ID NO: 2)	
MVLLWLTLILLIAPCLLQTKEDPNPPIITNLRLMKAKAQQLTWDLNRRVTDI	
ECVKDADY SMPAVNNNSYCQFGAISLCEVTNYTVR RVANPPF STWILFPENS	
GKPWAGAENLTCWIHDVDFLSCSWAVGPGAPADVQDYLYLNVANRRQQYE	
CLHYKTDAGQTRIGCRFDDISRLSSGSQSSHILVLRGRSAAPGIPCTDKFV	
VFSQIEILTPPNMTAKCNKTHSFMHWKMRSHFNRFYELQIQKRMQPV I	
TEQVRDRTSFQLLNPGTYTVQIRARERVYEFLSAWSTPQRFECQEEGAN	
TRAWRTSLLIALLGTLALVCFVICRRYLVMQRLFPRI PHMKDPIGDSFQ	
NDKLVVWEAGKAGLEECLVTEVQVVQKT	

TABLE 2C

VH/VL of CSL362		
Region	Sequence	SEQ ID NO:
VH	EVQLVQSGAEVKKPGESLKISCKGSGYS FTDYMKWARQMPGKGLEWMDIIPSNQ ATFYNQKFKGQVTISADKSI STTYLQWS SLKASDTAMYCARSHLLRASWFAYWQQ GTMVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSS	9
VL	EVQLVQSGAEVKKPGESLKISCKGSGYS FTDYMKWARQMPGKGLEWMDIIPSNQ ATFYNQKFKGQVTISADKSI STTYLQWS SLKASDTAMYCARSHLLRASWFAYWQQ GTMVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSS	10

TABLE 2D

VH/VL of 32716		
Region	Sequence	SEQ ID NO:
VH	QIQLVQSGPELKKPGETVKISCKASGYI FTNYGMNWKQAPGKSFKWMGWINTYTG ESTYSADFKGRFAPFLETSASTAYLHIN DLKNEEDTATYFCARSGGYDPMYDYGQGT SVTVSS	11
VL	DIVLTQSPASLAVSLGQRATISCRASES VDNYGNTFMHWYQQKPGQPPKLLIYRAS NLESQIPARFSGSGSRDFTLTINPVEA DDVATYYCQQSNEDPPTFGAGTKLELK	12

TABLE 2E

Example spacer sequences of crRNA for editing CD123 epitope							
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:			
I27	ABE	SpCas9	AGGTTTCGTGATTGGTGGGTT	229			
			TCCTTAGGTTTCGTGATTGGT	230			
			TTCATCCTTAGGTTTCGTGAT	231			
			GGTTCGTGATTGGTGGGTTT	232			
			CCTTAGGTTTCGTGATTGGTG	233			
			TCATCCTTAGGTTTCGTGATT	234			
			GTTCGTGATTGGTGGGTTTG	235			
			GTGATTGGTGGGTTTGGATCTT	236			
			TTCGTGATTGGTGGGTTTGGAT	237			
			GTTCGTGATTGGTGGGTTTGGGA	238			
			TAGGTTTCGTGATTGGTGGGTTT	239			
			ATCCTTAGGTTTCGTGATTGG	240			
	AtCas9	ABE	SpCas9	ACCCACCAATCACGAACCTA	241		
				ATCACGAACCTAAGGATGAA	242		
				ACCAATCACGAACCTAAGGA	243		
				CCCACCAATCACGAACCTAA	244		
				AGATCCAAACCCACCAATCA	245		
				AATCACGAACCTAAGGATGA	246		
				CAATCACGAACCTAAGGATG	247		
				CCAATCACGAACCTAAGGAT	248		
				CCACCAATCACGAACCTAAG	249		
				AACCCACCAATCACGAACCT	250		
				AAACCCACCAATCACGAACCC	251		
				ATCCAAACCCACCAATCACG	252		
GATCCAAACCCACCAATCAC	253						
GAAGATCCAAACCCACCAAT	254						
AtCas9	ABE	SpCas9	ACCAATCACGAACCTAAGGATG	255			
			AAGATCCAAACCCACCAATCAC	256			
			GAAGATCCAAACCCACCAATCA	257			
			CCACCAATCACGAACCTAAGGA	258			
			CAAACCCACCAATCACGAACCT	259			
			ATCCAAACCCACCAATCACGAA	260			
			CACCAATCACGAACCTAAGGAT	261			
			AACCCACCAATCACGAACCTAA	262			
			GATCCAAACCCACCAATCAC	263			
			L30	ABE	SpCas9	AGGTTTCGTGATTGGTGGGTT	264
						TCCTTAGGTTTCGTGATTGGT	265
						ATCCTTAGGTTTCGTGATTGG	266
TTCATCCTTAGGTTTCGTGAT	267						
CCTTAGGTTTCGTGATTGGTG	268						
TCATCCTTAGGTTTCGTGATT	269						
TGCTTTCATCCTTAGGTTTCG	270						
TTTGCTTTCATCCTTAGGTT	271						
AGCCTTTCGCTTTCATCCTTA	272						
GCTTTCATCCTTAGGTTTCGT	273						
AtCas9	CBE	SpCas9				TAGGTTTCGTGATTGGTGGGTTT	274
						TGAGCCTTTGCTTTCATCCTTA	275
			ATCCTTAGGTTTCGTGATTGG	276			
			GAACCTAAGGATGAAAGCAA	277			
			ACCCACCAATCACGAACCTA	278			
			AACCTAAGGATGAAAGCAA	279			
			ATCACGAACCTAAGGATGAA	280			
			ACCAATCACGAACCTAAGGA	281			
			CCCACCAATCACGAACCTAA	282			
			CGAACCTAAGGATGAAAGCA	283			
			ACGAACCTAAGGATGAAAGC	284			
			CACGAACCTAAGGATGAAAG	285			
AATCACGAACCTAAGGATGA	286						
CAATCACGAACCTAAGGATG	287						
CCACCAATCACGAACCTAAG	288						
AACCCACCAATCACGAACCT	289						
AAACCCACCAATCACGAACCC	290						
AtCas9	CBE	SpCas9	CACGAACCTAAGGATGAAAGCA	291			
			ACCAATCACGAACCTAAGGATG	292			
			ACCTAAGGATGAAAGCAAAGCC	293			
			CGAACCTAAGGATGAAAGCAA	294			

TABLE 2E-continued

Example spacer sequences of gRNA for editing CD123 epitope					
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:	
			GAACCTAAGGATGAAAGCAAAG	295	
			CAAACCCACCAATCACGAACCT	296	
			AACCCACCAATCACGAACCTAA	297	
			CACCAATCACGAACCTAAGGAT	298	
M32	ABE	SpCas9	TTCATCCTTAGGTTTCGTGAT	299	
			GAGCCTTTGCTTTCATCCTT	300	
			TGCTTTTCATCCTTAGGTTTCG	301	
			TTTGCTTTTCATCCTTAGGTT	302	
			AGCCTTTGCTTTTCATCCTTA	303	
			GCTTTTCATCCTTAGGTTTCGT	304	
			TGAGCCTTTGCTTTTCATCCT	305	
			TGAGCCTTTGCTTTTCATCCTTA	306	
			GAGCCTTTGCTTTCATCCTTAG	307	
			CTTTCATCCTTAGGTTTCGTG	308	
	ABE	SpCas9	GAACCTAAGGATGAAAGCAA	309	
			GATGAAAGCAAAGGCTCAGC	310	
			AAGGATGAAAGCAAAGGCTC	311	
			AACCTAAGGATGAAAGCAA	312	
			ATCACGAACCTAAGGATGAA	313	
			ACCAATCACGAACCTAAGGA	314	
			GGATGAAAGCAAAGGCTCAG	315	
			TAAGGATGAAAGCAAAGGCT	316	
			CGAACCTAAGGATGAAAGCA	317	
			ACGAACCTAAGGATGAAAGC	318	
AtCas9	Cpf1	AATCACGAACCTAAGGATGAA	319		
		CAATCACGAACCTAAGGATG	320		
		CCAATCACGAACCTAAGGAT	321		
		CACGAACCTAAGGATGAAAGCA	322		
		ACCAATCACGAACCTAAGGATG	323		
		ATGAAAGCAAAGGCTCAGCAGT	324		
		GATGAAAGCAAAGGCTCAGCAG	325		
		ACCTAAGGATGAAAGCAAAGGC	326		
		CGAACCTAAGGATGAAAGCAA	327		
		GAAACCTAAGGATGAAAGCAAAG	328		
CCACCAATCACGAACCTAAGGA	329				
CACCAATCACGAACCTAAGGAT	330				
W41	ABE	SpCas9	TAAGGTCCAGGTCAACTGC	331	
			CAGGTCAACTGCTGAGCCTT	332	
			AGGTCCAGGTCAACTGCTG	333	
			TGTTAAGGTCCAGGTCAAC	334	
			ACATTTCTGTTAAGGTCCCA	335	
			AAGGTCCAGGTCAACTGCT	336	
			TTCTGTTAAGGTCCAGGTTC	337	
			AtCas9	TTTCTGTTAAGGTCCAGGTCA	338
				CAGGTCAACTGCTGAGCCTTTG	339
				GTCCAGGTCAACTGCTGAGCC	340
		TTAAGGTCCAGGTCAACTGCT		341	
		GTTAAGGTCCAGGTCAACTGCT		342	
		Cpf1	TTTCTGTTAAGGTCCAGGTCA	343	
			ACATTTCTGTTAAGGTCCAGG	344	
			TGTTAAGGTCCAGGTCAAC	345	
E51	CBE		SpCas9	GTCTTTAACACACTCGATAT	346
				CTCGATATCGGTCAACATTC	347
		AACACACTCGATATCGGTCA		348	
		TTAACACACTCGATATCGGT		349	
		GGCGTCTTTAACACACTCGA		350	
		TCGGCGTCTTTAACACACTC		351	
		AtCas9		CGGTCTTTAACACACTCGATAT	352
				TAACACACTCGATATCGGTCA	353
				GTCTTTAACACACTCGATATCG	354
				GTCCGGCGTCTTTAACACACTCG	355
ACACACTCGATATCGGTCA	356				
ABE	SpG	ACACACTCGATATCGGTCA	357		
		ACACACTCGATATCGGTCA	358		
		ATCGAGTGTGTTAAAGACGC	359		
		GATATCGAGTGTGTTAAAGA	360		
		ACCGATATCGAGTGTGTTAA	361		

TABLE 2E-continued

Example spacer sequences of gRNA for editing CD123 epitope					
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:	
			AATGTGACCGATATCGAGTG	362	
			GAAATGTGACCGATATCGAG	363	
			AGTGTGTTAAAGACGCCGAC	364	
			TCGAGTGTGTTAAAGACGCC	365	
			CCGATATCGAGTGTGTTAA	366	
			GACCGATATCGAGTGTGTTA	367	
			TGACCGATATCGAGTGTGTT	368	
		AtCas9	GACCGATATCGAGTGTGTTAA	369	
			CGAGTGTGTTAAAGACGCCGAC	370	
			GATATCGAGTGTGTTAAAGACG	371	
			ACCGATATCGAGTGTGTTAAAG	372	
			GTGACCGATATCGAGTGTGTTA	373	
			CGATATCGAGTGTGTTAAAGAC	374	
			AAATGTGACCGATATCGAGTGT	375	
			ACAGAAATGTGACCGATATCGA	376	
C52	CBE ABE	SpCas9	GTCTTTAACACACTCGATAT	377	
			TCTTTAACACACTCGATATC	378	
			GTCGGCGTCTTTAACACACT	379	
			AACACACTCGATATCGGTCA	380	
			TTAACACACTCGATATCGGT	381	
			GGCGTCTTTAACACACTCGA	382	
			TCGGCGTCTTTAACACACTC	383	
			AtCas9	CGGTCTTTAACACACTCGATAT	384
				TAAACACTCGATATCGGTCA	385
				GTCTTTAACACACTCGATATCG	386
				GTCGGCGTCTTTAACACACTCG	387
				ACACACTCGATATCGGTCA	388
			Cpf1	CGGCGTCTTTAACACACTCGAT	389
				GAATAGTCGGCGTCTTTAACAC	390
				ACACACTCGATATCGGTCA	391
S59	CBE	SpCas9		ATTTACCGGCATAGAATAGT	392
				GACGCCGACTATCTATGCC	393
			TAAAGACGCCGACTATTCTA	394	
			TATTTATGCGCGTAAATCA	395	
			ACTATCTATGCGCGTAAAT	396	
			CCGACTATTCTATGCGCGTA	397	
			GCCGACTATTCTATGCGCGT	398	
			AtCas9	ACGCCGACTATTCTATGCGCGT	399
				TATTTATGCGCGTAAATCATA	400
				ACTATCTATGCGCGTAAATCA	401
CGACTATTCTATGCGCGTAAAT	402				
TGTTAAAGACGCCGACTATTCT	403				
ABE	SpCas9	AGACGCCGACTATTCTATGCCG	404		
		TTAAAGACGCCGACTATTCTAT	405		
		GTTAAAGACGCCGACTATTCTA	406		
		ATTTACCGGCATAGAATAGT	407		
		TTTACCGGCATAGAATAGTC	408		
		ATGATTTACCGGCATAGAAT	409		
		AATAGTCGGCGTCTTTAACA	410		
		AGAATAGTCGGCGTCTTTAA	411		
		ATAGAATAGTCGGCGTCTTT	412		
		AtCas9	CGGCATAGAATAGTCGGCGTCT	413	
AGAATAGTCGGCGTCTTTAACA	414				
ATAGAATAGTCGGCGTCTTTAA	415				
GCATAGAATAGTCGGCGTCTTT	416				
CGGCATAGAATAGTCGGCGTCT	417				
R84	CBE	SpCas9	ATTTACCGGCATAGAATAGTCG	418	
			ACCGGCATAGAATAGTCGGCGT	419	
			GAATAGTCGGCGTCTTTAACA	420	
			GGCCACTCGGACGGTGTAGT	421	
			TGGTGGGTTGGCCACTCGGA	422	
			GTTGGCCACTCGGACGGTGT	423	
			TGGGTTGGCCACTCGGACGG	424	

TABLE 2E-continued

Example spacer sequences of gRNA for editing CD123 epitope				
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:
			GGTGGGTTGGCCACTCGGAC	425
			GAATGGTGGGTTGGCCACTC	426
			GCCACTCGGACGGTGTAGTT	427
			ACTCGGACGGTGTAGTTGGT	428
			AATGGTGGGTTGGCCACTCG	429
		At Cas9	CTCGGACGGTGTAGTTGGTCAC	430
			CACTCGGACGGTGTAGTTGGTC	431
			GGCCACTCGGACGGTGTAGTTG	432
			TTGGCCACTCGGACGGTGTAGT	433
			TCGGACGGTGTAGTTGGTCACT	434
			GGTTGGCCACTCGGACGGTGT	435
P88	CBE	SpCas9	CCAACCCACCATTCTCCACG	436
			CAACCCACCATTCTCCACGT	437
			GGCCAACCCACCATTCTCCA	438
			AACCCACCATTCTCCACGTG	439
			GTGGCCAACCCACCATTCTC	440
			CGTCCGAGTGGCCAACCCAC	441
			CACCGTCCGAGTGGCCAACC	442
		At Cas9	CCACCATTTCTCCACGTGGATCC	443
			AACCCACCATTCTCCACGTGGA	444
			CCAACCCACCATTCTCCACGTG	445
			GCCAACCCACCATTCTCCACGT	446
			CCGAGTGGCCAACCCACCATT	447
			GTCCGAGTGGCCAACCCACCAT	448
			GTCCGAGTGGCCAACCCACCAT	449
			GTCCGAGTGGCCAACCCACCAT	450
F90	ABE	SpCas9	CCACGTGGAGAATGGTGGGT	451
			AGAAATGGTGGGTTGGCCACT	452
			GGATCCACGTGGAGAATGGT	453
			AAGAGGATCCACGTGGAGAA	454
			GAATGGTGGGTTGGCCACTC	455
			CACGTGGAGAATGGTGGGTT	456
			GATCCACGTGGAGAATGGTG	457
			AGAGGATCCACGTGGAGAAT	458
			AATGGTGGGTTGGCCACTCG	459
			GTGGAGAATGGTGGGTTGGC	460
		At Cas9	ACGTGGAGAATGGTGGGTTGGC	461
			GGAGAATGGTGGGTTGGCCACT	462
			CCACGTGGAGAATGGTGGGTTG	463
			ATCCACGTGGAGAATGGTGGGT	464
			GATCCACGTGGAGAATGGTGGG	465
			GGATCCACGTGGAGAATGGTGG	466
S91	ABE	SpCas9	CCACGTGGAGAATGGTGGGT	467
			GGATCCACGTGGAGAATGGT	468
			AAGAGGATCCACGTGGAGAA	469
			AGGATCCACGTGGAGAATGG	470
			CACGTGGAGAATGGTGGGTT	471
			GATCCACGTGGAGAATGGTG	472
			AGAGGATCCACGTGGAGAAT	473
			GTGGAGAATGGTGGGTTGGC	474
			GGGAAGAGGATCCACGTGGA	475
		At Cas9	ACGTGGAGAATGGTGGGTTGGC	476
			GGAGAATGGTGGGTTGGCCACT	477
			CCACGTGGAGAATGGTGGGTTG	478
			ATCCACGTGGAGAATGGTGGGT	479
			GATCCACGTGGAGAATGGTGGG	480
			GGATCCACGTGGAGAATGGTGG	481
		SpCas9	CCAACCCACCATTCTCCACG	482
			TCCACGTGGATCCTCTTCCC	483
			CCACGTGGATCCTCTTCCC	484
			AACCCACCATTCTCCACGTG	485
			GTGGCCAACCCACCATTCTC	486
		At Cas9	ACCATTTCTCCACGTGGATCCTC	487
			TCCACGTGGATCCTCTTCCCTG	488
			ACCATTTCTCCACGTGGATCCTC	489
			CACCATTTCTCCACGTGGATCCT	490
			CCACCATTTCTCCACGTGGATCC	491

TABLE 2E-continued

Example spacer sequences of gRNA for editing CD123 epitope				
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:
			AACCCACCATTCTCCACGTGGA	492
			CCAACCCACCATTCTCCACGTG	493
			GCCAACCCACCATTCTCCACGT	494
			TCTCCACGTGGATCCTCTTCCC	495
			ATTCTCCACGTGGATCCTCTTC	496
			CATTCTCCACGTGGATCCTCTT	497
W93	ABE	SpCas9	CCACGTGGAGAATGGTGGGT	498
			GGATCCACGTGGAGAATGGT	499
			AAGAGGATCCACGTGGAGAA	500
			CTCAGGGAAGAGGATCCACG	501
			CACGTGGAGAATGGTGGGTT	502
			GATCCACGTGGAGAATGGTG	503
			AGAGGATCCACGTGGAGAAT	504
			TCAGGGAAGAGGATCCACGT	505
			TTCTCAGGGAAGAGGATCCA	506
		At Cas9	GGAAAGAGGATCCACGTGGAG	507
			GGGAAGAGGATCCACGTGGA	508
			CAGGGAAGAGGATCCACGTG	509
			ACGTGGAGAATGGTGGGTTGGC	510
			CCACGTGGAGAATGGTGGGTTG	511
			ATCCACGTGGAGAATGGTGGGT	512
			GATCCACGTGGAGAATGGTGGG	513
			GTTTCTCAGGGAAGAGGATCCAC	514
			GGATCCACGTGGAGAATGGTGG	515
			TGTTCTCAGGGAAGAGGATCCA	516

TABLE 2F

Example spacer sequences of pegRNA for editing CD123 epitope			
Residue	Spacer	SEQ ID NO:	
R84, P88, F90, S91, W93	AACAATAGCTATTGCCAGTT	517	
	CATAGTCCTATGTCCTCTT	518	
	AAGACACAGCGAAGGCCGAGA	519	
	AAAGACACAGCGAAGGCCGAG	520	
	ACACAGCGAAGGCCGAGAGGG	521	
	TCTCACTGTTCTCAGGGAAG	522	
	CACAGCGAAGGCCGAGAGGGA	523	
	ACATTTTTCTCACTGTTCTC	524	
	CATTTTTCTCACTGTTCTCA	525	
	AAAGAAAAAGACACAGCGA	526	
	GGGAGAGAGGGAAGGAGGGA	527	
	AGGAGAGAGGGAAGGAGGGA	528	
	GGGAGGAGAGAGGGAAGGA	529	
	AGGAGGAGAGAGAGGGAAGG	530	
	GAGAGGAGAGAGAGAGGGA	531	
	AAGGCGAGAGGAGGAGGAGAG	532	
	AGGCAGAGAGGAGGAGAGAGA	533	
E51, C52, S59, P61	ACCCACCAATCACGAACCTA	534	
	AAAGGCTCAGCAGTTGACCT	535	
	CAAGGCTCAGCAGTTGACCT	536	
	GAACCTAAGGATGAAAGCAA	537	
I27, L30, M32, W41	GTCTTTAACACACTCGATAT	538	
	TATCGGTCACATTTCTGTTA	539	
I27, L30, M32	CACATTTCTGTTAAGGTCCC	540	
I27, L30	GAGCCTTTGCTTTCATCCTTAGG	541	

TABLE 3A

Epitope Residues in CD117	
Antibody	Target Residues in Epitope
Ab85	T67, K69, T71, S81, Y83, T114, T119, K129
Ab65	S236, H238, Y244, S273, T277, T279

TABLE 3B

CD117 Protein Sequence (SEQ ID NO: 3)
QPSVSPGEPSPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDEN
ENKQNEWI TEKAEATNTGKYTCNKHGLSNSIYVFVRDPAKFLVDRSLY
GKEDNDTLVRCPLTDPEVTNYSLKGCQKPLPKDLRFIPDPKAGIMIKSV
KRAYHRLCLHCSVDQEGKSVLSEKFIKVRPAFKAVPVVSVSKASYLLRE
GEEFTVCTIKDVS SSVYSTWKRENSQTKLQEKYNSWHHGDFNYERQATL
TISSARVNDSGVPMCYANNTFGSANVTTTLEVVDRKGFINIFPMINTTVFV
NDGENVDLIVEYEAFFKPEHQWIYMNRTFTDKWEDYPKSENE SNIRYVS
ELHLTRLKGTGGTYTFLVNSNDVNAAIAPNVVNTKPEILTYDRLVNGM
LQCVAAAGPEPTIDWYFCPGTEQRCSASVLPVDVQTLNSSGPPFGKLVVQ
SSIDSSAFKHNGTVECKAYNDVGKTSAYFNPAFKGNNKEQIHPHTLFTPL
LIGFVIVAGMMCIIVMILTYKYLQKPMYEVQKWVVEEINGNNVYIDPTQ
LPYDHKWEFPRNRLSFGKTLGAGAFGKVVVEATAYGLIKSDAAMTVAVKML
KPSAHLTHEREALMS ELKVLVSYLGNHMNI VNLGACTIGGPTLVITEYCCY
GDLLNFLRRKRDSFICSKQEDHAEALYKNLLHSKSSCS DSTNEYMDMK
PGVSYVVPKADKRRSVRIGSYIERDVT PAIMEDDELALDLEDLLSFSYQ
VAKGMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVV
KGNARLPVKWMAPE SIFNCVYTFESDVWSYGI FLWELFSLGSSPYGMPV
DSKFYKMIKEGFRML SPEHAPAEMYDIMKTCWDADPLKRPTFKQIVQLIE
KQISESTNHIYSNLANCS PNRQKPVVDHSVRINSV GSTASSQPLLVDHDD
V

TABLE 3C

VH/VL of Ab85		
Region	Sequence	SEQ ID NO:
VH	EVQLVQSGAEVKKPGESLKISCKGSGYS FTNYWIGVVRQMPGKLEWMAI INPRDS DTRYRPSFQGQVTISADKSI STAYLQWS SLKASDTAMYCARHGRGYEGYEGAFDI WGQGLTVTVSS	13
VL	DIQMTQSPSSLSASVGDRTITCRSSQG IRSDLGWYQQKPGKAPKLLIYDASNLET GVPSRFRSGSGSDFTLTISLQPEDF ATYYCQQANGFPLTFGGGTKVEIK	14

TABLE 3D

VH/VL of Ab67		
Region	Sequence	SEQ ID NO:
VH	EVQLVESGGGLVQPGGSLRLS CAASGFT FSDADMDWVRQAPGKLEWVGRTRNKAG SYTTEYAASVKGRFTISRDDSKNSLYLQ MNSLKTEDTAVYYCAREPKYIWIDFDLWG RGLTLVTVSS	15
VL	DIQMTQSPSSLSASVGDRTITCRASQS ISSYLNWYQQKPGKAPKLLIYAASSLQS GVPSRFRSGSGSDFTLTISLQPEDFA TYYCQQSYIAPYTFGGGTKVEIK	16

TABLE 3E

Example spacer sequences of gRNA for editing CD117 epitope				
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:
T67	ABE/ CBE	Sp cas9	aacaccggcaaat acacgtg	542
			ccaacaccggcaaat acacg	543
			caccaacaccggcaaat aca	544
			gccaccaacaccggcaaat a	545
			aagccaccaacaccggcaaaa	546
			aacaccggcaaat acacgtgca	547
			caccaacaccggcaaat acacg	548
	At cas9	accaacaccggcaaat acacgt	549	
		gccaccaacaccggcaaat aca	550	
		gcagaagccaccaacaccggca	551	
		ccaacaccggcaaat acacgtg	552	
		caacaccggcaaat acacgtgc	553	
		caccggcaaat acacgtgcacc	554	
		K69	ABE	Sp cas9
accggcaaat acacgtgcac	556			
ggcaaat acacgtgcaccaa	557			
gcaaat acacgtgcaccaa	558			
caaat acacgtgcaccaa	559			
cggcaaat acacgtgcaccaa	560			
T71	ABE/ CBE	Sp cas9	tacacgtgcaccaacaaca	562
			aat acacgtgcaccaacaaca	563
			acacgtgcaccaacaacaac	564
			aaatacacgtgcaccaacaac	565
			acacgtgcaccaacaacaacg	566
			S81	CBE
aattccatttatgtgtttgt	568			
agcaattccatttatgtgtt	569			
cttaagcaattccatttatg	570			
ggcttaagcaattccattta	571			
ataaatggaattgcttaagc	572			
aatggaattgcttaagccg	573			
ABE	At cas9	ggaattgcttaagccggtgt		574
		acacataaatggaattgctt		575
		aacacataaatggaattgct		576
		cacataaatggaattgctta		577
		caaacacataaatggaattgct		578
		aaacacataaatggaattgctt		579
		caaacacataaatggaattgct		580
Y83	ABE	Sp cas9	caattccatttatgtgtttgtt	581
			gcaattccatttatgtgtttgt	582
			gcttaagcaattccatttatg	583
			ttatgtgtttgttagaggta	584
			tttatgtgtttgttagagg	585
			atttatgtgtttgttagagg	586
			ccatttatgtgtttgttaga	587

TABLE 3E-continued

Example spacer sequences of qRNA for editing CD117 epitope				
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:
			tccatttatgtgtttgtag	588
			ttccatttatgtgtttgtag	589
			tctaacaacacataaaatgg	590
			ctctaacaacacataaaatg	591
			acctctaacaacacataaaa	592
		At cas9	ctctaacaacacataaaatgga	593
			atztatgtgtttgtagaggta	594
			gcaattccatttatgtgtttg	595
T114	ABE/ CBE	Sp cas9	ctcacagaccagaagtgc	596
			cctctcacagaccagaagt	597
			tcacagaccagaagtgc	598
			tctctcacagaccagaag	599
			tgctctctcacagaccaga	600
			ctgtctctctcacagaccag	601
			gctgtctctctcacagacca	602
			cgctgtctctctcacagacc	603
			cgctgtctctctcacagacc	604
		At cas9	ctgtctctctcacagaccagaa	605
			cacagaccagaagtgc	606
			tgctctctcacagaccagaag	607
			tctctcacagaccagaagtgc	608
			gctgtctctctcacagaccaga	609
			tccgtgtctctctcacagacc	610
T119	ABE/ CBE	Sp cas9	gtgaccaattattccctca	611
			gtgaccaattattccctcaa	612
			aagtgaccaattattccctc	613
			gtgaccaattattccctcaa	614
			tgaccaattattccctcaag	615
			gaccaattattccctcaagg	616
			gaagtgaccaattattccct	617
		At cas9	cagaccagaagtgc	618
			gaccagaagtgc	619
			acagaccagaagtgc	620
			gtgaccaattattccctcaag	621
			tgaccaattattccctcaagg	622
			agtgaccaattattccctcaag	623
K129	ABE	Sp cas9	ccaggggaagcctcttccca	624
			caggggaagcctcttcccaa	625
			aggggaagcctcttcccaag	626
			gaagcctcttcccaaggact	627
		CBE	ccttgggaagaggttcccc	628
			tgggaagaggttccccctgg	629
			aggcttccccctggcaccct	630
			ggcttccccctggcaccct	631
		At cas9	tgccaggggaagcctcttccca	632
			gggggtgccaggggaagcctctt	633
		CBE	ttgggaagaggttccccctggc	634
			cttgggaagaggttccccctgg	635
			ccttgggaagaggttccccctg	636
			agtcttgggaagaggttcccc	637
			aggcttccccctggcacccttg	638
			ggcttccccctggcacccttga	639
			aagaggcttccccctggcaccct	640
			agaggcttccccctggcaccct	641
S236	ABE	Sp cas9	aaatataatagctggcatca	642
			tataatagctggcatcacgg	643
			aaatataatagctggcatcac	644
			ataatagctggcatcacgg	645
			agaaatataatagctggcat	646
			aggagaaatataatagctgg	647
		CBE	gccagctattatatttctcc	648
			caccgtgatgccagctattat	649
			cagctattatatttctctctg	650
			agctattatatttctctctg	651
		At cas9	tataatagctggcatcacgg	652
			aaatataatagctggcatcacg	653

TABLE 3E-continued

Example spacer sequences of qRNA for editing CD117 epitope				
Res- idue	Ed- itor	Cas	Spacer	SEQ ID NO:
			caggagaaatataatagctggc	654
			tacaggagaaatataatagctg	655
			taatagctggcatcacggtgac	656
			tagctggcatcacggtgacttc	657
			ggagaaatataatagctggcat	658
		CBE	cggtagtccagctattatatt	659
			accgtgatccagctattatatt	660
			taccgtgatccagctattatatt	661
H238	ABE/ CBE	Sp cas9	agctggcatcacggtgacttc	662
			gctggcatcacggtgacttc	663
			ggcatcacggtgacttc	664
		At cas9	ggcatcacggtgacttc	665
			gcatcacggtgacttc	666
Y244	ABE	Sp cas9	tgacttcaattatgaacgtc	667
			ttatgaacgtcaggcaacgt	668
			caattatgaacgtcaggcaaa	669
			gacttcaattatgaacgtca	670
			acggtgacttcaattatgaa	671
			cataatgaagtcaccgtga	672
			gttcataatgaagtcaccg	673
			acgttcataatgaagtcac	674
			tgctgacgttcataatga	675
			cgctgctgacgttcataat	676
			ttcaattatgaacgtcaggc	677
			cttcaattatgaacgtcagg	678
			gtgacttcaattatgaacgt	679
			tcacggtgacttcaattatg	680
			ttcataatgaagtcaccgt	681
			ctgacgttcataatgaag	682
			ttgctgacgttcataatg	683
			gttgcctgacgttcataat	684
		At cas9	caattatgaacgtcaggcaacg	685
			tatgaacgtcaggcaacgttga	686
			tgacttcaattatgaacgtcag	687
			cggtgacttcaattatgaacgt	688
			gttcataatgaagtcaccgtg	689
			cataatgaagtcaccgtgatg	690
			cgcttcataatgaagtcaccgt	691
			tgctgacgttcataatgaag	692
			ttgctgacgttcataatgaa	693
			cgctgctgacgttcataatg	694
			tcaattatgaacgtcaggcaac	695
			atataatgaacgtcaggcaacgtt	696
			acggtgacttcaattatgaacg	697
			cacggtgacttcaattatgaac	698
			tcataatgaagtcaccgtgat	699
			acgttcataatgaagtcaccg	700
			gctgacgttcataatgaag	701
S273	CBE	Sp cas9	ggatcagcaaatgtcacac	702
			ttggatcagcaaatgtcac	703
			tttggatcagcaaatgtcac	704
			tttggatcagcaaatgtcac	705
			actttggatcagcaaatgt	706
			aatactttggatcagcaaa	707
			ataatactttggatcagca	708
			aataatactttggatcagc	709
			caataatactttggatcag	710
		ABE	gctgatccaaaagtattat	711
			tgatccaaaagtattattgg	712
			gctgatccaaaagtattatt	713
			atttgctgatccaaaagtat	714
			gacatttggctgatccaaa	715
			gtgacatttggctgatccaaa	716
			ttgtgacatttggctgatcc	717
			gttggacatttggctgatcc	718
			gttggacatttggctgatcc	719
			ttgtgacatttggctgatcc	720

TABLE 3E-continued

Example spacer sequences of qRNA for editing CD117 epitope					
Residue	Editor Cas	Spacer	SEQ ID NO:		
	ABE At cas9	at ttgtgatccaaaagtatta	721		
		ctgatccaaaagtattattggc	722		
		aataaacttttggatcagcaa	723		
		tttggatcagcaaatgtcaca	724		
		tttggatcagcaaatgtcaca	725		
		tacttttggatcagcaaatgtc	726		
		taacttttggatcagcaaat	727		
		ctgatccaaaagtattattggc	728		
		gatccaaaagtattattggc	729		
		tcagcaaatgtcacaacaacct	730		
		atacttttggatcagcaaatgt	731		
		aatacttttggatcagcaaatgt	732		
		ataacttttggatcagcaaaa	733		
		tttgtgatccaaaagtattat	734		
		tgctgatccaaaagtattattg	735		
		gttgtgacatttctgatccaa	736		
		acatttgctgatccaaaagtat	737		
		ggatcagcaaatgtcacaacaa	738		
		T277	ABE/ Sp cas9 CBE	agcaaatgtcacaacaacct	739
				gtcacaacaaccttggaaagt	740
cacaacaaccttggaaagt	741				
tgtcacaacaaccttggaaag	742				
aatgtcacaacaaccttggaa	743				
aaatgtcacaacaaccttgg	744				
caaatgtcacaacaaccttg	745				
gcaaatgtcacaacaacctt	746				
ggatcagcaaatgtcacaac	747				
cacaacaaccttggaaagt	748				
	At cas9	gcaaatgtcacaacaaccttgg	749		
		tgtcacaacaaccttggaaagt	750		
		atgtcacaacaaccttggaaagt	751		
T279	ABE/ Sp cas9 CBE	caacaaccttggaaagt	752		
		caacaaccttggaaagt	753		
		acaaccttggaaagt	754		
		caaccttggaaagt	755		
		aaccttggaaagt	756		
		caaccttggaaagt	757		
		acaaccttggaaagt	758		
			At cas9	acaaccttggaaagt	758

TABLE 3F

Example spacer sequences of pegRNA for editing CD117 epitope				
Residue	Spacer	SEQ ID NO:		
T67, K69, T71, S81, Y83	CTGATCCGGGCTTTGTCAAATGG	759		
	TACACGTGCACCAACAACACGG	760		
	CAAAATGGACTTTTGAGATCTGG	761		
	GAATGAATGGATCACGGAAAAGG	762		
	AAGGCAGAAGCCACCAACCCGG	763		
	ATGAGAATAAGCAGAATGAATGG	764		
	TAAGCAGAATGAATGGATCACGG	765		
	ATTGCTTAAGCCGTGTTTGTGTTG	766		
	TGTCATCCAAAATTAAGAGCAGG	767		
	GTTGGTGCACGTGTAATTTGCCGG	768		
	ACCTCTAACAAACACATAATGG	769		
	T114, T119, K129	TTGTTGACCGCTCCTTGATGTTGG	770	
		CTTGTGACCGCTCCTTGATGTTGG	771	
		GAAAGAAGACAACGACACGCTGG	772	
TTATTCCTCAAGGGGTGCCAGG		773		
TGACCAATATTCCCTCAAGGGG		774		
TATTCCTCAAGGGGTGCCAGG		775		
GTGACCAATATTCCCTCAAGGG		776		
			776	

TABLE 3F-continued

Example spacer sequences of pegRNA for editing CD117 epitope			
Residue	Spacer	SEQ ID NO:	
		ATTCCCTCAAGGGGTGCCAGGGG	777
		TTGATCATGATGCCCGCCTTGGG	778
		ATGCAGACAGAGCCGATGGTAGG	779
		TGATCATGATGCCCGCCTTGGG	780
		TTTGATCATGATGCCCGCCTTGG	781
		GCACCCCTTGAGGGAATAATTGG	782
		AACAATGCAGACAGAGCCGATGG	783
		GGGAATAATTGGTCACTTCTGGG	784
		AGGGAATAATTGGTCACTTCTGG	785
		AGGAATAAACCTCAAGTCTTGG	786
		ATGATGCCCGCCTTGGGGTCAGG	787
		CTTCCCTTGGCACCCCTTGAGGG	788
		GCTTCCCTTGGCACCCCTTGAGG	789
		AACCTCAAGTCTTGGGAAGAGG	790
		GGAATAAACCTCAAGTCTTGGG	791
S236, H238, Y244		AAACCAGCAGACTAAACTACAGG	792
		TACAGGAGAAATATAATAGCTGG	793
		AAATATAATAGCTGGCATCACGG	794
		GATTCTGAATATAAATA	795
		TATGG	
		TGCTGATCCAAAAGTATTATTGG	796
S273, T277, T279		TCAGCGAGAGTTAATGATTCTGG	797
		TGACTTCAATTATGAACGTGAGG	798
		TGTTATGCCAATAATACTTTTGG	799
		GTATTTACTACTACTTCCAAGG	800
		TAATTTAAACATTCCTATAGAGG	801

TABLE 4A

Epitope Residues in CLL-1	
Antibody	Target Residues in Epitope
Hu6E7.N54A	142 to 158 (DSCYFLSDDVQTWQESK) of SEQ ID NO: 4

TABLE 4B

CLL-1 Protein Sequence (SEQ ID NO: 4)	
MSEEVTYADLQFQNSSEMEKIPEIGKFGKAPAPSHVWRPAALFLTL	
LLLLI LGLV LASM FHVTLK IEMK MNKLQNI SEELQRN I SLQLM SNMNI S	
NKIRNLSTTLQTIATKLCRELYSKEQEHKCKPCPRRWIWHK DSCYFLSDD	
VQTWQESK MACAAQNASLLKINNKNALEFIKSQSRSDYWLGLSPEEDST	
RGM RVDNI INSSAWVIRNAPDLNNMYCGYINRLVQYYHCTYKKRMI CEK	
MANPVQLGSTYFREA	

TABLE 4C

VH/VL of Hu6E7.N54A		
Region	Sequence	SEQ ID NO:
VH	EVQLVQSGAEVKKPGASVKVSKASGY	17
	SFTDYMHVWRQAPGQGLEWIGRINPY	
	AGAAFYSQNPKDRVTLTVDTSSTAYL	
	ELSSLRSEDYVYCAIERGADLEGYA	
	MDYWGQGLVTVSS	

TABLE 4C-continued

VH/VL of Hu6E7.N54A		
Region	Sequence	SEQ ID NO:
VL	DIQMTQSPSSLSASVGRVTITCRASQ SVSTSSYNYMHYQQKPKPKLLIKY ASNLESGVPSRFRSGSGSDFTLTISS LQPEDFATYYCQHSWEIPLTFGQGTKV EIK	18

TABLE 4D

Example spacer sequences of crRNA for editing CLL-1 epitope				
Res- idues	Ed- itor	Cas	Spacer	SEQ ID NO:
142-158	ABE	Sp cas9	taagtgatgatgtccaaca	802
			tgatgatgtccaacatggc	803
			aacatggcaggagagtaaaa	804
			atgtttggacatcatcactt	805
			ttttactctcctgccatggt	806
			aggacagctgttatttcccta	807
			gacagctgttatttccctaag	808
			agctgttatttccctaagtga	809
			tgttatttccctaagtgatga	810
			tgatgtccaacatggcagg	811
atgtccaacatggcaggag	812			
ggcaggagagtaaaatggcc	813			
caggagagtaaaatggcctg	814			
ggaaataacagctgtcctta	815			
atcacttaggaaataacagc	816			
atcatcacttaggaaataac	817			
gccattttactctcctgccca	818			
taaggacagctgttatttcc	819			
aaggacagctgttatttccct	820			
acagctgttatttccctaagt	821			
gctgttatttccctaagtgat	822			
atttccctaagtgatgatgtc	823			
ttcctaagtgatgatgtcca	824			
cctaagtgatgatgtccaaa	825			
atgatgtccaacatggcagg	826			
gatgtccaacatggcaggag	827			
gtccaacatggcaggagag	828			
tccaacatggcaggagaggt	829			
caaacatggcaggagagta	830			
gctgtccttatgccaaatc	831			
taacagctgtccttatgcca	832			
ataacagctgtccttatgcc	833			
aataacagctgtccttatgc	834			
catcatcacttaggaaataa	835			
gacatcatcacttaggaaat	836			
ttggacatcatcacttagga	837			
tttggacatcatcacttagg	838			
gtttggacatcatcacttag	839			
ctgccatgtttggacatcat	840			
ctcctgccatgtttggacat	841			
actctcctgccatgtttgga	842			
ttactctcctgccatgtttg	843			
aggccattttactctcctgc	844			
agctgttatttccctaagtgat	845			
agctgttatttccctaagtgat	846			
tttggcataaggacagctgtta	847			
ttaggaaataaacagctgtcct	848			
cttaggaaataaacagctgtcct	849			
tcatcacttaggaaataacagc	850			
tctcctgccatgtttggacatc	851			
taaggacagctgttatttcccta	852			
tgttatttccctaagtgatgat	853			
cctaagtgatgatgtccaaaca	854			
gtgatgatgtccaacatggca	855			
atgatgtccaacatggcagg	856			

TABLE 4D-continued

Example spacer sequences of crRNA for editing CLL-1 epitope				SEQ ID NO:
Res- idues	Ed- itor	Cas	Spacer	SEQ ID NO:
			tgtttggacatcatcacttagg	857
			cctgccatgtttggacatcatc	858
			ttactctcctgccatgtttgga	859
			attttactctcctgccatggtt	860
			ttatttccctaagtgatgatgtc	861
	ABE		tcctaagtgatgatgtccaaac	862
	ABE/CBE		ccaaacatggcaggagagtaaa	863
			caaacatggcaggagagtaaaa	864
			atggcaggagagtaaaatggcc	865
			gcaggagagtaaaatggcctgt	866
			ggacatcatcacttaggaaata	867
			ttggacatcatcacttaggaaa	868
			actctcctgccatgtttggaca	869
			tttactctcctgccatgtttgg	870
	CBE		cattttactctcctgccatggt	871
	ABE		gcataaggacagctgttatttc	872
			tttccctaagtgatgatgtccaa	873
	ABE/CBE		taagtgatgatgtccaaacatg	874
			tgatgatgtccaacatggcagg	875
			acttaggaaataaacagctgtcc	876
			tgccatgtttggacatcatcac	877
			ctgccatgtttggacatcatca	878
			gccattttactctcctgccatg	879

TABLE 4F

Example spacer sequences of pegRNA for editing CLL-1 epitope		
Residues	Spacer	SEQ ID NO:
142-158	TAAGTGATGATGTCCAACATGG	880
	TGATGATGTCCAACATGGCAGG	881
	ACAAATGTAAGCCTTGTCCAAGG	882
	CTTGTCCAAGGAGATGGATTGG	883
	GTAAGCCTTGTCCAAGGAGATGG	884
	AAGGAGATGGATTGGCATAAGG	885
	CCCATGATGGTAGAAACACCTGG	886
	CCATGATGGTAGAAACACCTGGG	887
	CACCCCTCTTATCCCATGATGG	888
	GTTGTTTATCTTCAACAGGCTGG	889
	ATGTTTGGACATCATCACTTAGG	890
	GCTGGCATTTGTGAGCAGCACAGG	891
	TTTTGTTGTTTATCTTCAACAGG	892
	TTTACTCTCTGCCATGTTTGG	893

[0133] The present disclosure is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects of the disclosure, and any compositions or methods which are functionally equivalent are within the scope of this disclosure. It will be apparent to those skilled in the art that various modifications and variations can be made in the methods and compositions of the present disclosure without departing from the spirit or scope of the disclosure. Thus, it is intended that the present disclosure cover the modifications and variations of this disclosure provided they come within the scope of the appended claims and their equivalents.

[0134] All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

SEQUENCE LISTING

Sequence total quantity: 897

SEQ ID NO: 1 moltype = AA length = 364
 FEATURE Location/Qualifiers
 source 1..364
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 1

MPLLLLLLPLL WAGALAMDPN FWLQVQESVT VQEGLCVLPV CTFPHPIPY DKNSPVHGYW 60
 FREGAIISRDP SPVATNKLDQ EVQEEETQGRF RLLGDPSPRN CSLSIVDARR RDNGSYFFRM 120
 ERGSTKYSYK SPQLSVHVTDL LTHRPKILIP GTLEPGHRSK LTCSVSWACE QGTPPIFSWL 180
 SAAPTSLGPR TTHSSVLIIT PRPQDHGTNL TCQVKFAGAG VTERTIQLN VTYVPQNPPT 240
 GIFPGDGSYK QETRAGVVHG AIGGAGVTAL LALCLCLIFF IVKTHRRKAA RTAVGRNDTH 300
 PTTGSASPKH QKSKLHGPT ETSSCSGAAP TVEMDEELHY ASLNPHGMNP SKDTSTEYSE 360
 VRTQ 364

SEQ ID NO: 2 moltype = AA length = 378
 FEATURE Location/Qualifiers
 source 1..378
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 2

MVLLWLTLLL IALPCLLQTK EDPNPPITNL RMKAKAQQLT WDLNRNVTDI ECVKDADYSM 60
 PAVNNSYQCF GAISSLCEVTN YTVRVANPPP STWILFPENS GKPWAGAENL TCWIHDVDFL 120
 SCSWAVGPGA PADVQYDLYL NVANRRQQYE CLHYKTDAGQ TRIGCRPDDI SRLSSGSQSS 180
 HILVRGRSAA FGIPCTDKFV VFSQIEILTP PNMTAKCNKT HSPMHWKMS HFNKRKFRYEL 240
 QIQKRMQPMVI TEQVRDRTSF QLLNPGTYTV QIRARERVYE FLSAWSTPQR FECDQEEGAN 300
 TRAWRTSLLI ALGTLALVC VFVICRRLV MQRLEPRIPH MKDPIGDSFQ NDKLVVWEAG 360
 KAGLEECLVT EVQVVQKT 378

SEQ ID NO: 3 moltype = AA length = 951
 FEATURE Location/Qualifiers
 source 1..951
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 3

QPSVSPGEPSP PPSIHPGKSD LIVRVGDEIR LLCTDPGFVK WTFEILDEN ENKQNEWITE 60
 KAEATNTGKY TCTNKHGLSN SIYVVRDPA KLFLVDRLY GKEDNDTLVR CPLTDPEVTN 120
 YSLKGCQKPK LPKDLRFIPD PKAGIMIKSV KRAYHRLCLH CSVDQEGKSV LSEKFIKVR 180
 PAFKAVPVVS VSKASYLLRE GEEFTVTCTI KDVS SVYST WKRENSQTKL QEKYNSWHHG 240
 DFNYERQATL TISSARVNDV GVFMCYANNT FGSANVTTL EVVDKGFINI FPMINTTVFV 300
 NDGENVDLIV EYEAFPKPEH QQWIYMNRTF TDKWEDYPKS ENESNIRYVS ELHLTRLKGT 360
 EGGTYTFLVS NSDVNAIAF NVVNTKPEI LTYDRLVNGM LQCVAAAGPE PTIDWYFCPG 420
 TEQRCSASVL PVDVQTLNNS GPPFGKLVVQ SSIDSSAFKH NGTVECKAYN DVGKTSAYFN 480
 PAFKGNNEKQ IHPHTLFTPL LIGFVIVAGM MCIIVMILTY KYLQKPMYEV QWKVVEEING 540
 NNYVYIDPTQ LPYDHWKPEP RNRLSPGKTL GAGAFGKVE ATAYGLIKSD AAMTVAVKML 600
 KPSAHLTERE ALMSELKVLV YLGNHMNIVN LLGACTIGGP TLVITEYCCY GDLNLFRRK 660
 RDSFICSQKE DHAEAAALYKN LLHSKSSCS DSTNEYMDMK PGVSYVVPK ADKRRSVRIG 720
 SYIERDVTQA IMEDDELALD LEDLLSFSYQ VAKGMAFLAS KNCIHRDLAA RNILLTHGRI 780
 TKICDFGLAR DKNDNSNYVV KGNARLPVKW MAPESIFNCV YTFESDVWSY GIFLWELFSL 840
 GSSPYGMPV DSKFYKMIKE GFRMLSPHA PAEMYDIMKT CWDADPLKRP TFKQIVQLIE 900
 KQISESTNHI YSNLANCSPN RQKPVVDHSV RINSVGTAS SSQPLLVDHDD V 951

SEQ ID NO: 4 moltype = AA length = 265
 FEATURE Location/Qualifiers
 source 1..265
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 4

MSEEVTYADL QFQNSSEMEK IPEIGKFGKE APPAPSHVWR PAALFLTLCL LLLLIGLGLV 60
 ASMFHVTLKI EMKMNKLQN ISEELQRNIS LQLMSNMNIS NKIRNLSTTL QTIATKLCRE 120
 LYSKEQEHKC KPCPRRWIWH KDSCYFLSDD VQTWQESKMA CAAQNASLLK INNKNALFEI 180
 KSQRSYDYW LGLSPEEDST RGMRVNDIIN SSAAVIRNAP DLNMYCYGI NRYLVQYYHC 240
 TYKKRMICEK MANPVQLGST YFREA 265

SEQ ID NO: 5 moltype = AA length = 118
 FEATURE Location/Qualifiers
 source 1..118
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 5

QVQLQQPGAE VVKPGASVKM SCKASGYTPT SYIIHWIKQT PGQGLEWVGV IYPGNDDISY 60
 NQKQKQKATL TADKSSSTAY MQLSSLTSED SAVYYCAREV RLRYFDVWGQ GTTIVTVSS 118

SEQ ID NO: 6 moltype = AA length = 113
 FEATURE Location/Qualifiers

-continued

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source                1..113
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 6
EIVLTQSPGS LAVSPGERVT MSCCKSSQSVF FSSSQKNYLA WYQQIPGQSP RLLIYWASTR 60
ESGVDRPFTG SGSGTDFTLT ISSVQPEDLA IYYCHQYLSS RTFGQGTKLE IKR 113

SEQ ID NO: 7         moltype = AA length = 116
FEATURE             Location/Qualifiers
source              1..116
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 7
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT DYNMHWRQA PGQGLEWIGY IYPYNGGTGY 60
NQKFKSKATI TADESTNTAY MELSSLRSED TAVYYCARGR PAMDYWGQGT LVTVSS 116

SEQ ID NO: 8         moltype = AA length = 111
FEATURE             Location/Qualifiers
source              1..111
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 8
DIQMTQSPSS LSASVGRVIT ITCRASESVD NYGISFMNWF QQKPGKAPKL LIYAASNQGS 60
GVPSRFRSGSG SGTDFTLTIS SLQPDDFATY YCQQSKEVPW TFGQGTKVEI K 111

SEQ ID NO: 9         moltype = AA length = 180
FEATURE             Location/Qualifiers
source              1..180
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 9
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT DYYMKWARQM PGKGLEWMGD IIPSNQATFY 60
NQKFKGQVTI SADKSISTTY LQWSSLKASD TAMYYCARSH LLRASWPAYW GQGTMTVTVSS 120
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSKV HTPPAVLQSS 180

SEQ ID NO: 10        moltype = AA length = 112
FEATURE             Location/Qualifiers
source              1..112
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 10
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT DYYMKWARQM PGKGLEWMGD IIPSNQATFY 60
NQKFKGQVTI SADKSISTTY LQWSSLKASD TAMYYCARSH LLRASWPAYW GQ 112

SEQ ID NO: 11        moltype = AA length = 118
FEATURE             Location/Qualifiers
source              1..118
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 11
QIQLVQSGPE LKKPGETVKI SCKASGYIFT NYGMNWRQA PGKSFKWMGW INTYTGESTY 60
SADFKGRPAF SLETSASTAY LHINDLKNED TATYFCARSG GYDPMQYWGQ GTSVTVSS 118

SEQ ID NO: 12        moltype = AA length = 111
FEATURE             Location/Qualifiers
source              1..111
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 12
DIVLTQSPAS LAVSLGQRAT ISCRASESVD NYGNTFMHWY QQKPGQPKL LIYRASNLES 60
GIPARFRSGSG SRTDFTLTIN PVEADDVATY YCQQSNEDPP TFGAGTKLEL K 111

SEQ ID NO: 13        moltype = AA length = 123
FEATURE             Location/Qualifiers
source              1..123
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 13
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT NYWIGWRQM PGKGLEWMAI INPRSDTRY 60
RPSFQGGVTI SADKSISTAY LQWSSLKASD TAMYYCARHG RGYEGYEGAF DIWQQGLTVT 120
VSS 123

SEQ ID NO: 14        moltype = AA length = 107
FEATURE             Location/Qualifiers
source              1..107
                    mol_type = protein

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                                organism = synthetic construct
SEQUENCE: 14
DIQMTQSPSS LSASVGRVIT ITCRSSQGIR SDLGWYQQKP GKAPKLLIYD ASNLETGVPS 60
RFGSGSGGTD FTLTISSLQP EDFATYYCQQ ANGFPLTFGG GTKVEIK 107

SEQ ID NO: 15      moltype = AA length = 121
FEATURE           Location/Qualifiers
source           1..121
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 15
EVQLVESGGG LVQPGGSLRL SCAASGFTFS DADMWVRQA PGKGLEWVGR TRNKAGSYTT 60
EYAASVKGGRF TISRDDSKNS LYLQMNLSLKT EDTAVYYCAR EPKYWIDFDL WGRGTLVTVS 120
S 121

SEQ ID NO: 16      moltype = AA length = 107
FEATURE           Location/Qualifiers
source           1..107
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 16
DIQMTQSPSS LSASVGRVIT ITCRASQGIS SYLNWYQQKP GKAPKLLIYA ASSLQSGVPS 60
RFGSGSGGTD FTLTISSLQP EDFATYYCQQ SYIAPYTFGG GTKVEIK 107

SEQ ID NO: 17      moltype = AA length = 122
FEATURE           Location/Qualifiers
source           1..122
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 17
EVQLVQSGAE VKKPGASVKV SCKASGYSPT DYYMHWRQA PGQGLEWIGR INPYAGAAFY 60
SQNFKDRVTL TVDTSTSTAY LELSSLRSED TAVYYCAIER GADLEGYAMD YWGQGLVTV 120
SS 122

SEQ ID NO: 18      moltype = AA length = 111
FEATURE           Location/Qualifiers
source           1..111
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 18
DIQMTQSPSS LSASVGRVIT ITCRASQSVS TSSYNYMHWY QQKPGKPPKL LIKYASNLES 60
GVPSRFGSGG SGTDFTLTIS SLQPEDFATY YCQHSWEIPL TFGQGTKVEI K 111

SEQ ID NO: 19      moltype = RNA length = 20
FEATURE           Location/Qualifiers
source           1..20
                 mol_type = other RNA
                 organism = synthetic construct

SEQUENCE: 19
gtgcagggca cgaggacgca 20

SEQ ID NO: 20      moltype = RNA length = 20
FEATURE           Location/Qualifiers
source           1..20
                 mol_type = other RNA
                 organism = synthetic construct

SEQUENCE: 20
aagtcaggg cagcaggacg 20

SEQ ID NO: 21      moltype = RNA length = 20
FEATURE           Location/Qualifiers
source           1..20
                 mol_type = other RNA
                 organism = synthetic construct

SEQUENCE: 21
gaaagtcag ggcacgagga 20

SEQ ID NO: 22      moltype = RNA length = 20
FEATURE           Location/Qualifiers
source           1..20
                 mol_type = other RNA
                 organism = synthetic construct

SEQUENCE: 22
aagaaagtc agggcacgag 20

SEQ ID NO: 23      moltype = RNA length = 20

```

-continued

FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 23		
gaagaaagtg cagggcacga		20
SEQ ID NO: 24	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 24		
ggaagaaagt gcagggcacg		20
SEQ ID NO: 25	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 25		
tggaagaaag tgcagggcac		20
SEQ ID NO: 26	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 26		
tgcagggcac gaggacgcac		20
SEQ ID NO: 27	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 27		
atggaagaaa gtgcagggca		20
SEQ ID NO: 28	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 28		
ggatggaaga aagtgcaggg		20
SEQ ID NO: 29	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 29		
tgggatggaa gaaagtgcag		20
SEQ ID NO: 30	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 30		
atggaagaaa gtgcagggca cg		22
SEQ ID NO: 31	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 31		
ggaagaaagt gcagggcacg ag		22
SEQ ID NO: 32	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

-continued

SEQUENCE: 32		
aagaaagtgc agggcacgag ga		22
SEQ ID NO: 33	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 33		
gaagaaagtg cagggcacga gg		22
SEQ ID NO: 34	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 34		
cggaaccagt aaccatgaac		20
SEQ ID NO: 35	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 35		
ggaaccagta accatgaact		20
SEQ ID NO: 36	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 36		
gaaccagtaa ccatgaactg		20
SEQ ID NO: 37	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 37		
accagtaacc atgaactggg		20
SEQ ID NO: 38	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 38		
aaccagtaac catgaactgg		20
SEQ ID NO: 39	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 39		
ccagtaacca tgaactgggg		20
SEQ ID NO: 40	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 40		
cttcccggaa ccagtaacca		20
SEQ ID NO: 41	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 41		
tcccggaacc agtaaccatg		20
SEQ ID NO: 42	moltype = RNA length = 20	

-continued

FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 42		
ttcccggaac cagtaaccat		20
SEQ ID NO: 43	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 43		
tccttcccgg aaccagtaac		20
SEQ ID NO: 44	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 44		
ggctccttcc cggaaccagt		20
SEQ ID NO: 45	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 45		
aaccagtaac catgaactgg gg		22
SEQ ID NO: 46	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 46		
ttcccggaac cagtaaccat ga		22
SEQ ID NO: 47	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 47		
tacgatgctc agggagcagt		20
SEQ ID NO: 48	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 48		
gtctacgatg ctcagggagc		20
SEQ ID NO: 49	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 49		
cgtctacgat gctcagggag		20
SEQ ID NO: 50	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 50		
ggcgtctacg atgctcaggg		20
SEQ ID NO: 51	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

-continued

SEQUENCE: 51			
tggcgtctac gatgctcagg			20
SEQ ID NO: 52	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 52			
ctggcgtcta cgatgctcag			20
SEQ ID NO: 53	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 53			
cctggcgtct acgatgctca			20
SEQ ID NO: 54	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 54			
tcttggegtc tacgatgctc			20
SEQ ID NO: 55	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 55			
ctcctggcgt ctacgatgct			20
SEQ ID NO: 56	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 56			
tctacgatgc tcaggagca gt			22
SEQ ID NO: 57	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 57			
ctacgatgct cagggagcag tt			22
SEQ ID NO: 58	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 58			
cgatgctcag ggagcagttg tt			22
SEQ ID NO: 59	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 59			
ggagggataa tggttcatac tt			22
SEQ ID NO: 60	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 60			
ggaggaggga taatggttca ta			22
SEQ ID NO: 61	moltype = RNA	length = 22	

-continued

FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 61		
aggaggaggg ataatggttc at		22
SEQ ID NO: 62	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 62		
ataatggttc atacttcttt		20
SEQ ID NO: 63	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 63		
gacgccagga ggagggataa		20
SEQ ID NO: 64	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 64		
ggaggagga taatggttca		20
SEQ ID NO: 65	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 65		
caggaggagg gataatggtt		20
SEQ ID NO: 66	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 66		
ttcactctt ttcggatgg		20
SEQ ID NO: 67	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 67		
tcatacttct ttcggatgga		20
SEQ ID NO: 68	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 68		
gttcatactt ctttcggatg		20
SEQ ID NO: 69	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 69		
ccgaaagaag tatgaacct		20
SEQ ID NO: 70	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

-continued

SEQUENCE: 70
aatggttcac acttctttcg ga 22

SEQ ID NO: 71 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 71
ggttcatact tctttcggat gg 22

SEQ ID NO: 72 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 72
catacttett tcggatggag ag 22

SEQ ID NO: 73 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 73
ccgaaagaag tatgaacct 20

SEQ ID NO: 74 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 74
catccgaaag aagtatgaac 20

SEQ ID NO: 75 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 75
ctctctccat ccgaaagaag 20

SEQ ID NO: 76 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 76
catccgaaag aagtatgaac ca 22

SEQ ID NO: 77 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 77
atccgaaaga agtatgaacc at 22

SEQ ID NO: 78 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 78
tccgaaagaa gtatgaacca tt 22

SEQ ID NO: 79 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 79
cgaaagaagt atgaaccatt at 22

SEQ ID NO: 80 moltype = RNA length = 22

-continued

FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 80		
ctctccatcc gaaagaagta tg		22
SEQ ID NO: 81	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 81		
caaatctccc cagctctctg		20
SEQ ID NO: 82	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 82		
tctcccagc tctctgtgca		20
SEQ ID NO: 83	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 83		
aatctcccga gctctctgtg		20
SEQ ID NO: 84	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 84		
tacaaatctc cccagctctc		20
SEQ ID NO: 85	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 85		
atctcccag ctctctgtgc at		22
SEQ ID NO: 86	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 86		
gttacaaatc tccccagctc tc		22
SEQ ID NO: 87	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 87		
atacagttac aaatctcccc ag		22
SEQ ID NO: 88	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 88		
aaatctcccc agctctctgt gc		22
SEQ ID NO: 89	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

-continued

SEQUENCE: 89		
acaaatctcc ccagctctct gt		22
SEQ ID NO: 90	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 90		
agaaatttgg atccatagcc		20
SEQ ID NO: 91	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 91		
tgcacttgca gccagaaatt		20
SEQ ID NO: 92	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 92		
agccagaaat ttggatccat		20
SEQ ID NO: 93	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 93		
cagccagaaa ttggatcca		20
SEQ ID NO: 94	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 94		
tgcagccaga aatttgatc		20
SEQ ID NO: 95	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 95		
cacttgcagc cagaaatttg		20
SEQ ID NO: 96	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 96		
gcacttgcag ccagaaattt		20
SEQ ID NO: 97	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 97		
tgcacttgca gccagaaatt tg		22
SEQ ID NO: 98	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 98		
tgcagccaga aatttgatc ca		22
SEQ ID NO: 99	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 99		
ccagaaattt ggatccatag cc		22
SEQ ID NO: 100	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 100		
cttgagcca gaaatttga tc		22
SEQ ID NO: 101	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 101		
aaacctctct gtaccgtcac		20
SEQ ID NO: 102	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 102		
cacaaacct cctgtaccgt		20
SEQ ID NO: 103	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 103		
acgcacaaac cctcctgtac		20
SEQ ID NO: 104	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 104		
aggacgcaca aacctcctg		20
SEQ ID NO: 105	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 105		
cgaggacgca caaacctcc		20
SEQ ID NO: 106	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 106		
gacgcacaaa ccctcctgta cc		22
SEQ ID NO: 107	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 107		
aaacctctct gtaccgtcac tg		22
SEQ ID NO: 108	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 108		
caaaccctcc tgtaccgtca ct		22
SEQ ID NO: 109	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 109		
cacaaacct cctgtaccgt ca		22
SEQ ID NO: 110	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 110		
cgaggacgca caaaccctcc tg		22
SEQ ID NO: 111	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 111		
aggaggcgga atctgcctg		20
SEQ ID NO: 112	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 112		
aaggaggcgg aatctgcctt		20
SEQ ID NO: 113	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 113		
aggcggaatc tgccttgagt ct		22
SEQ ID NO: 114	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 114		
gaatctgccc tgagtctct cc		22
SEQ ID NO: 115	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 115		
gaggcggaat ctgccctgag tc		22
SEQ ID NO: 116	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 116		
aggaggcgga atctgcctg ag		22
SEQ ID NO: 117	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 117		
aaggaggcgg aatctgcct ga		22
SEQ ID NO: 118	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 118		
ccaaggaggc ggaatctgcc ct		22
SEQ ID NO: 119	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 119		
aacaactgct ccctgagcat		20
SEQ ID NO: 120	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 120		
aggaacaact gctccctgag		20
SEQ ID NO: 121	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 121		
gtaggaacaa ctgctccctg		20
SEQ ID NO: 122	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 122		
agtaggaaca actgctccct		20
SEQ ID NO: 123	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 123		
cagtaggaac aactgctccc		20
SEQ ID NO: 124	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 124		
gggatcccag taggaacaac tg		22
SEQ ID NO: 125	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 125		
agtaggaaca actgctccct ga		22
SEQ ID NO: 126	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 126		
cccagtagga acaactgctc cc		22
SEQ ID NO: 127	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 127		
ggggatccca gtaggaacaa ct		22
SEQ ID NO: 128	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 128		
atcccagtag gaacaactgc tc		22
SEQ ID NO: 129	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 129		
ataatggttc atacttcttt		20
SEQ ID NO: 130	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 130		
ggaggaggga taatggttca		20
SEQ ID NO: 131	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 131		
ggagggataa tggttcatatc tt		22
SEQ ID NO: 132	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 132		
aggaggaggga ataatggttc at		22
SEQ ID NO: 133	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 133		
ataatggttc atacttcttt cg		22
SEQ ID NO: 134	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 134		
gggagatttg taactgtatt		20
SEQ ID NO: 135	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 135		
gagctgggga gatttgtaac		20
SEQ ID NO: 136	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 136		
gctggggaga tttgtaactg		20
SEQ ID NO: 137	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 137		
tctccccagc tctctgtgca		20
SEQ ID NO: 138	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 138		
caaatctccc cagctctctg		20
SEQ ID NO: 139	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 139		
tacaaatctc cccagctctc		20
SEQ ID NO: 140	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 140		
aatctccccca gctctctgtg		20
SEQ ID NO: 141	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 141		
atctccccag ctctctgtgc at		22
SEQ ID NO: 142	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 142		
acaaatctcc ccagctctct gt		22
SEQ ID NO: 143	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 143		
aaatctcccc agctctctgt gc		22
SEQ ID NO: 144	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 144		
agctggggag atttgtaact gt		22
SEQ ID NO: 145	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 145		
tggctatgga tccaaatttc tgg		23
SEQ ID NO: 146	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 146
aaatttctgg ctgcaagtgc agg 23

SEQ ID NO: 147 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 147
gcaggagtca gtgacggtac agg 23

SEQ ID NO: 148 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 148
ggagtcagtg acggtacagg agg 23

SEQ ID NO: 149 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 149
gagtcagtga cggtacagga ggg 23

SEQ ID NO: 150 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 150
gggagagggg ttgtcgggct ggg 23

SEQ ID NO: 151 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 151
gtgggcaggt gagtggctgt ggg 23

SEQ ID NO: 152 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 152
ggggagaggg gttgtcgggc tgg 23

SEQ ID NO: 153 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 153
tcgtttcccc acaggggccc tgg 23

SEQ ID NO: 154 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 154
ctgtggggag aggggttgtc ggg 23

SEQ ID NO: 155 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 155
ccccacaggg gccctggcta tgg 23

SEQ ID NO: 156 moltype = RNA length = 23

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FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 156		
gcaagtgcag gagtcagtga	cgg	23
SEQ ID NO: 157	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 157		
gctgaccctc gtttccccac	agg	23
SEQ ID NO: 158	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 158		
tgaccctcgt ttccccacag	ggg	23
SEQ ID NO: 159	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 159		
ctgaccctcg tttccccaca	ggg	23
SEQ ID NO: 160	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 160		
tgtgggcagg tgagtggctg	tgg	23
SEQ ID NO: 161	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 161		
tgggcaggtg agtggctgtg	ggg	23
SEQ ID NO: 162	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 162		
gctgtgggga gaggggtgt	cgg	23
SEQ ID NO: 163	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 163		
ccctgctgtg ggcaggtag	tgg	23
SEQ ID NO: 164	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 164		
gtgagtggct gtgggagag	ggg	23
SEQ ID NO: 165	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 165
 ggtgagtggc tgtggggaga ggg 23

SEQ ID NO: 166 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 166
 aggtgagtgg ctgtggggag agg 23

SEQ ID NO: 167 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 167
 ggggagttct tgctgtagta ggg 23

SEQ ID NO: 168 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 168
 tggggagttc ttgtcgtagt agg 23

SEQ ID NO: 169 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 169
 gttcttgtcg tagtaggga tgg 23

SEQ ID NO: 170 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 170
 ttcttgctgt agtagggtat ggg 23

SEQ ID NO: 171 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 171
 tggagagtcc ctggatataa tgg 23

SEQ ID NO: 172 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 172
 gaaccagtaa ccatgaactg ggg 23

SEQ ID NO: 173 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 173
 tgctgtagta gggtatggga tgg 23

SEQ ID NO: 174 moltype = RNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 174
 tggatataat ggctccttcc cgg 23

SEQ ID NO: 175 moltype = RNA length = 23

-continued

FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 175		
tgtggccact ggagagtccc tgg		23
SEQ ID NO: 176	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 176		
cggaaccagt aaccatgaac tgg		23
SEQ ID NO: 177	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 177		
ggaagaaagt gcagggcacg agg		23
SEQ ID NO: 178	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 178		
atgggatgga agaaagtgca ggg		23
SEQ ID NO: 179	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 179		
tatgggatgg aagaaagtgc agg		23
SEQ ID NO: 180	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 180		
ggaaccagta accatgaact ggg		23
SEQ ID NO: 181	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 181		
gacaagaact cccagttca tgg		23
SEQ ID NO: 182	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 182		
tggagagtcc ctggatataa tgg		23
SEQ ID NO: 183	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 183		
tggatataat ggctccttcc cgg		23
SEQ ID NO: 184	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 184		
tctagcttgt ttgtggccac tgg		23
SEQ ID NO: 185	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 185		
ttcttgatct agcttgtttg tgg		23
SEQ ID NO: 186	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 186		
tgtggccact ggagagtccc tgg		23
SEQ ID NO: 187	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 187		
gggaaggagc cattatatcc agg		23
SEQ ID NO: 188	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 188		
gcctccttgg ggatcccagt agg		23
SEQ ID NO: 189	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 189		
ggaaggagcc attatatcca ggg		23
SEQ ID NO: 190	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 190		
gctagatcaa gaagtacagg agg		23
SEQ ID NO: 191	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 191		
tatatccagg gactctccag tgg		23
SEQ ID NO: 192	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 192		
gaagtacagg aggagactca ggg		23
SEQ ID NO: 193	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 193		
agaagtacag gaggagactc agg		23
SEQ ID NO: 194	moltype = RNA length = 23	

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FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 194		
catggttact ggttccgga agg		23
SEQ ID NO: 195	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 195		
caagctagat caagaagtac agg		23
SEQ ID NO: 196	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 196		
agggcagatt cgcctcctt ggg		23
SEQ ID NO: 197	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 197		
cagttcatgg ttactgggtc cgg		23
SEQ ID NO: 198	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 198		
gggcagattc cgctccttg ggg		23
SEQ ID NO: 199	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 199		
agttcatggt tactggttcc ggg		23
SEQ ID NO: 200	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 200		
cagggcagat tccgcctcct tgg		23
SEQ ID NO: 201	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 201		
agggagcagt tggtcctact ggg		23
SEQ ID NO: 202	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 202		
gggagatttg taactgtatt tgg		23
SEQ ID NO: 203	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 203
caggagcag ttgttctac tgg 23

SEQ ID NO: 204 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 204
tgttcctact gggatcccca agg 23

SEQ ID NO: 205 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 205
tgaaccatta tccctcctcc tgg 23

SEQ ID NO: 206 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 206
tcctactggg atccccaagg agg 23

SEQ ID NO: 207 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 207
tcctggcgtc tacgatgctc agg 23

SEQ ID NO: 208 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 208
tactgggatc cccaaggagg cgg 23

SEQ ID NO: 209 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 209
cctggcgtct acgatgetca ggg 23

SEQ ID NO: 210 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 210
tgtcacatgc acagagagct ggg 23

SEQ ID NO: 211 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 211
gtcacatgca cagagagctg ggg 23

SEQ ID NO: 212 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 212
ctgtcacatg cacagagagc tgg 23

SEQ ID NO: 213 moltype = RNA length = 23

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FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 213		
gggagatttg taactgtatt tgg		23
SEQ ID NO: 214	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 214		
tgtcacatgc acagagagct ggg		23
SEQ ID NO: 215	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 215		
gtcacatgca cagagagctg ggg		23
SEQ ID NO: 216	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 216		
ctgtcacatg cacagagagc tgg		23
SEQ ID NO: 217	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 217		
tggttcatac ttctttcgga tgg		23
SEQ ID NO: 218	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 218		
gacgccagga ggagggataa tgg		23
SEQ ID NO: 219	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 219		
gcatcgtaga cgccaggagg agg		23
SEQ ID NO: 220	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 220		
ccctgagcat cgtagacgcc agg		23
SEQ ID NO: 221	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 221		
catcgtagac gccaggagga ggg		23
SEQ ID NO: 222	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 222			
tgagcatcgt agacgccagg agg			23
SEQ ID NO: 223	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 223			
ataatggttc atacttcttt cgg			23
SEQ ID NO: 224	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 224			
tacttctttc ggatggagag agg			23
SEQ ID NO: 225	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 225			
gtaccatga acttcccttg cgg			23
SEQ ID NO: 226	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 226			
tgtcacatgc acagagagct ggg			23
SEQ ID NO: 227	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 227			
gtcacatgca cagagagctg ggg			23
SEQ ID NO: 228	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 228			
ctgtcacatg cacagagagc tgg			23
SEQ ID NO: 229	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 229			
aggttcgtga ttggtgggtt			20
SEQ ID NO: 230	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 230			
tccttaggtt cgtgattggt			20
SEQ ID NO: 231	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 231			
ttcacacctta gggttcgtgat			20
SEQ ID NO: 232	moltype = RNA	length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 232		
ggttcgtgat tggtagggttt		20
SEQ ID NO: 233	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 233		
ccttaggttc gtgattgggtg		20
SEQ ID NO: 234	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 234		
tcatccttag gttcgtgatt		20
SEQ ID NO: 235	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 235		
gttcgtgatt ggtggggtttg		20
SEQ ID NO: 236	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 236		
gtgattgggtg ggtttggatc tt		22
SEQ ID NO: 237	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 237		
ttcgtgattg gtgggtttgg at		22
SEQ ID NO: 238	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 238		
gttcgtgatt ggtggggtttg ga		22
SEQ ID NO: 239	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 239		
taggttcgtg attggtgggt tt		22
SEQ ID NO: 240	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 240		
atccttaggt tcgtgattgg		20
SEQ ID NO: 241	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 241		
accaccaat cacgaaccta		20
SEQ ID NO: 242	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 242		
atcacgaacc taaggatgaa		20
SEQ ID NO: 243	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 243		
accaatcacg aacctaagga		20
SEQ ID NO: 244	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 244		
cccaccaatc acgaacctaa		20
SEQ ID NO: 245	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 245		
agatccaaac ccaccaatca		20
SEQ ID NO: 246	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 246		
aatcacgaac ctaaggatga		20
SEQ ID NO: 247	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 247		
caatcacgaa cctaaggatg		20
SEQ ID NO: 248	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 248		
ccaatcacga acctaaggat		20
SEQ ID NO: 249	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 249		
ccaccaatca cgaacctaag		20
SEQ ID NO: 250	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 250		
aaccaccaa tcacgaacct		20
SEQ ID NO: 251	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 251		
aaaccaccca atcacgaacc		20
SEQ ID NO: 252	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 252		
atccaaaacc accaatcacg		20
SEQ ID NO: 253	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 253		
gatccaaacc caccaatcac		20
SEQ ID NO: 254	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 254		
gaagatccaa accccaat		20
SEQ ID NO: 255	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 255		
accaatcacg aacctaagga tg		22
SEQ ID NO: 256	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 256		
aagatccaaa cccaccaatc ac		22
SEQ ID NO: 257	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 257		
gaagatccaa accccaat ca		22
SEQ ID NO: 258	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 258		
ccaccaatca cgaacctaag ga		22
SEQ ID NO: 259	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 259		
caaaccacc aatcacgaac ct		22
SEQ ID NO: 260	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 260		
atccaaacc accaatcacg aa		22
SEQ ID NO: 261	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 261		
caccaatcac gaacctaagg at		22
SEQ ID NO: 262	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 262		
aaccaccaa tcacgaacct aa		22
SEQ ID NO: 263	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 263		
gatccaaacc caccaatcac		20
SEQ ID NO: 264	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 264		
aggttcgtga ttggtgggtt		20
SEQ ID NO: 265	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 265		
tccttaggtt cgtgattggt		20
SEQ ID NO: 266	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 266		
atccttaggt tcgtgattgg		20
SEQ ID NO: 267	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 267		
ttcatcctta gggtcgtgat		20
SEQ ID NO: 268	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 268		
ccttaggttc gtgattggtg		20
SEQ ID NO: 269	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 269		
tcatccttag gttcgtgatt		20
SEQ ID NO: 270	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 270		
tgctttcatc cttaggttcg		20
SEQ ID NO: 271	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 271		
tttgctttca tccttagggt		20
SEQ ID NO: 272	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 272		
agcctttgct ttcacacctta		20
SEQ ID NO: 273	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 273		
gctttcatcc ttaggttcgt		20
SEQ ID NO: 274	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 274		
taggttcgtg attgggtgggt tt		22
SEQ ID NO: 275	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 275		
tgagcctttg ctttcacct ta		22
SEQ ID NO: 276	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 276		
atccttaggt tcgtgattgg		20
SEQ ID NO: 277	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 277		
gaacctaaagg atgaaagcaa		20
SEQ ID NO: 278	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 278		
accaccaat cacgaacctta		20
SEQ ID NO: 279	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 279		
aacctaaagga tgaagcaaaa		20
SEQ ID NO: 280	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 280		
atcacgaacc taaggatgaa		20
SEQ ID NO: 281	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 281		
accaatcacg aacctaaagga		20
SEQ ID NO: 282	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 282		
cccaccaatc acgaacctaa		20
SEQ ID NO: 283	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 283		
cgaacctaaag gatgaaagca		20
SEQ ID NO: 284	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 284		
acgaacctaa ggatgaaagc		20
SEQ ID NO: 285	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 285		
cacgaacctaa aggatgaaag		20
SEQ ID NO: 286	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 286		
aatcacgaac ctaaggatga		20
SEQ ID NO: 287	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 287		
caatcacgaa cctaaggatg		20
SEQ ID NO: 288	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 288		
ccaccaatca cgaacctaaag		20
SEQ ID NO: 289	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 289		
aaccaccaa tcacgaacct		20
SEQ ID NO: 290	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 290		
aaaccaccca atcacgaacc		20
SEQ ID NO: 291	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 291		
cacgaacctt aggatgaaag ca		22
SEQ ID NO: 292	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 292		
accaatcacg aacctaagga tg		22
SEQ ID NO: 293	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 293		
acctaaggat gaaagcaaag gc		22
SEQ ID NO: 294	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 294		
cgaaccttaag gatgaaagca aa		22
SEQ ID NO: 295	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 295		
gaaccttaagg atgaaagcaa ag		22
SEQ ID NO: 296	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 296		
caaaccacc aatcacgaac ct		22
SEQ ID NO: 297	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 297		
aaccaccaa tcacgaacct aa		22
SEQ ID NO: 298	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 298		
caccaatcac gaacctaagg at		22
SEQ ID NO: 299	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 299		
ttcacacctta ggctcgtgat		20
SEQ ID NO: 300	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 300		
gagcctttgc tttcacctt		20
SEQ ID NO: 301	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 301		
tgctttcatc cttagggttcg		20
SEQ ID NO: 302	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 302		
tttgctttca tccttaggtt		20
SEQ ID NO: 303	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 303		
agcctttgct ttcacacctta		20
SEQ ID NO: 304	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 304		
gctttcatcc ttaggttcgt		20
SEQ ID NO: 305	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 305		
tgagcctttg ctttcacctt		20
SEQ ID NO: 306	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 306		
tgagcctttg ctttcacctt ta		22
SEQ ID NO: 307	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 307		
gagcctttgc tttcacctt ag		22
SEQ ID NO: 308	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 308		
ctttcatcct taggttcgtg		20
SEQ ID NO: 309	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 309		
gaacctaaagg atgaaagcaa		20
SEQ ID NO: 310	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 310		
gatgaaagca aaggctcagc		20
SEQ ID NO: 311	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 311		
aaggatgaaa gcaaaggctc		20
SEQ ID NO: 312	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 312		
aacctaagga tgaaagcaaa		20
SEQ ID NO: 313	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 313		
atcacgaacc taaggatgaa		20
SEQ ID NO: 314	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 314		
accaatcacg aacctaagga		20
SEQ ID NO: 315	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 315		
ggatgaaagc aaaggctcag		20
SEQ ID NO: 316	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 316		
taaggatgaa agcaaaggct		20
SEQ ID NO: 317	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 317		
cgaacctaa gatgaaagca		20
SEQ ID NO: 318	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 318		
acgaacctaa ggatgaaagc		20
SEQ ID NO: 319	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 319		
aatcacgaac ctaaggatga		20
SEQ ID NO: 320	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 320		
caatcacgaa cctaaggatg		20
SEQ ID NO: 321	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 321		
ccaatcacga acctaaggat		20
SEQ ID NO: 322	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 322		
cacgaaccta aggatgaaag ca		22
SEQ ID NO: 323	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 323		
accaatcacg aacctaagga tg		22
SEQ ID NO: 324	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 324		
atgaaagcaa aggctcagca gt		22
SEQ ID NO: 325	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 325		
gatgaaagca aaggctcagc ag		22
SEQ ID NO: 326	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 326		
acctaaggat gaaagcaaag gc		22
SEQ ID NO: 327	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 327		
cgaacctaag gatgaaagca aa		22
SEQ ID NO: 328	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 328		
gaacctaagg atgaaagcaa ag		22
SEQ ID NO: 329	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 329		
ccaccaatca cgaacctaag ga		22
SEQ ID NO: 330	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 330		
caccaatcac gaacctaagg at		22
SEQ ID NO: 331	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 331		
taaggtccca ggtcaactgc		20
SEQ ID NO: 332	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 332		
caggtcaact gctgagcctt		20
SEQ ID NO: 333	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 333		
aggtcccagg tcaactgctg		20
SEQ ID NO: 334	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 334		
tgtaaggtc ccaggtcaac		20
SEQ ID NO: 335	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 335		
acatttctgt taaggtccca		20
SEQ ID NO: 336	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 336		
aaggtcccag gtcaactgct		20
SEQ ID NO: 337	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 337		
ttctgttaag gtcccaggtc		20
SEQ ID NO: 338	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 338		
tttctgttaa ggtcccaggt ca		22
SEQ ID NO: 339	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 339		
caggtcaact gctgagcctt tg		22
SEQ ID NO: 340	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 340		
gtcccaggtc aactgctgag cc		22
SEQ ID NO: 341	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 341		
ttaaggtccc aggtcaactg ct		22
SEQ ID NO: 342	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 342		
gttaaggtcc caggtcaact gc		22
SEQ ID NO: 343	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 343		
tttctgttaa ggtcccaggt ca		22
SEQ ID NO: 344	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 344		
acatttctgt taaggtccca gg		22
SEQ ID NO: 345	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 345		
tgtaaggtc ccaggtcaac		20
SEQ ID NO: 346	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 346		
gtctttaaca cactcgatat		20
SEQ ID NO: 347	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 347		
ctcgatatcg gtcacatttc		20
SEQ ID NO: 348	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 348		
aacacactcg atatcgggtca		20
SEQ ID NO: 349	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 349		
ttaacacact cgatatcggt		20
SEQ ID NO: 350	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 350		
ggcgtcttta acacactcga		20
SEQ ID NO: 351	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 351		
tcggcgtctt taacacactc		20
SEQ ID NO: 352	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 352		
gcgtctttaa cacactcgat at		22
SEQ ID NO: 353	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 353		
taacacactc gatatcggtc ac		22
SEQ ID NO: 354	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 354		
gtctttaaca cactcgatat cg		22
SEQ ID NO: 355	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	

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SEQUENCE: 355		
gtcggcgtct ttaacacact cg		22
SEQ ID NO: 356	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 356		
acacactcga tatcggtcac at		22
SEQ ID NO: 357	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 357		
acacactcga tatcggtcac at		22
SEQ ID NO: 358	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 358		
acacactcga tatcggtcac		20
SEQ ID NO: 359	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 359		
atcgagtgtg ttaaagacgc		20
SEQ ID NO: 360	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 360		
gatatcgagt gtgttaaaga		20
SEQ ID NO: 361	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 361		
accgatatcg agtgtgttaa		20
SEQ ID NO: 362	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 362		
aatgtgaccg atacgagtg		20
SEQ ID NO: 363	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 363		
gaaatgtgac cgatatcgag		20
SEQ ID NO: 364	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 364		
agtgtgttaa agacgccgac		20
SEQ ID NO: 365	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 365		
tcgagtgtgt taaagacgcc		20
SEQ ID NO: 366	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 366		
cggatatacga gtgtgttaaa		20
SEQ ID NO: 367	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 367		
gaccgatatac gagtgtgtta		20
SEQ ID NO: 368	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 368		
tgaccgatatac cgagtgtgtt		20
SEQ ID NO: 369	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 369		
gaccgatatac gagtgtgtta aa		22
SEQ ID NO: 370	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 370		
cgagtgtgtt aaagacgccg ac		22
SEQ ID NO: 371	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 371		
gatatacagat gtgttaaaga cg		22
SEQ ID NO: 372	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 372		
accgatatac agtgtgttaa ag		22
SEQ ID NO: 373	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 373		
gtgaccgata tcgagtgtgt ta		22
SEQ ID NO: 374	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	

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SEQUENCE: 374		
cgatcgcgag tgtgttaaag ac		22
SEQ ID NO: 375	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 375		
aaatgtgacc gatcgcgagt gt		22
SEQ ID NO: 376	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 376		
acagaaatgt gaccgatc ga		22
SEQ ID NO: 377	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 377		
gtctttaaca cactcgatat		20
SEQ ID NO: 378	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 378		
tctttaacac actcgatatc		20
SEQ ID NO: 379	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 379		
gtcgcgctct ttaacacact		20
SEQ ID NO: 380	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 380		
aacacactcg atatcgggtca		20
SEQ ID NO: 381	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 381		
ttaacacact cgatcgggt		20
SEQ ID NO: 382	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 382		
ggcgtcttta acacactcga		20
SEQ ID NO: 383	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 383		
tcggcgtctt taacacactc		20
SEQ ID NO: 384	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 384		
gcgtctttaa cacactcgat at		22
SEQ ID NO: 385	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 385		
taacacactc gatatcggtc ac		22
SEQ ID NO: 386	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 386		
gtctttaaca cactcgat at cg		22
SEQ ID NO: 387	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 387		
gtcggcgtct ttaacacact cg		22
SEQ ID NO: 388	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 388		
acacactcga tatecggtcac at		22
SEQ ID NO: 389	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 389		
cggcgtcttt aacacactcg at		22
SEQ ID NO: 390	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 390		
gaatagtcgg cgtctttaac ac		22
SEQ ID NO: 391	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 391		
acacactcga tatecggtcac		20
SEQ ID NO: 392	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 392		
atttaccggc atagaatagt		20
SEQ ID NO: 393	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	

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SEQUENCE: 393 gacgccgact attctatgcc		20
SEQ ID NO: 394 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 394 taaagacgcc gactattcta		20
SEQ ID NO: 395 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 395 tattctatgc cggtaaatca		20
SEQ ID NO: 396 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 396 actattctat gccggtaaat		20
SEQ ID NO: 397 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 397 ccgactattc tatgccggta		20
SEQ ID NO: 398 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 398 gccgactatt ctatgccgggt		20
SEQ ID NO: 399 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 399 acgccgacta ttctatgccg gt		22
SEQ ID NO: 400 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 400 tattctatgc cggtaaatca ta		22
SEQ ID NO: 401 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 401 actattctat gccggtaaat ca		22
SEQ ID NO: 402 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 402 cgactattct atgccggtaa at		22
SEQ ID NO: 403	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 403		
tgtaaagac gccgactatt ct		22
SEQ ID NO: 404	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 404		
agacgccgac tattctatgc cg		22
SEQ ID NO: 405	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 405		
ttaaagacgc cgactattct at		22
SEQ ID NO: 406	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 406		
gttaaagacg ccgactattc ta		22
SEQ ID NO: 407	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 407		
atttaccggc atagaatagt		20
SEQ ID NO: 408	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 408		
tttaccggca tagaatagtc		20
SEQ ID NO: 409	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 409		
atgatttacc ggcatagaat		20
SEQ ID NO: 410	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 410		
aatagtcggc gtctttaaca		20
SEQ ID NO: 411	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 411		
agaatagtcg gcgtctttaa		20
SEQ ID NO: 412	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 412			
atagaatagt cggcgtcttt			20
SEQ ID NO: 413	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 413			
cgcatagaa tagtcggcgt ct			22
SEQ ID NO: 414	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 414			
agaatagtcg gcgtctttaa ca			22
SEQ ID NO: 415	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 415			
atagaatagt cggcgtcttt aa			22
SEQ ID NO: 416	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 416			
gcatagaata gtcggcgtct tt			22
SEQ ID NO: 417	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 417			
eggcatagaa tagtcggcgt ct			22
SEQ ID NO: 418	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 418			
attaccggc atagaatagt cg			22
SEQ ID NO: 419	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 419			
accggcatag aatagtcggc gt			22
SEQ ID NO: 420	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 420			
gaatagtcgg cgtctttaa ac			22
SEQ ID NO: 421	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 421			
ggccactcgg acggtgtagt			20
SEQ ID NO: 422	moltype = RNA	length = 20	

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FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 422		
tggtgggttg gccactcgga		20
SEQ ID NO: 423	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 423		
gttgccact cggacgggtg		20
SEQ ID NO: 424	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 424		
tgggttgcc actcggacgg		20
SEQ ID NO: 425	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 425		
ggtgggttg cactcggac		20
SEQ ID NO: 426	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 426		
gaatggtggg ttggccactc		20
SEQ ID NO: 427	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 427		
gccactcgga cggtagtagt		20
SEQ ID NO: 428	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 428		
actcggacgg ttagttggt		20
SEQ ID NO: 429	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 429		
aatggtgggt tggccactcg		20
SEQ ID NO: 430	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 430		
ctcggacgg ttagttggtc ac		22
SEQ ID NO: 431	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	

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SEQUENCE: 431
cactcggacg gtgtagttgg tc 22

SEQ ID NO: 432 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 432
ggccactcgg acggtgtagt tg 22

SEQ ID NO: 433 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 433
ttggccactc ggacgggtga gt 22

SEQ ID NO: 434 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 434
tcggacggtg tagttggtca ct 22

SEQ ID NO: 435 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 435
ggttgccac tcggacggtg ta 22

SEQ ID NO: 436 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 436
ccaaccacc attctccacg 20

SEQ ID NO: 437 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 437
caaccaccca ttctccacgt 20

SEQ ID NO: 438 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 438
ggccaacca ccattctcca 20

SEQ ID NO: 439 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 439
aaccacccat tctccacgtg 20

SEQ ID NO: 440 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 440
gtggccaacc caccattctc 20

SEQ ID NO: 441 moltype = RNA length = 20

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 441		
cgtccgagtg gccaacccac		20
SEQ ID NO: 442	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 442		
caccgtccga gtggccaacc		20
SEQ ID NO: 443	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 443		
ccaccattct ccacgtggat cc		22
SEQ ID NO: 444	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 444		
aaccacccat tctccacgtg ga		22
SEQ ID NO: 445	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 445		
ccaaccacc atttccacg tg		22
SEQ ID NO: 446	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 446		
gccaaccac catttccac gt		22
SEQ ID NO: 447	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 447		
ccgagtgcc aaccacccat tc		22
SEQ ID NO: 448	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 448		
gtccgagtg ccaaccacc at		22
SEQ ID NO: 449	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 449		
gtccgagtg ccaaccacc at		22
SEQ ID NO: 450	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 450		
gtccgagtgg ccaacccacc at		22
SEQ ID NO: 451	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 451		
ccacgtggag aatggtgggt		20
SEQ ID NO: 452	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 452		
agaatggtgg gttggccact		20
SEQ ID NO: 453	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 453		
ggatccacgt ggagaatggt		20
SEQ ID NO: 454	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 454		
aagaggatcc acgtggagaa		20
SEQ ID NO: 455	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 455		
gaatggtggg ttggccactc		20
SEQ ID NO: 456	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 456		
cacgtggaga atggtggggt		20
SEQ ID NO: 457	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 457		
gatccacgtg gagaatggtg		20
SEQ ID NO: 458	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 458		
agaggatcca cgtggagaat		20
SEQ ID NO: 459	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 459		
aatggtgggt tggccactcg		20
SEQ ID NO: 460	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 460		
gtggagaatg gtgggttggc		20
SEQ ID NO: 461	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 461		
acgtggagaa tgggtgggtg gc		22
SEQ ID NO: 462	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 462		
ggagaatggt gggttggcca ct		22
SEQ ID NO: 463	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 463		
ccacgtggag aatggtgggt tg		22
SEQ ID NO: 464	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 464		
atccacgtgg agaatgggtg gt		22
SEQ ID NO: 465	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 465		
gatccacgtg gagaatgggtg gg		22
SEQ ID NO: 466	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 466		
ggatccacgt ggagaatggt gg		22
SEQ ID NO: 467	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 467		
ccacgtggag aatggtgggt		20
SEQ ID NO: 468	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 468		
ggatccacgt ggagaatggt		20
SEQ ID NO: 469	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 469			
aagaggatcc acgtggagaa			20
SEQ ID NO: 470	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 470			
aggatccaacg tggagaatgg			20
SEQ ID NO: 471	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 471			
cacgtggaga atggtggggt			20
SEQ ID NO: 472	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 472			
gatccaacgtg gagaatgggt			20
SEQ ID NO: 473	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 473			
agaggatcca cgtggagaat			20
SEQ ID NO: 474	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 474			
gtggagaatg gtgggtgggc			20
SEQ ID NO: 475	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 475			
gggaagagga tccacgtgga			20
SEQ ID NO: 476	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 476			
acgtggagaa tgggtgggtg gc			22
SEQ ID NO: 477	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 477			
ggagaatggt gggttggcca ct			22
SEQ ID NO: 478	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 478			
ccacgtggag aatggtgggt tg			22
SEQ ID NO: 479	moltype = RNA	length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 479		
atccacgtgg agaatggtgg gt		22
SEQ ID NO: 480	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 480		
gatccacgtg gagaatggtg gg		22
SEQ ID NO: 481	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 481		
ggatccacgt ggagaatggt gg		22
SEQ ID NO: 482	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 482		
ccaaccacc attctccacg		20
SEQ ID NO: 483	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 483		
tccacgtgga tcctcttccc		20
SEQ ID NO: 484	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 484		
ccacgtggat cctcttccct		20
SEQ ID NO: 485	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 485		
aaccacccat tctccacgtg		20
SEQ ID NO: 486	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 486		
gtggccaacc caccattctc		20
SEQ ID NO: 487	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 487		
accattctcc acgtggatcc tc		22
SEQ ID NO: 488	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 488
tccacgtgga tcctcttccc tg 22

SEQ ID NO: 489 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 489
accattctcc acgtgatcc tc 22

SEQ ID NO: 490 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 490
caccattctc cacgtggatc ct 22

SEQ ID NO: 491 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 491
ccaccattct ccacgtggat cc 22

SEQ ID NO: 492 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 492
aaccacccat tctccacgtg ga 22

SEQ ID NO: 493 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 493
ccaaccacc attctccacg tg 22

SEQ ID NO: 494 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 494
gccaaaccac cattctccac gt 22

SEQ ID NO: 495 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 495
tctccacgtg gatcctcttc cc 22

SEQ ID NO: 496 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 496
attctccacg tggatcctct tc 22

SEQ ID NO: 497 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 497
cattctccac gtggatcctc tt 22

SEQ ID NO: 498 moltype = RNA length = 20

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 498		
ccacgtggag aatggtgggt		20
SEQ ID NO: 499	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 499		
ggatccacgt ggagaatggt		20
SEQ ID NO: 500	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 500		
aagaggatcc acgtggagaa		20
SEQ ID NO: 501	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 501		
ctcaggaag aggatccacg		20
SEQ ID NO: 502	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 502		
cacgtggaga atggtgggtt		20
SEQ ID NO: 503	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 503		
gatccacgtg gagaatggtg		20
SEQ ID NO: 504	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 504		
agaggatcca cgtggagaat		20
SEQ ID NO: 505	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 505		
tcaggaaga ggatccacgt		20
SEQ ID NO: 506	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 506		
ttctcagga agaggatcca		20
SEQ ID NO: 507	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 507			
ggaagaggat ccacgtggag			20
SEQ ID NO: 508	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 508			
gggaagagga tccacgtgga			20
SEQ ID NO: 509	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 509			
caggaagag gatccacgtg			20
SEQ ID NO: 510	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 510			
acgtggagaa tgggtgggtg gc			22
SEQ ID NO: 511	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 511			
ccacgtggag aatggtgggt tg			22
SEQ ID NO: 512	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 512			
atccacgtgg agaatggtgg gt			22
SEQ ID NO: 513	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 513			
gatccacgtg gagaatggtg gg			22
SEQ ID NO: 514	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 514			
gttctcaggg aagaggatcc ac			22
SEQ ID NO: 515	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 515			
ggatccacgt ggagaatggt gg			22
SEQ ID NO: 516	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 516			
tgttctcagg gaagaggatc ca			22
SEQ ID NO: 517	moltype = RNA	length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 517		
ccacgtggag aatggtgggt		20
SEQ ID NO: 518	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 518		
tgtgaagtga ccaactacac		20
SEQ ID NO: 519	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 519		
gaccaactac accgtccgag		20
SEQ ID NO: 520	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 520		
aagtgaccaa ctacaccgtc		20
SEQ ID NO: 521	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 521		
gtgaccaact acaccgtccg		20
SEQ ID NO: 522	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 522		
agaatggtgg gttggccact		20
SEQ ID NO: 523	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 523		
aagaggatcc acgtggagaa		20
SEQ ID NO: 524	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 524		
ccaaccacc attctccacg		20
SEQ ID NO: 525	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 525		
catttttctc actgtttctca		20
SEQ ID NO: 526	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 526		
aaagaaaaa gacacagcga		20
SEQ ID NO: 527	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 527		
aggatccaag tggagaatgg		20
SEQ ID NO: 528	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 528		
ggatccacgt ggagaatggt		20
SEQ ID NO: 529	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 529		
tgaagtgacc aactacacgc tc		22
SEQ ID NO: 530	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 530		
ttatgtgaag tgaccaacta ca		22
SEQ ID NO: 531	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 531		
tccacgtgga gaatggtggg tt		22
SEQ ID NO: 532	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 532		
tcaggaaga ggatccacgt		20
SEQ ID NO: 533	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 533		
ctcactgttc tcaggaaga		20
SEQ ID NO: 534	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 534		
attaccggc atagaatagt		20
SEQ ID NO: 535	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 535		
cttaacagaa atgtgaccga		20
SEQ ID NO: 536	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 536		
cagaaatgtg accgatatcg		20
SEQ ID NO: 537	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 537		
gtcggcgtct ttaacacact		20
SEQ ID NO: 538	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 538		
gaaatgtgac cgatatcgag		20
SEQ ID NO: 539	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 539		
caatagagag tatgatttac		20
SEQ ID NO: 540	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 540		
agagtatgat ttaccggcat		20
SEQ ID NO: 541	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 541		
atgatttacc ggcatagaat		20
SEQ ID NO: 542	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 542		
aacaccggca aatacacgtg		20
SEQ ID NO: 543	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 543		
ccaacaccgg caaatacacg		20
SEQ ID NO: 544	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 544		
caccaacacc ggcaaataca		20
SEQ ID NO: 545	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	

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SEQUENCE: 545			
gccaccaaca cggcaata			20
SEQ ID NO: 546	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 546			
aagccaccaa caccggcaaa			20
SEQ ID NO: 547	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 547			
aacaccggca aatacacgtg ca			22
SEQ ID NO: 548	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 548			
caccaacacc ggcaataca cg			22
SEQ ID NO: 549	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 549			
accaacaccg gcaatacac gt			22
SEQ ID NO: 550	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 550			
gccaccaaca cggcaata ca			22
SEQ ID NO: 551	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 551			
gcagaagcca ccaacaccgg ca			22
SEQ ID NO: 552	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 552			
ccaacaccgg caatacacg tg			22
SEQ ID NO: 553	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 553			
caacaccggc aaatacacgt gc			22
SEQ ID NO: 554	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 554			
caccggcaaa tacacgtgca cc			22
SEQ ID NO: 555	moltype = RNA	length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 555		
ccggcaaata cacgtgcacc		20
SEQ ID NO: 556	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 556		
accggcaaat acacgtgcac		20
SEQ ID NO: 557	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 557		
ggcaataaca cgtgcaccaa		20
SEQ ID NO: 558	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 558		
gcaaatacac gtgcaccaac		20
SEQ ID NO: 559	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 559		
caaatacacg tgcaccaaca		20
SEQ ID NO: 560	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 560		
ccggcaaata cacgtgcacc aa		22
SEQ ID NO: 561	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 561		
ggcaaataca cgtgcaccaa ca		22
SEQ ID NO: 562	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 562		
tacacgtgca ccaacaaaaca		20
SEQ ID NO: 563	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 563		
aatacacgtg caccaaaaa		20
SEQ ID NO: 564	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 564		
acacgtgcac caacaaacac		20
SEQ ID NO: 565	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 565		
aaatacacgt gcaccaacaa ac		22
SEQ ID NO: 566	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 566		
acacgtgcac caacaaacac gg		22
SEQ ID NO: 567	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 567		
attccattta tgtgtttgtt		20
SEQ ID NO: 568	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 568		
aattccattt atgtgtttgt		20
SEQ ID NO: 569	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 569		
agcaattcca tttatgtgtt		20
SEQ ID NO: 570	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 570		
cttaagcaat tccatttatg		20
SEQ ID NO: 571	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 571		
ggcttaagca attccattta		20
SEQ ID NO: 572	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 572		
ataaatggaa ttgcttaagc		20
SEQ ID NO: 573	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 573		
aatggaatt gcttaagccg		20
SEQ ID NO: 574	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 574		
ggaattgctt aagccgtgtt		20
SEQ ID NO: 575	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 575		
acacataaat ggaattgctt		20
SEQ ID NO: 576	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 576		
aacacataaa tgggaattgct		20
SEQ ID NO: 577	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 577		
cacataaatg gaattgctta		20
SEQ ID NO: 578	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 578		
caaacacata aatggaattg ct		22
SEQ ID NO: 579	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 579		
aaacacataa atggaattgc tt		22
SEQ ID NO: 580	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 580		
caaacacata aatggaattg ct		22
SEQ ID NO: 581	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 581		
caattccatt tatgtgtttg tt		22
SEQ ID NO: 582	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 582		
gcaattccat ttatgtgttt gt		22
SEQ ID NO: 583	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 583		
gcttaagcaa ttccatttat gt		22
SEQ ID NO: 584	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 584		
ttatgtgttt gtttagagga		20
SEQ ID NO: 585	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 585		
tttatgtggt tgtttagaggt		20
SEQ ID NO: 586	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 586		
atztatgtgt ttgttagagg		20
SEQ ID NO: 587	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 587		
ccatttatgt gtttgtaga		20
SEQ ID NO: 588	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 588		
tccatttatg tgtttgtag		20
SEQ ID NO: 589	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 589		
ttccatttat gtgtttgtag		20
SEQ ID NO: 590	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 590		
tctaacaac acataaatgg		20
SEQ ID NO: 591	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 591		
ctctaacaaa cacataaatg		20
SEQ ID NO: 592	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 592		
acctctaaca aacacataaa		20
SEQ ID NO: 593	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 593		
ctctaacaaa cacataaatg ga		22
SEQ ID NO: 594	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 594		
atztatgtgt ttgttagagg ta		22
SEQ ID NO: 595	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 595		
gcaattccat ttatgtgttt gt		22
SEQ ID NO: 596	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 596		
ctcacagacc cagaagtgac		20
SEQ ID NO: 597	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 597		
cctctcacag acccagaagt		20
SEQ ID NO: 598	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 598		
tcacagacc agaagtgacc		20
SEQ ID NO: 599	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 599		
tcctctcaca gaccagaag		20
SEQ ID NO: 600	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 600		
tgtctctca cagaccaga		20
SEQ ID NO: 601	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 601		
ctgtctctc acagaccag		20
SEQ ID NO: 602	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 602 gctgtcctct cacagaccca		20
SEQ ID NO: 603 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 603 cgctgtcctc tcacagaccc		20
SEQ ID NO: 604 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 604 ccgctgtcct ctcacagacc		20
SEQ ID NO: 605 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 605 ctgtcctctc acagaccag aa		22
SEQ ID NO: 606 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 606 cacagaccca gaagtgacca at		22
SEQ ID NO: 607 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 607 tgtcctctca cagaccaga ag		22
SEQ ID NO: 608 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 608 tcctctcaca gaccagaag tg		22
SEQ ID NO: 609 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 609 gctgtcctct cacagaccca ga		22
SEQ ID NO: 610 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 610 tccgctgtcc tctcacagac cc		22
SEQ ID NO: 611 FEATURE source	moltype = RNA length = 19 Location/Qualifiers 1..19 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 611 gtgaccaatt attccctca		19
SEQ ID NO: 612	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 612		
gtgaccaatt attccctcaa		20
SEQ ID NO: 613	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 613		
aagtgaccaa ttattcctc		20
SEQ ID NO: 614	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 614		
gtgaccaatt attccctcaa		20
SEQ ID NO: 615	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 615		
tgaccaatta ttcctcaag		20
SEQ ID NO: 616	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 616		
gaccaattat tcctcaagg		20
SEQ ID NO: 617	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 617		
gaagtgacca attattcct		20
SEQ ID NO: 618	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 618		
cagaccaga agtgaccaat ta		22
SEQ ID NO: 619	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 619		
gaccagaag tgaccaatta tt		22
SEQ ID NO: 620	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 620		
acagaccag aagtgaccaa tt		22
SEQ ID NO: 621	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 621		
gtgaccaatt attccctcaa gg		22
SEQ ID NO: 622	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 622		
tgaccaatta ttccctcaag gg		22
SEQ ID NO: 623	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 623		
agtgaccaat tattccctca ag		22
SEQ ID NO: 624	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 624		
ccaggggaag cctcttccca		20
SEQ ID NO: 625	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 625		
caggggaagc ctcttcccaa		20
SEQ ID NO: 626	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 626		
aggggaagcc tcttcccaag		20
SEQ ID NO: 627	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 627		
gaagcctctt cccaaggact		20
SEQ ID NO: 628	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 628		
ccttggaag aggcttcccc		20
SEQ ID NO: 629	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 629		
tgggaagagg cttcccctgg		20
SEQ ID NO: 630	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 630		
aggettcccc tggcaccct		20
SEQ ID NO: 631	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 631		
ggcttcccct ggcaccctt		20
SEQ ID NO: 632	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 632		
tgccagggga agcctcttcc ca		22
SEQ ID NO: 633	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 633		
ggggtgccag ggaagcctc tt		22
SEQ ID NO: 634	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 634		
ttgggaagag gcttcccctg gc		22
SEQ ID NO: 635	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 635		
cttgggaaga ggcttcccct gg		22
SEQ ID NO: 636	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 636		
ccttgggaag aggcttcccc tg		22
SEQ ID NO: 637	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 637		
agtccttggg aagagcttc cc		22
SEQ ID NO: 638	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 638		
aggttcccc tggcaccctt tg		22
SEQ ID NO: 639	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 639		
ggcttcccct ggcaccctt ga		22
SEQ ID NO: 640	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 640		
aagaggcttc ccctggcacc cc		22
SEQ ID NO: 641	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 641		
agaggcttcc cctggcacc ct		22
SEQ ID NO: 642	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 642		
aaatataata gctggcatca		20
SEQ ID NO: 643	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 643		
tataatagct ggcacacgg		20
SEQ ID NO: 644	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 644		
aatataatag ctggcatcac		20
SEQ ID NO: 645	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 645		
ataatagctg gcatcacggt		20
SEQ ID NO: 646	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 646		
agaaatataa tagctggcat		20
SEQ ID NO: 647	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 647		
aggagaaata taatagctgg		20
SEQ ID NO: 648	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 648		
gccagctatt atatttctcc		20
SEQ ID NO: 649	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 649		
caccgtgatg ccagctatta		20
SEQ ID NO: 650	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 650		
cagctattat atttctcctg		20
SEQ ID NO: 651	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 651		
agctattata tttctcctgt		20
SEQ ID NO: 652	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 652		
tataatagct ggcatcacgg tg		22
SEQ ID NO: 653	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 653		
aatataata gctggcatca cg		22
SEQ ID NO: 654	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 654		
caggagaaat ataatagctg gc		22
SEQ ID NO: 655	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 655		
tacaggagaa atataatagc tg		22
SEQ ID NO: 656	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 656		
taatagctgg catcacggtg ac		22
SEQ ID NO: 657	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 657		
tagctggcat cacggtgact tc		22
SEQ ID NO: 658	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 658		
ggagaaatat aatagctggc at		22
SEQ ID NO: 659	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 659		
ccgtgatgcc agctattata tt		22
SEQ ID NO: 660	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 660		
accgtgatgc cagctattat at		22
SEQ ID NO: 661	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 661		
tcaccgtgat gccagctatt at		22
SEQ ID NO: 662	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 662		
agctggcatc acggtgactt		20
SEQ ID NO: 663	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 663		
gctggcatca cggtgacttc		20
SEQ ID NO: 664	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 664		
ggcatcacgg tgacttcaat		20
SEQ ID NO: 665	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 665		
ggcatcacgg tgacttcaat ta		22
SEQ ID NO: 666	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 666		
gcatcacggt gacttcaatt at		22
SEQ ID NO: 667	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 667		
tgacttcaat tatgaacgtc		20
SEQ ID NO: 668	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 668		
ttatgaacgt caggcaacgt		20
SEQ ID NO: 669	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 669		
caattatgaa cgtcaggcaa		20
SEQ ID NO: 670	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 670		
gacttcaatt atgaacgtca		20
SEQ ID NO: 671	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 671		
acggtgactt caattatgaa		20
SEQ ID NO: 672	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 672		
cataattgaa gtcaccgtga		20
SEQ ID NO: 673	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 673		
gttcataatt gaagtcaccg		20
SEQ ID NO: 674	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 674		
acgttcataa ttgaagtcac		20
SEQ ID NO: 675	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 675		
tgcctgacgt tcataattga		20
SEQ ID NO: 676	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 676		
cgttgcctga cgttcataat		20
SEQ ID NO: 677	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 677		
ttcaattatg aacgtcaggc		20
SEQ ID NO: 678	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 678 cttcaattat gaacgtcagg		20
SEQ ID NO: 679 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 679 gtgacttcaa ttatgaacgt		20
SEQ ID NO: 680 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 680 tcacggtgac ttcaattatg		20
SEQ ID NO: 681 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 681 ttcataattg aagtcaccgt		20
SEQ ID NO: 682 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 682 ctgacgttca taattgaagt		20
SEQ ID NO: 683 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 683 ttgcctgacg ttcataattg		20
SEQ ID NO: 684 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 684 gttgctgac gttcataatt		20
SEQ ID NO: 685 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 685 caattatgaa cgtcaggcaa cg		22
SEQ ID NO: 686 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 686 tatgaacgtc aggcaacggt ga		22
SEQ ID NO: 687 FEATURE source	moltype = RNA length = 22 Location/Qualifiers 1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 687 tgacttcaat tatgaacgtc ag		22
SEQ ID NO: 688	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 688		
cggtgacttc aattatgaac gt		22
SEQ ID NO: 689	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 689		
gttcataatt gaagtcaccg tg		22
SEQ ID NO: 690	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 690		
cataattgaa gtcaccgtga tg		22
SEQ ID NO: 691	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 691		
cgttcataat tgaagtcacc gt		22
SEQ ID NO: 692	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 692		
tgcctgacgt tcataattga ag		22
SEQ ID NO: 693	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 693		
ttgcctgacg ttcataattg aa		22
SEQ ID NO: 694	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 694		
cgttgcctga cgttcataat tg		22
SEQ ID NO: 695	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 695		
tcaattatga acgtcaggca ac		22
SEQ ID NO: 696	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 696		
attatgaacg tcaggcaacg tt		22
SEQ ID NO: 697	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 697
acggtgactt caattatgaa cg 22

SEQ ID NO: 698 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 698
cacggtgact tcaattatga ac 22

SEQ ID NO: 699 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 699
tcataattga agtcaccgtg at 22

SEQ ID NO: 700 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 700
acggtcataa ttgaagtcac cg 22

SEQ ID NO: 701 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 701
gcctgacgtt cataattgaa gt 22

SEQ ID NO: 702 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 702
ggatcagcaa atgtcacaac 20

SEQ ID NO: 703 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 703
tggatcagca aatgtcaca 20

SEQ ID NO: 704 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 704
tttggatcag caaatgtcac 20

SEQ ID NO: 705 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 705
ttttggatca gcaaatgtca 20

SEQ ID NO: 706 moltype = RNA length = 20
FEATURE Location/Qualifiers
source 1..20
 mol_type = other RNA
 organism = synthetic construct

SEQUENCE: 706
acttttggat cagcaaatgt 20

SEQ ID NO: 707 moltype = RNA length = 20

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 707		
aatacttttg gatcagcaaa		20
SEQ ID NO: 708	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 708		
ataaactttt tggatcagca		20
SEQ ID NO: 709	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 709		
aataaacttt ttggatcagc		20
SEQ ID NO: 710	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 710		
caataaact tttggatcag		20
SEQ ID NO: 711	moltype = RNA length = 19	
FEATURE	Location/Qualifiers	
source	1..19	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 711		
gctgatccaa aagtattat		19
SEQ ID NO: 712	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 712		
tgatccaaaa gtattattgg		20
SEQ ID NO: 713	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 713		
gctgatccaa aagtattatt		20
SEQ ID NO: 714	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 714		
atttgctgat ccaaaagtat		20
SEQ ID NO: 715	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 715		
gacatttgct gatccaaaag		20
SEQ ID NO: 716	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 716		
gtgacatttg ctgatccaaa		20
SEQ ID NO: 717	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 717		
tgtgacattt gctgatccaa		20
SEQ ID NO: 718	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 718		
ttgtgacatt tgctgatcca		20
SEQ ID NO: 719	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 719		
gttgtgacat ttgctgatcc		20
SEQ ID NO: 720	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 720		
tgttgtgaca ttgctgatcc		20
SEQ ID NO: 721	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 721		
at ttgctgat ccaaaagtat ta		22
SEQ ID NO: 722	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 722		
ctgatccaaa agtattattg gc		22
SEQ ID NO: 723	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 723		
aataatactt ttggatcagc aa		22
SEQ ID NO: 724	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 724		
ttttggatca gcaaatgtca ca		22
SEQ ID NO: 725	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 725		
tttggatcag caaatgtcac aa		22
SEQ ID NO: 726	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 726		
tacttttga tcagcaaatg tc		22
SEQ ID NO: 727	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 727		
taatactttt ggatcagcaa at		22
SEQ ID NO: 728	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 728		
ctgatccaaa agtattattg gc		22
SEQ ID NO: 729	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 729		
gatccaaaag tattattggc at		22
SEQ ID NO: 730	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 730		
tcagcaaatg tcacaacaac ct		22
SEQ ID NO: 731	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 731		
atacttttgg atcagcaaat gt		22
SEQ ID NO: 732	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 732		
aatacttttg gatcagcaaa tg		22
SEQ ID NO: 733	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 733		
ataatactttt tggatcagca aa		22
SEQ ID NO: 734	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 734		
tttgctgac caaaagtatt at		22
SEQ ID NO: 735	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 735		
tgctgatcca aaagtattat tg		22
SEQ ID NO: 736	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 736		
gttgtgacat ttgctgatcc aa		22
SEQ ID NO: 737	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 737		
acatttgctg atccaaaagt at		22
SEQ ID NO: 738	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 738		
ggatcagcaa atgtcacaac aa		22
SEQ ID NO: 739	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 739		
agcaaatgtc acaacaacct		20
SEQ ID NO: 740	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 740		
gtcacaacaa ccttgaagt		20
SEQ ID NO: 741	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 741		
cacaacaacc ttggaagtag		20
SEQ ID NO: 742	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 742		
tgtcacaaca accttgaag		20
SEQ ID NO: 743	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 743		
aatgtcaca caaccttga		20
SEQ ID NO: 744	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 744		
aaatgtcaca acaaccttgg		20
SEQ ID NO: 745	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 745		
caaatgtcac aacaaccttg		20
SEQ ID NO: 746	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 746		
gcaaatgtca caacaacctt		20
SEQ ID NO: 747	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 747		
ggatcagcaa atgtcacaac		20
SEQ ID NO: 748	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 748		
cacaacaacc ttggaagtag ta		22
SEQ ID NO: 749	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 749		
gcaaatgtca caacaacctt gg		22
SEQ ID NO: 750	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 750		
tgtcacaaca accttggag ta		22
SEQ ID NO: 751	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 751		
atgtcacaac aaccttggaa gt		22
SEQ ID NO: 752	moltype = RNA length = 19	
FEATURE	Location/Qualifiers	
source	1..19 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 752		
caacaacctt ggaagtagt		19
SEQ ID NO: 753	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 753		
caacaacctt ggaagtagta		20
SEQ ID NO: 754	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other RNA organism = synthetic construct	

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SEQUENCE: 754			
acaaccttgg aagtagtagg			20
SEQ ID NO: 755	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 755			
caaccttgga agtagtaggt			20
SEQ ID NO: 756	moltype = RNA	length = 20	
FEATURE	Location/Qualifiers		
source	1..20		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 756			
aaccttgga gtagtaggta			20
SEQ ID NO: 757	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 757			
caaccttgga agtagtaggt aa			22
SEQ ID NO: 758	moltype = RNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 758			
acaaccttgg aagtagtagg ta			22
SEQ ID NO: 759	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 759			
ctgatccggg ctttgc aaa tgg			23
SEQ ID NO: 760	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 760			
tacacgtgca ccaacaaa cgg			23
SEQ ID NO: 761	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 761			
caaatggact tttgagatcc tgg			23
SEQ ID NO: 762	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 762			
gaatgaatgg atcacggaaa agg			23
SEQ ID NO: 763	moltype = RNA	length = 23	
FEATURE	Location/Qualifiers		
source	1..23		
	mol_type = other RNA		
	organism = synthetic construct		
SEQUENCE: 763			
aaggcagaag ccaccaacac cgg			23
SEQ ID NO: 764	moltype = RNA	length = 23	

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FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 764		
atgagaataa gcagaatgaa tgg		23
SEQ ID NO: 765	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 765		
taagcagaat gaatggatca cgg		23
SEQ ID NO: 766	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 766		
attgcttaag ccgtgtttgt tgg		23
SEQ ID NO: 767	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 767		
tgtcatccaa aattaagagc agg		23
SEQ ID NO: 768	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 768		
gttggtgac gtgtatttgc cgg		23
SEQ ID NO: 769	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 769		
acctctaaca aacacataaa tgg		23
SEQ ID NO: 770	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 770		
ttggtgacc ctccttgtat ggg		23
SEQ ID NO: 771	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 771		
cttgttgacc gctccttcta tgg		23
SEQ ID NO: 772	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 772		
gaaagaagac aacgacacgc tgg		23
SEQ ID NO: 773	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 773
ttattccctc aaggggtgcc agg 23

SEQ ID NO: 774 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 774
tgaccaatta ttcctcaag ggg 23

SEQ ID NO: 775 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 775
tattccctca aggggtgccca ggg 23

SEQ ID NO: 776 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 776
gtgaccaatt attccctcaa ggg 23

SEQ ID NO: 777 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 777
attccctcaa ggggtgccag ggg 23

SEQ ID NO: 778 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 778
ttgatcatga tgcccgcctt ggg 23

SEQ ID NO: 779 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 779
atgcagacag agccgatggt agg 23

SEQ ID NO: 780 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 780
tgatcatgat gcccgcttg ggg 23

SEQ ID NO: 781 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 781
ttgatcatg atgccgcctt tgg 23

SEQ ID NO: 782 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 782
gcacccttg agggataat tgg 23

SEQ ID NO: 783 moltype = RNA length = 23

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FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 783		
aacaatgcag acagagccga tgg		23
SEQ ID NO: 784	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 784		
gggaataatt ggtcacttct ggg		23
SEQ ID NO: 785	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 785		
aggaataat tggtcacttc tgg		23
SEQ ID NO: 786	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 786		
aggaataaac ctcaagtct tgg		23
SEQ ID NO: 787	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 787		
atgatgcccg ccttggggtc agg		23
SEQ ID NO: 788	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 788		
cttcccctgg cacccttga ggg		23
SEQ ID NO: 789	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 789		
gcttcccctg gcacccttg agg		23
SEQ ID NO: 790	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 790		
aacctcaagt ccttgggaag agg		23
SEQ ID NO: 791	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 791		
ggaataaacc tcaagtcctt ggg		23
SEQ ID NO: 792	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 792
aaaccagcag actaaactac agg 23

SEQ ID NO: 793 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 793
tacaggagaa atataatagc tgg 23

SEQ ID NO: 794 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 794
aaatataata gctggcatca cgg 23

SEQ ID NO: 795 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 795
gattctgaat ataaattata tgg 23

SEQ ID NO: 796 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 796
tgctgatcca aaagtattat tgg 23

SEQ ID NO: 797 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 797
tcagcgagag ttaatgatcc tgg 23

SEQ ID NO: 798 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 798
tgacttcaat tatgaacgtc agg 23

SEQ ID NO: 799 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 799
tgttatgcca ataatacttt tgg 23

SEQ ID NO: 800 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 800
gtatttacct actacttcca agg 23

SEQ ID NO: 801 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 801
taatttaaac attcccatag agg 23

SEQ ID NO: 802 moltype = RNA length = 20

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 802		
taagtgatga tgcctcaaca		20
SEQ ID NO: 803	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 803		
tgatgatgtc caaacatggc		20
SEQ ID NO: 804	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 804		
aacatggcag gagagtaaaa		20
SEQ ID NO: 805	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 805		
atgtttgac atcatcactt		20
SEQ ID NO: 806	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 806		
ttttactctc ctgccatggt		20
SEQ ID NO: 807	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 807		
aggacagctg ttatttccta		20
SEQ ID NO: 808	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 808		
gacagctggt atttcctaag		20
SEQ ID NO: 809	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 809		
agctgttatt tcctaagtga		20
SEQ ID NO: 810	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 810		
tgttatttcc taagtgatga		20
SEQ ID NO: 811	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 811		
tgatgtccaa acatggcagg		20
SEQ ID NO: 812	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 812		
atgtccaac atggcaggag		20
SEQ ID NO: 813	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 813		
ggcaggagag taaaatggcc		20
SEQ ID NO: 814	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 814		
caggagagta aaatggcctg		20
SEQ ID NO: 815	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 815		
ggaaataaca gctgtcctta		20
SEQ ID NO: 816	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 816		
atcacttagg aaataacagc		20
SEQ ID NO: 817	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 817		
atcatcactt aggaaataac		20
SEQ ID NO: 818	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 818		
gccattttac tctcctgcc		20
SEQ ID NO: 819	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 819		
taaggacagc tgttatttcc		20
SEQ ID NO: 820	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 820		
aaggacagct gttatttcc		20
SEQ ID NO: 821	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 821		
acagctgtta ttcctaagt		20
SEQ ID NO: 822	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 822		
gctgtatatt cctaagtgat		20
SEQ ID NO: 823	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 823		
attcctaag tgatgatgtc		20
SEQ ID NO: 824	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 824		
ttcctaagtg atgatgtcca		20
SEQ ID NO: 825	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 825		
cctaagtgat gatgtccaaa		20
SEQ ID NO: 826	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 826		
atgatgtcca aacatggcag		20
SEQ ID NO: 827	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 827		
gatgtccaaa catggcagga		20
SEQ ID NO: 828	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 828		
gtccaaacat ggcaggagag		20
SEQ ID NO: 829	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 829		
tccaaacatg gcaggagagt		20
SEQ ID NO: 830	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 830 caaacatggc aggagagtaa		20
SEQ ID NO: 831 FEATURE source	moltype = RNA length = 19 Location/Qualifiers 1..19 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 831 gctgtcctta tgccaaatc		19
SEQ ID NO: 832 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 832 taacagctgt ccttatgcca		20
SEQ ID NO: 833 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 833 ataacagctg tccttatgcc		20
SEQ ID NO: 834 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 834 aataacagct gtccttatgc		20
SEQ ID NO: 835 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 835 catcatcact taggaaataa		20
SEQ ID NO: 836 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 836 gacatcatca cttaggaaat		20
SEQ ID NO: 837 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 837 ttggacatca tcacttagga		20
SEQ ID NO: 838 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 838 ttggacatc atcacttagg		20
SEQ ID NO: 839 FEATURE source	moltype = RNA length = 20 Location/Qualifiers 1..20 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 839 gtttggacat catcacttag		20
SEQ ID NO: 840	moltype = RNA length = 20	

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FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 840		
ctgccatggtt tggacatcat		20
SEQ ID NO: 841	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 841		
ctcctgcat gtttggacat		20
SEQ ID NO: 842	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 842		
actctcctgc catgtttgga		20
SEQ ID NO: 843	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 843		
ttactctct gccatgtttg		20
SEQ ID NO: 844	moltype = RNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 844		
aggccatttt actctcctgc		20
SEQ ID NO: 845	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 845		
agctgttatt tcctaagtga tg		22
SEQ ID NO: 846	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 846		
agctgttatt tcctaagtga tg		22
SEQ ID NO: 847	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 847		
ttggcataa ggacagctgt ta		22
SEQ ID NO: 848	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 848		
ttaggaaata acagctgtcc tt		22
SEQ ID NO: 849	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 849
cttaggaaat aacagctgtc ct 22

SEQ ID NO: 850 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 850
tcatcactta ggaataaca gc 22

SEQ ID NO: 851 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 851
tctcctgcca tgtttgaca tc 22

SEQ ID NO: 852 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 852
taaggacagc tgttatttcc ta 22

SEQ ID NO: 853 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 853
tgttatttcc taagtgatga tg 22

SEQ ID NO: 854 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 854
cctaagtgat gatgtccaaa ca 22

SEQ ID NO: 855 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 855
gtgatgatgt ccaaacatgg ca 22

SEQ ID NO: 856 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 856
atgatgtcca aacatggcag ga 22

SEQ ID NO: 857 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 857
tgtttgaca tcatcactta gg 22

SEQ ID NO: 858 moltype = RNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 858
cctgccatgt ttggacatca tc 22

SEQ ID NO: 859 moltype = RNA length = 22

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 859		
ttactctct gccatgtttg ga		22
SEQ ID NO: 860	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 860		
atcttactct cctgccatgt tt		22
SEQ ID NO: 861	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 861		
ttatttccta agtgatgatg tc		22
SEQ ID NO: 862	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 862		
tcctaagtga tgatgtccaa ac		22
SEQ ID NO: 863	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 863		
cctaacatgg caggagagta aa		22
SEQ ID NO: 864	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 864		
caaacatggc aggagagtaa aa		22
SEQ ID NO: 865	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 865		
atggcaggag agtaaaatgg cc		22
SEQ ID NO: 866	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 866		
gcaggagagt aaaatggcct gt		22
SEQ ID NO: 867	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 867		
ggacatcatc acttaggaaa ta		22
SEQ ID NO: 868	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	

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SEQUENCE: 868		
ttggacatca tcacttagga aa		22
SEQ ID NO: 869	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 869		
actctcctgc catgtttgga ca		22
SEQ ID NO: 870	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 870		
tttactctcc tgccatgttt gg		22
SEQ ID NO: 871	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 871		
cattttactc tcctgccatg tt		22
SEQ ID NO: 872	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 872		
gcataaggac agctgttatt tc		22
SEQ ID NO: 873	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 873		
tttcctaagt gatgatgtcc aa		22
SEQ ID NO: 874	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 874		
taagtgatga tgtccaaaca tg		22
SEQ ID NO: 875	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 875		
tgatgatgtc caaacatggc ag		22
SEQ ID NO: 876	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 876		
acttaggaaa taacagctgt cc		22
SEQ ID NO: 877	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 877		
tgccatgttt ggacatcatc ac		22
SEQ ID NO: 878	moltype = RNA length = 22	

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FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 878		
ctgccatggtt tggacatcat ca		22
SEQ ID NO: 879	moltype = RNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 879		
gccatttttac tctectgcca tg		22
SEQ ID NO: 880	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 880		
taagtgatga tgtccaaaca tgg		23
SEQ ID NO: 881	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 881		
tgatgatgtc caaacatggc agg		23
SEQ ID NO: 882	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 882		
acaaatgtaa gccttgtoaca agg		23
SEQ ID NO: 883	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 883		
ctgtccaag gagatggatt tgg		23
SEQ ID NO: 884	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 884		
gtaagccttg tccaaggaga tgg		23
SEQ ID NO: 885	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 885		
aaggagatgg atttggcata agg		23
SEQ ID NO: 886	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 886		
cccatgatgg tagaacacc tgg		23
SEQ ID NO: 887	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other RNA	
	organism = synthetic construct	

-continued

SEQUENCE: 887
ccatgatggt agaaacacct ggg 23

SEQ ID NO: 888 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 888
caccctctc tatcccatga tgg 23

SEQ ID NO: 889 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 889
gttgttatc ttcaacaggc tgg 23

SEQ ID NO: 890 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 890
atgtttgac atcatcactt agg 23

SEQ ID NO: 891 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 891
gctggcattc tgagcagcac agg 23

SEQ ID NO: 892 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 892
ttttgtggtt tatcttcaac agg 23

SEQ ID NO: 893 moltype = RNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other RNA
organism = synthetic construct

SEQUENCE: 893
ttttactctc ctgccatggt tgg 23

SEQ ID NO: 894 moltype = AA length = 378
FEATURE Location/Qualifiers
source 1..378
mol_type = protein
organism = synthetic construct

SEQUENCE: 894
MVLWLWTLTLL IALPCLLQTK EDPNPPITNL RMKAKAQQLT WDLNRNVTDI ECVKDADYSM 60
PAVNNSYCQF GAISLCEVTN YTVQIANPPF STWILFPENS GKPWAGAENL TCWIHDVDFL 120
SCSWAVGPGA PADVQYDLYL NVANRRQQYE CLHYKTDAQ TRIGCRPDDI SRLSSGSQSS 180
HILVRGRSAA FGIPCTDKFV VFSQIEILTP PNMTAKCNKT HSPFMHWKMRS HFNRKFRYEL 240
QIQKRMQPMVI TEQVRDRTSF QLLNPGTYTV QIRARERVYE FLSAWSTPQR FECDQEBEGAN 300
TRAWRTSLLI ALGTLALVC VFVICRRLV MQLRFPRIHP MKDPIGDSFQ NDKLWVWEAG 360
KAGLEECLVT EVQVVQKT 378

SEQ ID NO: 895 moltype = AA length = 378
FEATURE Location/Qualifiers
source 1..378
mol_type = protein
organism = synthetic construct

SEQUENCE: 895
MVLWLWTLTLL IALPCLLQTK EDPNPPITNL RMKAKAQQLT WDLNRNVTDI ECVKDADYSM 60
PAVNNSYCQF GAISLCEVTN YTVQIANPPF STWILFPENS GKPWAGAENL TCWIHDVDFL 120
SCSWAVGPGA PADVQYDLYL NVANRRQQYE CLHYKTDAQ TRIGCRPDDI SRLSSGSQSS 180
HILVRGRSAA FGIPCTDKFV VFSQIEILTP PNMTAKCNKT HSPFMHWKMRS HFNRKFRYEL 240
QIQKRMQPMVI TEQVRDRTSF QLLNPGTYTV QIRARERVYE FLSAWSTPQR FECDQEBEGAN 300

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TRAWRTSLLI ALGTLALVC VFVICRRLV MQLRFPRIIPH MKDPIGDSFQ NDKLVVWEAG 360
KAGLEECLVT EVQVVQKT 378
```

```
SEQ ID NO: 896      moltype = AA length = 378
FEATURE            Location/Qualifiers
source             1..378
                  mol_type = protein
                  organism = synthetic construct
```

```
SEQUENCE: 896
MVLWLTLTLL IALPCLLQTK EDPNPPITNL RMKAKAQQLT WDLNRNVTDI ECVKDADYSM 60
PAVNNSYQCF GAISLCEVTN YTVHIANPPF STWILFPENS GKPWAGAENL TCWIHDVDFL 120
SCSWAVGPGA PADVQYDLYL NVANRRQQYE CLHYKTDAQG TRIGCRFDDI SRLSSGSQSS 180
HILVRGRSAA FGIPTDKFV VFSQIEILTP PNMTAKCNKT HSPMHWKMRS HFNRKFRYEL 240
QIQKRMQPMV TEQVRDRTSF QLLNPGTYTV QIRARERVYE FLSAWSTPQR FECDQEEGAN 300
TRAWRTSLLI ALGTLALVC VFVICRRLV MQLRFPRIIPH MKDPIGDSFQ NDKLVVWEAG 360
KAGLEECLVT EVQVVQKT 378
```

```
SEQ ID NO: 897      moltype = AA length = 378
FEATURE            Location/Qualifiers
source             1..378
                  mol_type = protein
                  organism = synthetic construct
```

```
SEQUENCE: 897
MVLWLTLTLL IALPCLLQTK EDPNPPITNL RMKAKAQQLT WDLNRNVTDI ECVKDADYSM 60
PAVNNSYQCF GAISLCEVTN YTVHIANPPF STWILFPENS GKPWAGAENL TCWIHDVDFL 120
SCSWAVGPGA PADVQYDLYL NVANRRQQYE CLHYKTDAQG TRIGCRFDDI SRLSSGSQSS 180
HILVRGRSAA FGIPTDKFV VFSQIEILTP PNMTAKCNKT HSPMHWKMRS HFNRKFRYEL 240
QIQKRMQPMV TEQVRDRTSF QLLNPGTYTV QIRARERVYE FLSAWSTPQR FECDQEEGAN 300
TRAWRTSLLI ALGTLALVC VFVICRRLV MQLRFPRIIPH MKDPIGDSFQ NDKLVVWEAG 360
KAGLEECLVT EVQVVQKT 378
```

1. A mutant CD123 protein comprising a mutation at residue R84 according to SEQ ID NO:2, wherein the mutation is to an amino acid residue that is not lysine.

2. The mutant CD123 protein of claim 1, wherein the mutation is to glutamine (Q), asparagine (N) or histidine (H).

3. The mutant CD123 protein of claim 1, wherein the mutation is R84Q.

4. The mutant CD123 protein of claim 1, which further comprises a mutation at residue V85 according to SEQ ID NO:2.

5. The mutant CD123 protein of claim 3, wherein the mutation at residue V85 is to methionine (M), isoleucine (I), leucine (L), alanine (A), cysteine (C), glycine (G), or threonine (T).

6. The mutant CD123 protein of claim 4, wherein the mutations are selected from the group consisting of R84Q and V85I, R84Q and V85M, R84H and V85I, and R84H and V85M.

7. The mutant CD123 protein of claim 1, which comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 894, 895, 896 and 897.

8. A polynucleotide encoding the mutant CD123 protein of claim 1.

9. A cell comprising the mutant CD123 protein of claim 1 or a polynucleotide encoding the mutant CD123 protein.

10. A method for preparing a cancer patient for a therapy comprising an anti-CD123 antibody or antigen-binding frag-

ment thereof, comprising administering to the patient a cell expressing the mutant CD123 protein of claim 1 which has reduced binding to the anti-CD123 antibody or antigen-binding fragment thereof as compared to the corresponding wild-type CD123 protein.

11. The method of claim 10, wherein the cell is a stem cell.

12. The method of claim 11, wherein the stem cell is a hematopoietic stem and progenitor cell (HSPC).

13. The method of claim 10, wherein the therapy comprises the antibody, an antigen-binding fragment of the antibody, a chimeric antigen receptor (CAR) comprising the antigen-binding fragment, or an immune cell comprising the CAR.

14. The method of claim 10, wherein the cancer is leukemia.

15. The method of claim 10, wherein the cancer is acute myeloid leukemia (AML).

16. The method of claim 10, wherein the anti-CD123 antibody is CSL362 or 32716.

17. A method for preparing the polynucleotide of claim 8 in a cell, comprising introducing to the cell with a base editor comprising a gRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:229-516.

18. A method for preparing the polynucleotide of claim 8 in a cell, comprising introducing to the cell a prime editor and a pegRNA that comprises a spacer sequence selected from the group consisting of SEQ ID NO:517-541.

* * * * *